SIMULTANEOUS IMPROVEMENT OF LACTATION MILK AND PERSISTENCY

C. Y. Lin[1] and K. Togashi[2]

[1]Dairy and Swine Research and Development Centre, Agriculture and Agri-Food Canada
Correspondence: Dept. of Animal & Poultry Science, University of Guelph, Canada N1G 2W1
[2]National Agricultural Research Centre in Hokkaido, Toyohira-ku, Sapporo, Japan 062-8555

INTRODUCTION

Persistency commonly refers to the rate of decline after peak yield. Although there are many different measures of persistency as reviewed by Swalve and Gengler (1998), given the same total lactation yield a cow with a flatter curve is said to be more persistent. A more persistent cow has better use of cheap roughage (Solkner and Fuchs, 1987), suffers less stress due to high peak yield (Zimmermann and Sommer, 1975) and makes more profit (Dekkers *et al*., 1998). Random regression test day models not only improves the accuracy of genetic evaluations, but also provides a potential for evaluating persistency because the EBV for various parts of the lactation can be calculated (Schaeffer and Dekkers, 1994 ; Jamrozic *et al.*, 1997). Danell (1982) and Ferris *et al*. (1985) did empirical studies on selection for increased persistency where the economic weights were arbitrarily assigned. The objective of this study was to present two selection methods to simultaneously improve total lactation yield and persistency in dairy cows.

MATERIALS AND METHODS

It is theoretically possible, although impractical, to weight daily yield for each day in milk (DIM) across lactation to modify the lactation curve. Yields at adjacent DIM have high correlations and thus, it is reasonable to partition lactation period into different stages.

Index selection based on stage EBV. Animal test-day model with quartic regression (*i.e*., 5 RR coefficients) was assumed in this study. Lactation length was partitioned into five stages : say, stage 1 (DIM 1-30), stage 2 (DIM 31-60), stage 3 (DIM 61-170), stage 4 (DIM 171-280), and stage 5 (DIM 281-305). Note that the number of stages partitioned should be equal to the number of RR coefficients fitted. A "stage EBV" is calculated by summing the daily EBV within a stage. The index based on the EBV of the 5 stages is,

$$I = \sum_{j=1}^{5} b_j \, EBV_j = \sum_{j=1}^{5} b_j \sum_{t=m_j}^{n_j} \sum_{i=0}^{k-1} \phi_i(t)\alpha_i$$

where m_j and n_j are the first and the last day of the j^{th} stage, respectively; b_j is the index weight for the j^{th} stage; $\phi_i(t)$ is the i^{th} order of Legendre polynomial evaluated at day t standardized; and α_i is the i^{th} random (genetic) regression coefficient, k is the number of RR coefficients fitted. Legendre polynomial regression is used to model the shape of the lactation curve in this study. However, the same principles apply to other lactation curve functions. In matrix notation, $I = b'\theta$ where θ is a column vector containing the EBV of the 5 stages and b is a vector of index weights. The expected genetic gain (correlated response) in the i^{th} stage

due to selection on I is $\Delta G_i = b_{EBV_i \bullet I}(\text{sel. diff.}) = \text{Cov}(EBV_i, I)(\bar{i}/\sigma_I)$ where $\bar{i}$ is selection intensity. Consequently, the expected genetic gains for the 5 stages due to selection on I are,

$$\begin{bmatrix} \Delta G_1 \\ \Delta G_2 \\ \Delta G_3 \\ \Delta G_4 \\ \Delta G_5 \end{bmatrix} = \begin{bmatrix} \mathbf{1}'\Phi^1 K \Phi^{1'}\mathbf{1} & \mathbf{1}'\Phi^1 K \Phi^{2'}\mathbf{1} & \mathbf{1}'\Phi^1 K \Phi^{3'}\mathbf{1} & \mathbf{1}'\Phi^1 K \Phi^{4'}\mathbf{1} & \mathbf{1}'\Phi^1 K \Phi^{5'}\mathbf{1} \\ \mathbf{1}'\Phi^2 K \Phi^{1'}\mathbf{1} & \mathbf{1}'\Phi^2 K \Phi^{2'}\mathbf{1} & \mathbf{1}'\Phi^2 K \Phi^{3'}\mathbf{1} & \mathbf{1}'\Phi^2 K \Phi^{4'}\mathbf{1} & \mathbf{1}'\Phi^2 K \Phi^{5'}\mathbf{1} \\ \mathbf{1}'\Phi^3 K \Phi^{1'}\mathbf{1} & \mathbf{1}'\Phi^3 K \Phi^{2'}\mathbf{1} & \mathbf{1}'\Phi^3 K \Phi^{3'}\mathbf{1} & \mathbf{1}'\Phi^3 K \Phi^{4'}\mathbf{1} & \mathbf{1}'\Phi^3 K \Phi^{5'}\mathbf{1} \\ \mathbf{1}'\Phi^4 K \Phi^{1'}\mathbf{1} & \mathbf{1}'\Phi^4 K \Phi^{2'}\mathbf{1} & \mathbf{1}'\Phi^4 K \Phi^{3'}\mathbf{1} & \mathbf{1}'\Phi^4 K \Phi^{4'}\mathbf{1} & \mathbf{1}'\Phi^4 K \Phi^{5'}\mathbf{1} \\ \mathbf{1}'\Phi^5 K \Phi^{1'}\mathbf{1} & \mathbf{1}'\Phi^5 K \Phi^{2'}\mathbf{1} & \mathbf{1}'\Phi^5 K \Phi^{3'}\mathbf{1} & \mathbf{1}'\Phi^5 K \Phi^{4'}\mathbf{1} & \mathbf{1}'\Phi^5 K \Phi^{5'}\mathbf{1} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \\ b_5 \end{bmatrix} (\bar{i}/\sigma_I)$$

where K is the genetic covariance matrix of RR coefficients, matrix Φ^i contains the Legendre polynomials of the i^{th} stage, and **1** is a summing vector of 1 with a dimension equal to the number of days in the corresponding stage. The above equation can be written as $\underline{\Delta} = Gb(\bar{i}/\sigma_I)$ where vector $\underline{\Delta}$ contains the genetic gains for the 5 stages and G is the genetic covariance matrix of the 5 stages. Since $\bar{i}/\sigma_I$ is a constant for all stages and can be dropped, the solution to the index equations becomes $b = G^{-1}\underline{\Delta}$. Some countries such as Canada and Finland use random regression test day model in national genetic evaluations. Therefore, matrix G and vector $\underline{\Delta}$ can be determined to solve for vector b.

Selection for increased rate of ascent to the peak would result in a greater rate of descent after peak (Batra *et al*., 1987). Thus, the rate of ascent in stage 1 is restricted to zero change in order to improve persistency. Peak yield usually occurs in stage 2 where cows suffer negative energy balance. Therefore, the genetic change in stage 2 is set to zero to avoid extra stress. The last stage (days 281 to 305) is so short that it is restricted to zero change. Basically, the index is designed to improve stage 3 (days 61 to 170) and stage 4 (days 171 to 280) while holding zero changes in stages 1, 2 and 5. As an example, annual genetic gain is 140 kg EBV for milk yield in Canada (CDN website, 2001), we may improve stage 3 by 72 kg EBV and stage 4 by 68 kg EBV. Thus, the prespecified genetic changes for the 5 stages become $\underline{\Delta}' = [0 \quad 0 \quad 72 \quad 68 \quad 0]$ where the elements of $\underline{\Delta}$ sum to annual genetic gain of 140 kg EBV.

Index selection based on random regression coefficients. The shape of a cow's lactation curve is determined by a unique set of RR coefficients, thus offering a possibility of modifying the lactation curve by direct selection on the RR coefficients. Let S be a (5 x 5) matrix with (*i*,*j*) element equal to the sum of the j^{th} order Legendre polynomial (j = 0, 1, 2, 3 or 4) of the i^{th} stage (i = 1, 2, 3, 4 or 5). The i^{th} row of S is equal to $\mathbf{1}'\Phi^i$. Let α be a column vector containing $\alpha_0, \alpha_1, \alpha_2, \alpha_3$ and α_4 for the typical curve. The stage EBVs of a cow are $\theta = S\alpha$ and the lactation EBV is $\mathbf{1}'\theta = \mathbf{1}'S\alpha$. The index based on RR coefficients is defined as,

$$I^* = b_0^* \alpha_0 + b_1^* \alpha_1 + b_2^* \alpha_2 + b_3^* \alpha_3 + b_4^* \alpha_4 = \alpha' b^*$$

The expected response in α_i due to selection on I^* is $\Delta\alpha_i = \text{Cov}(\alpha_i, I^*)(\bar{i}/\sigma_{I^*})$. It follows that

$$\begin{bmatrix}\Delta\alpha_0\\ \Delta\alpha_1\\ \Delta\alpha_2\\ \Delta\alpha_3\\ \Delta\alpha_4\end{bmatrix} = \begin{bmatrix}\sigma^2_{\alpha_0} & \sigma_{\alpha_0\alpha_1} & \sigma_{\alpha_0\alpha_2} & \sigma_{\alpha_0\alpha_3} & \sigma_{\alpha_0\alpha_4}\\ \sigma_{\alpha_1\alpha_0} & \sigma^2_{\alpha_1} & \sigma_{\alpha_1\alpha_2} & \sigma_{\alpha_1\alpha_3} & \sigma_{\alpha_1\alpha_4}\\ \sigma_{\alpha_2\alpha_0} & \sigma_{\alpha_2\alpha_1} & \sigma^2_{\alpha_2} & \sigma_{\alpha_2\alpha_3} & \sigma_{\alpha_2\alpha_4}\\ \sigma_{\alpha_3\alpha_0} & \sigma_{\alpha_3\alpha_1} & \sigma_{\alpha_3\alpha_2} & \sigma^2_{\alpha_3} & \sigma_{\alpha_3\alpha_4}\\ \sigma_{\alpha_4\alpha_0} & \sigma_{\alpha_4\alpha_1} & \sigma_{\alpha_4\alpha_2} & \sigma_{\alpha_4\alpha_3} & \sigma^2_{\alpha_4}\end{bmatrix}\begin{bmatrix}b^*_o\\ b^*_1\\ b^*_2\\ b^*_3\\ b^*_4\end{bmatrix}(\bar{i}/\sigma_{I^*})$$

where $\Delta\alpha_i = \bar{\alpha}^*_i - \bar{\alpha}_i =$ mean difference in the i^{th} order RR coefficient after and before selection. This set of equations can be expressed as $\underline{\Delta}_\alpha = Kb^*(\bar{i}/\sigma_{I^*})$. Since $\bar{i}/\sigma_{I^*}$ is a constant and can be dropped, the index coefficients for I^* finally become $b^* = K^{-1}\underline{\Delta}_\alpha$ where

$$\underline{\Delta}_\alpha = \begin{bmatrix}\bar{\alpha}^*_0 & \bar{\alpha}^*_1 & \bar{\alpha}^*_2 & \bar{\alpha}^*_3 & \bar{\alpha}^*_4\end{bmatrix}' - \begin{bmatrix}\bar{\alpha}_0 & \bar{\alpha}_1 & \bar{\alpha}_2 & \bar{\alpha}_3 & \bar{\alpha}_4\end{bmatrix}' = \bar{\alpha}^* - \bar{\alpha}$$

After one cycle of selection based on I^*, the expected stage EBVs are $\bar{\theta}^* = S\,\bar{\alpha}^* = \bar{\theta} + \underline{\Delta}$ and the expected RR coefficients are $\bar{\alpha}^* = S^{-1}\bar{\theta}^* = S^{-1}(\bar{\theta} + \underline{\Delta})$. Therefore,

$$\underline{\Delta}_\alpha = \bar{\alpha}^* - \bar{\alpha} = S^{-1}\bar{\theta}^* - S^{-1}\bar{\theta} = S^{-1}(\bar{\theta}^* - \bar{\theta}) = S^{-1}\underline{\Delta}$$

This shows that the determination of $\underline{\Delta}_\alpha$ depends upon the prior information on $\underline{\Delta}$ and the genetic changes in RR coefficients and stage EBVs can be readily converted from each other.

Relationship between I and I^*. Because of $G = SKS'$, it follows that $K = S^{-1}GS'^{-1}$.

$$I^* = \alpha'\,b^* = \alpha'[K^{-1}\underline{\Delta}_\alpha] = \alpha'[(S^{-1}GS'^{-1})^{-1}(S^{-1}\underline{\Delta})] = \alpha'[S'G^{-1}\underline{\Delta}] = \alpha'[S'b] = \theta'b = I$$

This proved that the two selection procedures are equivalent and $b^* = S'b$ permits an easy conversion between vectors b^* and b.

RESULTS AND DISCUSSION

It is good practice to assign equal number of DIM to those stages under modification. For example, this study aims to modify stages 3 and 4 and thus, these two stages are assigned 110 days each. The varying length of the stages could be taken into account by using the average daily EBV of each stage. Since the goal is to reduce the rate of decline after the peak (stage 2), the average daily EBV of each stage should be in order of stage 2 > stage 3 > stage 4 > stage 5. There are numerous ways of partitioning the lactation length and distributing the genetic gains between different stages. Optimal combination of these two factors merits further study.

The derivation of the two selection procedures is based on prior knowledge of annual genetic gains from national genetic evaluations. When there is no prior knowledge of genetic gains, the relative proportion of genetic gains between stages could replace the actual genetic changes in $\underline{\Delta}$. For example, the use of $\underline{\Delta}' = [0 \quad 0 \quad 1.1 \quad 1 \quad 0]$ implies that there are zero genetic changes in stages 1, 2 and 5 and the rate of genetic improvement between stages 3 and 4 is 1.1:1. Proportional restriction needs to take into account the unequal interval of the stages.

Substituting the ratio of genetic gains among stages for $\underline{\Delta}$ would not alter the relative values of index coefficients or the rankings of animals.

The proposed procedures restrict genetic changes to certain specified lactation stages to improve persistency and total yield. The difference between the genetic changes used to construct the index and realized by its application provides an experimental check on the theoretical validity of the index. The smaller the difference is, the more realistic the restricted index. Because the RR coefficients change with genetic progress, it is important to assess the realized genetic gains due to the index and reconstruct the index on a routine basis. The realized correlated responses in different lactation stages offer biological insight into genetic manipulation of the lactation curves and further refinement of the restricted index. Theoretically, it is possible to derive a restricted index to meet any restrictions imposed, but the restrictions must be biologically reasonable to be achievable (Lin, 1985). Therefore, the validity of the developed procedures needs to be confirmed by experimental study.

CONCLUSION

Two equivalent methods were presented to simultaneously improve the lactation EBV and the shape of the lactation curve : 1) index selection on stage EBV and 2) index selection on random regression coefficients. Both indexes were developed based on the restriction of genetic gains to specified lactation stages to achieve the desired curves. Index selection on stage EBV appears more practical than index selection on random regression coefficients simply because the concept of EBV has been deeply implanted in the dairy industry. The developed methods provide a practical approach to manipulate the genetic changes in different stages of lactation at a prespecified rate. The optimal strategy to modify the lactation curve should take into account : 1) annual rate of genetic improvement, 2) proportion of genetic gains between stages, 3) genetic covariance matrix of stages, 4) choice of lactation curve functions, and 5) number and length of stages. This study has provided a theoretical framework to achieve the desired lactation curve. However, theoretical possibility needs to be confirmed by experimental study.

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