

New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website www.nzsap.org.nz

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

Share— copy and redistribute the material in any medium or format

Under the following terms:

Attribution — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

NonCommercial — You may not use the material for [commercial purposes](#).

NoDerivatives — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

Accounting for scale effects in genetic evaluation of dairy cattle

N. LOPEZ-VILLALOBOS, D.J. GARRICK, B.L. HARRIS¹ AND H.T. BLAIR

Department of Animal Science, Massey University, Palmerston North, New Zealand.

ABSTRACT

Lactation records of dairy cows calving between 1986 and 1989 were obtained from the Livestock Improvement Corporation of the New Zealand Dairy Board. There were milkfat yields from 2,004,854 lactations in 83,805 contemporary groups. The data were divided into three equal-sized subsets based on average level of production (scale) in the contemporary group; these being (kg milkfat \pm sd) High (H), 172 \pm 28; Medium (M), 152 \pm 26; and Low (L), 139 \pm 25. The objectives of this study were to provide evidence of heterogenous variance and to identify the best of three methods to stabilise the variance of milkfat yields for use in the genetic evaluation of New Zealand dairy cattle based on a best linear unbiased prediction procedure using an across breeds animal model which will be implemented in July 1996.

The methods investigated for the accounting of scaling were adjustment based on: contemporary group standard deviation (SD); contemporary group mean (MEAN); and logarithmic transformation (LOG) of milkfat yield. The overall correlation between contemporary group means and standard deviations was 0.44. This value was reduced to 0.31 in SD-transformed data, -0.27 (MEAN) and -0.24 (LOG).

Correlations between breeding values for sires estimated from the independent data sets using a mixed model but without adjustment for scale were 0.76, 0.73 and 0.78 in the L-M, L-H and M-H comparisons. These were lower than expected correlations of 0.85, 0.85 and 0.87, reflecting inaccuracies in sire evaluation when scaling is ignored. Calculated correlations were similar for SD and MEAN (0.78, 0.75 and 0.80; 0.78, 0.74 and 0.78), but LOG reduced the calculated correlations (0.73, 0.69 and 0.75).

Results confirm the problem of scaling on genetic evaluation of New Zealand dairy cattle and indicate other methods need to be studied to correct the scaling problem.

Keywords: animal model; BLUP; scaling effect.

INTRODUCTION

Homogeneity of variance is assumed in most currently applied models of genetic evaluation. However, numerous studies (Hill *et al.*, 1983; Brotherstone and Hill, 1986; Visscher *et al.*, 1991) have reported that variation in lactation yields tends to increase with average production. The effects of not considering this scale effect may reduce responses to selection (Hill, 1984; Vinson, 1987; Van Vleck, 1987; Garrick and Van Vleck, 1987; Visscher and Hill, 1992) as most cows identified as being elite will be located in herds with the greatest variation. Superior cows in low variance herds tend to be overlooked (Everett *et al.*, 1982; Vinson, 1987). Scaling may cause overestimation of genetic merit of those sires which have a higher proportion of daughters in high-variation herds and vice-versa (Van Vleck, 1987).

The correlation between breeding values of sires at different production levels, for milk and milkfat, has been reported near to unity (Robertson *et al.*, 1960; Danell, 1982; De Veer and Van Vleck, 1987; Boldman and Freeman, 1990; Carabaño *et al.*, 1990; Winkelman and Schaeffer, 1988; Dong and Mao, 1990), indicating that the progeny of sires tend to rank the same across production levels.

Best linear unbiased prediction (BLUP) with a multiple trait analysis (Henderson, 1984; Garrick and Van Vleck, 1987) is feasible with heterogeneous variance provided the parameter values are known for each contemporary group. Parameter values can be estimated using for example REML

but this requires large amounts of data for estimation within each contemporary group. A number of methods have been proposed to pre-adjust yields for the heterogeneity of variance. Logarithmic transformation is a computationally simple method and is a reasonable choice when the true correlation between the herd mean and herd standard deviation is unity (Visscher *et al.*, 1991). A similar method to the logarithmic transformation is scaling for the herd mean. The current system of sire evaluation in New Zealand overcomes the scaling effect by expressing the performance of the daughters as a proportion of the performance of the contemporaries (Wickham and Stichbury, 1980; Garrick *et al.*, 1993). Brotherstone and Hill (1986) suggested that heterogeneous variance can be accounted for by a weighted average of the estimated phenotypic standard deviation for the environment and the population estimate.

The objectives of this study were to provide evidence of heterogenous variance and its effects on the genetic evaluation of sires in the New Zealand dairy industry and to investigate three methods of accounting for heterogenous variance (correction by the mean, adjustment by the standard deviation and log transformation).

MATERIAL AND METHODS

Data

Lactation records of straight- and cross-bred dairy cows calving between 1986 and 1989 inclusive were obtained from

¹Livestock Improvement Corporation Ltd, Private Bag 3016, Hamilton, New Zealand.

the Livestock Improvement Corporation files of the New Zealand Dairy Board. After editing, there were 2,004,854 lactation milkfat yields.

Definition of levels of production

A contemporary group was defined as at least 6 cows of the same age calving in the same herd-year (HYA). In total there were 83,805 contemporary groups. The mean and the standard deviation for milkfat yield was calculated for each one of them. Contemporary groups were sorted on mean milkfat production and subsequently divided into three equal-sized subsets which were identified as low (L), medium (M) and high (H) producing levels.

Estimation of breeding values

Estimates of breeding values were only used in subsequent analyses for sires with more than 20 daughters in each production level. For each subset, breeding values of sires were obtained through the BLUP procedure (Henderson, 1973) using a single trait repeatability animal model across breeds, which is currently being developed for the future genetic evaluation of dairy cattle in New Zealand (Garrick *et al.*, 1993; Harris *et al.*, 1993). The statistical model for the analysis of milkfat yield (Harris *et al.*, 1993) included the fixed effects of contemporary group, heterosis, month of calving, induced lactation class, maternal breed, and genetic group, and the random effects of additive genetic value, permanent environment and residual error.

Methods to reduce heterogeneity of variance

Three methods to reduce heterogeneity of variance were investigated. First, assuming that within herd-year-age standard deviation is directly proportional to the herd-year-age mean, the records were scaled by the corresponding HYA mean (MEAN correction). Second, yields were adjusted using a pooled estimate of HYA standard deviation ($\tilde{\sigma}_{y_i}$) (SD adjustment) as $y_{ij}^{sd} = y_{ij} / \tilde{\sigma}_{y_i}$ where y_{ij} is the j^{th} milkfat yield in the i^{th} contemporary group and y_{ij}^{sd} is the adjusted record. $\tilde{\sigma}_{y_i}$ was obtained from a weighted combination of the population standard deviation (σ_y) and an estimate of within HYA standard deviation ($\hat{\sigma}_{y_i}$), i.e., $\tilde{\sigma}_{y_i} = w_1\sigma_y + w_2\hat{\sigma}_{y_i}$ for some w_1 and w_2 . An estimate of σ_y was approximated by the unweighted average of within HYA standard deviations and values for w_1 and w_2 were obtained by using a Bayesian regression approach (Brotherstone and Hill, 1986; Visscher and Hill, 1992). Finally, the natural logarithm of the lactation milkfat yields were taken (LOG transformation). Estimated breeding values of sires were obtained after transformations from each independent subset.

Measurement of the effect of heterogeneous variance

Relationship between mean and standard deviation. A significant correlation between HYA mean and HYA standard deviation would indicate some departures in the basic assumptions of homogeneous variance (Everett and Keown, 1984).

Correlations between estimated breeding values. An approximate method for validating the assumption of homogeneous variance involves comparing observed (r_o) and expected (r_e) correlations of breeding values of sires with progeny in different environments. Observed correlations are product-moment correlations between estimated breeding values in each subset and expected correlations would be obtained by using selection index theory. Garrick *et al.* (1989) showed that the correlation between estimated breeding values of sire k is $r_{\hat{u}_{1k}\hat{u}_{2k}} = r_{u_{1k}u_{2k}} r_{u_{1k}\hat{u}_{1k}} r_{u_{2k}\hat{u}_{2k}}$ where subscripts 1 and 2 define production levels, u_{ik} and \hat{u}_{ik} are true and estimated merit of the sire in environment i . Assuming a unit genetic correlation between true breeding values $r_{u_1u_2}$, then the expected correlation between evaluations is: $r_e = r_{u_{1k}\hat{u}_{1k}} r_{u_{2k}\hat{u}_{2k}}$, the product of correlations between true and estimated breeding value in each production level. For a well designed and implemented progeny test with $h^2 = 0.25$ and n_{ik} daughters of sire k in environment i , $r_{u_{ik}\hat{u}_{ik}} = \sqrt{n_{ik} / (n_{ik} + 15)}$. Using these results, the expected correlation between estimated breeding values of sample of m sires evaluated in different environ-

$$r_e = \left[\sum_{k=1}^m \left(\frac{n_{1k}}{n_{1k} + 15} \right) \left(\frac{n_{2k}}{n_{2k} + 15} \right) \right] / \left[\sqrt{\sum_{k=1}^m \left(\frac{n_{1k}}{n_{1k} + 15} \right)} \sqrt{\sum_{k=1}^m \left(\frac{n_{2k}}{n_{2k} + 15} \right)} \right]$$

ments (Hickman *et al.*, 1969) is:

Confidence intervals for observed correlations were constructed by using the Fisher's $Z = [1/2 \ln\{(1+r)/(1-r)\}]$ (Snedecor and Cochran, 1980) with variance $\approx (m-3)^{-1}$.

Genetic correlations. An estimate (\hat{r}_G) of the correlation between true breeding values ($r_{u_1u_2}$) may be obtained from the ratio of the calculated and the expected correlations between the expression of the same genotype in two environments (Danell, 1982; Notter and Diaz, 1993).

RESULTS

Table 1 shows the statistics for each level of production. The differences in milkfat yield between M-L, H-L and H-M production levels were 12.79, 32.97 and 20.18 kg, respectively. The corresponding differences in averages of standard deviations were: 1.02, 3.33, and 2.31. Thus, standard deviation increased with milk production. However, the change in the standard deviation was less than the change in mean milkfat production, such that the coefficient of variation decreased. This relationship was more clearly shown by the correlation coefficient between HYA means and standard deviations estimated as 0.44. This correlation was notably reduced by MEAN correction and LOG transformation with a change from positive to negative values (to -0.27 and to -0.24, respectively). SD adjustment slightly reduced this correlation to 0.31

The number of sires with more than 20 daughters in each subset was 486 with the average number of daughters per sire being 2,138. The observed (product-moment correlations) and expected correlations between breeding values estimated from the three subsets are shown in Table 2 for untransformed, MEAN-corrected, SD-adjusted and LOG-transformed data. For all the comparisons the observed correlations were significantly lower than the expected correlations. MEAN cor-

TABLE 1: Contemporary group numbers, means, standard deviations and coefficients of variation for milkfat yield overall and at three levels of production.

Variable	Production level			
	All	Low	Medium	High
Contemporary group number	83,805	27,935	27,935	27,935
Mean (kg)	154.29	139.32	152.11	172.29
Standard deviation (kg)	26.49	24.99	26.01	28.32
Coefficient of variation	17.17	17.94	17.10	16.44

TABLE 2: Expected (r_e) and observed (r_o) correlations between estimated breeding values for milkfat yield of sires at different production levels using untransformed and transformed data.

Transformation	Level of production compared					
	Low-Medium		Low-High		Medium-High	
	r_e	r_o	r_e	r_o	r_e	r_o
None	0.85	0.76*	0.85	0.73*	0.87	0.78*
MEAN correction	0.85	0.78*	0.85	0.74*	0.87	0.78*
SD adjustment	0.85	0.78*	0.85	0.75*	0.87	0.80*
LOG transformation	0.85	0.73*	0.85	0.69*	0.87	0.75*

*Significantly different to the expected value (P<0.05).

rection and SD adjustment slightly increased the observed correlations but still were significantly different to the expected correlations. LOG transformation, on the contrary, reduced the correlations.

Table 3 shows estimates of the correlations between true breeding values expressed in different production levels. For untransformed data, estimates ranged from 0.86 to 0.90. These values were increased by the MEAN correction and SD adjustment but reduced by the LOG transformation.

TABLE 3: Estimates of genetic correlations between expressions of the same genotype in different production levels using untransformed and transformed data.

Transformation	Level of production compared		
	Low-Medium	Low-High	Medium-High
None	0.89	0.86	0.90
MEAN correction	0.92	0.87	0.90
SD adjustment	0.92	0.88	0.92
LOG transformation	0.86	0.81	0.86

DISCUSSION

Correlation between mean and standard deviation

The correlation coefficient between HYA means and HYA standard deviations of 0.44 for milkfat found in this study agrees with the typical value of 0.4 to 0.5 reported in the literature between herd mean and herd (phenotypic) standard deviation for milk and milkfat yield (Hill *et al.*, 1983; Brotherstone and Hill, 1986; Visscher *et al.*, 1991). This study confirms the presence of heterogeneous variance for milkfat yield in New Zealand dairy cattle, i.e., HYA groups

with high levels of production tend to exhibit more variability than those with low levels of production. However, heterogeneity of variance is only partially explained by the scale effect because the estimates of the genetic correlation between environments were less than unity.

Correlation between estimated breeding values from independent datasets

The observed correlations between breeding values obtained from the three production levels were high but still significantly different to the expected correlations (Table 2). Thus, sires tended to rank differently across levels of production. These results differ to those correlations between estimated breeding values at different production levels reported in other countries, which were similar to the expected correlations (Robertson *et al.*, 1960; Danell, 1982). The validity of the comparisons between expected and observed correlations in this study is constrained by two assumptions. First, expected correlations were derived as a function of the true number of daughters in each producing level rather than effective number. Ideally, expected correlations would be obtained using accuracies of estimated breeding values computed from elements of the inverse matrix of the mixed model equations. Second, values of heritability were assumed constant across environments.

Genetic correlations

Estimates of genetic correlations between production levels are lower than those found in other countries for milk yield (Robertson *et al.*, 1960; Danell, 1982; Hill *et al.*, 1983; De Veer and Van Vleck, 1987; Boldman and Freeman, 1990; Carabaño *et al.*, 1990; Winkelman and Schaeffer, 1988; Dong and Mao, 1990) and for milkfat yield (Carabaño *et al.*, 1990), which have been very close to one. Lack of knowledge concerning the distribution of the obtained estimates of genetic correlations allows neither any accurate calculation of standard errors nor an objective statistical model to test whether or not the genetic correlations are significantly different from 1. However, the standard errors associated with the estimates of genetic correlations would be small, given that the average number of daughters per sire was large. This result suggests that if sires are genetically evaluated on the basis of daughters located predominantly in a small range of the production spectrum, responses to selection may be lower than expected.

Effect of methods to reduce heterogeneity of variance

LOG transformation changed the correlation between mean and standard deviation from a positive to a negative value, as found by Everett and Keown (1984) and Visscher *et al.* (1991), indicating that the heterogeneity of variance was overadjusted because the relationship is not unity. This overadjusting was reflected in a reduction of the observed correlations between breeding values estimated from the three subsets (Table 2) and in a reduction of estimated genetic correlations of production in different environments (Table 3). Similar effects of log transformation on genetic correlations were reported by De Veer and Van Vleck (1987).

The current system of genetic evaluation in New Zealand using the ratio of cow to herd mean performance is

comparable to the MEAN correction of this study. This method overadjusted the correlation between mean and standard deviation but the correlations between breeding values estimated from the three subsets (Table 2) and estimates of genetic correlation of production in different environments (Table 3) were similar to the untransformed data.

SD adjustment reduced the correlation between means and standard deviations from 0.44 to 0.31, i.e., the variances tended to be stabilised but not completely. A similar pattern was reported by Visscher et al. (1991) using an adjustment by a ratio between the estimated population standard deviation and the estimated herd-year-season phenotypic standard deviation. The correlations between estimated breeding values at different levels of production were slightly increased but still were significantly lower than the expected correlations (Table 2). Estimates of the genetic correlation between the expression of the same genotype in two environments were slightly increased compared to those from untransformed data (Table 3).

Practical implications

If variances increase with mean yield but are assumed to be homogeneous, animals could be misranked. Superior cows in herds with large variances would tend to be overevaluated (Vinson, 1987; Boldman and Freeman, 1990). Similarly, sires with a large percentage of their daughters in herds with large variances would tend to be overevaluated (Van Vleck, 1987; Garrick and Van Vleck, 1987). However, results from field data (Winkelman and Schaeffer, 1988) have indicated that modification of the mixed model equations to account for heterogeneous variances has little effect on the overall ranking of sires. The most important evaluations, however, are for the genetically superior sires and cows. The top sires are selected for extensive use throughout the cow population, and elite cows are candidates for producing young bulls for progeny testing. If the subsequent progeny test is random across production levels, sires out of overevaluated cows should be identified as inferior and culled (Boldman and Freeman, 1990). Hence, compared with sire selection, cow evaluation is more likely to be adversely affected by heterogeneous variances (Van Vleck, 1987; Vinson, 1987).

The results found here give an indication of the scaling problem, and it must therefore be considered in the genetic evaluation of sires and dams in the national herd. The question still remains as to what strategy should be used to deal with the problem of heterogeneity of variance between environments since the approaches considered in this study did not satisfactorily resolve the problem.

SUMMARY AND CONCLUSIONS

The overall correlation between contemporary group means and standard deviations was 0.44 providing evidence of heterogeneity of variance for lactation milkfat yield across contemporary groups. This suggests that a scale effect should be considered in the new genetic evaluation system.

The effect of this scaling problem was reflected in the genetic evaluation of sires across production levels. Product-

moment correlations between estimated breeding values for the three comparisons (low-medium, low-high, medium-high) were significantly lower than the expected correlations. These results indicate that if the scaling effect is not corrected for, superior cows in contemporary groups with large variances or sires with a large percentage of their daughters in contemporary groups with large variances, would tend to be overevaluated.

Estimates of genetic correlations of production in different environments suggest that the correlation between the true breeding values is slightly lower than unity. Thus, if sires are genetically evaluated on the basis of daughters located in only one level of production, responses to selection may be lower than the expected.

The methods investigated in this study to account for scale were not appropriate. The mean correction and log transformation tended to overadjust rather than stabilise the variance while standard deviation adjustment was only partially successful.

Therefore, alternative methods are required. A multiple-trait approach (treating each level of production as a different trait) seems theoretically best but it will require the collection of data for the estimation of appropriate genetic and phenotypic parameters for the different levels of production. A more practical approach would be to pre-adjust data for some estimate of the herd or herd-year-age phenotypic standard deviation. Further work is required to identify a suitable method for pre-adjustment.

REFERENCES

- Boldman, K. G.; Freeman, A. E. 1990. Adjustment for heterogeneity of variances by herd production level in dairy cow and sire evaluation. *Journal of Dairy Science* **73**: 503-512.
- Brotherstone, S.; Hill, W. G. 1986. Heterogeneity of variance amongst herd for milk production. *Animal Production* **42**: 297-303.
- Carabaño, M. J.; Wade, K. M.; Van Vleck, L. D. 1990. Genotype by environment interaction for milk and fat production across regions of the United States. *Journal of Dairy Science* **73**: 173-180.
- Danell, B. 1982. Interaction between genotype and environment in sire evaluation for milk production. *Acta Agriculturae Scandinavica* **32**: 33-46.
- De Veer, J. C.; Van Vleck, L. D. 1987. Genetic parameters for first lactation milk yields at three levels of herd production. *Journal of Dairy Science* **70**: 1434-1441.
- Dong, M. C.; Mao, I. L. 1990. Heterogeneity of (co)variance and heritability in different levels of intraherd milk production variance and of average. *Journal of Dairy Science* **73**: 843-851.
- Everett, R. W.; Keown, J. F. 1984. Mixed model sire evaluation with dairy cattle -experience and genetic gain. *Journal of Animal Science* **59**: 529-541.
- Everett, R. W.; Keown, J. F.; Taylor, J. F. 1982. The problem of heterogeneous within herd error variances when identifying elite cows. *Journal of Dairy Science (Suppl. 1)* **65**:100 (Abstr.)
- Garrick, D. J.; Harris, B. L.; Shannon, P.; Sosa-Ferreira, C. 1993. A prototype sire evaluation for New Zealand dairy cattle. *Proceedings of the New Zealand Society of Animal Production* **53**: 91-94.
- Garrick, D. J.; Pollak, E. J.; Quaas, R. L.; Van Vleck, L. D. 1989. Variance heterogeneity in direct and maternal weight traits by sex and percent purebred for Simmental-sired calves. *Journal of Animal Science* **67**: 2515-2528.
- Garrick, D. J.; Van Vleck, D. L. 1987. Aspects of selection for performance in several environments with heterogeneous variances. *Journal of Animal Science* **65**: 409-421.
- Harris, B. L.; Jackson, R. G.; Garrick, D. J. 1993. Animal Evaluation System for New Zealand Dairy Cattle. *Livestock Improvement, Hamilton*.

- Henderson, C. R. 1973. Sire evaluation and genetic trends. In: Proceedings of the Animal Breeding and Genetics Symposium held in Blacksburg, Virginia, pp 10-41. American Society of Animal Sciences, Champaign, Illinois.
- Henderson, C. R. 1984. *Applications of Linear Models in Animal Breeding*. University of Guelph, Guelph, Ont., Can.
- Hickman, C. G.; Lee, A. J.; Gravir, K. 1969. Genotype x season x method interaction in evaluating dairy sires from progeny records. *Canadian Journal of Animal Science* **49**: 151-155.
- Hill, W. G. 1984. On selection among groups with heterogeneous variance. *Animal Production* **39**: 473-477.
- Hill, W. G.; Edwards, M. R.; Ahmed, M. -K. A.; Thompson, R. 1983. Heritability of milk yield and composition at different levels and variability of production. *Animal Production* **36**: 59-68.
- Notter, D. R.; Diaz, C. 1993. Use of covariances between predicted breeding values to assess the genetic correlation between expressions of a trait in 2 environments. *Genetics Selection Evolution* **25**:353-372.
- Robertson, A.; O'Connor, L. K.; Edwards, J. 1960. Progeny testing dairy bulls at different management levels. *Animal Production* **2**:141-152.
- Snedecor, G. W.; Cochran, W. G. 1980. *Statistical Methods*. The Iowa State University Press, Ames, IA.
- Van Vleck, L. D. 1987. Selection when traits have different genetic and phenotypic variances in different environments. *Journal of Dairy Science* **70**: 337-344.
- Vinson, W. E. 1987. Potential bias in genetic evaluations from differences in variation within herds. *Journal of Dairy Science* **70**: 2450-2455.
- Visscher, P. M.; Hill, W. G. 1992. Heterogeneity of variance and dairy cattle breeding. *Animal Production* **55**: 321-329.
- Visscher, P. M.; Thompson, R.; Hill, W. G. 1991. Estimation of genetic and environmental variances for fat yield in individual herds and an investigation into heterogeneity of variance between herds. *Livestock Production Science* **28**: 273-290.
- Wickham, B. W.; Stichbury, J. W. 1980. Cow and Sire evaluation in New Zealand. *Proceedings of the Symposium on Dairy Cattle Sire Evaluation held in Warsaw*.
- Winkelman, A.; Schaeffer, L. R. 1988. Effect of heterogeneity of variance on dairy sire evaluation. *Journal of Dairy Science* **71**: 3033-3039.