THESIS

EVALUATION OF BREEDING OBJECTIVE FOR THAI INDIGENOUS CATTLE

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GRADUATE SCHOOL, KASETSART UNIVERSITY
2008

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GRADUATE SCHOOL, KASETSART UNIVERSITY

Doctor of Philosophy (Animal Science)
DEGREE

Animal Science
FIELD

Animal Science
DEPARTMENT

TITLE: Evaluation of Breeding Objective for Thai Indigenous Cattle

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THESIS

EVALUATION OF BREEDING OBJECTIVE FOR THAI INDIGENOUS CATTLE

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A Thesis Submitted in Partial Fulfillment of
the Requirements for the Degree of
Doctor of Philosophy (Animal Science)
Graduate School, Kasetsart University
2008

Wutipong Intaratham 2008: Evaluation of Breeding Objective for Thai Indigenous Cattle. Doctor of Philosophy (Animal Science), Major Field: Animal Science, Department of Animal Science. Thesis Advisor: Associate Professor Sornthep Tumwasorn, Ph.D. 106 pages.

Combined data of four lines of Thai indigenous cattle born between 1993 and 2004 were used to examine fixed effects for weight and body measurements i.e. birth, weaning and yearling age. The data were also used to estimate the (co)variances and genetic parameters. Analyses were carried out with univariate and bivariate animal models using average information restricted maximum likelihood procedure. Herd and line-year-season of calving and sex had significant influence on birth, weaning and yearling traits. Male calves had greater values for all traits than female calves. Age of dam had significant influence on birth and weaning traits ($P < 0.001$). Age of animal had a significant influence on weaning and yearling traits ($P < 0.001$).

The estimates of direct and maternal heritabilities for birth traits ranged from 0.09 to 0.30 and 0.09 to 0.18, respectively. The estimates of direct heritabilities and maternal permanent environmental effects for weaning traits ranged from 0.15 to 0.28 and 0.14 to 0.25, respectively. The estimates of direct heritabilities for yearling traits ranged from 0.26 to 0.43. The genetic correlations between weight and body measurements ranged from 0.34 to 0.98. Thus, the selection to increase weight traits would increase body size as well.

Production and economical data were used to develop profit function for breeding objective and selection traits. The breeding structures relevant to Thai indigenous cattle were evaluated for their genetic gains and economic parameters. A population with a nucleus herd of 1,500 cows, supplying bulls to a total population of 800,000 cows was assumed with the investment period of 20 years. The economic weights of breeding objective traits i.e. cow weaning rate, sale weight and mature cow weight were positive. The genetic gain per year for growth traits (WW, YW, CoW), body measurement (GIR4, HH4, STP4) were gained positive. For reproductive traits, SC and CoWR gain was positive. For DtoC and A1C gain was negative. The genetic gain per year for breeding objective was 96.85 baht. The total calculated returns, cost and profit per cow in the population from one round of genetic selection were 317.26, 22.27 and 294.99 baht, respectively.

Wutipong ______________________ 31 / 03 / 08

Student's signature Thesis Advisor's signature

ACKNOWLEDGEMENTS

I would like to express my sincere gratitude to *Assoc. Prof. Dr. Sornthep Tumwasorn,* chairman of my supervisory committee for his guidance, encouragement and support in the pursuit of this degree and in the preparation for my thesis. It has been both a pleasure and honor to share with him ideas and meaningful discussion on many subjects related to my research and program of study.

The special thank is extended to *Prof. Dr. Hans-Urich Graser*, my committee member for never-ending support on thesis work, impressive ideas on how Thai indigenous cattle should be. The high quality of supervision demonstrated by him is greatly appreciated. I am also grateful for his support in research facilities and valuable opportunities during my study at Animal Genetics and Breeding Unit, University of New England.

I would like to thank the other members of my supervisory committee, *Assist. Prof. Dr. Panwadee Sopannarath, Assist. Prof. Dr. Skorn Koonawootrittriron and Assist. Prof. Dr. Boonorm Chomtee*, and the representative of the Graduate School, *Dr. Piyama Tasanasuwan,* for their friendly attitude and valuable advice throughout this study and in the preparation for this manuscript.

Special thank goes to the Thailand Research Fund (TRF) for the financial support under the Royal Golden Jubilee Project from 2003 to 2006, the Department of Livestock Development for granting me study leave to undertake this course, Animal Husbandry Division for providing valuable Thai indigenous cattle data. Also thank to the staff and colleagues in the Department of Animal Science, Kasetsart University who contribute towards the completion of this thesis.

Finally, I would like to take this opportunity to express my thanks to my parents, Mr Plaiwat and Mrs Boonta Intaratham, who dedicated their lives to education. I would never have had a chance to study at this level without their teaching, support and encouragement during my childhood. I would like to express heartfelt gratitude to my wife, Nantaka, to my daughter, Warinrat and to my son, Lorpong. Without them this work would never be done.

Wutipong Intaratham
February 2008

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LIST OF ABBREVIATIONS

A1C = Age at first calving

(AI)-REML = Average information restricted maximum likelihood

BW = Birth weight

CoW = Mature cow weight

CoWR = Weaning rate

c^2 = Maternal permanent environmental effect

Dtoc = Day to calving

ΔG = Genetic gain for each trait

GIR = Hearth girth at birth

GIR2 = Hearth girth at weaning age

GIR4 = Hearth girth at yearling age

h^2 = Heritability

HH = Hip height at birth

HH2 = Hip height at weaning age

HH4 = Hip height at yearling age

m^2 = Maternal heritability

SDE = Standard discount expression

SC = Scrotal circumference

SW-d = Sale weight direct

STP = Body length, shoulder to pin at birth

STP2 = Body length, shoulder to pin at weaning age

STP4 = Body length, shoulder to pin at yearling age

WW = Weaning weight

YW = Yearling weight

EVALUATION OF BREEDING OBJECTIVE FOR THAI INDIGENOUS CATTLE

INTRODUCTION

Thai indigenous cattle play an important role in the subsistence, economic and social livelihoods of smallholders in Thailand. In the past, the Thai beef industry was never a major contributor to the country's meat supply since animals were basically used for draught purpose and culled when unable to work well enough. Presently, the change in the socio-economic pattern of the local farmers has gradually been absorbed by modern technology. Animals are replaced for their draught power by machinery. Consequently, farmers have no longer raised cattle for working but rather for beef production. To assist in the provision of more beef for the consumer demand it was considered necessary to increase output and therefore larger animals were preferred. This was generally achieved by importation of several different breeds. European breeds were brought in to provide fast growing livestock with improved meat yield and to develop synthetic breed within Thailand. Brahman cattle were also imported since it was recognized that these *Bos indicus* were better adapted to Thailand's environments. However, the importations were not completely successful although most of them have contributed some beneficial aspects to the future beef industry. The policy with Brahman was to use them to improve size of the local indigenous cattle and to increase output per animal. This program was developed mainly by artificial insemination (A.I.) and had limited success as it met difficulties in rural areas. The main problems were concerned with the provision of adequate feed, low level of management, disease and parasite challenge and poor marketing. These constraints are not a realistic long term option given the price of the beef produced.

In 2001, Department of Livestock Development (DLD) made the decision to plan and implement a national genetic improvement program for Thai indigenous cattle to improve the economic situation of small Thai beef cattle producers; secure a base supply of beef for Thai people from within country; utilize the adapted genotype of Thai beef cattle and conserve biodiversity in Thai beef cattle. The defined breeding objectives were to increase sale weight of live animal and fertility. Therefore, a breeding structure has been established with three herds: nucleus, multiplier and commercial herd. There are five key decision areas to be considered to make the breeding structure beneficial: definition of breeding objective, design of recording system, design of breeding program, genetic evaluation, selection and mating. The current structure within the Thai indigenous cattle population requires some direct involvement of DLD livestock centers to maintain and improve a nucleus of these cattle whose progress will be disseminated via a multiplier herd to the small commercial village farmers. The primary function of multiplier in villages is to expand the material of the elite nucleus into greater number of animals to pass onto the commercial herd. The breeding structure will also lead to *in-situ* genetic conservation of the indigenous cattle where low inputs combined with sustainable production systems will help meet local beef consumption demands.

Genetic improvement programs for livestock are businesses and involve more than one trait. Rates of improvement that are achieved in key economic traits typically are of the order of .5 to 2 % of the mean per annum. To obtain these long-term changes, the relative economic importance of changes in all traits in the breeding objectives should be known in order to appropriately weight the genetic evaluations for those traits and achieve maximum response (Gibson and Wilton, 1998). Emphasis in breeding programs of Thai indigenous cattle should be to evaluate and optimize gene flow principles to disseminate the improved genetics through the target industry which could be e.g. annual genetic gain for one round of selection, the cost and return including profit over the investment period.

OBJECTIVES

The objectives of this study were:

1. To examine fixed effects affecting weight and body measurements at birth, 200-day weight and 400-day weight of Thai indigenous cattle.

2. To estimate the genetic parameters for weight and body measurements at birth, 200-day weight and 400-day weight of Thai indigenous cattle.

3. To calculate economic weight of economically important traits such as sale weight, cow mature weight and fertility of Thai indigenous cattle.

4. To evaluate the returns of investment and predict annual genetic gains from one round of selection in a deterministic approach by using the estimated genetic parameters and economic weight of Thai indigenous cattle.

LITTERATURE REVIEW

1. Beef population and overview of beef industry in Thailand

According to DLD statistic (2006), Thailand had a total beef population of 5.2 million heads in 1997 and in 2006 possessed 8.0 million heads. These numbers of beef cattle were maintained by 1,226,005 households. The numbers of farmers who raised beef cattle for industry were 48,703 farmers. The distribution of beef cattle is predominantly in the northeastern part follow by northern, central and southern part of Thailand in proportions of 53.7, 19.5, 16.4 and 10.4%, respectively. The beef population consists mainly of indigenous cattle, 5.6 million heads which represent about 70.4% of the total. The number of farmers concerned with raising indigenous cattle was 944,453 and this represents 77.0% of all households with cattle. The rest of the beef population consists of purebred and crossbred Brahman, 2.4 million heads.

Table 1 Number of beef in different parts of Thailand (×1000) from 1997 to 2006

(unit: heads)

Year	Central	Northeast	North	South	Total
1997	1,060	2,302	1,046	882	5,291
1998	904	2,027	887	748	4,567
1999	855	2,219	875	685	4,635
2000	849	2,522	943	585	4,900
2001	1,022	2,573	1,025	606	5,227
2002	936	2,910	1,132	570	5,550
2003	984	3,078	1,297	556	5,916
2004	1,001	3,693	1,326	646	6,668
2005	1,296	4,092	1,636	770	7,796
2006	1,315	4,316	1,564	839	8,036

Source: Department of Livestock Development (2006)

The beef market in Thailand can be classified into three different groups of consumers (Opartpattanakit and Setthakul, 2005). The first group is the low market such as local market and meat ball market. This group contributes approximately 40% of the whole market value. Thai indigenous cattle are mostly classified in this system. The second group is the medium market such as Brahman crossbred fattening cattle (3-4 months for fattening periods). This group contributes 59% of the whole market value. The last group is the upper market such as European crossbred and high blood Brahman crossbred fattening cattle (more than 6 months for fattening periods). The consumer buys good quality meat for particular purpose, for example, for restaurants and hotel. This group contributes 1% of the whole market value.

The existing beef production does not match the present socio-economic trend. During the past fives years (2002 to 2006), Thailand imported both live cattle and frozen beef meat from other countries to secure meat supply within country (Table 2).

Table 2 Number of live cattle and frozen beef meat imported to Thailand

Year	Live cattle		Frozen beef meat	
	Quantity (head)	Value (baht)	Quantity (kg)	Value (baht)
2002	133,114	1,351,345,419	1,400,028	140,019,016
2003	71,844	581,183,405	1,183,456	149,823,418
2004	102,589	839,173,701	1,711,437	158,928,925
2005	83,784	607,820,111	1,581,115	170,803,926
2006	51,782	359,775,753	1,842,528	225,650,487

Source: Department of Livestock Development (2006)

In 2006, the domestic consumptions of beef meat were 160 million kilogram. The human population of Thailand stands at about 64 million. The average beef meat consumption per capita was 2.5 kilogram. The number of permitted slaughter cattle within the country was 448,176 heads. The numbers of permitted live cattle were imported to Thailand, 51,782 heads valued at 359 million baht mainly from neighboring countries such as Myanmar and Laos. However, Thailand had a lot of illegal slaughter houses. Thus, the exact numbers of slaughtered cattle had higher than permitted slaughter with the estimates of exact slaughtered cattle were 1.35 million heads (triple of permitted slaughter cattle). The estimates of permitted and non-permitted imported live cattle form neighboring country were expected to be 0.1 million heads.

As results, there were four main sources of beef meat supply in Thailand; First, the numbers of slaughtered cattle within the country came from indigenous and crossbred cattle (0.70 million heads), culled dairy cows (0.02 million heads), imported live cattle from neighboring country (0.025 million heads) and weaned male dairy calves (0.07 million heads). The total meat productions in this section were 73,360,000 kilogram. These meat products were supplied to low quality meat markets. Second, the fattening cattle came from Brahman-Native crossbred (0.42 million heads), imported live cattle from neighboring country and raised as fattening cattle (0.075 million heads) and fattening male dairy cattle (0.02 million heads). The total meat productions in this section were 81,790,000 kilogram. These meat products were supplied to medium quality meat markets. Third, the fattening cattle came from European-Brahman crossbred (15,000 heads/year). The total meat productions in this section were 3,476,000 kilogram. These meat products were supplied to high quality meat markets. Fourth, frozen beef meat for high quality meat markets was imported, 1,842,528 kilogram valued at 225 million baht, mainly from Australia, New Zealand, Argentina and United States of America. The domestic consumptions for frozen beef meat were 1,772,000 kilogram. The rest, 70,528 kilogram, were processed and re-exported (DLD, 2006).

2. Production system

Thai indigenous cattle can be categorized into four lines, i.e. Northern (Koaw Lumpoon), Northeastern (Kor Gee), Central (Kor Lan) and Southern lines (Kor Chon). They are different in color and external appearances depending on the regions (Akkahart, 2003; Tumwasorn, 2005). Thai indigenous cattle have small size and low growth rate because they have been selected over generations for survival under harsh environment. As a result, they have both high fertility and an ability to use low quality roughage (DLD, 2005). Historically, the cattle were mainly used for draught purposes and culled when unable to work well enough. Presently, the changes in the socio-economic patterns of the local farmer have gradually been absorbed by modern technology; the cattle are being replaced for their draught power by machinery. Consequently, farmers no longer raise cattle for working but rather for beef production (Tongthainan, 2002).

Most Thai indigenous cattle are used in cow-calf production system. The natural mating is widely practiced because cattle are gathered in a large herd. Bulls and cows are selected within herd and mated to produce male offspring for meat consumption and to produce female offspring for replacement (DLD, 2005). Na-Chiangmai (2002) reported that the production system could be referred to as subsistence production, involving smallholders in remote areas. There were great varieties in forms of husbandry and management techniques from region to region as a result of the natural conditions of the grazing area, the crop production system, the lifestyle and economic framework of the farmers. On the whole, the production system of Thai indigenous cattle could be classified as 3 types. The first type, the cattle were allowed to graze in public land during the day and were maintained in the pen during the night. This type was mostly practiced by smallholders (2-3 heads of cattle). In the second type, the cattle were allowed to graze in forest-hill areas during rice plantation periods. After rice harvesting, the cattle were allowed to graze in rice field area. In this type, during dry periods, the cattle were fed with rice straw and natural grasses in the field. In the last type, the cattle were allowed to graze in forest-hill areas throughout the year. The feed resources were native grass such as *Cynadon dactylon*, *Axonopus compressus*.

The selling of meat for local consumption and for to meat processing factories was normally from the abattoir where live animals were purchased directly from the villages. The sale weights of Thai indigenous cattle ranged from 150 to 200 kilogram. The average ages at selling were 1.5 to 2 years. Those animals were priced per head by individual appearances, depending on the size of the animal (Tongthainan, 2002).

3. Breeding objective

In the agricultural development plan of the country the DLD has been assigned the duty of research and experiments for Thai indigenous cattle. DLD has therefore launched a national genetic improvement project for Thai indigenous cattle under the responsibility of the Animal Husbandry Division (AHD). Since 1992, the initial project was conducted with purchasing northeastern and southern Thai indigenous cattle lines from farmers for genetic improvement at Chaiyapoom and Ubonrachatani Livestock Breeding Stations. In 1996, the northern line was purchased and raised at Payoa and Prae Livestock Breeding Stations. In 1997, the southern line was purchased and raised at the stations in southern part of Thailand i.e. Krabi, Yala, Thepa, Nakornsithamarat and Trang, respectively. Finally in 2001, the central line was purchased and raised at Udorntani and Nongkwang Livestock Breeding Stations as shown in Table 3 (DLD, 2005).

Table 3 Numbers of Thai indigenous cattle for genetic improvement in DLD's stations/centers

(unit: heads)

Station/Center	Sire	Dam	Performance test	Breed line
Ubonrachatani	10	250	17	Northeastern, Southern
Chaiyapoom	6	150	10	Northeastern
Udorntani, Nongkwang	6	150	10	Northeastern, Central
Payoa	7	175	11	Northern
Prae	7	175	11	Northern
Yala	3	75	7	Southern
Krabi	4	100	7	Southern
Thepa	7	175	11	Southern
Nakornsithamarat	3	75	5	Southern
Trang	7	175	11	Southern
Total	60	1,500	100	

Source: Department of Livestock Development (2005)

Animal breeding generally aims to obtain a successive generation of animals that will produce desired products more efficiently under future farm economic and social circumstances than the present generation of animals (Groen, 2000). Definition of the breeding objective was generally regarded as the primary step in the development of structured breeding programs (Ponzoni, 1986). Formal breeding objectives for subsistence production systems were scare in the tropics (Amer *et al.*, 1998). Detailed economic assessments of cost and revenues were rare. Likely factors contributing to this situation included illiteracy, lack of record keeping, small herd sizes and the many roles animals played in smallholder systems (e.g. as a form of insurance, banking reserve, source of prestige). This has forced animal breeders in the past to just define breeding objectives in purely biological terms (Franklin, 1986).

In 2001, AHD presented the plan and implements a genetic improvement program for Thai indigenous cattle. The breeding objectives were to increase sale weight of live animal and fertility to be suitable for subsistence production system, therefore, the traits for breeding objective are sale weight, mature cow weight and cow weaning rate. The traits for selections to achieve the breeding objective were measured as shown in Table 4 (DLD, 2005).

Table 4 Breeding objectives and selection traits of Thai indigenous cattle

Breeding objectives	Selection traits
Growth	Weight and body measurements at birth, 200, 400-day weight, mature cow weight
Fertility	Scrotum circumference, age at first calving, days to calving

The breeding structures were set up into 3 tiers; nucleus, multiplier and commercial herds (Figure 1). Nucleus herds are genetically elite herds in DLD's stations/centers throughout the country. The tier comprises 60 sires and 1,500 dams. The primary functions of the nucleus herds are to produce elite animals according to the breeding objective and to distribute them to multiplier herds. Sire and dam replacements are selected only from nucleus herds.

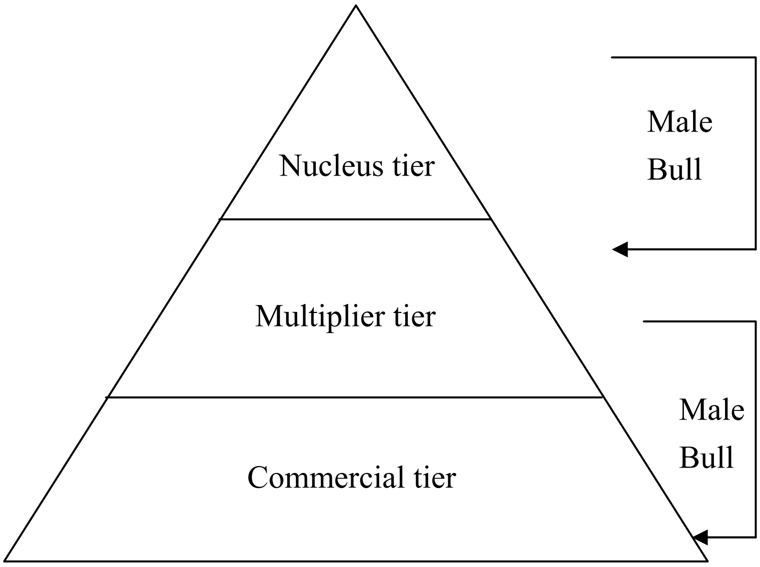

Figure 1 Breeding structure of Thai indigenous cattle

Source: Department of Livestock Development (2005)

Multipliers herds are owned by progressive farmers or contract farmers under the auspices of DLD. The function of the multiplier is to expand the genetic materials of the elite nucleus into greater numbers of animals to pass on to the commercial herds. Thus, the multiplier is a replicate of the original nucleus which develops into two tiers, one tier being the true nucleus while the other tier involves satellites of the nucleus. Bulls for performance testing are selected from nucleus herds. Breeding is done by natural mating. Dams mostly are the farmer’s cows. Commercial herds are those raised by smallholder farmers throughout the country. They normally lack good sires of their own and mating is by bulls from multiplier.

Graser (2002) outlined that the most difficult part in the planning of a breeding program for Thai indigenous cattle was the definition of a breeding objective which accounts for all economically important traits of animals in a village production system. Through natural and human selection indigenous cattle are well adapted to their environment and highly fertile. This adaptation and fertility has to be maintained or only reduced slightly while the production traits were improved. Van der Werf (2000) has summarized the roles of the different tiers in a livestock breeding structure. Generally, the central nucleus and multiplier herd generate sires for distribution to commercial farmers. A crucial point for the successful implementation of a breeding scheme in smallholder systems is adequate interaction between nucleus and farmers’ herd, in a technical as well as socio-economic sense. The nucleus breeding objectives impact on the whole scheme, therefore should be set up with the breeding objectives of the farmer in mind.

4. Fixed effects affecting weight and body measurements

Genetic evaluations are dependent on accurate adjustments for fixed effects of records of animals. If records are adjusted exactly, all known fixed effects would be adjusted for each record and accurate estimates of the genetic parameters can be obtained. There are two ways that data can be adjusted for fixed effects. First, these effects can be adjusted prior to analysis through the use of estimated adjustment factors or second, they can be adjusted simultaneously with the estimation of genetic parameters. If pre-adjusted, the magnitude of these effects must be estimated, whereas with simultaneous adjustment, the computational process estimates and adjusts during analysis (Rumph and Van Vleck, 2004).

4.1 Sex

Male calves generally grow faster than female calves (Setshwaelo *et al.*, 1990; Newman *et al.*, 1993; Ahunu *et al.*, 1997; Vargas *et al.*, 1999). In line bred

Hereford, Snelling *et al.* (1996) reported that male calves were heavier than female calves. Males were on averages 2.5 and 23.3 kg heavier than females for birth and weaning weight. In the study of four lines of Thai indigenous cattle (northern, northeastern, southern and central lines) and Brahman cattle in Thailand, the results concluded that growth traits and body measurements such as hip height (HH), heart girth (HG) and body length (STP) at birth, weaning and yearling ages of male were significantly higher than that of female (Akkahart, 2003; Chokchareon, 2003). Similarly, Pico (2004) reported that sex of the calf in Brahman cattle had a significant effect on growth traits. Males were on averages 1.77, 16.76 and 44.32 kg heavier than females for birth, weaning and yearling weight, respectively.

4.2 Herd, year, season

Herd, year and season also need to be accounted for in analysis because not only will animals in different herds and areas of the country be treated differently but groups of animals within a herd could also be treated differently. Animals with what could be considered preferential treatment would have an unfair advantage if adjustments were not made (Rumph and Van Vleck, 2004).

In the study of Landim and Africander cattle, Carvalheira *et al.* (1995) found that year-season of birth significantly affected birth and weaning weight ($P < 0.01$). Ahunu *et al.* (1997) reported that period (year grouping) significantly influenced birth and weaning weight of calves. Season of birth did not influence calf weight at birth but significant affected calf weaning weight. Krupa *et al.* (2005) concluded that herd-year-season significantly affected birth, weaning and yearling weight of beef cattle breeds raised in Slovakia. The proportion of variability of growth traits explained by herd-year-season effects were 42.9 to 71.6% of total variance. Similarly, Szabo *et al.* (2006) found that birth year, season had a significant effect on weaning weight in beef breeds.

4.3 Age of dam

First-calf heifers are not physically or biologically mature. Nutrients which they consume are partitioned not only into lactation, maintenance and gestation but also to their own growth. Therefore, calves from young cows are generally smaller both at birth and at weaning. Similarly, cows will reach peak production at a mature age and then decrease in performance as measured by weight of their calves.

These old cows are no longer as efficient as they were at younger ages and consequently their calves born at older ages would have smaller weights than calves born earlier in their life (Rumph and Van Vleck, 2004).

For birth weight, Tong (1983) concluded that for all breeds of beef cattle, birth weight steadily increases with dam age until maturity (≥ 5 years) with few exceptions. Four-year-old Maine-Anjou dams as well as four-year-old 1/2 Charolais dams showed slightly heavier birth weights than mature dams of the same breed compositions. Elzo *et al*. (1987) analyzed field records from Simmental calves. The result indicated that adjustment factors for age of dam should be different across the two sexes with adjustments for male calves being larger. Mature dams were assumed to be 5 to 8 years old and age-of-dam adjustment factors were positive for all other ages. Newman *et al*. (1993) reported that for a composite line of beef cattle, age of dam was important for all growth traits except post-weaning average daily gain. In general, growth of calves increased with increasing age of dam (2 to 5 years). Likewise, Archer *et al*. (1998) indicated that age of dam had a significant effect on birth weight and birth height in Angus with heifers having lighter and shorter calves than older cow. Van Vleck and Cundiff (1998) found that mature dams were considered to be 5 to 9 year old dams and solutions for effects of age consistently increased to maturity and then decreased for 10 year old and older dams, indicating that calves out of young and old dams were born smaller than calves out of mature dams.

Meyer (1998) fit linear and quadratic regression coefficients for age of dam on weight and body measurements at birth in Thai Brahman cattle. The estimates of the linear and quadratic regression coefficients were 0.04, -0.04; 0.30, -0.27; 0.10, -0.03; 0.08, -0.03 for birth weight, HH, HG and STP, respectively. Similarly, Akkahart (2003) reported that age of dam in Thai indigenous cattle had significant effects on birth weight, HH, HG and STP.

For weaning weight, age of dam had been found to be statistically significant ($P < 0.01$) for weaning weight of calves out of 4 to 9-year-old Angus and Hereford cows bred to Hereford, Angus, Red Poll, Brown Swiss, Gelbvieh, Maine-Anjou and Chianina sires (Gregory *et al*., 1978). Dams were classified in one of two age-of-dam groups: 4 years old or 5 years and greater. This result indicated that cows were still gaining in efficiency and have not fully matured through four years of age. Leigton *et al*. (1982) also found that weaning weight increased with age of dam until dams reached maturity at five to six years of age and then decreased for cows older than ten years of age.

In their study Elzo *et al.* (1987), using a sire-maternal grandsire model, found that age of dam was significant for weaning weight in Simmental field data which they attributed to differential milking abilities in mature cows relative to younger and older cows. Meyer (1998) fit linear and quadratic regression coefficients of age of dam on weight and body measurement at weaning in Thai Brahman cattle. The estimates of the linear and quadratic regression coefficients were 0.28, -0.31; 0.45, -0.55; 0.18, -0.07; -0.02, -0.06 for weaning weight, HH, HG and STP, respectively.

4.4 Age of animal

Goyache *et al.* (2003) fit linear and quadratic regression coefficient of age of animal on weaning weight in Asturiana de los Valles beef breed. The result indicated that only linear covariate influenced weaning weight significantly. Likewise, Krupa *et al.* (2005) fit linear regression coefficient of age of animal on weaning and yearling weight in six beef breeds (Aberdeen Angus, Blonde d'Aquitaine, Charolais, Hereford, Limousin and Simmental). The result showed that age of animal significantly affected both weaning and yearling weight ($P < 0.001$).

5. Genetic parameters for weight and body measurements

5.1 Direct and maternal heritabilities

Growth traits such as birth weight, weaning weight, yearling weight and mature cow weight are of primary economical importance in beef cattle production systems. Birth weight of an animal and its early growth rate, in particular till weaning, are determined not only by its own genetic potential but also by the maternal environments. These represent mainly the dam's milk production and mothering ability. The genotype of the dam, therefore affects the phenotype of the young through a sample of half her direct additive genes for growth as well as through her genotype for maternal effects on growth. Direct measures of milk production in beef cattle are not normally available. Thus, weaning weight of calf is the best available measure of a cows milking ability (Koch, 1972; Baker, 1980; Willham, 1980; Meyer, 1992).

Maternal ability is sex limited, occurs late in life of the female and lags by one generation. This leads to difficulties in assessing maternal effects because direct and maternal effects are at least partially confounded in calf's recorded performance. Studies on beef cattle growth traits have reported substantial genetic variation within breed in both direct and maternal effects. In many cases, the estimated genetic correlation between direct and maternal effects was moderate and negative (Baker, 1980). A negative genetic correlation indicates a tendency for animals with superior growth genes to have inferior maternal genes or the other way around. This suggests that genes which partition nutrients to increase body reserves (growth of a young calf) were partly incompatible with genes which partition away from the body to the mammary glands of a lactating cow (Garrick, 1990; Diaz *et al*., 1992).

For *Bos indicus*, Kries *et al.* (1991) estimated variance for growth traits of Brahman and Brahman-derivative cattle, the report concluded that direct heritabilities of birth weight and weaning weight ranged from 0.22 to 0.37 and 0.21 to 0.25, maternal heritabilities ranged from 0.12 to 0.55, 0.15 to 0.21, direct-maternal genetic correlation was negative for all breeds, except in Brahman cattle. In contrast, Meyer (1992) concluded that direct heritability, maternal heritability and direct-maternal genetic correlation of weaning weight for Zebu Cross cattle were 0.58, 0.36 and -0.78. Eler *et al.* (1995) estimated variance for growth traits of Nelore cattle in Brazil, the report concluded that direct heritabilities of birth weight, weaning weight and yearling weight were to be 0.22, 0.13 and 0.16, maternal heritabilities were to be 0.12, 0.13 and 0.10, direct-maternal genetic correlation were to be -0.72, -0.32 and 0.09, respectively.

Akkahart (2003) reported that direct heritabilities of birth weight, weaning weight and yearling weight ranged from 0.19 to 0.38, 0.18 to 0.30 and 0.18 to 0.22, maternal heritability and direct-maternal genetic correlation of weaning weight ranged from 0.14 to 0.17 and -0.58 to -0.93, respectively for four lines of Thai indigenous cattle. Chokchareon (2003) showed that direct heritabilities of birth weight, weaning weight and yearling weight were to be 0.39, 0.18 and 0.12, maternal heritability and direct-maternal genetic correlation were 0.04 and -0.16 for weaning weight of Brahman cattle in Thailand. Demeke *et al.* (2003) reported that direct heritabilities of birth weight, weaning weight were 0.14 and 0.08 for a mixed population of purebred *Bos indicus* and crossbred cattle. Results of this study also showed that estimate of variance components and genetic parameter suitable for general use can be obtained from mixed purebred and crossbred data after appropriately accounting for breed additive and nonadditive effects.

For *Bos taurus*, Robinson (1996) reported that direct heritabilities of birth weight, weaning weight and yearling weight of Australia Angus cattle were 0.35, 0.20 and 0.24, maternal heritabilities were 0.08, 0.09 and 0.06, direct-maternal genetic correlation were -0.61, -0.52 and -0.72, respectively. De Mattos *et al.* (2000) estimated variance and covariance of weaning weight for Hereford data from United States, Canada and Uruguay, using a complete animal model. Estimated direct heritability, maternal heritability and direct-maternal genetic correlation were 0.20 to 0.24, 0.16 to 0.20 and -0.35 to -0.50. The maternal heritability was nearly 50% smaller than the values which were estimated using sire-maternal grand sire model.

Maiwashe *et al.* (2002) studied Bonsmara cattle in South Africa, the report concluded that direct heritability, maternal heritability, maternal permanent environment effect and direct-maternal genetic correlation for weaning weight were 0.25, 0.18, 0.12 and -0.54. Splan *et al.* (2002) estimated direct and maternal genetic effects for weaning weight in crossbred cattle, the result showed that direct heritability, maternal heritability and direct-maternal genetic correlation were 0.14, 0.19 and -0.18. Phocas and Laloe (2004) concluded that direct heritabilities, maternal heritabilities and direct-maternal genetic correlation of French specialized beef cattle breeds ranged from 0.13 to 0.32, 0.09 to 0.13 and -0.09 to -0.41, respectively.

Mature cow weight is one economically importance trait. It affects many aspects of production, reproduction and cull cow value, and therefore the profitability of the cow-calf operation (McMorris and Wilton, 1989; Kaps *et al.*, 1999; Burrow, 2001). Because of impacts on many economic aspects of production, mature cow weight should be considered in selection programs. Cows with higher mature weight require more energy for maintenance, so increasing mature mass is generally not considered desirable for the breeding herd (Buttram and Willham, 1989; Fiss and Wilton, 1992).

Johnston *et al.* (1996) reported that repeatability of cow weight for Angus, Hereford and Poll Hereford were 0.43, 0.39 and 0.48, consistent with the estimates for other *Bos tauras* cows (Meyer, 1995; Meyer and Carrick, 1995; Kaps *et al.*, 1999; Choy *et al.*, 2002). In contrast, Burrow (2001) reported that direct heritability for cow mature weights at calf weaning in a composite breed of tropical beef cattle was 0.82. Rumph *et al.* (2002) estimated variance component for mature cow weight of Hereford cattle using models including maternal effects and weights taken at various time during the year, the result showed that direct heritabilities, maternal heritabilities and direct-maternal genetic correlation ranged from 0.53 to 0.79, 0.09 to 0.21 and -0.16 to -0.67. The result also showed that mature cow weight was a highly heritable trait and could be included in selection programs, maternal effects should not be ignored when analyzing mature cow weight data.

5.2 Phenotypic and genetic correlations

Burrow (2001) reported that phenotypic correlations between birth weight and weaning weight and yearling weight of tropical beef breed ranged from were 0.35 to 0.73. The genetic correlations ranged from 0.53 to 0.90. Akkahart (2003) concluded that genetic correlation on growth traits of Thai indigenous cattle ranged from 0.29 to 0.92. The genetic correlation on body measurement ranged from 0.04 to 0.93. Most genetic correlations were positive and should be implemented in multiple traits selection to improve Thai indigenous cattle. Chokchareon (2003) reported that phenotypic correlations between birth weight, weaning weight and yearling weight of Brahman cattle ranged from 0.27 to 0.67. The genetic correlations ranged from 0.60 to 0.75.

For other beef breeds, Meyer *et al.* (1993) indicated that phenotypic correlations between birth weight, weaning weight and yearling weight for Hereford ranged from 0.37 to 0.76. Ahunu *et al.* (1997) concluded that the phenotypic and genetic correlations between birth and weaning weight for purebred and crossbred Ndama and West African Shorthorn cattle were 0.24 and 0.48. The genetic correlations ranged from 0.66 to 0.97. Roughsedge *et al.* (2005) found that genetic correlation between weaning and yearling weight for Aberdeen Angus, South Devon, Limousin and Simmental ranged from 0.81 to 0.92.

6. Genetic parameters for fertility traits

Scrotal size is used as a measure of male reproductive performance. For the female, the measurement of reproductive is days to calving i.e. number of days between the times when the cow was first exposed to a bull in natural mating and when she subsequently calves (McDonald, 1992). Gregory *et al.* (1995) found that direct heritability of scrotal circumference in composite beef cattle was 0.43.

Similarly, Keeton *et al.* (1996) reported that direct heritability of scrotal circumference in Limousin cattle was 0.46. Mwansa *et al.* (2000) reported that direct heritabilities of scrotal circumference in crossbred bulls were 0.45, 0.49, 0.57 and 0.66 at 6, 8, 10 and 12 months of age, respectively. Moser *et al.* (1996) concluded that selection using scrotal circumference EPD was more effective than phenotypic selection.

Several studies have shown favorable relationships between scrotal circumference in bulls and reproductive traits in female. Meyer *et al.* (1991) concluded that genetic correlation between scrotal circumference and days to calving for Hereford, Angus and Zebu crosses were low but favorable, being -0.25, -0.28 and -0.41, respectively. Vargus *et al.* (1998) reported that genetic correlation between scrotal circumference and age at puberty of heifer in Brahman cattle was -0.32. Evans *et al.* (1999) concluded that genetic correlation between scrotal circumference and heifer pregnancy in Hereford cattle was 0.002. Similarly, Eler *et al.* (2004) found that genetic correlation between scrotal circumference and heifer pregnancy was 0.20. The results also recommended that EPD for heifer pregnancy can be used to select bulls for the production of precocious daughters and will be more effective than selecting on scrotal circumference EPD in Nellor cattle.

Burrow (2001) reported that strong negative genetic correlations of scrotal circumference for tropical beef cattle at weaning, 12 and 18 months (ranging from -0.52 to -0.75) existed between direct-maternal genetic effects. Pregnancy rate and days to calving were lowly heritable (0.04 and 0.07, respectively). Genetic correlation between scrotal circumference and day to calving was 0.32. In contrast to other research, Martinez-Velazquez *et al.* (2003) concluded that genetic correlation between scrotal circumference and age at puberty of heifer in *Bos taurus* was low, being -0.15. These results suggest that genetic response in female reproductive traits through sire selection on yearling scrotal circumference is not effective.

7. Economic values

The breeding objective involves calculation of economic values for all biological traits that had an impact upon profitability (James, 1982). In selection index theory, the aggregate genotype (i.e. the breeding objective) is usually defined as a linear function of traits to be improved, each multiplied by its economic value, which is the value of a unit change in the trait while keeping other traits in the aggregate genotype constant (Hazel, 1943). Several methods can be used to calculate economic values (Brascamp *et al.*, 1985; Smith *et al.*, 1986; Ponzoni, 1988; Groen, 1989). Deriving the economic values from the difference between costs and revenues (profit equation) has the advantage of simplicity (Ponzoni, 1988). In the biological definition, costs and revenues are expressed in energy and/or protein terms, and in the economic definition the expression is usually in terms of money. The biological definition is not ideal because not all costs and revenues can be expressed in terms of energy and/or protein (Groen, 1989).

In the tropics, an analysis conducted by Upton (1985) suggested that in small ruminant, the most critical area, where improvements were most needed, was that of reducing mortality i.e. increasing survival. Variation in growth rate had only a relatively small impact. The second most influential factor on overall economic performance was reproduction rate. Similarly, Baker and Rege (1994) pointed out that in many subsistence tropical farming systems, survival in the face of multiple stresses was one of the most important economic traits, while increasing growth rate was of less economic value. Greeff *et al.* (1995) reported that high reproductive and survival rates played an important role in increasing efficiency of lamb production. Likewise, Kosgey (2004) studied in small ruminants (sheep), the report revealed that litter size and lambing frequency had the most impact upon profitability in a breeding objective for smallholder production.

In contrast, for the temperate, MacNeil *et al.* (1994) found that the economic values for male, female fertility and survival were small compared to the economic values of growth rates. Post-weaning growth rate was the trait with the highest economic value. Phocas *et al.* (1998) reported that breeding traits, for French purebred beef cattle, especially maternal effects on weaning weight and calving success, were identified as the most economically important traits requiring improvement. Fernandez-Perea and Alenda Jimmenez (2004) suggested that selection index would select animal with lower mature cow weight and pre-weaning growth and bigger post-weaning daily gain and carcass performance. The results also suggested that improvement of fertility, post-weaning daily gain and carcass performance traits had positive effect on profitability in beef cattle production system.

8. Annual genetic gain

Nitter *et al*. (1994) evaluated industry breeding program for Australian beef cattle from an example population with a breeding unit of 10,000 cows, supplying bulls to a total population of 200,000 cows. Selection criteria considered to be birth weights, 200, 400 and 600-days weights. The result showed that the annual genetic gain, return per cow, total cost per cow and profit per cow were 1.43, 8.14, 1.33 and 6.81 dollars, respectively. Likewise, Graser *et al.* (1994) evaluated industry breeding program for Australian beef cattle with different levels of performance recording of young cattle. The result showed that breeding schemes which utilized performance recording beyond weight measurements were more profitable. The fertility measures such as day to calving and scrotal circumference were the most cost effective additional selection criteria. For the fertility measures, costs increased by 0.90 dollars per cow in the breeding unit, while profit per cow in the total population increased by 2.17 dollars.

Intaratham (2002) evaluated breeding program for Thai indigenous cattle from an example population with a breeding unit of 1,300 cows, supplying bulls to a total population of 800,000 cows. There were three levels of performance recording such as basic (weight, fertility), basic plus carcass scanning and basic plus carcass scanning and adaptation. The result showed that basic plus carcass scanning and adaptation provided the best overall response. The annual genetic gain, return per cow, total cost per cow and profit per cow were 108.1, 395.6, 8.1 and 387.5 baht, respectively.

MATERIALS AND METHODS

General management

1. Animal and pasture management

Records of four lines of Thai indigenous cattle population from 1993 through 2004 were obtained from ten stations of Animal Husbandry Division, Department of Livestock Development (DLD). In overalls, the animal and pasture management systems in stations were divided into two periods i.e. wet and dry periods.

The wet period, started from May to November, covered a period of 6 months. During this period, the cattle in each station were maintained to graze in pasture during the day without concentrate supplementation. The pasture was improved by using of ruzi grass (*Brachilia ruziziensis*) and verano stylo (*Stylosanthes spp.*). The rotational grazing was introduced to provide both quantity and quality of grasses for cattle (Figure 2).

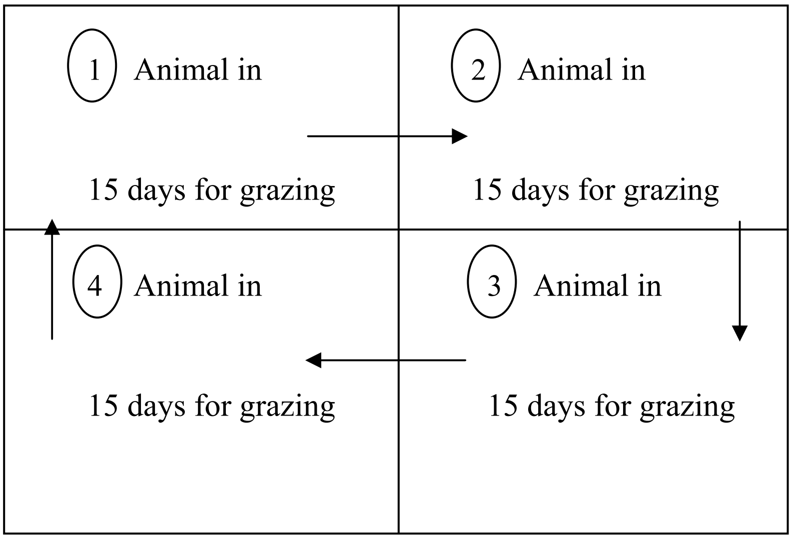

Figure 2 The rotational grazing system of Thai indigenous cattle during wet periods in stations

The pasture was divided into 4 small paddocks using electric fence. The cattle were allowed to graze each paddock for 15 days. The paddock was then allowed to rest and recovery before being grazed again. Therefore, in one cycle for rotational grazing, the rest times for grasses were 45 days. The stocking rates were calculated depending on animal unit (AU). The animal unit calculation for bull, cow, growing cattle and calf were equal to 0.9, 0.5, 0.3 and 0.1 with the equivalent weights of 400, 250, 135 and 45 kilograms, respectively. After pregnancy test, the cattle were grouped to be 25-35 heads per herd according to the stage of production such as nursing and pregnant cows, replacement herd etc. Each year, one animal unit used total pasture area of 0.48 hectare, 0.32 hectare for rotational grazing during wet period and 0.16 hectare reserved for making hay and silage during dry period.

The dry period, from December to April, covers a period of approximately 6 months. During this period, the cattle were confined in large pens throughout. Hay and silage were fed ad libitum and supplemented with 0.5 kilogram of 14% crude protein concentrate feed. Dry lick mineral blocks and drinking water were fed for each herd in large pens.

2. Mating

Natural mating was used at the ratio of 1 bull per 25-35 cows. The mating periods were allocated into 2 periods (Figure 3). For each mating period, the cows would be weighed at joining, at calving and at weaning of their calves. The first mating period started from 5th of May to 1st of September and covered a period of 4 months. In late October a pregnancy test was performed. The second mating period started from 3rd of November to 2nd of March also a period of 4 months. The females were allowed to be a herd according to the state of production such as heifer, pregnant, nursing and dry cows. Cows were randomized into new paddocks between mating periods. In late April a pregnancy test would be performed again prior to the start of the next mating period. The culling was on the basis of pregnancy test at this time.

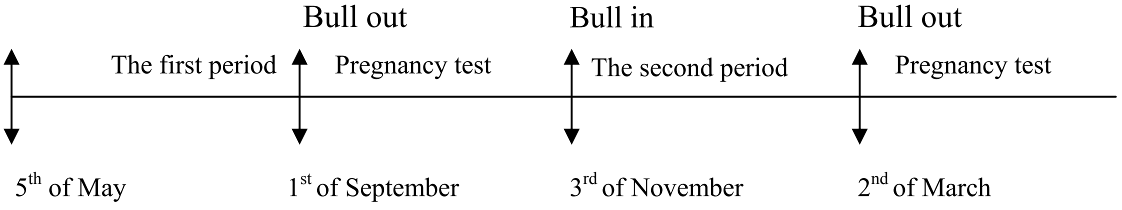

Figure 3 The mating period of Thai indigenous cattle

After birth, calves were weighed within 24 hours and were identified at birth. They were dehorned and treated against internal parasites and vaccinated against foot and mouth disease at 3-4 month of age. The calves were reared full time with their dams until weaning (approximate 7 months of age). The calves were selected as replacements after a performance test from weaning to yearling age.

Trial I

Fixed effects affecting weight and body measurements at birth, 200-day weight and 400-day weight of Thai indigenous cattle

1. Data description

The data set comprised weight and body measurements at birth, weaning and yearling weight of four lines of Thai indigenous cattle (Northern, Northeastern, Central and Southern lines). There were kept in the stations of DLD throughout the country such as Chaiyapoom, Ubonrachtani, Udonthani, Phare, Payoa, Nongkwang, Trang, Nakornsithammarat, Yala and Thepa Livestock Research and Breeding stations during 1993 to 2004. Environmentally, production conditions were characterized as hot humid climatic zone with minimum and maximum temperature of 25 and 38 degree Celsius. The annual rainfall ranged from 1,200 to 1,500 millimeter. There were three seasons: the winter season (from November to February), the summer season (from March to June) and the rainy season (from July to October). The data were validated by checking pedigrees to ensure all parents were born at appropriate times before their offspring. Other basic editing involved consistency checks for sex, age at weighing and age of dam. Birth weight, weaning weight, yearling weight and body measurements were checked for outlier using SAS (1996).

After editing, the total final data set of Thai indigenous cattle comprised 4,579, 4,479, 4,525, and 4,478 records for birth weight, heart girth (GIR), hip height (HH) and body length (STP) at birth, respectively. The weaning weight, GIR2, HH2 and STP2 at weaning were 3,336, 2,705, 2,696 and 2,693 records. The yearling weight, GIR4, HH4 and STP4 were 1,052, 907, 894 and 891 records. Characteristic of the data set of each line and total data were summarized and presented in table 5, 6 and 7, respectively.

Table 5 Birth trait data structure for Thai indigenous cattle

Trait[1/]	Line				Total
	Northeastern	Central	Northern	Southern	
BW					
No. of records	1,922	266	953	1,438	4,579
Mean ± std (kg)	16.7 ± 2.4	16.6 ± 3.7	18.3 ± 2.9	14.3 ± 2.3	16.3 ± 2.9
Minimum (kg)	7.0	8.0	8.0	7.0	7.0
Maximum (kg)	27.0	28.0	28.0	23.0	28.0
GIR					
No. of records	1,849	262	933	1,435	4,479
Mean ± std (cm)	58.1 ± 3.9	55.9 ± 5.1	61.3 ± 4.0	55.1 ± 3.8	57.5 ± 4.6
Minimum (cm)	40.0	43.0	45.0	40.0	40.0
Maximum (cm)	73.0	72.0	73.0	68.0	73.0
HH					
No. of records	1,892	263	942	1,428	4,525
Mean ± std (cm)	62.6 ± 3.7	61.4 ± 4.6	67.7 ± 4.9	60.8 ± 3.5	63.1 ± 4.7
Minimum (cm)	45.0	47.0	47.0	48.0	45.0
Maximum (cm)	76.0	77.0	79.0	75.0	79.0
STP					
No. of records	1,838	260	946	1,434	4,478
Mean ± std (cm)	45.8 ± 3.6	43.2 ± 4.3	54.1 ± 4.6	47.1 ± 4.3	47.8 ± 5.3
Minimum (cm)	33.0	31.0	33.0	34.0	31.0
Maximum (cm)	63.0	56.0	66.0	63.0	66.0
Age of dam					
No. of records	1,922	266	953	1,438	4,579
Mean ± std (years)	4.9 ± 1.4	3.7 ± 0.9	6.1 ± 2.4	4.9 ± 0.7	5.0 ± 1.6
Minimum (years)	1.6	2.0	2.0	1.7	1.6
Maximum (years)	14.9	5.4	11.8	8.0	14.9

[1/] BW = birth weight, GIR = heart girth at birth
HH = hip height at birth, STP = body length, shoulder to pin at birth

Table 6 Weaning trait data structure for Thai indigenous cattle

Trait[1/]	Lines				Total
	Northeastern	Central	Northern	Southern	
WW					
No. of records	1,486	75	747	1,028	3,336
Mean ± std (kg.)	91.9 ± 19.3	84.7 ±17.9	102.7 ± 22.9	63.6 ± 15.3	85.5 ± 24.4
Minimum (kg.)	39.0	36.0	47.0	31.0	31.0
Maximum (kg.)	157.0	123.0	172.0	116.0	172.0
GIR2					
No. of records	955	72	707	931	2,705
Mean ± std (cm.)	102.9 ± 7.4	98.3 ± 8.2	109.7 ± 9.2	92.5 ± 8.1	100.9 ± 10.6
Minimum (cm.)	78.0	77.0	79.0	70.0	70.0
Maximum (cm.)	125.0	119.0	139.0	115.0	139.0
HH2					
No. of records	1,001	66	695	934	2,696
Mean ± std (cm.)	92.6 ± 4.7	89.1 ± 4.9	100.4 ± 6.2	85.1 ± 5.6	91.9 ± 8.0
Minimum (cm.)	78.0	79.0	81.0	70.0	70.0
Maximum (cm.)	105.0	101.0	120.0	100.0	120.0
STP2					
No. of records	983	71	708	931	2,693
Mean ± std (cm.)	80.5 ± 6.6	74.3 ± 6.2	94.8 ± 8.3	75.9 ± 7.4	82.5 ± 10.6
Minimum (cm.)	64.0	63.0	69.0	59.0	59.0
Maximum (cm.)	102.0	91.0	122.0	101.0	122.0
Age of animal					
No. of records	1,486	75	747	1,028	3,336
Mean ± std (days)	201.9 ± 16.7	205.1 ± 21.6	204.1 ± 18.3	200.0 ± 18.2	201.8 ± 17.7
Minimum (days)	133.0	170.0	155.0	137.0	133.0
Maximum (days)	287.0	262.0	285.0	247.0	287.0

[1/] WW = weaning weight, GIR2 = heart girth at weaning
HH2 = hip height at weaning, STP2 = body length, shoulder to pin at weaning

Table 7 Yearling trait data structure for Thai indigenous cattle

Trait[1/]	lines				Total
	Northeastern	Central	Northern	Southern	
YW					
No. of records	331	70	261	390	1,052
Mean ± std (kg.)	125.3 ± 22.5	111.4 ±18.5	137.5 ± 25.8	92.7 ± 17.8	115.3 ± 28.4
Minimum (kg.)	79.0	75.0	84.0	66.0	66.0
Maximum (kg.)	200.0	162.0	227.0	170.0	227.0
GIR4					
No. of records	152	69	245	441	907
Mean ± std (cm.)	106.4 ± 11.5	111.4 ± 6.5	121.5 ± 8.4	103.5 ± 8.4	109.5 ± 11.7
Minimum (cm.)	84.0	94.0	95.0	80.0	80.0
Maximum (cm.)	129.0	128.0	152.0	130.0	152.0
HH4					
No. of records	153	68	245	429	894
Mean ± std (cm.)	100.8 ± 4.7	97.8 ± 7.4	109.6 ± 5.3	93.4 ± 5.6	99.4 ± 8.8
Minimum (cm.)	88.0	84.0	95.0	81.0	81.0
Maximum (cm.)	112.0	117.0	122.0	112.0	122.0
STP4					
No. of records	149	62	245	435	891
Mean ± std (cm.)	99.7 ± 11.1	81.5 ± 5.9	104.1 ± 6.4	87.1 ± 7.3	93.5 ± 11.3
Minimum (cm.)	76.0	70.0	86.0	71.0	70.0
Maximum (cm.)	119.0	96.0	127.0	107.0	127.0
Age of animal					
No. of records	331	70	261	390	1,052
Mean ± std (days)	401.9 ± 28.6	426.9 ± 29.3	410.1 ± 29.4	399.9 ± 19.6	404.8 ± 26.8
Minimum (days)	326.0	376.0	307.0	343.0	307.0
Maximum (days)	494.0	492.0	497.0	444.0	497.0

[1/] YW = yearling weight, GIR4 = heart girth at yearling
HH4 = hip height at yearling, STP4 = body length, shoulder to pin at yearling

2. Test for fixed effects

In order to determine the fixed effects to be included in the model, preliminary analyses were performed using the PROC MIXED in SAS (1996). The fixed effects included in the analyses were herd and line, year, season of calving and sex. Age of dam and age of animal were fitted as covariate. If fixed effects and interactions were not-significant, they would be eliminated out of the initial model. Only significant effects and interactions would be remained. The final model for analysis of fixed effects was:

2.1 For birth traits;

$$y_{ijkl} = \mu + H\text{-}L{\times}Y{\times}S_i + Sex_j + b_1Aod + b_2Aod^2 + Sire_k + \varepsilon_{ijkl} \qquad [1]$$

where

y_{ijkl} = observation of birth traits (BW, GIR, HH and STP)
μ = overall mean
$H\text{-}L{\times}Y{\times}S_i$ = herd and line×year×season of calving ($i = 1$ to 151)
Sex_j = sex (j = male, female)
b_1, b_2 = the linear and quadratic regression coefficients of birth traits on age of dam
$Sire_k$ = random effect of sire ($k = 1$ to 122)
ε_{ijkl} = random residual effect ($\varepsilon_{ijkl} \sim NID\ (0, \sigma^2_e$)

2.2 For weaning traits**;**

$$y_{ijkl} = \mu + H\text{-}L{\times}Y{\times}S_i + Sex_j + b_1Aod + b_2Aod^2 + b_3Age + Sire_k + \varepsilon_{ijkl} \qquad [2]$$

where

y_{ijkl} = observation of weaning traits (WW, GIR2, HH2, STP2)

μ = overall mean

$H\text{-}L\times Y\times S_i$ = herd and line×year×season of calving (i = 1 to 125)
Sex_j = sex (j = male, female)
b_1, b_2 = the linear and quadratic regression coefficients of weaning traits on age of dam
b_3 = the linear regression coefficient of weaning traits on age of animal
$Sire_k$ = random effect of sire (k = 1 to 110)
ε_{ijkl} = random residual effect ($\varepsilon_{ijkl \sim \text{NID}\,(0,}\,\sigma^2_e$)

2.3 For yearling traits;

$$y_{ijkl} = \mu + H\text{-}L\times Y\times S_i + Sex_j + b_1Age + Sire_k + \varepsilon_{ijkl} \qquad [3]$$

where

y_{ijkl} = observation of yearling traits (YW, GIR4, HH4, STP4)
μ = overall mean
$H\text{-}L\times Y\times S_i$ = herd and line×year×season of calving (i = 1 to 73)
Sex_j = sex (j = male, female)
b_1 = the linear regression coefficient of weaning traits on age of animal
$Sire_k$ = random effect of sire (k = 1 to 84)
ε_{ijkl} = random residual effect ($\varepsilon_{ijkl \sim \text{NID}\,(0,}\,\sigma^2_e$)

Trial II

Estimate the genetic parameters such as weight and body measurements at birth, 200-day weight, 400-day weight of Thai indigenous cattle

1. Data description

The single-record contemporary groups (herd and line-year-season of calving, HLYS) of each line were checked and deleted. The classifications of the data structure for each line were performed. A summary of the pedigree structure and descriptive statistics were presented in Table 8, 9 and 10, respectively.

For birth traits, the numbers of data for birth weight, GIR, HH and STP were 4,572, 4,518, 4,472 and 4,471 records, respectively. The numbers of data for weaning traits were 3,328, 2,968, 2,688 and 2,685 records, and for yearling traits there were 1,046, 902, 889 and 885 records, respectively.

Table 8 Birth traits data structure and descriptive statistic

Trait	Line				Total
	Northeast	Central	North	South	
BW					
No. of animals in pedigree	2,292	375	1,155	2,066	5,888
No. of records	1,922	266	949	1,435	4,572
No. of sires	48	7	31	38	124
No. of dams	584	116	300	675	1,675
- 1 calf	84	25	68	195	372
- 2 calves	158	36	57	256	507
- 3 calves	165	51	74	172	462
- 4 calves	56	4	38	48	146
- 5 calves and higher	121	-	63	4	188
No. of dams with own record	234	13	114	76	437
No. of contemporary groups	51	12	35	46	144
Mean ± std (kg)	16.7 ± 2.4	16.6 ± 3.7	18.3 ± 2.9	14.3 ± 2.3	16.3 ± 3.0
GIR					
No. of animals in pedigree	2,224	371	1,133	2,062	5,790
No. of records	1,849	262	929	1,432	4,472
No. of sires	48	7	30	38	123
No. of dams	584	116	300	672	1,672
- 1 calf	107	27	74	195	403
- 2 calves	170	36	58	252	516
- 3 calves	134	49	67	172	422
- 4 calves	54	4	38	49	145
- 5 calves and higher	119	-	63	4	186
No. of dams with own record	229	13	113	77	432
No. of contemporary groups	47	12	33	46	138
Mean ± std (cm.)	58.1 ± 3.9	55.9 ± 5.1	61.3 ± 4.0	55.1 ± 3.7	57.6 ± 4.6

Table 8 (Continued)

Trait	Line				Total
	Northeast	Central	North	South	
HH					
No. of animals in pedigree	2,265	372	1,142	2,055	5,834
No. of records	1,892	263	938	1,425	4,518
No. of sires	48	7	30	38	123
No. of dams	581	116	304	672	1,673
- 1 calf	83	26	77	199	385
- 2 calves	160	37	59	249	505
- 3 calves	166	49	68	172	455
- 4 calves	56	4	37	49	146
- 5 calves and higher	116	-	63	3	182
No. of dams with own record	228	13	117	77	435
No. of contemporary groups	51	12	33	46	142
Mean ± std (cm.)	62.6 ± 3.7	61.4 ± 4.6	67.6 ± 4.9	60.8 ± 3.5	63.0 ± 4.7
STP					
No. of animals in pedigree	2,214	369	1,146	2,060	5,789
No. of records	1,838	260	942	1,431	4,471
No. of sires	48	7	30	38	123
No. of dams	583	116	305	672	1,676
- 1 calf	107	26	77	194	404
- 2 calves	176	40	59	254	529
- 3 calves	127	46	69	171	413
- 4 calves	54	4	37	49	144
- 5 calves and higher	119	-	63	4	186
No. of dams with own record	227	13	117	77	424
No. of contemporary groups	47	12	33	46	138
Mean ± std (cm.)	45.8 ± 3.6	43.2 ± 4.3	54.1 ± 4.6	47.1 ± 4.3	47.8 ± 5.3

Table 9 Weaning trait data structure and descriptive statistic

Trait	Line				Total
	Northeast	Central	North	South	
WW					
No. of animals in pedigree	1,826	133	944	1,611	4,514
No. of records	1,485	75	743	1,025	3,328
No. of sires	44	5	26	35	110
No. of dams	524	53	254	579	1,410
- 1 calf	128	31	57	235	451
- 2 calves	200	22	71	256	549
- 3 calves	53	-	44	75	172
- 4 calves	49	-	34	12	95
- 5 calves and higher	94	-	48	1	143
No. of dams with own record	201	-	73	25	299
No. of contemporary groups	44	6	30	37	117
Mean ± std (kg)	91.9 ± 19.3	84.7 ± 17.9	102.8 ± 22.9	63.6 ± 15.3	85.5 ± 24.4
GIR2					
No. of animals in pedigree	1,342	129	904	1,493	3,868
No. of records	995	72	703	928	2,698
No. of sires	38	5	26	35	104
No. of dams	438	51	252	550	1,291
- 1 calf	167	31	64	254	516
- 2 calves	115	20	72	227	434
- 3 calves	78	-	46	57	181
- 4 calves	45	-	29	11	85
- 5 calves and higher	33	-	41	1	75
No. of dams with own record	115	-	70	18	203
No. of contemporary groups	29	6	30	37	102
Mean ± std (cm.)	102.9 ± 7.4	98.3 ± 8.2	109.7 ± 9.2	92.4 ± 8.1	100.9 ± 10.6

Table 9 (Continued)

Trait	Line				Total
	Northeast	Central	North	South	
HH2					
No. of animals in pedigree	1,354	118	895	1,497	3,864
No. of records	1,000	66	691	931	2,688
No. of sires	38	5	26	35	104
No. of dams	441	47	252	551	1,291
- 1 calf	154	28	65	250	497
- 2 calves	135	19	72	235	461
- 3 calves	79	-	48	54	181
- 4 calves	43	-	28	11	82
- 5 calves and higher	30	-	39	1	70
No. of dams with own record	111	-	67	18	196
No. of contemporary groups	30	6	30	37	103
Mean ± std (cm.)	92.6 ± 4.7	89.1 ± 4.9	100.4 ± 6.2	85.2 ± 5.6	91.9 ± 8.0
STP2					
No. of animals in pedigree	1,328	127	905	1,495	3,855
No. of records	982	71	704	928	2,685
No. of sires	38	5	26	35	104
No. of dams	435	51	252	552	1,290
- 1 calf	169	31	63	255	518
- 2 calves	110	20	73	231	434
- 3 calves	80	-	46	54	180
- 4 calves	44	-	29	11	84
- 5 calves and higher	32	-	41	1	74
No. of dams with own record	113	-	70	18	201
No. of contemporary groups	28	6	30	37	101
Mean ± std (cm.)	80.5 ± 6.6	74.3 ± 6.2	94.8 ± 8.3	75.9 ± 7.4	82.5 ± 10.6

Table 10 Yearling traits data structure and descriptive statistics

Trait	Line				Total
	Northeast	Central	North	South	
YW					
No. of animals in pedigree	518	139	435	718	1,810
No. of records	328	70	258	390	1,046
No. of sires	30	5	23	27	85
No. of dams	202	64	170	306	742
No. of contemporary groups	19	4	23	21	67
Mean ± std (kg)	125.1 ± 22.3	111.4 ± 18.5	137.4 ± 25.5	92.7 ± 17.8	115.1 ± 28.3
GIR4					
No. of animals in pedigree	292	137	410	799	1,638
No. of records	151	69	242	440	902
No. of sires	23	5	20	24	72
No. of dams	124	63	164	335	686
No. of contemporary groups	6	4	21	20	51
Mean ± std (cm.)	106.3 ± 11.5	111.4 ± 6.5	121.5 ± 8.4	103.5 ± 8.4	109.4 ± 11.7
HH4					
No. of animals in pedigree	289	135	410	780	1,614
No. of records	150	68	242	429	889
No. of sires	22	5	20	24	71
No. of dams	123	62	164	327	676
No. of contemporary groups	6	4	21	20	51
Mean ± std (kg)	100.9 ± 4.6	97.9 ± 7.5	109.7 ± 5.3	93.4 ± 5.6	99.4 ± 8.8
STP4					
No. of animals in pedigree	284	125	410	787	1,606
No. of records	147	62	242	434	885
No. of sires	23	5	20	24	72
No. of dams	120	58	164	329	671
No. of contemporary groups	6	4	21	20	51
Mean ± std (cm.)	99.8 ± 11.2	81.5 ± 5.9	104.1 ± 6.4	87.1 ± 7.3	93.5 ± 11.3

2. Variance and covariance analysis

Fixed effects taken into account for all traits were contemporary groups (Herd and line-year and season of calving) and sex. For birth traits, ages of dam were fitted as covariate. In addition, ages of animal were fitted as covariate for weaning weight. For yearling traits age of animal was the only covariate fitted.

2.1 Univariate analyses

In preliminary studies, univariate analyses for each trait (birth and weaning traits) were carried out considering six different models to establish which model fitted best. These models were the same as considered by Meyer (1992, 1993). For yearling traits only a simple animal model was considered.

Model 1 was a simple animal model, ignoring all maternal effects.

$$y = X\beta + Zu + \varepsilon \,; \qquad \varepsilon \sim (0, R);\, u \sim (0, G) \qquad [4]$$

The first moment for the model was as followed:

$$E[y] = X\beta \qquad [5]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & 0 \\ 0 & I\sigma^2{}_\varepsilon \end{bmatrix} \qquad [6]$$

Model 2 allowed for maternal permanent environmental effect in addition.

$$y = X\beta + Zu + Spe + \varepsilon \qquad [7]$$

The first moment for the models was:

$$E[y] = X\beta \qquad [8]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ pe \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & 0 & 0 \\ 0 & I\sigma^2{}_{pe} & 0 \\ 0 & 0 & I\sigma^2{}_\varepsilon \end{bmatrix} \qquad [9]$$

Model 3 included a maternal genetic effect in addition to animals' direct genetic effect assuming these were uncorrelated.

$$y = X\beta + Zu + Wm + \varepsilon \qquad [10]$$

The first moment for the model was:

$$E[y] = X\beta \qquad [11]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ m \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & 0 & 0 \\ 0 & A\sigma^2{}_m & 0 \\ 0 & 0 & I\sigma^2\varepsilon \end{bmatrix} \qquad [12]$$

Model 4 was as Model 3 but allowed for a direct-maternal genetic covariance.

$$y = X\beta + Zu + Wm + \varepsilon \qquad [13]$$

The first moment for the models was:

$$E[y] = X\beta \qquad [14]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ m \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & A\sigma_{um} & 0 \\ A\sigma_{um} & A\sigma^2{}_m & 0 \\ 0 & 0 & I\sigma^2{}_\varepsilon \end{bmatrix} \qquad [15]$$

Model 5 fitted both maternal genetic and permanent environmental effects assuming direct-maternal covariance were uncorrelated.

$$y = X\beta + Zu + Wm + Spe + \varepsilon \qquad [16]$$

The first moment for the model was:

$$E[y] = X\beta \qquad [17]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ m \\ pe \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & 0 & 0 & 0 \\ 0 & A\sigma^2{}_m & 0 & 0 \\ 0 & 0 & I\sigma^2{}_{pe} & 0 \\ 0 & 0 & 0 & I\sigma^2{}_\varepsilon \end{bmatrix} \qquad [18]$$

Model 6, finally, was as Model 5 but allowed for a direct-maternal genetic covariance.

$$y = X\beta + Zu + Wm + Spe + \varepsilon \qquad [19]$$

The first moment for the model was:

$$E[y] = X\beta \qquad [20]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u \\ m \\ pe \\ \varepsilon \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_u & A\sigma_{um} & 0 & 0 \\ A\sigma_{um} & A\sigma^2{}_m & 0 & 0 \\ 0 & 0 & I\sigma^2{}_{pe} & 0 \\ 0 & 0 & 0 & I\sigma^2{}_\varepsilon \end{bmatrix} \qquad [21]$$

where

y = vector of observations (birth and weaning traits)

β = vector of fixed effects

u = vector of random animal genetic effects

m = vector of random maternal genetic effects

pe = vector of random maternal permanent environmental effects

ε = random residual error

X, Z, W and S were incidence matrices relating records to fixed, animal genetic, maternal genetic and permanent environment effects, respectively. A and I were numerator relationship and identity matrices. σ^2_u was the animal direct genetic variance, σ^2_m was the maternal genetic variance. σ_{um} was the direct-maternal covariance. σ^2_{pe} and σ^2_ε were the maternal permanent environmental variance and residual error variance, respectively.

2.2 Log likelihood ratio test of random effects

Models with different random components were compared using the log likelihood ratio test (LRT). Models 2 and 3 were tested against Model 1. Model 4 was tested against Model 3. Model 5 was tested against Model 2 and 3. Model 6 was tested against Model 5. The log likelihood ratio test was tested against the Chi-Square distribution with degrees of freedom being the difference in number of variance and covariance in the models. If the values were not significant different ($P > 0.05$), the model with the fewest number of variance was chosen (Gilmour *et al.*, 2002).

$$\text{Chi-Square } (\chi^2) = 2(\text{log likelihood of model j} - \text{likelihood of model i}) \quad [22]$$

2.3 Bivariate analyses

Bivariate analyses were carried out for each pair of traits recorded, fitting the previously determined best model from univariate analyses of each trait. The best fitted model for univariate analyses of each trait and bivaraite analyses were as followed:

2.3.1 Birth and weaning traits

The bivariate mixed model was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} S_1 & 0 \\ 0 & S_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} \qquad [23]$$

where

y_1 and y_2 = vector of observations for birth and weaning traits

β_1 and β_2 = vector of fixed effects for birth and weaning traits

u_1 and u_2 = vector of animal genetic effects for birth and weaning traits

m_1 and m_2 = vector of maternal genetic effects for birth and weaning weight

pe_1 and pe_2 = vector of maternal permanent environmental effects for birth and weaning traits

ε_1 and ε_2 = vector of residual effects for birth and weaning traits

X_1 and X_2 , Z_1 and Z_2 , W_1 and W_2 , S_1 and S_2 were incidence matrices relating records of birth and weaning traits to fixed, animal genetic, maternal genetic and maternal permanent environmental effects, respectively.

The first moment for the models was:

$$E\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} \qquad [24]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u_1 \\ u_2 \\ m_1 \\ m_2 \\ pe_1 \\ pe_2 \\ \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} = \begin{bmatrix} A\sigma^2_{u1} & A\sigma_{u12} & 0 & 0 & 0 & 0 & 0 & 0 \\ A\sigma_{u21} & A\sigma^2_{u2} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & A\sigma^2_{m1} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & A\sigma^2_{m2} & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2_{pe1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & I\sigma^2_{pe2} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & I\sigma^2_{\varepsilon1} & I\sigma_{\varepsilon12} \\ 0 & 0 & 0 & 0 & 0 & 0 & I\sigma_{\varepsilon21} & I\sigma^2_{\varepsilon2} \end{bmatrix} \quad [25]$$

where

A and I were numerator relationship and identity matrices. σ^2_{u1}, σ^2_{u2} and σ_{u12} were the animal genetic (co)variance for birth and weaning traits. σ^2_{m1} and σ^2_{m2} were the maternal genetic variance. σ^2_{pe1} and σ^2_{pe2} were the maternal permanent environmental variance. σ^2_{e1}, σ^2_{e2} and σ_{e12} were residual (co)variance for birth and weaning traits, respectively.

2.3.2 Birth and yearling traits

The bivariate mixed model was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix}\begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix}\begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} \quad [26]$$

where

y_1 and y_2 = vector of observations for birth and yearling traits

β_1 and β_2 = vector of fixed effects for birth and yearling traits

u_1 and u_2 = vector of animal genetic effects for birth and yearling traits

m_1 and m_2 = vector of maternal genetic effects for birth and weaning weight

ε_1 and ε_2 = vector of residual effects for birth and weaning traits

X_1 and X_2, Z_1 and Z_2, W_1 and W_2 were incidence matrices relating records of birth and yearling traits to fixed, animal genetic and maternal genetic effects.

The first moment for the model was:

$$E\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix}\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} \qquad [27]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u_1 \\ u_2 \\ m_1 \\ m_2 \\ \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_{u1} & A\sigma_{u12} & 0 & 0 & 0 & 0 \\ A\sigma_{u21} & A\sigma^2{}_{u2} & 0 & 0 & 0 & 0 \\ 0 & 0 & A\sigma^2{}_{m1} & 0 & 0 & 0 \\ 0 & 0 & 0 & A\sigma^2{}_{m2} & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2{}_{\varepsilon 1} & I\sigma_{\varepsilon 12} \\ 0 & 0 & 0 & 0 & I\sigma_{\varepsilon 21} & I\sigma^2{}_{\varepsilon 2} \end{bmatrix} \qquad [28]$$

where

A and I were numerator relationship and identity matrices. $\sigma^2{}_{u1,}$ $\sigma^2{}_{u2}$ and σ_{u12} were the animal genetic (co)variance for birth and yearling traits. $\sigma^2{}_{m1}$ and $\sigma^2{}_{m2}$ were the maternal genetic variance. $\sigma^2{}_{e1,}$ $\sigma^2{}_{e2}$ and σ_{e12} were residual (co)variance for birth and yearling traits, respectively.

2.3.3 Weaning and yearling traits

The bivariate mixed model was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix}\begin{bmatrix} u_1 \\ u_2 \end{bmatrix} + \begin{bmatrix} S_1 & 0 \\ 0 & S_2 \end{bmatrix}\begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} \qquad [29]$$

where

y_1 and y_2 = vector of observations for weaning and yearling traits

β_1 and β_2 = vector of fixed effects for weaning and yearling traits

u_1 and u_2 = vector of animal genetic effects for weaning and yearling traits

pe_1 and pe_2 = vector of maternal genetic effects for birth and weaning weight

ε_1 and ε_2 = vector of residual effects for birth and weaning traits

X_1 and X_2, Z_1 and Z_2, S_1 and S_2 were incidence matrices relating records of weaning and yearling traits to fixed, animal genetic and maternal permanent environmental effects.

The first moment for the models was:

$$E\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 \\ x_2 \end{bmatrix}\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} \quad [30]$$

The variance and covariance structure were:

$$Var\begin{bmatrix} u_1 \\ u_2 \\ pe_1 \\ pe_2 \\ \varepsilon_1 \\ \varepsilon_2 \end{bmatrix} = \begin{bmatrix} A\sigma^2{}_{u1} & A\sigma_{u12} & 0 & 0 & 0 & 0 \\ A\sigma_{u21} & A\sigma^2{}_{u2} & 0 & 0 & 0 & 0 \\ 0 & 0 & I\sigma^2{}_{pe1} & 0 & 0 & 0 \\ 0 & 0 & 0 & I\sigma^2{}_{pe2} & 0 & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2{}_{\varepsilon 1} & I\sigma_{\varepsilon 12} \\ 0 & 0 & 0 & 0 & I\sigma_{\varepsilon 21} & I\sigma^2{}_{\varepsilon 2} \end{bmatrix} \quad [31]$$

where

A and *I* were numerator relationship and identity matrices. σ^2_{u1}, σ^2_{u2} and σ_{u12} were the animal genetic (co)variance for weaning and yearling traits. σ^2_{pe1} and σ^2_{pe2} were the maternal permanent environmental variance. σ^2_{e1}, σ^2_{e2} and σ_{e12} were residual (co)variance for weaning and yearling traits, respectively.

2.4 Estimation of (co)variance components and genetic parameters

Estimates of variance and covariance components were obtained by the average information restricted maximum likelihood (AI) REML using ASREML (Gilmour *et al.*, 2002). The method involves maximizing the likelihood function (log *L*) given the data. Each complex model was restarted using the resulting estimates of the previous parameters as a new prior until changes in the function values were minimal, to ensure that a global rather than a local maximum likelihood have been reached, some genetic parameters were calculated using the previous formula as in the first study. The genetic parameters, genetic correlation (r_{am}) and total heritability were defined according to Willham (1972); Falconer and Mackay (1996).

Trial III

Calculate economic weight of economically important traits such as sale weight, mature cow weight and fertility of Thai indigenous cattle

1. General aspects of Production model

In this study a production model was developed to describe an Indigenous cattle enterprise. The model allowed to compute economic weights for a number of traits related to the production system. A schematic representation of the elements of the model is in Figure 4.

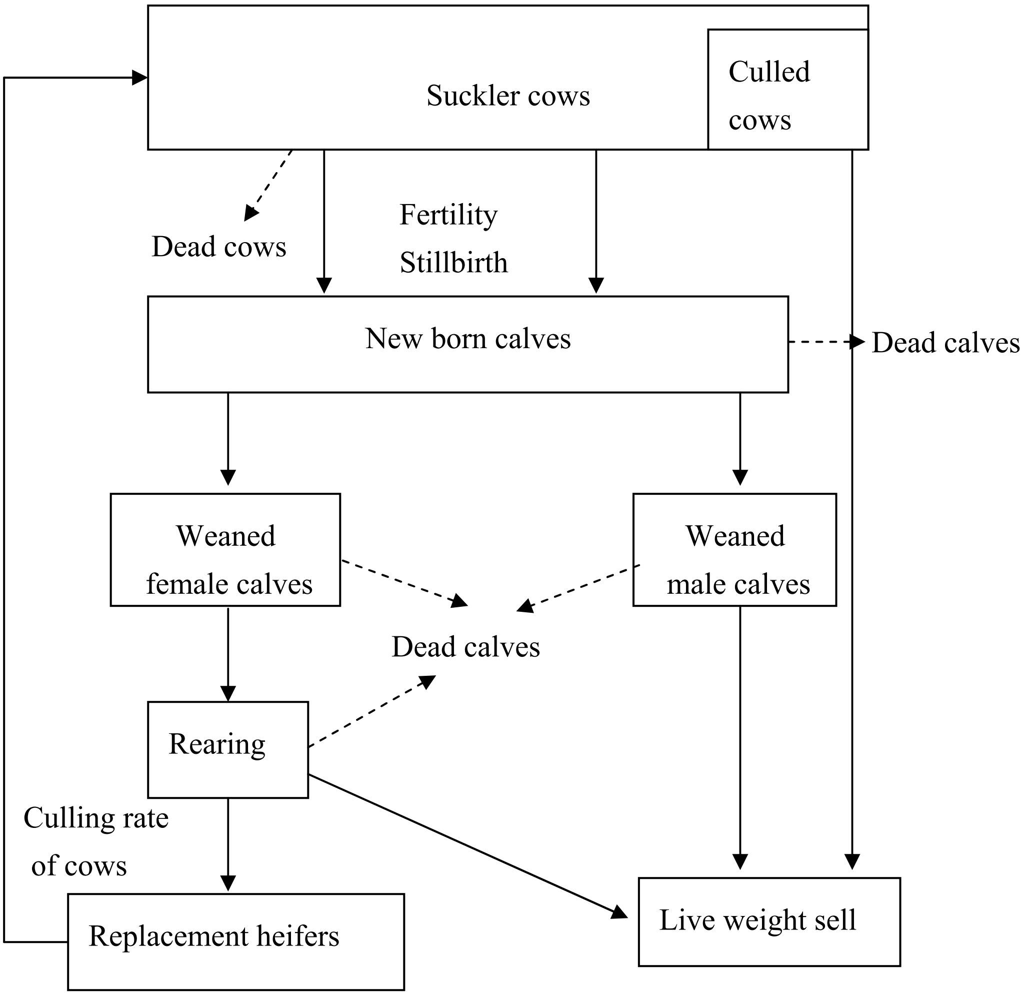

Figure 4 General representation of the elements of the model

The overall situations for Thai indigenous cattle were that average calving and weaning rate were 85.0% and 80.0%. The survival rate from birth to age at selling was 94.0%. Both male and female calves were sold at approximately 1.5 to 2 years of age, with average live weight of 185.5 kg. The replacement rate was 20.0% and the culled cow was average live weight of 250.0 kg. There were three major areas to increase the profitability of Thai indigenous cattle industry such as weaning rate (fertility), sale weight and mature cow weight. Therefore, these traits were appropriate to be incorporated into breeding objective. The production data and costs for calf, wet and dry cow were presented in Table 11.

Table 11 Production data and costs for calf, wet and dry cow of Thai indigenous cattle

Production data	
Calving rate, %	85.0
Weaning rate, %	80.0
Survival rate, % (from birth to sale weight)	94.0
Replacement rate, %	20.0
Sale weight, kg	185.5
Cow weight, kg	250.0
Cost of sale weight, baht/kg[1/]	17.91
Total cost of wet cow, baht[2/]	4,679.40
Cost of dry cow, baht/kg[3/]	16.99
Sale price of calf, baht/kg	65.00
Sale price of dry cow, baht/kg	45.00

[1/], [2/] and [3/] were presented in details in appendix 1, 2 and 3, respectively.

2. Profit Function

The function that best represented total herd profit was defined by Groen *et al.* (1989) as incomes minus costs. In this study, the total profit function considered was:

$$\text{Profit} = (\text{wean} \times \text{surr} - \text{repr}) \times \text{sw} \times \text{salca} + (\text{nocul} \times \text{swcul} \times \text{salco}) - (\text{nowcow} \times \text{costwet}) + (\text{nodrycow} \times (\text{swcul} \times \text{costdry/kg}) + (\text{wean} \times \text{sw} \times \text{costcal/kg}) \qquad [32]$$

where

wean = weaning rate

surr = survival rate

repr = replacement rate

sw = sale weight of calf

salca = sale price of calf/kg

nocul = number of culled cows

swcul = sale weight of culled cows

salco = sale price of culled cows/kg

nowcow = number of wet cows

costwet = total cost of wet cows

nodrycow = number of dry cow

costdry/kg = cost of dry cows/kg

costcal/kg = cost of calf/kg

3. Derivation of economic weights

Profit function was calculated under base conditions where every trait was on averages using Spreadsheet program (Exel, 2003). The economic weights of each trait such as weaning rate, sale weight and cow weight were calculated from the production model.

Trial IV

Evaluate the returns of investment and predict genetic gains per year from one round of selection of Thai indigenous cattle

1. Analysis for an example population structure

The ZPLAN program (Karras *et al*., 1993) was used to calculate the returns, annual genetic gains and profits from selection using a deterministic approach, employing selection index theory and gene flow methodology. Returns in the population as a whole that were generated from decisions taken in the nucleus herd were compared with the cost of selection.

Information about the basic breeding structure of Thai indigenous cattle population considered here is presented in Table 12. The number of cows in this analysis comprised 800,000 heads out of total mature females of 1.7 million heads (DLD, 2006). With 0.2% of which (1,500 cows of the total) were organized in a recording system and considered to be the nucleus herds of DLD. The multiplier herds comprised 6.5% of the total. This group would be established under the auspices of DLD as contract farming. The remaining, 93.3% were in the production herd throughout the country. The bulls used in the multiplier herd were selected from the nucleus herd. The bull used in commercial herd came from both the multiplier herd and home-bred bull. There was natural mating, with a bull to cow ratio of 1:25, 1:50 and 1:50 in nucleus, multiplier and production herd, respectively.

Table 12 Assumed characteristic of Thai indigenous cattle population

Character	Nucleus herd	Multiplier herd	Production herd
Number of cow, heads	1,500	52,000	746,500
Number of bull/cows, heads	25	50	50

2. Selection groups

To use gene flow methodology (Hill, 1974), the selection groups for Thai indigenous cattle were identified as the parent groups which contributed genes to the next generation. The nucleus herd was the tier of the population which generated genetic gain. There were ten selection groups, coded 1-10, in the population (Figure 5).

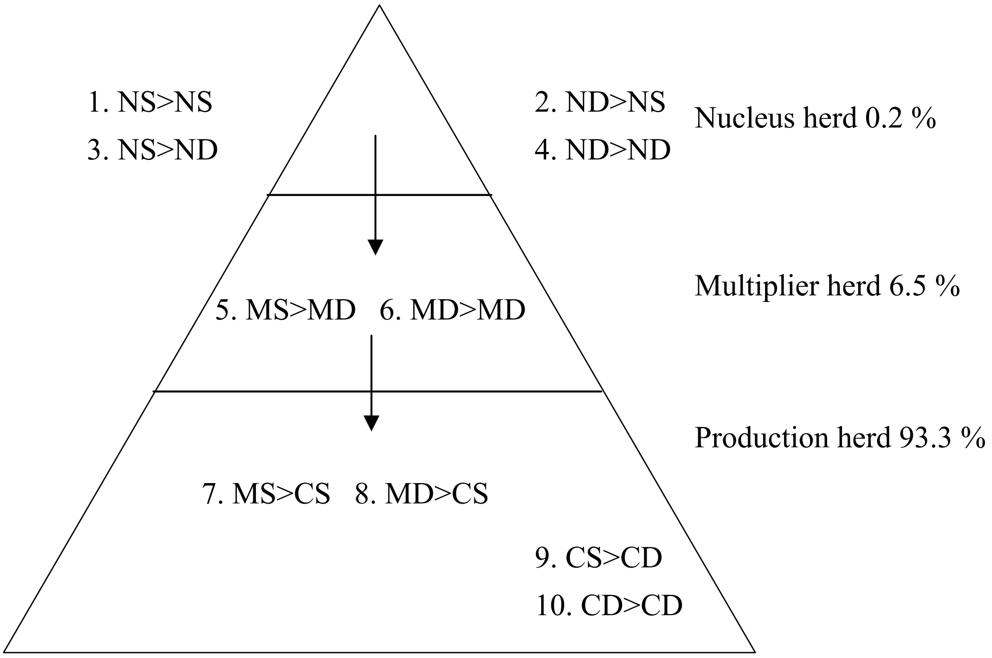

Figure 5 Breeding structure and selection groups of Thai indigenous cattle population. Code for selection groups correspond to their order in the transmission matrix

Four selection groups were defined in the nucleus herd, where bull selection occurred both to improve the sire used (sires to breed sire, NS>NS) and the female retained (sire to breed dam, NS>ND). Selection of females in the nucleus herd also occurred to improve both sire (dams to breed sire, ND>NS) and female (dams to breed dams, ND>ND). The bull from nucleus herd was used to produce cows in multiplier herd (sire to breed dams, MS>MD) and female (dam to breed dam, MD>MD). The bulls from multiplier herd bought for the production herd to improve the sire used (sire to breed sire, MS>CS) and female to produce sire (dam to breed sire, MD>CS). The last two selection groups involved home-bred sire and dam in the production herd that were used to produce dam (CS>CD and CD>CD).

3. Breeding objectives and selection criteria

The breeding objectives for Thai indigenous cattle were to increase weaning rate (CoWR), sale weight (SW-d) and mature cow weight (CoW). The selection criteria considered here were weaning weight (WW), yearling weight (YW), body measurement (i.e. GIR4, HH4, STP4) and scrotal circumference (SC) at yearling age, days to calving (Dtoc) and age at first calving (A1C). Economic values for one unit changes in each trait together with genetic and phenotypic parameters were shown in Table 13. These values were based on genetic and phenotypic parameters from the analysis of Thai indigenous cattle. However, some values such as heritabilities, genetic and phenotypic correlations for sale weight, fertility traits (SC, Dtoc and A1C) taken from a composite breed of tropical beef cattle (Burrow, 1999).

Table 13 Economic value for traits of the breeding objective, phenotypic standard deviation, heritabilities and genetic and phenotypic correlations

Traits	ν (baht) Per unit	σ_p	h^2	Genetic and phenotypic correlations[1/]											
				SW-d	WW	YW	CoW	GIR4	HH4	STP4	CoWR	SC	Dtoc	A1C	SW-m
SW-d, kg	21.81	32.62	0.25		0.60	0.70	0.80	0.60	0.60	0.60	0.05	0.43	-0.10	-0.10	0.00
WW, kg	-	14.64	0.28	0.64		0.80	0.60	0.70	0.75	0.70	0.05	0.33	-0.18	-0.10	0.00
YW, kg	-	15.74	0.43	0.87	0.71		0.80	0.65	0.65	0.65	0.05	0.50	-0.10	-0.10	0.00
CoW, kg	4.90	27.86	0.20	0.45	0.33	0.45		0.60	0.60	0.60	0.05	0.20	-0.15	-0.10	0.00
GIR4, cm	-	6.37	0.29	0.30	0.61	0.50	0.30		0.83	0.78	0.05	0.1	0.05	-0.10	0.00
HH4, cm	-	4.67	0.29	0.30	0.65	0.40	0.25	0.71		0.65	0.05	0.1	0.05	-0.10	0.00
STP4, cm	-	5.72	0.26	0.30	0.57	0.40	0.25	0.62	0.90		0.05	0.1	0.05	-0.10	0.00
CoWR, %	80.11	40.0	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.2	0.5	-0.20	0.00
SC, cm	-	3.98	0.34	0.38	0.32	0.48	0.01	0.00	0.00	0.00	0.00		-0.20	-0.10	0.00
Dtoc, day	-	26.44	0.07	-0.02	-0.03	0.01	-0.42	0.00	0.00	0.00	0.00	0.00		0.10	0.00
A1C, year	-	0.45	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.00
SW-m, kg	21.81		0.10	-	-	-	-	-	-	-	-	-	-	-	

[1/] Genetic correlations above and phenotypic correlations below diagonal

4. Biological and technical parameters

The estimates of productive lifetime, survival rate and age at first calving for various tiers were shown in Table 14. These biological parameters were vital for construction of transmission matrix. The other values shown were required to calculate the proportion of selected animal and selection intensities.

Table 14 Biological and technical parameters for Thai Indigenous cattle

Trait	Nucleus	Multiplier	Production
Production life time of sire, years	2.0	3.0	3.0
Age at first calving of sire, years	2.5	2.5	2.5
Production life time of dam, years	5.0	6.0	7.0
Age at first calving of dam, years	2.5	2.7	2.7
Survival rate of sire, %	80.0	80.0	70.0
Survival rate of dam, %	95.0	90.0	90.0
Survival rate to sale, %	94.0	94.0	94.0
Calves weaned/dam, %	80.0	78.0	78.0
Bull fit breed, %	90.0		

5. Investment parameter

The assumed investment parameters were shown in Table 15. The investment covers a period of 20 years, with 7.8 and 3.5 % for interest rate of return and cost.

Table 15 Investment parameters for Thai indigenous cattle

Parameter	
Investment period, years	20.0
Interest rate for returns, %	3.5
Interest rate for cost, %	7.8

6. Fixed costs

The fixed costs were assumed to be the overhead cost of a DLD's officer and its involvement in performance recording. The cost estimate were obtained for two populations, with 200 and 2,100 cows in nucleus herd and shown in Table 16. The estimates for the assumed 1,500 cows in nucleus herd were obtained by linear regression:

Fixed cost = fixed cost for the first population + b(number of assumed cows − number of cows in the first population) [33]

where

b = (fixed cost for the second population − fixed cost for the first population) / (number of cows in the second population − number of cows in the first population)

Table 16 Estimated overhead costs of DLD's officer servicing a nucleus herd of 200 or 2,100 cows

Elements (unit: baht)	Number of cows in nucleus herd (head)	
	200	2,100
Management costs		
Technical officer	253,920[1/]	507,840
Traveling	94,795	315,985
Material costs		
Heath	41,885	439,800
Feeding, Drafting	1,834,594	19,263,240
Data processing	29,524	310,000
Extra costs i.e. training and other office	304,821	3,200,630
Total	2,559,539	24,037,495

[1/] Employed part time

7. Variable cost

The assumed variable costs were those directly relating to performance and pedigree recording. Those variable costs occurred exclusively in the nucleus herd. Estimations were base on the routine work of DLD's farm labor. For instance, the recording of weaning weight took 13 minutes. The average minimum wage of Thai labor was 148.00 baht/day (8 hours). Therefore, the cost for recording weaning weight was equal to be 4.00 baht. For other performance and pedigree recording the same principle in estimation was used. The mating system in multiplier herds was natural mating. Progeny test was performed in nucleus herd for two stage selection. The variable costs were shown in Table 17.

Table 17 Estimated variable cost for Thai indigenous cattle

Recording parameters (unit: baht)	Variable cost
Weaning weight	4
Yearling weight	4
Body measurement at yearling	9
Scrotal circumference at yearling	5
Cost per cow	30
Days to calving	10
Cow weight	4
Transport bull from nucleus to multiplier herd	150
Transport bull from multiplier to production herd	100
Contract cow	250
Maintenance bull/year	4,000

8. Calculation of return and annual genetic gain

ZPLAN program (Karras *et al.*, 1993) was used to calculate the return and annual genetic gains from one round of selection in a deterministic way.

8.1 Selection intensities

The number of proven and selected animals in each selection group was calculated as:

$$i = i_{\infty} - \frac{N - n}{2n(N+1)\, i_{\infty}} \qquad [34]$$

where

i and i_∞ are the selection intensities for finite and infinite sample
N and n are the number of proven and selected animals.

8.2 Genetic gain per year

Annual genetic gain for breeding objective can be calculated as:

$$\Delta G_y = \frac{q'd}{q'1} \qquad [35]$$

where

q' is a 1 * *k* vector proportions contributed by the selection groups,
d is a *k* * 1 vector of genetic superiorities for the *k* selection groups in the breeding herd and
1 is a *k* * 1 vector of genetic intervals for the *k* selection groups in the breeding herd.

8.3 Number of discounted traits expressions

For calculating the return from genetic selection, the numbers of standard discounted expressions (SDE) for traits are most important. They are specific to each selection group and each type of trait. The number for each trait is calculated according to the formula:

$$SDE_{ij} = \sum_{t=1}^{T} h'_i m_{it} \left(\frac{1}{1+r}\right)^t \qquad [36]$$

where

T is the time horizon of the investment in years
h'_i is a 1 * s vector (realization vector) for trait *i,* where s is the number of sex/age classes
m_{it} is a s * 1 vector of gene proportions that the animals of the various sex-age classes carry from selection group *j* at time *t* and

r is the annual discount rate for returns.

8.4 Returns per selection group

In contrast to the calculation of genetic gain, where only the selection groups of the breeding herd contribute, selection groups of the multiplier or commercial herd also contribute to the returns from selecting for a single trait *i* in a selection group *j* (R_{ij}) and the total return for the selection group (R_j) are given by

$$R_{ij} = \Delta G_{ij}.SDE_{ij}.v_i \qquad [37]$$

$$R_j = \sum_{t=1}^{m} \Delta G_{ij}.SDE_{ij}.v_i \qquad [38]$$

where

ΔG_{ij} is the genetic superiority of trait i in selection group j

v_i is the undiscounted economic value of traits i, one of m traits contained in the breeding objective

8.5 Total returns from selection

The overall return from selection is obtained by summing over all selection groups (i.e., all k′ groups, considering all tiers) and over all m traits of the breeding objective:

$$R_{Overall} = \sum_{i=1}^{m} \sum_{j=1}^{k'} \Delta G_{ij}.SDE_{ij}.v_i \qquad [39]$$

8.6 Selection costs

The fixed and variable costs are specified together with their average time of occurrence, in years. The overall cost of the investment in one round of selection is calculated as:

$$C_{overall} = \sum_{t=0} \frac{c_t}{(1 + r^*)^t} \qquad [40]$$

where

T^* is the time of the latest cost from one round of selection
c_t are costs applying in year t, and
r^* is the annual discount rate for costs

8.7 Net present value

The net present value of the returns from one round of selection, or the overall profit, is obtained by subtracting the overall costs from the overall returns.

RESULTS AND DISCUSSION

Trial I

Fixed effects affecting weight and body measurement at birth, 200-day weight and 400-day weight of Thai indigenous cattle

1. Descriptive Statistic

The means BW, GIR, HH and STP for combined data were 16.3 kg., 57.5 cm, 63.1 cm and 47.8 cm, respectively. These records consisted of northeastern, southern, northern and central lines in the proportions of 42.0, 31.4, 21.8 and 5.8% out of the total records. The means age of dam were 5.0 years. More than 60% of age of dam ranged from 4 to 6 years.

The means WW, GIR2, HH2 and STP2 were 85.5 kg, 100.9 cm, 91.9 cm and 82.5 cm, respectively. The records consisted of northeastern, southern, northern and central lines in the proportions of 44.5, 30.8, 22.4 and 2.2% out of the total records. The means age of recording were 201.8 days with the ranges from 133 to 287 days. More than 40% of ages at weaning were recorded from 190 to 210 days.

The means YW, GIR4, HH4 and STP4 were 115.3 kg, 109.5 cm, 99.4 cm and 93.5 cm, respectively. The means age of recording were 404.8 days with the ranges from 307 to 497 days.

2. Birth traits

The levels of significant for all fixed effects were summarized in Table 18. Herd-line × year × season of calving (H-L×Y×S) and sex had significantly influenced on BW, GIR, HH and STP ($P < 0.001$). Age of dam had significantly influenced on all traits at linear and quadratic ($P < 0.001$).

Table 18 Fixed effects affecting birth traits of Thai indigenous cattle

Fixed effects	Birth traits			
	BW	GIR	HH	STP
H-L×Y×S	***	***	***	***
Sex	***	***	***	***
Age of dam				
Linear	***	***	***	***
Quadratic	***	***	***	***

*** = $P < 0.001$

The solutions for birth traits were presented in Table 19. The results indicated that male calves were on averages 1.06 kg heavier than female calves for BW and were on averages 1.13, 1.09 and 0.73 cm greater than female calves for GIR, HH and STP, respectively. The result was consistent with Akkahart (2003) who concluded that birth weight and body measurements such as GIR, HH and STP at birth of Thai indigenous male calves were significantly higher than female calves. In term of biology, testosterone (the male sex hormone) concentrations were higher during gestation in the peripheral circulation of dams with male fetuses than in dams with female fetuses. Therefore, male calves were heavier than female calves due to greater exposure to this hormone and had larger body measurements compared to female calves. The result was supported by many other authors (e.g. Setshwaelo *et al*., 1990; Newman *et al*., 1993; Chokchareon, 2003; Pico, 2004).

Table 19 Solution of birth traits of Thai indigenous beef cattle

Parameters	Birth traits[1/]			
	BW (kg)	GIR (cm)	HH (cm)	STP (cm)
Intercept	14.06 ± 0.56	54.61 ± 0.93	60.16 ± 0.91	49.42 ± 0.90
Sex difference	1.06 ± 0.07	1.13 ± 0.11	1.09 ± 0.11	0.73 ± 0.11
Age of dam				
Linear	0.42 ± 0.04	0.43 ± 0.07	0.36 ± 0.07	0.23 ± 0.07
Quadratic	-0.08 ± 0.01	-0.14 ± 0.03	-0.17 ± 0.03	-0.12 ± 0.03

[1/] estimate ± s.e.

With regard to age of dam, the solutions of the linear and quadratic regression coefficients were 0.42 and -0.08 kg for BW. The solutions of the linear and quadratic regression coefficients were 0.43, -0.14; 0.36, -0.17; 0.23, and -0.12 cm for GIR, HH and STP, respectively. The effects of age of dam on birth weight and body measurement were shown in Figure 6 and 7.

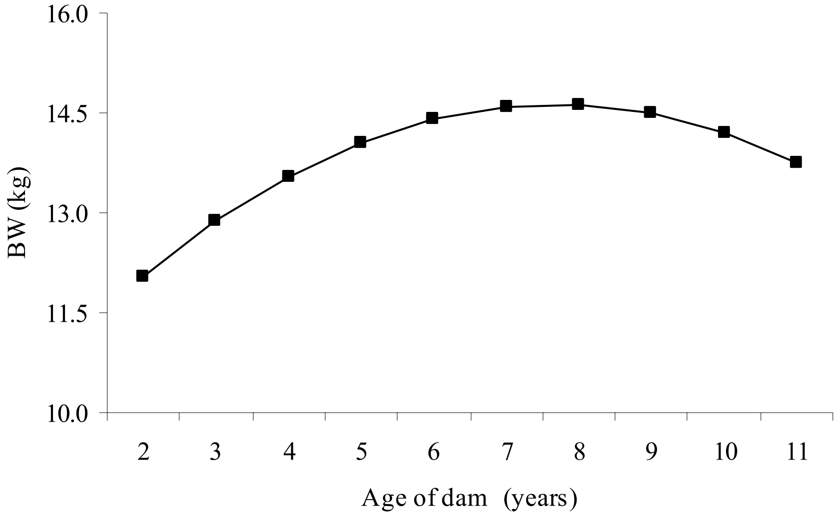

Figure 6 Effect of age of dam on birth weight of Thai indigenous cattle

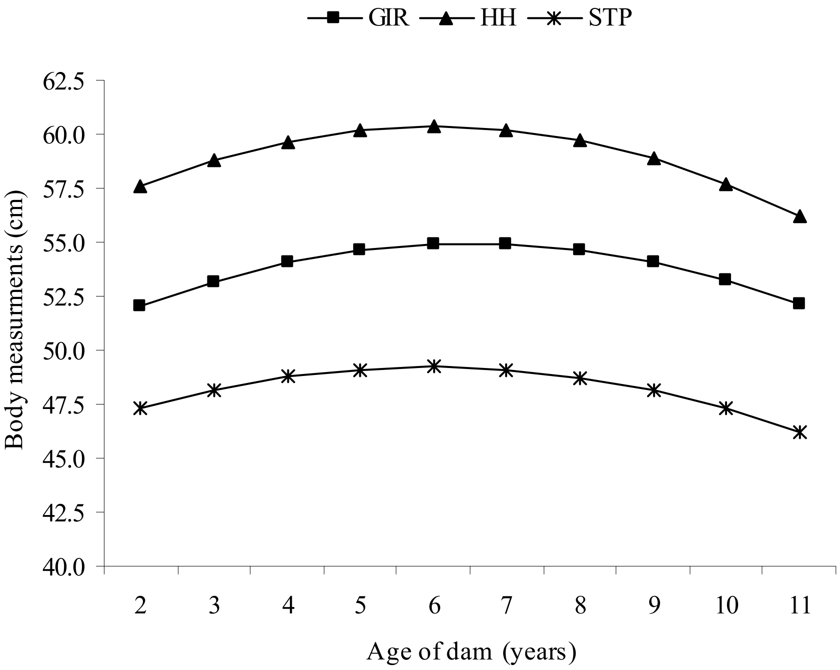

Figure 7 Effect of age of dam on body measurements at birth of Thai indigenous cattle

This result indicated that Thai indigenous calves from young dams (2 to 4 years) were generally smaller at birth. Dams at mature age (5 to 10 years), calves were higher for BW, GIR, HH and STP, respectively. For beef cattle, they have been well established that first-calf heifers were not physically mature. Nutrients they consume were partitioned not only into lactation, maintenance and gestation but also to their own growth. Therefore, calves from young dams were generally smaller both at birth and at weaning. Dams will reach peak production at a mature age (5 to 9 years) and then decrease in performance as measured by weight of their calves (Tong, 1983; Elzo et al, 1987; Newman *et al*, 1993; Archer *et al*, 1997; Rump and Van Vleck, 2004).

3. Weaning traits

The levels of significant for all fixed effects were summarized in Table 20. H-L×Y×S and sex had significantly influenced on WW, GIR2, HH2 and STP2 ($P < 0.001$). Age of dam had significantly influenced on all traits at linear and quadratic ($P < 0.001$). Age of animal had significantly on all traits at linear ($P < 0.001$).

Table 20 Fixed effects affecting on weaning traits of Thai indigenous cattle

Fixed effects	Weaning traits			
	WW	GIR2	HH2	STP2
H-L×Y×S	***	***	***	***
Sex	***	***	***	***
Age of dam				
Linear	***	*	***	***
Quadratic	***	***	***	***
Age of animal				
Linear	***	***	***	***

* = $P < 0.05$, *** = $P < 0.001$

The solutions for weaning traits were presented in Table 21. Male calves were on averages 5.59 kg heavier than female calves for WW and were on averages 1.46, 1.26 and 1.27 cm greater than female calves for GIR2, HH2 and STP2, respectively. In other studies, the results indicated in the same direction male calves generally grow faster than female calves (e.g. Setshwaelo *et al*., 1990; Newman *et al.,* 1993; Vargas *et al.,* 1999).

Table 21 Solution of weaning traits of Thai indigenous beef cattle

Parameters	Weaning traits[1/]			
	WW (kg)	GIR2 (cm)	HH2 (cm)	STP2 (cm)
Intercept	54.39 ± 3.49	91.31 ± 1.54	83.71 ± 1.03	84.48 ± 1.31
Sex difference	5.59 ± 0.49	1.46 ± 0.25	1.26 ± 0.17	1.27 ± 0.23
Age of dam				
Linear	1.66 ± 0.43	0.44 ± 0.20	0.49 ± 0.14	0.66 ± 0.12
Quadratic	-0.93 ± 0.15	-0.32 ± 0.08	-0.27 ± 0.05	-0.13 ± 0.04
Age of animal				
Linear	0.23 ± 0.02	0.10 ± 0.01	0.06 ± 0.01	0.08 ± 0.01

[1/] estimate ± s.e.

With regard to age of dam, the solutions of the linear and quadratic regression coefficients were 1.66 and -0.93 kg for WW. The solutions of the linear and quadratic regression coefficients were 0.44, -0.32; 0.49, -0.27; 0.66, and -0.13 cm for GIR2, HH2 and STP2, respectively. The effects of age of dam on WW and body measurement were shown in Figure 8 and 9.

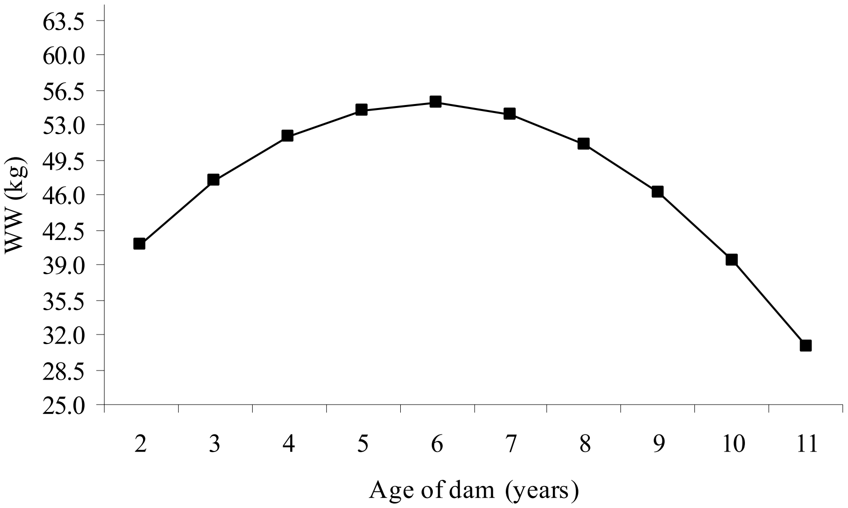

Figure 8 Effect of age of dam on weaning weight of Thai indigenous cattle

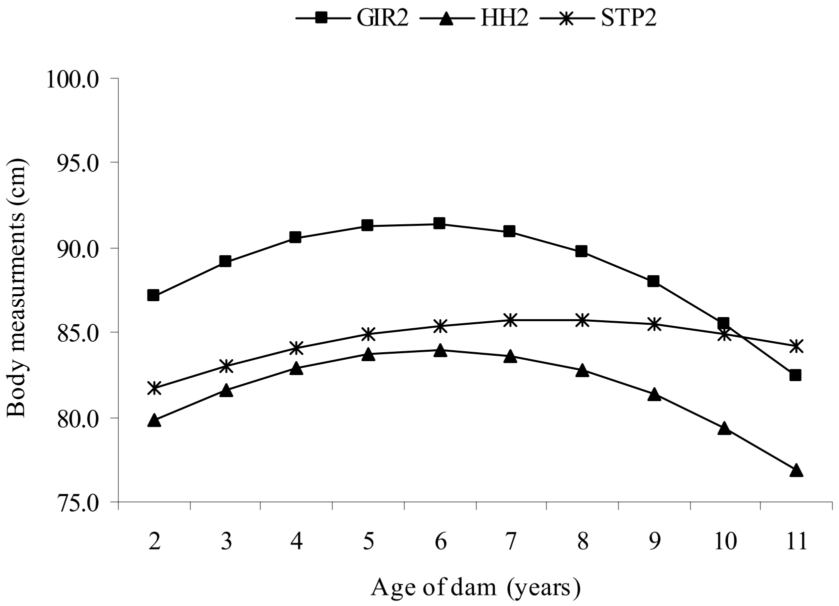

Figure 9 Effect of age of dam on body measurements at weaning of Thai indigenous cattle

This result indicated that WW and body measurement increased with age of dam until dams reached maturity at 5 to 8 years and then decreased for dams older than 9 years. This finding was in agreement with report of Van Vleck and Cundiff (1998), they concluded that mature dams were considered to be 5 to 9 years old and solutions for effects of age consistently increased to maturity and then decreased for 10 years and older dams, indicating that calves out of young and old dams were smaller than calves out of mature dams.

The solution for the linear regression coefficient of age of animal was 0.23 kg/day for WW. The solutions of the linear regression coefficients were 0.10, 0.06; 0.08 cm/day for GIR2, HH2 and STP2, respectively. Actually, age of animal within sex was fitted in preliminary analyses; however, the results were not significantly different between males and females. Therefore, such interaction was ignored from the model. This confirms previous study in Thai indigenous cattle (Akkahart, 2004). However, the solutions of this study were somewhat lower than estimate of other reports i.e. Meyer (1998) concluded that estimates of regression of weaning weight on age in Brahman cattle were 0.46 kg/day for male and 0.34 kg/day for female calves. Estimates of regression of GIR2, HH2 and STP2 were 0.13, 0.62 and 0.08 cm/day for male and 0.11, 0.48 and 0.07 cm/day for female calves, respectively.

4. Yearling traits

The levels of significant for all fixed effects on yearling traits were summarized in Table 22. H-L×Y×S and sex had significantly influenced on WW, HH4 and STP4 at the P < 0.001 significance level and at the P < 0.01 significant level for GIR4 and STP4. Age of animal was significant for all traits (P < 0.001).

Table 22 Fixed effects affecting yearling traits of Thai indigenous cattle

Fixed effects	Yearling traits			
	YW	GIR4	HH4	STP4
H-L×Y×S	***	**	***	**
Sex	***	***	***	***
Age of animal				
Linear	***	***	***	***

** = P < 0.01, *** = P < 0.001

The solutions for yearling traits were presented in Table 23. Male calves were on averages 7.14 kg heavier than female calves for YW and were on averages 1.40, 1.63 and 1.27 cm bigger than female calves for GIR4, HH4 and STP4, respectively. Age of dam was fitted in this model; however, the result was not significant different and therefore excluded. The solution of the linear regression coefficient for calf age was 0.22 kg/day for YW. The solutions of the linear regression coefficients were 0.09, 0.05 and 0.07 cm/day for GIR4, HH4 and STP4, respectively for both sexes.

Table 23 Solution of yearling trait of Thai indigenous beef cattle

Parameters	Yearling traits[1/]			
	YW (kg)	GIR4 (cm)	HH4 (cm)	STP4 (cm)
Intercept	75.95 ± 3.60	101.60 ± 1.31	91.38 ± 0.99	90.22 ± 1.16
Sex difference	7.14 ± 1.04	1.40 ± 0.46	1.63 ± 0.34	1.27 ± 0.42
Age of animal				
Linear	0.22 ± 0.03	0.09 ± 0.01	0.05 ± 0.01	0.07 ± 0.01

[1/] estimate ± s.e.

Trial II

Estimate the genetic parameters such as weight and body measurement at birth, 200-day weight and 400-day weight of Thai indigenous cattle.

1. Descriptive Statistis

For birth traits, calves were by 124 different sires and 1,675 different dams. The numbers of dam which had more than one progeny were approximate 75.9 to 77.8%. The numbers of dam with own record were approximate 25.3 to 26.1% of the total number of dam. The numbers of contemporary groups were 144, 138, 142 and 138 groups for BW, GIR, HH and STP, respectively.

For weaning traits, the numbers of dam which had more than one progeny were approximate 59.8 to 68.0%. The numbers of dam with own record were approximate 15.2 to 21.2% of the total number of dam. The numbers of contemporary groups were 117, 102, 103 and 101 groups for WW, GIR2, HH2, and STP2. The number of contemporary groups for YW, GIR4, HH4 and GIR4 were 67, 51,51 and 51 groups, respectively.

2. Variance components and genetic parameters

2.1 Birth traits

The variance components and genetic parameters together with the pertaining log likelihood (Log L) values for birth traits from fitting various univariate analyses were presented in Table 24.

The profiles of changes in estimates were different between model 1 and model 3. Ignoring maternal effects (model 1) provided substantially higher estimates of σ^2_a and h^2 than for other models. For BW, the estimate of h^2 for model 1 was 0.66. Fitting a maternal permanent environmental effect (model 2) increased value of Log L markedly over that of model 1. Maternal permanent environmental effect contributed 15% of σ^2_p in BW while reducing estimate of σ^2_a was 35%. Fitting a maternal genetic effect (model 3) increased value of Log L markedly over that of model 2. The estimate of σ^2_a also decreased in the same manner with model 2 and substantially decreased estimate of h^2. Maternal genetic effect contributed 18% of σ^2_p.

Table 24 Variance components and parameter estimates for birth traits from fitting various univariate analysis models

Model	Variance components						Parameter estimates[1/]				
	σ^2_u	σ^2_{pe}	σ^2_m	σ_{um}	σ^2_e	σ^2_p	h^2	m^2	c^2	r_{um}	Log L
BW, kg^2											
1	3.86	-	-	-	1.98	5.84	0.66	-	-	-	-5887.1
2	1.90	0.83	-	-	2.64	5.37	0.35	-	0.15	-	-5881.0
3	1.59	-	1.00	-	2.79	5.38	0.30	0.18	-	-	-5845.1
4	1.32	-	0.62	0.49	2.93	5.36	0.25	0.12	-	0.54	-5844.9
5	1.60	0.23	0.75	-	2.77	5.35	0.29	0.13	0.04	-	-5844.3
6	1.33	0.19	0.45	0.46	2.91	5.44	0.25	0.08	0.04	0.58	-5843.3
GIR, cm^2											
1	7.80	-	-	-	6.63	14.43	0.54	-	-	-	-7831.7
2	3.08	2.11	-	-	8.20	13.39	0.23	-	0.16	-	-7808.3
3	2.42	-	2.44	-	8.56	13.42	0.18	0.18	-	-	-7806.5
4	1.94	-	1.20	1.42	8.83	13.39	0.14	0.09	-	0.93	-7805.5
5	2.51	0.76	1.62	-	8.48	13.37	0.18	0.12	0.06	-	-7805.5
6						Not fitted					
HH, cm^2											
1	7.15	-	-	-	6.95	14.10	0.51	-	-	-	-7887.5
2	3.96	1.32	-	-	8.08	13.36	0.29	-	0.10	-	-7877.1
3	3.08	-	1.67	-	8.49	13.25	0.24	0.13	-	-	-7873.6
4						Not fitted					
5	3.09	0.22	1.45	-	8.47	13.23	0.23	0.11	0.02	-	-7873.4
6						Not fitted					
STP, cm^2											
1	3.15	-	-	-	9.96	13.11	0.24	-	-	-	-7851.8
2	1.45	0.97	-	-	10.37	12.79	0.11	-	0.07	-	-7844.6
3	1.12	-	1.15	-	10.51	12.78	0.09	0.09	-	-	-7842.3
4						Not fitted					
5						Not fitted					
6						Not fitted					

[1/] See list of abbreviations

For model 4 and 6, covariances between the direct-maternal genetic effects were also fitted, however, the log likelihood did not differ significantly from zero when compared to that of excluding the two (co)variances (model 3). As Log L values indicated, maternal effects on BW in this data set were almost entirely maternal genetic effect, i.e. model 3 was fitted for this trait.

For body measurements at birth i.e. GIR, HH and STP, the estimates of h^2 for model 1 were 0.24 to 0.54. Fitting maternal permanent environmental effects (model 2) also increased value of Log L markedly over that of model 1. Maternal permanent environmental effects contributed 7 to 16% of σ^2_p while reducing estimates of σ^2_a were 11 to 29%. Fitting maternal genetic effects (model 3) increased value of Log L markedly over that of model 2. Maternal genetic effects ranged from 9 to 18% of $\sigma^2_{p.}$ For GIR, covariances between the direct-maternal genetic effects were fitted (model 4), however, the log likelihood did not differ significantly from zero when compared to that of excluding the two (co)variances (model 3). Similarly, for HH and STP, covariance between the direct-maternal genetic effects were also included in the models (model 4 and 6), however, the models were not fitted. As Log L values indicated, model 3 were fitted for body measurements the same as BW.

With regard to the combined data structure in this study, the numbers of dam which had more than one progeny were approximate 75.9 to 77.8 %. The numbers of dam with own record were approximate 25.3 to 26.1 % of the total number of dam. This might reflect a problem of accurate partitioning of maternal effects in these data. Therefore, considerably more data across generations is required to investigate the maternal permanent environmental effects and the covariance between direct and maternal genetic effects further.

2.2 Variance components and genetic parameters for birth traits

The variance components and genetic parameters with their standard error from the best model for birth traits were presented in Table 25.

BW and body measurement i.e. GIR, HH and STP both direct and maternal genetic effects played an important role. The estimates of direct and maternal heritabilities were moderate to low. For BW, the estimates of direct and maternal heritabilities were significant, explaining 30% and 18% of the phenotypic variance. The maternal heritability amounted to 60% of that due to direct heritability.

The estimates were within the range generally found in beef cattle, identifying birth weight as moderately heritable trait (Kriese *et al*., 1991; Maiwasshe *et al*, 2002; Phocas and Laloe, 2004). However, Meyer (1993) and Robinson (1996) found that direct and maternal heritabilities were 43%, and 10% for Hereford and 35% and 8% for Angus, respectively. The maternal genetic effects were smaller in this analysis, with the maternal heritability amounting to about 23% of that due to direct heritability. Koot *et al*. (1994) and Keeton *et al*. (1996) stated that the differences between estimates might be attributed to differing levels of genetic variation between populations and the restricted nature and effects of selected data.

Table 25 Variance components and genetic parameters from the best model for birth traits of Thai indigenous cattle

Traits	σ^2_p	h^2	m^2	c^2
BW	5.38 ± 0.15	0.30 ± 0.05	0.18 ± 0.02	-
GIR	13.42 ± 0.33	0.18 ± 0.04	0.18 ± 0.02	-
HH	13.25 ± 0.34	0.23 ± 0.05	0.13 ± 0.02	-
STP	12.78 ± 0.29	0.09 ± 0.03	0.09 ± 0.02	-

For GIR, HH and STP both direct and maternal genetic effects were significant with the same pattern as birth weight. The direct and maternal heritabilities played an equally important role for GIR and STP, explaining 18% and 9% of the phenotypic variance. As found in other breeds, measures of body size in cattle were generally found to be moderately to highly heritable (Meyer, 1998; Bourdon, 2000). In this study, low estimate observed in STP might be attributed to inaccuracies in measurements. In contrast to HH, the results showed that direct and maternal heritabilities were moderately heritable. The direct and maternal heritabilities explained 23% and 13% of the phenotypic variance. The maternal heritability amounted to 56% of that due to direct heritability.

2.3 Weaning traits

The variance components and genetic parameters together with the pertaining log likelihood (Log L) values for weaning traits from fitting various univariate analyses were presented in Table 26.

Table 26 Variance components and parameter estimates for weaning traits from fitting various univariate analysis models

Model	Variance components						Parameter estimates[1/]				
	σ^2_u	σ^2_{pe}	σ^2_m	σ_{um}	σ^2_e	σ^2_p	h^2	m^2	c^2	r_{um}	Log L
WW, kg^2											
1	139.36	-	-	-	89.54	228.90	0.61	-	-	-	-10224.4
2	60.23	53.23	-	-	100.71	214.17	0.28	-	0.25	-	-10162.4
3	59.06	-	55.53	-	104.43	219.02	0.27	0.25	-	-	-10176.7
4	63.45	-	64.28	-10.60	102.11	219.24	0.29	0.29	-	-0.16	-10176.4
5						Not fitted					
6						Not fitted					
GIR2, cm^2											
1	22.41	-	-	-	24.24	46.65	0.48	-	-	-	-6289.4
2	9.07	10.78	-	-	24.41	44.26	0.20	-	0.24	-	-6239.6
3	9.18	-	10.53	-	25.07	47.78	0.21	0.24	-	-	-6248.9
4	11.32	-	17.28	-7.46	23.79	44.93	0.25	0.38	-	-0.53	-6247.9
5						Not fitted					
6						Not fitted					
HH2, cm^2											
1	12.51	-	-	-	9.57	22.08	0.51	-	-	-	-5262.0
2	4.83	4.56	-	-	11.29	20.68	0.29	-	0.10	-	-5235.6
3	4.82	-	4.46	-	11.59	20.87	0.23	0.13	-	-	-5241.9
4	4.98	-	4.95	-0.56	11.50	20.87	0.24	0.24		-0.11	-5241.9
5						Not fitted					
6						Not fitted					
STP2, cm^2											
1	10.57	-	-	-	24.93	35.50	0.29	-	-	-	-5981.3
2	5.27	4.79	-	-	24.62	34.68	0.15	-	0.14	-	-5967.3
3	5.23	-	4.33	-	25.21	34.77	0.15	0.12	-	-	-5970.7
4	5.43	-	4.75	-0.48	25.09	34.79	0.16	0.14	-	-0.09	-5970.7
5						Not fitted					
6						Not fitted					

[1/] See list of abbreviations

For weaning traits, in contrast to birth traits, both direct genetic and maternal permanent environmental effects played an important role. Fitting maternal permanent environmental effects (model 2) increased value of Log L markedly over model 1 and model 3. Allowing maternal genetic and covariance between the direct-maternal genetic effects (model 4) yield a negative estimate of -0.16, -0.53, -0.11 and -0.09 for WW, GIR, HH and STP, respectively. However, the model did not augment the likelihood significantly when compared to that of excluding the maternal genetic and the covariance. Therefore, the model with the direct-maternal covariance included was not used in this study. Model 5 and 6 were also included in the model for all weaning traits but the models were not fitted. As Log L values indicated, maternal effects on weaning traits in this data set were almost entirely non-genetic effects, i.e. model 2 was fitted for weaning traits.

As observed by many authors (e.g. Meyer, 1992; Meyer, 1993; Robinson, 1996), allowing for a model with covariance between the direct-maternal genetic effects yielded a large negative estimate for this parameter. The increasing estimate of both direct and maternal heritabilities dramatically augmented the likelihood significantly. The large negative estimate of direct-maternal genetic covariances did not reflect a marked adverse genetic correlation between growth and maternal performance. The negative values were associated with the management practice or environmentally induced negative dam-offspring covariances. In this study, the data structure for weaning traits consisted of the numbers of dam which had more than one progeny was approximate 59.8 to 68.0 %. The numbers of dam with own record were approximate 15.2 to 21.2 % of the total number of dam. This might reflect a problem of accurate partitioning of maternal effects in these data. Considerably more data across generations is required to investigate the negative covariance further.

2.4 Variance components and genetic parameters for weaning traits

The variance components and genetic parameters with their standard error from the best model for weaning traits were presented in Table 27.

For WW, the estimates of direct heritability and maternal permanent environmental effect played an equally important role, explaining 28% and 25% of the phenotypic variance. In Thai indigenous cattle, the direct heritability for weaning weight was considered moderate, genetic improvement through selection was therefore possible in this population. The estimate of direct heritability was well in agreement with the range of 0.21 to 0.30 (Meyer *et al*., 1993; Haile-Mariam and Kassa-Mersha, 1995; Roughsedge *et al*., 2005). However, the estimates were much higher than the estimate of direct heritability reported for tropical and Korean native cattle (Burrow, 2001; Choi *et al*., 2005).

With respect to maternal effects, the maternal permanent environmental effect was the main factor determining weaning weight. The maternal heritability which generally assumed to express the variation in milk production potential was unimportant in this study. Consequently, the improvement of weaning weight should be solely based on direct genetic effect. Similar results were observed by Meyer (1992), Meyer (1993) and Meyer *et al.* (1993) who reported that maternal permanent environmental effects in Hereford and Charolais were consistently more important than maternal genetic effect.

Table 27 Variance components and genetic parameters from the best model for weaning traits of Thai indigenous cattle

Traits	σ^2_p	h^2	m^2	c^2
WW	214.17 ± 6.45	0.28 ± 0.05	-	0.25 ± 0.03
GIR2	44.25 ± 1.39	0.20 ± 0.05	-	0.24 ± 0.03
HH2	22.70 ± 0.66	0.23 ± 0.06	-	0.22 ± 0.03
STP2	34.69 ± 1.03	0.15 ± 0.05	-	0.14 ± 0.03

For body measurement at weaning i.e. GIR2, HH2 and STP2, the estimates of direct heritability were moderate, explaining 15-23% of the phenotypic variance. The maternal permanent environmental effect played an equally important role, explaining 14-24% of the phenotypic variance. The genetic improvement for body size through selection was possible in this population.

2.5 Yearling traits

The variance components and genetic parameters with their standard error from univariate analyses for yearling traits were presented in Table 28.

For YW, the estimate of direct heritability was high, explaining 43% of the phenotypic variance. In general, maternal effects for this trait were considered negligible because the animals no longer depend on their mothers (Meyer, 1992). The estimate of this study was higher than the estimates reported by Makinnon *et al.* (1991) and Burrow (2000) who reported that the estimates of direct heritability in tropical cattle were moderate, explaining 25-31% of the phenotypic variance. However, relatively high estimates of maternal heritability at yearling age (0.11-0.20% of the phenotypic variance) were also reported by both authors. They recommended that for animals raised on pasture with little or no feed supplement, the length of time between weaning and yearling ages may not be enough to buffer maternal effects present at weaning. In Thai indigenous cattle, direct heritability played an important role. The genetic improvement through selection should be accomplished in this population.

Table 28 Variance components and genetic parameters from the simple model for yearling traits of Thai indigenous cattle

Traits	σ^2_p	h^2	m^2	c^2
YW	247.60 ± 12.78	0.43 ± 0.11	-	-
GIR4	40.52 ± 2.15	0.29 ± 0.12	-	-
HH4	21.79 ± 1.16	0.29 ± 0.11	-	-
STP4	32.74 ± 1.72	0.26 ± 0.11	-	-

For body measurement at yearling i.e. GIR4, HH4 and STP4, the estimates of direct heritability were moderate, explaining 26-29% of the phenotypic variance. On the whole, the direct heritabilities of body measurement were lower than that of YW. The direct heritabilities of body measurement amounted to 65% of that due to direct heritability. The genetic improvement through selection should also be accomplished for YW.

3. Phenotypic and genetic correlations

The estimates of phenotypic and genetic correlations between traits with their standard error from bivariate analyses were presented in Table 29.

3.1 Phenotypic correlation

The phenotypic correlations of the weight trait between BW, WW and YW were moderately positive, ranged from 0.35 to 0.71. The estimate in this study indicated that calves with high WW tended to be high YW. These results were in agreement with Burrow (2001) who reported that phenotypic correlations between

BW, WW and YW of tropical beef cattle ranged from were 0.35 to 0.73. Likewise, Chokchareon (2003) reported that phenotypic correlations between BW, WW and YW of Brahman cattle in Thailand ranged from 0.27 to 0.67. For other beef breeds, Meyer *et al*. (1993) indicated that phenotypic correlations between BW, WW and YW for Hereford ranged from 0.37 to 0.76.

The phenotypic correlations of body measurement at various ages were moderately to highly positive. The phenotypic correlations between GIR, GIR2 and GIR4 ranged from 0.43 to 0.66. The phenotypic correlations between HH, HH2 and HH4 ranged from 0.43 to 0.87 and for STP, STP2 and STP4 ranged from 0.30 to 0.47, respectively. The result showed that calves with high body size at weaning tended to be high body size at yearling age. The magnitudes of these correlations were the same pattern as weight traits.

The phenotypic correlations of traits measured the same ages were moderately to highly positive. The phenotypic correlations between BW, GIR, HH and STP ranged from 0.55 to 0.73. The phenotypic correlations between WW, GIR2, HH2 and STP2 ranged from 0.68 to 0.82 and for YW, GIR4, HH4 and STP4 ranged from 0.77 to 0.88, respectively. The estimate of this study indicated that calves with high BW, WW and YW tend to be high body size at birth, weaning and yearling ages.

3.2 Genetic correlation

The genetic correlations of the weight trait between BW, WW and YW were highly positive, ranged from 0.86 to 0.91. The correlations were uniform between traits. The estimate were higher than the estimate of Akkahart (2003) who concluded that genetic correlation on growth traits of Thai indigenous cattle ranged from 0.29 to 0.92. Somporn (2003) reported that the genetic correlations on growth traits of Brahman cattle ranged from 0.60 to 0.75. The fluctuations in the genetic correlation might be a reflection of different models used in the analysis. In both studies, WW was fitted as comprehensive model allowing maternal genetic and covariance between the direct-maternal genetic effects. In contrast, in this study, WW was fitted only with a direct genetic and maternal permanent environmental effect. However, the result of this study was consistent with Roughsedge *et al*. (2005) who found that genetic correlation between WW and YW for Aberdeen Angus, South Devon, Limousin and Simmental ranged from 0.81 to 0.92.

In general, genetic correlations between weight traits were higher than phenotypic correlations. High positive genetic correlation between WW and YW indicated that genetic improvement could be achieved by selection at WW or YW in this population. This is in agreement with other studies from tropical environments (e.g. Mackinnon *et al.*, 1991; Burrow, 2002).

The genetic correlations of body measurement at various ages were moderately positive. The genetic correlations between GIR, GIR2 and GIR4 ranged from 0.83 to 0.85. The genetic correlations between HH, HH2 and HH4 ranged from 0.82 to 0.86 and ranged from 0.79 to 0.88 for STP, STP2 and STP4, respectively. Similarly, the genetic correlations of traits measured at the same age were moderately to highly positive. The genetic correlations between BW, GIR, HH and STP ranged from 0.84 to 0.89. The genetic correlations between WW, GIR2, HH2 and STP2 ranged from for 0.79 to 0.98 and ranged from 0.94 to 0.98 for YW, GIR4, HH4 and STP4, respectively. The estimates were higher than the estimate of Meyer (1998) who reported that the correlation of traits measured the same age (WW, GIR2, HH2 and STP2) was 0.70 to 0.86.

On the whole, most genetic correlations were highly positive. The estimates of genetic correlations were high for both the same trait measured at different ages and the different traits measured at the same age. Therefore, selection to increase weight traits will increase the body size as well, which may be preferable and can be implemented in multiple traits selection to improve Thai indigenous cattle.

Table 29 Genetic (above diagonal) and phenotypic (below diagonal) correlations between traits of Thai indigenous beef cattle

Traits	BW	WW	YW	GIR	GIR2	GIR4	HH	HH2	HH4	STP	STP2	STP4
BW		0.86±0.04	0.83±0.07	0.86±0.04	0.84±0.05	0.72±0.10	0.89±0.04	0.90±0.04	0.89±0.06	0.84±0.07	0.93±0.05	0.87±0.12
WW	0.45±0.02		0.91±0.04	0.80±0.05	0.91±0.03	0.88±0.06	0.73±0.06	0.79±0.06	0.91±0.05	0.76±0.06	0.98±0.03	0.96±0.06
YW	0.35±0.04	0.71±0.02		0.82±0.07	0.74±0.06	0.97±0.02	0.59±0.08	0.65±0.08	0.94±0.03	0.55±0.09	0.70±0.08	0.98±0.02
GIR	0.73±0.01	0.40±0.02	0.39±0.05		0.85±0.05	0.83±0.08	0.61±0.01	0.45±0.02	0.91±0.12	0.71±0.11	0.83±0.06	0.93±0.08
GIR2	0.42±0.02	0.82±0.01	0.62±0.02	0.43±0.02		0.85±0.06	0.34±0.02	0.80±0.07	0.62±0.03	0.79±0.06	0.82±0.08	0.76±0.10
GIR4	0.49±0.05	0.61±0.02	0.88±0.01	0.65±0.07	0.66±0.02		0.57±0.07	0.57±0.03	0.83±0.09	0.66±0.09	0.79±0.07	0.78±0.13
HH	0.69±0.01	0.31±0.02	0.38±0.05	0.81±0.06	0.71 0.07	0.63±0.11		0.86±0.05	0.83±0.07	0.84±0.08	0.76±0.07	0.71±0.13
HH2	0.47±0.02	0.74±0.01	0.57±0.03	0.89±0.04	0.69±0.01	0.75±0.08	0.43±0.02		0.82±0.06	0.84±0.05	0.84±0.07	0.75±0.09
HH4	0.71±0.08	0.65±0.02	0.80±0.01	0.86±0.06	0.69±0.08	0.71±0.02	0.87±0.10	0.66±0.02		0.78±0.07	0.76±0.08	0.98±0.07
STP	0.55±0.01	0.29±0.02	0.32±0.05	0.44±0.01	0.30±0.02	0.45±0.09	0.49±0.01	0.35±0.02	0.75±0.12		0.85±0.06	0.79±0.10
STP2	0.37±0.02	0.68±0.01	0.45±0.03	0.33±0.02	0.56±0.01	0.48±0.03	0.28±0.02	0.61±0.01	0.50±0.03	0.30±0.02		0.88±0.07
STP4	0.41±0.04	0.57±0.02	0.77±0.02	0.51±0.06	0.54±0.03	0.62±0.02	0.43±0.06	0.49±0.03	0.65±0.02	0.47±0.06	0.47±0.03	

4. Residual correlations

The estimates of residual correlations between traits with their standard error from bivariate analyses were presented in Table 30.

The residual correlations of weight traits between BW and YW were low negative (-0.13) with high standard error and moderate positive between WW and YW (0.40). Similarly, the residual correlations of body measurement between GIR and GIR4 were low negative (-0.10) and moderate positive between GIR2 and GIR4 (0.46). The residual correlations of body measurement between STP, STP4 were negative (-0.15) and low negative between STP2 and STP4 (-0.09) with high standard error. The estimates suggested that the relationship between prenatal and postnatal environments was slightly negative. The environment experienced by a calf before it was born has relative little to do with the environment it would experience from birth to yearling age. In contrast, the genetic and environmental correlation between weaning and yearling traits was moderately positive. It indicated that caves at weaning were reared in the same environment resulting in high yearling traits.

The residual correlations of traits measured at the same ages were moderately positive. The residual correlations between BW, GIR, HH and STP ranged from 0.52 to 0.60. The residual correlations between WW, GIR2, HH2 and STP2 ranged from 0.53 to 0.71 and for YW, GIR4, HH4 and STP4 ranged from 0.29 to 0.67, respectively. The estimates from this study indicated that traits measured the same time and were reared in the same environment resulting in high other traits as well.

Table 30 Residual correlations between traits of Thai indigenous beef cattle

Traits	BW	WW	YW	HH	HH2	HH4	GIR	GIR2	GIR4	STP	STP2	STP4
BW		0.10±0.06	-0.13±0.11	0.52±0.03	0.07±0.06	-0.12±0.13	0.60±0.02	0.08±0.06	-0.05±0.12	0.43±0.02	-0.01±0.05	-0.07±0.09
WW2			0.40±0.08	0.01±0.05	0.60±0.03	0.46±0.07	0.06±0.05	0.71±0.02	0.41±0.08	-0.06±0.05	0.53±0.03	0.33±0.07
YW4				-0.09±0.10	0.51±0.12	0.51±0.15	-0.11±0.09	0.44±0.09	0.67±0.10	-0.15±0.09	0.13±0.11	0.29±0.19
HH					0.08±0.05	-0.06±0.11	0.46±0.03	0.08±0.06	-0.03±0.10	0.35±0.02	-0.00±0.05	-0.07±0.08
HH2						0.39±0.13	-0.00±0.06	0.51±0.03	0.39±0.13	-0.13±0.07	0.45±0.03	0.23±0.14
HH4							-0.21±0.15	0.56±0.09	0.65±0.06	-0.24±0.14	0.01±0.16	0.50±0.07
GIR								0.04±0.06	-0.10±0.12	0.29±0.02	0.02±0.05	-0.17±0.10
GIR2									0.46±0.09	-0.14±0.07	0.35±0.03	0.37±0.09
GIR4										-0.30±0.13	-0.11±0.16	0.56±0.07
STP											-0.07±0.05	-0.15±0.09
STP2												-0.09±0.14
STP4												

Trail III

Calculate economic weight of economically important traits such as sale weight, mature cow weight and fertility of Thai indigenous cattle.

1. Profit under base scenario

The profit from production model of Thai indigenous cattle under base scenario was presented in Table 31. The replacement and survival rates were kept as constants in this calculation. The total costs of calf from birth to sale weight were 17.91 baht/kg with the sale price of 65.00 baht/kg. The total costs of dry cow, cover a period of 1 year were 16.99 baht/kg with the sale price of 45.00 baht/kg. The total costs of wet cow, cover a period of 1 year were also taken into accounted in the production model with the total costs of 4,679.40 baht.

Table 31 Profit from production model of Thai indigenous beef cattle under base scenario

Traits	Average		
Weaning rate, %	80.0		
Sale weight, kg	185.5		
Mature cow weight, kg	250.0		
Constants			
Replacement rate, %	20.0		
Survival rate, %	94.0		
Prices		Cost	Income
Cost of calf, baht/kg		17.91	
Sale weight price, baht/kg			65.00
Cost of dry cow, baht/kg		16.99	
Mature cow weight price, baht/kg			45.00
Calculation of net income			
Profit, baht			1,429.42

The results from the analysis showed that the total costs for the overall production model of Thai indigenous cattle were 7,251.32 baht. These costs consisted of the total cost for dry cow, calf and wet cow were 849.70, 2,658.10 and 3,743.52 baht. The corresponding values in percentage units were 11.7, 36.7 and 51.6%, respectively. The total incomes were 8,680.74 baht. These incomes derived from the selling of culled cow and calf which were 6,655.74 and 2,025.00 baht. In the bottom line, the base profit form this production model was 1,429.42 baht per cow per year.

2. Economic weights of breeding objective traits

The economic weights of breeding objective traits i.e. weaning rate, sale weight and mature cow weight for Thai indigenous cattle were presented in Table 32.

Table 32 Profit due to an increase 1 extra unit of weaning rate, sale weight and mature cow weight

Traits	Average
Weaning rate, %	80.0
Sale weight, kg	185.5
Mature cow weight, kg	250.0
Calculation of net income	
Base profit, baht	1,429.42
Profit due to 1 extra unit of weaning rate, baht	80.11
Profit due to 1 extra unit of sale weight, baht	21.81
Profit due to 1 extra unit of mature cow weight, baht	4.90

The economic weights (not discount) in profit per cow per year were 80.11 baht per an increase of 1% of weaning rate, 21.81 baht per kg of sale weight and 4.90 baht per kg of mature cow weight, respectively. The results of this study suggested that improvement of weaning rate (fertility), sale weight and mature cow weight would have a positive effect on profitability of Thai indigenous cattle production system. However, the profit from improvements in weaning rate was higher than those from sale weight and mature cow weight.

The incomes, costs and profit for improvement of weaning rate from 80% to 100% were shown in Table 33 and Figure 10. The result indicated that an increase of 5% on weaning rate, from 80% to 85%, 90%, 95% and 100%, the expected changes in the income were 400.56, 801.14, 1,201.71 and 1,602.28 baht/cow, respectively. An improvement of 5% in weaning rate implied an average of 46.6% in profit increase.

Table 33 Income, costs and profit with different weaning rate

Parameter	Weaning rate				
	80%	85%	90%	95%	100%
Income, baht	8,680.74	9,247.44	9,814.15	10,380.85	10,947.55
Cost, baht	7,251.32	7,417.46	7,583.59	7,749.72	7,915.85
Profit, (baht/cow/year)	1,429.42	1,829.98	2,230.56	2,631.13	3,031.70
Profit difference, (baht/cow/year)	0	400.56	801.14	1,201.71	1,602.28

The relationships between profit and weaning rate were practically linear (Figure 10). This figures illustrated that an important increase in profit could be achieved by improvement in herd management.

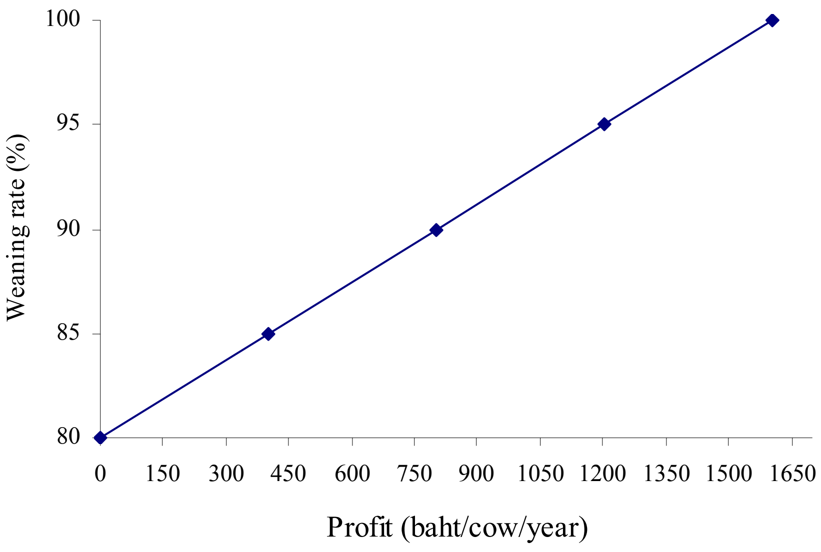

Figure 10 Relation between profit and weaning rate of Thai indigenous cattle

A direct comparison between the results of different studies was difficult because of differences in the biological, management, production system and breeds being examined. Further differences occurred in the definition of traits and in production constraints. Some general conclusions however were possible. Reviews by Upton (1985), Greeff *et al.* (1995) and Phocas *et al.* (1998) concluded that reproductive traits seem to be more important economically than growth. Likewise, among the reproduction traits success measured as weaning rate of females had high economic importance (Barwick, 1998; Urioste *et al*., 1998; Kahi *et al*., 2003). These results were supported in this study. In contrast, MacNeil *et al*. (1994) found that the economic weight for fertility and survival were small compared to the economic weight of growth rates. Post-weaning growth rate was the trait with the highest economic weight.

In this study, the main reason for the differences in economic weights between weaning rate and sale weight was that the age at selling of Thai indigenous cattle was 1.5 to 2 years of age. Thai indigenous cattle were reared under subsistence production systems. The growth rate was low, therefore the rearing periods from birth to sale weight were long to meet market requirement (150 to 200 kg of sale live weight). This would lower the profit due to total cost increases under economic conditions.

For mature cow weight, mostly negative economic weights have been reported (e.g. Fernandez-Perea and Alenda Jimmenez, 2004; Wolfova *et al*., 2005). Considering that the increase in mature cow weight affected only the cost of maintenance but no better performance in the feedlot. This value was negative because bigger animals required more maintenance energy. If forage was adequate, larger cows could consume enough to meet nutrient needs but larger cows might be penalize if forage was sparse.

In contrast, the results of Koots and Gibson (1998) and Hirooka *et al*. (1998) reported that the economic weights were positive for mature cow weight. In the first paper, the reason was the exclusion of a higher energy requirement for heavier cows because of a separate handling of feed intake in mature animals. In the second paper, the reason was due to assuming a lower rate of dystocia and lower calf losses in heavier cows as well as a relatively high price per kg slaughter. In Thai indigenous cattle, the economic weights of mature cow weight were positive in agreement with both studies. The reason however was that cow had small size. Therefore, they required less maintenance energy. The total costs for dry cow was low (4,248.50 baht or 16.99 baht/kg) as well as the reasonable sale price resulted in a positive profit. On the ground that weaning rate, sale weight and mature cow weight have a positive effect on profitability of Thai indigenous cattle production system, these traits should be included in the breeding objective to formulate selection indices used for ranking the animals.

Trial IV

Evaluate the returns of investment and predict genetic gains per year from one round of selection of Thai indigenous cattle

In preliminary studies for this part, productive life times of sired used in nucleus, multiplier and commercial herds were assumed to be 3, 4 and 5 years, respectively. However, the reproductive time could not be realized and there was no genetic gain. Therefore, the productive life time of sires used was varied in different tiers. The suitable productive life times to produce genetic gain for the whole breeding structure were 2, 3 and 3 years in nucleus, multiplier and commercial herds, respectively. Beside this, a study was also conducted to optimize the number of cows in the multiplier herds. The percentage of cows in multiplier herds was assumed to be 9 levels i.e. 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5 and 8.0% out of the total population (800,000 cows). The results indicated that the profit per cow was highest when 6.5% of cows were in the multiplier herds. Therefore, the suitable breeding structure in term of economical return should consist of 6.5% or 52,000 cows in multiplier herd according to result shown below.

1. Number of animal and selection intensity

The number of animal and selection intensity for the individual selection groups were present in Table 34. There were nine selection groups generating genetic gain. The last selection group involved dams to produce dams in the production herd (CD>CD) was not relevant, since all proven dams were all selected to use in commercial herd which resulted in a selection intensity of zero. Consequently, there was no genetic gain for this group.

The number of proven and selected animal for each group was calculated from the population parameter shown in table 12 and table 14. For instance, the number of proven animals in group 1 (NS>NS) and 3 (NS>ND) were 482 heads. They were the product of the number of dams in the breeding herd (1,500 heads), the percentage of calves weaned per dam (80.0%) and coefficients of the sex ratio (0.5), the survival rate of dam in nucleus (95%), the survival rate of calves at selling (94%) and the proportion of bull fitted for breeding (90%). The selected animal in these groups was calculated from the number of dams mated (1,500 heads) divided by the product of the sire's productive life time (2 years) and the bull/cow ratio (1:25). In other selection groups, i.e. group 2 (ND>NS) and 4 (ND>ND); group 5 (MS>MD) and 7 (MS>CS), the calculations were conducted in the same way.

Table 34 Number of animal and selection intensity for the individual selection groups

Character	1	3	2	4	5	7	6	8	9
	NS> NS	NS> ND	ND> NS	ND> ND	MS> MD	MS> CS	MD> MD	MD> CS	CS> CD
No. of proven animal	482		535		482		20,529		18,476
No. of selected animal	30		300		373		9,333		4,950
Selection proportion, %	6.20		56.00		77.40		45.50		26.80
Selection intensity, *i*	1.96		0.70		0.16		0.87		1.23
Generation interval, years	3.10		4.69		3.76		5.91		4.12
Accuracy of selection, r_{ai}	0.45		0.44		0.45		0.29		0.35

The selection intensity of the individual selection groups were 1.96, 0.70, 0.16, 0.87 and 1.23, respectively. Groups 5 and 7 were of pre-selected groups. In these groups the better proportion of males selected in the nucleus herd (30 heads), were used for mating in the herd of DLD (group 1 and 3) and it was only the remainder of selected males (373 heads) that were used in multiplier herd (group 5 and 7). Therefore, the selection intensity for group 1 and 3 was higher than those of other selection groups. As expected, the selection intensity for each selection groups decreased as number of selected animal increased. The selection intensity and the accuracy of selection for male in nucleus herd (group 1 and 3), in multiplier herd (group 5 and 7) and female in nucleus herd (group 2 and 4), in multiplier herd (group 6 and 8) were equal. The reason was that those animals were selected on the basis of the same information irrespective of their allocation to selection groups. The information sources used to calculate selection index for each selection group were presented in Table 35.

The accuracy of selection was the correlation between selection index and true aggregate breeding value. The accuracies of selection for this study ranged from 0.29 to 0.45. The accuracies of selection increased as information sources used correspondingly. The accuracies of selection for group 1, 3 and 5, 7; group 2 and 4; group 9; group 6 and 8 were 0.45, 0.44, 0.35 and 0.29. The information sources for each selection group were 20, 19, 9 and 8 sources, respectively. Group 1, 3 and 5, 7 had higher accuracies of selection than group 2 and 4 because these groups had scrotum circumference from individual information source in addition. Due to high genetic correlations between WW4 and body measurements, therefore, group 6 and 8 recorded only body measurements such as GIR4, HH4 and STP4. Group 9 had higher accuracy of selection than group 6 and 8 because this group had scrotum circumference from individual information source in addition. The results agreed well with the previous study of example Thai indigenous cattle (Intaratham, 2002). Beside from this, the study also found that the accuracy would increase with the intensity of performance recording from growth to reproduction, temperament and carcass. Similarly, Graser *et al.* (1994) concluded that the accuracy of selection for Australian beef cattle increased with increasing intensity of performance recording from growth, to reproduction and carcass (0.21 to 0.34).

Table 35 Information sources used to calculate selection index for each selection groups

Selection	Information	Selection traits[2/]								
groups	sources[1/]	WW	YW	GIR4	HH4	STP4	Co-W	DtoC	A1C	SC
1, 3 and 5, 7	Individual	√	√	√	√	√				√
	Dam	√	√	√	√	√	√	√	√	
	PHS	√	√	√	√	√				√
2 and 4	Individual	√	√	√	√	√				
	Dam	√	√	√	√	√	√	√	√	
	PHS	√	√	√	√	√				√
6 and 8	Individual			√	√	√				
	Dam			√	√	√		√	√	
	PHS									
9	Individual			√	√	√				√
	Dam			√	√	√		√	√	
	PHS									

[1/] PHS = paternal half sib
[2/] See list for abbreviations

The generation interval for the individual selection groups were 3.10, 4.69, 3.76, 5.91 and 4.12 years, respectively. The average generation interval of the nucleus herd in this study was 3.90 years. The selection group for males in group 1 and 3 had a shorter generation interval than those of males in group 5 and 7. The reason was that the productive life time of sires used in nucleus was shorter than in multiplier herds.

2. Genetic gain per generation for the individual selection groups

The genetic gain (ΔG) per generation occurring both for the breeding objective and for the component traits were presented in Table 36. These groups and parameters were relevant for calculating genetic gain per year.

Table 36 Genetic gain per generation for the individual selection groups

Character[1/]	1	3	2	4	5	7	6	8	9
	NS> NS	NS> ND	ND> NS	ND> ND	MS> MD	MS> CS	MD> MD	MD> CS	CS> CD
ΔG for the breeding objective, baht	563.83		190.91		69.09		161.42		303.01
ΔG for SW-d, kg	17.52		6.25		2.14		5.25		8.47
ΔG for WW, kg	8.61		3.24		1.06		2.97		4.17
ΔG for YW, kg	13.83		5.12		1.69		3.61		5.97
ΔG for CoW, kg	13.38		5.15		1.64		4.04		5.23
ΔG for GIR4, cm	3.61		1.35		0.44		1.66		1.85
ΔG for HH4, cm	2.59		0.99		0.32		1.09		1.23
ΔG for STP4, cm	2.85		1.08		0.35		1.25		1.40
ΔG for CoWR, %	1.45		0.36		0.18		0.34		1.16
ΔG for SC, cm	1.94		0.56		0.24		0.14		1.18
ΔG for Dtoc, day	-0.87		-0.26		-0.11		0.06		-0.58
ΔG for A1C, year	-0.03		-0.01		-0.00		-0.01		-0.02

[1/] See list of abbreviations for trait definitions

The genetic gain per generation in aggregate breeding objective was the sum of the genetic gain in the SW, CoW and CoWR weighted by their economic weight. For instance, the aggregate breeding objectives in nucleus herd (group 1 and 3) were 563.83 baht. They were the sum of the genetic gain of SW-d (17.52 kg), CoW (13.38 kg) and CoWR (1.45%), multiplied by economic weight of SW-d (21.81 baht), CoW (4.90 baht) and CoWR (80.11 baht), respectively. In other selection groups, the calculations were conducted in the same way. The genetic gains in single trait were required to calculate the contribution of selection groups to total returns.

The results showed that male selection groups 1 and 3 in the nucleus had higher genetic gain per generation for the breeding objective than those of other male selection groups (group 5 and 7 in multiplier herd and group 9 in commercial herd). The factors affecting the higher genetic gain in this selection group were higher selection intensity and higher accuracy of selection.

For the female selection groups, the result shown that group 2 and 4 in nucleus herd had higher genetic gain than those of group 6 and 8 in multiplier herd as well. Although, in group 6 and 8 had high selection intensity (0.87 vs 0.70) but the accuracy of selection (Table 34) was smaller resulting in lower genetic gain.

3. Standard discounted expression and total return

The standard discounted expression (SDE) and total return of breeding objective traits for the individual selection groups were presented in Table 37. The SDE in this study were specified to two types of trait. The first type was growth traits. The breeding objective traits in this type were SW-d and CoW. The second type was reproductive trait. The breeding objective trait in this type was CoWR. The result indicated that SDE for growth traits in CS>CD was 0.48, followed by MS>CS, NS>NS and MD>CS were 0.18, 0.16 and 0.15, respectively. The SDE for reproductive trait was lower than growth trait in the same selection groups. The SDE for reproductive were 0.30, 0.10 and 0.08 in CS>CD, MS>CS and MD>CS, respectively.

The SDE allowed total return per group to be determined. The return per selection group was the sum of the returns from genetic gain in single traits, multiplied by their SDE and economic weight. For example, the return for SW-d in NS>NS (group 1) was 63.43 baht which derived from 17.52 kg × 0.16 × 21.81 baht. The return for CoW was 10.49 baht (13.38 kg × 0.16 × 4.90 baht). The return for CoWR was 8.13 baht (1.45 % × 0.07 × 80.11 baht). Therefore, the total return for this group was 82.05 baht per generation. The result showed that the total return in CS>CD (group 9) was higher than those of other groups, follow by NS>NS (group 1) and NS>ND (group 3), respectively. The total return was high in CS>CD because this group was both high SDE for growth and for reproductive traits led to high return for

SW-d, CoW and CoWR, correspondingly.

Table 37 Standard discounted expression (SDE) and total return of breeding objective traits for the individual selection groups

Character[1/]	1 NS> NS	3 NS> ND	2 ND> NS	4 ND> ND	5 MS> MD	7 MS> CS	6 MD> MD	8 MD> CS	9 CS> CD
SDE for SW-d and CoW	0.16	0.05	0.13	0.04	0.09	0.18	0.08	0.15	0.48
SDE for CoWR	0.07	0.02	0.06	0.01	0.05	0.10	0.04	0.08	0.30
Total return, baht	82.05	24.31	23.32	6.30	6.13	11.20	11.47	22.12	129.65
SW-d, baht	63.43	19.17	18.32	5.05	4.63	8.29	8.93	16.98	89.25
CoW, baht	10.49	3.28	3.39	0.94	0.79	1.42	1.54	2.93	12.37
CoWR, baht	8.13	1.86	1.61	0.31	0.71	1.50	1.00	2.21	28.03

[1/] See list of abbreviations for trait definitions

4. Genetic gain per year, profit per cow

The genetic gain per year, return, cost and profit per cow in the population were presented in Table 38. Inserting the average generation interval (3.90 years) and the average genetic gain of selection groups achieved in the nuclease herd i.e. NS>NS, NS>ND; ND>NS and ND>ND, led to genetic gain per year for each trait. In this case the gene contributions of these four groups were equal at 25% for each group. The genetic gain per year of SW-d was 3.05 kg per year. It was the product of the average genetic gain (11.89 kg, (17.52+6.25)/2) divided by the average generation interval (3.90 years). The genetic gains per year for other single trait were calculated in the same way.

The results revealed that genetic gain per year for growth traits (SW-d, WW, YW, CoW) and body measurements (GIR4, HH4, STP4) were positive. These positive genetic gains were in the desirable direction to improve genetic of Thai indigenous cattle. For fertility, SC for male calves and CoWR for female cows trends were also positive, and for DtoC and A1C the trends were negative. The genetic gains of fertility traits were all favorable because shorter DtoC and lower A1C and higher for CoWR led to an overall increase in profit.

Table 38 Genetic gain per year, return, cost and profit per cow in the population

Trait[1/]	Genetic gain per year		Return per cow (baht)
SW-d, kg	3.05		234.02
WW, kg	1.52		-
YW, kg	2.43		-
CoW, kg	2.38		37.53
GIR4, cm	0.64		-
HH4, cm	0.46		-
STP4, cm	0.50		-
CoWR, %	0.23		45.71
SC, cm	0.32		-
DtoC, day	-0.14		-
A1C, year	-0.005		-
Δ G for breeding objective, baht	96.85		
Total return per cow, baht			317.26
Total costs per cow, baht		22.27	
Fixed costs per cow, baht		20.49	
Variable costs per cow, baht		1.78	
Profit per cow, baht		294.99	

[1/] See list of abbreviations for trait definitions

The genetic gain per year for breeding objective was 96.85 baht. This was the sum of the genetic gain per year of SW-d (3.05 kg), CoW (2.38 kg) and CoWR (0.23%), multiplied by economic weight of SW-d (21.81 baht), CoW (4.90 baht) and CoWR (80.11 baht), respectively.

With regard to return and cost, the returns per cow for SW-d, CoW and CoWR were 234.02, 37.53 and 45.71 baht, respectively. The total return per cow in the population of 800,000 cows was obtained by summing the return per cow from SW-d, CoW and CoWR which were 317.26 baht. The total costs of selection per cow were 22.27 baht. The total returns more the total costs gave the resulting profit. This was 294.99 baht per cow. On the whole, the total costs in the population of 800,000 cows were 17,816,000 baht. The profits in the investment period (20 years) were 235,992,000 baht.

CONCLUSIONS

Four investigations of this thesis involved evaluation of breeding objective for Thai indigenous cattle. The first study examined fixed effects affecting weight and body measurement at birth, 200, 400-day weight. The second study estimated the genetic parameters among studied traits. The third study calculated economic weights of breeding objective traits. The fourth study evaluated the returns of investment and genetic gains per year relevant to the breeding structure of Thai indigenous cattle. The following conclusions were drawn from the present investigations:

1. Herd and line-year-season of calving and sex had a significant influence on birth, weaning and yearling traits. Age of dam had significantly influenced birth and weaning traits at linear and quadratic levels. Age of animal had a significant influence on weaning and yearling trait at a linear level. Age of animal by sex interactions was not significant for both weaning and yearling traits. Male calves had greater birth, weaning and yearling traits than female calves.

2. Heritabilties of birth traits were low to moderate. Both direct and maternal genetic effects played an important role. In contrast, for weaning traits both direct and maternal permanent environment effects played an important role. The maternal genetic effects were not important. For yearling traits, the estimates of direct heritabilities were moderate to high. Due to direct heritabilities being moderate to high for weaning and yearling weight genetic improvement through selection for the two traits should be accomplished.

3. The phenotypic correlations of the weight traits and body measurement were moderately to highly positive. The calves with high weight traits tend to be high body size. The genetic correlation of the weight traits and body measurement were moderately to highly positive. On the whole, genetic correlations between weight traits were higher than phenotypic correlations. The residual correlations of birth and yearling traits were low and negative and between weaning and yearling traits were moderately positive. From the favorable genetic correlations between weight and

body measurement it was concluded that selection to increase weight traits would increase body size traits as well.

4. The base profit from production model of Thai indigenous cattle was 1,429.24 baht per cow per year. The economic weights of breeding objective traits i.e. cow weaning rate, sale weight and mature cow weight (not discount) were 80.11, 21.81 and 4.90 baht. The profit from improvement weaning rate was higher than those of sale weight and mature cow weight. However, the improvement of these breeding objective traits had a positive effect on profitability of Thai indigenous cattle production system. These traits should be included to formulate selection index used in selection.

5. The genetic gain per year for growth traits and body measurement relevant to breeding structures of Thai indigenous cattle were positive. For fertility, SC for male calves and CoWR for female cows, were positive. DtoC and A1C were negative. The genetic gains per year for all breeding objective and component traits were favorable direction led to the profit in overall. The genetic gain per year for breeding objective was 96.72 baht.

6. The total returns and costs in the population of 800,000 cows were 317.26 and 22.27 baht. The profit per cow was 294.99 baht for 20 years of investment period.

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APPENDIX

Appendix Table 1 The cost of production from birth to sale weight of Thai indigenous cattle

No	Stage of production	Cost (baht)
1	Birth to weaning	
	- concentrate feed (16% of crude protein) at 5.50 baht/kg, 0.25 kg/head/day for 55 days	75.63
	- roughage (hay) at 1.50 baht/kg, 1.6 kg/head/day for 55 days	132.00
	- roughage (pasture) at 0.50 baht/kg, 6.0 kg/head/day for 55 days	165.00
	- medicine and deworming	100.00
2	Weaning to yearling weight	
	- concentrate feed (14% of crude protein) at 4.00 baht/kg, 0.50 kg/head/day for 100 days	200.00
	- roughage (hay) at 1.50 baht/kg, 2.5 kg/head/day for 100 days	375.00
	- roughage (pasture) at 0.50 bath/kg, 9.0 kg/head/day for 100 days	450.00
	- medicine and labor cost	190.00
3	Yearling to sale weight	
	- concentrate feed (14% of crude protein) at 4.00 baht/kg, 0.50 kg/head/day for 100 days	200.00
	- roughage (hay) at 1.50 baht/kg, 3.8 kg/head/day for 100 days	570.00
	- roughage (pasture) at 0.50 baht/kg, 13.5 kg/head/day for 100 days	675.00
	- medicine and labor cost	190.00
	Total cost	3,322.63
	Cost/kg	17.91

Appendix Table 2 The cost of production for wet cow of Thai indigenous cattle

No	Stage of production	Cost (baht)
1	Rearing cow	
	- concentrate feed (14% of crude protein) at 4.00 baht/kg, 0.75 kg/head/day for 100 days	300.00
	- roughage (hay) at 1.50 baht/kg, 6.3 kg/head/day for 100 days	945.00
	- roughage (pasture) at 0.50 baht/kg, 22.0 kg/head/day for 100 days	1,100.00
	- medicine and labor	250.00
2	Cow from weaning to calving 165 days	
	- concentrate feed (14% of crude protein) at 4.00 baht/kg, 0.50 kg/head/day for 82 days	164.00
	- roughage (hay) at 1.50 baht/kg, 6.3 kg/head/day for 82 days	774.90
	- roughage (pasture) at 0.50 baht/kg, 22.0 kg/head/day for 83 days	913.00
	- medicine and labor	232.50
	Total cost	4,679.40
	Cost/kg	18.72

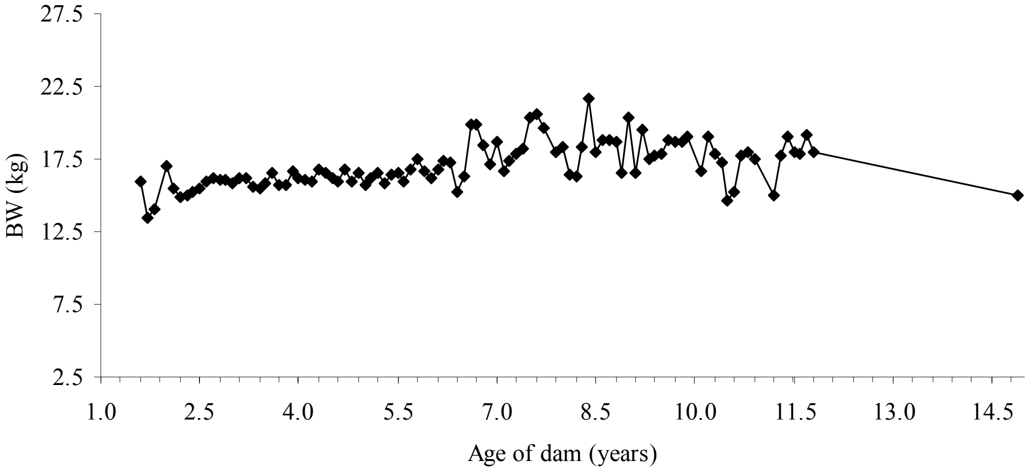
Appendix Table 3 The cost of production for dry cow of Thai indigenous cattle

No	Stage of production	Cost (baht)
1	Dry cow	
	- concentrate feed (14% of crude protein) at 4.00 baht/kg, 0.25 kg/head/day for 180 days	180.00
	- roughage (hay) at 1.25 baht/kg, 6.3 kg/head/day for 180 days	1,701.00
	- roughage (pasture) at 0.50 baht/kg, 22.0 kg/head/day for 185 days	2,035.00
	- medicine and labor cost	332.50
	Total cost	4,248.50
	Cost/kg	16.99

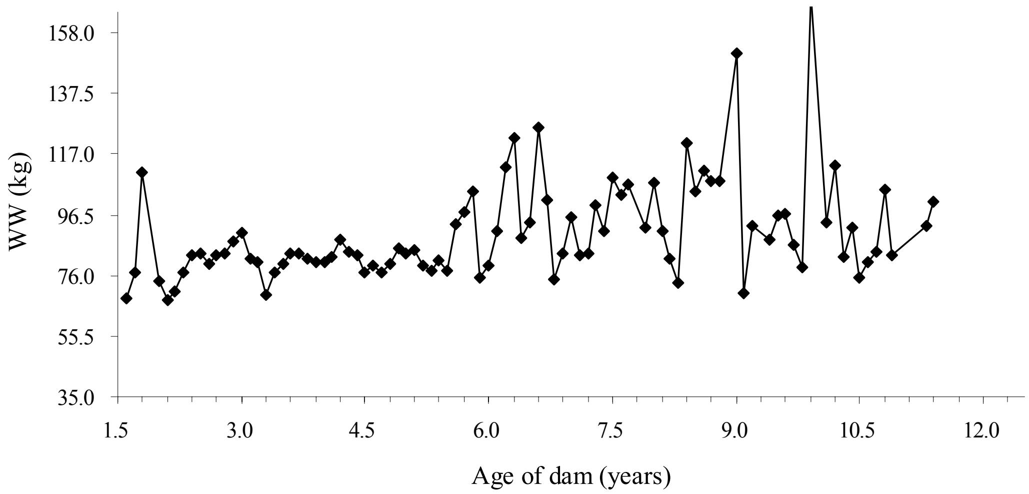
Appendix Table 4 Components of the transmission matrix of Thai indigenous cattle

	NS			ND						MD						CS					CD					
	x	x		x	x	x	x	x	x																	
NS	1																									
		1																								
			1																							
	x	x		x	x	x	x	x	x																	
				1																						
ND					1																					
						1																				
							1																			
								1																		
	x	x								x	x	x	x	x	x											
										1																
											1															
MD												1														
													1													
														1												
															1											
	x	x								x	x	x	x	x	x											
																1										
CS																	1									
																		1								
																			1							
																				1						
																x	x	x	x	x	x	x	x	x	x	x
																					1					
CD																						1				
																							1			
																								1		
																									1	
																										1

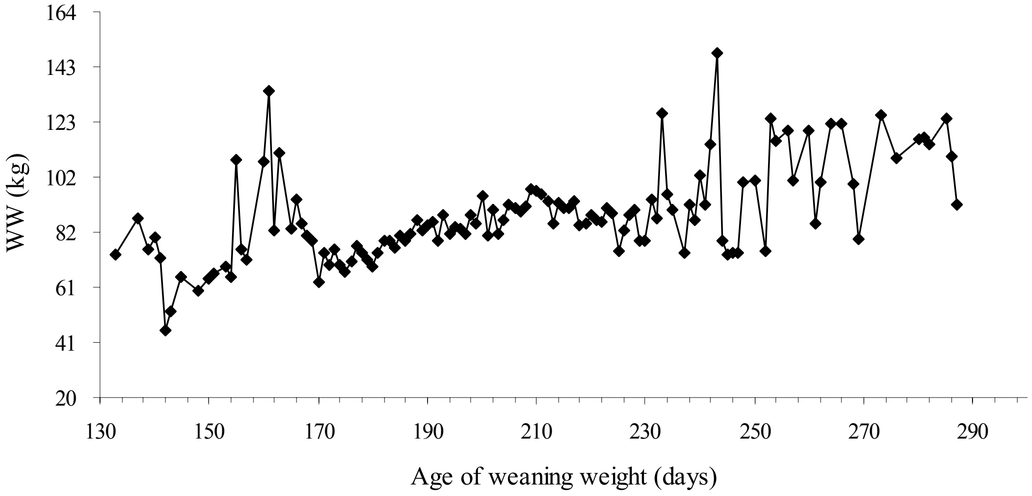
Appendix table 4 shows the required transmission matrix for Thai indigenous cattle population structure described. Cells are filled for the ten selection groups of Figure 5 with donor parents and their age classes heading the table. These are sires and dams are born in the nucleus herd (NS and ND), in the multiplier herd (MD) and those born in commercial herd (CS and CD). The rows of the table show the age classes of each group receiving gene (recipients). Age group 1 of males in the nucleus herd (NS) receives their genes from 2.5 to 3.5 year-old sire and from 2.5 to 8.5 years dams. These represent 0.5 of the gene of each parent, summing to 1. The table forming a diagonal of ones in five of the blocks, indicate the aging of animal.



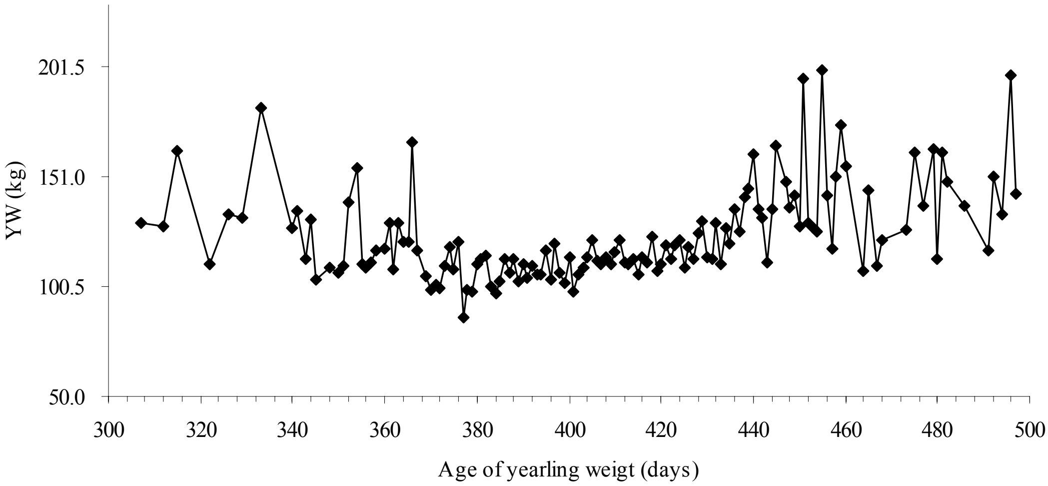
Appendix Figure 1 Means of birth weight at age of dam for Thai indigenous cattle



Appendix Figure 2 Means of weaning weight at age of dam for Thai indigenous cattle



Appendix Figure 3 Means of weaning weight at age recording for Thai indigenous cattle



Appendix Figure 4 Means of yearling weight at age recording for Thai indigenous cattle

CURRICULUM VITAE

Name: Wutipong Intaratham

Birth Date: October 5, 1960

Birth Place: Sisaket, Thailand

Education:

YEAR	INSTITUTE	DEGREE
1982	Khon kaen University	B.S. (Agriculture)
1996	Khon kaen University	M.S. (Agriculture)

Position / Title: Animal Scientist

Work Place: Division of Animal Husbandry, Department of Livestock Development, Payathai Road, Rachatewee District, Bangkok 10400, Thailand.

Scholarship: The Royal Golden Jubilee (RGJ) project (2003 -2006), Thailand Research Fund (TRF), Thailand.

PUBLICATIONS

Intaratham, W., S. Koonawootrittriron, P. Sopannarath, H-U Graser and S. Tumwasorn. 2008. Genetic Parameters and Annual Trends for Birth and Weaning Weights of a Northeastern Thai Indigenous Cattle Line. **Asian-Aust. J. Anim. Sci.** 21(4): 478-483.