Somatic Cells Count and Its Genetic Association with Milk Yield in Dairy Cattle Raised under Thai Tropical Environmental Conditions

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ABSTRACT: Somatic cells count (SCC), milk yield (MY) and pedigree information of 2,791 first lactation cows that calved between 1990 and 2010 on 259 Thai farms were used to estimate genetic parameters and trends for SCC and its genetic association with MY. The SCC were log-transformed (lnSCC) to make them normally distributed. An average information-restricted maximum likelihood procedure was used to estimate variance components. A bivariate animal model that considered herd-yr-season, calving age, and regression additive genetic group as fixed effects, and animal and residual as random effects was used for genetic evaluation. Heritability estimates were 0.12 (SE = 0.19) for lnSCC, and 0.31 (SE = 0.06) for MY. The genetic correlation estimate between lnSCC and MY was 0.26 (SE = 0.59). Mean yearly estimated breeding values during the last 20 years increased for SCC (49.02 cells/ml/yr, SE = 26.81 cells/ml/yr; p = 0.08), but not for MY (0.37 kg/yr, SE = 0.87 kg/yr; p = 0.68). Sire average breeding values for SCC and MY were higher than those of cows and dams (p<0.01). Heritability estimates for lnSCC and MY and their low but positive genetic correlation suggested that selection for low SCC may be feasible in this population as it is in other populations of dairy cows. Thus, selection for high MY and low SCC should be encouraged in Thai dairy improvement programs to increase profitability by improving both cow health and milk yield. (**Key Words:** Dairy Cattle, Milk Yield, Selection, Somatic Cell Count, Tropics)

INTRODUCTION

Mastitis is one of the most important diseases in the dairy industry, that causes widespread losses due to reduced milk production and milk quality, discarded milk, and increased health care costs. Thus, mastitis control programs have been implemented to prevent mastitis on farms through proper hygiene and management practices (The National Mastitis council (NMC), 2006). In addition, genetic selection has been used to prevent or resist mastitis of cows either directly or indirectly (de Haas et al., 2002; Ødegård et al., 2002). Direct methods involve selection based on appearance of clinical mastitis in individual animals. However, this method is not widely practiced because the appearance of clinical mastitis has very low heritability (0.02 to 0.05) and it is difficult to measure (Mrode and Swanson, 1996; Rupp and Boichard, 1999). Indirect methods use selection on indicator traits such as somatic cell count (SCC), which has a higher heritability

than the appearance of clinical mastitis (Rupp and Boichard, 1999). The genetic correlation between the appearance of clinical mastitis and SCC is high (0.7 to 0.8; e.g., Rupp and Boichard, 1999; Kadarmideen and Pryce, 2001; Carlén et al., 2004), thus selection to decrease SCC should increase resistance to mastitis (Shook and Schutz, 1994).

Lactation average of SCC is generally used for genetic improvement to prevent mastitis. Heritability estimates for lactation average of SCC ranged from 0.05 to 0.17 (e.g., Ødegård et al., 2002; Carlén et al., 2004). Genetic correlation estimates between SCC and milk yield have been found to be low and positive (0.13 to 0.22; Rupp and Boichard, 1999; Carlén et al., 2004). Emphasis by most dairy breeding programs on selection for milk yield alone may have resulted in an increase in cow mastitis. Including SCC in dairy breeding programs may counteract undesirable correlated responses resulting from selection for milk yield. Several studies have shown higher genetic gain for overall economic value when selection for mastitis resistance was included in breeding programs than by selecting for milk yield only (Rogers, 1993; Colleau and le Bihan-Duval, 1995).

Thailand is a tropical country in Southeast Asia whose weather usually has high temperatures and humidity (Thai

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Meteorological Department, 2006). Since 1957, milk production has been based on crossbred Holstein (H) cows resulting from the upgrade of local stock to H using genetics from imported sires (77%) as well as sires born in Thailand (23%). Sires have been selected primarily based on their ability for high milk production. However, SCC and mastitis have continued to increase in the Thai dairy population (11.36 cells/ml/yr-season; Yeamkong et al., 2010). Thus, the objective of this study was to estimate genetic parameters and trends for SCC and its association with milk yield using individual information from dairy cows raised in farms under Thai tropical environmental conditions.

MATERIALS AND METHODS

Animal and management

Data consisted of somatic cells count (SCC) and milk yield (MY) of 2,791 first lactation dairy cows that calved between 1990 and 2010 in 259 farms located in Thailand. All cows had their sires and dams identified and their expected breed composition was known (e.g., 3/4 Holstein, 1/8 Brahman, 1/16 Red Sindhi, 1/16 Sahiwal). Breeds represented in this population were Holstein (H), Brahman, Jersey, Red Dane, Red Sindhi, Sahiwal and Thai Native. Nearly all cows in this population (94%) were H crossbreds, and the remaining 6% were purebred H. The average H fraction of cows was 87.5% (minimum = 3%; maximum = 100%). Cows were the progeny of 624 sires and 2,407 dams. Sires represented in the population were H (520 sires), crossbred H (99 sires) and Jersey sires (5 sires). Most sires were imported (482 sires) and the rest were produced by the Dairy Farming Promotion Organization (DPO; 65 sires) and the Department of Livestock Development (DLD; 77 sires). Purebred and crossbred animals in this population were used as parents (a multibreed dairy population). However, it was unfeasible to consider all breeds in the genetic analysis due to the small size of the dataset and unbalanced breed compositions. Thus, following Koonawootrittriron et al. (2002b), breeds other than H were grouped together resulting in two breed groups: H and Other breeds (O).

Weather in Thailand is generally hot (17° to 36° Celsius) and humid (69 to 79% Relative Humidity). Rainfall is approximately 1,214 mm/yr. Weather characteristics are influenced by tropical monsoons (Thai Meteorological Department, 2006). Seasons are winter (November to February), summer (March to June), and rainy (July to October). Dairy cows were fed 12 to 15 kg/d of concentrate (15 to 40% of CP, 63 to 83% of NFE), equivalent to approximately 1 kg of concentrate per 2 kg of milk. Concentrate was either mixed by the farmers themselves or bought from local companies. Green roughage (*Penicum maximum*, *Brachiaria ruzziensis*,

Penisetum parpurium, and *Brachiaria mutica*) were cut and carried to animals only in the rainy season (July to October) and in irrigated areas. When green roughage was limited, especially in the dry season (November to June), silage (grass, corn, leucaena), crop residues, agricultural byproducts, and rice straw were given to cows. Cows were housed in open barns and some farms (less than 10%) used fans or sprinklers on the rooftops to reduce heat stress. Farmers bred their cows only by artificial insemination all year round. Semen was chosen based on availability, price or genetic ability mainly for increasing milk production. Culling was practiced when cows had health or reproductive problems.

Most dairy farms (66% of all farms; n = 171) in this study had less than 10 milking cows, 8% (n = 21) had 10 to 20 milking cows, and the remainder (26% farms; n = 67) had more than 20 milking cows. In each farm, cows were milked twice a day; firstly in the morning (05:00 to 7:00 am) and secondly in the afternoon (03:00 to 05:00 pm). Farmers milked their cows using a bucket-type system. Test-day milk yields were measured and samples taken from each individual cow once a month after calving until drying off. Monthly milk samples of cows were sent to a laboratory for quality analysis (fat, protein, solids not fat, total solids, lactose, and somatic cell count).

Data preparation and statistical analyses

Monthly test day SCC records collected after calving until the month of 305 d in milk were used to calculate the average SCC for 305-d. Unfortunately, the distribution of SCC was not normal (skewed distribution). Thus, SCC were transformed using natural logarithms (lnSCC = $\log_e$ [SCC]; Ali and Shook, 1980) and then the lnSCC were used to estimate variance components and to compute genetic predictions. Monthly test day milk yields of individual cows were used to calculate the accumulated 305-d MY using the test interval method following the computational expression below (Koonawootrittriron et al., 2002a):

$$MY305 = (P_1 \times D_1) + \sum_{i=2}^{k}\left[\left(\frac{P_i + P_{i-1}}{2}\right)\right] + (P_{k+1} \times D_{k+1})$$

Where MY305 is the milk yield of a cow adjusted to 305 d of lactation, P_1 is the milk yield of the test-day in the first month after calving, D_1 is the interval between five days after calving and the first day of the first month sampled, P_i is the test-day milk yield in month i (i = 2, …, k), P_{k+1} is the test-day milk yield in the month when 305 days in lactation was achieved, and D_{k+1} is the interval between the 305th d of lactation and the last day of the month prior to achieving 305 d of lactation. Population averages and SD were 496.72 (SD = 725.07)$\times 10^3$ cells/ml for SCC, 5.54 (SD = 1.16) for lnSCC, and 4,090.65 (SD =

1,127.53) kg for MY.

Contemporary groups were defined as groups of cows that calved in the same herd, year and season. There was a total of 746 connected contemporary groups with a mean of 4 cows per contemporary group (minimum = 2; maximum = 29). Connectedness between sires and contemporary groups was assessed using program THAICSET (Elzo, 2000) and contemporary groups with a single sire were eliminated. The resulting connected dataset had a minimum of 2 sires and a maximum of 14 sires per contemporary group.

Data were analyzed using a bivariate multibreed animal model that included contemporary group (i.e., herd-year-season), calving age and regression additive genetic group deviation (H - O) as fixed effects, and animal additive genetic and residual as random effects. Regression additive genetic groups were not estimable (i.e., neither H nor O were estimable). However, their difference (i.e., H - O) was estimable, thus the regression additive genetic group was defined as the difference between H and O. This was accomplished by setting the solution for O equal to zero when solving the mixed model equations, thus the expectation of the solution for H was H - O. Variance components were estimated using an Average Information-Restricted Maximum Likelihood procedure. Variance component estimates and genetic predictions were computed using ASREML (Gilmour et al., 2000). The bivariate multibreed animal model can be described as follows in matrix notation (1):

$$y = Xb + Z_{ga}g_a + Z_a a_a + e \qquad (1)$$

where,

y = vector of cow lnSCC and MY,

b = vector of contemporary groups (herd-year-season) and calving ages,

g_a = vector of regression additive genetic group deviations (i.e., H - O),

a_a = vector of animal additive genetic effects,

e = vector of residuals,

X = matrix of 1's, calving ages, and zeroes relating elements of vector y to vector b,

Z_{ga} = matrix of expected H fractions of cows relating elements of vector y to vector g_a,

Z_a = matrix of 1's and zeroes relating elements of vector y to vector a_a,

The assumptions of the model were (2):

$$\begin{bmatrix} y \\ a_a \\ e \end{bmatrix} \sim MVN \left(\begin{bmatrix} Xb + Z_{ga}g_a \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} Z_a G_a Z_a + R & Z_a G_a & R \\ G_a Z_a & G_a & 0 \\ R & 0 & R \end{bmatrix} \right) \qquad (2)$$

where, $G_a = G_0 \otimes A$, where G_0 is the matrix of additive genetic covariances between lnSCC and MY, A is the numerator relationship matrix and $\otimes$ represents direct product, and R = Residual covariance matrix.

The heritabilities of lnSCC and MY, and the genetic correlation between these 2 traits were computed using the estimated variances and covariances. The estimated breeding value ($\hat{u}_{aij}$) of each animal was computed as the sum of the predicted random additive genetic effect of the animal ($\hat{a}_{aij}$) plus the product of the estimated regression additive genetic group effect ($\hat{g}_a$) times the H fraction of the animal (Koonawootrittriron et al., 2002b). The SCC EBV of individual animals were computed by applying an exponential transformation to lnSCC EBV. Then, yearly mean EBV for SCC and MY for all animals, sires, dams and cows were computed. Regression coefficients of mean EBV for SCC and MY on calving years were estimated for animals, sires, dam and cows using the REG procedure in SAS (SAS, 2003). Least squares means (LSM) of sires (i.e., all sires, imported sires and local sires), dams and cows were computed and then they were used for comparison.

RESULTS AND DISCUSSION

Factors affecting SCC and MY

Least squares means (LSM) across herd-year-season subclasses ranged from 1.49 (SCC = 4.45×10^3 cells/ml) to 6.30 (SCC = 546.21×10^3 cells/ml) for lnSCC, and from 972.4 to 7,767.0 kg for MY. These values indicated large differences for both SCC (541.66×10^3 cells/ml) and MY (6,795 kg) between the best and worst management and environment conditions within particular herd-year-seasons. Cows that calved in the rainy season had higher SCC ($65.21 \pm 10.93 \times 10^3$ cells/ml) than cows that calved in summer ($46.37 \pm 11.66 \times 10^3$ cells/ml) and winter ($39.55 \pm 11.35 \times 10^3$ cells/ml). Conversely, cows that calved in the rainy season had lower MY ($3,498.42 \pm 60.09$ kg) than cows that calved in winter ($3,648.91 \pm 62.09$ kg) and summer ($3,858.30 \pm 62.60$ kg).

The undesirable results for both SCC and MY in the rainy season may have been associated with harsh environmental conditions during this season and management limitations of farmers. Although there was sufficient green roughage to feed cows in the rainy season, farmers had limited land and clean resting areas for their cows. Almost all farms in this population were small (i.e., had less than 10 milking cows) and the average farm size was 4 acres (SD = 6 acres). Most farms had problems with water drainage during the rainy season (Rhone et al., 2008). The floor of most resting areas was soil that became muddy when excess water could not be drained out. These conditions affected normal daily living, health status, and sanitation of cows. Cows that had to stand in mud were not able to have a normal life and behavior. These

environmental conditions increased chances for spreading of mastitis-causing organisms and created opportunities for teat infection and disease before and after milking times (Petersson et al., 2010). Cows lost their normal health status because they did not have enough rest and sleep. These results suggest that cow management needs to be improved, management variation among seasons should be reduced, and barns should be well bedded, dry, clean, and comfortable (NMC, 2006) in order to improve SCC and MY across lactations.

Level of H in cows was associated with SCC (p<0.01) but not with MY (p = 0.27). Cows with a high H fraction tended to produce more milk but they also had higher SCC. Regression coefficients of the two traits on additive genetic group (H-O) were $11.63\pm2.37\times10^3$ cells/ml for SCC and 172.00 ± 205.40 kg for MY. These results implied that upgrading dairy cows to H under these Thai environmental conditions was favorable for milk production but unfavorable in terms of mastitis resistance and health status. Among Thai H crossbreds, cows with high H fraction were found to have higher levels of heat stress especially cows with more than 93.7% H fraction (Boonkum et al., 2011). In order to achieve or maintain high levels of milk production under Thai tropical environmental conditions, H cows and cows with high H fractions would need more intensive care and management (feeding, housing, milking, health care) than cows with lower H fractions (Koonawootrittriron et al., 2009; Boonkum et al., 2011). These additional practices increase dairy production costs. Thus, farmers need to consider cows with H fractions that fit well with the nutritional, management, health, and physical environmental conditions of their farms in order to enhance the efficiency and profitability of their dairy operations.

Genetic variation and parameters

Variance components and genetic parameters for lnSCC and MY are reported in Table 1. Heritability estimates were 0.12 (SE = 0.19) for lnSCC and 0.31 (SE = 0.06) for MY. The heritability estimate for lnSCC in this dairy population

was within range values reported in other countries (0.10 to 0.17; Mrode and Swanson, 1996; Rupp and Boichard, 1999; de Hass et al., 2002). Although the heritability value for lnSCC was low, it suggested that this trait could be improved by genetic selection to improve mastitis resistance of cows. However, response to genetic selection for SCC in this population will likely be slow because of its low heritability. Thus, selection should be practiced in conjunction with improvements in management and environmental conditions. Unfortunately, data recording by farmers in Thailand (Yeamkong et al., 2010; Sarakul et al., 2011) and other tropical countries has been scarce (Mukisira, 1997; Chagunda, 2002). Thus, routine field data recording for SCC and other economically important traits needs to be increased. The heritability estimate for MY in this dairy population was close to values reported in other Thai dairy populations (0.33, Sanpote and Buaban, 2003; 0.34, König et al., 2005) and it was also within the range of values reported in other tropical countries (0.25 to 0.37; Costa et al., 2000; Cerón-Muñoz et al., 2004).

The genetic correlation between lnSCC and MY was 0.26 (SE = 0.59). This genetic correlation estimate was consistent with values reported in other populations (0.15 to 0.22; Rupp and Boichard, 1999; Carlén et al., 2004; Koivula et al., 2005). However, its standard error was high. This high standard error was likely due to the small dataset used here, thus it would need to be reconfirmed when a larger completed pedigree dataset is available. This positive genetic correlation also indicated that high producing cows tended to have high SCC, which is associated with mastitis occurrence (Koivula et al., 2005). Thus, upgrading to H and selection to increase milk production appears to have resulted in a decrease in resistance to mastitis in this Thai dairy population. However, simultaneous selection to decrease SCC and to increase MY could potentially improve overall profitability (Rogers, 1993; Colleau and le Bihan-Duval, 1995). Furthermore, culling of cows with high SCC and low milk production in the first lactation could help increase the number of cows in the population

Table 1. Variance components, phenotypic correlations, genetic correlations and heritabilities for natural logarithm of somatic cell count (lnSCC) and milk yield (MY) standard errors are in brackets

Parameter		lnSCC	lnSCC, MY	MY
Phenotypic	Variance	0.95 (0.08)		653,900 (21,620)
	Covariance		-54.97 (47.95)	
	Correlation		-0.07 (0.06)	
Genetic	Variance	0.12 (0.19)		202,945 (43,833)
	Covariance		40.50 (86.17)	
	Correlation		0.26 (0.59)	
Environmental	Variance	0.83 (0.19)		451,003 (40,054)
	Covariance		-95.47 (84.49)	
	Correlation		-0.16 (0.14)	
Heritability		0.12 (0.19)		0.31 (0.06)

that have high MY and low SCC in subsequent lactations (Koivula et al., 2005).

The phenotypic correlation estimate between lnSCC and MY was virtually zero (-0.07, SE = 0.06). This value indicated that there was no association between measurements of these two traits. Zero phenotypic correlation and low genetic correlation between lnSCC and MY and low heritability for SCC lends support to a combined strategy of selection for animals with high MY and low SCC accompanied by environmental improvements in management, nutrition, health, and housing conditions of cows in Thailand. To achieve this goal, dairy farmers would need to improve their record-keeping capabilities (pedigree, performance, health, and economic information) and use them to improve the genetic, environmental, and economic aspects of their business (Tomaszewski, 1993; Bishop et al., 2002; Rhone et al., 2008; Yeamkong et al., 2010).

Improvement in genetic ability

Genetic trends for SCC and MY of dairy cattle are illustrated in Figure 1. Means of yearly estimated breeding values (EBV) from 1991 to 2010 increased for SCC (49.02 cells/ml/yr, SE = 26.81 cells/ml/yr; p = 0.08) and for MY (0.37 kg/yr, SE = 0.87 kg/yr; p = 0.68). Yearly EBV means during this period ranged from 6.99 to 10.74×10^3 cells/ml for SCC, and from 106.67 to 189.39 kg for MY. Although yearly mean EBV tended to increase for MY between 1990 and 2001, they decreased continuously after 2001 until 2010, resulting in a near zero trend between 1990 and 2010. On the other hand, excluding 1990, yearly mean SCC steadily increased from 1991 and 2010. This is likely to be a reflection of a deterioration of the health of dairy cows, particularly due to mastitis. This genetic trend suggests an increase in mastitis susceptibility in the Thai cow population that will require better quality of management to maintain high milk production and sound health status. Although management and environmental control could
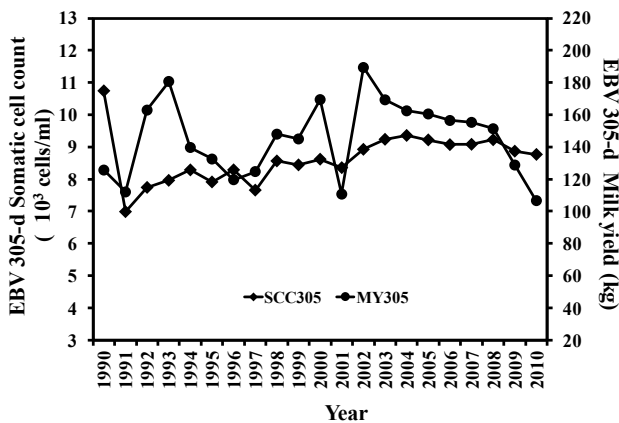
help decrease SCC for these cows (NMC, 2006), there would be an increase in the risk of mastitis and production costs. Thus, genetic trends in this population suggest that, in addition to MY, SCC should be considered for genetic selection.

The low genetic trend for MY could be due to low accuracy of selection. Most dairy farmers in this population were small holders (less than 10 milking cows per day) with a low level of education (primary school or no school education) and kept no records (Yeamkong et al., 2010). Most farmers did not know how to use genetic information (e.g., EBV) for selection, thus they got information and advice from artificial inseminators, semen sellers, consultants, and other farmers. A minority of farmers made their own decisions using their knowledge and experience rather than discussing with other farmers or consultants when choosing potential sires (Sarakul et al., 2009). However, sire selection in Thai dairy populations has been based primarily on semen availability, and secondarily on sire EBV for economically relevant traits (Koonawootrittriron et al., 2002a, b). Thus, to increase the genetic potential of dairy cattle for MY in Thailand, record keeping, selection accuracy and knowledge of genetic improvement of dairy farmers should continue to be improved.

Trends for yearly EBV means of cows, their sires and their dams for SCC from 1990 to 2010 are shown in Figure 2. Genetic trends were positive for cows (49.02 cells/ml/yr, SE = 26.81 cells/ml/yr; p = 0.08) and dams (99.84 SE = 41.66 cells/ml/yr; p = 0.03) but negative for sires (-66.08 cells/ml/yr, SE = 15.47 cells/ml/yr; p<0.01). Yearly EBV means of cows were highly associated with yearly mean EBV values of dams (r = 0.97; p<0.05) but lowly associated with yearly mean EBV values of sires (r = -0.18; p = 0.43).

The negative genetic trend of sires for SCC was related

Figure 1. Yearly means of EBV for somatic cell count and milk yield of cows from 1990 to 2010.
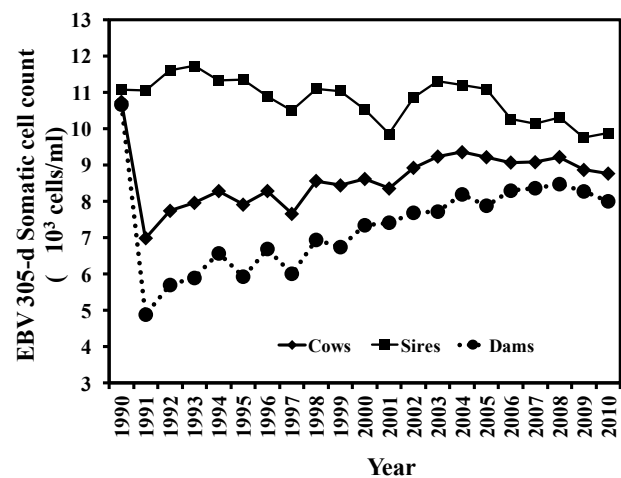
Figure 2. Yearly means of EBV for 305-d somatic cell count of cows, their sires and their dams from 1990 to 2010.

to the proportion of local and imported sires that were used in the population during the years of the study. The ratio of local sires to imported sires was 35:65 from 1990 to 2000, and it increased to 53:46 from 2001 to 2010. The mean EBV of all sires in the population was (10.80 cells/ml/yr, SE = 0.06×10^3 cells/ml/yr) for SCC. However, the mean EBV for SCC of local sires (9.66 cells/ml, SE = 0.13×10^3 cells/ml) was lower (p<0.01) than the mean EBV of imported sires (11.48 cells/ml, SE = 0.07×10^3 cells/ml). Similarly, the mean EBV for MY of local sires (123.15 kg, SE = 20.26 kg) was lower than that of imported sires (158.65 kg, SE = 11.00 kg), but not significantly (p = 0.12). Thus, the higher proportion of local sires used in this population from 2001 to 2010 helped decrease the EBV trend for SCC while simultaneously contributing to a decreasing trend in MY.

Almost all imported sires (96%) were purebred H and they were from temperate climate countries. In contrast, most local sires (83%) were crossbreds and born in Thailand. Holstein has been primarily selected for high MY under temperate conditions. It requires high nutritional levels, excellent management, and it is sensitive to climate, environmental conditions and diseases in tropical countries. In contrast, local sires (H and crossbred H) were bred and raised under Thai tropical conditions. These local sires were genetically evaluated for MY using progeny tests (accumulated 305-d milk yield). Local sires were not evaluated for SCC. Thus, the decrease of the genetic trend for SCC (favorable trend) of sires occurred by chance, and not by selection for the trait itself.

Cows and their dams were born within Thailand and they were the progeny of parents chosen primarily on MY. The upward genetic trends for SCC of cows and dams suggested an increase of their predisposition for mastitis. If dairy farmers continue to consider only MY and use imported sires, they will continue to increase the likelihood of having cows with higher incidence of mastitis infections. A reasonable strategy for farmers would be to consider both MY and SCC when choosing sires (local or imported), culling cows with high SCC and low MY, and exerting tight control over the quality of management that is the most appropriate for milk productions under their local conditions. Use of locally bred purebred and crossbred sires whose daughters have high milk production and are well adapted to hot and humid conditions would help farmers increase dairy production efficiency and profitability.

Somatic cell count and milk yield of dairy cattle raised under Thai tropical environmental conditions varied by herd-year-season and H fraction. Heritability estimates were low for lnSCC and medium for MY. Genetic correlation estimate between lnSCC and MY was low, and phenotypic correlation was near zero. Positive genetic trends existed for both SCC and MY, indicating a favorable genetic trend for MY, but an unfavorable trend for SCC. Sires had a downward trend of yearly mean EBV for SCC, whereas cows and dams had upward trends for this trait. Selection for high MY and low SCC should be encouraged in Thai dairy improvement programs to increase profitability by improving both cow health and milk yield.

REFERENCES

Ali, A. K. A. and G. E. Shook. 1980. An optimum transformation for somatic cell concentration in milk. J. Dairy Sci. 63:487-490.

Bishop, S., M. de Jong and D. Gray. 2002. Opportunities for incorporating genetic elements into the management of farm animal diseases: policy issues. Food and Agricultural Organization [FAO] study paper No. 18, Commission on Genetic Resources for Food and Agriculture, FAO Rome. pp. 1-36.

Boonkum, W., I. Misztal, M. Duangjinda, V. Pattarajinda, S. Tumwasorn and J. Sanpote. 2011. Genetic effects of heat stress on milk yield of Thai Holstein crossbreds. J. Dairy Sci. 94: 487-492.

Carlén, E., E. Strandberg and A. Roth. 2004. Genetic parameters for clinical mastitis, somatic cell score, and production in the first three lactations of Swedish Holstein cows. J. Dairy Sci. 87:3062-3070.

Cerón-Muñoz, M. F., H. Tonhati, C. N. Costa, D. Rojas-Sarmiento and C. S. Portilla. 2004. Variance heterogeneity for milk yield in Brazilian and Columbian Holstein herds. Livest. Res. Rural Dev. 16(4):http://ftp.sunet.se/wmirror/www.cipav.org.co/lrrd/lrrd16/4/cero16020.htm.

Chagunda, M. G. G. 2002. The importance of a national breeding policy-case for the Malawian dairy industry. Animal Genetics Training Resource: http://agtr.ilri.cgiar.org/agtrweb/index.php?option=com_content&task=view&id=155&Itemid=180

Colleau, J. J. and E. L. Bihan-Duval. 1995. A simulation study of selection methods to improve mastitis resistance of dairy cattle cows. J. Dairy Sci. 78:659-671.

Costa, C. N., R. W. Blake, E. J. Pollak, P. A. Oltenacu, R. L. Quaas and S. R. Searle. 2000. Genetic analysis of Holstein cattle populations in Brazil and United States. J. Dairy Sci. 83:2963-2974.

de Haas, Y., H. W. Barkema and R. F. Veerkamp. 2002. Genetic parameters of pathogen-specific incidence of clinical mastitis in dairy cows. Anim. Sci. 74:233-242.

Elzo, M. A. 2000. Manual for multibreed editing program CSET (cset.f90, version 12/07/2000). Animal Breeding Mimeo Series, No. 42, University of Florida, Gainesville, pp. 1-6.

Gilmour, A. R., B. R. Cullis, S. J. Welham and R. Thompson. 2000.

ASREML reference manual. NSW Agric., Australia.

Kadarmideen, H. N. and J. E. Pryce. 2001. Genetic and economic relationships between somatic cell count and clinical mastitis ad their use in selection for mastitis resistance in dairy cattle. Anim. Sci. 73:19-28.

Koivula, M., E. A. Mäntysaari, E. Negussie and T. Serenius. 2005. Genetic and phenotypic relationships among milk yield and somatic cell count before and after clinical mastitis. J. Dairy Sci. 88:827-833.

König, S., N. Chongkasikit and H. J. Langholz. 2005. Estimation of variance components for production and fertility traits in Northern Thai dairy cattle to define optimal breeding strategies. Arch. Tierz. 48:233-246.

Koonawootrittriron, S., M. A. Elzo and T. Thongprapi. 2009. Genetic trends in a Holstein×other breeds multibreed dairy population in Central Thailand. Livest. Sci. 122:186-192.

Koonawootrittriron, S., M. A. Elzo and S. Tumwasorn. 2002a. Multibreed genetic parameters and predicted genetic values for first lactation 305-d milk yield, fat yield, and fat percentage in a *Bos taurus×Bos indicus* multibreed dairy population in Thailand. Thai J. Agric. Sci. 36: 339-360.

Koonawootrittriron, S., M. A. Elzo, S. Tumwasorn and K. Nithichai. 2002b. Estimation of covariance components and prediction of additive genetic effects for first lactation 305-d milk and fat yield in a Thai multibreed dairy population. Thai J. Agric. Sci. 35:245-258.

Mrode, R. A. and G. J. T. Swanson. 1996. Genetic and statistical properties of somatic cell count and its suitability as an indirect means of reducing the incidence of mastitis in dairy cattle. Anim. Breed. Abst. 64:847-857.

Mukisira, E. A. 1997. Dairy recording in Kenya. In: International workshop on animal recording for smallholders in developing countries. Anand (India), 20-23 October 1997, ICAR Technical Series No. 1. pp. 147-153.

Ødegård, J., G. Klemetsdal and B. Heringstad. 2002. Variance components and genetic trend for somatic cell count in Norwegian cattle. Livest. Prod. Sci. 79:135-144.

Petersson, C. S., I. K. Mullarky and G. M. Jones. 2010. *Staphylococcus aureus* mastitis: cause, detection and control. Virginia Cooperative Extension. Publication No. 404-229: http://pubs.ext.vt.edu/404/404-229/404-229_pdf.pdf

Rhone, J. A., S. Koonawootrittriron and M. A. Elzo. 2008. Factors affecting milk yield, milk fat, bacterial score, and bulk tank somatic cell count of dairy farms in the central region of Thailand. Trop. Anim. Health Prod. 40:147-153.

Rogers, G. W. 1993. Index selection using milk yield, somatic cell score, udder depth, teat placement and foot angle. J. Dairy Sci. 76:664-670.

Rupp, R. and D. Boichard. 1999. Genetic parameters for clinical mastitis, somatic cell score, production, udder type trait and milking ease. J. Dairy Sci. 82:2198-2204.

Sanpote, J. and S. Buaban. 2003. Genetic evaluation of production traits for dairy cattle in Thailand. Thai J. Vet. Med. 33:80-90. (In Thai language).

Sarakul, M., S. Koonawootrittriron, M. A. Elzo and T. Suwanasopee. 2011. Factors influencing genetic change for milk yield within farm in Central Thailand. Asian-Aust. J. Anim. Sci. 24:1031-1040.

Sarakul, M., S. Koonawootrittriron, T. Suwanasopee, A. Hirunwong and T. Tongprapi. 2009. Situation of production and attitude for sire selection of dairy farmers in Thailand (2008). In: Proceeding of the 47th Kasetsart University Annual Conference. Bangkok, Thailand. pp. 174-181. (In Thai language).

SAS, 2003. SAS OnlineDoc 9.1.3. SAS institute Inc., Cary, North Carolina, USA.

Shook, G. E. and M. M. Schutz. 1994. Selection on somatic cell score to improve resistance to mastitis in the United States. J. Dairy Sci. 77:648-658.

Thai Meteorological Department, 2006. The Thai Meteorological Department: Climate of Thailand: http://www.tmd.go.th/en/archive/archive.php.

The National Mastitis Council 2006. NMC mastitis control program checklist updated. The NMC Newsletter: Udder Tropics 29(6): http://nmconline.org/newsletters/UT29-06.pdf

Tomaszewski, M. A. 1993. Record-keeping systems and control of data flow and information retrieval to manage large high producing herds. J. Dairy Sci. 76:3188-3194.

Yeamkong, S., S. Koonawootrittriron, M. A. Elzo and T. Suwanasopee. 2010. Milk quantity, quality and revenue in dairy farms supported by a private organization in Central Thailand. Livest. Res. Rural Dev. 22(2):http://www.lrrd.org/lrrd22/2/yeam22033.htm.