

INTERACTION DUE TO GENETIC AND ENVIRONMENTAL EFFECTS ON MILK PRODUCTION IN JAPANESE HOLSTEIN

M.Suzuki¹, J.A.Pereira¹, K. Kuchida¹, Y.Saito¹, Y. Ikeuchi²

¹ Department of Animal Science, Obihiro University of Agric. & Vet. Sci.
Obihiro, Hokkaido 080, Japan

² National Livestock Breeding Centre, Ministry of Agriculture, Forestry and Fisheries,
Nishigo, Fukushima 961, Japan

SUMMARY

The interaction between genetic and environment for milk and fat yields in Japanese Holstein cows was evaluated. Sire genetic level, Herd-year level, Parity, Area and their interactions were analysed for deviation data calculated from animal model BLUP analysis and actual yield data.

GLM, SAS procedure, showed that the coefficient of determination decreased clearly from actual data (0.4672 to 0.4578) to deviation data (0.0093 to 0.0057). Log-transformation was effectively to diminish the F value of herd level, sire level and their interactions.

Keywords: GxE Interaction, Milk production, Log-transformation, BLUP.

INTRODUCTION

Milk production of dairy cows is influenced by genetic and environmental effects, and some kinds of interaction of those effects. The study of this interaction has taken different kinds of forms. The expression of the sire genetic ability in different kinds of environment is not clearly defined, but if the interaction due to genetic and herd environment were of considerable size, sires with high genetic level will not express its genetic ability in the same way as if they were used in different herds level, bulls with outstanding performance in high herds level may not be outstanding in low herds level. On the other hand, due to the heterogeneous variance of the herds, a considerable difference among herd levels exists, even inside the same herd level. In the former statement, the problem regard on the sires, in the second the problem laid in the selection of females when considerable difference exists.

However, in fact many different kinds of environment exist, and the genetic estimation has to take account this problem. In this paper, the following four factors were considered: area (A), parity (P), and herd-year levels (H) were assumed as environmental factors, the sire genetic level (S) was assumed as a main genetic factor. The aim of this study was to reveal the size of the interaction due to genetic and environment for milk and fat yields.

MATERIAL AND METHODS

A total of 2,947,726 official records of milk and fat yields from 1,137,384 Japanese Holstein cows were available. These data were accumulated in the National Livestock Breeding Centre

since 1975 and used for the 1993 autumn Sire Evaluation.

The Mixed Linear Model was:

$$Y_{ijklm} = HY_i + M_j + A_k + g_l + p_l + e_{ijklm}$$

The subscripts of Y_{ijklm} represent the herd-year number (i), the calving month (j), the age at calving (k), and the cows milk and fat yield records (l). HY_i , M_j , A_k , are the i, j, and k fixed effects for herd-year, calving month, and age at calving respectively, g_l and p_l are the random effects for the additive genetic and permanent environment of the cows respectively, e_{ijklm} is the random residual effect for records. By this model the residual effects were calculated as a deviation record.

In the analysis by SAS system, years of calving were limited from 1981 through 1990. The sires' genetic level for milk yields were calculated using the data of more than 2,000 daughters per sire, these sire levels were classified based on their ETA's for milk yields in four groups, assuming that the genetic average is zero, the groups were: -400kg or less, -400kg to 0Kg, 0kg to 400kg, and 400kg or more, in a fifth special group the sires with genetic evaluation from less than 2,000 daughters were included (Level 0). Herds were divided in five groups according of their herd-year effects, from 6,000kg or less to 9,000kg or more, the interval between groups was 1,000kg. All Japan was evaluated divided in three regions: Hokkaido (The Biggest Northern Island), North and east (NE), and South and west (SW, including Honshu, Kyushu, and Okinawa). All the genetic and environmental interactions among the four main effects were analysed using the GLM procedure included in the SAS system.

RESULTS AND DISCUSSION

The number and percentage of records due to regional area, sire and herd level, and number of lactations are shown in table 1. The number of records was distributed in a proportion of 4:1:1: approximately among the three areas, Hokkaido, NE, and SW respectively. Analysing the sire levels due to regional areas, and confronting Hokkaido's data to the rest of Japan, a difference in the use of sires level was observed. In the NE and SW areas, a strong tendency of the use of unpopular young bulls (sires of level 0) were evident. In contrast, Hokkaido shows the use of more bulls of levels 1 to 4 (bulls with more than 2,000 daughters), particularly sires of levels 1 and 4 were more used in Hokkaido than in other areas. The sires in level 1 may have good type classification scores, and bulls of level 4 may have high milk yield ability. The intermediate sire levels (2 and 3) were a little higher in Hokkaido with 59.8%, compared with the NE and SW areas with 47.5% and 43.8% respectively.

The herd level by areas, shows that Hokkaido had higher number of herds with low and high levels than the rest of Japan, these areas (NE and SW) had more concentration of herds in the intermediate levels, particularly the SW area. The lactation number against the areas shows that Hokkaido had a tendency of more number of lactations per cow.

Table 1. Number and percentage of records due to regional area, genetic, level of sire's ETA (sire Level), production level of herd-year (herd year), and number of lactation.

		Regions			All
		Hokkaido	NE	SW	
No. of records		1,465,611	369,432	340,569	2,175,612
percentage to all (%)		67.4	17.0	15.7	
Sire Level					
	0 (others)	14.7	38.0	41.9	22.9
	1 (low)	14.3	8.2	7.8	12.3
	2	28.2	25.3	22.0	26.7
	3	31.6	22.2	21.8	28.5
	4 (high)	11.1	6.2	6.5	9.6
Herd level					
	-6000kg	16.1	6.6	9.9	13.5
	6000-7000	44.0	36.3	41.9	42.3
	7000-8000	31.2	45.3	40.7	35.1
	8000-9000	7.9	11.1	7.2	8.3
	9000-	0.9	0.8	0.3	0.8
Lactation					
	1	35.2	41.8	42.0	37.4
	2	26.1	26.3	26.5	26.2
	3	18.6	16.9	16.8	18.0
	4	12.5	9.8	9.7	11.6
	5	7.6	5.1	5.1	6.8
Average lactation no.		2.31	2.10	2.09	2.24

The table 2 contains the original and deviated data from actual (non transformed) and log-transformed data for milk yield. The four main factors were combined among them to analyse all the possible interactions in order to found the F values, mean square errors as well as the coefficient of determination.

Table 2 shows the decrease in size of F-values from the deviated data compared with the original data, but because the analysis was based on a large amount of data the deviated data still shows significant differences, except for herd, sire, and the A*S, and A*H*S interactions, which became non significant. In other words, the sires with a better gene combination for milk and fat production may express their genetic ability independently of herds level.

Table 2. F-values from analysis of variance in actual and deviations of milk yield by original and log-transformed scale.

Source	df	Originals		Deviations	
		Actual	Log	Actual	Log
Area (A)	2	406.90 **	269.47 **	27.55 **	27.52 **
Herd (H)	4	55942.00 **	47900.75 **	68.96 **	1.34 ns
Sire (S)	4	407.58 **	297.19 **	5.88 **	0.71 ns
Parity (P)	4	6945.39 **	5758.28 **	3.19 *	24.50 **
A*H	8	9.49 **	10.56 **	3.67 **	2.50 **
A*S	8	5.51 **	3.84 **	1.61 ns	0.98 ns
A*P	8	58.25 **	43.34 **	128.70 **	92.11 **
H*S	16	16.40 **	5.63 **	8.28 **	1.85 *
H*P	16	156.85 **	4.46 **	157.45 **	6.40 **
S*P	16	8.23 **	3.24 **	8.88 **	3.95 **
A*H*S	32	2.91 **	2.23 **	1.40 ns	1.04 ns
A*H*P	32	2.26 **	1.71 **	5.27 **	3.33 **
A*S*P	32	1.74 **	0.93 ns	2.09 **	1.34 ns
H*S*P	64	3.63 **	2.56 **	2.69 **	1.62 **
A*H*S*P	128	1.65 **	1.24 *	1.80 *	1.41 **
MSE		1169.3	0.1740	665.0	0.0987
R^2		0.4672	0.4578	0.0093	0.0057

* :Significant ($P < .05$) ** :Significant ($P < .01$)

ns : non significant.

The log-transformation decreased the F-values for almost all the factors involved in the analysis, but some of them did not change (Area and Parity) or in contrast increased in size.

But in general, deviation records from an animal model reduce the coefficient of determination from the actual data (0.4672 to 0.4578) to deviation data (0.0093 to 0.0057). Log-transformation was effectively to decrease the F value of herds and sire levels as well as their interactions.

REFERENCES

- Dimov, G., Keown, J. F., Van Vleck, L. D., and Norman, H. D. (1996) *J. Dairy Sci.* **79**:140-144
 Meuwissen, T. H. E., DE Jong, G., and Engel, B. (1996) *J. Dairy Sci.* **79**:310-316
 Suzuki, M., Kuchida, K., and Saito, Y. (1997) *Anim. Sci. Technol.(Jpn)* (in press).