Trends in Heritability of Daily Milk Yield by Periods in Korean Cattle*

J. G. Choi, K. J. Jeon, K. J. Na, C. W. Lee, J. B. Kim[1] and C. Lee**

Daekwanryeong Branch, National Livestock Research Institute, Kangwon-do 232-952, Korea

ABSTRACT : Korean cattle breeders have shown interest in genetic improvement of milking ability because poor milking ability and short suckling period of Korean cattle is a hindrance to growth of calves. In this study, daily milk yields by period in Korean cattle were analyzed with an animal model. The milk yields were actually measured at sequential intervals from 1 to 4 months after calving: daily milk yields from delivery to 1 month (DMY1), from 1 to 2 months (DMY2), from 2 to 3 months (DMY3), and from 3 to 4 months (DMY4). Genetic variance estimates gradually increased by the periods while environmental variance estimates gradually decreased. This resulted in a dramatic increase in the heritability by periods: 0.02 for DMY1, 0.11 for DMY2, 0.16 for DMY3, and 0.42 for DMY4. In multi-trait analyses with daily milk yield and body weight of calf, genetic correlation estimates between milk yield and body weight were quite small (-0.08 to 0.02 for birth weight and -0.10 to 0.00 for weaning weight). The trends of the heritability estimated in this study showed that the genetic effects were more influential when the milking period was longer, suggesting genetic evaluations with daily milk yield collected at a longer period. *(Asian-Aust. J. Anim. Sci. 2003, Vol 16, No. 9 : 1239-1241)*

Key Words : Genetic Correlation, Milking, Variance Components

INTRODUCTION

There has been a great concern on milk production among Korean beef cattle breeders because the body weight and the milk production of beef cattle have been positively correlated (Freking and Marshall, 1992; Miller et al., 1999), and Korean cattle are known to have an inferior milking ability (Kim and Lee, 2000). Beef cattle production in Korea relies heavily on Korean cattle. Thus learning about traits that may influence the milking ability becomes an important issue in Korea. Lee and Pollak (2002) estimated genetic and environmental correlations between body weight (birth weight, weaning weight, and yearling weight) of cow and daily milk yield at different periods in Korean cattle using a two-trait sire and maternal grandsire mixed model. They observed negative genetic correlation estimates between the body weight and the daily milk yield while environmental correlation estimates were positive. Further investigations of milk production in Korean cattle are in need to assess more accurate genetic ability of milking in Korean cattle.

The objective of this study was to analyze milk production data actually and intently collected from Korean cattle. Daily milk yields collected at sequential intervals

were separately analyzed to examine differences during the milking period.

MATERIALS AND METHODS

Data

Data Collection : Korean cattle data were collected from 1994 to 2000 at the Daekwanryeong branch of National Livestock Research Institute (NLRI), Korea. The data included daily milk yield and body weight of calf. The data were pre-adjusted for age of dam. The herd used in this study has been systematically managed by the NLRI.

Most Korean cattle have a suckling period of 4 months. The daily milk yield was measured every 2 weeks after delivery during the suckling period. Thus they were measured 8 times. The amount of milk was measured twice a day. Two quarters in a side were milked by machine while the other two in the opposite side were suckled by calves. Alternate sides were milked in order to reduce possible systematic errors (Lee et al., 1995). The five traits of milk yield were analyzed: daily milk yield from delivery to 1 month (DMY1), from 1 month to 2 months (DMY2), from 2 months to 3 months (DMY3), from 3 months to 4 months (DMY4), and average daily milk yield of DMY1, DMY2, DMY3, and DMY4 (MDMY). Birth weight and weaning weight of calves were measured. The weaning weight was recorded at about 4 months of age, and weaning weight was linearly adjusted to 120-day weight. A total of 203 records were available for both milk production and weight traits. Means and their corresponding standard errors for the 5 daily milk yield traits were 5.38±0.34 for DMY1, 5.31±0.38 for DMY2, 4.34±0.33 for DMY3, 4.63±0.39 for DMY4, and 4.96±0.43 for MDMY. They showed the largest milk yield for DMY1, and the milk yield was significantly

decreased (p<0.05) for DMY3 and DMY4.

Analytical models

The data for daily milk yield were analyzed using a mixed model. The analytical models used in this study was an animal model shown below:

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

where y represents a vector of n observations for the daily milk yield. β is a vector of year-season fixed effects. u is a vector of additive genetic random effects with the assumption of u-N(0. $A\sigma_U^2$) where A is numerator relationship matrix, and σ_u^2 is additive direct genetic variance component. e is a random vector of residuals with the assumption of e~N(0. $I\sigma_e^2$) where σ_e^2 is residual variance component. X and Z are known incidence matrices relating the fixed and random effects to their corresponding observations. Sex effects were excluded in the model because the effects were not significant (p>0.05) for daily milk yields (Choi. 2001).

In order to examine genetic and environmental correlations between daily milk yield and body weight of calf, additional analyses were performed using a two-trait mixed model. The analytical model was also an animal model as following:

$$\begin{bmatrix} y_w \\ y_m \end{bmatrix} = \begin{bmatrix} X_w & 0 \\ 0 & X_m \end{bmatrix} \begin{bmatrix} \beta_w \\ \beta_m \end{bmatrix} + \begin{bmatrix} Z_w & 0 \\ 0 & Z_m \end{bmatrix} \begin{bmatrix} u_w \\ u_m \end{bmatrix} + \begin{bmatrix} e_w \\ e_m \end{bmatrix}$$

where $y_{w(m)}$ represents a vector of n observations for the body weight (milk yield), $\beta_{w(m)}$ is a vector of year-season and sex fixed effects for the weight and of only year-season effects for the milk yield. $u_{w(m)}$ is a vector of additive genetic random effects with the assumption of

$$\begin{bmatrix} u_w \\ u_m \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, G_0 \otimes A \right) \text{ where } G_0 = \begin{bmatrix} \sigma_{u_w}^2 & \sigma_{u_{wm}} \\ \sigma_{u_{wm}} & \sigma_{u_m}^2 \end{bmatrix} \quad \sigma_{u_{w,}}^2 \text{ and }$$

$\sigma_{u_{wm}}$ are additive genetic variance and covariance components. and $\otimes$ is direct product (Searle. 1982). $e_{w(m)}$ is a random vector of residuals with the assumption of

$$\begin{bmatrix} e_w \\ e_m \end{bmatrix} \sim N \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, R_0 \otimes I \right) \text{ where } R_0 = \begin{bmatrix} \sigma_{e_w}^2 & \sigma_{e_{wm}} \\ \sigma_{e_{wm}} & \sigma_{e_m}^2 \end{bmatrix} \quad \sigma_{e_{w,}}^2 \text{ and }$$

$\sigma_{e_{wm}}$ are environmental variance and covariance components respectively. $X_{w(m)}$ and $Z_{w(m)}$ are known incidence matrices relating the fixed and random effects to their corresponding observations.

Table 1. Estimates of variance components and heritability for daily milk yield of Korean cattle

Trait	σ_u^2	σ_e^2	σ_{ph}^2	h^2
DMY1	0.018	1.128	1.146	0.02
DMY2	0.137	1.099	1.236	0.11
DMY3	0.203	1.087	1.290	0.16
DMY4	0.579	0.793	1.372	0.42
MDMY	0.221	0.575	0.796	0.28

σ_u^2 is genetic variance. σ_e^2 is environmental variance. σ_{ph}^2 is phenotypic variance, and h^2 is heritability.

Parameter estimation

When covariance between the body weight and the daily milk yield was estimated using multiple trait model. genetic and environmental variance components were set to fixed values that were their corresponding estimates obtained in single trait analyses. Derivative-free REML estimation of variance and covariance components was performed using MTDFREML (Boldman et al.. 1995). Stopping criterion was 10^{-10} of simplex variance. Cold restarts were conducted at least 3 times in every analysis.

RESULTS AND DISCUSSION

The estimates of variance components and heritabilities were obtained for the daily milk yield (Table 1). Phenotypic variance estimate was gradually increased from DMY1 to DMY4. which was unexpected, given the trend in the means of the daily milk yields (see Materials and Methods). That is. the daily milk yield was decreased by periods. but its variation increased. Genetic variance estimate was quite small for DMY1. and also gradually increased from DMY1 to DMY4. The gradual increase of genetic variance estimates indicated that the genetic effect of the daily milk yield was more influential when the milking period was longer. Furthermore, the importance of genetic evaluation at a longer period was emphasized in order to lengthen the suckling period.

On the other hand. environmental variance estimate was gradually decreased from DMY1 to DMY4. This might be that cows gradually adapted to stress related to measurement of the daily milk yield. The most serious stress tended to come from the separation between cows and calves one day prior to the measurement. The trends for genetic and environmental variance component estimates resulted in a dramatic increase of the heritability from DMY1 to DMY4 (Table 1). The estimate (0.28) of heritability for MDMY in this study was larger than the estimate (0.12) of heritability for milk yield of Herefords in Meyer et al. (1994). It was. however. comparable to the estimates (0.28. 0.26. and 0.35) obtained by Diaz et al. (1992). Fan et al. (1996). and Miller and Wilton (1999).

Genetic correlation estimates between the daily milk yield and the body weight of calf were obtained in Table 2.

Table 2. Estimates of genetic correlation between daily milk yield and body weight of calf in Korean cattle

	DMY1[1]	DMY2	DMY3	DMY4
Birth weight	-0.08	-0.05	0.02	-0.07
Weaning weight	-0.10	-0.03	-0.06	-0.00

[1]DMY1, DMY2, DMY3 and DMY4 are daily milk yields from delivery to 1 month, from 1 to 2 months, from 2 to 3 months, and from 3 to 4 months, respectively.

Genetic correlation estimates between the daily milk yield and the birth weight were smaller than the estimates (-0.08 to -0.16) of Lee and Pollak (2002). This might be due to lack of sufficient pedigree information to estimate the genetic correlation. Genetic correlation estimates between the daily milk yield and the weaning weight of calf were also smaller than the estimates of Lee and Pollak (2002). For example, Lee and Pollak's estimates were ranged from -0.10 to -0.21 except for that (-0.04) between weaning weight of cow and daily milk yield from 1 month to 2 months. Estimates obtained in the current study were, however, by and large corresponding to the estimates (-0.10 for Hereford and 0.00 for Wokalup) obtained by Meyer et al. (1994). Low negative genetic correlation estimate (-0.08) was also obtained between milk yield and 200-day weaning gain of calf in a multibreed beef herd (Miller and Wilton, 1999). This study also confirmed the hypothesis of Lee (2002) that, given the idea of partitioning nutrients by Bauman and Currie (1980), direct and maternal effects for the weaning weight of beef cattle is genetically antagonistic by considering the negative correlation between the body weight and the milk yield.

CONCLUSION

Korean cattle produce a small amount of milk and have an unusually short suckling period. The inferior milking ability leads to a low weaning weight of calves, and consequently results in lighter weights when they are sent to market. Strategic efforts to increase the amount and duration of milking deserves keen attention for improvement of meat production in Korean cattle. This study showed that genetic variance estimates increased gradually by periods, and environmental variance estimates decreased. Genetic evaluation with the daily milk yield collected at a longer period was recommended because genetic effects were more influential when the milking period was longer.

REFERENCE

Bauman, D. E. and W. B. Currie. 1980. Partitioning of nutrients during pregnancy and lactation: A review of mechanisms involving homeostasis and homeorhesis. J. Dairy Sci. 63:1514-1529.

Boldman, K. G., L. A. Kriese, L. D. Van Vleck, C. P. Van Tassell and S. D. Kachman. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variance and covariance [draft]. U.S. Department of Agriculture, Agricultural Research Service.

Choi, J. G. 2001. Genetic characteristics of body weight by growth periods for Hanwoo. Ph.D. Thesis, Kangwon National University, Chuncheon, Korea. (In Korean)

Diaz, C., D. R. Notter and W. E. Beal. 1992. Relationship between milk expected progeny differences of polled Hereford sires and actual milk production of their crossbred daughters. J. Anim. Sci. 70:396-402.

Fan, L. Q., J. W. Wilton and P. E. Colucci. 1996. Genetic parameters for feed intake and efficiency in lactating beef cows. Can. J. Anim. Sci. 76:81-87.

Freking, B. A. and D. M. Marshall. 1992. Interrelationships of heifer milk production and other biological traits with production efficiency to weaning. J. Anim. Sci. 70:646-655.

Kim, J. B. and C. Lee. 2000. Historical look at the genetic improvement in Korean cattle (Review). Asian-Aust. J. Anim. Sci. 13:1467-1481.

Lee, C. 2002. On the negative estimates of direct and maternal genetic correlation. Asian-Aust. J. Anim. Sci. 15:1222-1226.

Lee, C. and E. J. Pollak. 2002. Genetic antagonism between body weight and milk production in beef cattle. J. Anim. Sci. 80:316-321.

Lee, C., E. J. Pollak, R. W. Everett and C. E. McCulloch. 1995. Multiplicative factors for estimation of daily milk and component yields from single morning or afternoon tests. J. Dairy Sci. 78:221-235.

Meyer, K., M. J. Carrick and B. J. P. Donnelly. 1994. Genetic parameters for milk production of Australian beef cows and weaning weight of their calves. J. Anim. Sci. 72:1155-1165.

Miller, S. P. and J. W. Wilton. 1999. Genetic relationships among direct and maternal components of milk yield and maternal weaning gain in a multibreed beef herd. J. Anim. Sci. 77:1155-1161.

Miller, S. P., J. W. Wilton and W. C. Pfeiffer. 1999. Effects of milk yield on biological efficiency and profit of beef production from birth to slaughter. J. Anim. Sci. 77:344-352.

Searle, S. R. 1982. Matrix algebra useful for Statistics. John Wiley & Sons, New York.