

## HETEROGENEITY OF MILK PRODUCTION LEVELS IN KOREAN DAIRY HERDS

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### SUMMARY

Milk records were subdivided into low, medium, and high groups by herd-year averages. Mean milk yields and standard deviations of three production levels on the basis of ME milk yields of all cows freshening in the same herd-year were 7,284.68kg ~ 9,333.28Kg and 1,370.30 ~ 1,686.56, respectively and therefore showed the heterogeneity among three production levels of milk yield. When milk records were transformed to logarithms, average milk yields, standard deviations, and coefficients of variation for production levels were stable among sub-groups.

In case of transforming to logarithms, residual variance component of low group increased markedly and this result indicated that the ranks of genetic evaluations for bull-sires and bull-dams could be reversed.

REML estimates of heritability for low, medium, and high yield groups were 0.189, 0.234, 0.254, respectively, and multiple trait evaluation was necessary. Proportions of sires selected from groups by herd-year production levels corresponding to top 5% based on PTAM were 18.2%, 36.4%, 45.5% for low, medium, and high groups. In case of log transformation, proportions of sires selected from groups corresponding to top 5% of PTAM were 38.9%, 61.1%, 0.0% for low, medium, and high groups, respectively.

High genetic and rank correlations among sub-groups indicated that most of heterogeneity was due to environmental differences in Korean dairy herds.

### INTRODUCTION

The genetic improvement of dairy cattle is a primary concern for Korean dairy farmers nowadays due to the confrontation with many difficulties of dairy farming. This led to analyze the characteristics of milk production in dairy herds. Heterogeneity of genetic and residual variances for yield traits of dairy cattle is widely cited (Famula, 1989; Winkelman and Schaeffer, 1988). Most studies reported increasingly larger genetic and residual variances as herd average milk yield increased.

When choosing animals as future breeding stock across herds, a greater proportion of animals would be selected from the more variable herds ( De Veer and Van Vleck, 1987).

This led to be a problem for sire evaluation if the sires are not sampled across herds. A logarithmic transformation has been applied to milk records to adjust for the relationship between mean and variance (Everett, 1984).

The logarithmic transformation, however, resulted in residual variances being greatest for herds with smallest residual variances on the untransformed scale.

The objective of this study was to examine heterogeneous milk production and to implement correct model for genetic evaluation of dairy cattle in Korea.

## MATERIALS AND METHODS

A total of 1,933 milk records ranging 1985 to 1991 were used to find out heterogeneous characteristics of milk production in dairy herds. Mature equivalent 305day lactation records were divided into low, medium, and high groups by herd-year averages.

Number of observations, mean, standard deviation, and coefficient of variation for each group are in Table 1. A sire model was used to analyze the data.

Table 1. Limits(kg) for grouping herd-year subclasses by average of milk production and distribution of data in each of the groups.

Items	Groups		
	Low	Medium	High
Limits	< 7910	7910 - 8720	8720 <
Records	664	572	697
Milk			
Mean	7284.68	8325.84	9333.28
SD <sup>1</sup>	1370.30	1561.71	1686.56
CV <sup>2</sup>	18.81	18.76	18.07
Log(milk) <sup>3</sup>			
Mean	8.87489	9.00882	9.12405
SD	0.19717	0.19438	0.18992
CV	2.22162	2.15765	2.08154

1:Standard deviation, 2:Coefficient of variation,

3:Natural log transformation

The mixed linear model included random effects of sires, residual, a fixed contemporary group effect, and a genetic group of sire effect.

Genetic (co)variance components were estimated using REML procedure.

## RESULTS

Heterogeneity of variance components among groups was shown by Table 2. The value of residual components was higher than that of other study (Boldman, 1990). The result of this study indicated that most of milk variation was due to environmental differences.

Table 2. The convergence criterion  $10^{-8}$  was met in the estimation of sire and residual variance components by herd-year production levels.

Variables	Groups	$\hat{\sigma}^2_s$	$\hat{\sigma}^2_e$	$h^2$	S.E
		(kg <sup>2</sup> )			
Milk	Low	76966.25	1555731.75	0.189	0.129
	Medium	139031.25	2235514.84	0.234	0.133
	High	161584.33	2387083.87	0.254	0.117
Log(milk) <sup>1</sup>	Low	0.0015088	0.02980746	0.193	0.127
	Medium	0.0019477	0.03490261	0.211	0.126
	High	0.0018895	0.03066432	0.232	0.112

1 : Natural log transformation

Proportions of sires selected from groups by herd-year production levels when the top 5% and 10% of all sires were selected based on PTAM divided by its phenotypic and genetic standard deviation are in Table 3.

Proportions of sires selected from the top 5% PTAM for low, medium, and high groups were 16.7, 22.2, 61.1, respectively.

Proportions for low and medium groups were relatively stable when divided by its phenotypic and genetic standard deviations. When milk records were transformed to logarithms, proportions of sires selected from groups were reversed.

Genetic and rank correlations between sub-groups are in Table 4(not shown here). The genetic correlation between low and medium groups was highest.

Table 3. Proportions of sires selected from groups by herd-year production levels when the top 5% and 10% of all sires were selected based on PTA for milk yield divided by its phenotypic and genetic standard deviation.

Variables & groups	Average PTAM		No. of sires S. <sup>2</sup>		P. <sup>1</sup> of sires S. <sup>2</sup>	
	Top 5%	Top 10%	Top 5%	Top 10%	Top 5%	Top 10%
Milk						
Low	1715.66	1214.47	3	4	16.7	11.1
Medium	2189.04	1653.72	4	8	22.2	22.2
High	2878.12	2475.86	11	24	61.1	66.7
Milk/ $\sigma_p$						
Low	1.36578	0.95579	4	6	22.2	16.7
Medium	1.57583	1.21160	4	14	22.2	38.9
High	1.51570	1.36571	10	16	55.6	44.4
Milk/ $\sigma_g$						
Low	2.87268	1.99587	4	4	22.2	11.1
Medium	3.28550	2.57620	4	14	22.2	38.9
High	3.55497	3.13537	10	18	55.6	50.0

1 : Proportions, 2 : selected,  $\sigma_p$  = Phenotypic standard deviation for milk,  $\sigma_g$  = Genetic standard deviation for milk.

## DISCUSSION

Heterogeneity among three production levels of milk yield was shown markedly in Korean dairy herds. Higher values of residual components than those of other studies indicated that most of milk variations attributed the differences to be environmental. When milk records were transformed to logarithms, average milk yields, standard deviations, and coefficients of variation for production levels were stable.

Differences in within sub-groups can cause decreased accuracy of breeding value predictions, which may results in biased proportions of sires selected from different groups.

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