Factors Influencing Genetic Change for Milk Yield within Farms in Central Thailand*

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ABSTRACT : The objective of this study was to characterize factors influencing genetic improvement of dairy cattle for milk production at farm level. Data were accumulated from 305-day milk yields and pedigree information from 1,921 first-lactation dairy cows that calved from 1990 to 2007 on 161 farms in Central Thailand. Variance components were estimated using average information restricted maximum likelihood procedures. Animal breeding values were predicted by an animal model that contained herd-year-season, calving age, and regression additive genetic group as fixed effects, and cow and residual as random effects. Estimated breeding values from cows that calved in a particular month were used to estimate genetic trends for each individual farm. Within-farm genetic trends (b, regression coefficient of farm milk production per month) were used to classify farms into 3 groups: i) farms with negative genetic trend (b<-0.5 kg/mo), ii) farms with no genetic trend (-0.5 kg/mo≤b≤0.5 kg/mo), and iii) farms with positive genetic trend (b>0.5 kg/mo). Questionnaires were used to gather information from individual farmers on educational background, herd characteristics, farm management, decision making practices, and opinion on dairy farming. Farmer's responses to the questionnaire were used to test the association between these factors and farm groups using Fisher's exact test. Estimated genetic trend for the complete population was 0.29±1.02 kg/year for cows. At farm level, most farms (40%) had positive genetic trend (0.63±4.67 to 230.79±166.63 kg/mo) followed by farms with negative genetic trend (35%; -173.68±39.63 to -0.62±2.57 kg/mo) and those with no genetic trend (25%; -0.52±3.52 to 0.55±2.68 kg/mo). Except for educational background (p<0.05), all other factors were not significantly associated with farm group. (**Key Words :** Tropic, Dairy Cattle, Dairy Farmer, Selection, Breeding)

INTRODUCTION

Genetic improvement of dairy cattle for economically important traits, particularly milk yield, is an important component of an overall strategy to improve profitability and sustainability of dairy cattle operations. Characterization factors that affect genetic improvement, selection, and mating strategies in a population is essential to evaluate genetic improvement programs and determine areas that need to be improved.

Since commercial dairy production was begun in Thailand around 1960, number of dairy cattle and volume of milk yield has increased continuously. In 2009, the number of dairy cattle in Thailand was 483,899, and 42% of them were milking cows that produced 2,000 tons of milk per day (Department of Livestock Development, 2009). Efforts to increase milk production in Thailand combined with government policies resulted in widespread importation and use of Holstein (H) semen, and extensive use of high-percent H sires generated in Thailand by the Dairy Farming Promotion Organization (DPO) and the Department of Livestock Development (DLD). This mating strategy created the Thai multibreed dairy population. Currently, 90% of the population is over 75% H with small fractions of other breeds (Koonawootrittriron et al., 2002; 2009).

The level of genetic improvement of milk production in Thai dairy cattle populations during the last two decades has been small (less than 7 kg per year; Koonawootrittriron et al., 2004; Department of Livestock Development, 2008; Koonawootrittriron et al., 2009). These small genetic

changes for milk production suggest that selection and mating strategies used for genetic improvement in Thai dairy populations had limited success. However, these population estimates of genetic trends provide no information on genetic trends that occurred within individual farms. Genetic changes may vary among farms within a population. Within-farm genetic trends could be higher, similar, or lower than the genetic trend of the overall population. Factors that influence genetic improvement may vary across farms. Classification of farms according to the genetic trend of their cows would help identify factors that contributed to higher or lower milk production levels in individual herds. Differences among farmers (e.g., education background, experience, record keeping, decision making) were found to be important for farm milk production (Rhone et al., 2008; Sarakul et al., 2009; Yeamkong et al., 2010a). These differences among farmers may affect dairy genetic improvement within farms, and also genetic improvement of the whole population. Factors that affect the genetic improvement within farms will help identify common factors that influence genetic improvement across farms in Thai dairy populations. Inclusion of these factors in genetic evaluation models could improve the accuracy of genetic predictions and help increase the genetic trend toward higher production. Thus, the objective of this study was to characterize factors influencing genetic change for milk yield within farms in the multibreed dairy cattle population in Central Thailand.

MATERIALS AND METHODS

Animal and data

The dataset contained accumulated 305-day milk yield and pedigree information from 1,921 first lactation dairy cows that calved from 1990 to 2007 in 161 farms located in Central Thailand. The accumulated 305-day milk yield was calculated from monthly test-day milk yield using the test-interval method (Sargent et al., 1968; Koonawootrittriron et al., 2001). Monthly milk yields were computed using two consecutive test-day milk samples, and then added to obtain the accumulated 305-day milk yield. All cows in this dataset had their sire and dam indentified and complete information of breed composition, birth date, calving date, and drying of date. These 1,921 cows were the progeny of 488 sires and 1,649 dams.

Breeds presented in the population were Holstein (H), Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal, and Thai Native. Ninety two percent of cows in this population were crossbred, and the vast majority of them were composed of a large H fraction and a small fraction of other breeds. Furthermore, 81% of all cows in this population were more than 75% H. High H fraction cows were produced by artificial insemination of crossbred H cows with H sires

(83%) or high percent H crossbred sires (17%). The number of breeds represented in an individual cow ranged from 1 to more than 5. There were 160 cows (8%) composed of 1 breed, 372 cows (19%) composed of 2 breeds, 305 cows (16%) composed of 3 breeds, 512 cows (27%) composed of 4 breeds, 409 cows (21%) composed of 5 breeds, and 163 cows (9%) composed of more than 5 breeds. The extreme unbalancedness of breed representation in the population made it impossible to consider all breeds in the genetic analyses. Thus, following Koonawootrittriron et al. (2002) breeds were classified as Holstein (H) and other breeds (O), where O included all breeds other than H.

Climate, nutrition and management

The dairy farms that participated in this study were located in the Saraburi (Muaklek and Wang Muang), Lopburi (Pattananikom), and Nakorn Rachasima (Pak Chong) provinces, Central Thailand. The weather in this region was influenced by tropical monsoons. The southwest monsoon occurred from May to October, and the northeast monsoon occurred from October to February. During the years of the study (1990 to 2007), the average daily temperatures in this region ranged from 14.5°C to 34.2°C, the average relative humidity ranged from 33% to 97%, and the average rainfall was 1,112.5 mm per year. Seasons were classified as winter (November to February; cool (14.5°C to 31.6°C) and dry (65% RH, precipitation 50 mm/season)), summer (March to June; hot (20.8°C to 34.2°C) and dry (72% RH, precipitation 239 mm/season)) and rainy (July to October; hot (23.2°C to 31.8°C) and humid (77% RH, precipitation 624 mm/season)).

All farms in the study had less than 80 milking cows, except for one farm that had 190 milking cows. All farms kept cows in open barns. When weather was hot, some farmers (less than 10%) used fans inside the barn or sprinklers on top of the roof to reduce heat stress.

All dairy farms milked their cows twice a day. The first milking occurred early in the morning (04:00 to 04:30 AM), and the second milking was in the afternoon (02:30 to 03:00 PM). All farms used a bucket system for milking, except for one farm that used a pipeline system. Hand milking was used only for cows with colostrum or mastitis. All farms collected raw milk in 50 kg bulk tanks and then transported them to a dairy cooperative or to a private milk collection center after each milking (morning and evening).

Grasses used by farmers that participated in this study were Guinea (*Panicum maximum*), Ruzi (*Brachiaria ruziziensis*), Napier (*Pennisetum purpureum*), and Para (*Brachiaria mutica*). These grasses were produced within farms (56%), bought and cut and carried from other farms (20%), and from both sources (24%). Some farmers cut and carried Leucaena (*Leucaena leucocephala*; 18% to 22% CP and 55% to 73% TDN, DM basis), which generally grew

widely in public areas in this region, to supplement the ration of their cows (fresh, dried, or mixed with concentrate).

Most farmers (46%) preferred to purchase concentrate from commercial feed companies (The Charoen Pokpand Foods Public Co. Ltd., Bangkok, Thailand; Lee Feed Mill Public Co. Ltd., Bangkok, Thailand; Betagro Agro Group Co. Ltd., Bangkok, Thailand) rather than prepare concentrate themselves (35%), and only 19% of them did both (purchased concentrate and produced it in their farms). The concentrate contained from 15% to 19% CP and from 70% to 75% TDN (DM basis). Ingredients used in the concentrate ration were a protein source (e.g., palm meal, soybean meal, cotton seed meal, Leucaena), an energy source (e.g., cassava, rice bran, broken rice, fat from animals and plant, molasses), and mineral and vitamin sources (e.g., di-calcium, premixes).

Feed rations varied among farms, year and seasons. However, it was generally based on concentrate (12 to 15 kg/d, or considering 1 kg of concentrate per 2 kg of milk) and fresh grasses if available. Most farmers (56%) cut and carried green forage (approximately 22.10±17.19 kg/cow) from their own land or from public areas to feed cows, rather than let cows graze on pastures (20%). Lastly, 24% of farmers used both cut and carry green forage and direct pasture grazing.

Availability of forage in Central Thailand is limited, especially during the dry season (November to June). Number of days without rain in this region ranged from 25% (rainy; 30 days) to 43% (winter; 53 days). Water used for dairy farming in Central Thailand depends on water storage and underground water supply. When forage was not enough, rice straw, urea-treated rice straw, and crop residues (cassava leaves, corn cobs, and sugar cane tops) were used as sources of fiber. However, large amounts of concentrate were added to the ration in order to compensate the lack of good quality forage. All cows had free access to a mineral supplement throughout the year. Farmers bred their cows by artificial insemination all year round.

Genetic predictions

Accumulated 305-day milk yield and pedigree information of 1,921 first lactation cows were used for genetic prediction. A contemporary group was defined as a group of cows that were from the same farm, and calved in the same year and season. Calving age was calculated as the difference in months between calving and birth dates. All data (1,921 records) were genetically connected through sires with daughters in two or more contemporary groups.

Variance components were estimated by a Restricted Maximum Likelihood procedure (REML) using an average information algorithm (ASREML; Gilmour et al., 2000). The trait of interest, accumulated 305-day milk yield, was assumed to have only direct additive genetic effects. The model used was a single trait mixed animal model. Fixed environmental effects were contemporary group (herd-year-season) and regression of milk yield on calving age. Fixed additive genetic group effects were defined as the regression of milk yield on the H fraction of cows and it estimated the difference between H and O. Thus, the mixed animal model contained contemporary group, calving age, and additive genetic group as fixed effects, and animal additive genetic effects and residual as random effects. Random additive genetic effects were assumed to have mean zero and variance-covariance matrix equal to the matrix of additive relationships times the additive genetic variance for accumulated 305-day milk yield. Residual effects were assumed to have mean zero, a common variance, and be uncorrelated. Genetic predictions were computed using the ASREML software package (Gilmour et al., 2000). Estimated breeding values (EBV) for individual animals were computed as the sum of additive genetic group effects and random additive animal genetic effects (Koonawootrittriron et al., 2002).

Genetic trends

The genetic trend for the whole population was computed as the linear regression coefficient of yearly mean cow EBV on calving year using data from all farms. Genetic trends for individual farms were estimated as within-farm regression coefficients (b) of monthly mean cow EBV on month of calving within a farm. The REG procedure of the SAS program (SAS, 2003) was used to estimate regression coefficients. Within-farm regression coefficients (b) were used to classify farms into 3 groups: i) farms with negative genetic trend (b<-0.5 kg/mo), ii) farms with no genetic trend (-0.5 kg/mo≤b≤0.5 kg/mo), and iii) farms with positive genetic trend (b>0.5 kg/mo).

Questionnaire data and association tests

Questionnaires were used to gather information from individual farmers on educational background, herd characteristics, farm management, decision making practices, and opinion on dairy farming. Educational background was classified as primary school, high school, and bachelor degree. Experience was defined as number of years in dairy farming until 2009. Number of milking cows was used to classify farms into small (less than 10 milking cows), medium (10 to 19 milking cows) and large (more than 19 milking cows). Farm workers were classified into family members, hired persons, and both family members and hired persons. Data recording was defined as records kept or no records kept. The main roughages used were green grasses, rice straw, and silages (corn or grass). The systems used to feed roughage were cut and carry, pasture grazing, and both cut and carry and pasture grazing. Source

of roughage was classified as grown within farm, purchased, and both grown within farm and purchased. Decision making on sire selection was classified as without help and with help. Advisors for sire selection were classified as government officials, other farmers, academic people, and no one. Preferred breed group of sires were purebred H, crossbred H, and other breeds.

The questionnaires were distributed to 161 farms from March to April of 2009. A total of 31 farms completed and returned the questionnaires (19 percent return rate). This low return rate may have been because farmers were unable to understand and complete the questionnaire, incorrect farmer addresses, and farms in the mailing list that were out of business. Questions that were filled out improperly were followed up by phone calls to the farmers. Farmers' answers were then used to study what factors had influenced genetic improvement for milk production at farm level. The association between years of dairy experience, number of milking cows, and number of workers and farm group (farms with negative genetic trend, farms with no genetic trend and farms positive genetic trend) was evaluated with an F-test. The association between the classification levels of the remaining factors in the questionnaires (education, size of farm, type of worker, source of information, source of sires, data recording, milking type, type of roughage, roughage feeding system, source of roughage, decision making on sire selection, advisors for sire selection, and preferred breed group of sires) and the 3 farm groups was assessed using Fisher's exact test (Agresti, 1992).

RESULTS AND DISCUSSION

Genetic variances and genetic parameters

Variance component estimates for accumulated 305-day milk yield were $212,003\pm50,840$ kg^2 for genetic variance and $628,043\pm25,050$ kg^2 for phenotypic variance. These genetic and phenotypic variance estimates were higher than a study with data from farms across Thailand (Sanpote and Buaban, 2003; 181,220 kg^2 and 553,060 kg^2), but lower than a study using data from farms in Northern Thailand (König et al., 2005; 250,518 kg^2 and 711,704 kg^2). Although variance estimates differed among Thai dairy populations, estimated values suggested genetic selection for milk production would be feasible in these populations.

The heritability estimate for accumulated 305-day milk yield was 0.34 ± 0.08. The heritability estimate in Central Thailand was similar to values reported for other dairy populations in Thailand (h^2 = 0.33, Sanpote and Buaban, 2003; h^2 = 0.34, König et al., 2005) and within the range of estimates reported for other countries (h^2 = 0.21 to 0.45; e.g., Visscher and Goddard, 1995; Jakobsen et al., 2002; Muir et al., 2004; Perez-Cabal et al., 2006). The heritability estimate of 0.34 ± 0.08 obtained here suggested that genetic improvement of dairy cattle for milk production would be effective in Central Thailand. This would require dairy producers to select sires based primarily on their EBV for milk production.

Population genetic and phenotypic trends

Cow estimated breeding values (EBV) for accumulated 305-d milk yield ranged from 55.83 ± 40.48 kg (1991) to 132.21 ± 34.09 kg (1993). The estimated genetic trend from 1990 to 2007 was 0.29 ± 1.02 kg/year (Figure 1). On the other hand, cow estimated phenotypic values (EPV) for this trait ranged from $3,528.27\pm144.24$ kg (1993) to $4,423.80\pm124.35$ kg (2000). The estimated phenotypic trend from 1990 to 2007 was 14.57 ± 10.63 kg/year.

The genetic trend obtained here was similar to that reported by Seangjun et al. (2009; 0.55 kg/year from 1998
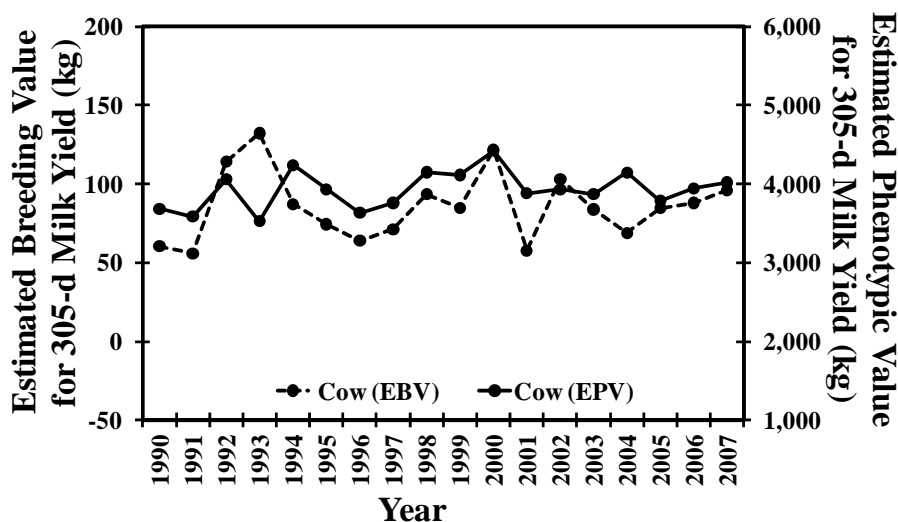

Figure 1. Genetic and phenotypic trends for 305-d milk yield of cows from 1990 to 2007.

Table 1. Genetic trends for 305-d milk yield (kg/mo) classified by farm group

Farm group	Number of farms (%)	Genetic trend for 305-d milk yield (kg/mo)	
		Minimum	Maximum
Farms with negative genetic trend	33 (35%)	-173.68±39.63	-0.62±2.57
Farms with no genetic trend	23 (25%)	-0.52±3.52	0.55±2.68
Farms with positive genetic trend	37 (40%)	0.63±4.67	230.79±166.63

to 2006), but it was lower than genetic trends reported by Department of Livestock Development (2008; 4.28 kg/year from 1989 to 2005) and Koonawootrittriron et al. (2009; 6.50 kg/year from 1991 to 2005). All estimated genetic trends for accumulated 305-d milk yield in Thai dairy populations were small compared to those reported for dairy cattle in other countries (120 to 173 kg/year; Legates and Myers, 1988; Burnside et al., 1992; Meinert and Pearson, 1992). The low estimate of genetic trend and its high standard error (0.29±1.02 kg/year) indicated that there was improvement for milk production from 1990 to 2007 in Central Thailand. Selection and mating strategies need to be improved in this population if milk production is to be increased. Higher levels of milk production will increase the competitiveness and sustainability of dairy farms in this region.

A large scale dairy genetic evaluation program in Thailand was created in 1996 with the involvement of the Dairy Farming Promotion Organization (DPO) and Kasetsart University. A multibreed genetic evaluation system was implemented in 2002 through collaboration with the University of Florida, USA. Estimated breeding values (EBV) for purebred and crossbred animals are routinely computed for economically important traits (milk yield, fat yield, fat percentage, lactation length, age at first calving, and lactation pattern) in the multibreed dairy population controlled by the DPO. The EBV are published and distributed to farmers in the yearly DPO Sire and Dam Summary (Dairy Farming Promotion Organization, 2009). The Department of Livestock Development (DLD) began to publish a dairy genetic evaluation in 2004 using data from farmers associated to 7 Artificial Insemination Services Centers located around the country. It currently evaluates animals for milk yield, fat yield, fat percentage, protein yield, protein percentage, age at first calving, and 17 type traits using animal models. These evaluations are published yearly in the DLD Dairy Sire Summary (Department of Livestock Development, 2008).

Genetic predictions published by these two genetic evaluation programs are useful for sire and dam selection under Thai environmental conditions. However, most Thai dairy farmers, especially small holders, cannot afford to have in-farm storage of semen of their preferred sires. Thus, sires used by farmers have been primarily those whose semen was available in the tanks of visiting artificial inseminators. This situation has prevented farmers from choosing sires based on their genetic ability for economically important traits (Koonawootrittriron et al., 2002). Consequently, the low genetic trend observed in Central Thailand was not related to availability of genetic prediction information of the sires, but to inadvisable choice of sires based on semen availability or suggestions by artificial inseminators. Increasing the level of training of artificial inseminators and dairy farmers on the use of EBV for sire selection would greatly help using of superior sires for milk production. The effectiveness of this training would be reflected in higher positive genetic trends for this trait in Central Thailand in future years.

Farm groups classified by genetic trends

Within farm genetic trends for accumulated 305-day milk yields ranged from -173.68±39.63 kg/mo to 230.79±166.63 kg/mo. The difference between the highest and the lowest genetic trend was approximately 404.47 kg/mo. Table 1 shows genetic trends by farm group. Most farms had a positive genetic trend (40%; 0.63±4.67 kg/mo to 230.79±166.63 kg/mo), followed by farms with a negative genetic trend (35%; -173.68±39.63 kg/mo to -0.62±2.57 kg/mo) and farms with no genetic trend (25%; -0.52±3.52 kg/mo to 0.55±2.68 kg/mo). Farms that had either a negative genetic trend (35%) or no genetic trend (25%) constituted 60% of the total (Figure 2). The similar proportion of farms with positive (40%) and negative
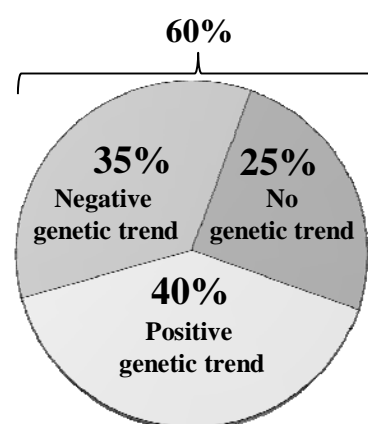

Figure 2. Frequency of groups of farms classified by genetic trend (negative genetic trend, no genetic trend, and positive genetic trend).

Table 2. Least squares means and standard errors for dairy experience, number of milking cows, and number of workers by farm group

Factor	Farm group			F-test
	Negative genetic trend	No genetic trend	Positive genetic trend	p-value
Dairy experience (yr)	21.64±2.06	22.00±2.71	17.00±2.56	0.3063
Number of milking cows	31.00±9.28	54.00±13.66	27.81±11.82	0.3069
Number of workers	3.28±0.64	4.87±0.84	3.13±0.84	0.2634

genetic trends (35%) largely determined the low overall genetic trend for milk production of the population.

Differences among individual farms explained from 30% and 52% of the total variation for milk yield per cow and per farm in Central Thailand (Yeamkong el al., 2010b). Thus, the 3 farm groups identified here should be supported differently. The same technology or strategy might not be suitable for all farmers to improve genetic for milk production of their dairy cattle. Farmer willingness or ability to accept new knowledge, entrepreneurial capability, experience, and access information resources may have influenced within-farm genetic trends. A genetic improvement strategy in Central Thailand could consider the promotion of farms with positive genetic trends as demonstration farms. Thus, although all farmers would benefit from continuous training and support from private, semi-private, or government organizations, personnel in farms with no or negative genetic trends should be provided with additional training and support in selection of sires and dams tailored to their dairy background and experience.

Education, herd characteristics, and farm management

Owners of farms with no genetic trend had the highest level of experience (22.00±2.71 years), number of milking cows (54.00±13.66 cows), and number of workers (4.87± 0.84 workers), followed by owners of farms with negative genetic trends and with positive genetic trends (Table 2). However, differences among the 3 farm groups were not statistically different. Farmers in the 3 farm groups (negative, no, and positive genetic trend) had farms of similar size, type of workers, sources of information, sources of sire semen, and data recording, but differed in their educational background (p<0.05; Table 3). In addition, farmers in the 3 farm groups employed a similar milking

Table 3. Frequency and percentage of farms by education, size of farm, type of worker, source of information, source of sire, and data recording×farm group combination

Factor	Farm group						Fisher's exact test
	Negative genetic trend		No genetic trend		Positive genetic trend		
	Freq.	%	Freq.	%	Freq.	%	p-value
Education							0.04
Primary school	10	71	1	13	6	67	
High school	1	7	3	37	2	22	
Bachelor degree	3	22	4	50	1	11	
Size of farm							1.00
Medium size	4	31	2	33	2	25	
Large size	9	69	4	67	6	75	
Type of worker							0.21
Family members	8	57	7	88	6	76	
Hired persons	0	0	0	0	1	12	
Both	6	43	1	12	1	12	
Source of information							0.76
Magazines and books	7	50	5	64	4	44	
Cooperative and milk center	1	7	1	12	2	22	
Consultant	0	0	1	12	1	12	
Government	2	14	0	0	0	0	
Other farmers	4	29	1	12	2	22	
Source of sires							0.78
Thailand	5	38	3	38	2	22	
Other countries	9	62	5	62	7	78	
Data recording							0.22
Records kept	10	71	3	37	7	78	
No records kept	4	29	5	63	2	22	

system, type of roughage, roughage feeding system, and source of roughage (Table 4).

Educational background was significantly associated (p<0.05) with farm groups (Table 3). The proportion of farmers that had primary school, high school and bachelor degree were 71%, 7%, and 22% for farms with a negative genetic trend, 13%, 37%, and 50% for farms with no genetic trend, and 67%, 22%, and 11% for farms with a positive genetic trend, respectively. Most owners of farms with negative genetic trends (71%) and positive genetic trends (67%) had primary school education. On the other hand, owners of farms with no genetic trend (50%) had a bachelor degree, the highest educational level of all farm groups. Thus, although there was an overall association between educational background and farm group, there appears to be no relationship between the level of formal education and farm genetic trends. However, it should be pointed out that bachelor degrees of all farmers in this study were unrelated to agriculture or dairy production (mechanics, accounting, management, and education).

Farms participating in this study were either medium size (10 to 19 milking cows) or large size (more than 19 milking cows). No farms in this study were small size (less than 10 milking cows). A similar proportion of farms with negative, no, and positive genetic trend was observed in medium size farms (31% with negative genetic trend, 33% with no genetic trend, and 25% with positive genetic trend; and in large size farms (69% with negative genetic trends, 67% with no genetic trends, and 75% with positive genetic trends; Table 3). Most farms employed family members as workers (57% farms with negative genetic trend, 88% farms

with no genetic trend, and 76% farms with positive genetic trend; Table 3).

The main sources of current dairy farming information and technology for dairy farmers were magazines and books (50% of farms with negative genetic trend, 64% of farms with no genetic trend, and 44% of farms with positive genetic trend; Table 3). Farmers that kept dairy records owned 29% of farms with negative genetic trends, 63% of farms with no genetic trend, and 22% of farms with positive genetic trends. Most farmers in all farm groups preferred foreign sires to Thai born sires (62% of farms with negative genetic trend, 62% of farms with no genetic trend, and 78% of farms with positive genetic trend).

Almost all farms in all farm groups used a bucket system for milking (93% of farms with negative genetic trend, 100% of farms with no genetic trend, and 100% of farms with positive genetic trend). Cows in the majority of farms with no genetic trend (Table 4) were fed green grasses (50%) and rice straw (50%). Most farmers in this group (50%) used both cut and carry and pasture grazing to feed roughage to their cows, and their primary source (50%) was roughage grown within their farms or purchased from an outside source (Table 4).

Most farms with positive (64%) and negative genetic trends (56%) used rice straw as the main type of roughage for their cows (Table 4). Farmers in these 2 farm groups used cut and carry as the primary mean to supply roughage feeding to cows (63% for farms with positive genetic trend and 64% for farms with negative genetic trend). Most of these farmers produced roughage within their farms (63% of farms with positive genetic trend and 64% of farms with

Table 4. Frequency and percentage of farms by milking type, main roughage, main roughage feeding and source of roughage factors×farm group combination

| Factor | Farm group | | | | | | Fisher's exact test p-value |
| | Negative genetic trend | | No genetic trend | | Positive genetic trend | | |
	Freq.	%	Freq.	%	Freq.	%	
Milking type							1.00
Bucket	13	93	8	100	9	100	
Pipeline	1	7	0	0	0	0	
Type of roughage							0.91
Green grasses	4	29	4	50	3	33	
Rice straw	9	64	4	50	5	56	
Corn or grass silage	1	7	0	0	1	11	
Roughage feeding system							0.44
Cut and carry	7	64	2	33	5	63	
Pasture grazing	3	27	1	17	1	12	
Both	1	9	3	50	2	25	
Source of roughage							0.44
Grown within farm	7	64	2	33	5	63	
Purchased	3	27	1	17	1	12	
Both	1	9	3	50	2	25	

negative genetic trend; Table 4).

Educational background of farmers, herd characteristics, and farm management in this study were similar to farms located in the Northeast (Sarakul et al., 2009), South (Sarakul et al., 2009), and Central regions of Thailand (Sarakul et al., 2009; Yeamkong et al., 2010b). Low genetic trends for milk production in Central Thailand suggested a problem in sire and dam selection at farm level. Considering the similarities among farm and farmers in Northeast, South, and Central Thailand, it is likely improvement in the strategy for sire and dam selection is needed in all these regions. Thus, a strategic plan to train and educate farmers, artificial inseminators, and supporting organizations on genetic selection of animals that encompasses all Thai regions may be a more effective approach than tackling this problem on a regional basis.

Decision making on sire selection

Farmers in most farms with negative (64%) and no genetic trends (62%) made decisions on sire selection by themselves rather than with input from other people (Table 5). Contrarily, farmers in farms with positive genetic trends made decisions on sire selection primarily based on outside input (75%). These different approaches to choosing sires may be related to the years of experience of farmers that owned farms with negative (21.64±2.06 years), no genetic trend (22.00±2.71 years), and positive genetic trend (17.00±2.56 years). Farmers with longer farm experience may have been more confident in their knowledge of animal breeding, thus they did not consult with other people, and they had less updated information on genetic selection of animals. However, the association between decision making on sire selection and farm groups was not significant. Decision making on sire selection was also found not to be

important for monthly milk production in Central Thailand (Yeamkong et al., 2010a). The proportion of farm owners with negative and no genetic trends that made sire selection decisions by themselves was twice as large as the proportion of farm owners that sought advice from other people. Further, Sarakul et al. (2009) reported that most farmers in North, Northeast, Central, and Southern Thailand had insufficient knowledge and options to appropriately select sires. These results reiterate the need to raise the understanding dairy farmers on the use of EBV for sire and dam selection through a program of training and dissemination of educational material. This program should also include training in data recording and its importance for genetic evaluation and selection of sires and dams as well as its impact on genetic trends within farms and in the complete population.

When farmers asked other people for help on sire selection, farmers with negative (36%) and positive genetic trends (67%) usually consulted with government officials rather than other farmers or academic people, or they sought input from no one (Table 5). A wide range of knowledge and understanding of genetic evaluation and sire selection by government officials that advised farmers on sire selection may help explain the large percent of farmers with negative genetic trends that sought their advice. Thus, periodic updating and training of government officials providing advice to farmers on genetic evaluation and selection of animals seems an appropriate part of an overall strategy for genetic improvement of dairy cattle in Thailand. In contrast, most farms with no genetic trend sought no outside help (43%; Table 5). Yeamkong et al. (2010a) reported that farmers that selected sires by themselves had higher monthly milk yield and revenue per farm and per cow than farmers that selected sires with help from other

Table 5. Frequency and percentage of farms by decision making on sire selection, advisors for sire selection, and preferred breed group of sires×farm group combination

Factor	Farm group						Fisher's exact test p-value
	Negative genetic trend		No genetic trend		Positive genetic trend		
	Freq.	%	Freq.	%	Freq.	%	
Decision making on sire selection							0.25
Without help	9	64	5	62	2	25	
With help	5	36	3	38	6	75	
Advisors for sire selection							0.77
Government officials	5	36	2	29	6	67	
Other farmers	3	21	1	14	1	11	
Academic people	2	14	1	14	0	0	
No one	4	29	3	43	2	22	
Preferred breed group of sires							0.77
Purebred Holstein	5	36	3	38	4	44	
Crossbred Holstein	9	64	4	50	5	56	
Other breeds	0	0	1	12	0	0	

people. Thus, this group of farmers appears to have developed an economically sound strategy for dairy production that involves semen, sires, and replacement heifers that fit their economic model rather than focusing on genetic progress. However, this group of farmers would benefit from external advice on choosing semen from sires that have higher EBV than similarly priced sires currently used in these herds.

The preferred group of sires in all farm groups (Table 5) was crossbred Holstein (64% of farms with negative genetic trend, 50% of farms with no genetic trend, and 56% of farms with positive genetic trend). This preference indicates that Thai dairy producers were seeking dairy cows with high percent H, but not 100% H, likely due to their superior milk production, adaptability and reproduction efficiency under Thai tropical environmental conditions. Koonawootrittriron et al. (2009) reported that cows between 75% H and less than 100% H had higher milk production than purebred H.

Thus, except for educational background, all 3 types of farms (negative genetic trend, no genetic trend, and positive genetic trend) had similar experience, number of milking cows, number of workers, type of worker, size of farm, source of information, data recording, source of sires, data recording, milking system, type of roughage, roughage feeding system, source of roughage, decision making on sire selection, advisor for sire selection, and preferred group of sire used by farmers. Lack of significance of these effects may have been partly due to the low number of returned questionnaires. Thus, this research needs to be repeated with a substantially larger number of questionnaire responses from Central Thailand to reevaluate results obtained here. This study needs also to be extended to all dairy regions in Thailand to gain a more thorough understanding on the factors associated with genetic improvement of dairy cattle within farms at both regional and national levels. Subsequently, information on factors associated with within-farm genetic trends could be regularly collected to aid in the development of more accurate genetic evaluation models and procedures to speed up genetic improvement for milk production under the hot and humid environmental conditions of Thailand.

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