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THESIS

GENETIC EVALUATION ON MILK PRODUCTION TRAITS USING RANDOM REGRESSION TEST-DAY MODEL IN A THAI MULTIBREED DAIRY CATTLE POPULATION

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A Thesis Submitted in Partial Fulfillment of
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Monthly test-day yields of 21,934 records from 2,321 first lactating cows were obtained from the Department of Livestock Development (DLD). Data were collected during the years 1993 and 2003. Test day yield were adjusted by the variation of herd-year-season of calving, Holstein Friesian (HF) breed fractions, calving age and first test-date after calving effects. In the first trial, the four functions included Wilmink exponential (WIL), Wood gamma (WD), Schaeffer and Dekkers (SHE) logarithm, and Legendre polynomials (LEG) functions were used to fit the mean and individual lactation curve. The results found that the WIL gave the best goodness of fit to mean and individual lactation curves and smaller values of residual errors than other functions. Also, WIL was therefore considered to be the most suitable function to describe the lactation curve in this population.

The second trial estimated genetic parameters of 305-d milk yield (305MY) and persistency of milk yield using WIL function. Three measures of persistency were calculated as 1) absolute value of regression coefficient from WIL function or parameter c (PER1), 2) the different of milk yield between days 60 and 280 (PER2) and 3) the ratio between accumulated yield from 201 to 305 days and 305MY (PER3). Multiple-trait animal model was performed using EM-REML to estimate genetic parameters. Heritability of 305MY was found to be 0.12, and persistency traits were low ranging from 0.01 to 0.03. Genetic correlations between 305MY and persistency traits were found to be range from 0.37 to 0.55. Ratio method in our study not only described persistency, but also was highly influenced by 305MY. Genetic correlations among three measurements of persistency were ranged from -0.07 to 0.99. The results showed that PER1 could be considered the suitable method to measure persistency because it was not complicated for computation, interpretation, heritable, and had low correlated with 305MY.

The third trial was carried out to evaluate genetic ability of milk yield using random regression test day model (RR-TDM). The model contained the random effect of herd-test date (HTD), fixed regression, and random regressions on the animal and the permanent environmental effects. The WIL function was nested as sub-models for both fixed and random parts. Residual and HTD variance was assumed constant during lactation. The results showed that heritability of 305MY was 0.47 which was higher than the lactation model (0.12). Heritabilities of daily yields varied from 0.40 to 0.59 and was generally highest at the mid lactation. The correlations of sires and cows occurred between RR-TDM and lactation model were moderate high. These results implied that RR-TDM could be used for routine genetic evaluation instead of lactation model. Moreover, the RR TDM can calculate genetic persistency at the same time. The RR-TDM was therefore suitable for routine evaluations on milk yield and persistency of dairy cattle under small farms and tropical conditions.

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Warangkana Kitpipit
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LIST OF ABBREVIATIONS

BLUP = Best Linear Unbiased Predictor

CGs = Contemporary groups

DIM = Day in milk

EBVs = Estimated breeding values

HF = Holstein Friesian

HTD = Herd test-date of recording

HYS = Herd year season of calving

LEG = Legendre polynomials

LM = 305-days lactation model

MMSE = Mean of mean square error

MSPE = Mean square prediction error

MAE = Means of absolute error

RMSE = Root mean square error

RR-TDM = Random regression test-day model
R^2 = coefficient of determination
SHE = Schaeffer and Dekkers mixed linear with logarithm
TD = test-day
TIM = test interval methods
WIL = Wilmink exponential
WD = Wood gamma
305MY = accumulated 305-d milk yield

GENETIC EVALUATION ON MILK PRODUCTION TRAITS USING RANDOM REGRESSION TEST-DAY MODEL IN A THAI MULTIBREED DAIRY CATTLE POPULATION

INTRODUCTION

Genetic evaluation on milk production of dairy cattle in Thailand has been based on 305-day milk yields (305MY) using traditional lactation model (LM). The accumulate 305MY was estimated from individual test-day (TD) records according to relatively simple rules giving from test interval method (TIM) by Sargent *et al.* (1968). The environmental changes within 305MY are usually ignored and a simple herd-year-season of calving (HYS) effect is often used to account for the average of environmental effects occurring on each TD records during the lactation. The accuracy of 305MY always varies depending on the number of TD samples and the procedure being used. It was also found that in computing accumulate 305MY, the short lactation on culled cows or records in progress have to be extended, which also may lead to bias (Anderson *et al.*, 1989; Jamrozik and Schaeffer, 1997). Biases from extending records may be occurred due to individual's shape of lactation pattern overestimate or underestimate (Shanks *et al.*, 1981).

In recent year, interest in TD records has increased among dairy geneticists and members of dairy cattle industry (Swalve, 2000). There have been numerous studies about applications of random regression test-day model (RR-TDM) to the genetic evaluation for milk production in many countries i.e. Belgium, Canada, Finland, Germany, Austria, Netherlands and Italy (Jamrozik *et al.*, 2002; Schaeffer, 2004). The RR-TDM accounted for each TD yields directly. The variation of TD yields for cow could be effected by many factors such as breed, management group within the same herd, day of the year (including weather conditions), day in milk (DIM), age at calving, pregnancy status, lactation number, medical treatment, and its own performance (Ptak and Schaeffer, 1993).

These factors usually change from one TD to the next and it would be difficult to account for 305MY model (Jamrozik and Schaeffer, 1997). In RR-TDM, contemporary groups are defined as sampling milk yield in the same herd on the same date (herd test date of recording, HTD) instead of HYS. Meyer *et al*. (1989) found that HTD effects reduced the overall residual variance of TD yields considerably over model with HYS effects, resulting in slightly greater heritability for TD yields. The estimation of the (co)variance between daily milk yields within a given time scale, including days that were not sampled, thereby enabling a more efficient utilization of TD records. The advantages of a RR-TDM are accounting for lactation pattern of individual animal through random regressions and have ability to account for short environmental effects of each TD, which increase the accuracy of genetic evaluation (Olori *et al*., 1999; Swalve, 2000). In addition, parameters such as initial yield, peak yield and persistency in the model could be explained for lactation pattern in phenotypic and genetic variations of individual cows.

Although several countries have been use a RR-TDM for the national genetic evaluation. However, most of these countries are in temperate region and milk productions come mainly from purebred cow. The assumption used in genetic evaluation would not be appropriate for Thai dairy cattle population, which majorities of cows are crossbred and raised under tropical conditions. In order to improve accuracy of genetic parameters and breeding values estimations and create more information for genetic selection of individual dairy cattle in Thailand, feasibility of using RR-TDM should be tested with a dataset from a Thai multibreed dairy population. If the RR-TDM has ability to make more benefit than the current strategies used in genetic evaluation, it would be proposed for using as a practical procedure of dairy genetic evaluation in Thailand.

OBJECTIVES

The objectives of this study were:

1. To compare four mathematical functions that would be the most suitable described lactation pattern in a Thai multibreed dairy cattle population.

2. To estimate genetic parameters for 305-d milk yield using LM and three measurements of persistency of milk yield from the suitable mathematical function describing lactation curve in a Thai multibreed dairy cattle population.

3. To estimate genetic parameters and to predict breeding value of 305-d milk yield and persistency using RR-TDM

4. To compare predicted breeding values obtained from RR-TDM and LM in a Thai multibreed dairy cattle population.

LITERATURE REVIEW

1. Dairy population in Thailand

In Thailand, dairy farming was promoted in early 1960s, several dairy development projects were tested in Thailand, including government projects by Department of Livestock Development (DLD) as well as some projects sponsored by foreign assistance, such as the Thai–Danish Dairy Farm in Saraburee province (changed their name into the Dairy Promotion Organization of Thailand, DPO) and the Thai–German Dairy Farm in Chiang Mai Province. Similarly, the Thai–German Dairy Farm was handed over to the DLD in 1977. These projects provided to establish a foundation for the new dairy industry. After the government's agricultural policies stated clearly a policy on the promotion of dairy production and extension. For this reason, the number of dairy cattle had increased rapidly because many farmers in various parts of country have decided to raise dairy cow to get into the dairy business (Sukhato and Kengvikkum, 2000).

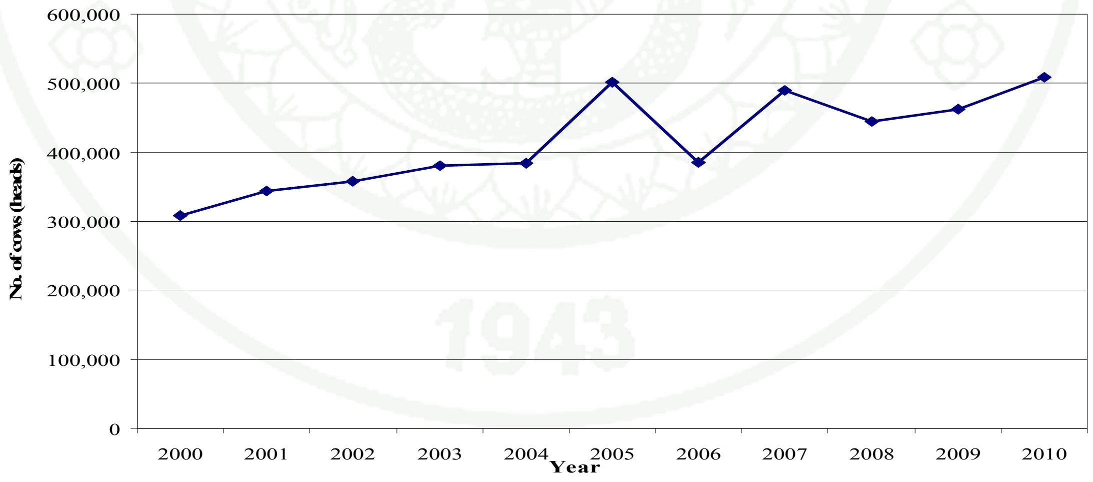

Figure 1 The number of dairy cattle in Thailand since 2000 to 2010

Source: Department of Livestock Department (2010)

The number of dairy cattle has consecutively increased in the past ten years. Recently, there are approximately 20,000 farmers that raised 508,642 heads of dairy cattle distributed in Thailand. The highest dairy raising were found in the Central part (323,489 heads) and the lowest dairy raising were found in the Southern part (4,005 heads) (Department of Livestock Development, 2010). The number of dairy cattle in Thailand from 2000 to 2010 was shown in Figure 1.

The majority of dairy farmers in Thailand (80%) are smallholder farmers with limited resources and education. There is some medium and large scale commercial production. Dairy cows production in Thailand has been based heavily on the feeding of concentrates because few small farmers occupy enough land to grow their own pasture. The lack of high quality forage crop and pasture technology are two other major constraints on raising a demanding ruminant such as dairy cow in a tropical environment like Thailand. The average milk yield is 10-12 kg per day. There is a wide range of milk producing ability from 7 to 8 kg per cow per day to over 20 kg per cow per day depending on the proportion of Holstein Friesian (HF) and farmers abilities. Several reports agree that high levels of HF produce more milk per lactation while 62.5% HF or lower show less reproductive failure (Buaban, 2005).

For breeding structure, crossbreeding has been proposed as a way to upgrade indigenous cattle to a high-producing breed (e.g. Holstein Friesian, Jersey, and Brown Swiss) or as a way to obtain the benefit of hybrid vigor (or heterosis effect) in the tropical countries. Upgrading had been applied in Thai dairy population since the local native cattle were mated with foreign sire in order to improve milk productions. However, upgrading the local to the foreign breeds had not been completed in many of Thai dairy farms. For some reasons, other foreign breeds or crossbreds were introduced to mate with crossbred cows. Results of mating with many types of purebred and crossbred animals created various breed fractions of animals in the population. It was estimated that the majority of cows were 90% of cows contained 75% HF and greater (Table 1). The characteristic of the dairy population like this, purebred and crossbred are equal to be chosen for being the parent of the new generation, is called multibreed dairy population (Koonawootrittriron *et al.*, 2002).

Table 1 Number and percentage of crossbred dairy cattle in Thailand

Fraction of Holstein Friesian	Number of dairy breed stock	
	Heads	**Percentage (%)**
50.00HF	3,685	1.80
62.50HF	13,107	6.41
75.00HF	63,386	30.99
87.50HF	86,139	42.12
93.75HF	32,880	16.08
100.00HF	2,923	1.43
Others	2,395	1.17
Total	204,515	100.00

Source: Buaban (2005)

2. Phenotypic performance for 305-d and TD milk yield in Thai dairy population

Currently, there are the annual sire and dam summary report by the Thai organizations (DLD and DPO). They report the annual summary about phenotypic value of 305MY and predicted breeding value for milk traits in Thai dairy population. In 2009, the DLD reported that the 305MY collected from 25,473 cows was 3,826.33±1,060.63 kg per lactation. That closed to report from Dairy Promotion Organization (2008). These milk production levels were in range of those reported by dairy organizations and other researchers in Thailand was shown in Table 2.

Furthermore, there were some reports in the private farms. Buaban (2000) reported 305MY in the commercial farm located in the western part was 3,767.91 kg. Duangjinda and Tramas (2002) reported that the 305MY in the commercial farm located in the North-Eastern was 3,753.04 kg. Boonkum (2003) reported that 305MY in the university’s farm was 2,752.00 kg per lactation. The difference of population structure, and management strategy in that particular population would be the main reason for the difference in 305MY among those populations (Elzo *et al.*, 2004).

Table 2 Means and standard deviation for 305MY of dairy cattle in Thailand

Source of data[1]	**305-d milk yield**		**Reference**
	No. of records	**Means±SD(kg)**	
DPO	2,059	4,914.95±1,607.98	Kuha *et al.* (2001)
DPO	1,921	3,956.23±1,082.86	Dairy Farming Promotion Organization (2008)
DLD	27,718	3,826.33±1,060.63	Department of Livestock Development (2009)
DPO	1,377	3,781.10±1,040.50	Koonawootrittriron *et al.* (2009)
DLD	10,111	3,759.89±983.63	Buaban and Sanpote (2010)

Note [1]DLD = Department of Livestock Development; DPO = Dairy Farming Promotion

Buaban and Sanpote (2010) reported the average TD yield was 12.39 in Thailand. Nevertheless, its lower than several studies in both tropical and temperate countries based on HF cows (Jamrozik and Schaeffer, 1997) and much lower than the average TD yield (22.90 kg) for the cow population in the Netherlands (de Roos *et al.*, 2004) and the 20.30 kg for Finland (Kettunen *et al.*, 2000). In Korea, Kim *et al.* (2009) reported the average TD yield was 28.25±6.24. In Japan, Togashi *et al.* (2008) reported the TD yield in Japanese HF was 26.20±5.75 kg and similarly, Bignadi *et al.* (2008) reported the average TD yield in HF cows was 27.45±7.61 kg in Brazil. However, the differences from these values may be due to feeding, management system and physiological property of cows in the particular populations.

3. Genetic evaluation of dairy cattle in Thailand

In Thailand, the genetic evaluation of dairy cattle for production traits using Best Linear Unbiased Prediction (BLUP) method was started in 1996 by DPO (DPO, 1996). The BLUP technology has been used for estimated breeding values (EBVs) based on 305-d lactation model (LM) (e.g Katkasame, 1996; Kanloung *et al.*, 1999; Kuha *et al.*, 2001; Dairy Farming Promotion Organization, 2008; Department of Livestock Development, 2009; Koonawootrittriron *et al.*, 2009). It is important to evaluate changing over time for economically important dairy traits. Hence, the main goal of genetic evaluation is the selection of sires and elite cows for improvement the genetic abilities of dairy cattle to the next generations. Recently, the routine genetic evaluation in Thailand has been continuously published by two organizations including DPO and DLD. The annual reports are necessary to predict individual abilities and to improve genetic abilities to the next generation.

Katkasame *et al*. (1996) estimated sire EBVs for dairy cows under the DPO farm operation. The records were collected during the year 1973 to 1993 for the estimation of genetic variance prier to fitting the Animal model. Henderson's method 3 was used to estimate variance component. The results of the analyses shown that the EBVs obtained from animal model were higher than those from use of sire model.

Kanloung *et al*. (1999) estimated breeding values for milk production traits using animal model. Field dataset was collected by the Artificial Insemination Division, DLD using Expectation Maximization Restricted Maximum Likelihood (EM-REML) method. They found that ranking EBVs showed no difference in average EBVs among cows of various blood levels of *Bos tuarus* and there was not difference ranking EBVs between single and multiple traits analysis.

Koonawootrittriron *et al*. (2009) applied a multibreed genetic evaluation strategy to predicted multibreed genetic value for milk production traits in a Thai multibreed dairy population. The genetic trends for 305MY was evaluated using monthly test-day records from first lactation cows collected from 1991 to 2005 in 92 farms located in Central Thailand. Average information restricted maximum likelihood (AI-REML) procedure was used to estimate variance components.

4. Lactation Curve

Lactation curve is a graphical representation of the rate of milk secretion after calving. Generally milk yield is increased until first 60 to 90 days during lactation, gets to peak and then relatively stable for a month. From this time the amount of milk produced daily decreases until the end of lactation. This general trend of the curve formed by amount of milk yield during the lactation was shown in Figure 2.

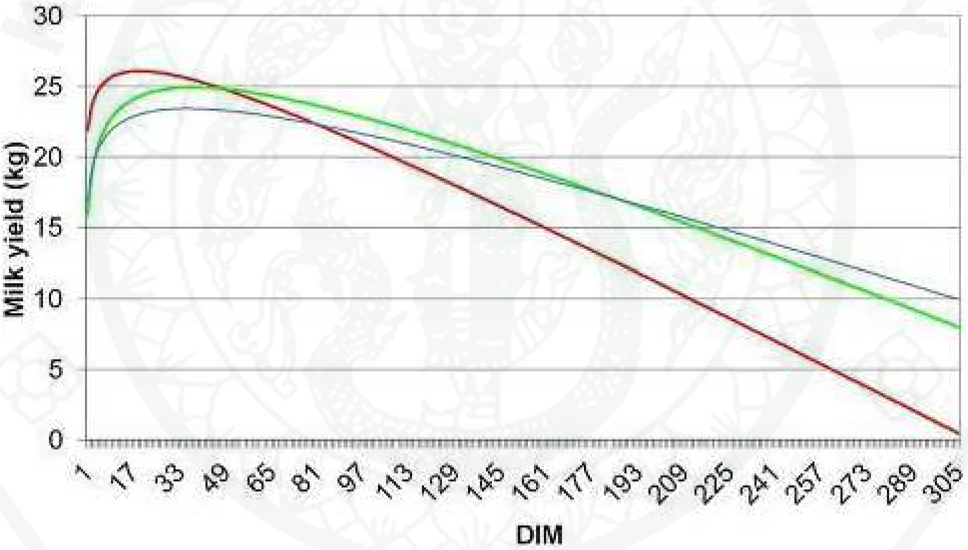

Figure 2 The typical lactation curve of dairy cow

Source: Horan *et al.* (2005)

Most of lactation curve studies always deal with average patterns of homogeneous groups of animals or individual curves. The knowledge of the shape of the lactation curve is valuable for breeding, feeding and economic management of a dairy herd. Lactation curves are especially important when making decisions that are time dependent. Knowing when to expect an animal to reach peak yield, would affect the feeding strategy followed, allowing economic management of feed to the extent that would satisfy the animal's requirement during various stages of lactation, reduce cost, and possibly maintaining peak yield for as long as possible (Tozer and Huffaker, 1999).

Lactation curves also allow for the identification of animals with a relatively constant yield throughout lactation, as well as animals with a high peak yield, but sudden decline thereafter. Information provided by lactation curves could also assist management, where decisions concerning aspects such as culling and milking strategies are concerned. It may for instance not be worthwhile to carry on milking an animal for an extended period of time, if it yields most of its milk early in lactation and then shows a sudden decline with respect to yield thereafter.

5. Factors affected to the shape of lactation curve

The lactation curve in dairy cattle is influenced by genetic ability (i.e breed, breed groups) (Ramirez *et al.*, 1994; Mekvilai, 1998; Olori *et al.*, 1999a; Koonawootrittriron *et al.*, 2001; Hansen *et al.*, 2006), and non-genetic abilities (i.e. herd-year and season of calving, age at calving, parity, days open, DIM, physiological state, nutritional status and environmental conditions) (Wood, 1967; Danell, 1982; Sölkner and Fuchs, 1987; Wilmink, 1987; Olori *et al.*, 1999a; Tekerli *et al.*, 2000; Rekik *et al.*, 2003).

Wood (1977) reported that differences in management of herds, including the intervals between milk extraction sessions, did not seem to really affect the shape of the lactation curve. He also noted that parity and season of calving were the two factors with the greatest influence on the lactation curve and as a result, inclusion of these two factors in a model would lead to more accurate prediction.

Ferris *et al.* (1985) reported that season of calving affected initial yield, peak yield, rise to peak and decline thereafter, and time of peak yield in dairy cows. Tekerli *et al.* (2000) reported that peak yield in dairy cows is higher when parturition taked place in autumn or winter. Season of calving is also expected to have a significant effect on total milk production. For cows, milk yields over the entire lactation seems to be higher when parturition takes place in autumn and decreases progressively when parturition occurs in winter, spring or summer. The reason for this is probably related to both temperature and the quality and availability of digestible feeds.

Tozer and Huffaker (1999) pointed out that almost all research to that point in time had been carried out on lactation records of animals that roam in the northern hemisphere, where environmental conditions and management practices are very different from that which occur in the southern hemisphere. They found that in the case of Australian HF dairy cows, the resulting lactation curve shapes and yield characteristics differ from the results obtained from studies of dairy cows in Europe, North America and the United Kingdom. They studied lactation curve was carried out on data acquired under South African conditions and will therefore make a valuable contribution to the knowledge of lactation curves under southern hemisphere conditions.

Koonawootrittriron *et al*. (2001) studied the seven models fitting the lactation pattern in a multibreed dairy herd. Monthly milk yields of 28,452 records from purebred HF and crossbred HF×Red Sindhi (HF-RS) were collected by the Sakon Nakorn Agricultural Research and Training Center between 1997 and 1999. They reported that purebred HF had a slightly convex curve whereas those crossbred 50HF50RS had a flat curve and 75HF25RS had a convex curve. However, the different three types of lactation curves among breed groups related to the fraction of HF genes in each group. Purebred HF and 75HF25RS contained the higher fractions of HF could produce milk yield more than 50HF50RS.

6. Mathematical function described the lactation curve

During the past few decades lactation curves have been modeled by many authors (Olori *et al*., 1999a; Vargas *et al*., 2000; Macciotta *et al*., 2005; Silvestre *et al*., 2006) intending to improve methods of predicting 305MY. Appropriate function provide useful information for breeding and management decisions at both industry and farm level, and also for the comparison of alternative production strategies in bio-economic modeling. To ensure accurate decisions pertinent to individual animals or herds it is essential that cumulative yield is predicted with minimum error and from relatively few test dates, the latter reducing the cost and inconvenience of milk recording.

The several mathematical functions have been suggested to describe lactation curve in many forms as logarithmic transformations of exponential, polynomial, linear and other nonlinear functions (Silvestre *et al.*, 2006). One of the first to give a reasonable fit of milk production during the whole lactation was the Wood gamma function (WD), as proposed by Wood (1967), which can be expressed as:

$$y_t = at^b\, exp^{-ct} \qquad (1)$$

where y_t is milk yield on days in milk (DIM) *t, a, b* and *c* are parameters describing the curve.

Nevertheless, the limitation of WD is the presence of atypical lactation (value for *b* and *c* are negatives) when nonlinear or log-linear methods are used to calculate individual parameters (Shanks *et al.*, 1981; Ferris *et al.*, 1985) and some parameters of the curve are difficult to interpret from the point of biology. Scott *et al.* (1996) found that WD overestimated milk production prior to peak and after mid-lactation and underestimated mid-lactation milk production. However, Varona *et al.* (1998) reported difference result from the previous studies. They found that WD and a hierarchical Bayesian analysis could reduce atypical curve from 29% to 0.25% in Spanish cows.

Wilmink (1987) developed the Wilmink exponential (WIL) function in the Netherlands. The general form can be express as:

$$y_t = a+bexp^{-kt}+ct \qquad (2)$$

where y_t is milk yield on DIM t, a, b and c are function parameters. Parameter k is related to the time of peak lactation. The factor k always depends on the time of peak yield (Wilmink, 1987). In the study of Olori *et al.* (1999a) estimated k equal 0.61. Moreover, the advantages of lactation parameters from WIL can also be easily related to the characteristics of the lactation curve such as initial, peak and declining rate of milk yield. Thus, the WIL function has been widely used to describe the shape of lactation curve in many countries (Schaeffer *et al.*, 2000; Ptak and Fracz, 2002; Mostert *et al.*, 2003).

Schaeffer and Dekkers (1994) developed the mixed linear with logarithm function (SHE). This function can be expressed as:

$$y_t = a+bln(305/t)+ct \qquad (3)$$

where y_t is milk yield on DIM t, a is initial yield, b and c are associated with the increasing and decreasing slope.

Moreover, the Legendre polynomials (LEG; Spiegel, 1971) have recently become very popular as having many advantages over other models (Kirkpatrick *et al.*, 1994). It is the orthogonal functions, easy to fit, and linear as functions of parameters (Pool *et al.*, 2000). It general form can be expressed as:

$$y_t =aL1+bL2+cL3 \qquad (4)$$

where y_t is milk yield on DIM t, a, b and c are parameters to be estimated, $L1$, $L2$, $L3$ and L are 1, $\sqrt{}3L$, $\sqrt{}5/4(3L^2-1)$ and $(-1)+2(t-1)/(305-1)$, respectively.

Ptak *et al.* (2004) fitted the standard lactation curve by LEG of the second, third and forth order polynomials. The result found that the forth order of LEG were the best-fitted lactation curve models, followed by the second order and the third order polynomials, showing that LEG of even orders were more suitable for fitting lactation curves. It was concluded that 305MY of heifers can be predicted with sufficient accuracy when the lactation curve parameters were derived using records from the first 200 DIM.

Quinn *et al.* (2005) studied the algebraic models to find a well-fitting, robust, single equation model to describe the shape of lactation curves for Irish dairy cows. The analysis was carried out on a total of 14,956 lactation records from commercial and experimental herds and included both autumn and spring calving animals. The goodness of fit and adherence of the various models to the assumptions of regression analysis were examined. The multicollinearity problem posed a severe problem in the application of the best-fit model as ALI function but omitting one of the variables from the estimation procedure reduced this effect.

Mekvilai (1998) studied the mathematical function fitting to lactation curve of first lactation crossbred cows in Thailand. The result showed that WD function most suitable describing the lactation curve in the population. Moreover, this function could explain the increasing and decreasing phase of milk production better than the others.

Koonawootrittriron *et al*. (2001) studied the eight functions included a gamma function, a mixed log second-degree polynomial model, and five polynomial regression models fitting the lactation curve in a multibreed dairy herd. Breed groups were defined as HF, 50HF50RS and 75HF25RS. Predicted 305MY were compared with actual yield within breed group×lactation number×age at calving and breed group×lactation number×season of calving subclasses. The result showed that the second degree polynomial was the best fit for the dataset. However, they commented that no procedure was uniformly better across all subclasses.

7. Persistency of milk yield

Persistency of milk yield is defined as the ability to maintain a constant milk yield in the high level through the lactation (Gengler, 1996) or the ability of a cow to continue producing milk at a high level after reaching the peak of her lactation (Jamrozik *et al.*, 1998). Therefore, persistency gives an indication of the flatness of the lactation curve and for ease of interpretation, should be independent of level of production (Jensen, 2001).

Improvement in persistency through selection allows for the possibility of using cheaper food around peak yield (Sölkner and Fuchs, 1987) and may reduce stress due to a high peak production. There is an advantageous relationship between flat lactation curves and a higher disease resistance. It is also often claimed that cows with a high persistency are less susceptible to nutritional disorders and perhaps as a result of this, more fertile (Dekkers *et al.*, 1998; Muir *et al.*, 2004). This could be the result of low energy needs at the onset of lactation, causing these cows to have lower negative energy balances. Thus, high persistent cows are considered to have more advantages for selection.

Gengler (1996) found that the reduction in feed costs gives persistency a relative economic weight of approximately 3% compared to yield. Dekkers *et al.* (1998) estimated the economic value of persistency in dairy cattle from the expected impact on feed cost and milk returns to be approximately 5% relative to the economic value of production traits. If the possible positive genetic relationship between persistency and disease resistance could be verified, the economic importance of persistency could be even higher (Jensen, 2001). According to Gengler (1996) the effect of a better persistency on health and reproductive costs would increase the relative economic weight of persistency to about 7% of the economic value of 305MY.

Muir *et al*. (2004) reported that genetic evaluation for persistency was available and could be used to increase the average level of persistency in the herd through sire selection in Canada. However, selection for persistency needs to be balanced against selection for 305MY and other economically important traits, which requires the knowledge of relationships between persistency and these other economically important traits (Dekkers *et al.*, 1998).

8. Measurement of persistency of milk yield

Several ways of calculating persistency traits have been published in the literatures. The methods found in the literature may be separated into four groups (Swalve and Gengler, 1999). The first group contains lactation parameters derived from mathematical function used to describe the lactation curve. The second group is measurement based on ratio between total, partial or other yields. The third group is formed by criteria measuring the variation of yield in the course of the lactation. The last group relatively new group has been suggested based on the application of random regression test-day model.

8.1 Measurement based on mathematical function used to describe the lactation curve

Measures of persistency based on mathematical lactation curve function have been described. A mathematical function to describe lactation curves and persistency should; 1) describe and fit all types of curves (even atypical curves), 2) contain parameters that are easy to estimate for every animal with sufficient number of measurements, and 3) must allow a persistency measure that can be computed for all lactations (Gengler *et al.*, 1995).

Some studies used three parameter models as WIL function (Wilmink, 1987). The general form can be expressed as (2). Parameter *c* from WIL function expresses as the slope or linear regression coefficient. Also, it could be considered as the declining rate of milk yield or persistency of milk yield.

Some researchers (Madsen, 1975; Shanks *et al.*, 1981; Ferris *et al.*, 1985; Rekaya *et al.*, 2000) have used parameters from WD functions to define a measure of persistency as following:

$$S = -(b+1)\ln c \tag{5}$$

As a by-product, some mathematical functions can be used to define criteria of persistency. The simplest function for the lactation curve would be a linear regression of TD yield on days in milk. Although obviously not really appropriate as a lactation curve function since the lactation curve for yield traits consist, at least clearly distinguishable for milk, of an ascending phase between calving and peak yield a more or less constant production around peak yield and a descending part after peak yield (Gengler, 1996). The regression coefficient could be viewed as a criterion of persistency.

8.2 Measurement based on ratio between total, partial or other yields

Measures based on ratios between total, partial, or other yields have been discussed since the work of Sanders (1930) cited by Danell (1982). He defined persistency as the ratio between mean and peak yield as follows:

$$\text{TOMAX} = \frac{\text{Average milk yield during 305 days}}{\text{Peak yield}} \tag{6}$$

In this sense, higher value of the criterion is associated with a higher persistency. Johansson and Hansson (1940) cited by Danell (1982) introduced ratios of partial yields in different stage of lactation. Depending on the parts of the lactation reflected in the ratios, either milk yields in the part of lactation are defined as:

$$\text{P2:1} = \frac{\text{Milk yield from days101 to 200 after calving}}{\text{Milk yield in the first 100 days of lactation}} \times 100 \tag{7}$$

$$\text{P3:1} = \frac{\text{Milk yield from days 201 to 305 after calving}}{\text{Milk yield in the first 100 days of lactation}} \times 100 \tag{8}$$

$$\text{P3:T} = \frac{\text{Milk yield from days 201 to 305 after calving}}{\text{Total milk yield during 305 days after calving}} \times 100 \tag{9}$$

For these types of measurement, higher values always indicate higher persistency. Contrary to this definition, Sölkner and Fuchs (1987) modified the new formulas to measure persistency from Sanders (1930). The general equations are express as:

$$\text{TOMAX2} = \frac{\text{Maximum milk yield from days 1 to 200 after calving}}{\text{Mean yield from days 1 to 200 after calving}} \tag{10}$$

$$\text{TOMAX3} = \frac{\text{Maximum milk yield from days 1 to 305 after calving}}{\text{Mean yield from days 1 to 305 after calving}} \tag{11}$$

In these sense, higher values indicate the lower persistency of milk yield (Sölkner and Fuchs, 1987).

8.3 Measurement based on variation of test-day yields

The simplest from the standard deviation of TD during the lactation is used by Sölkner and Fuchs (1987). They attempted to quantify persistency, as it is commonly defined. These measures consider variation of TD yields due to undesirable oscillations of the lactation curve. Sölkner and Fuchs (1987) analyzed two situations; lactations where the last TD occurred prior to 200 days in milk and lactations where the last TD occurred prior to 305 days in milk. In order to apply this measure, the lactation had to be completed. Measures based on statistical dispersion cannot be calculated independently of total or average daily yield and warrant caution when used because a given TD does not necessarily take place at the same stage of lactation and ideal sampling intervals would differ for different lactations (Gengler, 1996). This definition of persistency is independent of lactation length and values of the measure have a distribution that can be considered normal, although value of the measure nears zero with higher persistency (Gengler *et al.*, 1995). The calculated formulas are defined as:

SD2 = Standard deviation of TD milk yield from days 1 to 200 (12)

SD3 = Standard deviation of TD milk yield from days 1 to 305 (13)

TOMAX2 and TOMAX3 were modifications of the measure proposed by Snaders (1930). Measures (11) and (12) were calculated to obtain measurements comparable to P2:1, which should be less influenced abnormalities at the end of lactation (Sölkner and Fuchs, 1987).

8.4 Measurement based on the application of random regression test-day models

Schaeffer and Dekker (1994) proposed the used of random regression test-day model (RR-TDM) for genetic evaluation. The RR-TDM allows curve to be estimated for each lactation of every cow. Therefore, a measure of persistency based on the shape of the lactation curve after peak seems to be a natural way of describing potential to maintain the level of production (Jamrozik *et al.*, 1998).

There are measures of persistency of lactation based on EBVs for TD milk yield in different parts of lactation (interval, point and ratio) as from reviewing lliterature (Jamrozik *et al.*, 1997b; Jakobsen *et al.*, 2002; Cobuci *et al.*, 2007). The newest measure lactation persistency from RR-TDM widely used in several studies (Jamrozik *et al.*, 1997b; Jamrozik *et al.*, 1998; Jakobsen *et al.*, 2002; Cobuci *et al.*, 2006; Cobuci *et al.*, 2007).

In the Canadian RR-TDM, a relatively simple measure of persistency is computed. It is based on the decline in production from DIM 60 and DIM 280 of lactation. The advantage of this measure is that it is simple and easily understood by the end users (Schaeffer *et al.*, 2000).

Jamrozik *et al*. (1998) proposed persistency of production measuring the average slope of the animal's lactation curve between DIM 60 and 280 of lactation from RR-TDM. This called genetic persistency was also measured as a summation of deviation of estimated breeding value on days to attain peak yield from each days after days to attain peak yield to lactation length in dairy cattle. The advantages of this measure are that it is simple and easily understood by the end user (Jensen, 2001).

Jakobsen *et al*, (2002) compared several definitions of persistency and concluded that a measure similar to the one used in Danish HF cows was optimal if all TD in the period from 60 to 280 DIM was used in the prediction of persistency. Her criteria were the accuracy of predicted breeding values for persistency and a low genetic correlation between persistency and total lactation yield.

Cobuci *et al.* (2007) evaluated persistency of milk yield from RR-TDM. The RR-TDM for analyzing test day records including both fixed and random coefficients was applied to the genetic evaluation of first lactation HF cows. Data comprise 87,045 TD records calving between 1997 and 2001 in 10 regions in Brazil. Six persistency of lactation measures were evaluated using EBVs obtained by RR-TDM analyses. The WIL function was used as sub-model described the additive genetic and permanent environmental effects. Residual variance was assumed constant throughout lactation.

They found that ranking for animals did not change among criteria for persistency measurements, but ranking changes were observed when the EBV for persistency of lactation was contrasted with those estimated for 305MY. The rank correlation for persistency and 305MY were practically the same for sire and cows, and ranged from -0.45 to 0.69. The EBVs for milk yield during lactation for sires producing daughters with superior 305MY indicate genetic differences between sires regarding their ability to transmit desirable persistency of lactation traits. This suggested that selection for total lactation milk yield does not identify sires or cows that are genetically superior in regard to persistency of lactation. Genetic evaluation for persistency of milk yield is important for improving the efficiency of the milk production capacity of HF cows.

9. Factors affected to persistency of milk yield

In general, mixed model for the analysis of genetic and environmental influences on persistency are similar to models studying yield traits. Thus, factors that influence the persistency including both genetics and non-genetic effects such as HYS, age at calving, stage of lactation, day in milk at first test-date and days in milk (Wood, 1967; Choovatanapagon, 1975; Danell, 1982; Tekerli *et al.*, 2001; Dědková and Nèmcová, 2003; Fadlemoula *et al.*, 2007).

Breeds and breed groups were also found to have a significant effect on persistency (Choovatanapagon, 1975; Madsen, 1975; VanDoormal, 1999; Kitpipit, 2002). VanDoormaal (1999) reported the persistency of lactation is different across breeds based on genetic ability for milk yield at DIM 280 compared to DIM 60 represents the average persistency for each breed in Canada (Table 3). The average value of persistency of HF was 63% indicating that the genetic ability for milk yield at DIM 280 is 63% of the genetic ability at DIM 60. In contrast, several researches in the tropics (Sharma and Bhatnagar, 1981; Govindaiah *et al.*, 1996; Kitpipit, 2002) showed that crossbred cows were higher persistency than purebred cows.

Seasons of calving affect on the persistency (Choovatanapagon, 1975; Danell, 1982; Moon *et al.,* 1982; Ferris *et al.,* 1985; Sölkner and Fuchs, 1987; Zaman *et al.,* 1994; Gengler *et al.,* 1995; Tekerli *et al.*, 2001; Kitpipit, 2002; Fadlemoula *et al.,* 2007). The different seasons have been found that have a various effects on persistency. These finding should be attributed to differences in regions across the world and the specific management practices. In regions with distinct climatic seasons and especially in pasture-based system a strong seasonal effect is expected, while in regions with less climatic variations and operating in-door systems this effect may be negligible. Kitpipit (2002) showed that the cows which calved in the cold season had, more persistent than hot and rainy season in the tropical climate. The climate stress risk factors should strongly being affected.

Table 3 Average and minimum (Min) and maximum (Max) for lactation persistency by breed

Breed	**Persistency (%)**		
	Average	**Min**	**Max**
Ayrshire	51	41	61
Brown Swiss	62	54	70
Canadienne	50	42	58
Guersey	61	53	69
Holstein	63	53	73
Jersey	62	55	69
Milking Shorthorn	54	46	62

Source: VanDoormaal (1999)

Moreover, the criteria used present an important role. Criteria covering only specific parts of the lactation as opposed to the entire lactation will lead to different results with respect to seasonal differences (Sölkner and Fuchs, 1987).

Age at calving influences to the persistency traits. A slightly trend towards a reduction in persistency with increasing age is observed (Gengler, 1996). This may be attributed to the same relationship between persistency and yield. Within certain limits, it is well known that yields increase with age at calving. Persistency declines with age and age within lactation number. From this, a more developed mammary gland of older cows should also lead to sharper peaks of the lactation curve.

10. Genetic parameter for persistency

10.1 Heritabity (h^2)

Estimation of heritability of persistency was as numerous as type of measures. The heritability was in the wide range from reviewing. Heritabilities of persistency ranged from 0.02 to 0.59 were showed in Table 4. These reviews were restricted only the first lactation and to criteria of persistency that have been used by several authors. The variation may be depended on the measurement method, analyze methods, data structure and varied according to definition of persistency (Gengler, 1996).

Sölkner and Fuchs (1987) estimated the heritability of persistency from different methods ranged from 0.14 and 0.21, with higher estimates for measures pertaining to the whole lactation rather than shorter intervals. Gengler (1996) reported the heritability of persistency of milk yield (ratio of partial lactation yield) found to be 0.01 and 0.30. According to Muir *et al*. (2004) studied the relationships between persistency and reproductive performance in first lactation Canadian HF. They found that the heritability of persistency (parameter *c* form WIL function) was found to be 0.18.

More recent measures using random regression models tend to have higher heritability. Jamrozik *et al*. (1998) showed that heritability of persistency was 0.30 in Canadian HF using RR-TDM. Jamrozik *et al*. (2000) estimated the heritability of persistency to be 0.34 in Canadian Jersey. Jakobsen *et al*. (2002) reported heritabilities of 0.14-0.24 for milk persistency using several different measures in the first lactation in Danish HF (Table 4). These results may be due to overestimate by not accounting for effects of pregnancy in later lactation (Swalve, 1995b).

Table 4 Heritability of persistency of milk yield

Breed of cows	Measure[a]	h^2	Note[b]	Reference
HF	S	0.08	HS,SM	Wood (1967)
Red Dane, RedDane crossbred	Meanmax B	0.09±0.05 0.07±0.05	HS	Choovatanapagon (1975)
Red Danish	B	0.40±0.13	HS,SM	Madsen (1975)
	P2:1	0.59±0.15		
	P3:1	0.47±0.14		
	S	0.35±0.13		
Brown Swiss	P2:1	0.22±0.01	HS,SM	Schneeberger (1981)
	P3:1	0.29±0.01		
	P3:2	0.26±0.01		
Simmental	P2:1	0.14	DD,SM	Sölkner and Fuchs (1987)
	P3:1	0.19		
	SD2	0.17		
	SD3	0.21		
Canadian HF	P1	0.30	RR-TDM	Jamrozik *et al*. (1998)
Canadian Jersey	P1	0.34	RR-TDM	Jamrozik *et al*. (2000)
HF	S	0.17	AM	Rekaya *et al*. (2000)
HF	P3:1	0.14±0.03	AM	Roughsedge *et al*. (2000)
	SD3	0.12±0.03		
Dutch HF	*c*	0.13	AM	Van der Linde *et al*. (2000)
	P1	0.15	RR-TDM	
Polish HF	P1	0.17	RR-TDM	Strabel *et al*. (2001)

Table 4 (Continued)

Breed of cows	Measure[a]	h^2	Note[b]	Reference
Danish HF	P1	0.14	RR-TDM	Jakobsen *et al*. (2002)
	P2	0.24		
	P3	0.20		
HF, HFCrossbred	*c*	0.14	AM	Kitpipit (2002)
	P3:1	0.10		
	P3:T	0.07		
	P1	0.14	RR-TDM	
	P2	0.30		
	P4	0.42		
Canadian HF	*c*	0.18	AM	Muir *et al*. (2004)
HF, HFCrossbred	S	0.11	AM	Seangjun and Koonawootrittriron (2007)

Note [a]Meanmax = ratio between mean and maximum monthly yield, B = linear regression of on DIM

P2:1= ((milk yield from days 100 to 200)/(milk yield first 100 days))x100

P3:1= ((milk yield from days 201 to 305)/(milk yield first 100 days))x100

P3:2= ((milk yield from days 201 to 305)/(milk yield first 100 days))x100

P3:T= ((milk yield from days 201 to 305)/(total milk yield during 305 day))

c = lactation parameter from WIL function

S =-(b +1)ln c

P1= The difference of the lactation curve between DIM 60 and 280 (Canadian expression)

P2= The area under the lactation curve from day 1 to 100 subtracted from the area under the lactation curve from day 101 – 200

P3= The area under the lactation curve from day 1 to 100 subtracted from the area under the lactation curve from day 201 – 300

P4= The area under the lactation curve from day 201 to 305 subtracted from the area under the lactation curve from day 1 – 305

[b]HS=half sib analysis, DD=regression of offspring analysis, SM=sire model, AM=animal model, RR-TDM=random regression test-day model

10.2 Genetic correlations (r_g) between criteria of persistency for milk yield

Genetic correlations between different persistency traits have rarely been reported. Madsen (1975) reported the genetic correlations between B, P2:1, P3:1, TOMAX and S ranged from 0.31 to 0.94. Schneeberger (1981) fitted WD function to describe lactation curve in Swiss Brown in the United State. They found genetic correlations between P2:1, P3:1, P3:2 were around 0.90. Sölkner and Fuchs (1987) also reported the correlations between P2:1 and P3:1 was 0.89. Interestingly, they also found an extremely strong negative correlation (close to -1.0 due to their definitions of persistency) between P2:1 or P3:1 and measuring the standard deviation of TD yields in the course of lactation.

Gengler *et al*. (1995) studied the seven measurement of persistency in the first lactation Belgian HF cows. They found that genetic correlations were positive among all persistency measures ranged from 0.12 to 0.95. They suggested that the correlations are naturally high between measures that use the same formula but for different period.

In Thailand, Choovatanupagon (1975) found that correlation between Meanmax and regression coefficient of declining rate was 0.61. Kitpipit (2002) studied the persistency in crossbred dairy cattle in Thailand. Results showed that the correlation between parameter *c* from WIL function and P3:1 and P3:T were high raged between 0.94 and 0.88, when correlation between P3:1 and P3:T was 0.87. These genetic relationships between measurements method appear to be very strong.

10.3 Genetic correlations (r_g) between persistency and 305-d milk yield

Gengler (1996) stated that a good persistency measure should be independent of the level of production. Rekaya *et al*. (2000) defined persistency as S = c * exp(-(b+1)), they found an antagonistic genetic correlation between persistency and 305 MY. Danell (1982) and Sölkner and Fuchs (1987) also reported antagonistic genetic correlations between total yield and persistency defined as ratio of partial lactation yields, of 0.55 and 0.50 respectively. When persistency was corrected for yield, heritability of persistency and genetic correlations between yield and persistency decreased indicating that yield explained a portion of the genetic variation in persistency. Gengler *et al*. (1995) reported that the variation method used to measure persistency had negative correlation with 305MY and ratio methods had positive correlation. Measures of persistency based on variation of TD yields tended to have a negative correlation with 305MY, such that higher 305MY seemed to be associated with higher variation in TD yields (Swalve and Gengler, 1999).

Genetic correlations of persistency (calculated as a by-product from the RR-TDM) with their respective 305MY were found to be low (Jamrozik *et al*., 1998). Similarly, Jakobsen *et al*. (2002) compared five measures of persistency derived from parameters of lactation curves using RR-TDM in Danish HF. They found that genetic correlations with 305MY and five persistency measures (P1, P2, P3, P4 and P5) were in the wide ranged from 0.00 to 0.47.

Some authors have concluded that persistency is not expected to deteriorate when selecting for higher yields (Danell, 1982; Swalve, 1995b) even though significant genetic correlations existed between the two traits. Ferris *et al.* (1985) reported that selecting for ascent to peak and peak yield did not decrease 305MY, but attempts to decrease peak yield and increase persistency decreased milk yield greatly. Clearly relationships exist between the shape of the lactation curve, and total production. Total 305MY always measures as the area below the lactation curve, and the yield at everyday of the lactation is a function of that curve. A measure of persistency should describe the degree of flatness of the lactation curve irrespective of the overall height of the curve.

For two lactation curves with the same peak yield, a flatter lactation curve after peak yield would indicate a higher total yield for the entire lactation (for the same DIM) than a steeper lactation curve. Cows with really high peak yields will tend to have a steeper slope after peak compared to a lower producer, therefore creating an inevitable relationship between yield and persistency.

Therefore, milk yield is already included in the breeding goal, the value of selection for increased persistency should be derived, for a given 305MY, from its impact on health, reproduction and food efficiency (Dekkers *et al.*, 1998). The correlations between 305MY and different measures of persistency most commonly reported in the literature were shown in Table 5.

Table 5 The genetic correlation between various measurement of persistency and 305-d milk yield

Measure[a]	**Calculation method**	**Details**	**Correlation with 305MY**	**Reference**
S	Fit Wood curve to TD yields	Describes the shape of the descending phase of lactation curve;	0.52	Ferris *et al.* (1985)
		Hard to understood exponential function	0.33	Rekaya *et al.* (2000)
parameter *c* from Wilmink	Fit Wilmink curve to TD yields	Describes the slope of the curve after peak; Phenotypic expression; Easily understood linear function and applicable	0.21	Muir *et al.* (2004)
P2:1 P3:1	Fit curve to TD yields; sum yields for intervals; Calculate ratio	Numerator and denominator can both vary, therefore weak statistical properties; Lactation needs to be complete;	0.50	Sölkner and Fuchs (1987)
		Using production records with standard lengths thus accounts for time	0.48 -0.56	Swalve (1995)
SD2 SD3	Calculate standard deviation of TD yields; Does not require curve to be fitted	Distribution close to normal; Phenotypic expression; Easily calculated; Same scale as milk yield; Phenotypic expression; Covers the entire lactation; Independent of time;	0.36	Sölkner and Fuchs (1987)
		Expression difficult to interpret	0.38	Swalve (1995)

Table 5 (Continued)

Measure[a]	Calculation method	Details	Correlation with 305MY	Reference
P	Random regression model with 3 or 5 parameters; EBV for different intervals summed and then expressed as ratios or deviations	More easily interpreted than other RRM expressions, but still requires genetic evaluation	0.18	Jakobsen *et al.* (2002)
P2			0.47	
P3			0.33	
D280 – D60			0.38	
P	Random regression model using 3 Wilmink parameters as covariables; EBV for 2 days compared by difference, or ratio method	Flexible; EBV available for every day in milk therefore any two days or intervals can be used for comparison;	-0.10	Jamrozik *et al.* (1998)
		Genetic expression hard to interpret; More heritable than ratio measures; Requires genetic evaluation	0.25	Van der Linde *et al.* (2000)

Note [a] S = c * exp(-(b+1)); P2:1 = ((milk yield second 100 days)/(milk yield first 100 days))x100; P3:1 = ((milk yield third 100 days)/(milk yield first 100 days))x100; SD2 = Standard deviation of test day yields (200 days); SD3 = Standard deviation of test day yields (305 days)

D280 – D60 = Additional genetic yield (gained or lost) from DIM 60 to DIM 280 relative to an average animal having the same yield on DIM 60;

P = Average slope of the animal's lactation curve between DIM60 and DIM280 (Canadian expression); P2 = The area under the lactation curve from day 1 to 100 subtracted from the area under the lactation curve from day 101 – 200; P3 = The area under the lactation curve from day 1 to 100 subtracted from the area under the lactation curve from day 201 – 300; P5 = Summation of the contribution for each day in milk for the period of DIM60 to 279 as a deviation from DIM280

11. Test-day models (TDM)

Test-day models (TDM) have been widely studied in recent years as alternative to previous LM for genetic evaluation of milk yield traits. Nowadays, TDM are widely applied both in cosmopolitan (Schaeffer *et al.*, 2000) or in small and less diffused breeds (Lidauer *et al.,* 2003), due to many advantages they involve as compare with LM (Schaeffer *et al.,* 2000). Different types of TDM have been developed, and many functions describing the shape of the lactation curve analyzed (Silvestre *et al.*, 2006).

The using of appropriate method for genetic evaluation of dairy animals is an important aspect of dairy cattle production. Traditional 305-d LM does not account for the changes in environmental factors within 305-d LM and may involve unjustified projection of incomplete lactations. The using of TDM in the recent past has made it possible to economize the genetic evaluation with a better accuracy. Jamrozik and Schaeffer (1997) found that TD yields for HF dairy cows affected by factors such as breed, region, how the herd is managed, day of the year (including weather conditions), lactation number, age at calving, month of calving, days in milk, pregnancy status, medical treatments and number of milking times per day. All of these factors above are necessary to consider the changes of lactation curve.

The analysis of TD records entails the analysis of repeated records on an individual. Test-day models are the statistical procedures that consider all genetic and environmental effects directly on a TD basis (Ptak and Schaeffer, 1993). A summary of effects that can influence a TD record can be found in Swalve (1995). Many of those effects were the same as those that influence lactation yields (Swalve, 2000). However, special attention needed to be given to stage of lactation that often was modeled using some kind of sub-model (Grossman and Koops, 1988; Danell, 1990; Guo and Swalve, 1995). Swalve (2000) divided TDM in the following classes:

11.1 The two - step of TDM

The two-step TDM is model in which the TD records are corrected for TD environmental effects. Typically using a model with fixed effects only and then residual from this model are combined into lactation measures that can be analyzed with traditional model for lactation yields. These models are routinely used in Australia and New Zealand (Jensen, 2001).

11.2 The one-step of TDM with fixed regression model

The one-step TDM has been derived from repeatability animal model under which the TD records within lactation are taken as repeated measurements. The theoretical framework for the fixed regression model and its application for the analysis of longitudinal data such as TD milk production traits were presented by Ptak and Schaeffer in 1993. The model involved the use of individual TD records, thereby avoiding the problem of explicitly extending TD yields into the accumulated 305MY, and accounted for the effects peculiar to all cows on the same TD within herds (herd–test–date; HTD) effects. Therefore corrections for temporary environmental effects on the day of test are more precise compared to evaluations based on 305-day yields. The model also accounted for the general shape of the lactation curve for groups of cows of similar age, calving in the same season and region. In general scalar notation the model is described as:

$$y = HTD + \sum b_i X_i + a + p + e$$

where HTD is the fixed herd test date effects, *a* is the random additive genetic effect, *p* is the random permanent environment effect associated with each cow, and *e* is the random effect. The lactation curve is modeled using the regression parameters b_i, and X_i is the corresponding covariates. The regressions are typically nested within classes of fixed effects such as age and season of calving. Considering the random effects, the model is a simple repeatability model that assumes constant additive genetic and permanent environment variances throughout the lactation. This model assumed standard shapes to lactation curve for all cow in the same age-season of calving subclass, and the estimated additive genetic effects of animals reflected differences in the height of these curves. Therefore, differences in persistency of individual cow were ignored (Schaeffer and Dekkers, 1994).

11.3 The one-step of TDM with random regression model

The random regression test-day model (RR-TDM) has become common for the analysis of longitudinal data or repeated records on individuals over time (Schaeffer, 2004). These repeated records on the same animal can be described by a curve. It has been referred to as longitudinal data. The RR-TDM is extended from fixed regression model, and assumed that the shape of lactation curve is also influenced by random genetic and permanent environment effects. Furthermore, the model can accommodate heterogeneous additive genetic and permanent environment variance during the lactation (Jensen, 2001). In general scalar notation the model can be described as:

$$y = HTD + \sum b_i X_i + \sum a_j X_j + \sum p_k X_k + e$$

where a_j is the additive genetic effect corresponding to regression coefficient j, X_j are the corresponding covariates, and similarly for the permanent environmental effect subscripted by k. The different subscripts indicate that the covariates in different parts of the model are not necessarily the same. The covariates X_i can in principle be any covariate but are usually relatively simple functions of DIM such as polynomial, orthogonal polynomials (e.g. LEG function) or the parameters of the WIL function (Wilmink, 1987) as following:

$$x_1 = 1,\ x_2 = DIM,\ x_3 = \exp(-0.05DIM)$$

Another approach to model TD yields and get evaluations on the shape of the lactation would be to fit an individual lactation curve for each animal within the model of evaluation. Lactation curves could be used to calculate persistency of milk production, total milk yield per lactation, or other measures of milk production.

Lactation curves could be estimated by including regressions on functions of DIM for each animal. These regression coefficients are associated with individual animals and should, therefore, be random variables (Schaeffer and Jamrozik, 1996). The general concept of using random regression model (RRM) in an animal breeding was suggested by Henderson (1982) and have been suggested for use in genetic evaluation by Schaeffer and Dekkers (1994).

Ptak and Schaeffer (1993) used various combinations of linear, quadratic, and logarithm functions of DIM. Jamrozik *et al*. (1997a) found small practical differences when using the Ali and Schaeffer function (ALI; Ali and Schaeffer, 1987) or the WIL function (Wilmink, 1987) in RR-TDM in all respect; however, the function with higher number of parameters, the ALI, had a slight advantage.

Moreover, the ALI function was found strong multicollinearity exist. When multicollinearity exists two problems may occur: the computation of the parameter estimates may be slow and non-convergent, and the parameter estimates may have inflated variances (Belsley *et al.*, 1980). In several cases, authors have attempted to develop function that describes the lactation curves based on biological knowledge of the milk secretion process (e.g. Wood, 1967; Wilmink, 1987). In most cases, however, the functions used in genetic evaluation of dairy cattle have been based on relatively simple polynomial functions that are known to fit the data reasonably well.

Therefore cows must be grouped according to the shape of lactation curve when employing TDM (Ptak and Schaeffer, 1993) for the genetic evaluation of dairy cattle. The lactation curve of cows belonging to the same subclass is modeled by one joint fixed regression and additional random regressions describing the genetically based deviations of individual cows from the average lactation curve of the subclass (Schaeffer and Dekkers, 1998).

This model allows the effect of short-term environmental factor specific to individual yields, such as the effect of gestation stage (Olori *et al.*, 1997), to be accounted directly by including them in the model. Many of those effects are the same as those that influence lactation yields. Recently, several researches have been studied TD yield and random regression model in genetic evaluation instead using LM. Ptak and Schaeffer (1993); Jamrozik *et al.* (1997a) applied this function with RR-TDM to evaluate the genetic ability using TD records in Canada.

12. Genetic parameters form RR-TDM

The methodologies used for estimation of parameters included REML in the form of derivative-free, expectation-mazimization, or average-information algorithms and Bayesian via Gibbs sampling. In REML, the stopping point is well established. Because of computing limitations, the largest estimations of parameters were on fewer than 20,000 animals. However, the second method is simpler and uses less memory but may need many rounds to produce posterior samples (Misztal *et al.*, 2000).

Genetic parameters from RR-TDM were estimated using either REML (Olori *et al.*, 1999b; Lidauer *et al.*, 2000; Jakobsen *et al.*, 2002; Gengler *et al.*, 2004; Druet *et al.*, 2005; Strabel *et al.*, 2005; Melo *et al.*, 2007; Costa *et al.*, 2008; Faro *et al.*, 2008; Santellano-Estrada *et al.*, 2008; Buaban and Sanpote, 2010; Sesana *et al.*, 2010) or Bayesian Gibbs sampling methods based on Markov Chain Monte Carlo (MCMC) method, popularly called Gibb sampling (Jamrozik *et al.*, 1997a; Jamrozik *et al.*, 1997b; Rekaya *et al.*, 2000; Jamrozik *et al.*, 2002; Zavadilová *et al.*, 2005; Muir *et al.*, 2007; Hammami *et al.*, 2008).

Genetic parameters have been estimated for TD milk yields using various methods, sub-models and various data sets show great variability in both average values and shapes. Several authors estimated genetic parameters using RR-TDM, they observed that the heritability of TD milk yields remained low during early or late lactation because of greater residual variation and was higher during mid lactation (Meyer *et al.*, 1989; Swalve, 1995a; Jamrozik *et al.*, 1997a; Strabel and Miztal, 1999; Brotherstone *et al.*, 2000; Druet *et al.*, 2003; Hammami *et al.*, 2008).

Jakobsen *et al*. (2002) estimated (co)variance components for milk, fat and protein yield using RR models by REML in the Danish HF cows. They assumed the fixed part of the model was held constant, whereas four different functions were applied to model the additive genetic effect and the permanent environment effect and homogenous residual variance throughout lactation. They found heritabilities were the lowest in the beginning of the lactation. Moreover, they reported that estimated heritability under the RR-TDM using REML for 305MY (0.42) was higher than heritability 305MY that was estimated with a LM (0.28; Jamrozik *et al*., 1997a). Lidauer and Mäntysaari (1999) obtained estimates 0.30, which was slightly lower than estimates obtained in another researcher. Druet *et al*. (2003) reported that the maximum heritability was close to 0.39 and was maximum found at DIM 200, and Olori *et al*. (1999b) who found heritability higher than 0.50 for some part of lactation curve.

Strabel *et al*. (2005) selected the model for routine genetic evaluation of dairy cattle in Polish Black and White cows, Poland. This population is characterized by small herd size, low level of production, and relatively early peak of lactation. The characteristic in population that consist the number of cows under milk recording but the average herd size was still small. This resulted in a large proportion of cows without or with only a few contemporaries. Observations from such classes have limited value for genetic evaluation, and they reduce the reliability of estimates (de Roos *et al.*, 2004).

Therefore, the HTD effects were treated as random effect in the model. Since small herds usually lead to small HTD classes, and the problem of small contemporary groups remains. In such a case, increasing the size of the contemporary group or treating the herd-time effect as random are among the methods that can improve the quality of genetic evaluation by reducing the variances of residuals and prediction error (Visscher and Goddard, 1993). The model with a random HTD gave the smallest ratio of error to total variance, and was the best in predicting future records. Similarly, Lidauer *et al.* (2003) modeled the herd effect for the Finnish dairy population by fixed herd-year and random HTD components. Mayers *et al.* (2002) found that the combination of random HTD and fixed herd-years gave protection against the negative consequences of HTD groups that were too small (de Roos *et al*, 2004).

Hummani *et al.* (2008) estimated genetic parameter for Tunisian HF using a RR-TDM. The model included HTD, age × season of calving × stage of lactation, production sector ×stage of lactation (classes of 5 DIM) as fixed effects, and random regression coefficients for additive genetic, permanent environmental, and HYS of calving effects, which were defined as modified constant, linear, and quadratic LEG coefficients. They found the heritability of 305MY estimated from RR-TDM was 0.17 and heritabilities of TD milk for selected DIM were higher in the middle than at the beginning or the end of lactation.

Santellano-Estrada *et al*. (2008) estimated genetic parameters using RR-TDM in Tropical Milking Criollo cattle in Mexico and compared five RR-TDM using WIL and LEG in sub model. Estimation of heritability of TD yields ranged from 0.18 to 0.45 for the period spanning from DIM 6 to 400. Genetic correlation between days in milk 10 and 400 was around 0.50 but greater than 0.90 for most pairs of TD.

In Thailand, Buaban (2000) estimated genetic parameters and predicted breeding value using RR-TDM for first lactation. The expected maximization restricted maximum likelihood (EM-REML) and BLUP procedure was used for estimating variance components and predicting breeding value prediction, respectively. The residual variance assumed constant through the lactation. They found that residual variance from a RR-TDM were found to be less than LM.

Genetic correlations between adjacent TD records have been shown to be high and to decrease as interval between TD increases (Swalve, 1995a). The high genetic correlations have been due partially to the shape of the lactation curve, which has been ignored in many analyses. Estimated breeding values have been estimated using TD milk yield and these values were compared to the EBVs obtained from 305MY in many studies.

Swalve (1995a) estimated breeding values for 305-d and TD yields and comparison of both sets of breeding values indicated only minor changes in sire rank, but more drastic re-ranking for individuals. Schaeffer *et al.* (2000) observed a strong positive correlation of yield EBVs with previous 305LM EBVs for HF bulls (0.97) and cows (0.93). Similarly, there was a strong positive rank correlation observed between ranking of sire and cows on the basis of TD yield and 305MY (Kaya *et al.*, 2003; Sawalha *et al.*, 2005).

13. Advantages and disadvantages between random regression test day and 305 lactation model

Applying RR-TDM to TD records allows evaluation of cows for parameters associated with shape of the lactation curve, including persistency, simultaneously with production level. In general, using TD models could have advantages over a LM (Jamrozik *et al.*, 1997b; Schaeffer *et al.*, 2000);

13.1 Early evaluations of sires and cows for production traits could lead to a reduction in generation interval, and more selection response per unit of time in progeny testing and juvenile multiple ovulation and embryo transfer (MOET) nucleus herd programs in comparison to 305LM (Pander *et al.*, 1992).

13.2 Early genetic evaluation through TD models would identify cows and bulls with low EBVs. Discarding the low merit animals earlier than with 305LM evaluations, would result in reduced costs for progeny testing programs in comparison to 305LM.

13.3 Increasing in the number of records by including TD yields less than 90 DIM which are not currently used in 305LM due to the low genetic correlation between yield in first 3 months and 305-d milk yields.

13.4 Increasing in selection intensity by having more eligible animals for evaluation due to using al1 TD records, In comparison to 305LM evaluations, for which some incomplete lactation records are discarded.

13.5 A reduction in bias due to using records of heifers which have been culled before 90 days in milk.

13.6 To facilitate implementation of dairy cattle breeding programs in developing countries, where paucity of suitable methodology and necessary infrastructure for recording milk yield and TD manipulation are major limiting factors. In most developing countries, the milk recording facilities are inadequate to put an appropriate portion of their dairy cattle population into recording systems. Keeping and using all records (i.e. TD records before 90 DIM) in these countries is mare important than developed countries with a substantial amount of collected records for economic traits.

13.7 No need for extension factors or methods to combine TD yields into 305MY. Permits more detailed formulation of systematic effects in the models than LM (i.e. HTD instead of HYS), which could result in reduction in residual variance.

13.8 Permits evaluation of lactation curves and persistency for individual cow.

However, the RR-TDM has some disadvantages that are the EBVs should be converted to a 305-d scale because the direct results on daily yields are not familiar to farmers. More computer capacity is required in comparison to the LM. Changing the lactation curve in an undesirable way if selection is done only based on TD related to a specific part of lactation.

MATERIALS AND METHODS

Analysis I: Comparison of four mathematical functions fitting the individual lactation curve in a Thai multibreed dairy cattle population

The objective of this trial was to compare the four mathematical functions that would be the most suitable fitting the individual lactation curve in a Thai multibreed dairy cattle population.

Data structure

Total of 21,934 monthly TD records form 2,321 first lactating cows was provided by the bureau of Biotechnology in Livestock Production, Department of Livestock Development (DLD). Data were collected during the year 1993 to 2003 on 343 farms in several part of Thailand (i.e. Northern, Northeastern, Central, Eastern, and Western). All farms corporate into the Master Bull Project operated by DLD. Cows were mated with frozen semen using the artificial insemination (AI) technique by AI officers. They visit each farm to gather yield of milk productions once a month. Then, all the records are processed by the central data processing system of DLD.

The milk recording program measures yield of each cows being milked at the 5th after calving until dry off. All cows were milked twice a day, once in the morning (approximately 4.00 a.m.) and once in the afternoon (approximately 2.00 p.m.). Therefore, the amounts of monthly TD yields were summed from morning and afternoon yield in order to represent the sampling of monthly TD yield. In the particular farms, animals received the same nutritional (concentrate and roughage) and management systems. Dry lick mineral blocks and fresh water were fed *ad libitum.* Data included the cow's identification number, the farm code, breed fractions, calving date, birth date, the test date and TD milk yields.

Breed composed in a Thai multibreed population were Holstein Friesian (HF), Red Dane, Red Sindhi, Sahiwal and Native cattle. However, the majority of cows were composed of a large fraction of HF and a small fraction of other breeds. Therefore, two breed groups were defined: HF and other breeds (O), where O included all breeds other than HF.

Contemporary groups were defined as herd-year-season of calving (HYS). Single record contemporary groups were eliminated. The records were then checked for direct sire connectedness across contemporary groups with disconnected contemporary groups eliminated (Bertrand and Lee, 1999). The effects of age at first calving and first test-date of recording were considered as covariate variables in the analysis model. The data structure after editing was summarized in Table 6.

Table 6 The data structure for the analysis

Information	Number
Total TD records	21,934
No. of cows (heads)	2,321
No. of sires (heads)	475
No. of farms (farms)	343
No. of herd-year-season of calving (groups)	885
Average of TD records per cow (records)	9.40
Average TD yield ± SD (kg)	13.09 ± 4.45

Seasons of calving were classified in three groups as summer (March to June), rainy (July to October), and winter (November to February) by Thai meteorological department (2002). Lactation lengths were required to be more than 240 days. Age at first calving (AGE) ranged from 19 to 48 months. The interval from calving to first recording (FTD) was restricted between 5 and 35 days. Because delays intervals always increase atypical curves especially for cows which reach their early peak yield in the lactation and an attempt to describe the peak yield (Rekik and Gara, 2004). If the model for analysis of FTD had no variable to account for DIM, then the estimate of h^2 could be biased. The TD yields unreasonable (the TD yield less than 1 kg. or rather than 40 kg) were eliminated.

From preliminary analysis, monthly TD yields were pre-adjusted for the fixed effects included HYS, breed fractions, age at first calving and first test-date of recording. After that, all TD records were fitted the four mathematical functions for estimating individual lactation parameters. All of these functions were fitted to the whole and individual data.

Fitting mathematical function to the mean and individual lactation cow

In the current study, four mathematical functions were applied to fit and compared the whole and individual lactations included the Wilmink function (WIL) was developed in the Netherlands by Wilmink (1987) and it is the original function used to describe the shape of the lactation curve in the official program of genetic evaluation of Canada (Schaeffer *et al*., 2000). Wood gamma function (WD) was developed by Wood (1967) and it has been used by a numerous studies, most recently by Varona *et al*. (1998). The Schaffer and Dekkers (SHE) mixed linear logarithm function developed by Schaeffer and Dekkers (1994) is based on 3 parameters that has been used in subsequent studies (Schaeffer and Dekkers, 1994; Boonkum, 2003; Buaban and Sanpote, 2010). Recently, several researchers have begun to apply general mathematical tools, including Legendre polynomials (LEG) (Macciotta *et al.*, 2005; Silvestre *et al.*, 2006), to lactation curve modeling. These four functions have the common characteristic of being developed specifically for lactation curves. The descriptions of functions were shown in Table 7.

Table 7 Descriptions of functions considered in the analysis

Reference	Function form[1]		Abbreviation
Wilmink (1987)	$y^{*}_{t} = a+b\exp^{(-0.06t)}+ ct$	(9)	WIL
Wood (1967)	$y^{*}_{t} = at^{b}\exp^{-ct}$	(10)	WD
Schaeffer and Dekkers (1994)	$y^{*}_{t} = a+b\ln(305/t)+ct$	(11)	SHE
Spiegel (1971)	$y^{*}_{t} = aL1+bL2+cL3$	(12)	LEG

Note [1] y^{*}_{t} = predicted monthly TD yield on the day t adjusted with fixed effects;
t = days in milk;
$L1 = 1$; $L2 = \sqrt{3}L$; $L3 = \sqrt{5/4}(3L^{2}-1)$; $L = (-1)+2(t-5)/(305-5)$;
a, b and c= parameters of the functions to be estimate; exp = base of natural logarithm

Equations (9) to (12) were fitted to mean and individual lactation curves by non-linear regression procedure (PROC NLIN) providing least-square estimates of the parameters a, b and c. The estimation parameters of individual cows obtained were used to calculate the predicted individual lactation yield.

Comparison criteria for the lactation curve functions

The analysis of residuals is a common technique in the comparison of functions in which a residual for a given record of monthly TD yield is the difference between the observed and predicted values by the function equations. All the calculation were carried out with SAS (1996) program. The following criteria were used to compare all functions:

1. The coefficient of determination (R^{2}) of non-linear was as following (Neter *et al.*, 1996; Quinn *et al.*, 2005);

$$R^2 = 1 - \frac{SSE}{CSS} \tag{13}$$

where SSE = sum squares error, CSS = the corrected total sum squares

2. Root mean square error (RMSE);

$$RMSE = \sqrt{\frac{SSE}{n - p - 1}} \tag{14}$$

where SSE = sum squares error, n = number of observations, and p = number of parameters in each function.

3. Means of absolute error (MAE);

$$MAE = \frac{1}{n}\sum_{t=1}^{n} \left| y^{*}_{t} - \hat{y}^{*}_{t} \right| \tag{15}$$

where n = number of observation, y^{*}_{t} = actual TD yield and $\hat{y}^{*}_{t}$ = predicted TD yield

4. Mean of mean square error (MMSE);

$$MMSE = \frac{1}{N} \times (MSE) \tag{16}$$

where N = number of animal, MSE = mean square error

5. Mean square prediction error (MSPE), which determines the error in absolute terms (Guo and Swalve, 1995) without recognizing its variation through the lactation as following;

$$\mathrm{MSPE} = \frac{1}{n}\sum_{t=1}^{n}(y^{*}_{t} - \hat{y}^{*}_{t})^{2} \qquad (17)$$

where n = number of observation, y^{*}_{t} = actual TD yield and $\hat{y}^{*}_{t}$ = predicted milk yield of individual cows.

Criteria (13) and (14) were used to consider the average lactation curve, whereas criteria (15), (16) and (18) were used to consider the individual lactation curves. The function providing in higher R^2 and smaller RMSE were considered to be superior. Subsequently, the relative size of the MAE, MMSE and MSPE were used to compare the individual lactation curve.

Means comparison of MAE, MMSE and MSPE among each functions were used PROC GLM (SAS, 1996) to test significance difference among the functions.

Residuals were obtained for each function and plotted against lactation stage to determine the pattern of bias in predicting yields at different stages of lactation using Microsoft Excel 2000 (Dodge and Stinson., 1999).

Analysis II: Estimation of genetic parameters for 305-day milk yield and persistency of milk yield in a Thai multibreed dairy cattle population

The objective of this trial was to estimate the genetic parameters of 305MY and persistency of milk yield in a Thai multibreed dairy cattle population.

Data structure

This trial used the same dataset as described in Trial I. Breeds were therefore considered into two groups as HF and other breeds. Calving seasons were classified into three seasons as summer (March to June), rainy (July to October) and winter (November to February). Age at first calving ranged from 19 to 48 months. First test-date of recording was restricted from 5 to 35 days. In the analysis, both age at first calving and first test-date effects were considered as covariate effects in the model. Pedigree information included sire, dam, and birth date. Unknown parents were eliminated. Also, the pedigree file included 4,023 animals. The contemporary group was defined as HYS of calving. The structure of data was summarized in Table 6.

In the analyses, the dataset was prepared in three steps: 1) to calculate accumulated 305MY predicted from test-interval method (TIM) and mathematical function selected from trial I and 2) calculated individual persistency of milk yield and 3) checking connectedness by considering representation sires across contemporary groups. The largest contemporary group was used for estimating (co)variance components and genetic parameters.

Prediction of individual accumulation 305-day milk yield

Two methods were used to predict individual 305MY in this trial. The first method was test-interval method (TIM; Sargent *et al.*, 1968). This method is currently used to calculate individual 305MY by the dairy organization of Thailand (DLD, 2009). The 305MY calculated from TIM was defined as TIM_305MY.

The second method was calculated from lactation function selected from trial I. From the Trial I, the WIL function (Wilmink, 1987) was considered to be the most suitable function to describe and fit the individual lactation curve in this population. Then, the WIL function was used for interpolation and was therefore modeled on the TD records in order to calculated individual 305MY and persistency traits for every cows in the dataset. Total milk yield per lactation estimated form equation (10) was defined as WIL_305MY. The general formula was as following:

$$y^{*}_{t} = a + b\exp^{(-0.06t)} + ct$$

where y^{*}_{t} is monthly TD yield on day t of lactation, a is a regression coefficient related to the maximum daily level of production, b is a regression coefficient related to the production increase towards peak and c is a regression coefficient related to decrease yield after peak. In this study, the estimated parameters k = 0.06 (Table 9). It was obtained form mean lactation curve and used to fix the peak lactation day for all animal and those obtained from individual lactation curves were used to calculate the predicted yields.

Estimation of lactation parameters (a, b and c) for individual cow were obtained by a non-linear regression procedure (PROC NLIN) using Marquardt iteration in SAS program (SAS, 1996). Afterward, all parameters a, b and c were used to predict daily milk yield of individual cows from WIL function. Then, WIL_305MY was calculated by summing milk yield from DIM1 to DIM305.

Calculation of individual persistency of milk yield

Persistency of milk yield is always expressed in the term that is easily the expression can be interpreted. The WIL function was fitted to TD yield of each cow to explain the continuous curve. Therefore, daily milk yields were predicted using this function from each day starting from calving to drying off. Individual 305MY and partial yields were calculated based on accumulated daily yields during DIM1 to DIM305.

Three measurements of persistency were used in the present study. The first measurement (PER1) was based on absolute parameter c from WIL function. This parameter usually considered as the linear regression coefficient, decline rate of milk yield per unit or the slope of the lactation curve. It is estimated in negative for all cows. However, to easy and convenience for understanding it was assigned to be the absolute value for all cows (Madsen, 1975). Many reports also revealed PER1 parameter using this method (Muir *et al.*, 2004; Van der Linde *et al.*, 2000). The PER1 was calculated as following:

$$\text{PER1 (kg/day)} = \text{absolute value of parameter c from WIL function} \qquad (18)$$

The second measurement (PER2) was calculated as the difference between daily milk yield at DIM60 and DIM280 of the lactation. These two reference points during lactation were chosen to represent a DIM following peak yield and another towards the last TD available within 305-d lactation length. The advantage of this measurement is easy to compute (Jensen, 2001). This new method has been widely used in several researches (Cobuci *et al.*, 2007; Jakobsen *et al.*, 2002; Jamrozik *et al.*, 1997). The PER2 was calculated as following:

$$\text{PER2 (kg)} = \text{milk yield at (DIM60–DIM280)} \qquad (19)$$

The third measurement (PER3) was measured the ratio of milk yield in several part of lactation. Therefore, the PER3 was calculated as the ratio of daily yield during DIM201 to DIM305 and accumulative 305MY (Dekkers *et al.*, 1998; Sölkner and Fuchs, 1987). The PER3 was calculated as following:

$$\text{PER3 (\%)} = \frac{\sum_{t=201}^{305} \hat{y}_t^*}{\sum_{t=1}^{305} \hat{y}_t^*} \times 100 \qquad (20)$$

From the definition of persistency of milk yield measurements, the lower values of PER1 and PER2 and higher values of PER3 indicated the good persistency of milk yield.

Statistical analysis

Descriptive statistics of 305MY and persistency of milk yield were obtained by using MEANS procedure in the SAS program (SAS, 1996). In this study, fixed and covariate effects were examined for their significance influence (P<0.05) in single trait analysis using GLM procedure in SAS (SAS, 1996) as shown in Table 8.

Table 8 The fixed effects included in the statistical models

Traits[1]	**Fixed effects**[2]			
	CG	**BF**	**AGE**	**FTD**
TIM_305MY	**	*	**	ns
WIL_305MY	**	*	**	ns
PER1	**	**	*	*
PER2	**	**	*	**
PER3	**	**	*	*

Note ** P < 0.01, * P < 0.05, ns = not significant

[1] TIM_305MY=305-d milk yield calculated from test-interval method (TIM), WIL_305MY=305-d milk yield calculated by the WIL function, PER1=the absolute value of parameter c from WIL function, PER2=the different of milk yield between DIM60 and DIM280, PER3=the ratio of accumulated yield from days 201 to days 305 and 305-d milk yield

[2] CG=herd-year-season of calving, BF=breed fraction of HF, AGE=age at first calving, FTD=first test-date of recording

Estimation of (co)variance components

The (co)variance components were estimated by the restricted maximum likelihood (REML) method using the expected maximization algorithm (EM) of the BLUPF90 *DairyPack*2 program (Duangjinda *et al.*, 2004). The prior values for estimation of co(variance) in multiple-traits analysis values obtained from single-trait analysis in the same dataset. The convergence criterion for the iterative estimation procedure was set at 10^{-10} for stopping the iteration process.

The five-trait animal models were employed to estimate genetic parameters. These models included two production traits (TIM_305MY and WIL_305MY) and three persistency measurements (PER1, PER2 and PER3) were used in the analysis. The fixed effects were CGs, age at first calving, and first test-date of recording. The regression additive genetic effects were considered as HF and other breed fraction. The random genetic effects were additive genetic effects and residuals. The matrix notation can be written as following:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{\mathbf{ga}}\mathbf{g}_{\mathbf{a}} + \mathbf{Z}_{\mathbf{a}}\mathbf{a}_{\mathbf{a}} + \mathbf{e}$$

where

$\mathbf{y}$ = the vector of the observations of the five traits (TIM_305MY, WIL_305MY, PER1, PER2 and PER3),

$\mathbf{b}$ = the vector of fixed effects,

$\mathbf{g}_{\mathbf{a}}$ = the vector of regression additive genetic deviations,

$\mathbf{a}_{\mathbf{a}}$ = the vector of additive genetic effects,

$\mathbf{X}$ = the incidence matrix that related records to elements of vector **b**,

$\mathbf{Z}_{\mathbf{ga}}$ = the incidence matrix related cow records to element of vector $\mathbf{g}_{\mathbf{a}}$,

$\mathbf{Z}_{\mathbf{a}}$ = the incidence matrix related to element of vector $\mathbf{a}_{\mathbf{a}}$,

$\mathbf{e}$ = the vector of residuals.

The assumptions of the model were:

$$\begin{bmatrix} y \\ a_a \\ e \end{bmatrix} \sim MVN\left(\begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} Z_a G_a Z_a' + R & Z_a G_a & R \\ G_a Z_a & G_a & 0 \\ R & 0 & R \otimes I \end{bmatrix} \right)$$

Where

G_a = $G_o \otimes A$ where G_o is the additive genetic (co)variance matrix of five traits; A is the numerator relationship matrix; ⊗ is the Kronecker product,

I = Identity matrix,

R = the residual (co)variance matrix.

Estimation of additive genetic, and phenotypic variance were used to calculate heritability (h_i^2) for each trait. Heritability was calculated as following:

$$h_i^2 = \frac{\sigma_{ai}^2}{\sigma_{pi}^2} \tag{21}$$

Estimation of variance and (co)variance components were used to calculate genetic and phenotypic correlation among five traits as following:

$$r_{a_{ij}} = \frac{\text{cov}_{a_{ij}}}{\sqrt{\sigma_{a_i}^2 \sigma_{a_j}^2}} \tag{22}$$

$$r_{p_{ij}} = \frac{\text{cov}_{p_{ij}}}{\sqrt{\sigma_{p_i}^2 \sigma_{p_j}^2}} \tag{23}$$

The terms in equation (21), (22) and (23) are:

h_i^2 = heritability of trait i

$r_{a_{ij}}$ = genetic correlation between trait i and trait j

$r_{p_{ij}}$ = phenotypic correlation between trait i and trait j

$cov_{a_{ij}}$ = genetic (co)variance between trait i and trait j

$cov_{p_{ij}}$ = phenotypic (co)variance between trait i and trait j

$\sigma_{a_i}^2, \sigma_{a_j}^2$ = additive genetic variance of trait i and trait j

$\sigma_{p_i}^2, \sigma_{p_j}^2$ = phenotypic variance of trait i and trait j

Analysis III: Genetic evaluation of milk yield using lactation model and random regression test-day model in a Thai multibreed dairy cattle population

The objectives of this trial were to estimate genetic parameters and to predict breeding value of 305MY and persistency traits using lactation model and random regression test-day model

Data structure

This study used the same dataset as described in analysis I and II. In briefly, total 21,934 TD records from 2,321 first lactation cows calved during the years 1993 to 2003 were analyzed. Data was obtained from the bureau of Biotechnology in Livestock Production, DLD.

Breed fractions were classified into two groups as HF and other breeds (O). Calving seasons were classified into three seasons as summer (March to June), rainy (July to October) and winter (November to February). Age at first calving and first test-date of recording were considered as covariate effect in the model. In random regression test day model (RR-TDM), the contemporary groups were defined as herd-test-date of recording (HTD) in 10,878 classes. Pedigree information included sire, dam, and birth date. Unknown parents were deleted. Two dataset were used in the study included 2,321 records of 305MY and 21,934 monthly TD records. The animals in TD data file were in common with animal in 305MY data set for comparing results between RR-TDM and lactation model (LM). The structure of data is summarized in Table 6.

Lactation model (LM)

A single trait LM was set up for estimating genetic parameters and breeding values. The statistical model for 305MY composed both fixed and random effects. The fixed effects were included contemporary group (herd-year-season of calving), age at first calving defined as covariate and breed fractions was defined as regression additive genetic effect in the model. The random effects were direct additive genetic and residual effects.

In matrix notation could be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{\mathbf{ga}}\mathbf{g}_{\mathbf{a}} + \mathbf{Z}_{\mathbf{a}}\mathbf{a}_{\mathbf{a}} + \mathbf{e} \tag{24}$$

where

$\mathbf{y}$ = the vector of individual 305MY observations,

$\mathbf{b}$ = the vector of fixed effects,

$\mathbf{g}_{\mathbf{a}}$ = the vector of fixed regression additive genetic deviations,

$\mathbf{a}_{\mathbf{a}}$ = the vector of animal additive genetic effects,

$\mathbf{X}$ = the incidence matrix related cow records to elements of $\mathbf{b}$,

$\mathbf{Z}_{\mathbf{ga}}$ = the matrix of breed fraction of HF that related cow records to element of $\mathbf{g}_{\mathbf{a}}$,

$\mathbf{Z}_{\mathbf{a}}$ = the incidence matrix related cow records to elements of $\mathbf{a}_{\mathbf{a}}$,

$\mathbf{e}$ = the vector of residuals.

The expectations of the random variables are:

$$E(y) \quad = \quad Xb + Z_{ga}g_{a}$$

The (co) variance matrices of random effect factors in **a** and **e** were assumed to be:

$$V\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_{a}^{2} & 0 \\ 0 & I\sigma_{e}^{2} \end{bmatrix}$$

Where

A = the additive genetic relationship matrix between animals,

I = the identity matrix,

σ_{a}^{2}, σ_{e}^{2} = the additive genetic and residual variance, respectively.

The (co) variance components were estimated with the expected maximization restricted maximum likelihood (EM-REML) method using the BLUPF90-*DairyPack*2 program (Duangjinda *et al.*, 2004). The prior values for estimation of (co)variance in this study were obtained from Trial II. The convergence criterion for the iterative estimation procedure was set at 10^{-8} for stopping the iteration process. Estimation of (co) variance components were calculated for heritability (h_{i}^{2}) as followed equation (21).

Random regression test-day model (RR-TDM)

Using TD measurements for estimating variance components and genetic evaluation was one of this study's objectives. In this study TD records were modeled with HTD subclasses rather than HYS. Because of the small herd sizes, the small herd usually led to small HTD classes, and the problem of contemporary group remains. In such a case, treating the HTD effect as random is the methods that can improve the quality of genetic evaluation by reducing the variance of residuals and predicted error

(Visscher and Goddard, 1993). Lidauer *et al.* (2003) modeled the herd effect for the Finnish dairy population by fixed herd-year and random HTD components. Similarly, Strabel *et al*. (2005) compared RR-TDM for Polish Black and White cattle in Poland. They treated HTD as random effects in RR-TDM.

The single trait, random regression animal model was used for estimating genetic parameters and for genetic evaluation. In this study combination of year-seasons of calving were used as classes for fixed regression coefficients. Note that that the mathematical function for modeling both fixed and random was WIL function. The sub model of WIL function contained with three for fixed (associated with a common lactation curve to animals within a subclass) and random regression coefficients (associated with each individual's genetic lactation curve) was chosen to be applied to TD measurements for milk yield.

In matrix notation the model can be written as:

$$\mathbf{y} = \mathbf{Hc} + \mathbf{Xb} + \mathbf{Z}_{\mathbf{ga}}\mathbf{g}_{\mathbf{a}} + \mathbf{Z}_{\mathbf{a}}\mathbf{a}_{\mathbf{a}} + \mathbf{Wp} + \mathbf{e} \tag{25}$$

Where

$\mathbf{y}$ = the vector of observations,

$\mathbf{c}$ = the vector of random HTD effect,

$\mathbf{b}$ = the vector of fixed regression coefficients,

$\mathbf{g}_{\mathbf{a}}$ = the vector of fixed regression additive genetic deviations,

$\mathbf{a}_{\mathbf{a}}$ = the vector of random regression coefficients for animal genetic effects,

$\mathbf{p}$ = the vector of animal permanent environment effects,

$\mathbf{H}$ = the incidence matrix related to the herd test-date effects,

$\mathbf{Z}_{\mathbf{ga}}$ = the matrix of breed fraction of HF that related cow records to element of $\mathbf{g}_{\mathbf{a}}$,

$\mathbf{X}$, $\mathbf{Z}_{\mathbf{a}}$ and $\mathbf{W}$ = the incidence and (co)variance matrices related to DIM,

$\mathbf{e}$ = the vector of residual effects for TD records.

The assumption of these components are:

$$E(y) \quad = \quad Xb + Z_{ga} g_a$$

The (co)variance structure for models with random HTD effect was defined as following:

$$V\begin{bmatrix} c \\ a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} I\sigma_c^2 & 0 & 0 & 0 \\ 0 & G \otimes A & 0 & 0 \\ 0 & 0 & P \otimes I & 0 \\ 0 & 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

where

G = the genetic co(variance) matrix among the random regression coefficients,

P = the permanent environment co(variance) matrix among the random regression coefficients,

A = the matrix of additive genetic relationship among animals,

$\otimes$ = Kronecker product function,

σ_c^2 = the HTD effects variance

σ_e^2 = the residual variance

I = the identity matrix.

After estimating the random regression coefficients (co)variance matrix ($\hat{G}$), the genetic variance for DIM t ($\hat{\sigma}_{a(t)}^2$) was calculated as:

$$\hat{\sigma}_{a(t)}^2 = Z_t' \hat{G} Z_t \qquad (26)$$

The genetic (co)variance between yields on day t and s ($\hat{\sigma}^2_{a(t,s)}$) was estimated as:

$$\hat{\sigma}^2_{a(t,s)} = Z'_t \hat{G} Z_s \tag{27}$$

where

$\hat{G}$ = the (co)variance matrix for the random regression coefficients,

Z_t, Z_s = the vectors of covariates derived from WIL function at DIM t and s

For RR-TDM, heritabilities for DIM t, (h^2_t) through the lactation were calculated as Jakobsen *et al.* (2002).

$$h^2_t = \frac{\sigma^2_{a(t)}}{\sigma^2_{a(t)} + \sigma^2_{pe(t)} + \sigma^2_{HTD} + \sigma^2_e} \tag{28}$$

where $\sigma^2_{a(t)}$ and $\sigma^2_{pe(t)}$ are additive genetic and permanent environmental variances for DIM t.

Heritability for 305MY ($h^2_{305\,MY}$) was computed as the ratio of the genetic variances to the sum of the genetic, permanent environmental, HTD, and residual variances. This formula was modified from Jakobsen *et al.* (2003) as following:

$$h^2_{305MY} = \frac{\sigma^2_{a(305MY)}}{\sigma^2_{a(305MY)} + \sigma^2_{pe(305MY)} + 305\sigma^2_{HTD} + 305\sigma^2_e} \tag{29}$$

where $\sigma^2_{a(305MY)}$ and $\sigma^2_{pe(305MY)}$ were additive genetic and permanent environmental variances for 305MY. Residual term on different days are usually assumed to be independent, i.e. cov (DIM_i, DIM_j) = 0. Therefore, total variance of accumulated 305MY from RR-TDM was $305\sigma^2_e$ (adapted from Khorshidie *et al*, 2012).

The solutions for the additive genetic random regression coefficients of animal k were represented as following:

$$\hat{a}'_k = (\hat{a}_{1k}, \quad \hat{a}_{2k}, \quad \hat{a}_{3k}) \tag{30}$$

Also, the estimated breeding values (EBVs) at DIM t of animal k obtained as follows:

$$EBV_{tk} = \hat{a}_{1k} + \hat{a}_{2k}\exp^{-0.06\,t}\,t + \hat{a}_{53k}t \tag{31}$$

The breeding value for total 305MY (EBV_{305MY}) of animal k was obtained by summing the EBVs form DIM1 to DIM305 as following:

$$\begin{aligned} EBV_{305MY} &= \sum_{t=1}^{305} EBV_t \\ &= \sum_{t=1}^{305}\left[\hat{a}_{1k} + \hat{a}_{2k}\exp^{-0.06\,t} + \hat{a}_{3k}t\right] \\ &= \left[\sum_{t=1}^{305} 1\right]\hat{a}_{1k} + \left[\sum_{t=1}^{305}\exp^{(-0.06t)}\right]\hat{a}_{2k} + \left[\sum_{t=1}^{305} t\right]\hat{a}_{3k} \\ &= \left[305 \quad 16.17 \quad 46{,}665\right]\hat{a}_k \end{aligned} \tag{32}$$

Breeding values were predicted with BLUP method, using BLUPF90-DairyPack2 package (Duangjinda *et al*., 2004). The additive genetic value (EBVs) of animal ij as follow:

$$\hat{u}_{a_{ij}} = p_{ij} \overset{o}{g}_{a_i} + \hat{a}_{a_{ij}} \tag{33}$$

Where

$\hat{u}_{a_{ij}}$ = predicted additive genetic value (EBVs) of animal ij,

p_{ij} = the HF fraction for animal ij,

$\overset{o}{g}_{a_i}$ = the regression coefficient of additive genetic group effect,

$\hat{a}_{a_{ij}}$ = predicted the random additive genetic effect of animal ij.

Comparison of predicted breeding values from LM and RR-TDM

The impact of the different model on ranking of animals based on EBVs for LM and RR-TDM were used to get ranking of sires and cows. Bulls were grouped into sires, having daughters in at least 10 herds, and Unproven Sires, having daughters in less than 10 herds. Only measured cows were compared. The ranking of sires and cows from both LM and RR-TDM was compared using Pearson and Spearman rank correlation by PROC CORR procedure (SAS, 1996).

Calculation persistency from RR-TDM

The solutions for the additive genetic random regression coefficients equation (33) of animal *j* were used to calculate daily EBVs and then used to calculate the genetic persistency (P). The RR-TDM allows the estimation of individual lactation curve, also it could be calculated as a by product of RR-TDM (Jamrozik *et al.*, 1997b). Three different measures of genetic persistency (P) based on EBVs for TD yield in different periods were evaluated as following:

P1: The calculation of P1 was based on the individual random genetic regression coefficient from WIL function of that obtained from equation (30).

$$\text{P1} = \text{the genetic random regression coefficient } (\hat{a}_{3k}) \tag{34}$$

P2: The difference between daily EBVs between DIM 60 and 280

$$\text{P2} = (\text{EBV}_{60} - \text{EBV}_{280}) \tag{35}$$

P3: The area under individual lactation curve from DIM 201 to 305 divide by the area under individual lactation curve from DIM 201 to 305.

$$\text{P3} = \left(\frac{\sum_{t=201}^{305} \text{EBV}_t}{\sum_{t=1}^{305} \text{EBV}_t} \times 100 \right) \tag{36}$$

According to these expressions lower values of P1 and P2 and higher value of P3 indicated greater genetic persistency.

The solutions for random regression coefficients for each animal were obtained by the restricted maximum likelihood method using the expectation maximization algorithm (EM-REML) of the BLUPF90-DairyPack program (Duangjinda *et al.*, 2004). The convergence criterion was 10^{-8}.

RESULTS AND DISCUSSION

Analysis I: Comparison of four mathematical functions to describe the lactation pattern in Thai multibreed dairy cattle population

Estimation of the average lactation

The root mean square error (RMSE) values and the coefficient of determination (R^2) were used to consider the best suitable function of the whole data. The results showed the quite small differences in RMSE. The WIL and WD function gave the best fit with a RMSE value of 2.57, while LEG gave the poorest fit (RMSE value of 2.59). The ranking of the functions with different criteria were presented in Table 9.

Based on the R^2 values, the fit of the functions was rather poor, with about 40% of the curves. The WIL and WD function gave the R^2 values higher than both the LEG and SHE. Results implied that a great difficult in modeling individual deviations around the mean curve for milk yield in this population.

However, R^2 values obtained in the current study were in the range of estimation in the literature. Guo and Swalve (1997) reported the R^2 values obtained from three different farms were 0.55 by the WD, 0.57 by the WIL function, 0.57 by the Guo and Swalve function, and 0.56 by the Ali and Schaeffer (ALI) function. Mekvilai (1998) found the R^2 was 0.22 fitted from WD functions of dairy cows raised the Government Dairy Promotion Project in Thailand. Olori *et al*. (1999) reported R^2 were 0.66 by the WD function, 0.65 by the Nelder-Yadav function, 0.67 by the Guo and Swalve function and 0.69 by the WIL function. Quinn *et al*. (2004) also reported that the ALI function gave better fit than the WD, WIL, and Guo and Swalve function. Similarly reported by Koçak and Ekiz (2008) reported that the highest R^2 was found for ALI function.

The ranking base on R^2 was the same as for RMSE. Also for these two criteria, some differences between curves were marginal. With criteria based on goodness-of-fit, it is not trivial to conclude which of these curves is the best and different rankings might be obtained across samples or studies. Moreover, a compromise often based on subjective grounds, must be accepted between goodness-of-fit and other properties such as flexibility, robustness and computational considerations. These explain the large variation in models across studies and countries (Druet *et al*, 2003).

However, the accuracy of predicting average curve was not repeated for most individual lactations, for which there was wide variability in the fit (Olori *et al.*, 1999). The variation in fit was almost totally between cows rather than between functions. This suggested that the suitability of fitting function does not depend on the mathematical function form alone but rather more on the biology nature of the lactation itself, which varies randomly between cows.

Table 9 Estimation of average lactation curve parameters, root mean square error (RMSE), and coefficient of determination (R^2) of four mathematical functions from 21,934 monthly TD records of 2,321 cows.

Function	**Estimated equation**[1]	**RMSE**	**R^2**
WIL	$\hat{y}^*_t = 17.366 - 2.901\exp^{-0.06t} - 0.027t$	2.57	0.41
WD	$\hat{y}^*_t = 13.033t^{0.083}\exp^{-0.003t}$	2.57	0.41
SHE	$\hat{y}^*_t = 18.569 - 0.769\ln(305/t) - 0.032t$	2.58	0.40
LEG	$\hat{y}^*_t = 12.926 - 2.155L2 - 0.113L3$	2.59	0.40

Note [1] t = days in milk

$L2 = \sqrt{3}L$; $L3 = \sqrt{5/4}(3L^2-1)$; $L = (-1)+2(t-5)/(305-5)$

WD=Wood function, WIL=Wilmink exponential function, SHE=Schaeffer and Dekkers function and LEG=Legendre polynomial function

The estimation lactation curve parameters for the different function of the average yield were presented in Table 9. Estimation of parameters were different markedly to those found in research in temperate countries such as Macciotta *et al.* (2005) and Quinn *et al.* (2005). Hence, it could not directly compare the results generated in this study with other studies due to the different of time intervals of record, breeds of cows, feeding, and managements of those studies (Rowlands *et al.*, 1982; Tozer and Huffaker, 1999).

The average patterns of predicted yield over the lactation were shown in Figure 3. Although the mathematical functions forms were different, but they could fit the average monthly yields quite well. All functions could represent curves with increasing and decreasing phrase in the same trends. Both WIL and WD could predict the actual lactation fairly well in early lactation. In addition, any record in the mathematical function will influence the whole curve. However, the WD overestimated milk yield after peak until end of lactation. In contrast, the LEG and SHE cannot fit well in the initial phase of lactation curve. Also problem in using LEG usually yield very large estimates of variances at the beginning and at the end of lactation that tend to increase with the order of the polynomials (Lopez-Romero and Carabano, 2003). These results were similarly to research in Italian Simmental cows reported by Macciotta *et al.* (2005). Overall, the WIL performed better statistically and biologically, as they more closely resembles the underlying process for this data set.

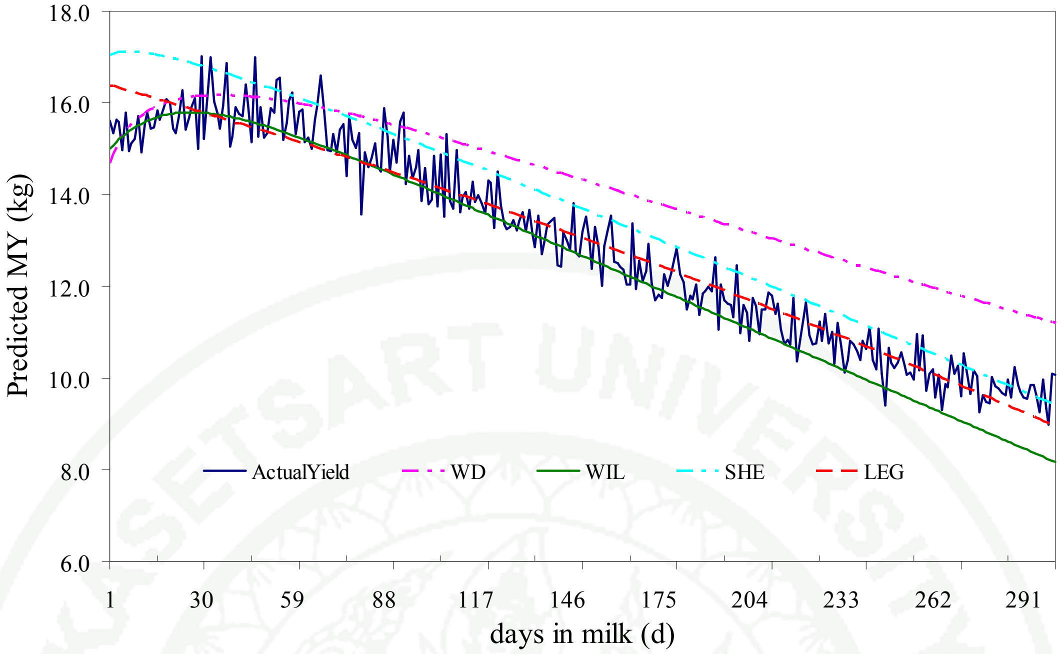

Figure 3 The average actual and predicted lactation curve form Wilmink (WIL), Wood (WD), Schaeffer and Dekkers (SHE) and Legendre (LEG) functions.

Prediction of the individual lactation

The comparison between the predictive ability of the different models is summarized in Table 10. The statistical criteria as MAE, MMSE and MSPE were tested functions of individual cows. The small values of all statistical criteria were considered the best fit of function.

The MAE values were significantly different among four functions (P<0.05). The WIL function provided the smallest value of MAE (0.86), while the LEG provided the largest value (0.93).

The MMSE and MSPE values were not significantly different among functions (WIL, WD and SHE, P<0.05), excepted the LEG function. The WIL gave the smallest values both MMSE (2.26) and MSPE (1.54) while, the LEG gave the largest values both MMSE (2.58) and MSPE (1.75) values.

Table 10 Means comparison of the goodness of fit (MAE, MMSE, MSPE) of the functions fitted to 2,321 individual curves.

Functions[1]	**Goodness of fit**[2]		
	MAE	**MMSE**	**MSPE**
WIL	0.86^{a}	2.26^{a}	1.54^{a}
WD	0.87^{ab}	2.37^{a}	1.63^{a}
SHE	0.88^{b}	2.40^{a}	1.61^{a}
LEG	0.93^{c}	2.58^{b}	1.75^{b}

Note ^{a,b,}and ^{c} means within the column with different superscripts differ ($P<0.05$)

[1] WD=Wood function, WIL=Wilmink function, SHE=Schaeffer and Dekkers function and LEG= Legendre polynomial function

[2] MAE = means of absolute error; MMSE = means of mean square error; MSPE = means of square prediction error

Figure 4 shows the trends of the mean residuals over DIM for milk yield in the first lactation of different functions. The residuals were scattered about the horizontal axis. These results indicated the WIL function was considered as a satisfactory description of the lactation curve and an adequate representation of the data by the proposed model. A similar trend of mean residuals over DIM was observed from WD. Both WIL and WD functions could predict milk yield in early slightly better than the other functions. However, the fluctuations around zero were slightly higher in SHE and LEG, which can be explained by providing more variation of residual than the others, especially they predicted milk yield overestimation in early lactation (as in Figure 3). It was indicating that the LEG was not able to model all the variation of the curve in this population.

Similarly, Olori *et al*. (1999) also found that the use of ALI and WIL assured the best fit compared with other functions (WD, Inverse quadratic polynomial, and Mixed log) in the single herd dairy cows using weekly records. However, all functions tested predicted the patterns of mean herd lactation well, with little difference in fit.

Quinn *et al.* (2005) reported that the ALI function gave the best fit to their data compared to the WIL and Guo and Swalve functions, based on MSPE in the Irish dairy population.

Therefore, the evaluation of functions to fit individual effects (genetic and permanent environmental) is usually based on predictive ability of the model (Pool and Meuwissen, 2000); and mathematical features such as correlations among parameters, and scale of parameters.

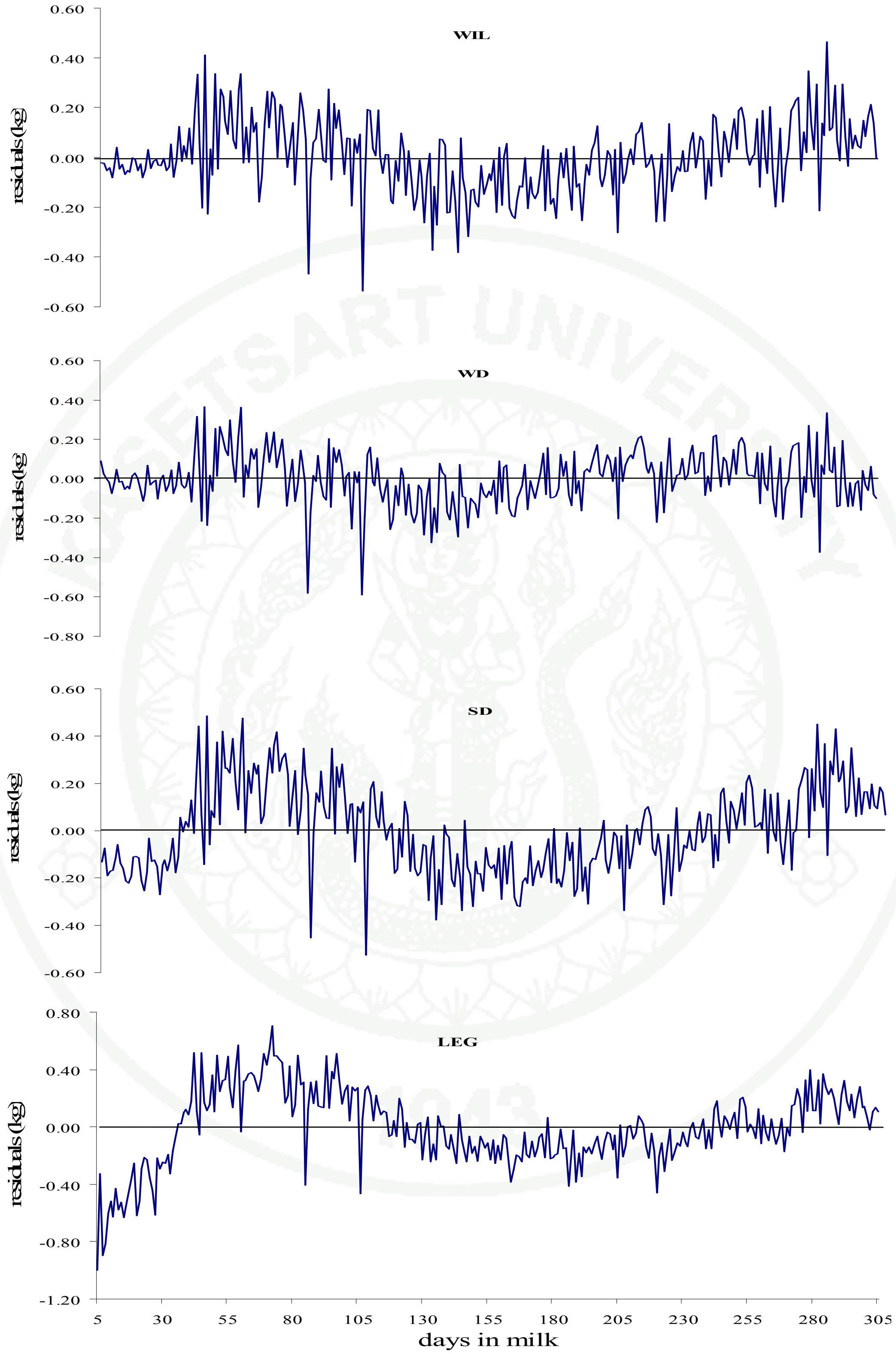

Figure 4 Residuals (kg/d) plots for Wilmink (WIL), Wood (WD), Schaeffer and Dekkers (SHE), and Legendre polynomial (LEG) functions

The results obtained in this study indicated that the variations of monthly TD yield during the lactation of a Thai multibreed dairy cows would be accurately explained by WIL function. Because it was found to be the best flexible function and goodness of fit for predicting both average and individual lactation curve. Also, WIL seem to be more robust and affordable under this criterion. These are the great importance for genetic evaluation of dairy cows and sires when prediction of their EBVs is base on TD records rather than 305-d yield. Therefore, in the RR-TDM such this function could be used to take account of the shape of lactation curve.

Estimation of individual 305-d milk yield

The Estimation of 305MY predicted from TIM and the four functions were compared in Table 11. The means of 305MY were not significantly different among four functions. It implied that all function could predict 305MY to be very similar amount. Total 305MY predicted from WIL function was 3,926.91 kg which lower than 305MY predicted from the TIM equal 1.08 kg (0.03%). On the other hand, the WD function provided the highest different yield from TIM method (DIFF=20.25 kg or 0.52%). Similarly, Guo and Swalve (1997) reported that the differences between actual and estimated lactation milk yield from the ALI, WIL, and Guo and Swalve models were very similar, and the superiority of these models to the WD were significant ($P<0.05$). The result indicated that WIL function was used as a lactation curve model, mean 305MY as well as those calculated with routine method.

Table 11 Means, standard deviation (SD), minimum (Min) and maximum (Max) for accumulate 305MY from four mathematical functions for 2,321 cows

Estimated function	Means (kg)	SD (kg)	Min (kg)	Max (kg)	DIFF^1 (kg)	Percentage deviation^2 (%)
TIM	3,927.98	1,017.84	1,103.40	9,586.50	0.00	0.00
WIL	3,926.91	478.82	1,537.43	6,427.43	-1.08	0.03
WD	3,948.23	473.15	1,631.85	6,483.61	20.25	0.52
SHE	3,936.26	473.27	1,524.28	6,487.52	8.28	0.21
LEG	3,930.80	472.12	1,454.73	6,539.31	2.81	0.07

Note [1] values express as a difference of predicted 305MY between four mathematical function and TIM method

[2] the percentage deviations resulting from comparing the 305MY predicted function with the TIM

However, the results were found in this study differed from several researches especially in the temperate regions (i.e. USA, Canada, Australia, Italy and etc). Most previous investigations on RR-TDM have recommended patterns and functions characterized by a high flexibility as parametric and non-parametric functions as sub model in RR-TDM. Due to most all researches to that point in time had been carried out on lactation records of animals that raised in the temperate regions, where environmental conditions and management practices are very different from that which occurs in the tropical regions. Our study of lactation was carried out on data gathered from multibreed dairy cows under Thailand conditions and will therefore make a valuable contribution to the knowledge of lactation curves under tropical conditions. Applicability vs economic dairy production in the tropics impacts might be the most appropriated dairy genetic know-how among Thai's dairy farmers.

Analysis II: Estimation of Genetic Parameters of Milk Production and Persistency of Milk Yield in a Thai Multibreed Dairy Population

Descriptive statistics

Means and summary statistics of 305MY predicted from both TIM and WIL function were presented in Table 12. These values were similar to previous analyses of the Thai multibreed dairy population (DPO, 2008; DLD, 2009).

Table 12 Mean, standard deviation (SD), minimum (Min) and maximum (Max) of 305MY and persistency of milk yield form 2,321 first lactating cows

Traits	Mean	SD	Min	Max
TIM_305MY, (kg)	3,927.98	1,017.84	1,103.40	9,586.50
WIL_305MY, (kg)	3,926.91	478.82	1,537.43	6,427.43
PER1, (kg/d)	0.03	0.02	0	0.11
PER2, (kg)	6.26	3.56	0.02	20.95
PER3, (%)	27.27	4.52	6.48	46.25

Note TIM_305MY=305-d milk yield calculated by test interval method (TIM), WIL_305MY=305-d milk yield calculated from the WIL function, PER1=absolute 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 305MY

Means of PER1, PER2 and PER3 were 0.03±0.016 kg/d, 6.26±3.56 kg and 27.27±4.52%, respectively (Table 12). These values were in the ranged of previous study Kitpipit (2002) reported the means of PER1 and PER3 of -0.03 kg/d and 26.10% in the commercial farm in Thailand. These values were similar to those reported by 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. By definition of the measurements, low values of PER1 and PER2 stand for good persistency but it stand for poor persistency with PER3 measure. Thus, it is not possible to directly compare the persistency traits obtained by the various measures, although there seems to be general consensus with respect to the effect of different biological and environmental factors on the various measurements of persistency of milk yield.

Heritability of 305MY

Estimated all variance components of 305MY and persistency measures were shown in Table13. Heritabilities of TIM_305MY and WIL_305MY were found to be 0.12. These values were lower than previous reports. Department of Livestock Development (2009) showed the high heritability of 0.41 for TIM_305MY. Koonawootrittriron *et al.* (2009) reported 0.38 for TIM_305MY in the DPO dataset and 0.33 were reported by Albarrán-Portillo and Pollott (2008) in HF cows raised in commercial herds in the United Kingdom. Nevertheless, Van der Linde *et al.* (2000) and Muir *et al.* (2004) reported the heritability of 305MY predicted from WIL function were 0.34 in Dutch HF cows and 0.45 in Canada HF. However, differences in population, model calculation and recording system may cause to the various heritabilities in several studies.

Table 13 Estimation of variance components and heritabilities for 305-d milk yield and persistency of lactation traits

Parameters	**TIM_305MY**	**WIL_305MY**	**PER1**	**PER2**	**PER3**
σ^2_a, (kg^2)	51,900.00	48,300.00	0.000005	0.19	0.03
σ^2_e, (kg^2)	373,000.00	360,000.00	0.000158	7.07	12.50
σ^2_T, (kg^2)	424,900.00	408,300.00	0.000163	7.26	12.53
h^2	0.12	0.12	0.03	0.03	0.01

Note σ^2_a= additive genetic variance, σ^2_e = residual variance, σ^2_T= phenotypic variance, h^2= heritability

Heritability of persistency

Heritabilities for persistency measures in the present study were range from 0.01 to 0.03 (Table13). The PER1 and PER2 were 0.03 more heritable in comparison with PER3 (0.01). The results showed that the PER3 trends to exhibit slightly lower heritability in study listed. In addition, persistency traits generally have low heritable than production traits. The estimates were within the range of previous measures ranged from 0.01 to 0.30 (Gengler, 1996; Kitpipit, 2002; Muir *et al.*, 2004; Seangjun and Koonawootrittriron, 2007; Sölkner and Fuchs, 1987; Van der Linde *et al.*, 2000; Weller *et al.*, 2006). Moreover, the extremely high heritabilities were ranged from 0.40 to 0.57 reported by Madsen (1975) in Danish cows. They explained that the common environment effects of progeny sire in the testing station may affect to the apparent heritabilities (Madsen, 1975).

The low heritability obtained form persistency of milk yield may be due to low additive genetic variance and large environmental variance on the phenotypic variance in the population. Therefore, the environmental effects (i.e. management, roughage quality, temperature, culture of farmers and availability of digestible feeds) change all bring about change in persistency trait. For examples, the effect of nutrition on heifer's requirement and days open always affect to persistency (Sölkner and Fuchs, 1987).

From the reviewing, heritabilities were found in tropical lower than reported in temperate countries. These results may be due to the different of the definitions of persistency, biological efficiency of measurement, population’s structure, environmental conditions, managements and estimation procedures (Cole and VanRaden, 2006; Madsen, 1975; Weller *et al.*, 2006).

Correlation between TIM_305MY and WIL_305MY

The relationships between TIM_305MY and WIL_305MY were extremely high (0.99 for genetic and 0.97 for phenotypic) were shown in Table14. These results indicated that both TIM_305MY and WIL_305MY showed good agreement by relationship. The accumulated 305MY predicted from TIM and WIL function were showed equivalently amount of lactation yield in this population. Also, the 305MY predicted from mathematical function could be used to consideration if it could estimate lactation yield similarly to the TIM.

As has been previously described, Ptak and Fracz (2002) fitted the WIL function as a lactation curve model, mean 305MY, as well as their ranges were also greater than those calculated with routine method. Schaeffer and Jamrozik (1996) compared two methods using to predict 305MY (i.e. the using of standard lactation curves *vs* the TIM) and concluded that they did not differ significantly when the TD records were regularly intervals of recording. Correlation between predicted and true 305MY increased with increasing number of TD records (from 0.62-0.65 for one record to 0.99-1.00 for nine records). In almost all cases the correlation coefficients exceeded 0.90 when the prediction was based on at least four records.

There were many comparisons of predicting 305MY using various methods. They concluded that the routine method (i.e. TIM) was satisfactory as long as its assumptions are fulfilled (Schaeffer and Jamrozik 1996, Ptak and Frącz 2002). On the other hand, methods based on lactation curve models (e.g. WIL function) have some advantages over those used routinely, as they deliver statistics useful in management, such as persistency of lactation, day of peak milk yield, as well as peak milk yield, and average curves for herds' production. The latter could be used to make within-herd comparisons. From an economic point of view, all those statistics could be valuable sources of information. Moreover, knowledge of cows' lactation curves may help detecting TD yields that are too high or too low compared with previous tests, as well as correcting yields relatively easily.

Table 14 Estimation of genetic (r_g, above diagonal) and phenotypic (r_p, below diagonal) correlations for all traits for the first lactation cows

r_g / r_p	**Production traits**[1]		**Persistency traits**[2]		
	TIM_305MY	**WIL_305MY**	**PER1**	**PER2**	**PER3**
TIM_305MY		0.99	0.34	0.29	0.55
WIL_305MY	0.97		0.33	0.29	0.56
PER1	0.28	0.23		0.97	0.30
PER2	0.24	0.21	0.94		0.26
PER3	0.12	0.17	-0.73	-0.82	

Note [1]TIM_305MY=305-d milk yield calculated by test interval method, WIL_305MY=305-d milk yield calculated by the WIL function

[2]PER1=absolute parameters c from the WIL function, PER2=the different yield between DIM60 and DIM280, PER3=the ratio between yield from 201 to 305 days and 305MY

Correlation between 305MY and persistency

The genetic correlations among 305MY and persictency measures ranged from 0.29 to 0.56 were shown in Table14. The phenotypic correlations ranged from 0.12 to 0.28. These relationships indicated that selection for increasing 305MY would affect to decrease PER1 and PER2, while PER3 was increased. From these relationships, we can class persistency trait in two groups as 1) ratio method (PER3) with positive genetic correlation and 2) methods based on declining phase of yield (PER1 and PER2) with negative correlations. The positive correlations indicated that the PER3 was not only measures persistency traits, but are in the fact highly related to 305MY.

Several researchers have found correlations (positive and negative) of persistency and 305MY ranging from 0 to over 0.60, varying with the way persistency was defined (Ferris *et al.*, 1985; Jamrozik *et al.,* 1998; Rekaya *et al.,* 2000; Van der

Linde *et al.,* 2000; Jakobsen *et al.,* 2002; Muir *et al.*, 2004). Gengler (1996) recommended the use of a measure of persistency that is genetically independent of 305MY; however, in this study, moderate positive genetic correlations were estimated between 305MY and persistency trait, indicating that selection for increased 305MY would slightly decreased PER1 and PER2, except for increasing PER3. Clearly, relationships exist between the shape of the lactation curve and total production. Minimizing this relationship will allow more efficient selection for 305MY and persistency trait simultaneously (Gengler,1995; Muir *et al.*, 2004).

Moreover, selection cows provide moderate level of 305MY and good persistency of milk yield have less stress, better health, better reproductive performances and more efficient use of cheap roughage than cows with high 305MY and low persistency (Grossman *et al.*, 1999; Muir *et al.*, 2004; Sölkner and Fuchs, 1987). Similarly reported by Muir *et al.* (2004) suggested that selection for increased persistency might increase total yields without increasing disease occurrence or reproductive failure. Recent studies have been more optimistic as to the possibility of joint selection for milk yield and persisitency trait (Togashi and Lin, 2004). If persistencycould be increased, considerable benefits would be preferable to dairyman.

Correlation between the persistency measurements

The correlations between different measures of persistency were showed in Table14. The genetic correlations were ranged from 0.26 to 0.97. The phenotypic correlations were high ranged from -0.73 to 0.94. Correlations were high positive for PER1 and PER2 because they measure the same parts of lactation. Hence, selection PER1 or PER2 could provide the same results. On the other hand, they were low related for PER3. It implied that selection for decrease PER1or PER2 would not affect PER3 in this population. The results were similarly to report from other researches (Gengler *et al.*, 1995; Madsen, 1974; Sölkner and Fuchs, 1987). There were long been study reports in Thailand by Choovatanapagon (1975) on persistency to have a moderate value of 0.61. Kitpipit (2002) reported the correlation between regression coefficient (parameter c from WIL function) and PER3 to be 0.88. As the results, the genetic relationship between measurement of persistency appear to be very strong. Consequently, the definition this trait should be defined and declare clearly.

Among the different measures, PER1 may be preferred to select and imply in the genetic evaluation, especially for cow evaluation, because of its higher heritable than others, low related to 305MY, easy to calculate, and stable statistical properties in parameter estimation. Moreover, PER3 may not be preferable because it was influenced by the irregularities at the end of lactation, especially for the long length of lactation (Madsen, 1975). Similarly, Muir *et al.* (2004) proposed the regression of the lactation curve after peak, as derived from the WIL function (Wilmink, 1987). These results implied that selection for higher 305MY might not result in selection of sires and cows that are genetically higher in lactation persistency and therefore, simultaneous evaluation for milk yield and lactation persistency would be necessary.

Analysis III: Genetic evaluation of milk yield using 305-d lactation and random regression test-day model in a Thai multibreed dairy cattle population

The (co)variance and correlations between genetic (a_i) and permanent environmental (p_i) random regression coefficients were given in Table15. The is a_1 coefficient corresponds to the initial milk production, the a_2 is coefficient represents the rate of increase in milk production gain until peak yield and the a_3 is coefficient expresses the rate of decline in milk production after peak yield. The results showed that the additive genetic variances of a_1 and permanent environmental of p_1 regression coefficients were larger than other coefficients indicating that they had the contribution in describing the variation of observations (Khorshidie *et al.*, 2012). On the other hand, other (co)variances of regression coefficients were close to zero. These finding was different from reported by Jamrozik and Schaeffer (1997) using WIL with a_3 = 0.05 in Canadian HF and Brotherstone *et al.*(2000) using WIL with a_3 = 0.10 and 0.06 in HF cows in UK.

Table 15 Estimation of additive genetic and permanent environmental variances (diagonal), (co)variances (upper diagonal) and correlations among coefficients (lower diagonal) for random regression coefficients.

	Additive genetic				**Permanent environment**		
	a_1	**a_2**	**a_3**		**p_1**	**p_2**	**p_3**
a_1	5.74	-0.02	-0.004	p_1	10.50	-0.03	-0.031
a_2	-0.91	0.10E-03	0.16E-04	p_2	-0.88	0.13E-03	0.62E-04
a_3	-0.79	0.69	0.52E-05	p_3	-0.72	0.41	0.17E-03

Note a_i = random regression coefficient of additive genetic effect to i^{th} WIL function.
p_i= random regression coefficient of permanent environmental effect to i^{th} WIL function.

Estimation of correlations between random regression coefficients for additive genetic effects and permanent environmental effects had same trends. Correlations between genetic regressions coefficients ranged from -0.91 (a_1, a_2) to 0.69 (a_2, a_3). Similarly, the correlations of permanent environmental regression coefficients ranged from –0.88 (p_1, p_2) to 0.41 (p_2, p_3). Genetic and permanent environment correlations between the initial regression coefficient and the regression coefficient of decreasing were all negative, suggesting that increasing the initial of production would increase persistency. In general, correlations between genetic coefficients varied from almost null to high and higher than those between permanent environmental coefficients. The results obtained in the present study were also similarly to observe by Olori *et al.* (1999), Zavadilová *et al.,* (2005) and El Faro *et al.* (2008) in several countries. Zavadilová *et al.,* (2005) reported that the correlations were stronger for the genetic component than for the permanent environmental effect, especially for the single-trait analyses.

Estimation of variance components of 305-d milk yield

Lactation model

Estimation variance components for 305MY were estimated from LM animal model using the BLUPF90 DairyPack package ((Duangjinda *et al*., 2004) via EM-REML algorithm. Estimation of variance components of additive genetic (σ^2_a), residual (σ^2_e) and total (σ^2_T) variances were found to be 51,900, 373,000 and 424,900 kg^2, respectively (Table16). The additive genetic variance was found to be lower that other reports in Thailand. Buaban and Sanpote (2010) studied data set from the same population, they reported the variance components (σ^2_a=129,000 kg^2, σ^2_e=492,000 kg^2, σ^2_T=621,000 kg^2) were higher than those values obtained from the present study. The differences may be cause from the different of defining the CGs as fixed effects in analytical model and editing criteria. Buaban and Sanpote (2010) defined the CGs as AI unit-year-season of calving, but actual herd-year-season of calving was defined in this study.

Table 16 Heritability (h^2), genetic, permanent environmental, HTD and residual variances (kg^2) for 305-d milk yield estimated from LM and RR-TDM form 21,934 TD records for 2,321 cows

Parameters	LM	RR-TDM
σ^2_a, (kg^2)	51,900.00	422,264.30
σ^2_{pe}, (kg^2)	-	477,187.20
σ^2_{HTD}, (kg^2)	-	408.70
σ^2_e, (kg^2)	373,000.00	613.05
h^2	0.12	0.47

Koonawootrittriron *et al.* (2002) estimated variance component in a HF×Other breeds in DPO multibreed dairy population in Central Thailand. They reported the additive genetic variance was 255,068 kg^2. However, all estimates of additive genetic and phenotypic variances for MY in multibreed population were lower than estimates for HF cows in Brazil (Costa *et al.,* 2000), Colombia (Ceron-Muñoz *et al*., 2001), and Mexico (Cienfuegos-Rivas *et al.,* 1999).

Random regression test-day model

Estimation variance components for 305MY predicted from RR-TDM were showed in Table17. The value of additive genetic variance was higher than the results from Buaban and Sanpote (2010) using the same data set and Jamrozik and Schaeffer (1997) using Canadian HF, but other components were lower than that reported. Additionally, additive genetic variance estimated from RR-TDM was greater obtained by LM. Differences between the estimates from the present study and other studies may be due to the different models (LM vs RR-TDM), analytical methods (Gibbs vs REML), assumptions of the individual study and fixed effects account in the models. The residual variance will be very small compared to the genetic variance and the permanent environmental variance. This is caused by the implicit assumption that a cow is measured 305 times, and the residual of each measurement is independent of the residuals of all other measurements.

Differences between the estimates from the present study and other studies may be due to the following reasons:

- Using different models for example RR-TDM vs 305-d LM, including functions related to changes in lactation curve in the model, and sire model vs animal model.

- Including HTD in the model to account for fixed or random effects related to each TD instead of HYS, which has been used in models using 305-d measurements. Previous work (Meyer *et al*., 1989; Pander *et al*., 1992; Ptak and Schaeffer, 1993;

Swalve, 1995) has shown a reduction in residual variance as a result of replacing HYS by HTD in the model.

- Using different assumptions (i.e. homogeneous residual variance vs heterogeneous residual variance across the lactations).

- Converting or extending TD or part lactation measurements to 305-d measurements with the same extension factors for all cows with different levels of production eliminated some genetic variance in production. Direct use of TD measurements in the variance component estimation could prevent this problem and finally could increase the estimates of genetic variance in comparison to using 305-d extended measurements.

Estimation of variance components of daily milk yield

Estimation of additive genetic, permanent environment, HTD and residual variances were presented in Table17 and Figure 5. Genetic and permanent environment variances throughout the lactation were calculated from the estimated (co)variance coefficients matrixes (Jamrozik and Schaeffer, 1997).

Estimation of daily additive genetic variances was generally larger at the beginning and decreased along lactation. The similar trends were reported by many authors in Brazil (Costa *et al.*, 2008; El Faro *et al.*, 2008), Mexico (Santellano-Estrada *et al.*, 2008) and Thailand (Buaban and Sanpote, 2010). Buaban and Sanpote (2010) applied the WIL function nested in additive genetic and permanent effects, but the LEG was applied in fixed part in the same data set. However, the additive genetic trend also as same as in the present study. These finding indicated that the different of submodels in the fixed part does not effect to the additive genetic part.

These results were disagreement with those reported by Jamrozik *et al.* (1997), who found that the daily genetic variance decreased from the beginning to the 25th DIM of lactation and then stability to the end of lactation in Canadian HF. Melo *et al.* (2007) showed the different trend of additive genetic variance estimates for the WIL function, increasing from 9.47 kg^2 on the 5th DIM to 171.27 kg^2 at the end of lactation. Pool *et al.* (2000) and Druet *et al.* (2003) found the genetic variance was highest in the mid part of lactation. In those studies, RR-TDM was applied and the LEG function was used to describe random curve.

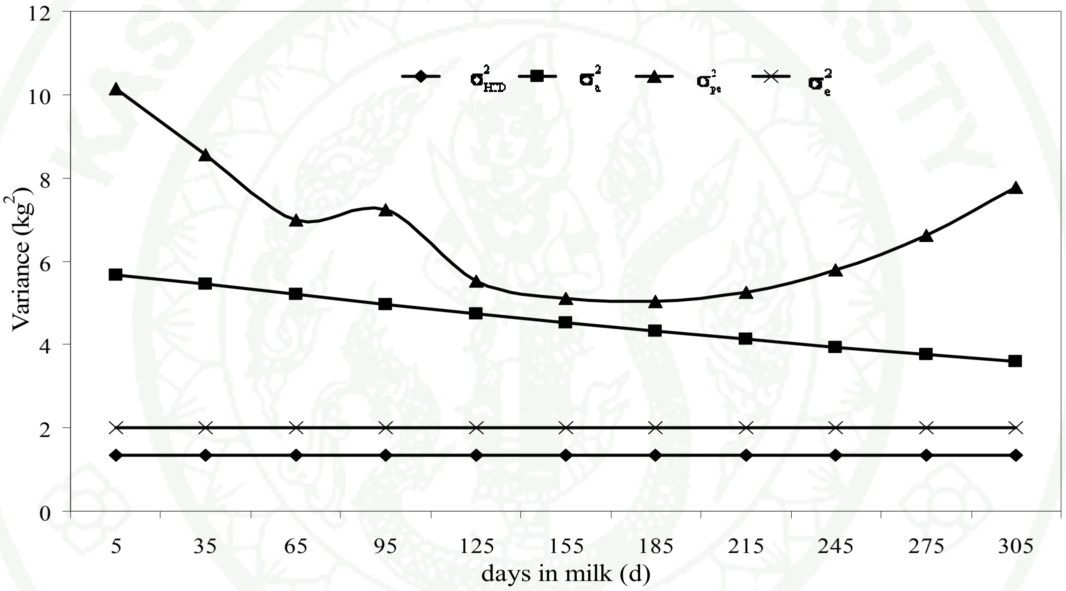

Figure 5 Additive genetic (σ^2_a), permanent environmental (σ^2_{pe}), herd-test-date (σ^2_{HTD}) and residual (σ^2_e) variances of milk yield estimated form RR-TDM in a Thai multibreed dairy population.

The permanent environmental variances were more mostly extremes observed at the beginning and the end of lactation. Small differences were observed at the mid-lactation. The permanent environmental variances were consistently higher than other variances. It seem to be a U-shape. The same pattern were also reported in previous studies (Pool *et al.*, 2000; López-Romero and Carabaño., 2003; Druet *et al.*, 2005; Strabel *et al.*, 2005; Zavadilová *et al.*, 2005; Fujii and Suzuki, 2006; Bignardi *et al.*, 2008; Costa *et al.*, 2008; Hammami *et al.*, 2008; Togashi *et al.*, 2008).

This finding could be caused from residual variance assumed as homogeneity does not appear to compromise the accuracy of the estimates of the other variance components and genetic parameters. This occurrence should influence to estimate permanent environmental variance (Olori *et al.*, 1999; Strabel *et al.*, 2005; Hammami *et al.*, 2008; Buaban and Sanpote, 2010). The moderate high value of permanent environment variance obtained in the present study indicated that to improve the management go together with intensive selection and mating should be improve dairy production and genetic under Thai conditions.

The estimated of HTD variance was found to be 1.34 kg2. It was the smallest compared with the other sources of variances. In the study, the HTD variance was assumed constant throughout the lactation as same as the residual variance. As expected from previous studies (Strabel *et al.,* 2005; Hammami *et al.,* 2008). Similar trend of HTD variance was also reported by Strabel *et al.* (2005) in Polish black and white cows and Hammami *et al*. (2008) in Tunisian HF. They defined the HTD effect as random effect in the analytical model. Because of the characteristic of population in this study have a small herd size and low level of production (de Roos *et al*., 2004; Strabel *et al.,* 2005). Small herds usually lead to small HTD classes, and the problem of small CGs remains, especially under Thailand conditions.

Table 17 Estimation of genetic (σ^2_a), permanent environmental (σ^2_{pe}), residual (σ^2_e), herd-test-date (σ^2_{HTD}) variance and heritabilities (h^2) for selected days in milk.

DIM	σ^2_a	σ^2_{pe}	σ^2_e	σ^2_{HTD}	h^2
5	5.67	10.15	2.01	1.34	0.32
35	5.44	8.55	2.01	1.34	0.34
65	5.20	7.23	2.01	1.34	0.36
95	4.97	7.23	2.01	1.34	0.35
125	4.74	5.51	2.01	1.34	0.39

Table 17 (Continued)

DIM	σ^2_a	σ^2_{pe}	σ^2_e	σ^2_{HTD}	h^2
155	4.52	5.12	2.01	1.34	0.39
185	4.32	5.03	2.01	1.34	0.38
215	4.12	5.25	2.01	1.34	0.36
245	3.93	5.78	2.01	1.34	0.34
275	3.75	6.62	2.01	1.34	0.30
305	3.58	7.77	2.01	1.34	0.27

Hence, increasing the size of the CGs or treating as random are among the methods that can improve the quality of genetic evaluation by reducing the variances of residuals and prediction error (Visscher and Goddard, 1993; Strabel and Szwaczkowski,1999). Similarly, Lidauer *et al.* (2003) modeled the herd effect for the Finnish dairy population by fixed herd-year and random HTD components. The model with a random HTD gave the smallest ratio of error to total variance, and was the best in predicting future records.

Mayers *et al.* (2002) found that the combination of random HTD and fixed herd-years gave protection against the negative consequences of HTD groups that were too small. The different effects of CGs of recording (HTD as fixed and HTD as random) were important to the applied in the genetic evaluation model. The CGs formation of HTD as random effect slightly increased the additive genetic variance but decreased the permanent environment variance (Strabel *et al.*, 2005). However, no literature is available defined the HTD effects as random effects in Thai multibreed population. Therefore, it is difficult to compare the result to others.

Residual variance was found to be 2.01 kg^2. In the analysis, residual variance was assumed to be constant during the lactation. This value was lower than other population as in Korea HF (7.03 kg^2; Kim *et al.* 2009); in Tunisian HF (2.98 kg^2; Hammami *et al.*, 2008), in Brazilian HF (5.41 kg^2; Costa *et al.*, 2008) and in Japanease HF (4.32 kg^2; Togashi *et al.*, 2008), but higher than found from Santellano-

Estrada *et al*. (2008) in Mexico (1.33 kg^2). Generally residual variance was larger in the beginning and decreased along lactation when assumed to vary between classes of lactation period.

Many authors found that the residual variance were not constant during the lactation (Jamrozik and Schaeffer, 1997; Olori *et al*., 1999a, 1999b; Brotherstone *et al.,* 2000; Misztal *et al.,* 2000; Rekaya *et al*., 2000). The heterogeneous of residual variance should reduce the permanent environmental variation at the beginning and end of lactation, but no apparent effect of genetic variation. Therefore, the further development of variance component estimation using RR-TDM included heterogeneity of residual variance during the lactation will be applied to evaluating genetic performance of dairy cattle in this population because it affects to estimate the heritability accurately. In contrast, Fujii and Suzuki, (2006) reported the antagonistic results from previous studies. They compared homogeneous and heterogeneous of residual variance using RR-TDM for first lactation Japanese HF. They found that there was not necessary to consider heterogeneous of residual variance in the genetic evaluations, because heterogeneous of residual variance over the year did not affect the ranking of top sires and cows.

López-Romero and Carabaño (2003) investigated 22 alternative RR-TDM using HF data in Spain. Differences in variances among models were more mostly observed at the extremes of lactation. All the models assumed homogeneous of residual variance along lactation. The model of choice was the most complex one, a LEG of order six. However, they pointed out that submodels with a lower order polynomial for the genetic than for the permanent environmental component would be sufficient to account for the variability of these effects.

Heritability of 305-d milk yield

Lactation model

Estimated heritability of 305MY from LM was found to be 0.12 (Table17). This value was close to the value found from Kim *et al.* (2009) in HF cows in Korea (0.14). These values were lower than estimates obtained form other studies in tropical and temperate countries (i.e Buaban and Sanpote, 2010; Department of Livestock Development, 2009; Koonawootrittriron *et al*, 2009; Albarrán-Portillo and Pollott, 2008; Van der Linde *et al,* 2000; Muir *et al.,* 2004).

Low estimates heritability from this data might be explained by limited production levels in the state and cooperative herds (Rekik *et al.*, 2003), incomplete and/or inaccurate pedigree information on imported semen of some sires. Similarly, Thomas and Hill (2000) showed that complete pedigree information is necessary to avoid decreasing biased estimation of genetic parameters. Differences in estimates of heritability in this study with other results could be due to different models, population, data structure, management and environmental factors.

Random regression test-day model

Heritability of 305MY estimated from RR-TDM was found to be 0.47 (Table17). This value was greater than the result obtained from LM (0.13). Due to the RR-TDM provided the higher genetic variance than LM. Similar results were found from many studies. Buaban and Sanpote (2010) reported the heritability estimated from LM lower than using RR-TDM on the same population used in this study. Similarly, Kim *et al*. (2009) showed the heritability estimated using the RR-TDM was higher than that finding from the LM. These results were in agreement of several studies (Pool *et al*., 2000; Jakobsen *et al*., 2002; de Roos *et al*., 2004; Druet *et al.*, 2005; Muir *et al*., 2007). In contrast, There were some researches reported the small values obtained from RR-TDM as 0.18 in Poland HF (Strabel *et al.*, 2005) and 0.17 in Tunisian HF (Hammami *et al.*, 2008).

These values are relatively high because the RR-TDM accounted better for temporary environmental effects on a test-day basis as compared to the LM (Jensen, 2001). Due to use of the RR TDM approach allows a more detailed statistical model to be developed, which accounts for environmental variation specific to individual TD yields and genetic effects associated with individual animals. It offers the opportunity to directly account for short-term environmental factors specific to individual yields such as gestation period. The RR-TDM also overcomes the need to predict 305-day yields or for projection of incomplete lactations. Furthermore, the TDM allows for precise definition of the CGs. With the TD approach, definition of CGs including test-month improves the properties of the statistical model. Solutions emanating from such CGs effects can be utilized to improve herd management.

Heritabilities of daily milk yield

Heritabilities for selected DIM were given in Table17, and for all DIM in Figure 6. Heritability estimates ranged from 0.27 to 0.39. The range for heritabilities obtained in this study was similar to obtained by Buaban and Sanpote (2010) for the same population. These values were in the same ranged in previous studies (Jamrozik and Schaeffer, 1997; Olori *et al.*, 1999; Druet *et al.*, 2005; Melo *et al.*, 2007; Santellano-Estrada *et al.*, 2008; Kim *et al.*, 2009). On the contrary, some authors reported the lower values from the present study (Strabel and Miztal, 1999; Brotherstone *et al.*, 2000; Hammami *et al.*, 2008). They showed a wide variability in comparison with other studies.

Regarding Zebu breeds, e.g. Gyr, heritability estimates have been higher than those obtained for Holstein cattle. Costa *et al.* (2005) presented estimates ranging from 0.71 at the earlier to 0.27 at the end of lactation. The explanation for this difference could be due to differences in sub models, data structures, breed of cows and management.

The pattern of heritability showed low in early and late lactation, but it was higher in mid-lactation. The extremely value at the mid lactation was due to the small permanent environmental variation in the mid lactations, while the additive genetic variance was rather constant during the lactation. The similar trends were reported by many authors (Rekaya *et al.*, 1999; Pool *et al.*, 2000; Jakobsen *et al.*, 2002; Druet *et al.*, 2003; Kaya *et al.*, 2003; Silvestre *et al.*, 2005; Bilal *et al.*, 2008; Costa *et al.*, 2008; Hammami *et al.*, 2008). On the contrary, some authors found the opposite trends of the study (Jamrozik and Schaeffer, 1997; Olori *et al.*, 1999; Strabel and Miztal, 1999; Kettunen *et al.*, 2000; Bignardi *et al.*, 2008; El Faro *et al.*, 2008). They reported high heritabilities at the beginning and end of lactation. In this study the HTD and residual variance were assume constant for all TD during the lactation, which were not a realistic assumption, and has resulted in increasing permanent environmental variance. The applicable of these heriabilities seem as selection criteria.

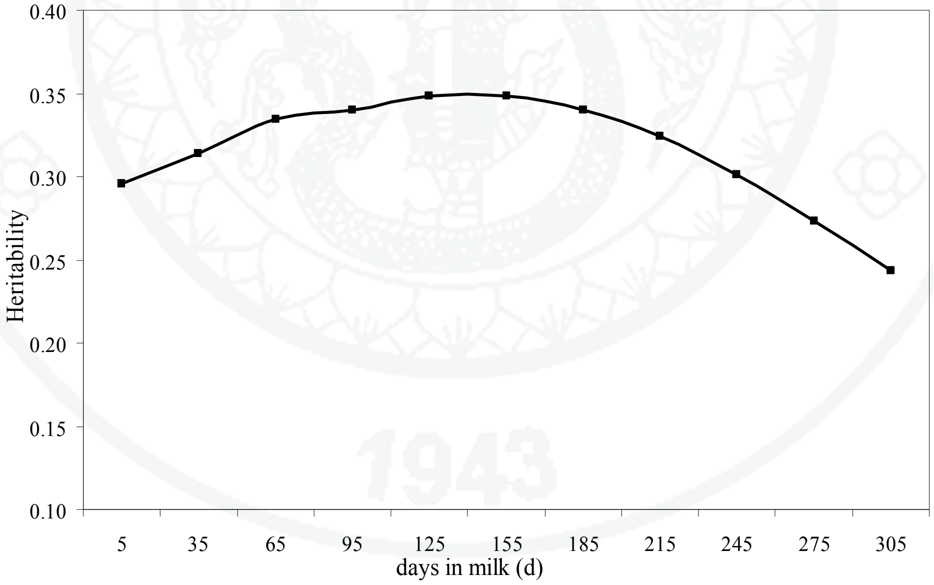

Figure 6 The heritability trends for milk yield obtained from RR-TDM

Random regression models lead to various results for the level and pattern of daily milk yield heritability; this was discussed by Misztal *et al.* (2000), and confirmed in more recent studies. The shape of the heritability curve with lower values at the beginning and end of lactation, as obtained by Druet *et al.* (2003) for example, seems most desirable, as these periods are strongly influenced by nongenetic effects cumulated before calving and associated with the farmer’s decision about drying off (Strabel *et al.*, 2005).

Genetic and permanent environment correlations

Genetic correlation between adjacent DIM were moderate high and close to unity (Figure 7; most of them greater than 0.96). Similar result was obtained by Strabel and Miztal (1999). Many researches have been reported the same trends, however, those correlation were not the moderate high as in this study (Swalve, 1995; Jamrozik and Schaeffer, 1997; Brotherstone *et al.*, 2000; Kettunen *et al.*, 2000; Eslamil *et al.*, 2004; Strabel *et al.*, 2005; Melo *et al.*, 2007).

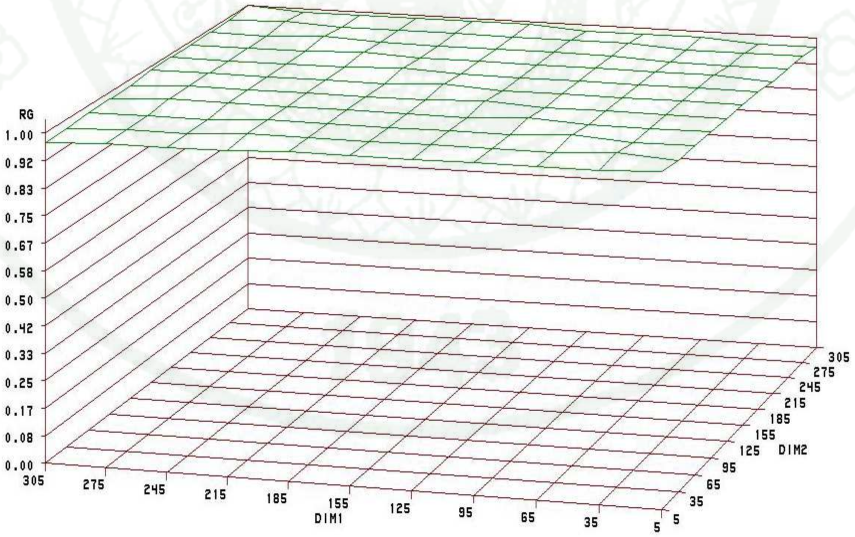

Figure 7 Estimates of genetic correlations between DIM obtained from RR-TDM

The negative genetic correlation estimates were observe between early and late TD records and have also been reported by Rekaya *et al*. (1999), Brotherstone *et al*. (2000), Kettunen *et al.* (2000); López-Romero & Carabaño (2003) and Bignardi *et al*. (2009). Those could be explained by the difficulty of modeling the initial production controls using the LEG as submodels had difficulty to model records at early and late lactation. The post calving cow's stress during the first weeks of lactation may influence these results because generally cows show negative energy balance during early lactation. Brotherstone *et al.* (2000) using LEG and WIL functions obtained negative genetic correlation between initial and further DIM.

Permanent environmental correlations among selected TD records were shown in Figure 8. The permanent environmental correlations decreased from 0.99 to 0.13 between days 5 and 305. The lowest correlations within lactation were between the 5th and the 305th day of lactation. This was in agreement with other studies, in which the lowest permanent environmental correlations were between MY at the most distant TD (Jamrozik and Schaeffer, 1997; Brotherstone *et al.*, 2000). Low correlations between distant DIM would reduce the possibility of selection based on few records from the beginning of lactation. In general, genetic correlations were higher than permanent environmental correlations, but estimates decreases more drastically with the increase in days between records.

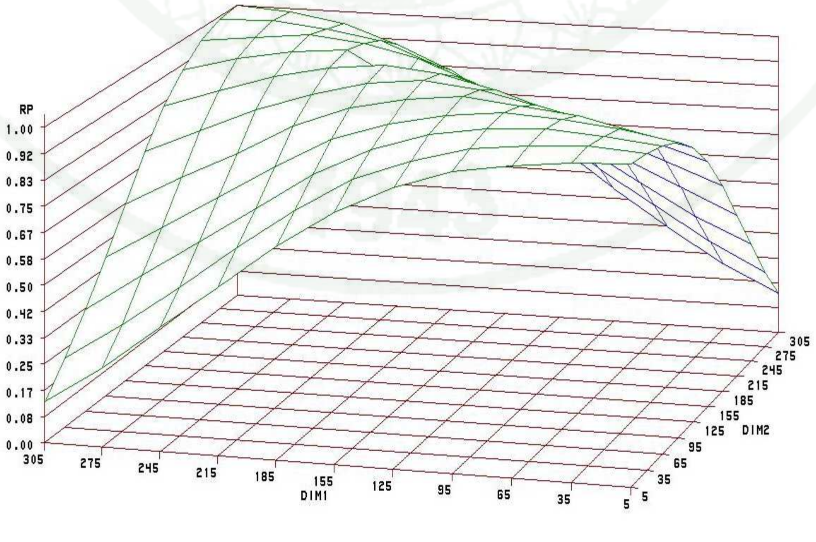

Figure 8 Estimates of permanent environment correlations between DIM obtained from RR-TDM

Strabel and Miztal (1999) suggested that the high genetic correlations between adjacent DIM in their study, the repeatability model could be a good approximation of the alternative model. Differences in shape of lactation curves for different ages and season could be partly accounted for by pre-adjustments. Additionally, it is the simplest model and has less permanent effects in the model. However, the finding of the present study showed that the permanent environmental variance were not unity between adjacent DIM. Therefore, RR-TDM is still the best choice to select for evaluating genetic ability in the population. Additionally, assumed the residual variance constant throughout the lactation may be caused the high genetic correlation. So, further study could investigate whether fitting this variance through random regressions results in better modeling accuracy.

Estimated Breeding Values

Means and standard deviations (SD) of estimated breeding values (EBVs) obtained from LM and RR-TDM were presented in Table18. Mean differences in EBVs were smallest between the RR-TDM and LM, but the SD of 305MY EBVs from RR-TDM was higher than LM. These results indicated that RR-TDM would model more variability between animals. From these results, using RR-TDM for genetic evaluation might increase the genetic gain by reducing the chance to select the poor genetic of sires and cows to be the parents and transfer genetic abilities to the next generations.

As expected, the increasing in SD of EBVs was higher for cows than for bulls. This reflects that the RR-TDM has most effect in improved EBVs of cows. Schaeffer *et al.* (2000) and Lidauer *et al*. (2000) have suggested that replacing the LM with the RR-TDM has a large impact on EBVs of cows but less impact on EBVs of bulls. Because of the RR-TDM can account environmental effects better than LM, which will improve the accuracy of cows' EBVs. Bulls that have the large number of daughters receive accurate EBVs also with traditional LM. Thus, the advantage of RR-TDM is more visible in EBVs of bulls with a small number of daughters. In most studies the model comparisons are not accurate because the genetic parameters in the different models are not comparable.

Table18 Means±standard deviation (kg) of estimated breeding values for milk yield with 305-d lactation yield model (LM) and random regression test-day model (RR-TDM)

	No. of animal (heads)	LM	RR-TDM
Sires	475	89.98±98.28	33.94±271.89
Cows	3,547	12.05±101.29	-2.04±373.39
All	4,023	0.00±106.17	2.21±363.07

The random regression coefficients of EBVs solutions for selected bulls were presented in Table19. There showed the variability among sires in the random regression coefficients. Therefore, the shape of individual sires and cows were variable. These EBVs for random regression coefficients are not useful for ranking or selecting animal directly, but function of these EBVs using WIL function can provided useful information to breeder for selection decisions.

Table 19 Estimated breeding values of random regression coefficients for milk yield for top five sires with more than 25 daughters from a random regression test-day model.

Sires	No. of daughters (heads)	$\hat{a}_{1k}$	$\hat{a}_{2k}$	$\hat{a}_{3k}$
71HO1064	199	3.63	0.0027	-0.0014
A72	164	2.42	0.0074	0.0000
71HO1083	153	4.00	0.0012	-0.0010
73HO1529	144	4.52	-0.0008	-0.0018
M124	109	4.20	0.0003	-0.0013

Note $\hat{a}_{1k}$, $\hat{a}_{2k}$ and $\hat{a}_{3k}$ = EBVs for the random regression coefficients

Correlations of EBVs between LM and RR-TDM

Correlations of 305MY EBVs between LM and the RR-TDM were shown in Table 20. Pearson and Spearman's rank correlation of animals for EBVs from the two models was compared. The Pearson correlations were 0.78 and 0.75 for sires and cows, while rank correlations were 0.69 and 0.65 for sires and cows, respectively. Correlation between both EBVs and ranking of sires and cows according to EBVs were found significantly (P<0.01). Generally, sires had stronger rank correlation compared to cows. Correlations estimated in this study are lower than reported value by Jamrozik *et al.*, (1997); Van Doormaal and Kistemaker, (1999); Schaeffer *et al.*, (2000) and Buaban and Sanpote, (2010).

Lidauer *et al.* (2003) reported high correlations between active bulls' breeding values (0.99 for milk) obtained from the LM and RR-TDM. However, the animals and data of their study were carefully selected to be the same across different models in contrast to the other mentioned publications. For young cows, the corresponding correlations were about 0.88, which led to significant re-ranking of cows. Other rankings reported in the literature were all in the range of 0.87-0.97 (Swalve, 1995; Jamrozik *et al.*, 1997; Lidauer *et al.,* 2000). The different correlations may be caused from the different both fixed and random effects in the particular model. Also, comparison of EBVs from the different models does not appropriate to indicate which model is better for ranking purpose. In most studies the model comparisons are not accurate because the genetic parameters in the different models are not comparable.

Table 20 Pearson and Spearman rank correlations between breeding values between LM and RR-TDM

	Pearson correlations	**Spearman rank correlation**
Sires	0.78	0.69
Cows	0.75	0.65

Genetic persistency of milk yield

Means, standard deviation (SD) and range of the EBVs for each measure of persistency and random regression coefficients of the 475 sires included in the analyses were given in Table 21. From the definition of persistency measurements, the lower values of P1 and P2 and higher values of P3 indicated the good persistency of milk yield that preferable to breeder.

The large variation in the magnitude of the genetic random regression coefficients of the WIL function for milk yield was observed among sires, indicating the possible presence of genetic variation in the shape of the lactation curves of sires and daughters. The $\hat{a}_{1k}$ coefficient corresponds to the initial milk production, the $\hat{a}_{2k}$ coefficient represents the rate of increase in milk production gain until peak yield and the $\hat{a}_{3k}$ coefficient represents the rate of decline in milk production after peak yield.

Table 21 Means, standard deviation (SD) and range of estimated breeding values for persistency of milk yield (P1 to P3) and random regression coefficients (a_1, a_2 and a_3) of WIL function for sires of the Thai multibreed population using RR-TDM

Traits	Mean	SD	Range
$\hat{a}_{1k}$	4.47	1.00	-0.28 to 7.94
$\hat{a}_{2k}$	-0.0005	0.0038	-0.0139 to 0.0176
$\hat{a}_{3k}$	0.0018	0.0007	-0.0043 to 0.0019
P1 (kg/d)	0.0018	0.0007	-0.0043 to 0.0019
P2 (kg)	0.39	0.16	-0.42 to 0.95
P3 (kg)	34.24	25.93	32.38 to 598.79

Note $\hat{a}_{1k}$, $\hat{a}_{2k}$ and $\hat{a}_{3k}$ = EBVs for the random regression coefficients; P1 = the EBV of random regression coefficient related to decrease yield after peak ($\hat{a}_{3k}$); P2 = the EBV at DIM 60 minus EBV at DIM 280; P3 = the ratio of accumulated genetic yield from days 201 to days 305 and 305MY calculated from RR-TDM

Correlations

Estimates of genetic correlations between 305MY and different genetic persistency measurements were presented in Table 22. The genetic correlation among P1 and P2 were high and positive which can be due to the similarity in their definition and in the same manner. Also, P1 and P2 could be considered as the same traits. The cows that have a high genetic ability to maintain MY in the high level after peak (P1) could reflect to the less different of MY between DIM 60 and DIM 280. Therefore, both P1 and P2 could be used for select to obtain the similar results. The P3 in contrast to P1 and P2 represents an area under the lactation curve at specified time interval that has been corrected for milk yield at the end of that interval. For a cow with normal lactation curve, the values of P2 and P3 are positive.

Table 22 Correlations for different genetic persistency and 305MY obtained from RR-TDM for sires (upper diagonal) and cows (below diagonal)

	305MY	**P1**	**P2**	**P3**
305MY		0.97	0.97	-0.23
P1	0.98		1.00	0.24
P2	0.98	1.00		-0.24
P3	-0.55	0.57	-0.57	

The lowest correlation estimates between persistency of lactation and 305MY were obtained for P3, for both sires (-0.23) and cows (-0.55), and, as expected, agree with the results of Cobuci *et al*. (2004). These estimates demonstrate the weak association between production and persistency of lactation; thus, cows with the same milk production may present different levels of persistency of lactation (Gengler, 1996; Jamrozik et al., 1998; Van der Linde et al., 2000). These estimates also indicate that animals with larger EBVs for persistency of lactation are not exactly the same as those with larger EBVs for 305MY.

Of the three genetic persistency measures evaluated in this study, the performance of P3 appeared as the most appropriate when applied to describe the milk persistency in a Thai multibreed dairy cattle. Because it had a lowest correlation with 305MY. Many researches supported this occurrence. Khorshidie *et al*. (2012) suggested that selection for higher 305MY might not result in selection of sires that are genetically higher in lactation persistency and therefore, simultaneous evaluation for milk yield and lactation persistency would be necessary. Jakobsen *et al.* (2002) compared several definitions of persistency and concluded that a measure similar to the one used in Canada was optimal if all TD in the period from 60 to 280 DIM was used in the prediction of persistency. Her criteria were the accuracy of predicted breeding values for persistency of milk yield and a low genetic correlation between persistency of milk yield and total lactation yield.

CONCLUSION AND RECOMMENDATIONS

Conclusion

The general conclusions are summarized from the three trials in this research. In the first trial, the WIL function was found to be the most suitable to describe the means and individual lactation curves in a Thai multibreed dairy population. The WIL function provided the best goodness of fit both mean and individual curves. Overall, the WIL performed better statistically and biologically, as they more closely resembles the underlying process for this data set.

However, the results were found in this study may differ from several researches especially in the temperate regions (i.e. USA, Canada, Australia, Italy and etc). Most previous investigations on RR-TDM have recommended patterns and functions characterized by a high flexibility as parametric and non-parametric functions. Due to most all researches to that point in time had been carried out on lactation records of animals that raise in the temperate regions, where environmental conditions and management practices are very different from the tropical regions. Our study of lactation was carried out on data gathered from multibreed dairy cows under Thailand conditions and will therefore make a valuable contribution to the knowledge of lactation curves under tropical conditions.

The second trial was to estimate genetic parameters of 305MY and persistency of milk yield using WIL function. Three measures of persistency calculated were 1) regression coefficient from WIL function or parameter c (PER1), 2) the different of milk yield between days 60 and 280 (PER2) and 3) the ratio between accumulated yield from 201 to 305 days and 305MY (PER3). The heritabilities of persistency were generally low and moderately related to 305MY. The highest correlation between PER1 and PER2 was observed (close to one). They were considered the same trait. Among persistency measures examined in this study, PER1 and PER2 behaved as independent measure from 305MY production, PER1 had equal heritability with PER2 and thus it is suggested that PER1 could be used for measuring persistency under conditions in Thailand. Due to PER1 is easy to calculate, stable statistical properties in parameter estimation and less correlate with 305MY.

The last trial was to estimate genetic parameters and predict breeding value of 305MY and persistency traits using LM and RR-TDM. The variance components for milk yield were estimated by applying both LM to 305-d measurements and RR-TDM to TD measurements. The estimated genetic variances for milk yield from RR-TDM were higher than the estimated values from the LM. The daily heritabilities for milk yield were highest at the mid of lactation, which might be due to the model assumption regarding permanent environment variance. Because the daily genetic variance slightly constant during lactation. The highest heritability in the mid lactation indicated selection dairy in this period could be done under these conditions.

Additionally, RR-TDM showed the higher means and SD of EBVs than LM. These results indicated that RR-TDM would model somewhat more variability between the animals. Implementation of RR-TDM to estimate breeding values for milk yield caused significant re-ranking of especially cows and sires. Consequently, the use of RR-TDM for genetic evaluation may increase the rate of genetic gain by reducing the chance of selecting genetically poor sires and cows.

Genetic persistency is obtained as by product from RR-TDM and usually considered as economic trait with an important impact on milk production. The daily EBVs changes across the whole lactation period showed differences among cows for persistency. Three alternative criteria for genetic persistency and their relationship with 305MY were studied. The correlation of a persistency criterion (P3) with 305-d and part lactation measurements for milk was the criteria for evaluating persistency criteria in this study.

The use of appropriate method for genetic evaluation of dairy animals is an important aspect of dairy cattle production. Traditionally, 305-d LM does not account for the changes in environmental factors within 305-day lactation and may involve unjustified projection of incomplete lactations. The use of RR-TDM in the recent past has made it possible to economize the genetic evaluation with a better accuracy. This research studies and develops in genetic evaluation of dairy cattle in the developed production set ups and explores the possibility of using RR-TDM for genetic evaluation of dairy cattle in Thailand.

Recommendations

The RR-TDM have been suggested as the method of choice for the analysis of milk yield traits in order to maximize the use of all available information. This method becomes even more important in countries with smaller herd size and without well-established milk recording schemes. In fact, the RR-TDM appears to be a better alternate of LM because early selection on the basis of TD could reduce generation interval. It could economize the genetic evaluation of dairy animals and improve accuracy of evaluation. However, under Thailand condition (i.e the small herd size pedigree information is not always available and breed variation is high at the farm level) applied the RR-TDM to genetic evaluation could be aware.

In further study, the HTD and residual variance for any animal might change across the lactation as the genetic variance change, so a variable residual variance across the lactation with function(s) of DIM could be investigated in the model.

Additionally, in the tropics countries, the values of THI could be associated with RR-TDM. Thus, THI could be considered in the further study.

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APPENDIX

PARAMETER FILE

```
# Generated by RENUMMAT; must be edited
DATAFILE
sss.prn
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
12
OBSERVATION(S)
7
WEIGHT(S)
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS
TYPE_OF_EFFECT  [EFFECT NESTED]
1 10878 cross          # HTD
3 1 cov                #BF
5 1 cov                #AGE
12 33 cross            #YS1
8 33 cov 12            #YS2
6 33 cov 12            #YS3
2 2321 cross           #pe1
8 2321 cov 2           #pe2
6 2321 cov 2           #pe3
2 4023 cross           #ag1
8 4023 cov 2           #ag2
6 4023 cov 2           #ag3
RANDOM_RESIDUAL VALUES
2.01
RANDOM_GROUP
7 8 9
RANDOM_TYPE
diagonal
FILE
```

```
(CO)VARIANCES
10.5 -0.329E-01 -0.307E-01
-0.329E-01 0.134E-03 0.620E-04
-0.307E-01 0.620E-04 0.172E-03
RANDOM_GROUP
10 11 12
RANDOM_TYPE
add_an_upg
FILE
redatped.prn
(CO)VARIANCES
5.75      -0.220E-01  -0.435E-02
-0.220E-01   0.102E-03   0.160E-04
-0.435E-02   0.160E-04   0.523E-05
RANDOM_GROUP
1
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
1.34
```

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