

# Estimation Of Genetic Parameters Of Persistency Of Milk Yield In A Thai Multibreed Holstein Population Using Multiple-trait Animal Model

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## Introduction

Persistency of milk yield is defined as the ability of cow to maintain a constant milk yield in the high level through the lactation (Gengler, N., Keown, J. F., and VanVleck, L. D. (1995)). Cows with high PER (flat curve) are always considered to have more advantages for selection. Persistency of milk yield is economically important because it is associated with feed cost, health, and fertility (Sölkner and Fuchs (1987); Dekkers, J. C. M., Hag, J. H. T., and Weersink, A. (1998)). Sölkner and Fuchs (1987) found that more persistent cow has lesser feed cost. They found that a high persistent cow requires lesser energy for lactation than a low one which eventually increases farm profitability.

There were several reports on PER were also reported by different authors elsewhere (Madsen, (1975), Van der Linde, R., Groen, A., and Jong. G. D. (2000); Muir, B. L., Fatehi J., and Schaeffer, L. R. (2004)). It was found that the heritability estimates of PER had a wide range between 0.01 and 0.54. Most of these genetic parameters of PER varied greatly and were mostly obtained from a single breed population raised in the temperate environment. Currently, the dairy cattle population in Thailand is composed of purebred Holstein (HF) and a high percentage of H animals with various fractions of other *Bos taurus* (Brown Swiss, Jersey, Red Dane) and *Bos indicus* (Brahman, Red Sindhi, Sahiwal) breeds (O). Parents in this population are chosen from HF, crossbred HF and O breed groups, resulting in a multibreed population composed of animals with a variety of breed compositions. Thus, using those genetic parameters directly in the population that contains the different infrastructures may not appropriate and may be bias for implementation. The objectives of this study were to estimate the genetic parameters of three different measures of persistency of milk yield, and to consider the suitable method that should be implied as routine in a multibreed dairy population under the tropical environment of Thailand.

## Material and methods

Records of 21,800 monthly test day yields from 2,308 first lactation cows calved during the years 1993 to 2003 were analyzed in the study. Data were obtained from the bureau of Biotechnology in Livestock Production, Department of Livestock Development (DLD), Thailand. The Wilmink function ( $y_t = a + b \times \exp^{-0.06 \times t} + c \times t$ ; Wilmink, (1987) was used for interpolation and fitted to unadjusted test day yield in order to estimate parameters ( $a$ ,  $b$  and  $c$ ) for every cows. After that these parameters of individual cows were used to predict daily milk yield and calculate persistency traits for each cows.

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Three measurements of persistency of milk yield were expressed as 1) the linear regression coefficient of milk yield on days in milk or parameter  $c$  of WIL function (PER1). Thus, PER1 is a measure of absolute decreasing of yield during the lactation, 2) the difference between daily milk yield at days 60 and days 280 of the lactation and 3) the ratio of milk yield in several part of lactation. Both measures of persistency were available as output from fitting WIL function to individual test day records. For the analysis, parameter  $c$  for every cow was estimated in a negative value because this value always represents a declining of milk yield. To easily understand and calculate, parameter  $c$  was considered in absolute value for all cows. Hence, the small values of PER1 and PER2 represent the low persistency, while a large value of PER3 indicates the high persistency of milk yield.

After reaching these criteria, all measures of persistency traits were merged to the production information of individual cows. Data were classified calving seasons as summer (Mar to Jun), rainy (Jul to Oct) and winter (Nov to Feb). Age at first calving ranged from 19 to 48 months. Lactation having the date of first test greater than 35 days was excluded. The contemporary groups (CG) were defined as herd-year-season of calving (HYS). The models included the direct genetic as random effect and the fixed effects were contemporary groups, breed fraction, first test date and age at first calving. The records were checked for direct sire connectedness across CG and the disconnected CG data were eliminated. Cows without a known sire and dam were discarded.

The Multiple-trait animal model was employed to estimate genetic parameters. Three persistency of milk yield (PER1, PER2 and PER3) were analyzed as followed:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_{ga}\mathbf{g}_a + \mathbf{Z}_a\mathbf{a}_a + \mathbf{e}$$

where,  $\mathbf{y}$  is a vector of the observations for persistency traits (PER1, PER2 and PER3),  $\mathbf{b}$  is the vector of fixed effects,  $\mathbf{g}_a$  is the vector of regression additive genetic groups deviations,  $\mathbf{a}_a$  is the vector of additive genetic effects,  $\mathbf{X}$  is the incidence matrix that related cow records to elements of vector  $\mathbf{b}$ ,  $\mathbf{Z}_{ga}$  is the incidence matrix of expected breed fraction of HF that related cow records to element of  $\mathbf{g}_a$  and  $\mathbf{Z}_a$  is the incidence matrix that related to element of vector  $\mathbf{a}_a$  and  $\mathbf{e}$  is the vector of residuals. The assumptions of these components were:

$$\mathbf{E}[\mathbf{y}] = \mathbf{X}\mathbf{b} + \mathbf{Z}_{ga}\mathbf{g}_a, \mathbf{V}(\mathbf{a}_a) = \mathbf{G} \otimes \mathbf{A}, \mathbf{V}(\mathbf{e}) = \mathbf{R} \otimes \mathbf{I}$$

where,  $\mathbf{G}$  is co(variance) matrices between additive genetic effects,  $\mathbf{A}$  is the relationship matrix between individuals,  $\otimes$  is the Kronecker product,  $\mathbf{R}$  is a diagonal of residual variances and  $\mathbf{I}$  is identity matrix. The (co)variances components were estimated by expected maximization restricted maximum likelihood (EM-REML) methodology from the BLUPF90 *DairyPack2* program (Duangjinda, M., Miztal, I., and Tsuruta, S. (2004)). Heritabilities were calculated between the ratio of additive genetic variance ( $\sigma_a^2$ ) and total variance ( $\sigma_T^2$ ). The additive genetic correlations were calculated as  $\sigma_{a(i,j)} / \sigma_{a(i)} \sigma_{a(j)}$ , where  $\sigma_{a(i,j)}$  was the covariance between trait  $i$  and trait  $j$ , respectively, and  $\sigma_{a(i)}, \sigma_{a(j)}$  were the standard deviations of trait  $i$  and trait  $j$ , respectively.

## Results and discussion

Means and summary statistics for all PER traits are in Table 1. The means of PER1, PER2 and PER3 were  $0.029 \pm 0.016$  kg/d,  $6.26 \pm 3.56$  kg and  $27.27 \pm 4.52\%$ , respectively. These results were similar to previous reports. Kitpipit (2002) reported the means of PER1 and PER3 of 0.03 kg/d and 26.10% in the commercial farm located central Thailand. Muir et al. (2004) reported the mean of PER1 in Canadian HF was 0.039 kg/d. Dekkers et al. (1998) reported the mean of PER3 of 29.2% in Canadian HF population.

**Table 1 Number of records, mean, standard deviation (SD), minimum (Min), and maximum (Max) of persistency of milk yield traits**

Trait <sup>1</sup>	No. of records	Mean	SD	Min	Max
PER1 (kg/d)	2,308	0.029	0.016	0	0.108
PER2 (kg)	2,308	6.26	3.56	0.02	20.95
PER3 (%)	2,308	27.27	4.52	6.48	46.25

<sup>1</sup>PER1=absolute value of parameter-c from the WIL function, PER2=the different of milk yield between DIM60 and DIM280, PER3=the ratio between yield from 201 to 305 days and total yield of lactation

Heritabilities for PER measures were found to range from 0.01 to 0.03 are shown in table 2. These lower heritabilities of PER indicated that there were greater environmental effects on these traits than the non-genetic ones. The values obtained were in the range of those reported by Swalve, H.H. and Gengler, N. (1999). In the tropical researches, Kitpipit (2002) reported the heritabilities for PER range between 0.07 and 0.14. Weller et al. (2006) reported the heritability of PER to be 0.17 in Israeli HF cows. The study of PER1 heritability in the temperate zone in Dutch HF cows by Van der Linde, R., Groen, A., and Jong, G. D. (2000) was 0.13 and was in the same range. Muir et al. (2004) also reported heritability for PER1 to be 0.18 in Canadian HF. The higher heritabilities were reported by Madsen (1975) in Danish cows (0.40 to 0.57). The extremely high heritabilities were explained by the common environment effects because the Danish progeny testing system progeny from sires were bought together in one testing station.

The result indicated the variation of environmental factors (management, roughage quality, climate, and culture of farmers) and cow's performance have much larger effects on PER traits (Cole and VanRaden (2006)). In addition, it may be due to the low adaptability of dairy cows under the tropical environment. Grossman et al. (1999) stated that selection PER directly on phenotypic value might not be appropriate.

Genetic and phenotypic correlations among measures of PER are shown in Table 2. The genetic correlations were found to be wide ranged from -0.09 (PER2 and PER3) to 0.99 (PER1 and PER2). The correlations between PER1 and PER2 were very high (0.99). It indicated that these can be considered as the same trait. In contrast, they were low relationship with PER3. This reflects the fact that PER1 and PER2 express the absolute decrease of milk yield after peak. On the other hand, PER3 relate to total lactation yield (Madsen, (1975)). Therefore, different measures express the shape of lactation curve in different ways (Gengler, N., Keown, J. F., and VanVleck, L. D. (1995)). The results were the same as reported by many studies (Madsen, (1975); Schneeberger, (1981); Sölkner and

Fuchs (1987)). Madsen (1975) reported the lower genetic correlations (0.31). There were long been study report in Thailand by Kitpipit (2002) reported the correlation between PER1 and PER3 to be 0.88. The correlation coefficients were in high levels as reported by Gengler, N., Keown, J. F., and VanVleck, L. D. (1995). In routine work, PER1 could be preferable than other methods because it was easy to interpret, calculation and understanding (Muir, B. L., Fatehi J., and Schaeffer, L. R. (2004)).

**Table 2 Estimation of heritabilities (on diagonal), genetic correlations ( $r_g$ , above diagonal) and phenotypic correlations ( $r_p$ , below diagonal) for persistency of milk yield in a Thai multibreed dairy population**

$r_p$	$r_g$	Measures of persistency of milk yield		
		PER1	PER2	PER3
PER1		0.03	0.99	-0.07
PER2		0.99	0.03	-0.09
PER3		-0.69	-0.74	0.01

## Conclusion

The heritabilities of PER were quite low. These results in the study were not conformed to those finding in the temperate environment which might be due different in population structure, feed, feeding, health care, and management systems. The correlation between PER1 and PER2 was very high. On the contrary, they negative correlated with PER3. In practical working, PER1 was preferable to measure PER of milk yield because this method was easily to calculate, understand, biological interpretation and only represented three parameters. Therefore, the results of this study should be implied that PER1 could be considered as the suitable method better than other methods in the population.

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