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THESIS

ESTIMATION OF DIRECT GENETIC EFFECT OF MILK YIELD AND LACTATION LENGTH AND GENOTYPE BY REGION INTERACTION IN DAIRY COWS IN THAILAND

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Two studies were conducted with the objectives to estimate the direct genetic effect of actual milk yield and lactation length in the Aownoi dairy cooperative and to examine the existence of genotype by region interaction on milk production traits of Holstein crossbred dairy cows in Thailand.

The estimation of the direct genetic effects on actual milk yield and lactation length showed the significant effect ($P < 0.05$) of lactation number on actual milk yield. Breed group of cow, lactation number and year-season of calving had no significant effect on lactation length. Estimates of heritability for the actual milk yield and lactation length were 0.22 ± 0.08 and 0.26 ± 0.09, respectively.

From the interaction of genotype and environmental effect, breed group of cow had significant effect ($P < 0.05$) on 305-d milk yield and highly significant ($P < 0.01$) on actual total milk yield and adjusted 305-d milk yield while the effect of year-season of calving and region had significant effects ($P < 0.001$) for all studied traits. Breed group by region had significant interaction ($P < 0.01$) for milk production traits. The presence of genotype by region interaction, this intern had inconsistent performance and ranking shift of genotypes across regions. Moreover, Sire by region had significant interaction ($P < 0.01$) on actual total milk yield and adjusted 305-d milk yield but not on 305-d milk yield. The results caused the ranking shift of sire's estimated breeding value across regions. The estimated heritability for milk production traits ranges between 0.17 to 0.24 for Central region and 0.29 to 0.57 for Eastern region.

Student's signature	Thesis Advisor's signature	/ /

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Mohammed Endris
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LIST OF ABBREVIATIONS

AIREML	=	Average information algorithm
AJ305	=	Adjusted 305-day milk yield
ANOVA	=	Analysis of variance
ATMY	=	Actual total milk yield
BG	=	Breed group
BG×R	=	Breed group by region interaction
CPD	=	Cooperative promotion department
DLD	=	Department of livestock development
DPO	=	Dairy promotion organization of Thailand
EBV	=	Estimated breeding value
G×E	=	Genotype by environment interaction
GLM	=	General linear model
h^2	=	Heritability
MME	=	Mixed model equation
MOAC	=	Ministry of agriculture and cooperative
MY305	=	305-day milk yield
NRM	=	Numerator relationship matrix
SAS	=	Statistical analysis software
SE	=	Standard error
TH	=	Thai Holstein
THI	=	Temperature humidity index
YS	=	Year- season of calving

ESTIMATION OF DIRECT GENETIC EFFECT OF MILK YIELD AND LACTATION LENGTH AND GENOTYPE BY REGION INTERACTION IN DAIRY COWS IN THAILAND

INTRODUCTION

Many countries in Asia are located in the tropical and sub-tropical zones. Most people in tropical Asia are involved in agriculture. Livestock is generally an integral part of mixed farming systems. Beef and dairy production have been economically important sectors of livestock. All countries in tropical Asia are economically classified as developing countries where most beef and dairy production is derived from smallholder farmers. Large-scale commercial production of beef and dairy is generally very limited due to various constraints especially those concerning economic aspects (Bazy *et al*., 2011). The improvement of performance of livestock in the tropics has been through the crossbreeding of local native animals to superior exotic breeds. In 2011, 90% of dairy cattle population in Thailand averages between 75 to 93% of Holstein Friesian blood. There is 80 kg of milk yield increased from 20 years upgrading breeding program and 90% of the total variation is associated with the environment (Tumwasorn, 2012).

Genetic improvement of milk production traits in dairy cattle in Thailand is based on phenotype selection. For more than 40 years, superior dairy sires and dam were identified using quantitative genetic evaluations and BLUP method was only introduced for selection in the past 15 years (Tumwasorn, 2000). Selective use of these animals improved phenotypic measures for milk production and milk components in Thai Holstein dairy crossbred (TH) population of Thailand. However, there are some limitations on predicting breeding values of the individual using quantitative analysis (Sanpote *et al.,* 2010). The trend of dairy cattle population size has been increasing by producing within the country with AI more than importing live animals from the foreign countries (MOAC, 2005). Most of dairy cows are crossbreds of native and/ or some Brahman origin with varying degrees of Holstein Frisian. Thailand has tried several crossbreeding programs with various *Bos taurus* genetics such as Red Dane, Brown Swiss, Jersey and Holstein Friesian as well as some dairy breeds of *Bos indicus* origin like Sahiwal, Red Sindhi, Shorthorn and Thai native. Efforts to increase milk production in Thailand combined with government policies resulted in widespread importation and use of Holstein semen, and widespread use of high-percent Holstein sires generated in Thailand (Department of Livestock Development, 2006). Through genetic selection and improved feeding and management practices, Thai farmers are averaging 305 day milk yield values from 3,000 to 4,000 kg. However despite these improvements, there is still a need to develop improved nutritional value in feedstuffs, milking management practices, genetic selection of animals through use of Estimated Breeding Values (EBV) and crossbreeding by use of complementation of breed types.

Dairy farmers across the world are motivated to increase profits by improving traits of economic importance such as milk yield, lactation length, calving interval, age at first calving, fat, protein yield and life time production. All these traits are affected in some measure by genetic, environment and genotype by environment interaction. Once genotype has been fitted to the existing environment or region, then there would be less variation for more improvement through upgrading due to stress and high temperature humidity index (THI) level affecting survival of high milking cow. Also the marginal improvement from improving feeding and management tended to be greater than that of genetic improvement (Tumwasorn, 2012). The improvement in milk production can be considered as being environmental or genetic. Both environmental and genetic factors contribute to variation in milk production. There are environmental and genetic limitations of production through the limiting tropical environment (Wilcox *et al*. 2003).

Moreover, despite a consorted effort being made to enhance the production and productivity of the dairy sector through breeding programs, management systems such as feed and feeding, housing and health care systems do vary across different regions of Thailand. Accordingly, farmers in the central region feed all sources of fiber mainly fruit waste from factory and rice straw. Equivalently, those in the north region feed mainly rice straw, waste from sweet corn factory, concentrate and waste from tapioca flour and cassava by product. Dairy farmers in the northeast feed their cows with concentrate, silage from sweet corn, pineapple waste and rice straw and finally in the south waste from pineapple factories with additional rice straw are main feed. Such variability in management systems and breed compositions will obviously have an influence on the dairy productive potential of the different breed compositions in the country. There are major differences considering the production system i.e. feed and feeding and herd management. The study of the magnitude of genotype by region or environment interaction (G × E) on milk production traits in Holstein crossbred cows across regions of Thailand is of significance importance. The interaction between an animal's genotype by region or environment interaction can play a major role in the expression of the phenotype of productive traits and is very important when estimating breeding value (Kang, 2002).

Efforts have been made to address this issue in most regions of Thailand except the dairy cows in Aownoi and very interesting to investigate genetic parameters of these cows which had not been reported before in Thailand. Similarly, information related to the performance of the different breed fractions or genotypes under the prevailing different feed and feeding management systems generally has not been addressed. Estimating the direct genetic effects of the ongoing efforts being made in improving the dairy sector in Thailand through AI will help objectively quantify their genetic effect. So do, examination of this improved dairy cattle performance across regions where the feed and feeding system, housing, and health care and climatic condition differences are clearly observed. Therefore, it is vital to estimate direct genetic effects for the genetic progress in a dairy breeding program targeted at improving milk production traits and genotype by region interaction which will help identify genotypes that better perform under the existing different management environments or regions (Tumwasorn, 2012).

OBJECTIVES

1. To estimate direct genetic effects on milk yield and lactation length of Holstein crossbred dairy cows in Aownoi dairy cooperative

2. To examine the existence of genotype by region interaction on milk production traits of Holstein crossbred dairy cows in Thailand

LITERATURE REVIEW

Overview of Thailand

Thailand is located in the Southeastern part of Asia, and it lies between 5° 35' to 20° 30' latitude, North and 97° 20' to 105° 40' longitude, East and is bordered by Cambodia to the East, Laos to the Northeast, Myanmar to the West, Malaysia to the South and also borders two main bodies of water, the Gulf of Thailand to the South and the Indian Ocean to the west (Royal Thai Embassy, 2004). Thailand is approximately 513,115 sq. km in size, and is comprises of 76 provinces that are subdivided into districts, sub-districts, and villages (Tourism Authority of Thailand, 2005). The topography of Thailand is divided into four main regions, the north, a mountainous area, the central plains, and the main rice producing area, the Northeast Plateau, an arid region, and the South peninsula, a major rubber producing area in Thailand (Public Relations Department, 2006). With a population of 62 million people, Thailand is comprised of 80% ethnic Thai, while the remaining 20% is made up of minority groups, with Chinese making up 10%, Malaysian 3%, and the remaining population made up of other minority groups such as the Mons, Khmers, and hill tribes (Tourism Authority of Thailand, 2005).

Climate of Thailand

The climate of Thailand is tropical and can be divided into three climatic seasons: a rainy (mid May to mid October), a winter (mid October to mid February) and a summer (mid February and mid May) season (Methodological Department, 2002). The winter season is characterized by cool and dry, summer as hot and dry, and the rainy season as hot and humid. The weather in Thailand is heavily influenced by monsoonal weather patterns. The southwest monsoon, beginning in May brings streams of moist air from the Indian Ocean which results in plenty of rain from May through October (Methodological Department, 2002). A second monsoon, the northeast monsoon, begins in October and brings colder air from the north, particularly in the north and northeast areas (Methodological Department, 2002). Annual rainfall in most areas of Thailand ranges from 1200 to 1600 mm (Methodological Department, 2002).

Figure 1 Regional Map of Thailand

Source: Maps-Thailand.com (2012)

Breeding History of Dairy Industries in Thailand

Thailand is the tropical country under the influence of monsoon climate. Most of the people in rural areas are farmers. They have a remarkable tradition in plant growing such as rice, sugar cane, corn and specific fruits. Raising of animals up to very recently was predominantly subsistence oriented based on native types of chicken, buffalo, cattle, duck, swine, and goat, depending on the differing demands in each area and the appropriation of land. In the north and northeast parts of the country e.g. there is a pronounced demand for beef from cattle and buffalos. In middle part, there is a dominating demand for pork and in south part for meat from goats and chicken. Whilst for several plant products like rice and tapioca established markets have developed also for export purposes market oriented animal production has reached a significant impact not before the recent decades. This holds especially for poultry and swine production. Although the first recordings of dairy farming in Thailand were in 1700 AD by Indian farmers, the introduction of developed dairy breeds, such Holstein Friesian in 1961, and the beginning of commercial dairying didn’t begin until 1962 (Chinwala and Umrod, 1988). Through cooperation from the Danish and German governments as well as the United Nations in starting many dairy development and school milk programs, dairy production began to develop and expand during the 1970’s and 80’s (Chinwala and Umrod, 1988). From 1999 to 2003 the Thai milk market increased 21.6% reaching an estimated value of 438 million (USD), a growth rate of 5% per year during that period (Datamonitor, 2004).

According to Ministry of Agriculture and Cooperatives, in 2004, there were 408,350 head of dairy cattle in Thailand raise by 23,000 farm households, with an average farm size of 17.5 head/farm producing 12 kg of raw milk per cow per/day (MOAC, 2005). Moreover, Rabobank (2004) reported that, assuming farmers are replacing animals at a 10% rate, average annual milk yield per cow would be approximately 2,100 kg, which is relatively low compared to most major milk producing countries such as the US with 8,400 kg and New Zealand that averages 3,300 kg (Rabobank, 2004). The result of low yields may be the results of the fact that 70% of Thai Dairy farmers have less than 10 head of cattle, where dairying maybe just one of many important farm activities. The small size of farms and other factors such as low nutritional content in feed, less productive management decisions, and keeping cow's for a long time after their peak milk production season has passed may be also the causes of lower milk yields (Rabobank, 2004). However on larger dairy farms in Thailand where farmers have 20 or more cows, reports have shown milk yields per cow up to 4,000 kg per year (Rabobank, 2004). The majority of dairy cattle in Thailand are high percentage, 75% or higher, Holstein Friesian cows (MOAC, 2005), with other percentages coming from breeds such as Red Sindhi, Brahman, Jersey, and Red Dane (Koonawootrittriron *et al*., 2002).

Table 1 Distribution of dairy cattle, milk production and farmers classified by regions

Regions	Male	Female	Milk production	Total	Farmers
Northern	683	45,605	201,656	46,288	1,697
Northeast	2,942	98,329	508,350	101,271	3,723
Central	17,719	315,179	1,370,990	332,898	12,240
Southern	317	3,125	12,426	3,442	177
All regions	21,661	462,238	2,093,371	483,899	17,837

Source: (DLD, 2011)

Dairy development in Thailand

So far several dairy development projects were organized by the government of Thailand. For example, the Department of Livestock Development (DLD) and the

Ministry of Agriculture and Cooperatives (MOAC) formed links with foreign groups to establish the Thai– Danish Dairy Project in Muak Lek (Saraburi Province) and the Thai–German Dairy Project in Chiang Mai Province, so that by the early 1970s, the government's agricultural policies were clearly aimed at the promotion of dairy products (Chantalakhana, 1995). The responsibility for this promotion then passed to the newly established Dairy Promotion Organization (DPO) of Thailand, a state-owned enterprise under MOAC and, in 1977, the Thai–Germany Dairy Project was handed over to the Department of Livestock Development (DLD). Both DPO and DLD provided local milk producers with access to facilities for milk processing and their roles also involved in research and the education of farmers with regard to the production of milk with an acceptable hygienic quality (Itsaranuwat and Robinson, 2003). Not only this the DPO also provided training to farmers on dairy production activities, but they also provide artificial insemination services and preventative and treatment of disease of animals to farmers (DPO, 2006). These activities are all part of the government's policies to stimulate and promote not only dairy production but also consumption of dairy products of the Thai population (Itsaranuwat and Robinson, 2003).

On the other hand, Department of Livestock development (DLD) also involve and cover all livestock species, they also work in cooperation with dairy farmers to improve areas in animal breeding, nutrition of animals, developing extension activities to farmers, and research and development and transfer technology in animal health and production. Furthermore, other governmental organization that has an influence on the Thai dairy industry is the Cooperative Promotion Department (CPD) which has responsible for supporting and strengthening cooperatives in order to increase the influence and reach of their business and the efficiency of their operation (CPD, 2006). It is also an outlet of information and help for dairy cooperatives in Thailand to become a self-reliant, thriving successful business in order to have a better socio-economic standard of living for farmers that are members of dairy cooperatives (CPD, 2006).

Dairy cooperative in Thailand

Although milk collection in Thailand is performed primarily by dairy cooperatives that buy milk from farmers and then sell the milk to milk processing companies, although a few cooperatives such as Nong Pho and Wang Nam Yen process the milk themselves. Approximately 80% of milk collected at the farm level is by cooperatives, while 20% is collected by private milk collectors (Department of Livestock Development, 2011). Based on the report by DL D (2011) the Ban Bueng, Muak Lek, Nong Pho, Pak Chong, Phi Mai and Wang Nam Yen cooperatives are among the largest dairy cooperatives in Thailand. In 2001 there were a total of 114 milk collection cooperatives mainly located in the central region of Thailand in the provinces of Saraburi, Ratchaburi, Nakhon Pathom and Chiang mai (Itsaranuwat and Robinson, 2003). The main activities of Thai dairy cooperatives are to operate milk collection centers where cooperatives purchase milk from farmers at a base price, plus price adjustments for milk quality and also sell other services. When purchasing and selling milk, farmers usually receive between 10.5 and 11.5 Baht/kg, depending on the quality of the milk, and when selling most cooperatives receive the standard price of 12.5 Baht/kg, stated by the government (Rabobank, 2004).

Table 2 Top ten cooperatives with highest number of dairy cows in Thailand.

Cooperative	Province	No. of Farmers	No. of Cows
Nongpho Dairy Coop. Ltd.	Ratchaburi	4,505	71,952
Wangnamyen Dairy Coop. Ltd.	Sakaeo	1,687	29,551
Muaklek Dairy Coop. Ltd.	Saraburi	1,262	27,456
Lamphayaklang Reform Land Dairy Coop. Ltd.	Saraburi	958	14,121
Pattananikom Dairy Coop. Ltd.	Lopburi	729	11,325
Pakchong Dairy Coop. Ltd.	Nakhon Ratchasima	1,046	11,250
Thai -Denmark Dairy Coop. Fed Ltd. (Aow Noi)	Prachuapkhirikhan	387	8,443
Kamphaengsaen Dairy Coop.	Nakhon Phatom	614	7,256
Nakhon Phatom Dairy Coop.	Nakhon Phatom	345	6,536
Thai -Denmark Dairy Coop. Fed. Ltd. (Pattananikom)	Lopburi	377	5,799

Source: Pattaraprakorn *et al*. (2010)

Traits of economic importance in Dairy cattle

Dairy cattle's breeding has been improved markedly during the last decade between the years 2000 to 2010 (Behmaran and Aslaminjad, 2010). In most countries, the primary selection objective in dairy cattle breeding has been milk production. Recently, other important traits such as reproduction and health traits have received increased focus because of biological, economical, ethical reasons and animal welfare concerns. However, the purpose of most animal breeding programs is to improve the benefit from the animal. This often includes simultaneous improvements in multiple traits (Andersen-Ranberg *et al*., 2005).

Dairy cattle performance is generally described by production, reproduction and longevity. The economic impact of these traits on a dairy production enterprise is examined by considering their effects on profitability of the enterprise. These traits are related both in phenotype and genotype and therefore breeding programs. Selection for improvement of these traits in a production system is influenced by the production environment, ease of expression and market conditions (Wasike, 2006). Traits of economic interest are biologically complex and usually assumed to be determined by a large number of alleles each having a very small effect. The type of information collected on economically important traits in dairy cattle (milk yield, lactation length, fat percent, and protein percent) has changed little over the last thirty years (Tumwasorn *et al*., 2000; Andersen-Ranberg *et al*., 2005).

Productive Performances

In dairy cattle farming, the main components of production performance are milk yield, lactation length, fat yield, and protein yield and milk contents. The objectives of many breeding plans are directed towards increasing these traits. In developed countries for example Germany, U.S.A. and Canada, the genetic trends of productive performance are steadily increasing. Canada dairy commission (2001) reported that in 1999 dairy cows, one of the imported sources of Thai Holstein genetic input in official milk recording produced an average of 8,738 kilograms of milk. This reflects a steady increase of 1,574 kg milk since 1988 or of 143 kg per cow per year. In Thailand several reports are available for production performance of dairy cattle (Chokchai dairy farm, 1992; Tumwasorn *et al.*, 1993; Suwannee 1994; Katkasame *et al*., 1996; Chongkasikit 2002).

Tumwasorn *et al.* (1993) reported that the milk yield and lactation length of imported Sahiwal x Friesian crossbreds of Thailand in the first and second lactation were 1,223.20 kg, 1,429.40 kg and 193.2 days and 173.66 days. Suwannee (1994) also reported that milk yield, lactation length and days dry of Holstein Friesian upgrades in Chachiangchao province, east of Bangkok were 2,802.4 kg, 256.87 days and 194.67 days, respectively. Chokchai dairy farm (1992) reported that milk yield and lactation length of Sahiwal crossbreds from New Zealand were 2,979.55 kg and 281.50 days, respectively. Similarly, Sureerat *et al.* (1997) reported that average milk yield and lactation length of Sahiwal x Friesian crossbreds from 16 provinces of Thailand were 2,336 kg and 295 days, respectively. Dahlin *et al.* (1998) reported that average lactation length of 256 days for large data set on Sahiwal cattle in Pakistan, while Ahmad (1999) reported that an average lactation length of 281 ± 55 days in Sahiwal cattle for the data set of 1968-94. Changkasikit (2002) reported that the average milk yields adjusted for calving age at 100, 305 days and in total average in lactation number 1 and 2 of Holstein breeding in Northern Thailand were 1101.45 ± 12.50 and 3359.45 ± 38.14, 1439.44 ± 29.63 and 4390.29 ± 90.37 and 1267.89 ± 20.94 and 3867.07 ± 63.86 respectively.

From literature reviewed it can be concluded that the dairy cattle performance in the tropics especially in Thailand is still much behind the performance level of dairy cattle in temperate countries, which to a great deal most likely is caused by non-genetic rather than by genetic factors (Changkasikit, 2002). The milk performance of Friesian upgrades under the tropical conditions of Thailand is significantly lower than of the Friesian cows in the countries of origin by at least 30% (Changkasikit, 2002). This also can be considered as an adaptive response to the tropical heat stress and the shortcomings in feeding and management.

Reproductive performance

The reproductive activity of cows in dairy operations is an important factor in milk production. The more frequently a dairy cow calves the greater is the amount of milk produced in her lifetime (Raheja *et al.*, 1989). The calving interval should not be longer than 1 year for obtaining lower costs, profitability and optimum viability of the dairy enterprise (Kamdasamu *et al.,* 1993). In the past, dairy animals have been mainly selected on the basis of their milk yield without giving consideration to other traits. The real merit of dairy animals, however, depends on many traits that need to be considered simultaneously for performance evaluation. Reproductive traits such as age at first calving and calving interval should be taken into consideration in a selection program (Shafig *et al.,* 1992; Mustafa and Gundogan, 2005).

The performance of animals depends not only on their genetic merits, but also on other factors such as nutrition, management, health, and environment. Many factors influence the reproductive performance of lactating dairy cows. Management factors such as accuracy of heat detection, use of proper inseminating techniques, proper semen handling, and appropriate herd health policies can directly influence the reproductive performance of a dairy herd (Shafig *et al.,* 1992; Walker *et al.,* 2001; Mustafa and Gundogan, 2005). Low reproductive performance is one of the major reproductive problems that cause a significant economic loss in dairy farming (Hall *et al.,* 2004). Virakul (2001) investigated the reproductive performance in dairy cattle across Thailand and found that reproductive performance in dairy cattle in Thailand was relatively poor with an average 183 days open in cows and an average age at first conception of 32 months in heifers. Furthermore, four reproductive parameters for dairy cows in Thailand as reported by (DLD, 2004) that the conception rate at first service, total conception rate, days open and age at first calving of 45.5%, 38.5%, 196% and 33.8 ± 6.6 months, respectively. Although there are a lot of works have been done on the reproductive performance of dairy cows in Thailand (Madsen *et al*., 1975; Tumwasorn *et al*., 1993, 1994, 1995, 1996; Suwannee, 1994; Changkasikit, 2002; Pongpiachan *et al*., 2003; Koonawootrittriron *et al*., 2006).

Components of an individual phenotypic performance

The most important economical characteristic of an animal is its production or performance associated with genotypes. For each performance trait we can observe or measure a certain level which is called the phenotype. An animal has as many phenotypes as there are traits to be observed or measured on this animal. In selection it is important to increase the phenotypic value which is possible through genetic and / or environmental improvement (Falconer and Mackay, 1996).

Variance components

Biological variation is an important aspect of genetic progress since the aim of selective breeding is reliable identification of animals with superior genes to form parents of the next generation (Falconer and Mackay, 1996). Since the actions of the individual genes are largely unknown, quantitative methods based on the minute model have been designed to analyze the effects of genes and partition phenotypic variance into its components. Classically, variance components were partitioned into genetic and environmental components. However, their inefficiency to explain the variance structure have spurred the use of more complex models which attribute variance to both direct and indirect sources (Falconer and Mackay, 1996). This has resulted in genetic and environmental variance being partitioned into direct additive, maternal additive genetic variance and direct permanent, maternal permanent and random environmental variance, respectively.

Genetic variance

Genetic variance is a component of phenotypic variance attributable to the genetic composition of the animal. It is a source of variation due to the sample of the genes that an animal receives from its parents (1/2 from either parent) and how they interact (Bourdon, 2000). This component of variation can be partitioned into additive and maternal genetic variance due to individual animal genetic and maternal genetic effects, respectively. Direct Additive genetic effects are effects on performance of the animal that can be attributed to its own genes. They are effects due to the average parental genes and constitute the breeding value of the animal. Since these effects are heritable, they form the core component of genetic improvement due to their ability to be selected for (Falconer and Mackay, 1996).

Environmental variance

Environmental variance is a component of phenotypic variance that is due to the effects of the environment where the animals live. The effects range from physical factors such as climatic factors to nutrition and general management factors. It can be partitioned into permanent, common and residual (measurement error) variances each resulting from different effects. In successively recorded traits, several records/observations are made on an individual. For instance, milk yield records in different lactations or same lactation in dairy cattle and weight records from an animal at different times in beef cattle are observations taken repeatedly on the same individual at different times. The variations that arise from such observations are partly related and thus constitute a permanent variance that is due to the environment (Mrode, 2005). In analysis of production and reproduction traits, the environmental variance is partitioned in order to accurately estimate the residual variance, which estimates the effect of the environment on the measurement. The permanent environmental effects are modeled as random effects since they are peculiar to the animals. The sum of these effects and the breeding value of the animal represent an estimated future performance of the animal in the same herd (Mrode, 2005).

Residual variance is the component of phenotypic variation due to all other factors that cannot be accounted for in the analysis. These consist of all modes of gene interactions such as dominance and epistasis and the random environmental effects (Mrode, 2005). This component of variance is an important indicator of the accuracy of the estimates and thus has a great influence on the reliability of the results. Residual variance is influenced by the structure of the data. Its value is overstated when the data has missing records and several outliers (Aziz *et al*., 2002; Maniatis and Pollott, 2003). All these components of variance are important in the estimation of genetic parameters for use in genetic improvement programs, consequently their accuracy is essential for high genetic progress.

Genetic parameters and their importance in dairy cattle

Successful breeding programs depend on the accuracy of genetic and phenotypic parameter estimates, which include heritability, repeatability and correlation between traits (Burrow, 2001). These parameters are ratios of (co) variance components described above and are important in performance evaluation and selection of dairy animals. Parameters for productive, reproductive and adaptive traits have been estimated for tropical dairy cattle. However, in Thailand many researchers have been reported on genetic parameters of dairy cows (Himarat *et al*., 2000; Topanurak *et al*., 2001; Koonawootrittriron *et al*. 2002).

Heritability and Repeatability

Heritability is defined as the proportion of phenotypic variance that is due to heredity. Another definition of heritability is a measure of the degree to which a trait such as milk yield is genetically determined. Although not all of the genetic contribution is included, essentially all which is available to a breeder who is trying to select within a breed is included. Obviously heritability is an important factor among the several factors determining how much genetic improvement can be made in any characteristic. Heritability estimates show a high level of variability. This variation is as a result of the differences in the population structure of the herds that provided the data, the model fitted for the analysis, the breed and the environment where the data was obtained. As a result, it is important that estimates from one population are treated with caution when used in other populations. These estimates are partitioned into maternal and direct heritability attributed to maternal and individual animal genetic effects (Wasike, 2006). In many cases, several measurements are taken on an individual for a particular trait. For instance, daily milk recorded in a lactation of dairy cattle and weekly weight gain measured in beef cattle. These measurements are related and thus constitute a covariance between them due to permanent environmental factors (Mrode, 2005). To account for this covariance in measurements as a component of phenotypic variance, a parameter, repeatability is estimated (Lynch and Walsh, 1998). It is treated as within individual variance and computed as correlation between the repeated measurements (Falconer and Mackay, 1996). If the repeatability estimate is large, it implies the variability in measurements is genetically influenced while small estimates indicate high environmental influence on the measurements.

Interaction between Genotype and Environment (G × E)

In dairy farming, differences between the production environments are significantly influencing the performance especially between temperate and tropical countries, which brings up the question of a possible genotype environment interaction between two completely different production environments.

Genotype by environment interaction (G x E) is a term used to describe the phenomenon that occurs when a set of genotypes change their relative performance in different environments. The most commonly described situation is where two breeds are kept in two environments and change their ranking for a given trait in those two environments. However, several studies have extended this concept to consider how a group of genotypes varies in several environments. The estimation of a variance component to describe the additional variance in the population due to the genotype × environment effect is one approach (Meyer, 1987). Recent developments in the use of random regression models have led to the suggestion that the genotype × environment effect can be systematically investigated by regressing sire breeding values on some measure of the environments in which their offspring are found (Kolmodin *et al*., 2002). G × E occurs when performances of different genotypes are not equally affected by different environments (Hammami *et al*., 2009). When the same genotypes develop different phenotypes in different environments, then there is G × E. When the differences between genotypes vary between environments without changes in their ranking there is scaling effect. However, if the genotypes rank differently in different environment, the effect of G × E is re-ranking of individuals. G × E is of less importance if only scaling effect is obtained because the best selected individuals in one environment would still perform the best in other environments (Hammami *et al*., 2009).

According to Calus (2006) genotype × environment interaction results in three possible effects: 1) heterogeneity of genetic variances across environments (also known as scaling effects), 2) re-ranking of animals across environments based on estimated breeding values, and 3) heterogeneity of correlations between two or more traits across environments. The G × E is usually considered to be unimportant if only scaling effects and no re-ranking occurs. Typically, estimated genetic correlations across environments are used to estimate the degree of re-ranking. In a situation where the genetic covariance between environments is not known, sometimes the correlation or rank correlation between estimated breeding values in both environments is used (Calus, 2006).

Sire by environment interaction (S × E)

Interaction of sire and herd occurs when the differences among progeny groups are not the same in different herds. Such an interaction implies that the genetic correlations among expressions of the same genotype in different herds are less than unity. Interaction variance also may be a consequence of heterogeneous variances across herds (Sopannarath, 2002). According to Nephawe *et al.* (1999), if an animal changes rank in performance or breeding value across environment, it indicates the presence of genotype by environment interaction, suggesting that individuals selected in one environment may not retain their full genetic superiority when transferred to other environment.

MATERIALS AND METHODS

Analysis I: Estimation of Direct Genetic Effect on Milk Yield and Lactation Length in the Aownoi Dairy Cooperative

Animals and Data

The data used for this study were collected from small farms under the Aownoi Dairy Cooperative in Prachuap Khiri Khan Province of Thailand. The data comprised a total of 869 lactation records from 850 cows that had calved during 2009–2010. The data were edited, with wrong and missing information excluded from the dataset. All cows had their sire and dam identified for the analysis of genetic value and, based on this information, the cows represented the daughters of 216 sires and 651 dams. The total numbers of animals in the pedigree was 1,590.

Cows were assigned to one of three breed groups based on the percentage of Holstein genetics (H) namely: $0.87 \leq H \leq 0.90625$, $0.90625 < H \leq 0.9375$ and $H > 0.9375$. Lactation records represented from the first to the fifth and more lactation numbers. Animals were grouped within year-season of calving (YS) contemporary groups. Contemporary groups are groups of cows from the same herds that calved in the same year and in the same season. The fixed factors evaluated during this research were year-season of the calving contemporary group, the breed group of cows and the lactation number. The investigated traits were the actual milk yield and lactation length.

Location and climate

The Aownoi Dairy Cooperative is located in Prachuap Khiri Khan Province, in the lower central region of Thailand, 281 km south of Bangkok and 93 km south of Hua Hin. The area is situated around latitude 11°49'N and longitude 99°47'E and is divided into seven districts and a sub district. The minimum and maximum temperatures range between 23 and 34 ºC, respectively, the relative humidity ranges from 67 to 70% and the average annual rainfall is 1,164 mm. The driest weather is in December when an average of 31 mm of rain falls and the wettest weather is in October when an average of 253 mm of rain falls (Meteorological Department, 2009). Calving months were grouped into three seasons: winter (November to February), summer (March to June) and the rainy season (July to October) following the work of Koonawootrittriron *et al*. (2009).

Animal feeding and other management practices

All animals were vaccinated against foot and mouth disease twice a year and farms treated their cows with antihelmintics twice a year. Feeding and nutritional management varied among seasons. Grasses fed to dairy cattle included *Brachiaria mutica* (para grass), *Brachiaria ruziziensis* (ruzi grass), *Pennisetum purpureum* (napier grass) and *Panicum maximum* (guinea grass). On the other hand, during the dry seasons (cold and hot), grasses were usually insufficient because of the lack of irrigation. Thus, rice straw, hay and silage were used as supplements (Yeamkon *et al*., 2010). Additionally, dairy farmers normally fed animals with waste from pineapple factories and concentrate. A roughage mixture composed mainly of pineapple waste and rice straw was supplied daily which is different from the feeding practices in other parts of the country. Milking occurred twice a day in the morning at 0500 hours and in the afternoon at 1400 hours. The farmers stop milking when the cows were drying off and when cows entered the late stage of pregnancy. Milk was collected from each household and delivered to the milk collection center at the Cooperative office. Feed and additives were distributed to the farmers by the Cooperative where milk yield was collected daily.

Model description and Statistical analysis

The data were subjected to analysis of variance in order to determine the significant sources of variation affecting production traits (actual milk yield and lactation length). The analysis of variance was employed using the GLM procedure of statistical analysis system (SAS, 2002). The model set up is therefore classified as follows:

$$Y_{ijkl} = \mu + YS_i + LN_j + BG_k + b(L_{ijkl} - \overline{L}) + e_{ijkl}$$

Where,

Y_{ijkl} = dependent variable (actual milk yield and lactation length)

μ = overall population mean,

YS_i = the fixed effect due to the i^{th} year- season of calving (i = 1, 2, 3,…,6)

LN_j = the fixed effect due to j^{th} lactation number (j = 1, 2, 3,…,5),

b = the coefficient of linear regression on lactation length applicable to analysis of actual milk yield

BG_k = the fixed effect due to the k^{th} breed group (k = 1, 2, and 3), and

e_{ijkl} = random residual error distributed as N $(0, \sigma_e^2)$

In this study, all cows had single record and these records are either of the five lactation number indicated in the model.

Model for estimation of genetic parameters

The variance components and genetic parameters of milk yield and lactation length of Thai- Holstein crossbred dairy cows were estimated using the single trait animal model and the restricted maximum likelihood methods and applying Average Information Algorithm (AIREML) using ASREML program (Gilmour *et al*., 2000). The solutions for the fixed and random effects were obtained by solving the mixed models equations (MME). Heritability (h^2) was determined as the ratio of additive genetic variance to the total phenotypic variance. The statistical model used was the same for all observation in a data set and expressed in matrix notation as follows:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Za} + \mathbf{e}$$

Where**,**

y = Vector of observations
β = the vector of fixed effects including lactation number, breed group and year- season of calving
a = the vector of random direct additive genetic effect
e = the vector of random residual effect

X and Z are incident matrices of fixed and random effect to the observation.
The assumptions about the variances of the random effects were $\mathbf{var}(a) = \mathbf{A}\sigma_a^2$ where $\mathbf{A}$ is the numerator relationship matrix (NRM) and $\mathrm{var}(e) = \mathbf{I}\sigma_e^2$ where $\mathbf{I}$ is the identity matrix.

Analysis II: Genotype by Region Interaction on Milk Production Traits of Holstein Crossbred Dairy Cows in Thailand

Animals and data

The data were comprised of 1,561 first lactation records from 1,561 Holstein crossbred cows that calved during the years 1993 to 2007. The data was collected by the Department of Livestock Development (DLD) of Thailand from 5 regions (Central, Eastern, North, Northeast and West). Average age at first calving of the cows was 32 months and animals without records were excluded from the data set. All cows had their sires and dams identified for the analysis of genetic value and therefore cows were from the daughters of 12 sires and 1,561 dams. All sires were commonly distributed in all regions and each sire had progenies ranges from 20 to 310.

Moreover, all cows were assigned to the 5 breed groups (genotypes) based on percentage of Holstein fractions: $H \leq 0.75$ (BG1), $0.75 < H < 0.875$ (BG2), $0.875 \leq H < 0.9375$(BG3) and $0.9375 \leq H < 0.9687$ (BG4) and $H \geq 0.9687$ (BG5). Calving months were grouped into three seasons: winter (November to February), summer (March to June) and rainy seasons (July to October). Animals were assumed to be grouped within year-season of calving contemporary group (a group of cows from the same herd that calved in the same year and in the same seasons). The fixed effects included were region, year-season of calving contemporary group and genetic group. The investigated traits were actual total milk yield (ATMY), 305-d milk yield (MY305) and adjusted 305-d milk yield (AJ305), respectively.

Animal feeding and management practices

Dairy cattle in Thailand are raised in small farm environment with varying feed and feeding methods. Farmers in the north feed their animal mainly with rice straw, waste from sweet corn factory, and concentrate whereas waste from tapioca flour and cassava by product are another source of fiber. In contrary, dairy farmers in the central feed their dairy cows with all sources of fiber found and vary from season to season. It is significantly found that farmers normally use fruit waste from factory as the main fiber source with rice straw as important fiber throughout the year. Fruit waste from pineapple factory and sweet corn factory are the main roughage feed covering up to 90% of daily feed especially in Prajuabkirikhan, Chiangmai, and Kanchanaburi provinces. Farmers in the northeast rely their feed on rice straw and small cash crop residue in the farm. Feeding method of dairy farmers also vary from regions to regions. In the south where pineapple factories exist, farmers feed 30-40 kg of pineapple waste with 5-10 kg of concentrate feed per cow per day with additional 2-3 kg of rice straw. In the central and northern parts, farmers feed their cow with 5-10 kg concentrate, 20-30 kg of silage from sweet corn and pineapple waste, 3-5 kg of rice straw, and 2-3 kg of waste from the ethanol factory. In the northeast, farmer feed their cows with 5-10 kg concentrate, 20-30 kg from silage from sweet corn and pineapple waste, 4-6 kg of rice straw, and 3-5 kg of waste from tapioca factory. Silage of mixed grass variety from backyard is given in small amount and available only in the wet season.

Model description and statistical analysis

The data were subjected to analysis of variance in order to determine the significant source of variation affecting the traits (ATMY, MY305 and AJ305). Two sets of analyses were performed; 1) Breed group by region interaction and 2) sire by region interaction effect. The fixed factor in the model includes year-season of calving, region, breed group (genotype), and breed group by region interaction. Similarly, for the analyses of sire by region interaction the same model was used except that breed group replaced by sire. Ages at first calving and lactation length were included as a covariate in the model. Therefore, the general linear model analysis was done using the GLM procedure of the Statistical Analysis System (SAS, 2002). It was assumed that with varying feed and feeding methods given to dairy cattle in each region, performance of animal should significantly differ within the same genetic group or there is genotype by region interaction. The model set up is therefore classified as follow.

$$y_{ijkl} = \mu + YS_i + R_j + BG_k + (BG*R)_{jk} + b_1(L_{ijkl} - \overline{L}) + b_2(A_{ijkl} - \overline{A}) + e_{ijkl}$$

Where,

y_{ijkl} = the observation of l^{th} animal

μ = the overall mean

YS_i = the fixed effect of i^{th} year-season of calving

BG_j = the fixed effect of j^{th} breed group (j = 1, 2, 3,…,5)

R_k = the fixed effect of k^{th} region (k = 1, 2, 3,…,5)

$(BG*R)_{jk}$ = the fixed effect of breed group by region interaction

b_1 = the coefficient of linear regression of actual total milk yield (ATMY) on lactation length

b_2 = the coefficients of linear regression of actual total milk yield (ATMY), 305-day milk yield (MY305) and adjusted 305-d milk yield (AJ305) on age at 1st calving

e_{ijkl} = residual error effect with $\mathbf{e_{ijkl} \sim N(0, \sigma_e^2)}$

Variance components and genetic parameter estimates for the investigated traits (ATMY, MY305 and AJ305) for Holstein crossbred dairy cows were made using the single trait animal model. The included fixed effects year-season of calving, breed group and region and random effects of animal and residual and Restricted Maximum Likelihood Methods and applying Average Information Algorithm (AIREML) using ASREML program (Gilmour *et al.*, 2000). The solutions for the fixed effects and simultaneously for the random effects were obtained by solving the mixed models equations (MME). Heritability (h^2) was determined as the ratio of additive genetic variance to the total phenotypic variance. The statistical model being used for the same for all traits, as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{a} + \mathbf{e}$$

Where,

y = Vector of observations

β = the vector of fixed effects including year-season of calving, region and breed group of cow

a = the vector of random direct additive genetic effect

e = the vector of random residual effect

X and Z are incident matrices of fixed and random effect to the observation. The assumptions about the variances of the random effects were $\mathrm{var}(a) = \mathbf{A}\sigma_a^2$ where $\mathbf{A}$ is the numerator relationship matrix (NRM) and $\mathrm{var}(e) = \mathbf{I}\sigma_e^2$ where $\mathbf{I}$ is the identity matrix.

RESULTS AND DISCUSSION

Analysis I: Estimation of Direct Genetic Effect on Milk Yield and Lactation Length in the Aownoi Dairy Cooperative

The results from the analysis of variance (Table 4) indicated that the overall means (± SE) for actual milk yield and lactation length were 4,484.84 ± 13.60 $kg.cow^{-1}.lactation^{-1}$ and 376.94 ± 0.34 d, respectively. All factors had no significant effects on the traits except for lactation number ($P < 0.05$) on actual milk yield.

Table 3 Descriptive statistical analysis of actual milk yield and lactation length per breed group of cow

	Breed group		
Trait	$0.87 \leq H \leq 0.906$	$0.906 < H \leq 0.9375$	$H > 0.9375$
Lactation length (days)			
Mean	376.4	377.3	377.5
SD	10.0	10.5	9.4
Minimum	350.0	345.0	355
Maximum	395.0	395.0	395
Actual milk yield (kg)			
Mean	4,461.8	4,509.9	4,475.9
SD	374.9	419.1	417.2
Minimum	3,700.0	3,600.0	3,650.0
Maximum	6,205.0	6,080.0	6,840.0

The overall least squares mean for milk yield (4,484.84 ± 13.60 kg) obtained in the present study was higher than those estimates reported for other sets of Holstein crossbreed cows in Thailand (Chongkasikit, 2002; Koonawootrittriron *et al*., 2009) but lower than those reported by Adel *et al*. (2005) in Egypt, Ajili *et al*. (2007) in Tunisia and Hashemi *et al*. (2009) in Iran. The overall mean lactation length in the present study was higher than those reported by other researchers in Thailand

(Tumwasorn *et al.,* 1993; Suwannee, 1994). The mean lactation length in the present study was in agreement with the findings of Amasaib *et al*. (2008) in Sudan (376.93 ± 122.96 day). In the present study all cows had lactation length greater than 305-d lactation; this could indicate that the cows had low conception rate. Hence farmers continued milking for longer period of time.

The least squares mean for milk yield per breed group of cow in the present study was 4,492.95 ± 23.02, 4,530.47 ± 23.10 and 4,493.21 ± 36.93 kg for cows in breed groups $0.87 \leq H \leq 0.90625$, $0.90625 < H \leq 0.9375$ and $H > 0.9375$, respectively. Furthermore, the corresponding least squares mean for lactation length was 376.65 ± 0.59, 377.66 ± 0.59 and 377.97 ± 0.95 (Table 4), respectively. The results from the present study were similar to the findings in other studies in Thailand (Katkasame, 1996; Koonawootrittriron *et al*., 2001, 2009; Konig *et al*., 2005). The non significant effect of the breed group of cow on the actual milk yield and lactation length in the present study was in agreement with the reports of Badi *et al*. (1985) and Konig *et al*. (2005). In contrast, a significant effect of the breed group on various milk production traits has been reported by other authors (Lakshmi *et al*., 2009; Bazy and Alipanah, 2011).

Table 4 Least Squares means (± SE) for actual milk yield and lactation length by breed group of cow, lactation number and year-season of calving

Factor	Actual Milk yield (kg.cow^{-1}.lactation^{-1})	Lactation length (day)
Minimum	3,600	345
Maximum	6,840	395
Over all mean	4,484.84 ± 13.60	376.94 ± 0.34
Breed group of cow	ns	ns
$0.87 \leq H \leq 0.90625$	4,492.95 ± 23.02	376.65 ± 0.59
$0.90625 < H \leq 0.9375$	4,530.47 ± 23.10	377.66 ± 0.59
$H > 0.9375$	4,493.21 ± 36.93	377.97 ± 0.95
Lactation number	*	ns
1	4,417.03 ± 31.13^{c}	377.35 ± 0.80
2	4,472.44 ± 23.77^{b,c}	376.44 ± 0.61
3	4,479.75 ± 27.22^{a,b,c}	376.45 ± 0.69
4	4,557.09 ± 41.83^{a,b}	379.53 ±1.07
5 and more	4,601.40 ± 56.87^{a}	377.35 ±1.46
Year-season of calving	ns	ns
1	4,476.61 ± 43.16	377.11 ± 1.11
2	4,531.74 ± 42.64	377.67 ± 1.01
3	4,471.66 ± 36.12	377.03 ± 0.92
4	4,512.30 ± 32.50	378.22 ± 0.83
5	4,511.05 ± 33.75	377.08 ± 0.86
6	4,529.88 ± 29.70	377.44 ± 0.76
Linear regression on lactation length (days)	7.13 ± 1.33***	-

^{a,b,c} least square means in a column with different letters within factors and traits are significantly different (* $P < 0.05$), (*** $P < 0.001$), ns = non significant

The effect of lactation number on the actual milk yield in the present investigation was significant ($P < 0.05$) which might have been due to variations in the age of the cows in different lactations. Moreover, management differences could also contribute to the variation to which the cows were exposed during different lactation numbers. Additionally, the influence of lactation number on various milk production traits was reported by other authors (Mustafa *et al*., 2002; Zafar *et al*., 2008; Lakshmi *et al*., 2009). The non significant effect of the year-season of calving on the actual milk yield in the present investigation was in close agreement with Bajwa *et al*. (2004) in Pakistan.

Heritability and the variance components estimation

The variance components were estimated after the non-genetic factors affecting milk yield and lactation length of graded Friesian cows were identified and accounted for in the mixed model equations. Table 5 shows the results of single trait analysis with respect to additive genetic, residual, phenotypic variance and the resulting heritabilities.

The additive genetic, the residual and phenotypic variances and heritabilities were 33,342.20, 121,582.00, 154, 92.50 kg^2 and 0.22 ± 0.08 for the milk yield, respectively. For the lactation length, an additive genetic variance, the residual variance phenotypic variance and heritability were 26.56, 76.50, 103.06 day^2 and 0.26 ± 0.09, respectively. The estimates of additive genetic variance and phenotypic variance for the milk yield in the present study were lower than those estimates reported from other researchers across Thailand (Konig *et al*., 2005; Koonawootrittriron *et al*., 2009; Sarakul *et al*., 2011) but larger than those reported by a few authors (Javed *et al*., 2001; Prempree *et al*., 2010).

Table 5 Variance components and heritability estimates (±SE) for actual milk yield and lactation length

Traits	Variance components			Heritability
	σ^2_a	σ^2_ε	σ^2_p	
Actual milk yield (kg^2)	33,342.20	121,582.00	154,924.20	0.22 ± 0.08
Lactation length (day^2)	26.56	76.50	103.06	0.26 ± 0.09

σ^2_a= Direct additive genetic variance, σ^2_ε = Residual variance, σ^2_p = Phenotypic variance.

The differences between the variance component estimates in the present study and those in other literature results could be due to the variation among herds. The milk yield used was not adjusted for any difference in the lactation length and the small number of records might have also contributed to the variation.

The estimates of heritability for the milk yield and lactation length in the present study were 0.22 and 0.26, respectively. The standard errors of the estimates found in this study showed normal ranges as reported by Tumwasorn *et al.* (2000). These estimates were in close agreement with the figure reported by Topanurak *et al.* (2001) who found the heritability estimate for milk yield to be 0.19 in Thailand. However, higher estimates of 0.37 to 0.56, 0.45, 0.43 and 0.34 for the milk yield in Thai Holstein dairy cows were also reported by Tumwasorn *et al.* (2000), Koonawootrittriron *et al.* (2003), Seangjun *et al.* (2009) and Sarakul *et al.* (2011), respectively.

The estimates of heritability for lactation length in the present study were in close agreement with those estimates of Bakir *et al.* (2004), Chander *et al.* (2008) and

Effa *et al*. (2011) who reported heritability estimates of 0.27, 0.14 and 0.25 in Turkey, India and Ethiopia, respectively. The highest heritability estimate for lactation length was reported to be 0.49 (Rahman *et al*., 2007) in Friesian × local cows in Bangladesh. However, this estimate was not in agreement with the results of the present study. The differences in the estimated heritability in the present study and those of other investigations could be due to breed, herd and environmental conditions as well as the method of estimation. The low estimate indicated that the variation due to additive gene action was small and that the variation due to the environmental factor was important.

Analysis II: Genotype by Region Interaction on Milk Production Traits of Holstein Crossbred Dairy Cows in Thailand

Factor affecting milk production traits

To assess the effects of breed group (genotype), region and breed group by region interaction, a combined analysis of variance (ANOVA) was performed on ATMY, 305MY and AJ305 (Table 6). Accordingly, breed group of cow had shown significant ($P < 0.05$) effect on MY305 and highly significant effect ($P < 0.01$) on actual total milk yield (ATMY) and adjusted 305-day milk yield (AJ305). ANOVA results of these milk production traits across region had shown highly significant ($p < 0.001$) differences while the effect of year-season of calving had significant effect ($P < 0.001$) for all the studied traits. In addition, the results revealed that the linear regression on lactation length had a significant ($P < 0.001$) effect on actual total milk yield (ATMY) while age at first calving had shown significant effect ($P < 0.01$) for actual total milk yield (ATMY), 305-d milk yield (MY305) and adjusted 305-d milk yield (AJ305).

Results of the combined ANOVA had also shown highly significant breed group by region interactions ($P < 0.01$) for all studied traits (Table 6). Obviously the presence of such sizeable of G×E interactions (differences) will lead to changes in the ranking of genotypes; hence, certain genotypes exhibited their highest performance in selected regions while others in their respective favorite regions.

Table 6 Analysis of variance for actual total milk yield (ATMY), 305-day milk yield (MY305) and adjusted 305-d milk yield (AJ305) by the effect of region, breed group by region interaction and year- season of calving

		Mean squares of traits			
Effect	DF	ATMY (kg)	DF	MY305 (kg)	AJ305 (kg)
Breed group	4	2, 216,109**	4	2,086,377*	3,377,785**
Region	4	4,849,115***	4	5,534,540***	7,220,020***
Year-season of calving	37	1,801,769***	37	1,860,893***	2,071,751***
Breed group by region interaction	16	1,721,317**	16	1,887,740**	2,075,295**
Lactation length	1	485,510,804***		-	-
Age at 1st calving	1	5,545,359**	1	8,880,559**	60,77,848**
Residual	1,497	640,724	1,498	837,901	791,665

***, ** and * indicate statistical significance at 0.001, 0.01 and 0.05 probability level, respectively, ns = non significant

The graphical presentation of genotype performance in actual total milk yield (ATMY), 305-d milk yield (MY305) and adjusted 305-d milk yield (AJ305) across Central, Eastern, Northern, Northeastern, and Western regions on two dimensional plots in which milk traits are plotted on y-axis while genotypes on x-axis, had shown a clearly observable oscillating performances of genotypes in the different region interaction that brought ranking differences among genotypes (Figure 2, 3 & 4).

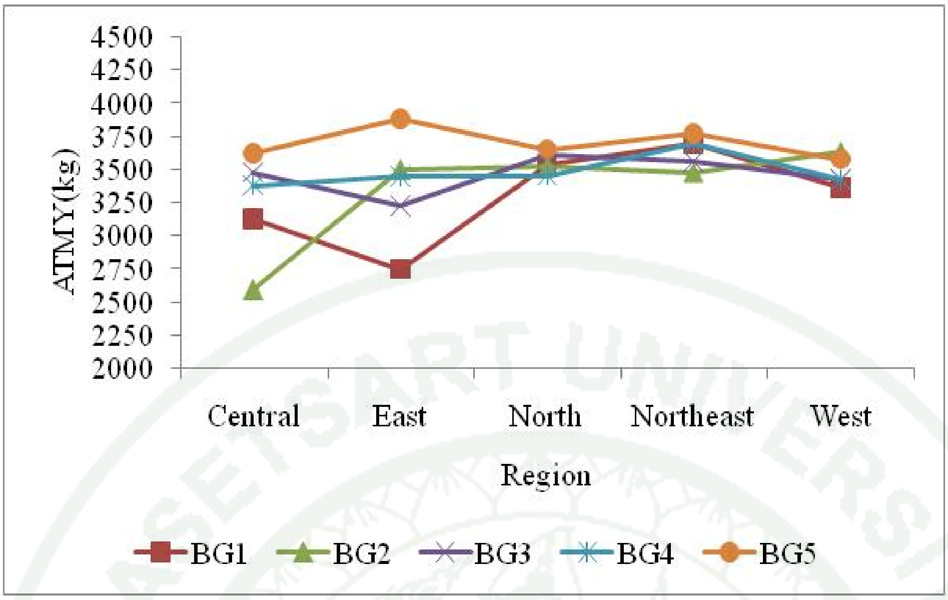

Figure 2 Least squares means of actual total milk yield (ATMY) for breed group (BG) by region interaction

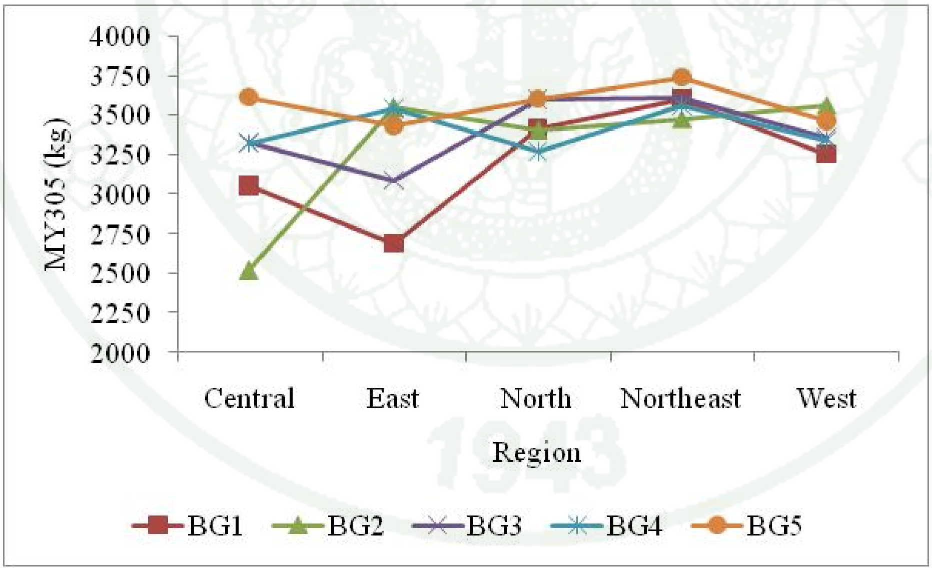

Figure 3 Least squares means of 305- day milk yield (MY305) for breed group (BG) by region interaction

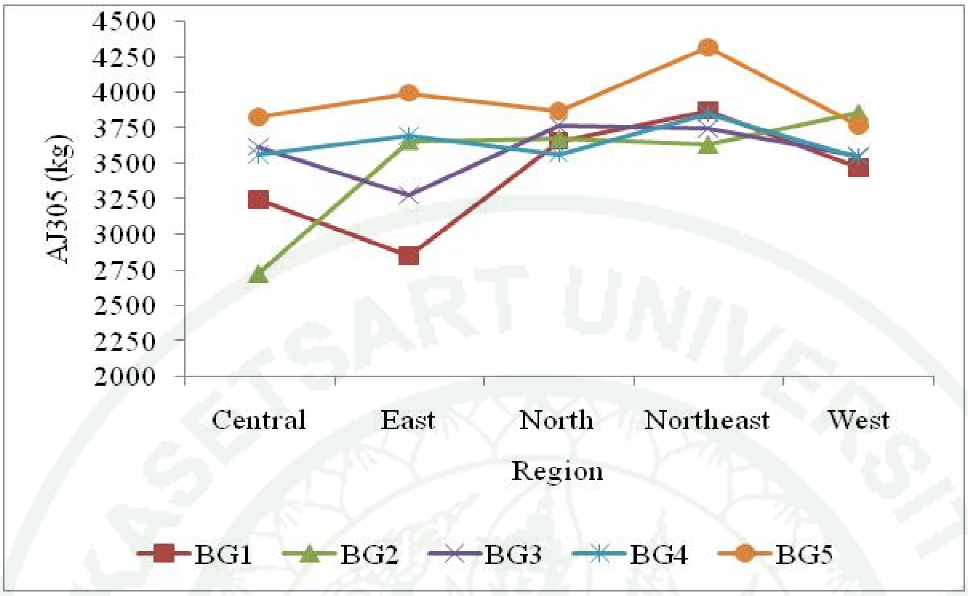

Figure 4 Least squares means of adjusted 305- day milk yield (AJ305) for breed group (BG) by region interaction

Overall, BG 5 had exhibited remarkably stable performance across all the regions considered in this particular study. BG 4 followed BG5 with its relatively stable performance or minimum oscillating trends (Figure 2, 3 & 4). Conversely, BG1 displayed the highest fluctuations of performance in all milk yield traits, the lowest of all of them being recorded in the Eastern region. BG1 gave its highest performance in the central region. Interestingly, all the remaining genotypes gave a relatively low actual total milk yield (ATMY), 305-d milk yield (MY305) and adjusted 305-d milk yield (AJ305) in the central region (Figure 2, 3 & 4). Thus, BG 2 seems to be ideal for central and western region as it had a relatively better performance in the milk yield traits compared to other blood groups. Contrarily, promotion of this genotype in the Eastern does not reward livestock holders in this region as clearly noted from its poor performance. Such inconsistent performance of genotypes in milk yield traits across different regions had been reported by Parra-Bracamon *et al.* (2005) and Prempree *et al.* (2010).

Although several factors could be attributed for such performance oscillation, the contribution of feed and feeding management systems practiced in those regions worth mention. In the current study this factor has shown a clear effect on all the breed groups. This has been clearly manifested in the estimation of genetic parameters. A clear estimates was obtained only for Central and Eastern regions genotypes had shown significant interactions (differences) unlike North, Northeast and Western regions where all genotypes had shown almost similar performance tendency. Generally, BG4 and BG5 on actual total milk yield (ATMY) and Adjusted 305-d milk yield (AJ305) didn't show cross over interaction or qualitative interaction but do show quantitative interaction or scaling effect which means there is no ranking shift among them (Figure 2).

The overall means (± standard errors) for actual total milk yield, 305-d milk yield and adjusted 305-d milk yield were 3,590 ± 25.8 kg, 3,499 ± 24.1 kg and 3,767 ± 23.7 kg, respectively (Table 7).

The highest 305-d milk yield of 3,526 ± 139, actual total milk yield of 3,653 ± 121and adjusted 305-d milk yield was recorded from BG5 while the lowest of all the above milk yield traits were recorded from BG1 (Table 7). Thus, this trend clearly revealed the strong and positive link between Holstein blood fraction and milk yield traits. The mean values for milk production traits per breed group of cow (Table 7) are within the range reported by other investigators in Thailand (Koonawootrittriron *et al.*, 2009, 2012; Konig *et al.*, 2005; Puangdee *et al.*, 2012). Highest mean milk yield traits of ATMY (3,607 ± 73.8 kg), MY305 (3,557 ± 84.6 kg) and AJ305 (3849 ± 82.1kg) for cow's had been obtained in the northeast region. The lowest AJ305 and MY305 were recorded from cows in the eastern region. The lowest ATMY of 3,238 ± 72.8 kg was obtained for cows in the central region (Table 7).

Table 7 Least squares means (± SE) for milk production traits (ATMY, MY305 and AJ305) of Holstein crossbred cows by region and breed group of cow

		Traits		
Factor		ATMY(kg)	MY305(kg)	AJ305 (kg)
Overall mean	N	3,590 ± 25.8	3,499 ± 24.1	3,767 ± 23.7
Region				
Central	335	3,238 ± 72.8^{c}	3,174 ± 83.5^{c}	3,391 ± 81.1^{c}
East	202	3,242 ± 121^{bc}	3,132 ± 138^{c}	3,369 ± 134^{c}
North	277	3,496 ± 96.8^{ab}	3,406 ± 111^{ab}	3,636 ± 107^{ab}
Northeast	314	3,607 ± 73.8^{a}	3,557 ± 84.6^{a}	3,849 ± 82.1^{a}
West	433	3,392 ± 83.4^{bc}	3,318 ± 95.7^{bc}	3,543 ± 92.8^{bc}
Breed group of cow				
$H \leq 0.75$ (BG1)	278	3,170 ± 94.6^{c}	3,095 ± 108^{b}	3,276 ± 105^{c}
$0.75 < H < 0.875$ (BG2)	107	3,315 ± 86.1^{bc}	3,252 ± 98.8^{a}	3,470 ± 95.8^{bc}
$0.875 \leq H < 0.9375$ (BG3)	546	3,408 ± 63.8^{b}	3352 ± 73.1^{a}	3,542 ± 70.9^{b}
$0.9375 \leq H < 0.9687$ (BG4)	463	3,429 ± 75.4^{ab}	3,363 ± 86.4^{a}	3,595 ± 83.8^{b}
$H \geq 0.9687$ (BG5)	167	3,653 ± 121^{a}	3,526 ± 139^{a}	3,905 ±135^{a}

^{a,b,c} Least square means within the same column with different superscripts are different

The least squares means values for milk yield traits estimated by region were in agreement with the findings of Parra-Bracamon *et al.* (2005) in Mexico and Prempree *et al.* (2010) in Thailand. In general, Vaccaro *et al.* (1992) reported significant differences between localities in Venezuela for economically important traits in dairy herds. They associated these differences with management and availability of feed and feeding. However, differences were also attributed to breed group composition of the herds and differences in herd management. In Northeastern region of Thailand most herds had high percentage of Holstein genetics and the better management and milking cows in the Northeastern region were it seems that the motives for this region having the highest values for ATMY, MY305 and AJ305 than the corresponding regions.

Sire by region interaction (S × R) effect

Analysis of variance (Table 8) indicated that the effect of region had highly significant effect ($P < 0.01$) on 305-d milk yield and adjusted 305-d milk yield while significant effect ($P < 0.05$) on actual total milk yields. The effect of year-season of calving had significant ($P < 0.001$) influences on all studied traits. The significant effect of year-season of calving on milk yield was in close agreement with the reports of (Musa *et al*., 2005 and Cilek, 2009) in Sudan and turkey. The effect of sire of cow was significant ($P < 0.05$) for actual total milk yields and highly significant ($P < 0.01$) for 305-d milk yield and adjusted 305-d milk yield. The significant effect of sire on milk yield had been reported by (Pandey *et al*., 2001) in India.

Moreover, the effect of Sire by region interaction was highly significant for actual total milk yield and adjusted 305-d milk yield but not significant for 305-d milk yield. The non significant effect of sire by district interaction had been reported by (Chongkasiki *et al*., 2002) in Holstein Friesian cows in Northern Thailand.

Table 8 Analysis of variance for actual total milk yield (ATMY), 305-day milk yield (MY305) and adjusted 305-d milk yield (AJ305) by the effect of region, Sire by region interaction and year- season

Effect	DF	ATMY (kg)	DF	MY305(kg)	AJ305 (kg)
		Mean squares of traits			
Region	4	1,592,477*	4	3,771,771**	3,240,107**
Year-season of calving	37	1,571,538***	37	1,815,367***	1,821,237***
Sire	11	1,295,808*	11	1,918,562**	1,848,116**
Sire by region	44	1,152,738**	44	1,109237^{ns}	1,265,623**
Lactation length	1	484,993,151***		-	-
Age at 1st calving	1	2,806,139*	1	5,627,787**	2,319,984**
Residual	1462	635,376	1,463	839,146	793,926

***, ** and * indicate statistical significance at 0.001, 0.01 and 0.05 probability level, respectively, ns = non significant

Variances and heritabilities within region analyses

Variance components and heritability were estimated after the non-genetic factors affecting the traits were identified and accounted for in the mixed model equations (MME). Tables 8 and 9 indicated that the results of single trait analysis with respect to additive genetic, residual, phenotypic variance and heritability using univaraite animal model. The overall estimated phenotypic, additive genetic and residual variances as well as heritability are presented in (Table 9).The overall heritability estimates of ATMY, MY305 and AJ305 were 0.20 ± 0.13, 0.24 ± 0.12 and 0.37 ± 0.11, respectively (Table 9). The heritability estimate found in this study for milk yield traits was lower than those reported by other authors in Thailand

(Tumwasorn *et al*., 2000; Topanurak *et al*., 2001; Koonawootrittriron *et al*., 2003, 2009; Seangjun *et al*., 2009; Sarakul *et al*., 2011) but the estimates was in close agreements with the findings of (Asaad *et al*., 2011; Usman *et al*., 2012). The heritability estimates of the present study different from other investigations due to fluctuation in feed availability and quality and herd management levels could also lead to considerable improvement. They also environmental factors could also contribute to the variation.

Table 9 Estimates of variance components and heritability for ATMY, MY305 and AJ305 of Holstein crossbred cows

Traits	Variance component [1]			Heritability
	σ_a^2	σ_ε^2	σ_p^2	
ATMY, kg^2	195,657	786,802	982,459	0.20 ± 0.13
MY305, kg^2	207,135	648,213	855,348	0.24 ± 0.12
AJ305, kg^2	301,373	507,652	809,025	0.37 ± 0.11

[1] σ_a^2= additive genetic variance, σ_e^2 = residual variance, σ_p^2 = phenotypic variance

The phenotypic variance of milk yield traits obtained (Table 9) was larger than those reported by (Sanpote and Buaban, 2003; 553,060 kg^2, Koonawootrittriron *et al*., 2009; 663,652.0 kg^2) in Thailand but the estimates of phenotypic variance was in close agreement with the findings of other countries (Boujenane, 2002; 846,641.5 kg^2, Amimo *et al.,* 2007; 658,516 kg^2 and Hashemi *et al*., 2009; 799,598.5 kg^2).

The result revealed that the estimated phenotypic variance (σ_p^2) for milk production traits within region analysis ranges from 699,160 to 100, 6065 kg^2 (Table 9). The findings of this phenotypic variance for milk production traits had been within the range reported by Nauta *et al*. (2006) and Sofla *et al*. (2011) in the Netherland and

Iran. In addition, the result revealed that the estimated heritability for milk production traits ranges between 0.17 to 0.24 for Central region and 0.29 to 0.57 for Eastern region (Table 9). The result of this research was similar to the findings of Prempree *et al*. (2010), who estimated heritability for milk production traits in different regions of Thailand. The heritability estimate of ATMY was 0.19 for Central region and 0.29 for Eastern region. The heritability of MY305 was 0.17 for Central and 0.37 for Eastern region. Similarly, the estimated heritability of AJ305 was 0.24 for central and 0.57 for Eastern region. The higher standard error of heritability estimates for all the traits under study indicated that these traits were highly influenced by environmental factors and management of the herd such as feed and feeding and health care could also contribute to the variation. The high standard error of the heritability estimates for milk yield was reported by Usman *et al.* (2012) in Holstein Friesian cattle in china, who estimates the heritability of 0.26 ± 0.33.

The estimated heritability of milk yield traits in Eastern region conditions were higher than in Central regions. The main reason for this was the residual variance (σ_e^2) of milk yield traits, which was lower for central region. Also, the estimate for the additive genetic variance (σ_a^2) of yield traits was higher under Eastern region than for central region (Table 9). Fikse *et al*. (2003) evaluated first lactation dairy cows' records of four countries (Australia, Canada, the United States and South Africa) to determine the genotype by environment interaction for milk production, using different statistical models. They reported the heritability of milk production as 0.33 for univariate model and 0.4 and 0.25 for multivariate models between countries, respectively. The estimated heritability for milk yield traits in the present investigation was within the range of Sofla *et al*. (2011), who estimated heritability of 0.48, 0.39, 0.59 and 0.70 for milk yield in conventional, preorganic, converting- organic and organic production environments.

Table 10 Estimates of additive genetic variances (σ_a^2), residual variance **(**σ_e^2**)**, phenotypic variance **(**σ_p^2**)** and heritabilities (h^2 ± SE) of milk production traits within regions analyses.

		Regions (Environments)	
Traits	Parameters	Central (Region1)	East (Region 2)
ATMY(kg^2)	σ_a^2	160,940	263,458
	σ_e^2	706,446	639,092
	σ_p^2	867,338	902,550
	h^2	0.19 ± 0.19	0.29 ± 0.25
MY305(kg^2)	σ_a^2	176,056	293,778
	σ_e^2	830,009	502,239
	σ_p^2	1006,065	796,017
	h^2	0.17 ± 0.18	0.37 ± 0.27
AJ305(kg^2)	σ_a^2	235,180	395,395
	σ_e^2	736,001	303,765
	σ_p^2	971,181	699,160
	h^2	0.24 ± 0.27	0.57 ± 0.34

Results (Figure 5 and 6) shows sire Estimated Breeding value (EBV) for milk production traits across regions. The result (Figure 5) showed that the estimated breeding value of 12 sires of actual total milk yield (ATMY) was ranges from -370 to +325 kg recorded from Central region and -593 to +693 kg from Eastern region while for adjusted 305-d milk yield ranges from -576 to +453 kg and -775 to +941 kg recorded from Central and Eastern region, respectively (Figure 6). The estimated breeding value of sires for milk yield traits in the present study was within the range reported in Thailand (Tumwasorn *et al*., 2000; Koonawootrittriron *et al*., 2009; Kitingern and Chongkasikit, 2011).

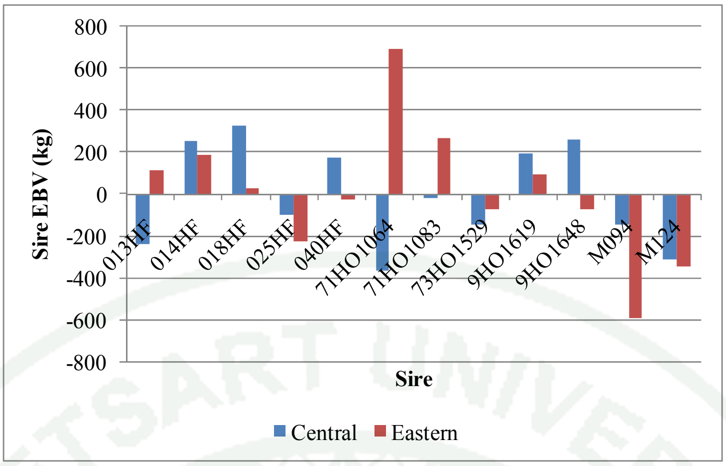

Figure 5 Sire Estimated Breeding Value (EBV) for actual total milk yield (ATMY) in Central and Eastern regions

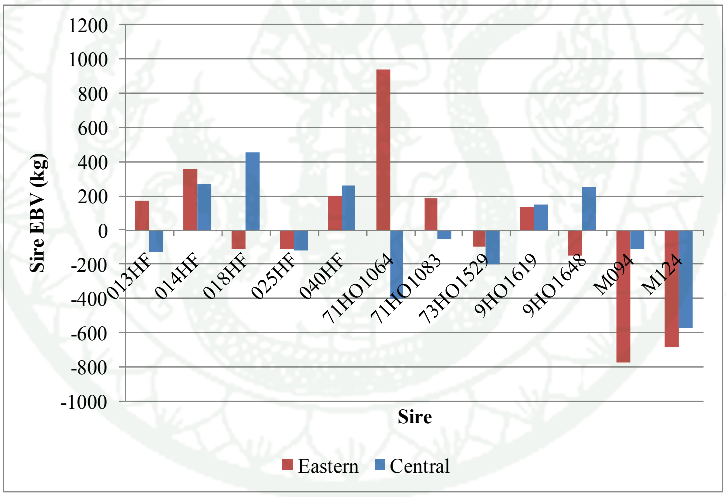

Figure 6 Sire Estimated Breeding Value (EBV) for adjusted 305day milk yield (AJ305) in Central and Eastern regions

The result revealed that the best performed sire for Central region was “018HF” with an EBV of +325 kg for actual total milk yield (ATMY) and + 453 kg for Adjusted 305-d milk yield. In addition, the best performed sire obtained from Eastern region was “71HO1064” with an EBV of +693 kg for Actual total milk yield and +941 kg for adjusted 305-d milk yield. This sire was not recommended in the central region (Figure 5 and 6). The ranking shift of sire's estimated breeding value obtained from this current study clearly indicated that there is a genotype by environment interaction or sire by region interaction. Nephawe *et al*. (1999) reported that, if an animal changes rank in performance or breeding value across environment, it indicates the presence of genotype by environment interaction, suggesting that individuals selected in on environment may not retain their full genetic superiority when transferred to other environment. The spearman rank correlation between estimated breeding values of common sire's for actual total milk yield and adjusted 305-d milk yield found to be 0.03 ($p > 0.05$) and 0.11 ($P > 0.05$). Using this rank correlation for estimation of correlation between sire's breeding values for two traits was different and showed significant genotype by environment interaction across two regions of Thailand.

Fikse *et al*. (2003) reported that genetic correlation between four countries namely Australia, Canada, the United States and South Africa as 0.87 to 0.92, using multivariate model; their results showed that the variance in different production environments is not the same and it is ranked based on the environment type. The spearman rank correlation between breeding values of common sires for milk production traits in the present investigation was in close agreement with the findings of Sofla *et al*. (2011) in different climates of Holstein milk production traits in Iran. In general, due to ranking of sire's based on estimated breeding value across regions, the performance of sires' EBV for Eastern region was probably higher estimates than Central region.

CONCLUSIONS AND RECOMMENDATIONS

The results of this trial (Estimation of the direct genetic effect on actual milk yield and lactation length) had the significant effect of lactation number on actual milk yield. Breed group of cow, lactation number and year-season of calving had no significant effect on lactation length. The direct, additive genetic variances of milk yield and lactation length were 33,342.20 and 26.56 kg^2, respectively. The heritability estimates of milk yield and lactation length were found in normal range of 0.22 to 0.26. The estimate obtained in this study shows the need to undertake similar studies for different areas with different management practices.

From the interaction of genotype and environmental effect, the presence of significant genotype by region interaction effect had shown. This intern had resulted in inconsistent performance and ranking shift of genotypes across regions. Nevertheless, BG 5 had exhibited remarkably stable performance across all the regions considered in this particular study. In addition, BG4 followed BG5 with its relatively stable performance or minimum oscillating trends. Hence, we recommend the further promotion of these two groups considered in this study. BG2 is also specifically recommended to be advanced in the Western region. Sire by region had also shown significant interaction on actual total milk yield and adjusted 305-d milk yield but not on 305-d milk yield. The results caused the ranking shift of sire's estimated breeding value across regions. Thus, it was recommended that the best performed sire based on estimated breeding value existed in the Eastern region was "71HO1064"and "018HF" in the Central Region. The estimated heritability of milk yield traits in Eastern region was higher than in Central region.

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