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ACCOUNTING FOR SCALE EFFECTS IN GENETIC EVALUATION OF NEW ZEALAND DAIRY CATTLE

A thesis presented in partial fulfilment
of the requirements for the degree
of Master of Agricultural Science
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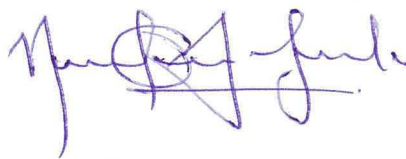
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ABSTRACT

It is well known that variation in lactation yields tends to increase with average production. Failure to account for this scale effect may cause overestimation of genetic merit for sires with a majority of daughters in high-variation herds and vice-versa. The current system of sire evaluation in New Zealand overcomes this problem by expressing daughters performance as a proportion of contemporary average performance. The objectives of this study were to quantify the magnitude of scaling (heterogeneous variance), and to identify methods to stabilise the variance of milkfat yields for use in the genetic evaluation system of dairy cattle through best linear unbiased prediction (BLUP) using an animal model across breeds.

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 (herd-year-age; HYA). The data were divided into three equal-sized subsets based on HYA mean; these being (kg milkfat \pm sd) High (H), 172 ± 28 ; Medium (M), 152 ± 26 ; and Low (L), 139 ± 25 .

The methods investigated for the accounting of scaling were: adjustment by the HYA sd (SD-adjustment); scaling by the HYA mean (MEAN-correction); and natural logarithmic transformation (LOG-transformation) of milkfat yield. The overall correlation between HYA means and HYA sd's was 0.44. This value was reduced to 0.31 in SD-adjusted, -0.27 in the MEAN-corrected and -0.24 in the LOG-transformed data. Ideally, the transformed data should exhibit independence between the mean and standard deviation.

Breeding values of sires were separately estimated from each data subset using a mixed model. Product-moment and rank correlations between breeding values for sires estimated from the independent subsets and with variable minimum number of daughters were in the overall comparisons (L-M, L-H and M-H) lower than expected correlations, reflecting inaccuracies in sire evaluation when scaling is ignored. Product-moment and rank correlations were similar for SD-adjustment and MEAN-correction, but LOG-transformation reduced the calculated correlations in the L-M, L-H and M-H comparisons.

Estimates of the genetic correlations between production in pairs of environments were obtained from the ratio of observed to expected correlations. These estimates ranged from 0.82 to 1.01 for the linear yields. Estimates of genetic correlations were similar for SD-adjusted and MEAN-corrected data, but for LOG-transformed data these were reduced, especially in the L-H comparison which ranged from 0.77 to 0.87.

Results confirm the problem of scaling on genetic evaluation of New Zealand dairy cattle. MEAN-correction and LOG-transformation methods are not appropriate because they tend to overcorrect the scaling problem. SD-adjustment is not satisfactory but seems to be more appropriate than no adjustment. An alternative method is proposed based on a Bayesian approach, which takes into account any relationship between variance and mean.

Keywords: dairy cattle, BLUP, scaling effect.

TABLE OF CONTENTS

	Page
ACKNOWLEDGEMENTS.....	ii
ABSTRACT	iv
TABLE OF CONTENTS	vi
LIST OF TABLES	ix
1. INTRODUCTION	1
2. DAIRY FARMING IN NEW ZEALAND	3
2.1 Climatic Conditions.....	3
2.2 Dairy Industry Structure.....	3
2.2.1 Milk Production Systems	4
2.2.1.1 Town Supply Dairy Farms	4
2.2.1.2 Seasonal or Factory Supply Dairy Farms.....	4
2.2.2 Operating Structures.....	4
2.2.3 Herd Production Statistics	5
2.3 Pasture Production.....	5
2.4 Calving Date	6
2.5 Stocking Rate	7
2.6 Grazing Management	8
2.7 Genetic Improvement.....	9
2.7.1 Herd testing	9
2.7.2 National Database.....	10
2.7.3 Artificial Insemination	11
2.7.4 Breeding Program.....	12
2.8 Sire evaluation	13
2.8.1 Sire Evaluation up to 1969.....	14
2.8.2 Current Sire Evaluation.....	16
2.8.3 A Prototype Sire Evaluation.....	19
3. BEST LINEAR UNBIASED PREDICTION.....	20
3.1 Linear Model	20
3.2 Mixed Model Equations	24
3.3 Variance of BLUE and BLUP	26
3.4 The Numerator Relationship Matrix	28
3.5 Genetic Groups	30
3.6 Computing Strategies to Solve the Mixed Model Equations	33
3.6.1 Absorption.....	33

3.6.2. Gauss Elimination	34
3.6.3 Cholesky Decomposition	35
3.6.4 Iterative Methods.....	36
3.6.5 Block Iteration.....	38
3.7 Example of the use of the BLUP procedure.....	40
3.8 Heterogeneous Variance	51
3.8.1 Effects of Heterogeneous Variance	52
3.8.1.1 Accuracy of Selection.....	52
3.8.1.2 Mass Selection	52
3.8.1.3 Sire Selection	53
3.8.1.4 BLUP.....	55
3.8.1.5 Correlations Between Breeding Values Estimated at Different Environments.....	56
3.8.1.6 Genetic Correlations.....	59
3.8.2 Methods to Account for Heterogeneous Variance	61
3.8.2.1 Logarithm Transformation	61
3.8.2.2 Scaling	62
3.8.2.3 Weighting.....	64
3.8.2.4 Multiple Trait Analysis	66
3.8.2.5 Multiplicative Model.....	67
3.8.3 Example of the Brotherstone and Hill Method.....	67
4. MATERIAL AND METHODS.....	71
4.1 Material	71
4.2 Methods.....	71
4.2.1 Estimation of Breeding Values	71
4.2.2 Definition of Levels of Production	78
4.2.3 Methods to Reduce Heterogeneity of Variance	78
4.2.3.1 Mean Correction	78
4.2.3.2 Standard Deviation Adjustment	79
4.2.3.3 Logarithmic Transformation	80
4.2.4 Measurement of the Effect of Heterogeneous Variance	81
4.2.4.1 Relationship Between Mean and Standard Deviation	81
4.2.4.2 Correlations Between Breeding Values.....	81
4.2.4.3 Significant Deviations.....	85
4.2.5 Genetic Correlation.....	86

5. RESULTS.....	87
5.1 Means and Standard Deviations and their Correlation.....	87
5.2 Averages and Standard Deviations of Estimates of Breeding Values.....	88
5.3 Correlation Between Estimated Breeding Values.....	92
5.3.1 Product-Moment Correlations.....	92
5.3.2 Rank Correlations.....	96
5.3.3 Product-moment versus Rank Correlations.....	99
5.4 Genetic Correlations.....	99
5.5 Significantly Deviating Breeding Values.....	100
6. DISCUSSION.....	106
6.1 Correlation Between Mean and Standard Deviation.....	106
6.2 Correlation Between Estimated Breeding Values from Independent Datasets.....	106
6.3 Genetic Correlations.....	108
6.4 Significantly Deviating Breeding Values.....	110
6.5 Effect of Methods to Reduce Heterogeneity of Variance.....	111
6.5.1 Mean Correction.....	111
6.5.2 Standard Deviation Adjustment.....	112
6.5.3 Log Transformation.....	112
6.6 Practical implications.....	114
6.7 Alternative Methods.....	116
SUMMARY AND CONCLUSIONS.....	120
REFERENCES.....	121
APPENDIX I.....	136
APPENDIX II.....	139

LIST OF TABLES

Table	Page
3.1 Milkfat yield of cows in different lactations for the example of genetic evaluation through BLUP procedure.	40
3.2 Estimates of breeding values for lactation milkfat yield and their prediction error variances and reliabilities for animals in the example of genetic evaluation through BLUP procedure.	48
3.3 Estimates of producing abilities for lactation milkfat yield and their prediction error variances and reliabilities for the cows with records in the example of genetic evaluation through BLUP procedure.	50
3.4 Milkfat yield of first calving cows in nine herds for the example of the Brotherstone and Hill method to correct for heterogeneity of variance.	68
3.5 Estimates of phenotypic standard deviations for herds considered in the example of the Brotherstone and Hill method to correct for heterogeneity of variance.	70
5.1 Contemporary group numbers, averages of HYA means and within-HYA standard deviations and coefficient of variation for milkfat production overall and at three levels of production.	87
5.2 Averages and standard deviation of herd-year-age (HYA) means and within-HYA standard deviations and correlations between them for milkfat production using untransformed and transformed data.	89
5.3 Averages and standard deviations of breeding values for milkfat yield of sires evaluated at three levels of production and with different minimum number of daughters. Untransformed data.	90
5.4 Averages and standard deviations of breeding values for milkfat yield of sires evaluated at three levels of production and with different minimum number of daughters. Data corrected by the HYA mean.	90

Table	Page
5.5 Averages and standard deviations of breeding values for milkfat yield of sires evaluated at three levels of production and with different minimum number of daughters. Data adjusted by the HYA sd.	91
5.6 Averages and standard deviations of breeding values for milkfat yield of sires evaluated at three levels of production and with different minimum number of daughters. Data after log transformation.	91
5.7 Expected and product-moment correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Untransformed data.	94
5.8 Expected and product-moment correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Data corrected by the HYA mean.	94
5.9 Expected and product-moment correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Data adjusted by the HYA sd.	95
5.10 Expected and product-moment correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable number of daughters. Data after log transformation.	95
5.11 Expected and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Untransformed data.	97
5.12 Expected and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable number of daughters. Data corrected by the herd-year-age mean.	97
5.13 Expected and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Data adjusted by the HYA sd.	98

Table	Page
5.14 Expected and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with different minimum number of daughters. Data after log transformation.	98
5.15 Estimates of correlations between true breeding values expressed in different production levels and with variable minimum number of daughters. Untransformed data.	101
5.16 Estimates of correlations between true breeding values expressed in different production levels and with variable minimum number of daughters. Data corrected by the HYA mean.	101
5.17 Genetic correlations between the expression of the same genotype in different production levels. Data adjusted by the HYA sd.	102
5.18 Estimates of correlations between true breeding values expressed in different production levels and with variable minimum number of daughters. Data after log transformation.	102
5.19 Expected and observed number of sires with significantly deviating breeding values for milkfat yield estimated at three levels of production and with variable minimum number of daughters. Untransformed data.	104
5.20 Expected and observed number of sires with significantly deviating breeding values for milkfat yield estimated at three levels of production and with variable minimum number of daughters. Data corrected by the HYA mean.	104
5.21 Expected and observed number of sires with significantly deviating breeding values for milkfat yield estimated at three levels of production and with variable minimum number of daughters. Data adjusted by the HYA sd.	105

Table	Page
5.22 Expected and observed number of sires with significantly deviating breeding values for milkfat yield estimated at three levels of production and with variable minimum number of daughters. Data after log transformation.	105
I.1 Product-moment and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable minimum number of daughters. Untransformed data.	137
I.2 Product-moment and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable minimum number of daughters. Data corrected by the HYA mean.	137
I.3 Product-moment and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable minimum number of daughters. Data adjusted by the HYA sd.	138
I.4 Product-moment and rank correlations between breeding values for milkfat yield of sires evaluated at different levels of production and with variable minimum number of daughters. Data after log transformation.	138
II.1 Number of sires and averages and standard deviations of breeding values for milkfat yield estimated at different levels of production and with different minimum number of daughters for sires with significantly deviating breeding values. Untransformed data.	140
II.2 Number of sires and averages and standard deviations of breeding values for milkfat yield estimated at different levels of production and with different minimum number of daughters for sires with significantly deviating breeding values. Data corrected by the HYA mean.	141
II.3 Number of sires and averages and standard deviations of breeding values for milkfat yield estimated at different levels of production and with different minimum number of daughters for sires with significantly deviating breeding values. Data adjusted by the HYA sd.	142

Table	Page
II.4 Number of sires and averages and standard deviations of breeding values for milkfat yield estimated at different levels of production and with different minimum number of daughters for sires with significantly deviating breeding values. Data after log transformation.	143