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THESIS

GENETIC ANALYSES FOR WEANING TO FIRST SERVICE INTERVAL IN A THAI COMMERCIAL SWINE POPULATION

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A Thesis Submitted in Partial Fulfillment of
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Genetic analysis for weaning to first service interval (WSI) and litter traits (i.e., number of piglets born alive, NBA; litter weight at birth of live piglets, LBW; number of piglets at weaning, NPW and litter weight at weaning, LWW) were evaluated base on the pedigree and phenotypic data from a commercial swine herd in Northern Thailand. The original data contained 1,341 Landrace (L) and 795 Large White (W) and reciprocal crossbred sows (163 LW and 169 WL) were collected during 1989 to 2008. Primiparous sows had a longer WSI than multiparous sows ($P < 0.0001$). Crossbred sows had longer WSI than purebreds sows ($P < 0.0001$), whereas WSI between L and W sows were no difference. Variance-covariance components were estimated with an animal model for WSI and a sire-dam model for litter traits. Heritabilities for direct genetic effects were low for WSI (0.04 ± 0.02) and litter traits (ranged from 0.05 ± 0.02 to 0.06 ± 0.02). Maternal heritabilities for litter traits were 20% to 50% lower than their direct genetic heritabilities. Repeatabilities for WSI was similar to its heritability, whereas repeatabilities for litter traits ranged from 0.15 ± 0.02 to 0.18 ± 0.02. Direct genetic correlations between WSI and litter traits were close to zero, contrarily with positive and high correlation among litter traits (except between litter traits at birth and LWW). Thus, a single trait analysis could be used for WSI, whereas litter traits must be multiple traits analysis. Boar genetic trends were small and significant only for NBA ($P = 0.0042$). Sow genetic trends were small, negative and significant for WSI ($P = 0.0113$), NBA ($P = 0.0071$), LBW ($P = 0.0109$), NPW ($P = 0.0234$) and LWW ($P = 0.0034$). In addition, one polymorphism and 2 alleles of the adiponectin (ADIPOQ; G and A) and follicle stimulating hormone receptor (FSHR; C and T) genes were studied for allele substitution and genotypic effects. Neither allelic nor genotypic effects were significant for either the ADIPOQ or the FSHR gene. Thus, the ADIPOQ and FSHR genes will be of little help for selecting pigs in this population.

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LIST OF ABBREVIATIONS

AD	=	Additive direct genetic effects
ADIPOQ	=	Porcine adiponectin gene
AM	=	Additive maternal genetic effects
AF	=	Age at farrowing of sow
BGD	=	Breed group of sow
BGS	=	Breed group of boar
°C	=	Degree Celsius
⊗	=	Direct product of matrices
EPD	=	Expected progeny differences
FSHB	=	Porcine follicle stimulating hormone beta sub-unit
FSHR	=	Porcine follicle stimulating hormone receptor
FYS	=	Frrowing year-season combinations
HD	=	Heterosis difference
HP	=	Heterosis percentage
LBW	=	Litter weight of living piglets at birth
LL	=	Lactation length
LSMs	=	Least squares means
LWW	=	Litter weight of living piglets at weaning
NBA	=	Number of live piglets at birth per litter
NPD	=	Non-productive sow day
NPW	=	Number of live piglets at weaning per litter
%	=	Percentage
PED	=	Sow permanent environmental deviations
PR	=	Parity group of sow
SD	=	Standard deviation
SE	=	Standard error
SNP	=	Single nucleotide polymorphism
WCI	=	Weaning to conception interval
WEI	=	Weaning to first estrus interval
WSI	=	Weaning to first service interval

GENETIC ANALYSES FOR WEANING TO FIRST SERVICE INTERVAL IN A THAI COMMERCIAL SWINE POPULATION

INTRODUCTION

Increasing number of survival piglets per sow per year is the first aim of commercial swine production in Thailand. The number of those piglets can be increased by improving performance of litter traits, such as number born alive (NBA), number of piglets at weaning (NPW), litter weight of live piglets at birth (LBW) and litter weaning weight (LWW), and increasing sow efficiency. The sow efficiency can be improved by decreasing the period of non-productive interval, which was measured as non-productive sow day (NPD), for example, weaning to first service interval (WSI), weaning to first estrus interval (WEI) and weaning to conception interval (WCI). Non-productive sow days is the economically important trait for commercial swine production because longer in this period increases maintenance and other fixed costs in production system and lead to decrease sow efficiency.

However, sow efficiency and reproductive performance were reflected from NPD management, which depended on several factors. Therefore, characterization of factors affecting NPD can be used to determine and indicate sow efficiency. For instance of factors affecting NPD were temperature and humidity variations, which prolonged WSI in the hot and rainy season (for crossbred Landrace × Yorkshire sows, Suriyasomboon *et al.*, 2006). Breed group effects were reported in different length of WEI that were longer in crossbred compared with purebred (Suwanasopee *et al.*, 2005a). Primiparous sow had a longer WSI than multiparous sows because of insufficient body energy reserves (Tantasuparuk *et al.*, 2001a). Lactation length prolonged WSI indirectly depend on body weight losses during lactation above 5% in primiparous sows and 10% in multiparous sows (Thaker and Bilkei, 2005). Non-productive sow day is the interval of sow from the date at weaning to the date at first insemination after weaned. The studies for NPD usually focused on WSI because it was measured clearly than the others NPD. However, the studies for NPD in Thailand

had mostly done in the populations which raised in the closed system (Suwanasopee *et al*., 2005a; Suwanasopee *et al*., 2005b; Imboonta *et al*., 2007). Thus, studying to decrease WSI in swine that raised in the hot-humid conditions, such as in Thailand, would help the commercial swine producers in the tropical country to decrease production costs and increase sow efficiency.

Commercial swine producers in Thailand have considered both production and reproduction traits in sow selection program. The production traits, such as NBA, NPW, LBW and LWW were normally used to cull or select sows for replacement herd. Recently, commercial swine producers in Thailand have begun to use WSI in their selection program. Thus, estimating of genetic variability and genetic association between WSI and litter traits need to be achieved for effective genetic improvement programs for these traits in Thailand. Reported heritability for WSI was low, which ranged from 0.03 (Holm *et al*., 2005) to 0.20 (Ehlers *et al*., 2005). Corresponding results of low heritability for WSI and litter traits were reported in Thailand that were 0.17 ± 0.03 for WSI with logarithmically transformed data (Imboonta *et al*., 2007), 0.11 ± 0.04 for NBA and 0.08 ± 0.03 for LBW (Pholsing *et al*., 2009) and 0.01 ± 0.02 for NPW and 0.08 ± 0.03 for LWW (Suwanasopee, 2006). However, the information of genetic trends and genetic associations between WSI and litter traits in the hot-humid environmental conditions of Thailand have not been investigated in the swine populations consisted of purebred and crossbred together.

According to low heritabilities for WSI and litter traits suggesting that the progress of genetic improvement based on quantitative selection is expected to be slow. For this obstruction can be solved by increasing the accuracy of selecting which animals contained the relevant genes associating good performance for WSI and litter traits. Using genotypic information of the genes with known effects that related to WSI and litter traits for classifying relevant animals would increase the accuracy of selection. Unfortunately, the genes play the major role affecting WSI and litter traits cannot be determined. Moreover, the studies for investigating the candidate genes that related to WSI have never been reported. However, there are some studies in temperate regions reported the associated genes for WEI and litter traits, i.e.,

adiponectin (ADIPOQ) and adiponectin receptor-2 (ADIPOR2) for WEI and NBA (Houde *et al.*, 2008), follicle stimulating hormone β-subunit (FSHB) for WEI (Li *et al.*, 2008) and follicle stimulating hormone receptor (FSHR) for litter size (Jiang *et al.*, 2002). Studies belong to associations between specific allele of these candidate genes in the hot-humid environmental conditions such as in Thailand have never been done. Using genotypic information combine with quantitative selection may increase the accuracy for selecting the animal that contained superior genetic and high performance. Therefore, the relevant genotypic polymorphism of genes related to WSI and litter traits need to be classified especially in the population that raised in the tropical environments.

OBJECTIVES

The objectives of this study were:

1. To characterize the factors affecting and determine heterosis effects for WSI and litter traits in a Landrace - Large White commercial swine population raised in an open-house system in Thailand.

2. To estimate genetic parameters and trends for WSI and litter traits in an open-house commercial swine population composed of purebred Landrace, Large White and reciprocal crossbred (Landrace × Large White and Large White × Landrace) in Thailand.

3. To estimate the allele frequencies of previously identified polymorphisms of candidate genes (adiponectin and follicle stimulating hormone receptor genes) and to evaluate the association between specific genotypes and reproductive traits in a commercial swine population composed of purebred Landrace, Large White and crossbred (Landrace × Large White and Large White × Landrace) in Thailand.

LITERATURE REVIEW

1. Non-productive sow days

Non-productive sow days (NPD) were defined as the period that a primiparous or multiparous sow was not in gestating or lactating (Polson *et al.*, 1993). This period can be measured as a number of days from weaning to gestation or culling. Sows with longer NPD would impact to decrease its efficiency and increase the maintenance and other fixed costs. This period composed of three intervals during the date at weaning to the date at pregnancy or culling (Figure 1). These components were the WSI, first-service to gestation and first-service to culling (Figure 1; Koketsu, 2005).

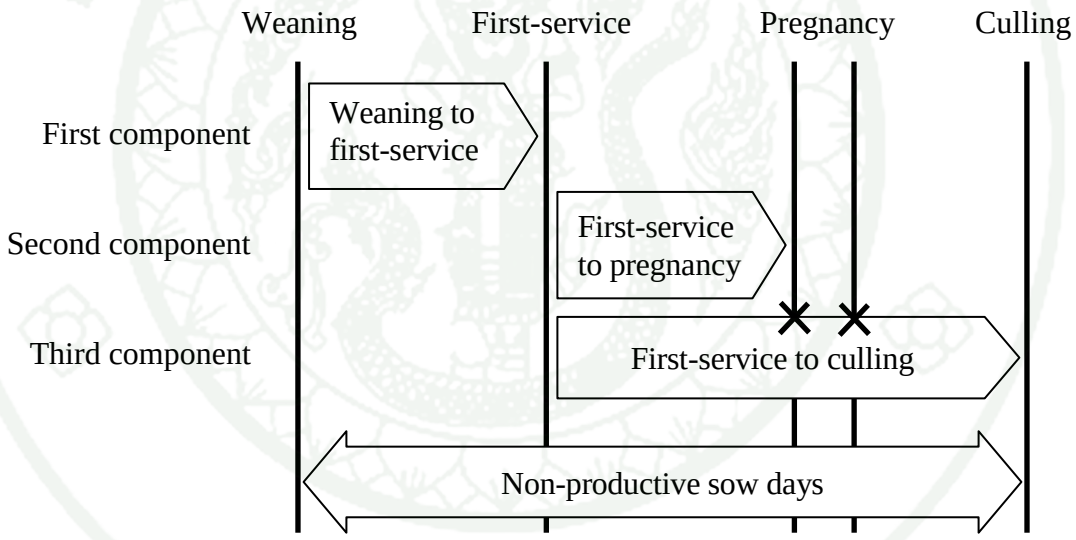

Figure 1 The components of non-productive sow days

The parameters for NPD were reported as weaning to estrus interval (WEI; Ten Napel *et al*., 1995; Koketsu and Dial, 1997), weaning to first service interval (WSI; Koketsu and Dial, 1997), weaning to conception interval (WCI; Le Cozler *et al*., 1997), weaning to farrowing interval (WFI; Ten Napel and Johnson, 1997) and farrowing to conception interval (FCI; Koketsu and Dial, 1997). These traits were importance economically trait because longer this period decreased sow efficiency and increased opportunity for those sow to be culled. However, the studies for NPD

were mostly used WSI to measure this period (Koketsu and Dial, 1997; Adamec and Johnson, 1997; Hanenberg *et al*., 2001; Ehlers *et al*., 2005; Imboonta *et al*., 2007), because it is measured clearly than the others NPD.

Thailand is a tropical country that has high temperature and humidity. These environmental conditions have directly impacted to NPD, because the animals raised under hot and humid conditions were hard to observe and delay estrus expression (Myer and Bucklin, 2001). Thus, the animals that raised in this weather, especially in the open-house system, usually presented a longer period of NPD. However, there are studies that reported several factors affecting NPD, such as, breed group (Tantasuparuk *et al.*, 2000a; Suwanasopee *et al*., 2005a), parity, seasonal (Koketsu and Dial, 1997; Tantasuparuk *et al.*, 2000a), lactation length (Mabry *et al.*, 1996; Tantasuparuk *et al*., 2000b), body weight loss in lactation (Tantasuparuk *et al.*, 2001a), ovulation time, hormone and stress (Patterson *et al.*, 2008). Unfortunately, the studies in the past for NPD in Thailand were underlined on management, reproductive and nutritional aspects. Few studies had considered NPD from a genetic selection perspective and none of them were in open-house systems (Imboonta *et al*., 2007; Suwanasopee *et al*., 2005a; Suwanasopee *et al*., 2005b). Consequently, factors affecting NPD in the weather of open-house system could be considered and characterized for commercial swine production in Thailand.

2. Factors affecting the weaning to first service interval

2.1 Breed or breed group

Breed and breed group were the importance factors for variation of WSI in swine population. Ten Napel and Johnson (1997) reported the longer interval from weaning to farrowing of Landrace compared to Large White sows ($P < 0.05$) in the United States. Moeller *et al*. (2004) compared the serviced interval after weaned of six crossbred commercial swine maternal lines in the United States. They found this interval was significant differences among dam lines ($P < 0.001$). In the hot-humid weather, purebred Yorkshire have a shorter WSI than Landrace ($P < 0.001$) in three

commercial swine herds in the central region Thailand (Tantasuparuk *et al*., 2000a). The concordant result was reported by Suwanasopee *et al*. (2005a) they reported purebred Large White had a shorter WEI than Landrace ($P < 0.05$) and crossbred swine had longer WEI than purebred ($P < 0.05$) in a commercial swine population in Central Thailand. The similar result for longer WSI in crossbred was found in the Lithuanian White × Danish Landrace crossbred than purebred Danish Landrace ($P < 0.01$) in Lithuanian pig herds (Karvelienè *et al.*, 2008).

2.2 Parity

Effects of parity were the results of the relationship between physiology status of reproduction and age effects. Primiparous sows have longer WSI ($P < 0.05$; Koketsu and Dial, 1997) and WEI ($P < 0.05$; Suwanasopee *et al*., 2005a) than multiparous sows. Moreover, the longer WSI in primiparous sows mostly presented in those were born from primiparous sows ($P < 0.05$; Tummaruk *et al*., 2001). Because primiparous sows would have to allocate nutrients for balancing high energy and protein requirements for milk production and their growth during lactation period of them (Einarsson *et al*., 1998).

2.3 Seasonal

Farrowing season was significant effects to longer WSI in summer (June to August) than spring (April to May) in the United States ($P < 0.05$; Koketsu and Dial, 1997). However, in the hot-humid environmental conditions, longer WSI was occurred in the hot and rainy weaning season (March through October) in three commercial herds of purebred Yorkshire and Landrace population in Thailand ($P < 0.05$; Tantasuparuk *et al.*, 2000a), and the similar result was in six commercial herds of three-crossbred swine population (Large White × Landrace × Duroc) in Central Thailand ($P < 0.001$; Suriyasomboon *et al*., 2006). These probably resulted from the weather higher than 25°C for the lactating period of sow performed a large of body weight loss and decreased the ability of sow to return to production after weaning (Myer and Bucklin, 2001).

2.4 Body weight loss during lactating period

Lactation feed intake, lactation weight loss and body condition were the reflections of metabolic energy status of lactating sows that affecting reproductive performance after weaning (Koketsu and Dial, 1997; Tummaruk *et al*., 2000; Thaker and Bikei, 2005). Increasing feed intake during early and mid lactation (4 to 12 days after farrowing) could improve the WEI ($P = 0.03$; Koketsu, 1999). Moreover, Crenshaw *et al*. (2007) reported the results for increasing protein supplement diet in younger lactating sows in the summer period increased lactation feed intake ($P < 0.01$) and tend to reduced WEI ($P = 0.06$) . In addition, fewer sows distinctly showed estrous appearance within 7 days after weaning if those sows were extended feed intake with low energy diet during lactation ($P < 0.01$; Reese *et al*., 1982). These implied that feeding for lactating sows would have to be considered increasing in both of quantity and quality aspects for reducing body weight loss during lactation.

Greater body weight loss during lactation affected to prolong WSI ($P < 0.05$) in two commercial purebred herds of Landrace and Yorkshire in central Thailand (Tantasuparuk *et al*., 2001a). The resemble result was reported by Thaker and Bilkei (2005) for quadratic association between lactation weight loss and WSI ($P < 0.01$) for crossbred Landrace × Yorkshire populations in German and Slovakia. And moreover, the significant extension of WSI was found when sows lost their body weight during lactation greater than 5% ($P < 0.05$) for primiparous sows and 10% ($P < 0.05$) for multiparous sows (Thaker and Bilkei, 2005). On the other hand, backfat thickness during lactation was used to be indicator to measure body weight loss. Tummaruk *et al*. (2001a) reported gilts with higher backfat thickness at 100 kg of body weight were shorter WSI than gilts with thinner backfat ($P < 0.01$) in purebred Swedish Landrace and Yorkshire population. These suggested that high body weight loss was associated with longer WSI. Body weight loss can be found in animal that is in the insufficient nutrients intake conditions. This status push those sows have to allocate nutrients intake for maintenance itself and milk production for nursling her piglets. Thus the number of piglets in lactating period and the length of lactation

would be the important factors to loss her body weight in large scale that impact to extend WSI (Eissen *et al*., 2003; Schenkel *et al*., 2010).

2.5 Lactation length

Longer lactation period in primiparous or multiparous sows were advantage for reducing WSI ($P < 0.05$) in the multiline crossbred of Landrace, Large White, Duroc and Hamshire in the United States that belong to the study of Xue *et al*. (1993). Similarly results were reported that lactation length less than 7 to 12 days affecting longer WSI than those sows weaned at 17 to 21 days (Koketsu and Dial, 1997; Marsteller *et al*., 1997). However, none significant result for WSI under effects of lactation length was reported in three purebred Landrace and Yorkshire sow herds from Thailand (Tantasuparuk *et al*., 2000b).

Since, longer lactation period push the primiparous or multiparous sows to overburden for nursling her piglets by extended period for milk production. This moment resulted to increase body weight loss of sows during lactation and may extend to WSI. Moreover, the association between lactation length and WSI were not only linear effects. Mabry *et al*. (1996) reported the quadratic effects of lactation length on WSI across parity in crossbred and purebred sows from 13 commercial herds of the United States suggesting that the lowest WSI related to the optimal range of lactation length. According to this optimal range of lactation length was reported as 22 to 27 days after weaning (Mabry *et al*., 1996), 22 to 25 days (Costa *et al*., 2004) and 21 to 28 days (Le Cozler *et al*., 1997).

2.6 Hormonal of reproduction

Increasing of gonadotropin releasing hormone (GnRH) secretion from hypothalamus leads to increase follicular size and estrogen. Estrus expression was reflected from the role of estrogen (Hafez and Hafez, 2000). Therefore, estrus appearance in sows was controlled by ovarian follicular growth after weaning. Thus, the numbers of smaller diameter of follicles at weaning were the indicator to prolong

WEI (Bracken *et al*., 2006). Because a large number of small follicles at weaning need to have extended time to reach the preovulatory follicle size. Thus, any inhibitor that can decrease the GnRH secretion would delay the showing of estrus appearance to prolong WSI. However, Sechin *et al*. (1999) found shorter WSI in primiparous sow when treated them with equine chorionic gonadotropin (PMSG), and the significant quadratic effects on the association between PMSG and WSI was found ($P < 0.05$) in sow at the first and second parities of three crossbred herds in Southern Brazil. This suggested that the lowest WSI related to most favorable of PMSG treatment (750 IU for sow at the first parity).

3. Genetic parameters for weaning to first service interval

3.1 Heritability and repeatability

A WSI is an important indicator of sow reproductive efficiency in pig industry. Theoretical period of WSI was 4 to 8 days post-weaning (Mabry *et al*., 1996), and optimal period of WSI was 4 to 6 days post-weaning (Hoshino and Koketsu, 2008). Estimates genetic parameters for WSI has been investigated in several populations with low value of heritabilities and repeatabilities. Rydhmer (2000) concluded the value of heritability for WSI closed to 0.1. However, heritabilities for WSI were reported in Dutch Landrace population (0.07 ± 0.005 to 0.14 ± 0.005; Hanenberg *et al*., 2001) and in Norwegian Landrace population (0.03 to 0.08; Holm *et al*., 2005), whereas higher heritabilities for WSI were reported in purebred Czech Landrace - Large White population (0.14; Adamec and Johnson, 1997), in purebred Yorkshire, 2 crossbred Yorkshire × Hampshire and 3 crossbred Yorkshire × Hampshire × Landrace in the United States (0.21 for purebred to 0.24 for crossbred; Ehlers *et al*., 2005) and in purebred Landrace population in Eastern Thailand (0.16 ± 0.03 to 0.18 ± 0.04; Imboonta *et al*., 2007). Remarkably, higher heritabilities were usually found in the primiparous sows.

Estimates repeatabilities for WSI were reported in few studies in the temperate region as 0.19 (Adamec and Johnson, 1997; Czech Republic) and $0.19 \pm$

0.005 (Hanenberg *et al*., 2001; Netherland). In Thailand has never reported the repeatability for WSI. The only study for repeatability involved NPD was performed for WEI by Suwanasopee *et al*. (2005b). They reported low heritability and repeatability (0.03 and 0.06 respectively) in purebred Landrace - Large White - Duroc commercial herds in Central Thailand. Moreover, a negative effect of heterosis of WEI (5.98%) was found in crossbred Landrace × Large White sows in Thailand (Suwanasopee *et al*., 2007).

3.2 Genetic correlation and traits association

Weaning to first service interval was associated to other production and reproduction traits. Holm *et al*. (2005) reported high genetic correlation between WSI and return rate of sow (0.93), WSI in first parity and WSI in other parities (0.78), but genetic correlation between WSI and NBA was close to zero in Norwegian Landrace population. This may explain the result of Koketsu and Dial (1997) for WSI did not affect from litter size. Moreover, genetic correlations for association between WSI and subsequent litter size were close to zero in purebred Landrace population in eastern Thailand (Imboonta *et al*., 2007). Contrarily result of Ehler *et al*. (2005) reported moderate genetic correlation between WSI and NBA (0.24) and WSI and adjusted litter weight (0.05). However, WSI was reported with high genetic correlation for relating to age at first insemination as 0.31 in Dutch Landrace population (Hanenberg *et al*., 2001) and 0.24 in purebred Norwegian Landrace population in Norway (Holm *et al*., 2005).

In addition, the association between WSI and production traits were reported by Imboonta *et al*. (2007) found negative genetic correlations between WSI and average daily gain (ADG) (-0.08 ± 0.09 to -0.03 ± 0.10) and between WSI and backfat thickness (-0.27 ± 0.09 to -0.11 ± 0.10) in purebred Landrace in eastern Thailand. However, gilts with higher growth rate had shorter WSI ($P < 0.05$), larger litter size ($P < 0.05$) and higher farrowing rate ($P < 0.05$) than those with lower growth rate for all parity in purebred Swedish Landrace-Large White herds (Tummaruk *et al*., 2001). Tantasuparuk *et al*. (2001b) found the association of longer longevity in

sow that shorter WSI (within 9 days) in purebred and within 5 days for crossbred swine in purebred Landrace and Yorkshire and crossbred herds in Thailand.

4. Candidate genes related to the weaning to first service interval

The major genes that play the role to regulate WSI are now unknown. Many evidences of genes related to sow reproduction were reported, e.g. gonadotropin gene and gonadotropin receptor gene (Li *et al*., 2008), estrogen receptor gene (Isler *et al*., 2002), leptin gene, leptin receptor gene (Summer *et al*., 2009), melanocotin receptor gene (Rempel *et al*., 2008), adiponectin gene and adiponectin receptors gene (Houde *et al*., 2008). Gonadotropin and gonadotropin receptor genes are involved estrus expression of swine. Follicle stimulating hormone (FSH) and luteinizing hormone (LH) are the results of gonadotropin gene expression in anterior pituitary gland (Li *et al*., 1997). Consequence, folliculogenesis has risen in the ovary and has generated the estrogen hormone as a product. Signs of estrus are the result of estrogen hormone expression. Therefore, the estrus expression is depended on gonadotropin and gonadotropin receptor genes expression. The results of these genes affected to NPD. Li *et al*. (2008) found the variation of WEI in the different follicle stimulating hormone β subunit (FSHB) microsatellite polymorphism of pigs in China ($P < 0.05$). In addition, transcriptional activation of ESR is induced by FSH, which is regulated by FSH receptor (FSHR). The relationship between FSH and ESR in the granulosa cell of follicle has synergistic effects to oocyte development (Ulloa-Aguirre *et al*., 2007). However, the estrus expression can be occurred in sows under mild negative metabolic energy condition (Barb *et al*., 2008). Thus, lactating sows with restricted feed intake are forced into energetic challenges, which affecting to prolong the length of lactation and postweaning anestrus (Schneider, 2000).

Leptin (LEP) and leptin receptor have also known in the role of maintain energy balance, dietary energy intake and indirectly control reproduction in sows (Spicer, 2001; De Rensis *et al*., 2005; Barb *et al*., 2008). However, there are no relationship between the concentration of LEP and reproductive performance of sows after weaning (De Renis *et al*., 2005). The study of Barb *et al*. (2008) found that LEP

concentration was associated with backfat depth. And loss of backfat was associated with reproductive performance at postweaning (Thummaruk *et al.*, 2001). Thus, LEP may plays the importance role of metabolic signal that influenced the regulation of reproductive in the post-partum sows via the regulation of food intake and energy balance (Benoit *et al*., 2000; Barb *et al*., 2008).

The melanocotin (i.e., alpha-melanocyte stimulating hormone, α-MSH; and melanocortin receptor type 4, MC4R) and agouti-related protein (AgR) system are an importance homeostatic regulation of body energy stores by controlling appetite (Benoit *et al*., 2000). Under the negative energy balance condition, low level of plasma LEP concentration, activates appetite control center to increase food intake through AgR and neuropeptide-Y (NPY) system (Matteri, 2001; Barb *et al*., 2008). The effects for NPY activation would also suppress the GnRH secretion (Barb *et al*., 2008). This suppression would be negative effects for the reproduction response. Contrarily, melanocortin system decreases food intake without NPY collaboration in the positive energy balance conditions (Matteri, 2001; Barb *et al*., 2008). Therefore, the factors that suppress for GnRH secretion would be disappeared. This would indicate the favorable conditions for the reproduction response of sows. The association between MC4R polymorphisms and WEI ($P < 0.01$) was reported by Rempel *et al*. (2008) in Landrace × Duroc × Yorkshire composite population in the United States.

Adiponectin and adiponectin receptors are importance factors for fatty acid catabolism and glucose homeostasis, which led to decreased the tissue triglyceride content in muscle and stimulated glucose uptake (Yamauchi *et al*., 2002; Kadowaki and Yamauchi, 2005; Lord *et al*., 2005). However, Houde *et al*. (2008) studied the association between reproductive traits and the polymorphisms of adiponectin (ADIPOQ) and adiponectin receptor (ADIPOR1 and ADIPOR2) genes in purebred Landrace sows in the United States. They found the ADIPOQ and ADIPOR2 polymorphisms associated with shorter WEI ($P < 0.05$; Houde *et al*., 2008).

MATERIALS AND METHODS

Herd management and data description

1. Animal herd and management

Swine commercial herd in this study was located in Chiang Mai province, Northern Thailand (18° 28' 39.74" North, 98° 47' 53.53" East; elev. 292 m). The average temperature from 1989 to 2009 was 26.2°C (12.4°C to 38.4°C) and the average humidity was 71.6% (44.0% to 90.0%; Thai Meteorological Department, 2009). Season was classified as winter (November to February: cool and dry), summer (March to June: hot and dry) and rainy (July to October: hot and humid). Average temperature by season was 23.2°C (3.8°C to 37.7°C) in winter, 28.3°C (13.8°C to 42.4°C) in summer and 27.1°C (14.0°C to 39.0°C) in the rainy season (Thai Meteorological Department, 2009). Average humidity by season was 68.7% (49.0% to 83.0%) in winter, 65.0% (44.0% to 84.0%) in summer and 81.2% (74.0% to 90.0%) in the rainy season (Thai Meteorological Department, 2009). Field data from this population were collected from 1989 to 2008. This population was composed of purebred (Landrace, L and Large White, W) and crossbred (L × W, LW and W × L, WL) that provided pedigree and reproductive performance records. Dataset was collected from primiparous and multiparous sows in the breeder and farrowing unit. The original sources of genetic of those sows were Scandinavian swine and original own. This commercial herd has been maintained as a closed population since 2002. Replacement gilts were recruited within their own population. Thus, sows in this population have been related. Therefore, they had connectedness through their sire.

All primiparous and multiparous sows were managed in an open-housing condition, the weather had ranges from 3.8°C to 38.4°C for temperature and from 44.0% to 90.0% for relative humidity (Thai Meteorological Department, 2009), and received sismilar management, nutrition, health care, mating and culling. Cooling systems were fogger for the breeders sows (gilts and non-lactating sows) and dipper

for the farrowing-nursling sows. Breeder boars were kept in a close-house system with evaporative cooling. Feeding for boars, gilts and non-lactating sows, were divided and fed twice a day (7:00 and 13:00) with approximate 2.5 kilogram per sow daily (breeder diet: 16% crude protein and 3,200 to 3,500 kcal/kg metabolic energy). The farrowing-nursling sows were fed 4 times a day (7:00, 10:00, 13:00 and 15:00) with 5 to 6 kilograms per sow daily due to sow condition (lactating diet: 17 to 18% crude protein and 4,060 kcal/kg metabolic energy).

Replacement gilts were inseminated for the first time at 8 to 9 months of age or 140 kg of body weight. A purebred boar (L or W) might be used to produce purebred (L or W) and crossbred (LW or WL) piglets with the same boar. Thus, all breed groups of sows were connected through their sire. After mating and conception, pregnant sows were placed into an individual stall until approximately 104 days of gestation then sows were taken to farrowing barn and placed into an individual farrowing pen. Some cross-fostering were perform in case of lactating over load. Piglets were weaned at 26 to 30 days of age due to piglets' condition (roughly 7 kg of individual weight). Weaned sows would be turned to the breeder unit and received breeder diet until first estrus was detected. Estrus detection of primiparous and multiparous sows were performed by boar exposure daily. The artificial insemination 2 times with the same boar were inseminated, first insemination at 12 hours after detection of visible estrus and second at 12 hours after the first insemination.

2. Traits and measurement

The original data (12,974 litter records) contained the major trait of weaning to first service interval (WSI, days). Meaning of this trait was a number of days between weaning date to service date at the first onset of estrus after weaning. Range of WSI in the original data was from 0 day to 89 days including 1,211 records of missing information. Other traits were litter traits, i.e., number of piglets born alive (NBA, piglets), litter weight at birth of live piglets (LBW, kg), number of piglets at weaning (NPW, piglets) and litter weight at weaning (LWW, kg).

Number of piglets born alive was described in this study as a number of total live piglets per litter at birth without cross-fostering piglets. The number of total piglets survival per litter at weaning date was determined as NPW. Both litter weight at birth and weaning (LBW and LWW) were measured as a total weight of all live piglets in their litter at birth and at weaning respectively. Range of these litter traits in the original data were 0 to 21 piglets for NBA, 0.5 to 39.7 kg for LBW, 0 to 20 piglets for NPW and 3.0 to 138.6 kg for LWW.

3. Data description and classification

The original dataset were collected from 1989 to 2008 that consisted of pedigree (i.e., sow identifying number, ID; ID of sire and dam), sows attribute (i.e., breed groups, parity of sow, age at farrowing and sow status), point of time (i.e., service date, farrowing date and weaned date), period of time (i.e., pregnant period, lactation length and WSI) and litter performance (i.e., total piglets born, NBA, LBW, NPW and LWW). This dataset contained 12,974 litter records with 3,310 sows and 612 sires appeared in this dataset. The erroneous and incomplete information were eliminated.

Breeds of swine in this study were L and W. Thus, breed group of sows (BGD) were L, W and reciprocal crossbred groups (LW and WL). Breed group of boars (BGS) were L and W. Classification for parity group of sows (PR) fell into 7 categories, i.e., 1, 2, 3, 4, 5, 6 and 7 parity groups, ranged from first parity (parity group 1) to eighteenth parities (parity group 7). Age at farrowing (AF) of sows ranged from 10 months (parity group 1) to 98 months (parity group 7). Lactation length (LL) ranged from 0 to 44 days (mean = 25.08 days, SD = 3.04 days). Contemporary groups were defined as year-season combination at farrowing (FYS; 56 categories for original dataset).

Trial 1: Characterization of factors affecting and determination of heterosis effects for weaning to first service interval

1. Dataset description and editing data

The original dataset (12,974 litter records) was edited to eliminate the records which contained missing data and erroneous for WSI, NPW and LL. Lactation length less than 7 days were deleted. Thus, edited dataset was obtained with 11,737 litter records from 2,468 sows. The study trait for this trial was WSI. Breed groups of sows were purebred L, W and reciprocal crossbred groups LW and WL. Parity of sows was classified as groups 1 (the first parity) to 7 (the seventh parities and older). Means, standard deviations (SD) and ranges for WSI by breed groups of sow were shown in Table 1.

Table 1 Number of sows, number of observations and descriptive statistics for weaning to first service interval (days) by breed groups of sow

Breed group of sow [1]	Number of sows (heads)	Number of observations (litters)	Weaning to first service interval			
			Means (days)	SD	Minima (days)	Maxima (days)
L	1,341	5,729	6.61	5.99	0	85
W	795	4,126	6.18	5.49	0	53
LW	163	935	6.35	5.52	0	87
WL	169	947	6.97	7.07	0	89
Total	2,468	11,737	6.47	5.88	0	89

[1] L, purebred Landrace; W, purebred Large White; LW, Landrace × Large White; WL, Large White × Landrace

2. Statistical analysis

The tested factors affecting WSI were FYS, PR, BGD, LL for first order and second order, NPW, and AF. The WSI data were analyzed using following linear model:

$$y_{ijkl} = \mu + FYS_i + PR_j + BGD_k + b_1 LL_{ijkl} + b_2 LL2_{ijkl} + b_3 NPW_{ijkl} + \varepsilon_{ijkl} \quad (1)$$

where

y_{ijkl} = the phenotypic observation for WSI,
μ = population mean for WSI,
FYS_i = farrowing year-season effects (i = 1 to 56),
PR_j = parity of sow (j = 1 to 7),
BGD_k = breed groups of sow (k = 1 to 4),
LL_{ijkl} = lactation length,
$LL2_{ijkl}$ = square of lactation length,
b_1 = linear regression of WSI on lactation length,
b_2 = quadratic regression of WSI on lactation length,
NPW_{ijkl} = number of piglets weaned,
b_3 = linear regression of WSI on number of piglets weaned,
ε_{ijkl} = random residuals effects

Random residual effects were assumed to zero mean, common variance and uncorrelated. Significance of the factors affecting were computed by using the MIXED procedure of SAS (SAS, 2008) and Bonferroni t-test was used to compare the least squares means (LSMs) for each subclass of the factors affecting.

The WSI difference between crossbred and purebred sows was estimated as the heterosis effects, which were represented with heterosis difference (HD) and heterosis percentage (HP). Heterosis difference was calculated as the difference

between LSMs for each reciprocal crossbred group by subtracting their LSMs (LW or WL) from the average of the LSMs of the parental breeds ($0.5 \times (L + W)$).

$$HD = (\text{LSMs for LW or WL}) - (0.5 \times (L + W)) \quad (2)$$

And heterosis percentage was computed as 100 times the ratio of HD to the parental average.

$$HP = \frac{HD}{(0.5 \times (L+W))} \times 100 \quad (3)$$

Trial 2: Estimation of variance components, genetic parameters and trends for weaning to first service interval and litter traits

1. Dataset description

The edited dataset 4,339 records were edited for eliminating the erroneous and incomplete information for five interesting traits (WSI, NBW, LBW, NPW and LWW) from the original dataset of 12,974 records. All of identified cross-fostered records were deleted.

Breed group of sows for this population composed of purebred (L and W) and crossbred animals (LW and WL), and BGS were L and W (Table 2). There were 356 boars and 1,852 sows represented in the dataset. The pedigree file contained 3,081 animals (660 boars and 2,421 sows). Number of observations by breed group of sows for WSI were majority in L sows (61.2%) and descend in W sows (29.5%), LW sows (5.7%) and WL sows (3.6%), whereas, number of boar records were similarity 46.8% for L and 53.2% for W. Number of observations by mating types for litter traits (NBA, LBW, NPW and LWW) were 1,162 (26.4%) records for the purebred mating (L×L and W×W), 2,827 (64.3%) records for crossbred mating (L×W and W×L) and 410 (9.3%) records for the backcrosses mating of purebred boars and crossbred sows (L×LW, L×WL, W×LW and W×WL).

Contemporary groups for this study were 56 categories of farrowing year-season. Parity of sows was classified into 7 parity groups, group 1 (sows in the first parity) to group 7 (sow in the seventh parities and older). Numbers of records for parity groups 1 to 7 were 954 (21.7%), 794 (18.0%), 681 (15.5%), 594 (13.5%), 516 (11.7%), 400 (9.1%) and 462 (10.5%), respectively. Age at farrowing of sows ranged from 10 months to 76 months. Lactation length ranged from 12 to 37 days (mean = 25.14 days, SD = 2.85 days). Means, SD, minima and maxima values for WSI, NBA, LBW, NPW and LWW were presented in Table 3.

Table 2 Number of boars and sows and number of observations by breed group of sow

Breed group of sow [1]	Number of boars	Number of sows	Number of observations	
			Breed group of boar	Breed group of sow
L	190	1,094	2,059	2,691
W	166	571	2,340	1,298
LW	-	81	-	160
WL	-	106	-	250
Total	356	1,852	4,399	4,399

[1] L, purebred Landrace; W, purebred Large White; LW, Landrace × Large White; WL, Large White × Landrace

Table 3 Descriptive statistics for weaning to first service interval and litter traits

Trait[1]	Number of observations	Means	SD	Minima	Maxima
WSI (days)	4,399	6.52	5.15	1.00	60.00
NBA (piglets)	4,399	10.49	2.76	1.00	21.00
LBW (kg)	4,399	16.05	4.66	0.60	39.70
NPW (piglets)	4,399	8.57	2.46	1.00	16.00
LWW (kg)	4,399	59.39	19.12	3.50	138.60

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

2. Estimation of variance and covariance components

Estimation of variance and covariance components for WSI, NBA, LBW, NPW and LWW were performed by using restricted maximum likelihood procedure (Harville, 1977) with average information algorithm (Gilmour *et al.*, 1995).

Computations for these components were carried out with ASREML program (Gilmour *et al*., 2006). Bivariate analyses were conducted for all traits. Therefore, ten pair-wise analyses were performed (WSI-NBA, WSI-LBW, WSI-NPW, WSI-LWW, NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW and NPW-LWW). The matrix notation models for ten pair-wise were shown as bellows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Zg_1 & 0 \\ 0 & Zg_2 \end{bmatrix} \begin{bmatrix} g_1 \\ g_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (4)$$

where

y_i = vector of phenotypic records for trait i (i = 1, 2; where traits 1 and 2 were the first and another trait in each pair-wise analyses),

b_i = vector of fixed environmental effects for trait i,

g_i = vector of fixed genetic group effects for trait i,

a_i = vector of random genetic effects for trait i,

p_i = vector of random permanent environmental effects for trait i,

e_i = vector of random residuals for trait i,

X_i = incidence matrix related records to environmental fixed effects for trait i,

Zg_i = incidence matrix related records to genetic groups effects for trait i,

Z_i = incidence matrix related records to random genetic effects for trait i, and

W_i = incidence matrix related records to permanent environmental effects for trait i.

An animal model (Quaas and Pollak, 1980) with genetic groups effects was used for WSI that consisted of FYS (49 farrowing year-season combinations) as fixed contemporary groups and PR (7 parity groups) as fixed subclass effects. Age at farrowing and LL of sow were determined as fixed covariates. Breed group of sow (4 groups; L, W, LW and WL) were fixed genetic group effects. Sow genetic effect, permanent environment of sow and residual were random effects.

A sire-dam model (Henderson, 1984) with genetic group effects was used for litter traits (NBA, LBW, NPW and LWW). These models composed of fixed environmental effects as FYS, PR, AF and LL for NPW and LWW, whereas fixed effects for NBA and LBW were FYS, PR and AF. Fixed genetic group effects for litter trait models were BGS, BGD and heterosis effects (probability of alleles in piglet that received from different breed between boar and sow; Elzo, 1990; Elzo and Wakeman, 1998). Boar and sow genetic effects, maternal permanent environmental effects and residual were random effects for all litter trait models.

The pair-wise analyses between WSI and litter traits (WSI-NBA, WSI-LBW, WSI-NPW and WSI-LWW) created the variances and covariances matrix of random genetic effects which was equal to $A \otimes V_{d,sd}$ where A is an additive relationship matrix among animals in the pedigree file and $V_{d,sd}$ was a 3×3 matrix of additive variances and covariances between sow genetic effects for trait 1 (WSI) and boar and sow genetic effects for trait 2 (litter traits; NBA, LBW, NPW and LWW). Where, sow genetic effects for trait 1 was equal to additive direct sow genetic effects. For trait 2, boar genetic effects was equal to a half of additive direct boar genetic effects and sow genetic effects were composed of a half of additive direct sow genetic effects and additive maternal genetic effects. The $V_{d,sd}$ matrix for traits 1 and 2 was as follows:

$$V_{d,sd} = \begin{bmatrix} \text{var}(\text{sow}_1) & \text{cov}(\text{sow}_1,\text{boar}_2) & \text{cov}(\text{sow}_1,\text{sow}_2) \\ \text{cov}(\text{boar}_2,\text{sow}_1) & \text{var}(\text{boar}_2) & \text{cov}(\text{boar}_2,\text{sow}_2) \\ \text{cov}(\text{sow}_2,\text{sow}_1) & \text{cov}(\text{sow}_2,\text{boar}_2) & \text{var}(\text{sow}_2) \end{bmatrix} \quad (5)$$

where the elements of $V_{d,sd}$ matrix in term of additive direct (AD; σ^2_{AD}) and additive maternal (AM; σ^2_{AM}) genetic effects were:

$$\text{var}(\text{sow}_1) = \sigma^2_{AD_1}$$

$$\text{var}(\text{boar}_2) = \frac{1}{4}\sigma^2_{AD_2}$$

$$\text{var}(\text{sow}_2) = \frac{1}{4}\sigma^2_{AD_2} + \sigma_{AD_2,AM_2} + \sigma^2_{AM_2}$$

$$\text{cov}(\text{sow}_1,\text{boar}_2) = \frac{1}{2}\sigma_{AD_1,AD_2}$$

$$\text{cov}(\text{sow}_1,\text{sow}_2) = \frac{1}{2}\sigma_{AD_1,AD_2}+\sigma_{AD_1,AM_2}$$

$$\text{cov}(\text{boar}_2,\text{sow}_2) = \frac{1}{4}\sigma^2_{AD_2}+\frac{1}{2}\sigma_{AD_2,AM_2}$$

$$\text{cov}(\text{boar}_2,\text{sow}_1) = \frac{1}{2}\sigma_{AD_2,AD_1}$$

$$\text{cov}(\text{sow}_2,\text{sow}_1) = \frac{1}{2}\sigma_{AD_2,AD_1}+\frac{1}{2}\sigma_{AM_2,AD_1}$$

$$\text{cov}(\text{sow}_2,\text{boar}_2) = \frac{1}{4}\sigma^2_{AD_2}+\frac{1}{2}\sigma_{AM_2,AD_2}$$

The variance of the random genetic effects for the pair-wise analyses involving litter traits (NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW and NPW-LWW) were equal to $A \otimes V_{sd,sd}$, where A is an additive relationship matrix among animals in the pedigree file (boars and sows) and $V_{sd,sd}$ was a 4×4 matrix of variances and covariances among boar and sow genetic effects for traits 1 and 2. Where, boar genetic effects were equal to a half of additive direct boar genetic effects and sow genetic effects were composed of a half of additive direct sow genetic effects and additive maternal genetic effects. The $V_{sd,sd}$ matrix for litter traits was as follows:

$$V_{sd,sd} = \begin{bmatrix} \text{var}(\text{boar}_1) & \text{cov}(\text{boar}_1,\text{boar}_2) & \text{cov}(\text{boar}_1,\text{sow}_1) & \text{cov}(\text{boar}_1,\text{sow}_2) \\ \text{cov}(\text{boar}_2,\text{boar}_1) & \text{var}(\text{boar}_2) & \text{cov}(\text{boar}_2,\text{sow}_1) & \text{cov}(\text{boar}_2,\text{sow}_2) \\ \text{cov}(\text{sow}_1,\text{boar}_1) & \text{cov}(\text{sow}_1,\text{boar}_2) & \text{var}(\text{sow}_1) & \text{cov}(\text{sow}_1,\text{sow}_2) \\ \text{cov}(\text{sow}_2,\text{boar}_1) & \text{cov}(\text{sow}_2,\text{boar}_2) & \text{cov}(\text{sow}_2,\text{sow}_1) & \text{var}(\text{sow}_2) \end{bmatrix} \quad (6)$$

where the elements of $V_{sd,sd}$ matrix in term of AD (σ^2_{AD}) and AM (σ^2_{AM}) genetic effects were:

$$\text{var}(\text{boar}_1) = \frac{1}{4}\sigma^2_{AD_1}$$

$$\text{var}(\text{boar}_2) = \frac{1}{4}\sigma^2_{AD_2}$$

$$\text{var}(\text{sow}_1) = \frac{1}{4}\sigma^2_{AD_1}+\sigma_{AD_1,AM_1}+\sigma^2_{AM_1}$$

$$\text{var}(\text{sow}_2) = \frac{1}{4}\sigma^2_{AD_2}+\sigma_{AD_2,AM_2}+\sigma^2_{AM_2}$$

$$\text{cov}(\text{boar}_1,\text{boar}_2) = \frac{1}{4}\sigma_{AD_1,AD_2}$$

$$\text{cov}(\text{boar}_1,\text{sow}_1) = \frac{1}{4}\sigma^2_{AD_1} + \frac{1}{2}\sigma_{AD_1,AM_1}$$

$$\text{cov}(\text{boar}_1,\text{sow}_2) = \frac{1}{4}\sigma_{AD_1,AD_2} + \frac{1}{2}\sigma_{AD_1,AM_2}$$

$$\text{cov}(\text{boar}_2,\text{sow}_1) = \frac{1}{4}\sigma_{AD_2,AD_1} + \frac{1}{2}\sigma_{AD_2,AM_1}$$

$$\text{cov}(\text{boar}_2,\text{sow}_2) = \frac{1}{4}\sigma^2_{AD_2} + \frac{1}{2}\sigma_{AD_2,AM_2}$$

$$\text{cov}(\text{sow}_1,\text{sow}_2) = \frac{1}{4}\sigma_{AD_1,AD_2} + \frac{1}{2}\sigma_{AM_1,AD_2} + \frac{1}{2}\sigma_{AD_1,AM_2} + \sigma_{AM_1,AM_2}$$

$$\text{cov}(\text{boar}_2,\text{boar}_1) = \frac{1}{4}\sigma_{AD_2,AD_1}$$

$$\text{cov}(\text{sow}_1,\text{boar}_1) = \frac{1}{4}\sigma^2_{AD_1} + \frac{1}{2}\sigma_{AM_1,AD_1}$$

$$\text{cov}(\text{sow}_1,\text{boar}_2) = \frac{1}{4}\sigma_{AD_1,AD_2} + \frac{1}{2}\sigma_{AM_1,AD_2}$$

$$\text{cov}(\text{sow}_2,\text{boar}_1) = \frac{1}{4}\sigma_{AD_2,AD_1} + \frac{1}{2}\sigma_{AM_2,AD_1}$$

$$\text{cov}(\text{sow}_2,\text{boar}_2) = \frac{1}{4}\sigma^2_{AD_2} + \frac{1}{2}\sigma_{AM_2,AD_2}$$

$$\text{cov}(\text{sow}_2,\text{sow}_1) = \frac{1}{4}\sigma_{AD_2,AD_1} + \frac{1}{2}\sigma_{AD_2,AM_1} + \frac{1}{2}\sigma_{AM_2,AD_1} + \sigma_{AM_2,AM_1}$$

Unfortunately, the dataset did not permit the computation of covariances between boar and sow genetic effects (pair-wise analyses failed to converge with ASREML). Thus, all covariances between boar and sow genetic effects were assumed to be zero. This assumption rendered $V_{sd,sd}$ block diagonal with two 2×2 blocks. The first block contained variances and covariances of a half of additive direct boar genetic effects between traits 1 and 2. The second block contained the variances and covariances of a half of additive direct sow genetic effects and additive maternal genetic effects between traits 1 and 2. Consequently, the $V_{sd,sd}$ matrix with these assumptions was as bellows:

$$V_{sd,sd} = \begin{bmatrix} \text{var}(\text{boar}_1) & \text{cov}(\text{boar}_1,\text{boar}_2) & 0 & 0 \\ \text{cov}(\text{boar}_2,\text{boar}_1) & \text{var}(\text{boar}_2) & 0 & 0 \\ 0 & 0 & \text{var}(\text{sow}_1) & \text{cov}(\text{sow}_1,\text{sow}_2) \\ 0 & 0 & \text{cov}(\text{sow}_2,\text{sow}_1) & \text{var}(\text{sow}_2) \end{bmatrix} \quad (7)$$

The permanent environmental matrix of variances and covariances for all pair-wise analyses was equal to $I \otimes V_{pe}$, where I is an identity matrix, and V_{pe} is a matrix of

variances and covariance between permanent environmental effects of the sow for traits 1 and 2. Notice that permanent environmental effects of the sow are from direct genetic effects for WSI and from maternal genetic effects for litter traits. Thus, V_{pe} matrices for all traits were as bellows:

$$V_p = \begin{bmatrix} \sigma^2_{pe_1} & \sigma_{pe_1,pe_2} \\ \sigma_{pe_2,pe_1} & \sigma^2_{pe_2} \end{bmatrix} \quad (8)$$

The residual variance matrix for all pair-wise analyses was equal to $I \otimes V_e$, where I is an identity matrix, and V_e is a matrix of variances and covariance between residual effects for traits 1 and 2. Thus,

$$V_e = \begin{bmatrix} \sigma^2_{e_1} & \sigma_{e_1,e_2} \\ \sigma_{e_2,e_1} & \sigma^2_{e_2} \end{bmatrix} \quad (9)$$

3. Estimation of genetic parameters

Computations of genetic parameters (i.e., heritabilities, repeatabilies and correlations), and their standard errors (SE) were carried out using the ASREML program (Gilmour *et al*., 2006).

3.1 Heritabilities

Estimates of heritabilities for direct genetic effects (h^2_{AD}) for WSI, NBA, LBW, NPW and LWW were computed as the ratio of their respective additive direct genetic (σ^2_{AD}) to phenotypic variances (σ^2_{Ph}) for each trait.

Estimates of additive direct genetic variances (σ^2_{AD}) for WSI were the sow variance, while phenotypic variances for WSI were computed as the sum of sow genetic (sow variance), sow direct permanent environment (σ^2_{pe}) and residual variances (σ^2_e). Thus, additive direct heritability for WSI was shown as follows:

$$h^2_{AD} = \frac{var(sow)}{var(sow) + \sigma^2_{pe} + \sigma^2_e} \quad (10)$$

For litter traits, the estimates of additive direct genetic variances (σ^2_{AD}) were equal to four times the boar variance, while phenotypic variances were estimated as the sum of boar genetic, sow genetic, sow maternal permanent environment (σ^2_{pe}), and residual variances (σ^2_e). Thus, additive direct heritabilities for litter traits were shown as bellows:

$$h^2_{AD} = \frac{4var(boar)}{var(boar) + var(sow) + \sigma^2_{pe} + \sigma^2_e} \quad (11)$$

Estimates of heritabilities for maternal genetic effects (h^2_{AM}) for NBA, LBW, NPW and LWW were computed as the ratio of their respective additive maternal genetic variances (σ^2_{AM}) to phenotypic variances which were equal to the sum of boar genetic, sow genetic, sow maternal permanent environment (σ^2_{pe}) and residual variances (σ^2_e). Estimates of maternal genetic variances were equal to the sow variance minus the boar variance for each litter trait. The heritabilities for maternal genetic effects were expressed as the equation bellows:

$$h^2_{AM} = \frac{var(sow) - var(boar)}{var(boar) + var(sow) + \sigma^2_{pe} + \sigma^2_e} \quad (12)$$

3.2 Repeatabilities

Estimates of repeatabilities (t) were equal to the ratio of the sum of additive direct genetic plus permanent environment variances over phenotypic variances corresponding to WSI and litter traits. Where, estimates of repeatabilities for WSI and litter traits were shown in the equations 13 and 14 respectively,

$$t_{WSI} = \frac{var(sow) + \sigma^2_{pe}}{var(sow) + \sigma^2_{Pe} + \sigma^2_e} \quad (13)$$

$$t_{\text{litter traits}} = \frac{4\text{var(boar)} + \sigma^2_{pe}}{\text{var(boar)} + \text{var(sow)} + \sigma^2_{pe} + \sigma^2_{e}} \quad (14)$$

3.3 Genetic and phenotypic correlations

Estimates of additive direct genetic correlations (r_{AD}) were equal to the ratio of additive direct genetic covariances between two traits over the square root of the product of the additive direct genetic variances of these traits.

Additive direct genetic correlations between WSI and litter traits were estimated as the ratio of two times covariance between sow (for WSI) and boar (for litter trait i) over the square root of sow variance for WSI multiplied by four times of boar variance for litter trait i, where litter trait i were NBA, LBW, NPW and LWW. Thus, additive direct genetic correlations between WSI and litter traits were bellows:

$$r_{AD} = \frac{2\text{cov}(\text{sow}_{WSI}, \text{boar}_i)}{\sqrt{\text{var}(\text{sow}_{WSI}) \times 4\text{var}(\text{boar}_i)}} \quad (15)$$

Estimates of additive direct genetic correlations for litter traits were equal to the ratio of the boar covariance between traits 1 and 2 divided by the square root of the product of the boar variances for traits 1 and 2. The additive direct genetic correlations between litter traits were shown as bellows:

$$r_{AD} = \frac{\text{cov}(\text{boar}_1, \text{boar}_2)}{\sqrt{\text{var}(\text{boar}_1) \times \text{var}(\text{boar}_2)}} \quad (16)$$

Estimates of maternal correlations (r_{AM}) for litter traits were equal to the ratio of maternal covariances between trait 1 and 2 divided by the square root of the product of the maternal variances for these traits. These estimations were shown as follows:

$$r_{AM} = \frac{\sigma_{AM_1, AM_2}}{\sqrt{\sigma^2_{AM_1} \times \sigma^2_{AM_2}}} \quad (17)$$

As with maternal variances, maternal covariances were estimated as the difference between sow covariances and boar covariances that were shown as bellows:

$$\sigma^2_{AM_1} = var(sow_1) - \frac{1}{4}\sigma^2_{AD_1} - \sigma_{AD_1,AM_1}$$

$$= var(sow_1) + var(boar_1) - 2cov(boar_1,sow_1)$$

$$\sigma^2_{AM_2} = var(sow_2) - \frac{1}{4}\sigma^2_{AD_2} - \sigma_{AD_2,AM_2}$$

$$= var(sow_2) + var(boar_2) - 2cov(boar_2,sow_2)$$

$$\sigma_{AM_1,AM_2} = cov(sow_1,sow_2) - \frac{1}{4}\sigma_{AD_1,AD_2} - \frac{1}{2}\sigma_{AM_1,AD_2} - \frac{1}{2}\sigma_{AD_1,AM_2}$$

$$= cov(sow_1,sow_2) + cov(boar_1,boar_2) - cov(sow_1,boar_2) - cov(boar_1,sow_2)$$

Permanent environmental correlations and phenotypic correlations for all traits were estimated as the ratio of their respective covariances divided by the square root of their variances.

4. Genetic and phenotypic trends

Weighted means of expected progeny differences (EPD) by farrowing years were computed for boar and sow EPD for WSI, boar EPD for litter traits, and sow EPD for litter traits. Boar and sow EPD were computed as the sum of a breed group effect plus a random genetic deviation. Boar breed groups (L and W) and sow breed groups (L, W, LW and WL) were deviated from L. Random genetic deviations were the random boar and sow genetic effects. In addition, weighted means of sow permanent environmental deviations (PED) by farrowing years were also computed for WSI and litter traits. Weighted means of EPD and PED were plotted against farrowing year numbers. A linear regression was fitted to the set of means of boar EPD, sow EPD and sow PED for each trait and regression coefficients computed to assess trends over time using the regression procedure of SAS (SAS, 2008).

Environmental changes over time were visualized by plotting farrowing years least squares solutions for each trait against farrowing years. Regression coefficients of farrowing years solutions on farrowing years were used to evaluate environmental trends. Computations were carried out with the regression procedure of SAS (SAS, 2008).

Trial 3: Estimation of allele frequencies for ADIPOQ and FSHR genes and evaluation of association between specific genotypes and reproductive traits

1. Dataset description and editing data

This dataset was consisted of 363 current sows with corresponding 619 litter records from 2006 to 2009. All records contained information for WSI, NBA, LBW, NPW and LWW. Sows in this study were placed into an open-house system that belonging to 4 breed groups, L (120 sows), W (120 sows), LW (26 sows) and WL (97 sows). This dataset was edited for erroneous and incomplete information for all traits. In addition, LWW and NPW for sows with larger litter sizes at weaning than at birth were discarded because they were assumed to contain cross-fostered piglets. Thus, the final dataset had 470 records for WSI and litter traits at birth (NBA and LBW) and 330 records for litter traits at weaning (NPW and LWW). Table 4 contains means, SD, minima and maxima for WSI, NBA, LBW, NPW and LWW.

Table 4 Descriptive statistics for weaning to first service interval and litter traits

Trait[1]	Number of observations	Mean	SD	Minima	Maxima
WSI (days)	470	7.23	4.54	1.0	30.0
NBA (piglets)	470	10.18	2.89	1.0	18.0
LBW (kg)	470	16.94	4.89	1.5	29.6
NPW (piglets)	330	9.24	2.01	4.0	13.0
LWW (kg)	330	68.96	18.52	22.5	117.0

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

Parities of sows were classified in 4 parity groups, group 1 for primiparous sows and group 4 for multiparous sows in the fourth parities and more. Collecting data from

2006 in winter to 2009 in summer produced 11 categories for FYS. Age at farrowing of sow ranged from 10 to 37 months (mean = 16.59 months, SD = 5.19 months). Lactation length ranged from 20 to 31 days (mean = 24.83 days, SD = 2.16 days).

2. Blood Sampling and DNA Extraction

Whole blood specimens were collected from 363 sows. Blood specimens (5 ml) were collected from the jugular vein and transferred to 6 ml tubes containing EDTA as anticoagulant. Blood samples were placed on ice after collection. The chilled blood samples were taken to the laboratory for extraction of the genomic DNA using a DNA purification kit protocol (MasterPure™ DNA Purification Kit for Blood; EPICENTRE® Biotechnologies, Madison, Wisconsin, USA). The extracted DNA was kept at -20°C.

3. DNA Amplification and Fragmentation

The porcine adiponectin gene (ADIPOQ; GenBank accession No. AJ849536) was amplified by using the following forward: 5′-TCAGGATGCTGTTG TTGGGA-3′ and reverse: 5′-CCCTGTGAATAGGCCTTTGG-3′ primers (Table 5; Houde *et al*., 2008). The total volume of the PCR mixture was 12.6 μl, including 1x PCR buffer, 1.6 mM $MgCl_2$, 0.2 mM dNTP, 1.0 μM of each primer and 0.04 U *Taq* polymerase (Fermentas, USA). Subsequently, 1.0 μl of genomic DNA was added to the PCR mixture. The PCR cycle protocol used the following program, a pre-denature at 94°C for 5 min, 35 cycles of 3 steps (denaturing at 94°C for 45 sec, annealing at 55°C for 1 min and elongation at 72°C for 45 sec) and an extending elongation at 72°C for 5 min. The PCR reaction amplified DNA fragments of 326 bp long. Restricted fragment length polymorphism (RFLP) was applied to recognize and digest the amplified PCR products of ADIPOQ at position 178 neucleotide by using the *Bsa*HI restriction enzyme (Houde *et al*., 2008).

Table 5 Primer sequences used to amplify PCR product for swine adiponectin (ADIPOQ) and follicle stimulating hormone receptor (FSHR) genes

Gene[1]	Primer Sequences (5′to 3′)	Position (nt)	GenBank Acc No.
ADIPOQ	F: TCAGGATGCTGTTGTTGGGA	1537 - 1557	AJ849536
	R: CCCTGTGAATAGGCCTTTGG	1842 - 1862	
FSHR	F: GCAACAAATCTATTTTAAGGCAAGA	911 - 935	AF025377
(outer)	R: GATGCTCACCTTCATGTAGCTG	1562 - 1584	
FSHR	F: ATGGTTTATTAGTATCCTTGCCAC[2]	1143 - 1166	AF025377
(inner)	R: AGCACTATGATGTTCCCAGTGA	1166 - 1187	

[1] ADIPOQ, adiponectin gene; FSHR, follicle stimulating hormone receptor gene

[2] Underlined letter were C/T nucleotide substitution at position 1166

The porcine follicle stimulating hormone receptor gene (FSHR; GenBank accession No. AF025377) was amplified by the method of Jiang *et al*. (2002). Briefly, the forward primer for FSHR (outer primer) was 5′-GCAACAAATCTATTTTAA GGCAAGA-3′ and the reverse primer (outer primer) was 5′-GATGCTCACCTTCA TGTAGCTG-3′ (Table 5). These outer primers amplified a DNA fragment of 674 bp long. A bidirectional PCR amplification of specific alleles (Bi-PASA; Liu *et al*., 1997) was applied to identify single nucleotide polymorphisms (SNP) in the FSHR gene. The inner primers were designed based on a SNP located at position 1166 (C/T) of the porcine FSHR gene. These inner primers were: forward primer 5′-ATGGTTTA TTAGTATCCTTGCCAC-3′ (positions 1143 nt to 1166 nt) and reverse primer 5′-AG CACTATGATGTTCCCAGTGA-3′ (positions 1166 nt to 1187 nt). The inner forward primer and the outer primers were used to detect a C nucleotide at position 1166 of the FSHR gene (allele C), and it produced DNA fragments of 674 bp and 442 bp long. On the other hand, the inner reverse primer and the outer primers were used to detect a T nucleotide at position 1166 of the FSHR gene (allele T) and produced DNA fragments that were 674 bp and 277 bp long. The PCR mixture was composed of 1x PCR buffer, 0.1 mM dNTPs, 1.2 mM $MgCl_2$, 0.04U *Taq* polymerase and 0.25 μM for

4 primers (outer and inner FSHR primers; Table 5) and it had a total volume of 10.07 µl. After that, 1.0 µl of genomic DNA was added to the PCR mixture. The PCR amplification protocol was consisted of the following steps, an initial denaturing period at 94°C for 5 min, 30 amplifying cycles of 3 steps (denaturing at 94°C for 1 min, annealing at 60°C for 1 min and elongation at 72°C for 1 min) and an additional elongation period of 5 min at 72°C.

4. Genotyping

Separation of the products of digestion process for the SNP of the ADIPOQ (Houde *et al*., 2008) was carried out using 2% agarose gel (1x TBE buffer) electrophoresis (100 volt) for 35 min. DNA fragments were compared against a low range DNA ladder under ultraviolet (UV) light after being stained with ethidium bromide (Fermentas, USA). The ADIPOQ polymorphism was identified at SNP AJ849536: g.1716G>A, which corresponds to SNP c.178G>A in Houde *et al*. (2008), using the RFLP technique with the *Bsa*HI restriction enzyme. Animals having the GG genotype present 2 bands of 145 bp and 181 bp, whereas those having the GA genotype show 3 bands of 326 bp (for the uncut portion), 145 bp and 181 bp (Figure 2; Houde *et al*., 2008).

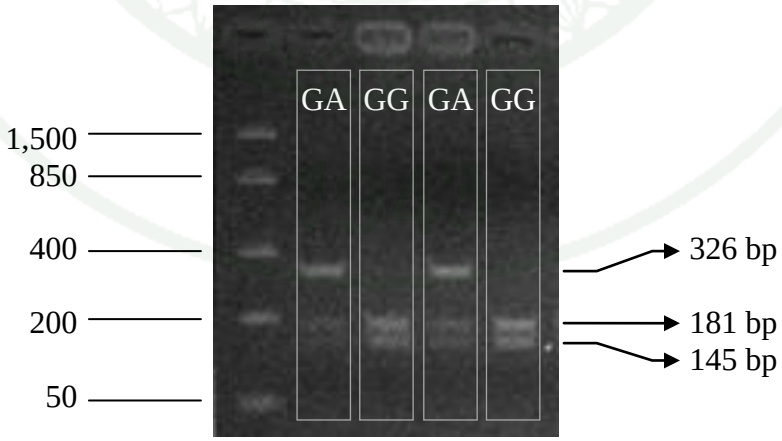

Figure 2 Genotyping for ADIPOQ polymorphisms (GG genotype presents 2 bands of 145 bp and 181 bp, GA genotype show 3 bands of 326 bp, 145 bp and 181 bp)

Substitution of nucleotide T for C at position 1166 nt of the FSHR gene (AF025377: g.1166C>T; Jiang *et al*., 2002) was elucidated by Bi-PASA genotyping technique (Liu *et al*., 1997). Outer and inner PCR products for FSHR generated three genotypes (CC, CT and TT; Jiang *et al*., 2002). Bands of outer and inner PCR products were detected by using 1.2% agarose gel (1x TBE buffer) electrophoresis (100 volt) for 35 min, stained with ethidium bromide and compared against a 100 bp DNA ladder under UV light (Fermentas, USA). The presence of 2 DNA fragments of 442 bp and 674 bp was associated with the CC genotype, whereas 3 fragments of 277 bp, 442 bp and 674 bp were observed in CT animals. Finally, the TT genotype was identified with the presence of 2 fragments of 277 bp and 674 bp (Figure 3).

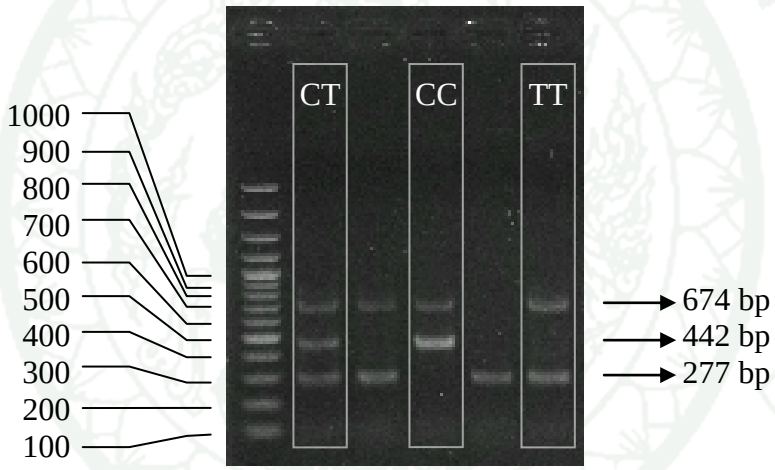

Figure 3 Genotyping for FSHR polymorphisms (CC genotype show 2 bands of 442 bp and 674 bp, CT genotype show 3 bands of 277 bp, 442 bp and 674 bp and TT genotype present 2 bands of 277 bp and 674 bp)

5. Statistical analysis

A Chi-square test was used to test Hardy-Weinberg equilibrium for ADIPOQ and FSHR genes and genotypes using the FREQ procedure of SAS (SAS, 2008). In addition, allele and genotype frequencies for ADIPOQ and FSHR among breed groups were compared using Chi-square tests. The four comparisons of interest were:

L vs. W, LW vs. WL, L vs. crossbred groups (LW and WL), and W vs. crossbred groups (LW and WL).

The SNP effects for WSI and litter traits were estimated as regressions of traits on number of G alleles for the ADIPOQ and number of T alleles for the FSHR in a linear model that accounted for fixed genetic and environmental effects. The linear model included FYS (11 categories of farrowing year-season combinations), PR (group 1 to group 4) and BGD (L, W, LW and WL) as fixed subclass effects; AF, LL (excepted for NBA and LBW), NPW (for WSI), number of G alleles in the ADIPOQ locus or number of T alleles in the FSHR locus as fixed covariates; and residual as a random effect. Residuals were assumed to have a mean equal to zero, a common variance and to be uncorrelated. Computations were carried out using the MIXED procedure of SAS (SAS, 2008).

Differences between genotypic effects for the ADIPOQ and FSHR genes were estimated using a linear model similar to the one above, except that ADIPOQ genotypes (AG and GG) and FSHR genotypes (CC, CT and TT) were substituted for the number of G and number of T alleles at the ADIPOQ and FSHR loci, respectively. Thus, the linear model contained the subclass fixed effects (i.e., FYS, PR, BGD, genotype of the sow at the ADIPOQ locus or genotype of the sow at the FSHR locus), the covariate effects, AF, LL (for WSI, NPW and LWW) and NPW (for WSI), and random residual effects.

RESULTS AND DISCUSSION

Trial 1: Characterization of factors affecting and determination of heterosis effects for weaning to first service interval

Means, SD, minimum and maximum values for WSI by BGD sow are shown in Table 1. The dataset had a larger proportion of purebred sows (54.34 % L and 32.21 % W) than crossbred sows (6.60 % LW and 6.89 % WL). The overall mean for WSI in this Landrace-Large White swine population was 6.47 days, the SD was 5.88 days, the minimum value was 0 day and the maximum value was 89 days. The mean WSI by breed group ranged from 6.18 days for W to 6.97 days for WL, whereas the SD ranged from 5.49 days for W to 7.07 days for WL. Large White had the shortest range (0 to 53 days), WL the longest range (0 to 89 days) and L and LW had range similar to WL. Means for L and W breeds in this Northern Thai herd were smaller (6.61 days for L and 6.18 days for W) than those reported in Central Thailand (7.90 days for Landrace and 8.20 days for Yorkshire) by Tantasuparuk *et al.* (2001a). On the other hand, the mean and SD for the combined LW and WL crossbred groups (mean = 6.66 days; SD = 6.36 days) was higher than that obtained for Landrace × Yorkshire crossbred sows in Central Thailand (mean = 5.90 days; SD = 4.60 days; Suriyasomboon *et al.*, 2006).

The largest fraction of information in this dataset was observed from primiparous sows (2,417 records; 20.59 %), followed by decreasing percentages for second and later parities. Means and SD for WSI by PR were larger for the first parity (mean = 8.49 days, SD = 8.59) than for subsequent parities (mean ranged from 5.70 to 6.13 days and SD ranged from 4.34 to 4.87 days). The WSI range was longer in first parity (0 to 87 days) than in later parity sows and it tended to decrease over time, except those seventh parity or older. Similarly, first parity sows in a larger Landrace population had larger mean (8.03 days) and SD (7.98 days) than second (mean = 5.72 days; SD = 4.25 days) and third (mean = 5.47 days; SD = 4.12 days) parities under Thai tropical conditions (Imboonta *et al.*, 2007).

1. Farrowing year-season

Least squares means for WSI fluctuated substantially across FYS (Figure 4). The shortest WSI occurred in winter of 1991 (4.38 ± 0.67 days; P < 0.0001) and the longest WSI was in the winter season of 1990 (10.08 ± 1.01 days; P < 0.0001). Least squares means for WSI within seasons across years ranged from 4.38 ± 0.67 days (P < 0.0001) in 1991 to 10.08 ± 1.01 days (P < 0.0001) in 1990 for winter, from 4.50 ± 0.67 days (P < 0.0001) in 1991 to 8.16 ± 0.46 days (P < 0.0001) in 1996 for summer and from 4.62 ± 0.62 days (P < 0.0001) in 1991 to 9.68 ± 1.14 days (P < 0.0001) for the rainy season.

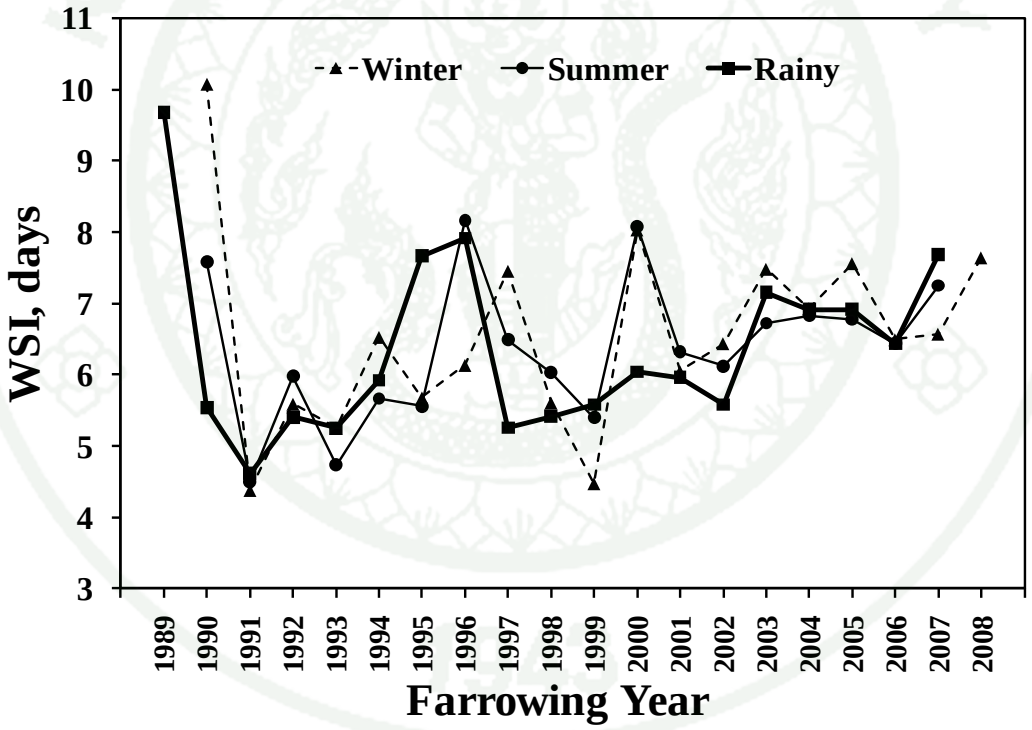

Figure 4 Least squares means for weaning to first service interval (WSI) by season across years from 1989 to 2008

Although LSMs for WSI within seasons tended to increase from 1989 to 2008, none of the coefficients of regression of WSI on years within seasons was significant (winter: 0.04 ± 0.06 days, P = 0.4408; summer: 0.07 ± 0.04 days, P = 0.1502; rainy:

0.02 ± 0.05 days, P = 0.6497). Differences between coefficients of regression of WSI on years within seasons were also non-significant. Thus, season was not a major source of variation for WSI in this swine population. This means that sows farrowed piglets in winter, summer and rainy seasons had similar WSI values. Thus, it appears that differences in temperature and humidity in the Chiang Mai area during the years of the study were not severe enough to have a significant effect on WSI. This appears not to have been the case in a Landrace and Yorkshire swine population in Central Thailand (Tantasuparuk *et al.*, 2000a), where WSI was reported to have been longer from April to August (part of summer and rainy seasons) than during the rest of the year. Similarly, Suriyasomboon *et al.* (2006) found that crossbred sows (Landrace × Yorkshire) that weaned piglets in May to August (late summer and early rainy seasons) tended to have longer WSI than sows that weaned piglets between September and April.

2. Parity

Least square means of WSI by PR are shown in Figure 5. Sow at first parity had longer WSI (8.54 ± 0.14 days) than second and later parity (range from 5.80 ± 0.19 to 6.33 ± 0.14 days; P < 0.0001). Non-significant LSMs for WSI found in multiparous sows. Accordingly, sows in this herd were separated into two distinct groups, primiparous sows with longer WSI and multiparous sows with shorter WSI. This was reported by Koketsu and Dial (1997), Tantasuparuk *et al*. (2000a), Imboonta *et al.* (2007). Longer WSI in primiparous sows may have been related to difficulties in balancing their higher energy and protein requirements for growth and production of milk for nursling their piglets than those of multiparous sows (Reese *et al*., 1982; Einarsson *et al*., 1998). These higher nutritional demands for growth and milk production for their first litter may have strained their ability to return estrus as quickly as multiparous sows after weaning. Follicles in lactating primiparous sows may have taken longer to mature because of their metabolic requirements took longer to be met than older sows (Quesnel *et al.*, 2007). Multiparous sows, being more mature than primiparous sows, may have had more energy reserves to generate mature follicles and return to estrus sooner than primiparous sows after weaning.

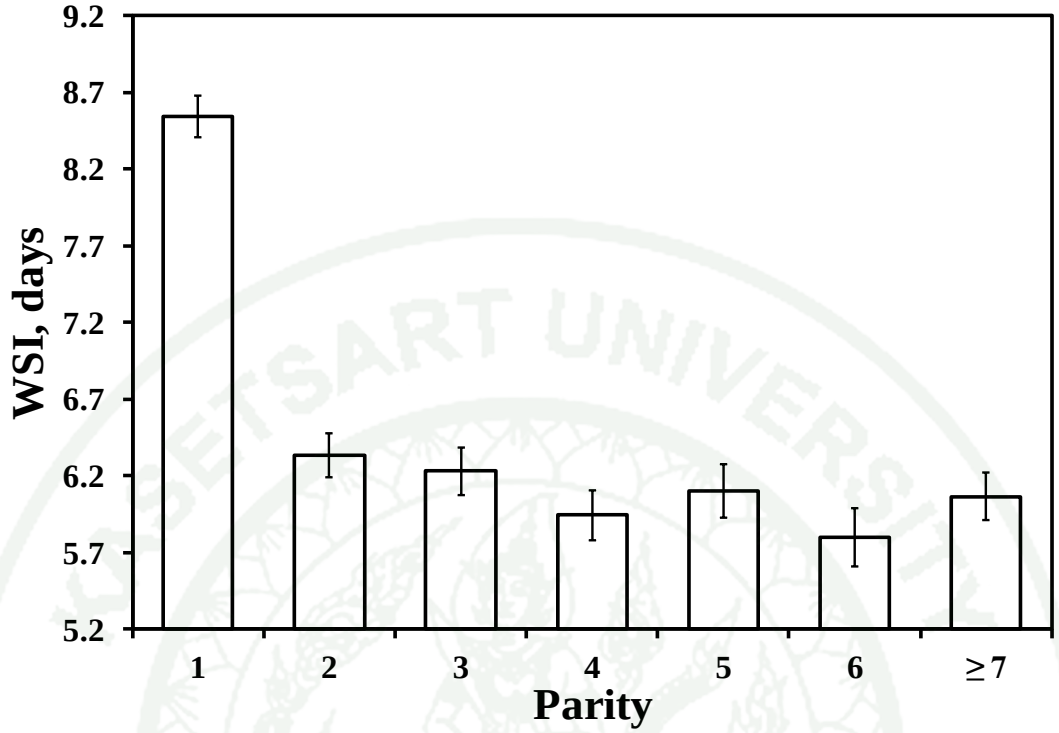

Figure 5 Least squares means for weaning to first service interval (WSI) by parity of sow

In addition, body weight losses during lactation may have also contributed to longer WSI for primiparous sows in this study. Thaker and Bilkei (2005) found that WSI increased ($P < 0.05$) when primiparous sows lost more than 5% of their body weight, whereas a 10% body weight loss was required for multiparous sows. Lastly, estrous detection may have played a role if primiparous sows showed less evident signs of estrous than multiparous sows. Missed estruses in primiparous sows may have affected service date, potentially making their WSI longer.

3. Breed groups and heterosis

Breed group of sows and heterosis LSMs for WSI are shown in Figure 6. Purebred L sows had similar WSI (6.10 ± 0.10 days) to W sows (6.14 ± 0.10 days) in the open-house system of this swine herd in Northern Thailand. Tantasuparuk *et al.* (2000a) also found WSI to be similar in purebred Landrace (8.20 days) and Yorkshire

(7.90 days) under an open-house system in Central Thailand. On the other hand, Suwanasopee (2006) found longer WEI ($P < 0.05$) in purebred Landrace (5.53 ± 0.07 days) than Large White (5.19 ± 0.07 days) under a closed-house system temperature and humidity control in Thailand.

Crossbred LW sows (6.43 ± 0.20 days) and WL sows (7.04 ± 0.20 days) had longer WSI than purebreds sows (1.22 ± 0.30 days; $P < 0.0001$), and LW crossbreds had shorter WSI than their reciprocal WL crossbreds ($P = 0.0235$). The only evidence for comparing NPD between crossbred sows and purebred sows in Thailand was reported by Suwanasopee (2006). Crossbred Landrace × Large White (5.69 ± 0.07 days) and Large White × Landrace (5.63 ± 0.07 days) had longer WEI than purebred sows ($P < 0.05$). However, contrary to results in this study, LSMs of WEI for the two reciprocal crossbred groups (Landrace × Large White and Large White × Landrace) were similar. Genetic characteristics of the purebred and crossbred animals in the two swine populations as well as differences environmental conditions (e.g., differences in temperature and humidity) may have contributed to LW and WL being different in the open-house system in Northern Thailand, but not in the closed-house system in Central Thailand.

Heterosis estimates for WSI were 0.31 ± 0.20 days ($P = 0.1228$) for LW sows, 0.91 ± 0.20 days ($P < 0.0001$) for WL sows and 0.61 ± 0.15 days ($P < 0.0001$) for the combined LW and WL crossbred groups. Heterosis estimates for WSI in Thailand were unavailable. However, Suwanasopee *et al.* (2007) reported WEI heterosis values for Landrace × Large White (0.36 ± 0.04 days), Large White × Landrace (0.26 ± 0.05 days) and the combined Landrace × Large White and Large White × Landrace crossbred group (0.32 ± 0.04 days) that were comparable to the LW heterosis estimate for WSI in this study.

Longer WSI in crossbred than in purebred sows (1.22 ± 0.30 days; $P < 0.0001$) may be an indication that crossbreds were less adapted than purebreds under Northern Thailand tropical conditions. However, crossbred sows had larger (0.34 ± 0.13 piglets; $P = 0.0092$) and heavier (2.8 ± 0.92 kg/litter; $P = 0.0025$) litters than purebred

sows. Crossbred sows may have dedicated a larger fraction of nutrients to produce the higher level of milk production required to feed larger litters of piglets than purebred sows. This reallocation of nutrients in crossbred sows may have lowered their energy reserves to such a degree that a longer period was required to produce mature follicles and return to estrous after weaning. Purebred and crossbred were under the same nutritional regime. Perhaps a higher level of nutrition for crossbred sows would have decreased WSI to lengths comparable to those of purebred sows.

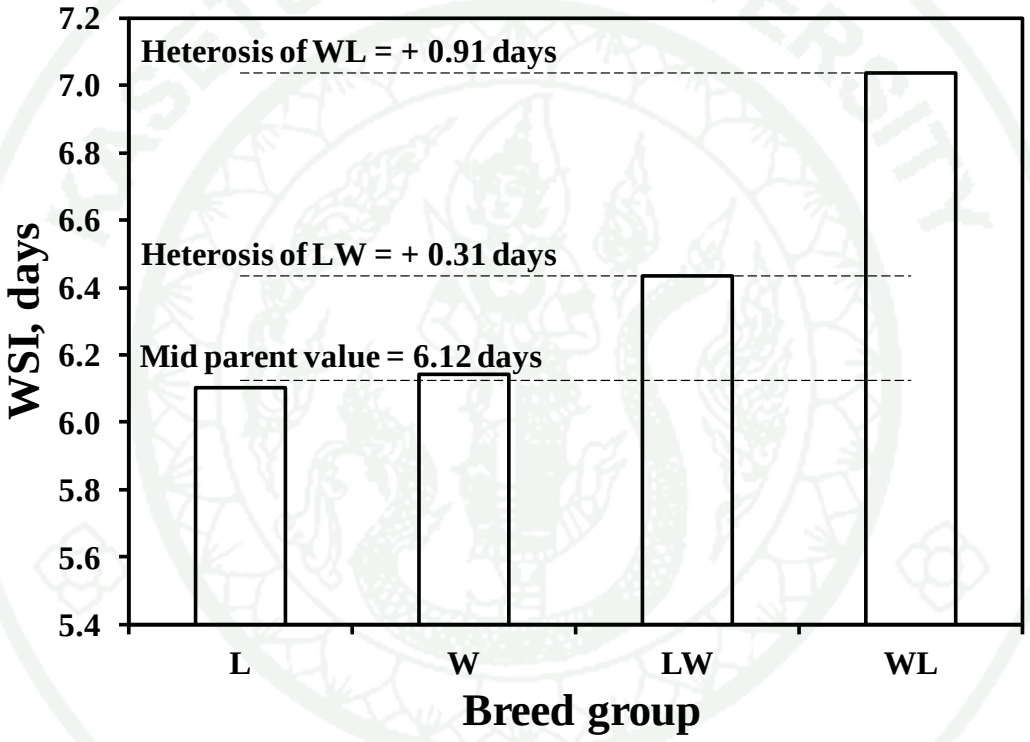

Figure 6 Breed group and heterosis least squares means for weaning to first service interval (WSI); L, purebred Landrace; W, purebred Large White; LW, Landrace × Large White; WL, Large White × Landrace

4. Lactation length

There was a quadratic association between WSI and LL. The estimate of the linear regression coefficient was negative (-0.80 ± 0.17 days WSI per days LL; $P < 0.0001$) and the estimate of the quadratic regression coefficient was positive (0.014 ± 0.003 days WSI per days^2 LL; $P < 0.0001$). Contrarily, LL had no significant effect

on WSI in a Landrace and Yorkshire swine population in Central Thailand (Tantasuparuk *et al.*, 2000b). Similarly, LL was not an important effect for WEI in a population of Landrace, Large White and reciprocal crossbred groups in central Thailand (Suwanasopee *et al.*, 2005a). However, swine studies in temperate countries have found LL significantly affected for WSI (Karvelienè *et al.*, 2008) and WEI (Koketsu and Dial, 1997; Belstra *et al.*, 2004).

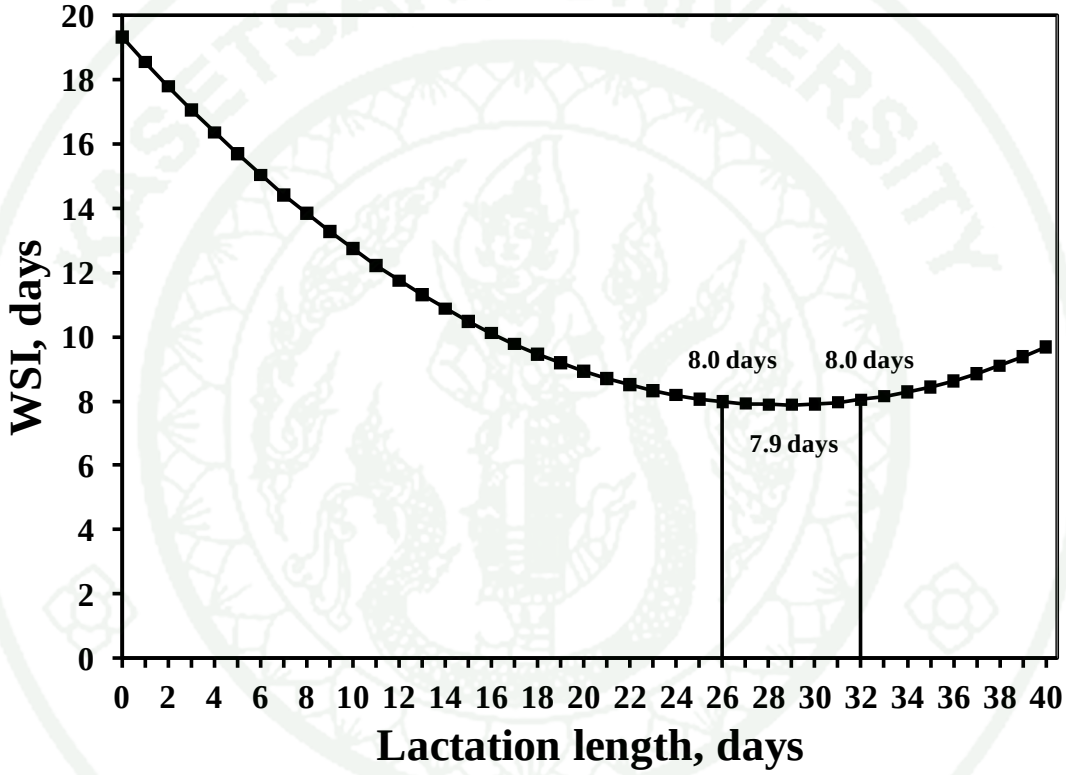

Figure 7 Relationship between predicted weaning to first service interval (WSI) and lactation length (LL) between 1 day and 40 days. Predicted WSI = Intercept + linear regression coefficient times LL + quadratic regression coefficient times LL squared. Vertical lines indicate the LL (26 to 32 days) corresponding to the lowest WSI values (7.9 to 8.0 days)

The estimated regression coefficients in this swine herd produced a concave line when predicted WSI were plotted against LL. Figure 7 shows the relationship between predicted WSI values computed using the intercept from the fixed effect model plus linear and quadratic regression coefficients for LL ranging from 1day to

40 days. The lowest values of WSI in occurred between 26 days and 32 days (vertical lines in Figure 7; predicted WSI values from 7.9 to 8.0 days). This concave relationship between WSI and LL was similar to one found in a large study in the United States (13 commercial herds, 178,519 litters from crossbred and purebred sows; Mabry *et al.*, 1996). However, in the United States study the smallest WSI values occurred somewhat earlier in the lactation (between 22 days and 27 days). The management system in this Thai herd required sows to have a maximum LL of 35 days. These results suggesting that maximum LL for 35 days could be decreased to 32 days were to help reducing WSI values and sow production costs.

Year-season of farrowing, PR, BGD and LL were all important factors affecting WSI in this population ($P < 0.0001$), except NPW was not significance effect for WSI ($P = 0.1207$). However, these factors have also affected on both litter traits at birth and weaning such as NBA, LBW, NPW and LWW. Therefore, the single trait analysis for genetic evaluation for WSI may influence on these litter traits variation. Thus, the studies of associations between these traits in terms of phenotypic and genetic need to be investigated. Unfortunately, the study for association between WSI and these litter traits in Thailand have not been reported. The only study of Imboonta *et al*. (2007) reported the genetic correlation between WSI and total number of piglet born (0.07 ± 0.27) in purebred Landrace population, and other study were involved on relations between WEI and NBA (-0.01), WEI and NPW (0.51 ± 0.47) and WEI and LWW (0.01 ± 0.24) in Large White and Landrace populations (Suwanasopee *et al*., 2005b; Suwanasopee, 2006). Consequently, estimates genetic parameters and correlations between WSI and these litter traits need to perform for improving the reproductive and these litter traits of sows in Thailand.

Trial 2: Estimation of variance components, genetic parameters and trends for weaning to first service interval and litter traits

1. Environmental fixed effects

Farrowing year-season was an important effect ($P < 0.0001$) for all traits. Estimates ranged from 2.7 ± 3.9 days ($P = 0.4800$) to 10.8 ± 1.7 days ($P < 0.0001$) for WSI, from 7.5 ± 1.6 piglets ($P < 0.0001$) to 12.9 ± 0.7 piglets ($P < 0.0001$) for NBA, from 10.4 ± 1.2 kg ($P < 0.0001$) to 19.5 ± 1.1 kg ($P < 0.0001$) for LBW, from 5.9 ± 1.6 piglets ($P < 0.0001$) to 11.3 ± 1.5 piglets ($P < 0.0001$) for NPW and from 23.9 ± 11.4 kg ($P < 0.0001$) to 59.1 ± 5.7 kg ($P < 0.0001$) for LWW. Estimates fluctuated more across FYS for WSI than for litter traits, and all of them tended to increase from 1989 to 2008.

Ranges of estimates for FYS found in this study were similar to those obtained in other Thai swine populations for WSI (Tantasuparuk *et al*., 2001b; Suriyasomboon *et al*., 2006; Imboonta *et al*., 2007), NBA (Suwanasopee *et al*., 2005b; Pholsing *et al*., 2009), LBW (Pholsing *et al*., 2009) and NPW and LWW (Suwanasopee, 2006). Variation among estimates of FYS for WSI and litter traits was the result of the combined effects of climate (seasonal fluctuations in temperature and humidity), nutrition (composition and nutritional content of diets) and management during the years of the study. Lack of adaptation of sows that were progeny of imported boars from temperate countries may have been a contributing factor for low FYS means.

Parity was also an important factor ($P < 0.0001$) for all traits. First parity sows had: a) longer WSI than parity groups 2 to 6 [from 2.2 ± 0.3 days (longer than parity 2 sows, $P < 0.0001$) to 2.8 ± 0.8 days (longer than parity 6 sows, $P < 0.0001$)]; b) smaller NBA than parities 2 to 6 [from -0.9 ± 0.1 piglets (less than parity 2 sows, $P < 0.0001$) to -1.7 ± 0.2 piglets (less than parity 3 sows, $P < 0.0001$)]; c) lighter LBW than parities 2 to 6 [from -2.2 ± 0.6 kg (lighter than parity 6 sows; $P = 0.0003$) to -3.4 ± 0.3 kg (lighter than parity 3 sows, $P < 0.0001$)]; d) smaller NPW than any other

parity group [from -1.3 ± 0.1 piglets (less than parity 2 sows, $P < 0.0001$) to -1.8 ± 0.3 piglets (less than parity 5 sows, $P < 0.0001$)]; and e) lighter LWW than all other parity groups [from -11.7 ± 1.0 kg (less than parity 2 sows, $P < 0.0001$) to -15.8 ± 1.3 kg (less than parity 3 sows, $P < 0.0001$)]. Second and later parity sows had similar WSI values. However, sows from parity 2 had smaller NBA than sows from parities 3 (-0.7 ± 0.1 piglets, $P < 0.0001$) and 4 (-0.7 ± 0.2 piglets, $P = 0.0004$), lighter LBW than parity 3 sows (-0.8 ± 0.2 kg, $P = 0.0001$), smaller NPW than parity 3 sows (-0.5 ± 0.1 piglets, $P = 0.0010$) and lighter LWW than parity 3 sows (-4.1 ± 1.0 kg, $P < 0.0001$).

Parity estimates for WSI and litter traits in this study had a similar pattern to those reported for other Thai swine populations (Suriyasomboon *et al*., 2006; Imboonta *et al*., 2007). Primiparous sows had larger parity values for WSI and smaller ones for litter traits than multiparous sows, likely because of their need to allocate a fraction of the energy and protein from ingested nutrients to body growth in addition to allocating nutrients for gestation, lactation and maintenance (Reese *et al*., 1982; Whittemore, 1996; Pluske *et al*., 1998).

Age of sow was unimportant for all traits. This means that the range of ages within parity had no major effect in this dataset. Lactation length was relevant for LWW (0.7 ± 0.1 kg/d, $P < 0.0001$) indicating that longer lactations resulted in heavier LWW, but not for either WSI or NPW. Conversely, Tantasuparuk *et al*. (2000b, 2001b) found lactation length to be non-significant for WSI, NPW and LWW in purebred and crossbred Landrace and Large White herds in Central Thailand. Lactation length effects on WSI were mixed in temperate regions. Longer lactation lengths increased WSI in a Landrace-Hampshire-Yorkshire population ($P < 0.05$; Ehlers *et al*., 2005), but decreased WSI in commercial United States swine populations ($P < 0.05$; Koketsu and Dial, 1997) and in Swedish Landrace and Yorkshire ($P < 0.0001$; Tummaruk *et al*., 2000). Extended lactations increased LWW in commercial swine farms in the United States ($P < 0.05$; Koketsu and Dial, 1997) and in Large White and Hybrid populations in Canada, but had no influence on NPW ($P < 0.0001$; Willis *et al*., 2003).

2. Genetic fixed effects

Breed group of boar was non-significant for all litter traits suggesting that L and W sires used in this population were similar genetic value for NBA, LBW, NPW and LWW. This suggests that boars in this population were chosen using similar criteria regardless of breed (L and W) throughout the length of the study. On the other hand, breed group of sow was significant for WSI ($P = 0.0028$), NBA ($P = 0.0007$), LBW ($P = 0.0002$), NPW ($P = 0.0304$) and LWW ($P = 0.0368$). Crossbred WL sows had longer WSI than purebred L (1.3 ± 0.4 days, $P = 0.0018$) and W (1.6 ± 0.4 days, $P = 0.0002$), larger NBA than L (0.8 ± 0.2 piglets, $P = 0.0002$) and W (0.9 ± 0.2 piglets, $P < 0.0001$), heavier LBW than L (1.1 ± 0.3 kg, $P = 0.0002$), W (1.4 ± 0.3 kg, $P < 0.0001$) and LW (1.1 ± 0.4 kg, $P = 0.0084$), larger NPW than L (0.6 ± 0.2 piglets, $P = 0.0034$) and W (0.5 ± 0.2 piglets, $P = 0.0057$) and heavier LWW than L (3.5 ± 1.4 kg, $P = 0.0125$) and W (3.9 ± 1.4 kg, $P = 0.0058$). Sows from breed groups L, W and LW had similar WSI, NBA, LBW, NPW and LWW. These results indicate that, as with boars, the same phenotypic culling and selection criteria were applied to all sows regardless of their breed composition. The outcome was a group of purebred L and W sows of similar mean additive genetic performance for WSI and litter traits and WL crossbred sows that were superior to both LW crossbred and purebred L and W sows.

Tantasuparuk *et al*. (2000a) found longer WSI ($P < 0.0001$) and larger ($P < 0.0001$) NBA in Landrace than Large White in Central Thailand. In addition, Suwanasopee (2006) found longer WEI in Landrace than Large White ($P < 0.05$), and in crossbred groups (Landrace × Large White and Large White × Landrace) than purebred (Landrace and Large White; $P < 0.05$). On the other hand, Suwanasopee (2006) also found no differences between Landrace and Large White for NPW and LWW. However, in crossbred groups had larger NPW and LWW than purebred Landrace and Large White. It should be mentioned that the model in Suwanasopee (2006) did not separate additive and non-additive effects for crossbred groups, thus comparisons of crossbred and purebred groups include both additive and non-additive effects, not only additive effects as in the models for litter traits used in this study.

Heterosis had positive effects on all traits, thus they were disadvantageous for WSI, but advantageous for litter traits. Heterosis effects tended to increase WSI (0.9 ± 0.3 days; P = 0.0070), NBA (0.2 ± 0.1 piglets, P = 0.0541), LBW (0.4 ± 0.2 kg, P = 0.0076), NPW (0.2 ± 0.1 piglets, P = 0.0607) and LWW (1.5 ± 0.7 kg, P = 0.0324) between 1989 and 2008. The estimate of heterosis for WSI was computed as the difference between the mean of the solutions for crossbred groups (WL and LW) minus the mean of the solutions for the parental breeds (W and L), whereas estimates of heterosis for litter traits were equal to the solutions for heterosis as functions of heterozygosities. Positive heterosis estimates were also found for WEI (0.4 ± 0.1 days for WL and 0.4 ± 0.1 days for LW), NPW (1.5 ± 0.2 piglets for WL and 1.6 ± 0.2 piglets for LW) and LWW (15.3 ± 1.2 kg for WL and 15.6 ± 1.0 for LW) in a Landrace-Large White Thai population (Suwanasopee, 2006). These values were estimated as differences between crossbred and purebred least squares means, thus they accounted for intra-locus and inter-loci interactions, whereas heterosis estimates in this study only include intra-locus interactions.

3. Genetic parameters for additive direct genetic effects

Variances and heritabilities for additive direct genetic effects for WSI and litter traits were all low (Table 6). Upper diagonal elements in Table 6 show estimates of heritabilities and lower diagonal elements are estimates of additive direct genetic variances. The direct heritability (0.04 ± 0.02) and genetic variance (0.90 ± 0.51 d^2) for WSI were estimated from the WSI-NBA analysis (this was the only 2-trait analysis involving WSI that converged without constraints in ASREML). Estimates of direct heritabilities for litter traits were equal for the three 2-trait analyses for NPW (0.06 ± 0.03), LWW (0.05 ± 0.02) and LBW (0.06 ± 0.02). The estimate of direct heritability for NBA ranged from 0.05 ± 0.02 to 0.06 ± 0.02.

Imboonta *et al*. (2007) estimated substantially higher values of heritability for WSI (0.16 ± 0.03 to 0.18 ± 0.04 for the first three parities) in a purebred Landrace population using logarithmically transformed WSI data (Ten Napel *et al*., 1995).

Estimates of similar magnitude were also obtained by Ehlers *et al*. (2005) in a Landrace-Hampshire-Yorkshire population in the United States (0.20) and by Hanenberg *et al*. (2001) for first parity sows in Dutch Landrace (0.14 ± 0.01) using similarly transformed WSI data. Contrarily, Suwanasopee *et al*. (2005b) estimated a heritability of 0.03 ± 0.01 for WEI in Landrace-Yorkshire population in Central Thailand similar to Northern Thai population used in this study. Similarly, Hanenberg *et al*. (2001) estimated a much lower heritability for WSI in parities 2 to 6 (0.07 ± 0.01). These last two estimates were similar to the estimate obtained in this population (0.04 ± 0.02) using WSI data from all parities.

Table 6 Direct heritabilities (upper diagonals), direct genetic variances (lower diagonals), direct genetic correlations (above diagonal) and direct genetic covariances (below diagonal) for weaning to first service interval and litter traits

Trait [1]	WSI	NBA	LBW	NPW	LWW
WSI	0.04 ± 0.02[2] 0.92 ± 0.51	0.05 ± 0.71	0.09 ± 0.00[4]	0.29 ± 0.00[4]	0.05 ± 0.00[4]
NBA	0.03 ± 0.39	0.05 ± 0.02[3] 0.33 ± 0.15	0.73 ± 0.13	0.85 ± 0.11	0.08 ± 0.02
LBW	0.08 ± 0.00[4]	0.38 ± 0.20	0.06 ± 0.02 0.82 ± 0.33	0.56 ± 0.20	0.06 ± 0.02
NPW	0.13 ± 0.00[4]	0.29 ± 0.13	0.29 ± 0.18	0.06 ± 0.03 0.30 ± 0.14	0.95 ± 0.05
LWW	0.18 ± 0.00[4]	0.19 ± 0.09	0.21 ± 0.12	1.98 ± 0.94	0.05 ± 0.02 14.50 ± 7.00

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

[2] Heritability and direct genetic variance from WSI-NBA analysis

[3] Minimum heritability value of three pairwise estimates (upper element) and corresponding average for direct genetic variance (lower element)

[4] Constrained estimate; ASREML provided no standard error

Heritabilities reported for litter traits in Thailand were low and comparable to estimates in this study. Pholsing *et al*. (2009) estimated heritabilities of 0.11 ± 0.04 for NBA and 0.08 ± 0.03 for LBW in a Pietrain-Large White population. Suwanasopee *et al*. (2005b) estimated a heritability of 0.07 for NBA, and Suwanasopee (2006) computed heritabilities of 0.01 ± 0.02 for NPW and 0.08 ± 0.03 for LWW in a Large White, Landrace and Duroc population. Imboonta *et al*. (2007) estimated a heritability of 0.03 ± 0.02 for total number of piglets born. Heritability values for litter traits in temperate regions were also low, ranging from 0.08 to 0.15 for NBA, 0.05 to 0.07 for NPW and 0.08 to 0.09 for LWW in populations of Landrace, Yorkshire, Duroc and Hampshire pigs in the United States and The Netherlands (Hanenberg *et al*., 2001; Chen *et al*., 2003; Ehlers *et al*., 2005).

Additive direct genetic covariances and direct genetic correlations between WSI and litter traits were all close to zero (Table 6). Only the direct genetic covariance and correlation between WSI and NBA converged without constraints, and had a large SE. Additive direct genetic correlations among litter traits were all positive (Table 6). The near zero direct genetic correlations between WSI and litter traits indicated that using a multiple trait analysis involving WSI and litter traits would yield no increase accuracy of prediction over a single-trait analysis for WSI. Thus, animals in this population could be evaluated for WSI using single trait genetic evaluation procedures without detrimental impact on the accuracy of their genetic predictions for WSI.

As expected, high and positive estimates of additive direct genetic correlations were obtained between NBA and LBW (0.73 ± 0.13) and NPW and LWW (0.95 ± 0.05) indicating a close positive association between the number of live piglets per litter at birth and at weaning and the weight of the litter at these times. There was also a high positive association between direct genetic effects for NBA and NPW (0.85 ± 0.11) and a moderate association between direct genetic effects for LBW and NPW (0.56 ± 0.20). Correlations between NBA and LWW and between LBW and LWW were near zero. These genetic correlation estimates among litter traits suggest that a

multiple trait analysis for litter traits would be advantageous to increase accuracies of prediction in this population.

Direct genetic correlations between WSI and litter traits in this study were unavailable in other Thai studies. However, Imboonta *et al*. (2007) estimated a genetic correlation between WSI and total number of piglets born (0.07 ± 0.27) in a Landrace population in Eastern Thailand that was similar to the correlation between WSI and NBA estimated in this study. Similarly, low values of correlations were estimated between WEI and NBA (-0.01), WEI and NPW (0.51 ± 0.47) and WEI and LWW (0.01 ± 0.24) in Landrace and Large White herds in Central Thailand (Suwanasopee *et al*., 2005b; Suwanasopee, 2006). There was general agreement between correlation estimates in this study and those from swine populations in temperate regions. Genetic correlations between WSI and NBA were similar to values in this study in Norwegian Landrace (0.05 ± 0.04 for first parity; 0.03 ± 0.07 for later parities; Holm *et al*., 2005), and higher in a Landrace-Hampshire-Yorkshire population in the United States (0.15 to 0.16; Ehlers *et al*., 2005). Genetic correlations were also found to be low between WSI and NPW (0.13) and between WSI and LWW (0.16) in a Landrace-Large White population in the Czech Republic (Adamec and Johnson, 1997). Genetic correlations between NBA and NPW (0.14 to 0.19) were lower than the estimate obtained in this study, but comparable between NBA and LWW (0.14 to 0.15) and NPW and LWW (0.75) in a Landrace-Yorkshire population in the United States (Chen *et al*., 2003).

4. Genetic parameters for maternal genetic effects

Estimates of maternal heritabilities for litter traits (Table 7) were from 20% to 50% lower than heritabilities for additive direct heritabilities for NBA (0.04 ± 0.02), LBW (0.03 ± 0.02) and NPW (0.03 ± 0.02). Only the maternal heritability for LWW (0.06 ± 0.02) was 20% higher than its direct counterpart. Estimates of maternal heritabilities were the same for the three pair-wise analyses for NBA and LWW, whereas estimates ranged from 0.03 ± 0.02 to 0.04 ± 0.02 for LBW and NPW.

Table 7 Maternal heritabilities (upper diagonals), maternal variances (lower diagonals), maternal correlations (above diagonal) and maternal covariances (below diagonal) for litter traits

Trait [1]	NBA	LBW	NPW	LWW
NBA	0.04 ± 0.02 0.22 ± 0.14	0.78 ± 0.15	0.54 ± 0.29	0.03 ± 0.03
LBW	0.26 ± 0.18	0.03 ± 0.02[2] 0.46 ± 0.29	0.50 ± 0.31	0.04 ± 0.03
NPW	0.11 ± 0.11	0.15 ± 0.16	0.03 ± 0.02[2] 0.18 ± 0.12	0.94 ± 0.06
LWW	0.06 ± 0.08	0.13 ± 0.12	1.68 ± 0.87	0.06 ± 0.02 17.77 ± 6.92

[1] NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

[2] Minimum heritability value of three pairwise estimates (upper element) and corresponding maternal genetic variance (lower element)

Estimates of maternal heritabilities for litter traits in Thailand were unavailable. However, estimates of maternal heritabilities obtained in this population were within the range of estimates from swine populations in temperate regions. Maternal heritabilities for NBA, NPW and LWW were found to be either zero or near zero (0.00 to 0.02) in a Landrace-Yorkshire swine population in the United States (Chen *et al*., 2003) and for NBA and NPW in Czech Landrace and Large White (Adamec and Johnson, 1997). Somewhat higher estimates of maternal heritability were computed for NBA and NPW in Polish Large White (0.03 to 0.10; Kaplon *et al*., 1991) and Canadian Landrace and Yorkshire (0.04 ± 0.04 to 0.08 ± 0.04; Southwood and Kennedy, 1990), and for LWW in Czech Landrace and Large White (0.05; Adamec and Johnson, 1997).

Lower values of maternal than direct heritabilities for litter traits indicate that more genetic progress could be achieved by selecting for direct than maternal effects in this population. However, selection for maternal effects should also be considered

as an integral part of a selection program because of its impact on both birth and weaning litter traits. Thus, selection of boars and sows with high EPD for direct and maternal effects would likely produce the most desirable changes in direct and maternal genetic values in the population. Because of the larger selection intensity that can be applied to boars, their impact on genetic progress could be substantially larger than that of sows. In addition, becarse Thai swine farmers frequently import L and W boars, it would be advantageous to choose these boars using direct and maternal genetic information to speed up genetic progress for WSI and litter traits in Thailand.

Estimates of maternal correlations among litter traits were all positive and had the same pattern as additive direct genetic correlations. The highest estimates of maternal correlations occurred between NBA and LBW (0.78 ± 0.15) and NPW and LWW (0.94 ± 0.06), whereas moderate maternal correlations existed between NBA and NPW (0.54 ± 0.29) and LBW and NPW (0.50 ± 0.31), and near zero maternal correlations between NBA and LWW, and between LBW and LWW. These correlations suggest that the relationship between the maternal ability of sows at birth and at weaning is primarily associated with the survival of piglets from birth to weaning, but not with the weight of the litter at weaning. This result LW seems reasonable because maternal ability for birth traits is primarily determined by the ability of the sow to provide an appropriate intrauterine environment, whereas maternal ability for weaning traits is largely associated with a milk production and nursing behavior.

Maternal correlations among litter traits in Thailand were unavailable. Kaplon *et al.* (1991) estimated correlations between sow genetic effects of 0.91 between NBA and NPW, 0.68 between NBA and LWW, and 0.80 between NPW and LWW in Polish Large White. In addition, contrary to the positive medium size correlation between NBA and NPW in this study, estimates in temperate regions ranged from negative to positive for Landrace and Yorkshire. Lund *et al*. (2002) estimated maternal correlations between %NBA and %NPW of 0.25 ± 0.09 in Landrace and -0.48 ± 0.31 in Yorkshire, whereas Su *et al*. (2008) estimated maternal correlations of -0.14 ± 0.18

for Landrace and -0.03 ± 0.21 for Yorkshire. Factors that likely contributed to differences in correlation estimates in these studies include differences in statistical methodology and genetic characteristics of each swine population.

5. Repeatabilities, permanent environmental correlations and phenotypic correlations

The estimate of repeatability for WSI (0.04 ± 0.02) was equal to the estimate of heritability suggesting that permanent environment was irrelevant for this trait. On the other hand, repeatability estimates for all litter traits were from 60% to 100% larger than the combined direct genetic and maternal to phenotypic ratios suggesting that permanent maternal environmental effects were important for litter traits in this population. Repeatability estimates from the three 2-trait analyses were equal for NBA (0.18 ± 0.02), LBW (0.18 ± 0.02) and NPW (0.15 ± 0.02) and ranged from 0.15 ± 0.02 to 0.16 ± 0.02 for LWW. These low repeatability estimates emphasize the importance of obtaining several records per sow for WSI and litter traits to improve the accuracy of prediction for sows' future records as well as to increase the accuracy of prediction for sow EPD, boar EPD and progeny EPD in Thai swine populations.

Suwanasopee *et al*. (2005b) estimated repeatabilities for WEI (0.06) and for NBA (0.15) in a swine population in Central Thailand that were similar to the repeatabilities estimated in this study for WSI and NBA. No other repeatability estimates for WSI or litter traits were available in Thailand. However, in the humid subtropics of Southern Brazil, Siewerdt and Cardellino (1995) estimated repeatabilities in Landrace and Large White herd for NBA (0.16 ± 0.01 for L and 0.14 ± 0.01 for W), LBW (0.19 ± 0.02 for L and 0.15 ± 0.01 for W), NPW (0.15 ± 0.02 for L and 0.12 ± 0.01 for W) and LWW (0.15 ± 0.02 for L and 0.13 ± 0.01 for W) that were very close to the ones estimated in this study. Somewhat lower estimates of repeatability were estimated in temperate regions by Adamec and Johnson (1997) in Czech Landrace and Large White (0.11 for NBA, 0.10 for NPW and 0.11 for LWW) and by Chen *et al*. (2003) in the United States Landrace and Yorkshire pigs (0.14 to 0.17 for NBA, 0.08 to 0.11 for NPW and 0.12 to 0.14 for LWW).

Direct permanent environmental correlations as well as phenotypic correlations between WSI and litter traits were close to zero (Table 8). These correlations lend support to the statement above that WSI could be analyzed separately from litter traits without detriment to the accuracy of genetic predictions. Near zero phenotypic correlations also were found in Thailand between weaning to first estrous interval and NBA (Suwanasopee *et al*., 2005b) and between WSI and litter traits in the United States (NBA, LBW; Ehlers *et al*., 2005). Maternal permanent environmental correlations and phenotypic correlations among litter traits (Table 8) followed the same pattern as direct genetic and maternal correlations. Higher estimates of maternal permanent environmental correlations existed between NBA and LBW (0.80 ± 0.05), NBA and NPW (0.82 ± 0.08), LBW and NPW (0.78 ± 0.09) and NPW and LWW (0.94 ± 0.04). Similarly, moderate to high phenotypic correlation estimates were computed between NBA and LBW (0.83 ± 0.01), NBA and NPW (0.63 ± 0.01), LBW and NPW (0.55 ± 0.01) and NPW and LWW (0.88 ± 0.00). Maternal permanent environment and phenotypic correlations between NBA and LWW, and between LBW and LWW were close to zero.

Similar estimates of phenotypic correlations to the ones computed in this study were obtained by Kaplon *et al*. (1991) between NBA and NPW (0.88) and NPW and LWW (0.86) in Polish Large White and by Chen *et al*. (2003) between NBA and LWW (0.06 to 0.07) and between NPW and LWW (0.78 to 0.80). However, Kaplon *et al*. (1991) also reported a substantially higher phenotypic correlation between NBA and LWW (0.75) and Chen *et al*. (2003) obtained a much lower phenotypic correlation between NBA and NPW (0.05 to 0.06) than corresponding estimates in this study.

Table 8 Repeatabilities, permanent environmental correlations (above diagonal) and phenotypic correlations (below diagonal) for weaning to first service interval and litter traits

Trait [1]	WSI	NBA	LBW	NPW	LWW
WSI	0.04 ± 0.02[2]	0.24 ± 0.33	0.06 ± 0.01	0.03 ± 0.00	0.03 ± 0.00
NBA	-0.00 ± 0.03	0.18 ± 0.02	0.80 ± 0.05	0.82 ± 0.08	0.08 ± 0.01
LBW	0.01 ± 0.01	0.83 ± 0.01	0.18 ± 0.02	0.78 ± 0.09	0.09 ± 0.01
NPW	-0.00 ± 0.01	0.63 ± 0.01	0.55 ± 0.01	0.15 ± 0.02	0.94 ± 0.04
LWW	-0.00 ± 0.02	0.05 ± 0.00	0.05 ± 0.00	0.88 ± 0.00	0.15 ± 0.02[3]

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

[2] Repeatability from WSI-NBA analysis

[3] Minimum repeatability value of three pairwise estimates

6. Genetic and environmental trends

Genetic trends for boar EPD, sow EPD and permanent environmental trends for sows are shown in Figure 8 for WSI, Figure 9 for NBA and Figure 10 for LBW. Figures of genetic trends for NPW and LWW (not shown) were similar to those for litter traits at birth.

Boar genetic trend was significant for NBA (P = 0.0042), but not-significant for WSI and other litter traits. Regression coefficients for WSI and litter traits were 0.012 ± 0.008 days/year (P = 0.1348) for WSI, -0.015 ± 0.005 piglets/year (P = 0.0042) for NBA, 0.008 ± 0.017 kg/year (P = 0.6391) for LBW, -0.015 ± 0.016 piglets/year (P = 0.3836) for NPW and -0.006 ± 0.011 kg/year (P = 0.5542) for LWW. Genetic trends for sows were negative and significant for all traits. Thus, sow genetic trends were favorable only for WSI and unfavorable for all litter traits. Regression

coefficients were -0.036 ± 0.013 days/year (P = 0.0113) for WSI, -0.017 ± 0.005 piglets/year (P = 0.0071) for NBA, -0.015 ± 0.005 kg/year (P = 0.0109) for LBW, -0.019 ± 0.008 piglets/year (P = 0.0234) for NPW and -0.022 ± 0.006 kg/year (P = 0.0034) for LWW.

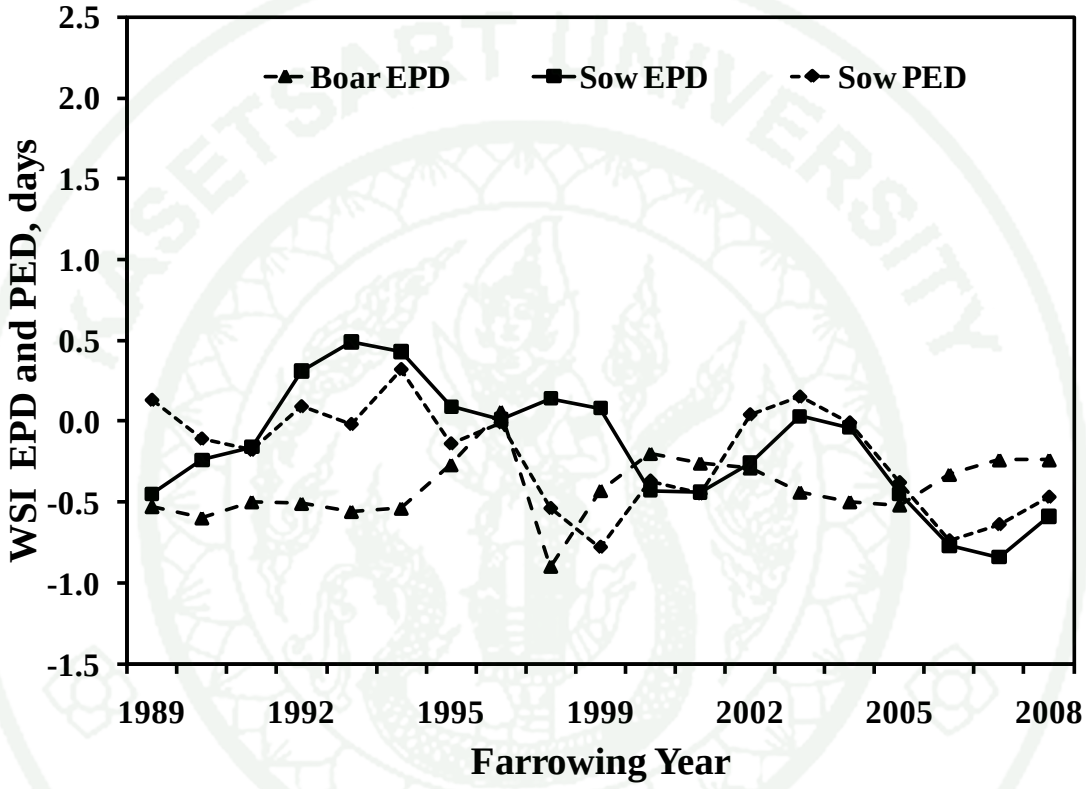

Figure 8 Mean weaning to first service interval (WSI) boar and sow direct expected progeny differences (EPD) and sow direct permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were 0.012 ± 0.008 days/year (P = 0.1348) for boar EPD on FY, -0.036 ± 0.013 days/year (P = 0.0113) for sow EPD on FY and -0.028 ± 0.011 days/year (P = 0.0205) for sow PED on FY

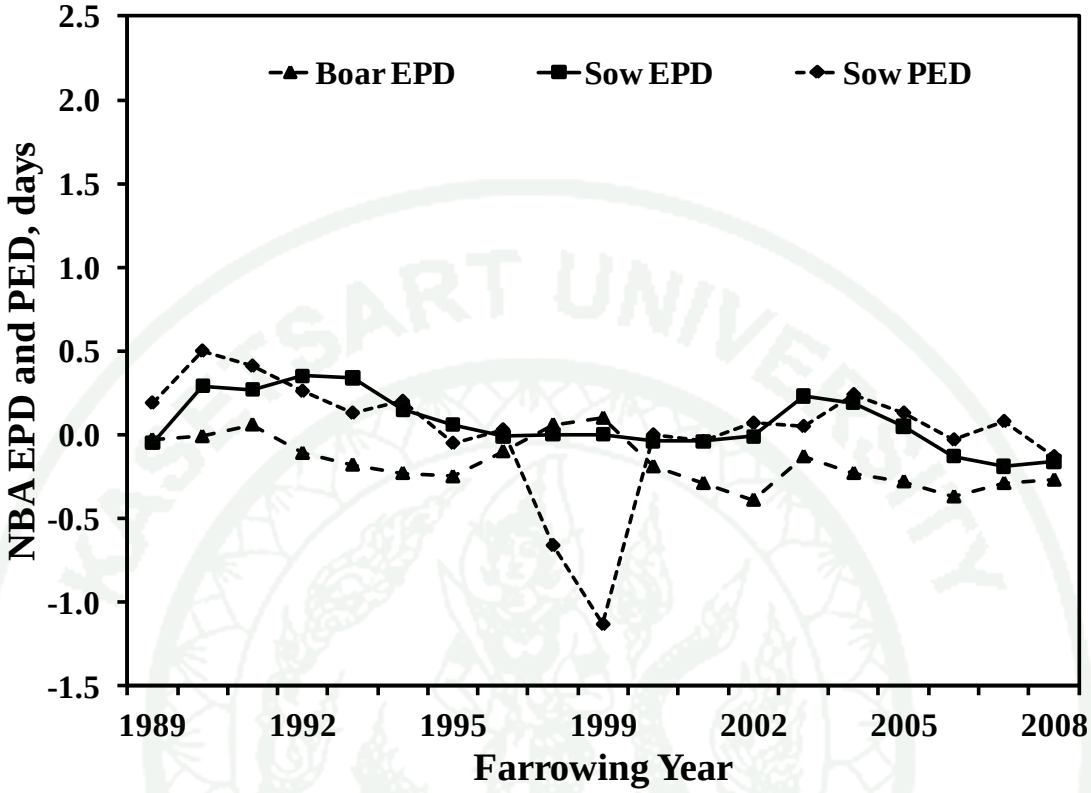

Figure 9 Mean number of piglets born alive (NBA) boar direct expected progeny differences (EPD), sow direct plus maternal EPD, and sow maternal permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were -0.015 ± 0.005 piglets/year (P = 0.0042) for boar EPD on FY, -0.017 ± 0.005 piglets/year (P = 0.0071) for sow EPD on FY and -0.015 ± 0.014 piglets/year (P = 0.2931) for sow PED on FY

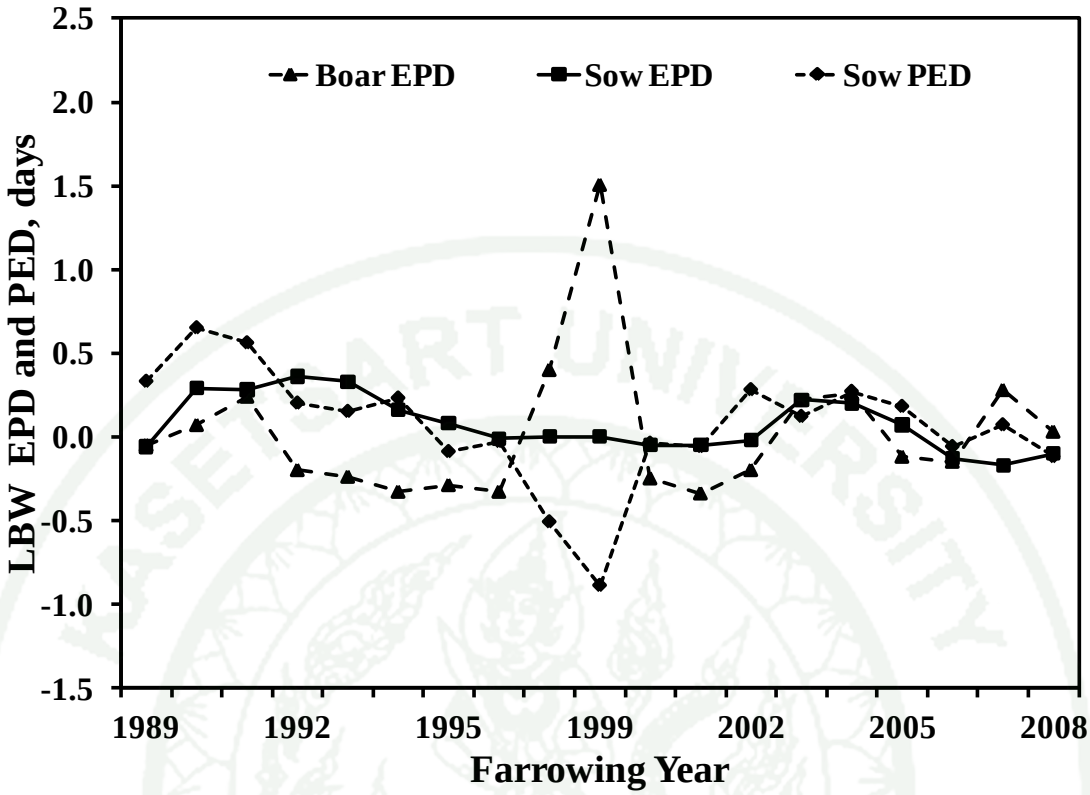

Figure 10 Mean litter weight of live piglets at birth (LBW) boar direct expected progeny differences (EPD), sow direct plus maternal EPD, and sow maternal permanent environmental differences (PED) by farrowing year (FY). Regression coefficients were 0.008 ± 0.017 kg/year (P = 0.6391) for boar EPD on FY, -0.015 ± 0.005 kg/year (P = 0.0109) for sow EPD on FY and -0.019 ± 0.013 kg/year (P = 0.1732) for sow PED on FY

Boars and sows in this herd were selected based on phenotypic information for litter traits only (Cherdsatirakul, P., personal contact). The low significant negative values for boar NBA genetic trend and sow genetic trends for all litter traits suggesting that the phenotypic information used was insufficient to successfully identify the best boars and sows for litter traits in this herd. The end result LW was low boar and sow genetic trends for all litter traits. Considering the low positive direct genetic correlations between WSI and litter traits estimated in this population, the favorable negative sow genetic trend for WSI may have been a correlated response to the negative selection pressure exerted on litter traits by the phenotypic selection used in this herd.

Reports of genetic trends in Thailand were few. Imboonta *et al*. (2007) obtained a genetic trend of zero for WSI in a Thai Landrace herd in Eastern Thailand and Suwanasopee *et al*. (2005b) estimated a negative genetic trend (-0.07 days/year) for WEI and a positive genetic trend for NBA (0.026 piglets/year) in a Landrace-Large White-Duroc population in Central Thailand. When expressed as sow EPD per FY, the sow trend for weaning to first estrous interval of Suwanasopee *et al*. (2005b) becomes -0.035 days/year which is nearly identical to the sow trend found in this study. Contrarily, the NBA sow trend of Suwanasopee *et al*. (2005b) becomes 0.013 piglets/year, a value close to the opposite of the negative sow trend of -0.017 ± 0.005 piglets/year found in this study for NBA.

Permanent environmental trends for sows were also negative for all traits, but significant only for WSI. The favorable PED trend for WSI was -0.028 ± 0.011 days/year (P = 0.0205) and the unfavorable PED trends for litter traits were -0.015 ± 0.014 piglets/year (P = 0.2931) for NBA, -0.019 ± 0.013 kg/year (P = 0.1732) for LBW, -0.019 ± 0.022 piglets/year (P = 0.3915) for NPW and -0.023 ± 0.013 kg/year (P = 0.0940) for LWW. Considering that several records per sow were likely used in the culling and selection process of multiparous sows, it is not surprising that sow permanent environmental effects showed the same pattern of trends as sow genetic effects.

Environmental trends expressed in terms of least squares solutions for FY over time were positive for all traits. Regression coefficients were 0.035 ± 0.059 days/year (P = 0.5640) for WSI, 0.165 ± 0.059 piglets/year (P = 0.0119) for NBA, 0.376 ± 0.084 kg/year (P = 0.0003) for LBW, 0.088 ± 0.048 piglets/year (P = 0.0799) for NPW and 1.121 ± 0.303 kg/year (P = 0.0018) for LWW. Trends of FY means over time are shown in Figure 11 for NBA and NPW, and Figure 12 for LBW and LWW. The lowest FY means for NBA and NPW in Figure 11 appear to have been due to lack of adaptation of daughters of imported boars to the hot and humid conditions in the farm at that time.

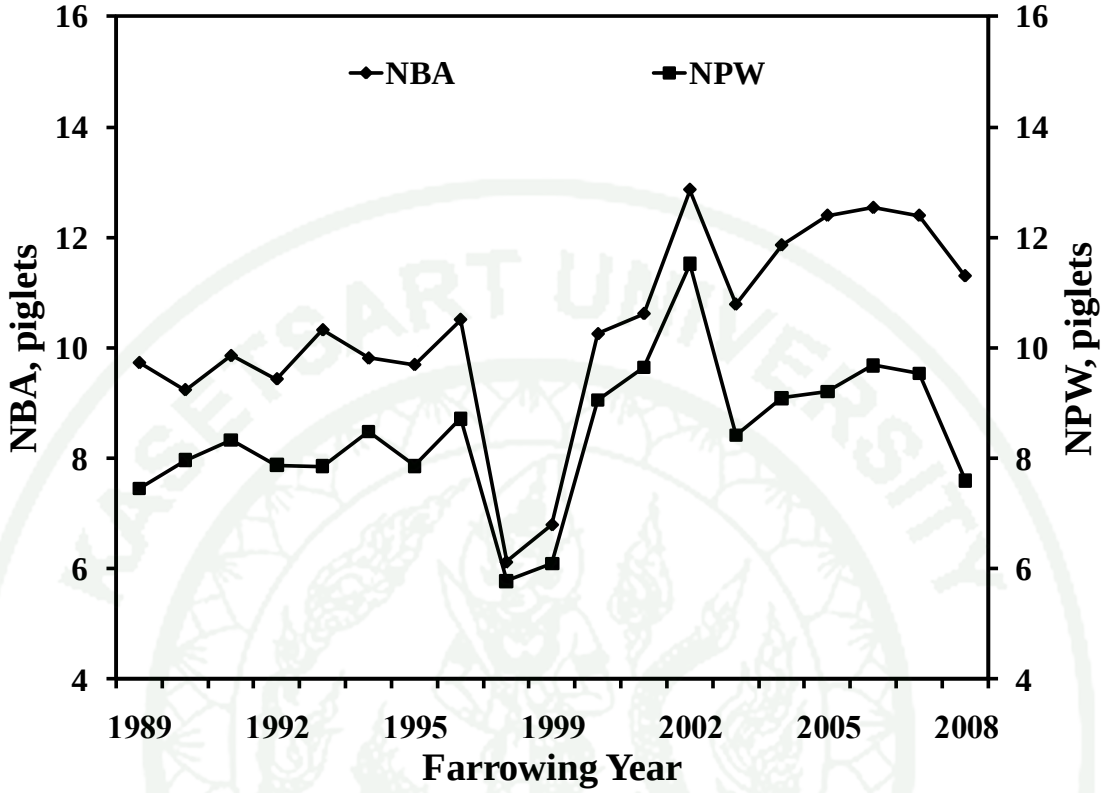

Figure 11 Least squares solutions for number of piglets born alive (NBA) and number of piglets at weaning (NPW) by farrowing year (FY). The regression coefficients of solutions on FY were 0.165 ± 0.059 piglets/year (P = 0.0119) for NBA and 0.088 ± 0.048 piglets/year (P = 0.0799) for NPW

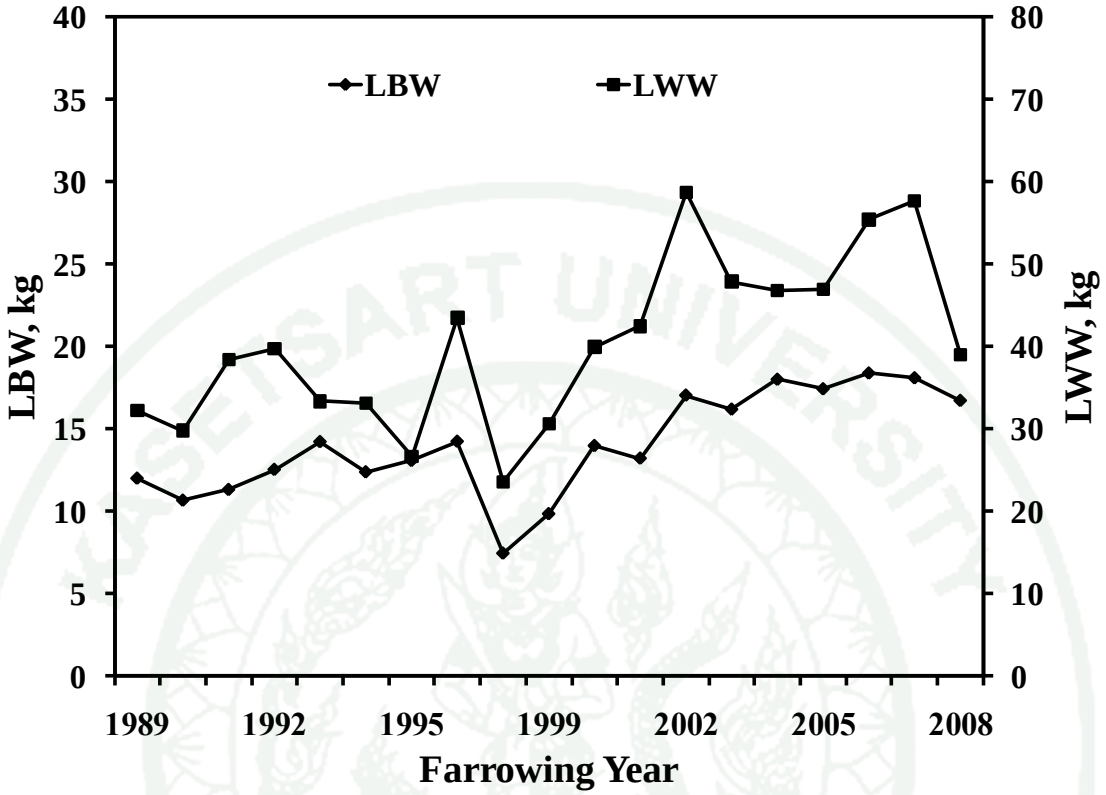

Figure 12 Least squares solutions for litter weight of live piglets at birth (LBW) and litter weight at weaning (LWW) by farrowing year (FY). The regression coefficients of solutions on FY were 0.376 ± 0.084 kg/year (P = 0.0003) for LBW and 1.121 ± 0.303 kg/year (P = 0.0018) for LWW

The positive environmental trends for litter trait means between 1989 and 2008 indicated that the level of nutrition, management and health care of animals in this swine herd improved over time. The substantially larger regression estimates for environmental than for genetic trends suggesting that chosen sows to remain in the herd based on superior phenotypic records for litter traits primarily were reflected from environmental rather than genetic effects. Thus, it would be advisable to implement a selection program based on predicted additive direct and maternal genetic values to improve the identification of superior replacement animals in this herd. If the selection goal continued to be the improvement of litter traits, then a multiple trait genetic evaluation involving all litter traits would be an appropriate

alternative. A multiple trait analysis system involving NBA, LBW, NPW and LWW would increase the accuracy of prediction of all animals for all four traits simultaneously, thus increasing the accuracy of identification of superior animals for all traits and the likelihood of favorable genetic trends for all litter traits. If the selection program also included WSI, a single-trait analysis could be used. As indicated above, evaluation of WSI in a multiple trait system with litter traits would provide no advantage over a single trait analysis because of the low genetic correlations between WSI and litter traits estimated in this population. This new genetic evaluation system would require an accurate and timely data collection and data management system.

Although low estimated genetic parameters for WSI and litter traits were estimated in this study, they were similar to values found in other swine populations in Thailand and in other countries. However, genetic trends were also low and mostly in the opposite direction to the goals of the selection program in the swine farm. Thus, the current phenotypic evaluation and selection program needs to be replaced with one based on multiple traits genetic prediction for litter traits and single trait genetic predictions for WSI. It would also be desirable if several farms joined efforts to create a larger breeding population in this region. This would increase the likelihood of identifying extraordinary animals, thus genetic trends may be improved with including the extended population.

However, the low value of heritabilities for WSI and litter traits in this study suggested that environmental factors were substantial effects for these traits. Consequently, the selection of superior animals would be obtained with low accuracy and slow genetic progress for WSI and litter traits. Thus, if associated genes with known effects on WSI and litter traits (e.g., ADIPOQ and FSHR) are used to predict the genetic value of animals for these traits, then the accuracy of prediction and genetic progress for these traits will be increased.

Trial 3: Estimation of allele frequencies for ADIPOQ and FSHR genes and evaluation of association between specific genotypes and reproductive traits

1. Allele and genotype frequencies

Allele and genotype frequencies for the ADIPOQ and FSHR genes are shown in Table 9. All breed groups and the whole population were in Hardy-Weinberg equilibrium.

The frequency of the G allele for the ADIPOQ gene was over 0.9 in all breed groups (from 0.93 in L to 0.99 in W), whereas the frequency of the A allele was close to zero (from 0.01 in W to 0.07 in L). These allele frequencies resulted in substantially higher frequency of GG genotypes (91.2%) than GA genotype (8.8%; $P < 0.0001$). The AA genotype was absent from the population tested in the current study. The higher frequency of GG sows in this population was similar to that found in a Landrace and Large White population in China (100%; Dai *et al*., 2006) and a purebred Landrace population in Canada (88%; Houde *et al*., 2008). Among breed groups, W sows had the lowest proportion of GA genotypes (1.7%; $P = 0.0015$ to 0.0032; Table 9). The other 3 breed groups (L, LW and WL) had similar frequencies of GA sows (11.6 to 12.9 %; Table 9). Homozygote sows for the AA genotype of the ADIPOQ gene have been reported only in Chinese pig breeds (Dai *et al*., 2006).

The frequency of allele C for FSHR was higher (0.72) than the frequency of allele T (0.28) in the whole population (Table 9). The frequency of allele C ranged from 0.64 for L sows to 0.79 for W and LW sows. On the other hand, W and LW sows had the lowest frequency of T alleles (0.21) and L the highest frequency (0.36) among breed groups of sows (Table 9). As with ADIPOQ, all breed groups of sows and the whole population (all breed groups) were in Hardy-Weinberg equilibrium for FSHR. The frequency of CC and CT genotypes was similar across breed groups of sows. On the opposite, the frequency of TT genotypes was higher in L sows (15.3%; $P = 0.0181$ to 0.0353; Table 9) than in sows from the other 3 breed groups (4.9% for W, 5.3% for LW and 5.6% for WL).

Table 9 Allele and genotype frequencies for adiponectin (ADIPOQ) and follicle stimulating hormone receptor (FSHR) genes

Genotype	Frequency by breed group of sow[1]				
	L[2]	W	LW	WL	All groups
Adiponectin (ADIPOQ)[2]					
Number of pigs	116	117	25	95	353
GA	15 (12.9)[a]	2 (1.7)[b]	3 (12.0)[a]	11 (11.6)[a]	31 (8.8)
GG	101 (87.1)	115 (98.3)	22 (88.0)	84 (88.4)	322 (91.2)
Allele A	0.07	0.01	0.06	0.06	0.05
Allele G	0.93	0.99	0.94	0.94	0.95
Follicle stimulating hormone receptor (FSHR)[2]					
Number of pigs	111	102	19	72	304
CC	49 (44.1)	65 (63.7)	12 (63.2)	35 (48.6)	161 (52.9)
CT	45 (40.5)	32 (31.4)	6 (31.6)	33 (45.8)	116 (38.2)
TT	17 (15.3)[c]	5 (4.9)[d]	1 (5.3)[d]	4 (5.6)[d]	27 (8.9)
Allele C	0.64	0.79	0.79	0.72	0.72
Allele T	0.36	0.21	0.21	0.28	0.28

[a,b] Genotypic frequencies within a row with unequal superscripts differ ($P < 0.01$)

[c,d] Genotypic frequencies within a row with unequal superscripts differ ($P < 0.05$)

[1] Numbers in parenthesis ( ) correspond to percentages

[2] L, purebred Landrace; W, purebred Large White; LW, Landrace × Large White; WL, Large White × Landrace

Jiang *et al*. (2002) reported frequencies for the C and T alleles in Chinese Erhualian pigs (0.39 for allele C and of 0.61 for allele T) that were the opposite of those found in this study. This resulted in lower genotypic frequencies for CC (0.16), similar genotypic frequency for CT (0.45) and higher genotypic frequency for TT (0.39) than those computed in this study for all breed groups. On the other hand, Jiang *et al*. (2002) obtained allele frequencies (C = 0.73 and T = 0.27) and genotype

frequencies (CC = 0.54, CT 0.39 and TT = 0.07) for German Landrace that were similar to W and LW breed groups in this study.

2. Allele substitution effects

Regression of traits on number of G alleles for the ADIPOQ gene and number of T alleles for the FSHR gene were used to estimate allele substitution effects. Regression coefficients for traits on number of ADIPOQ G alleles yielded non-significant positive estimates for WSI and NPW, and non-significant negative estimates for NBA, LBW and LWW (Table 10). Thus, substitution of an A nucleotide for a G nucleotide in SNP AJ849536: g.1716G>A of the ADIPOQ gene had no significant effects on all studied traits in this population. Similarly, estimates of regression coefficients for traits on number of FSHR T alleles were non-significant (close to zero for NBA and positive WSI, LBW, NPW and LWW; Table 10). This indicates that the substitution of a T nucleotide for a C nucleotide in SNP AF025377: g.1166C>T had no significant effects on WSI and litter traits in this swine population. There are no literature values were available for comparison with allelic effects in this study for either ADIPOQ or FSHR.

3. Genotypic effects

The difference between ADIPOQ genotypes GA and GG was non-significant for WSI and all studied litter traits (Table 11) in this swine population. Comparison with other Thai studies could not be done because this is the first association study between WSI and litter traits and ADIPOQ SNP polymorphisms in Thailand. However, in temperate zones, Houde *et al*. (2008) found in an Landrace population that GA sows had shorter WEI than GG sows ($P < 0.05$), but these two sow groups had similar NBA. Results from Houde *et al*. (2008) are in agreement with the non-significant estimates of the difference between GA and GG sows obtained in this study for the NBA trait (Table 11). Studies dealing with the association between SNP (AJ849536: g.1716G>A) and LBW, NPW and LWW are not available in the literature.

Table 10 Regression coefficient (± SE) of weaning to first service interval (WSI) and litter traits (NBA, LBW, NPW and LWW) on number of G alleles in the adiponectin (ADIPOQ) locus and number of T alleles in the follicle stimulating hormone receptor (FSHR) locus

Trait[1]	Locus	Regression coefficient	P value[2]
WSI (days)	ADIPOQ	0.85 ± 0.73	0.2429
	FSHR	0.32 ± 0.32	0.3218
NBA (piglets)	ADIPOQ	-0.06 ± 0.46	0.8999
	FSHR	-0.04 ± 0.20	0.8394
LBW (kg)	ADIPOQ	-0.32 ± 0.74	0.6664
	FSHR	0.11 ± 0.32	0.7419
NPW (piglets)	ADIPOQ	0.22 ± 0.35	0.5235
	FSHR	0.10 ± 0.16	0.5166
LWW (kg)	ADIPOQ	-0.91 ± 3.08	0.7686
	FSHR	1.80 ± 1.40	0.1979

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

[2] Presented P values base on null hypothesis that no significant difference from zero for corresponding regression coefficient

Table 11 Least squares means differences (± SE) between ADIPOQ and FSHR genotypes for weaning to first service interval (WSI) and litter traits (NBA, LBW, NPW and LWW)

Trait[1]	ADIPOQ	FSHR	
	GA - GG	CC - TT	CT - TT
WSI (days)	-0.90 ± 0.73 (P = 0.2173)[2]	-0.59 ± 0.72 (P = 0.4109)	-0.24 ± 0.72 (P = 0.7424)
NBA (piglets)	0.08 ± 0.45 (P = 0.8617)	0.23 ± 0.45 (P = 0.6082)	0.34 ± 0.45 (P = 0.4532)
LBW (kg)	0.42 ± 0.73 (P = 0.5709)	0.00 ± 0.73 (P = 0.6082)	0.33 ± 0.73 (P = 0.4532)
NPW (piglets)	-0.23 ± 0.35 (P = 0.5106)	-0.25 ± 0.35 (P = 0.4737)	-0.20 ± 0.35 (P = 0.5709)
LWW (kg)	0.90 ± 3.10 (P = 0.7728)	-3.67 ± 3.08 (P = 0.2337)	-1.96 ± 3.09 (P = 0.5266)

[1] WSI, Weaning to first service interval; NBA, Number of piglets born alive; LBW, Litter weight of live piglets at birth; NPW, Number of piglets at weaning; LWW, Litter weight at weaning

[2] Number in parenthesis ( ) refer to P values base on null hypothesis that no significant difference from zero for corresponding LSMs difference

Allele G of the porcine adeponectin (ADIPOQ) was associated with decreased fat deposition in body and carcass (Dai *et al*., 2006). Substitution of A to G (A178G) of this gene resulted in the changing of amino acid isoleucine with valine at location 60 of the amino acid sequence (Ile60Val) in the collagenous domain, which might cause a significant change of the adiponectin function (Dai *et al*., 2006). Furthermore, polymorphisms in ADIPOQ were found to have association with weaning to estrus interval and stillborn piglets in a Landrace sow population by Houde *et al*. (2008). Association studies relating swine prenatal and pre-weaning growth and ADIPOQ polymorphisms are unavailable. However, Dall'Olio *et al*. (2009) reported that GA

Duroc pigs had higher postweaning average daily gain (P = 0.003) and lower feed conversion ratio (P = 0.033), from 30 to 155 kg live weight, than GG Duroc pigs.

As with the ADIPOQ gene, estimates of differences between genotypes for the FSHR gene (CC – TT and CT – TT) were non-significant for WSI and all litter traits (Table 11). No association studies between FSHR gene and WSI or litter traits are available in Thailand. However, Jiang *et al*. (2002) found that CC and CT sows had larger (P = 0.0499) total piglet born than TT sows in German Landrace. The opposite was found for Chinese Erhualian sows, where TT sows had larger (P = 0.0137) litter sizes than CC and CT sows. This indicates interaction between breed of sow and FSHR gene. A model with genotype of sow nested within breed group of sow (L, W, LW and WL) for FSHR was analyzed in this study. Differences between CC and TT and between CT and TT for NBA were non-significant differences in all breed groups of sows. Non-significant differences between genotypes (CC, CT and TT) of the FSHR gene for NBA in European (Duroc, Large White and Landrace) and Chinese (Small Meishan, Qingping and Jinhua) sow lines were reported by Yuan *et al*. (2007).

Jiang *et al*. (2002) indicated that the SNP AF025377: g.1166C>T was a substitution of a T for a C at position 1166 in exon 10 of the FSHR gene. This replacement of a C with a T resulted in a change from isoleucine 377 to threonine in the FSHR protein (Ile377Thr; Jiang *et al*., 2002). The position of this substitution is in the conserve motif of ILAITGN that found in the transmembrane-1region of the FSHR protein (Jiang *et al*., 2002; Ulloa-Aguirre *et al*., 2007). Therefore, this missense mutation may have not affected to changes in the functionality of the FSHR protein. This may have been the reason for CC, CT and TT sows in this study to have similar estimates of WSI and numbers of piglets at birth and at weaning. Lack of differences among breed groups in this study may have been influenced by genetic similarity among animals because this population has remained closed since 2002, thus all replacement boars and sows in this population are produced within the herd.

CONCLUSIONS

Farrowing year-season, PR, BGD and LL were all important factors affecting WSI in this population ($P < 0.0001$), whereas NPW was not significance effect. Although, the combination of FYS would be an important factor affecting WSI in this population, the differences between regressions coefficients of WSI on year in each season were not significant. Therefore, WSI in this population from 1989 to 2008 were not substantially increased for all season. The longer WSI in primiparous sows than multiparous sows ($P < 0.0001$) were probably resulted from higher nutritional requirements for growth and lactation. Thus, unmet of nutrition managements of primiparous sows with the same condition of multiparous sows could be seriously considered. Least square means WSI for purebred L and W sows had similar, but lower than LW and WL crossbred sows ($P < 0.0001$). The WL sows had the longest WSI of all breed groups ($P < 0.0001$). The significant quadratic relationship between WSI and LL ($P < 0.0001$) suggested that the lowest WSI value was occurred with LL from 24 to 32 days for this population, thus perhaps the maximum LL allowed in this population could be lowered from 35 to 32 days.

Estimates of genetic parameters estimated in this study for WSI and litter traits were low; direct genetic heritabilities were 0.04 ± 0.02 for WSI, 0.05 ± 0.02 for NBA, 0.06 ± 0.02 for LBW, 0.06 ± 0.03 for NPW and 0.05 ± 0.02 for LWW; maternal heritabilities were 0.04 ± 0.02 for WSI, 0.03 ± 0.02 for NBA, 0.03 ± 0.02 for LBW and 0.06 ± 0.02 for LWW. Estimated repeatability for WSI (0.04 ± 0.02) was equal to the estimate of heritability suggesting that permanent environment effects was irrelevant for this trait in this population. However, 60% to 100% of repeatability estimates for litter traits were larger than both genetic and maternal heritabilities. Estimates repeatabilities for litter traits were 0.18 ± 0.02 for NBA, 0.18 ± 0.02 for LBW, 0.15 ± 0.02 for NPW and 0.03 ± 0.00 for LWW. In addition, direct genetic and maternal correlations between WSI and litter traits were close to zero, whereas the direct genetic correlations among litter traits were all positive with high values, except the correlations between LWW and litter trait at birth. These implied that multiple trait

analysis for WSI and litter traits were not gained the accuracy for estimating genetic parameters in this population.

Although, low values of genetic parametersn were estimated in this study, they were similar to values found in other swine populations in Thailand and in other countries. However, genetic trends were also low and mostly in the opposite direction of goals for the selection program in swine farm. Thus, the current phenotypic evaluation and selection program needs to be replaced with one based on multiple trait genetic predictions for litter traits and single trait genetic predictions for WSI. Increasing the number of animal with several farms joined efforts to create a larger breeding population would be established to increase probability of indentifying extra ordinary animals for improving genetic trends in those populations. The proposed system could also serve as a model for future regional and national swine genetic improvement programs in Thailand.

According to low heritabilities for WSI and litter traits would create the problem that concerned about low accuracy of selecting animal and slow genetic progress, if the program of genetic improvement based on the only quantitative selection. However, selecting the animals contained the relevant genes associating good performance for WSI and litter traits would increase the accuracy of animal selection. Using genotypic information of the genes with known effects (e.g., ADIPOQ and FSHR genes) that related to WSI and litter traits for classifying the relevant animals need to be considered to elevate the accuracy of animal selection.

Two alleles (G and A) and two genotypes (GA and GG) were identified for the ADIPOQ gene. Similarly, two alleles (C and T) and three genotypes (CC, CT and TT) were identified for the FSHR gene. Allele and genotype frequencies of the ADIPOQ and FSHR genes for all breed groups and the whole population were in Hardy-Weinberg equilibrium. Regression coefficients of traits on number of G alleles for the ADIPOQ gene and on number of T alleles for the FSHR gene were non-significant for WSI and litter traits. Thus, the change of a G to an A nucleotide in position 1716 of the ADIPOQ gene and the substitution of a T for a C in position 1166 of the FSHR gene

had little impact on reproductive traits in this population. Differences between genotypes for the ADIPOQ gene (GA – GG) and the FSHR gene (CC – TT and CT – TT) were all non-significant. These suggesting that the ADIPOQ and FSHR genes will be little help for selecting pigs for WSI and litter traits in this population. Low numbers of animals, tropical environmental conditions and genetic similarity among animals due to intra-herd replacement of boars and primiparous sows during the period of the study may have contributed to the lack of significant differences among allelic and genotypic effects in this population. Estimates of ADIPOQ and FSHR gene effects may change with a larger dataset and several herds. Thus, it would be advantageous to repeat this study with a larger and more representative sample of the Thai swine population.

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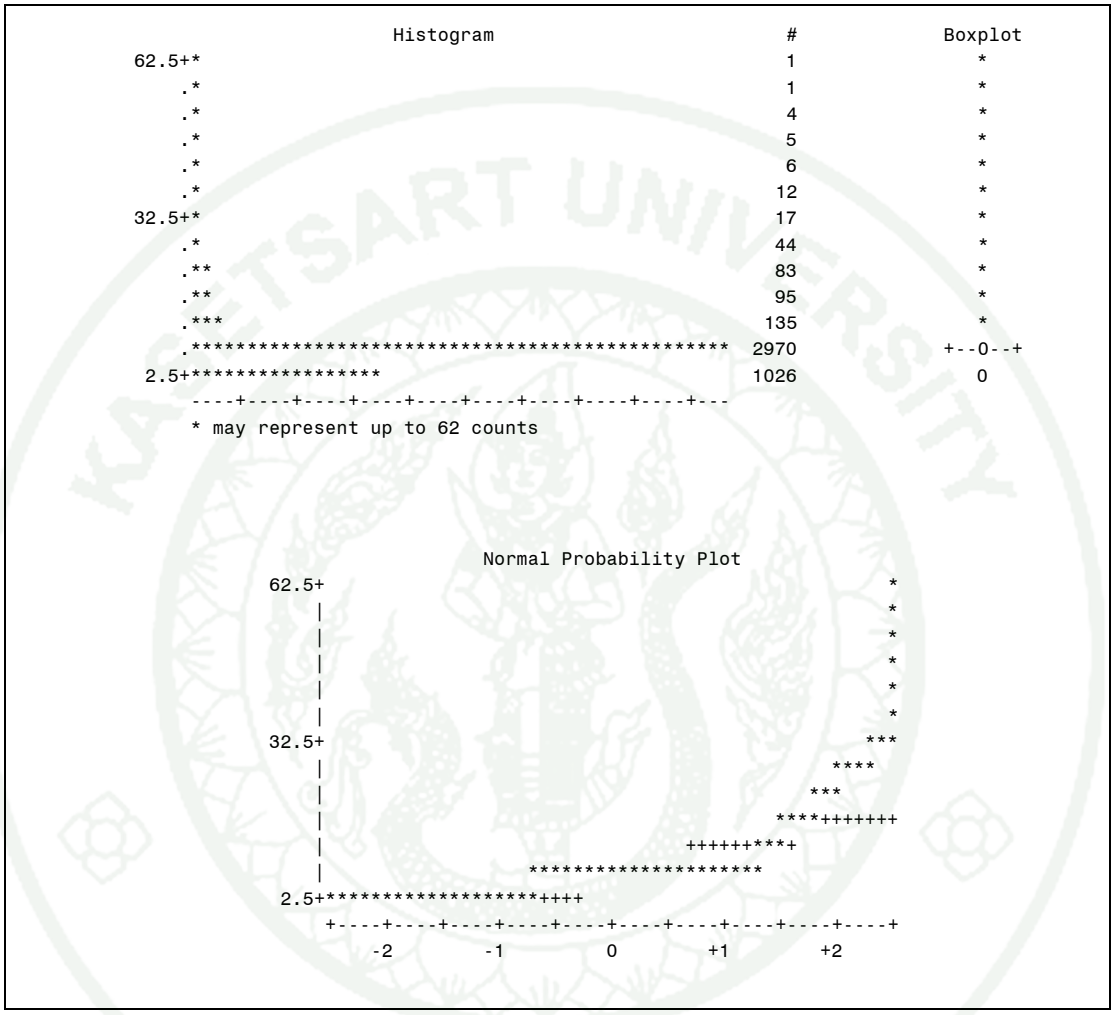
APPENDICES

Appendix A

Statistical method for genetic evaluation

The UNIVARIATE Procedure for Genetic Analysis

Variable: WSI



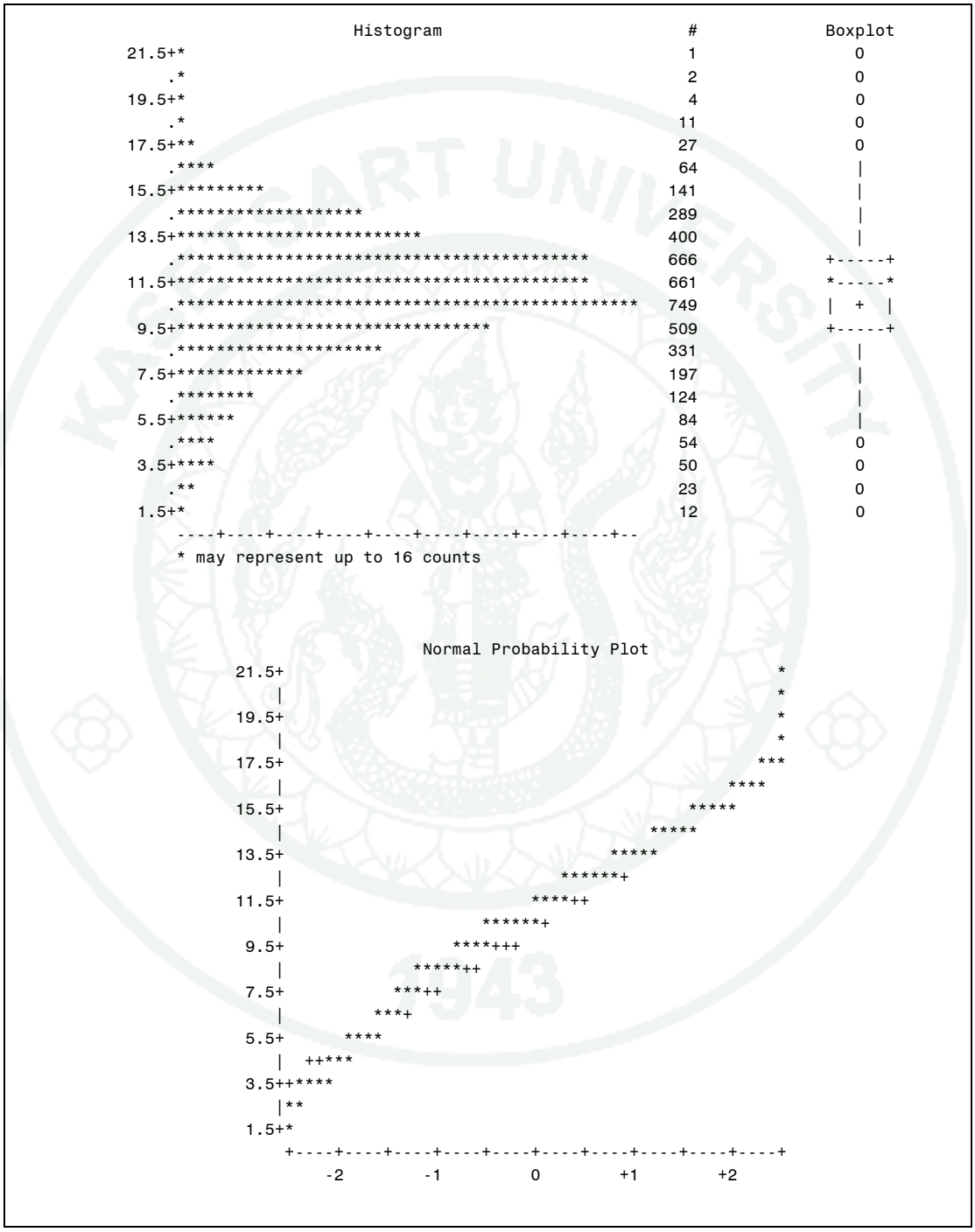
Appendix Figure A1 Histogram, box plot and normal probability plot for weaning to first service interval (WSI) ranged from 1 to 60 days

Appendix Table A1 Basic and descriptive statistical values for weaning to first service interval (WSI) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (days)	6.52
Median (days)	5.00
Mode (days)	5.00
Std Deviation (days)	5.15
Variance ($days^2$)	26.54
Range (days)	59.00
Distribution parameters	
Number of observations	4,399.00
Mean (days)	6.52
Std Deviation (days)	5.15
Variance (days2)	26.54
Sum Weights (days)	4,399.00
Sum Observations (days)	28,662.00
Skewness	4.30
Kurtosis	23.94
Uncorrected SS ($days^2$)	303,480.00
Corrected SS ($days^2$)	116,730.68
Coefficient of Variation (%)	79.07
Std Error Mean (days)	0.08

The UNIVARIATE Procedure for Genetic Analysis

Variable: NBA



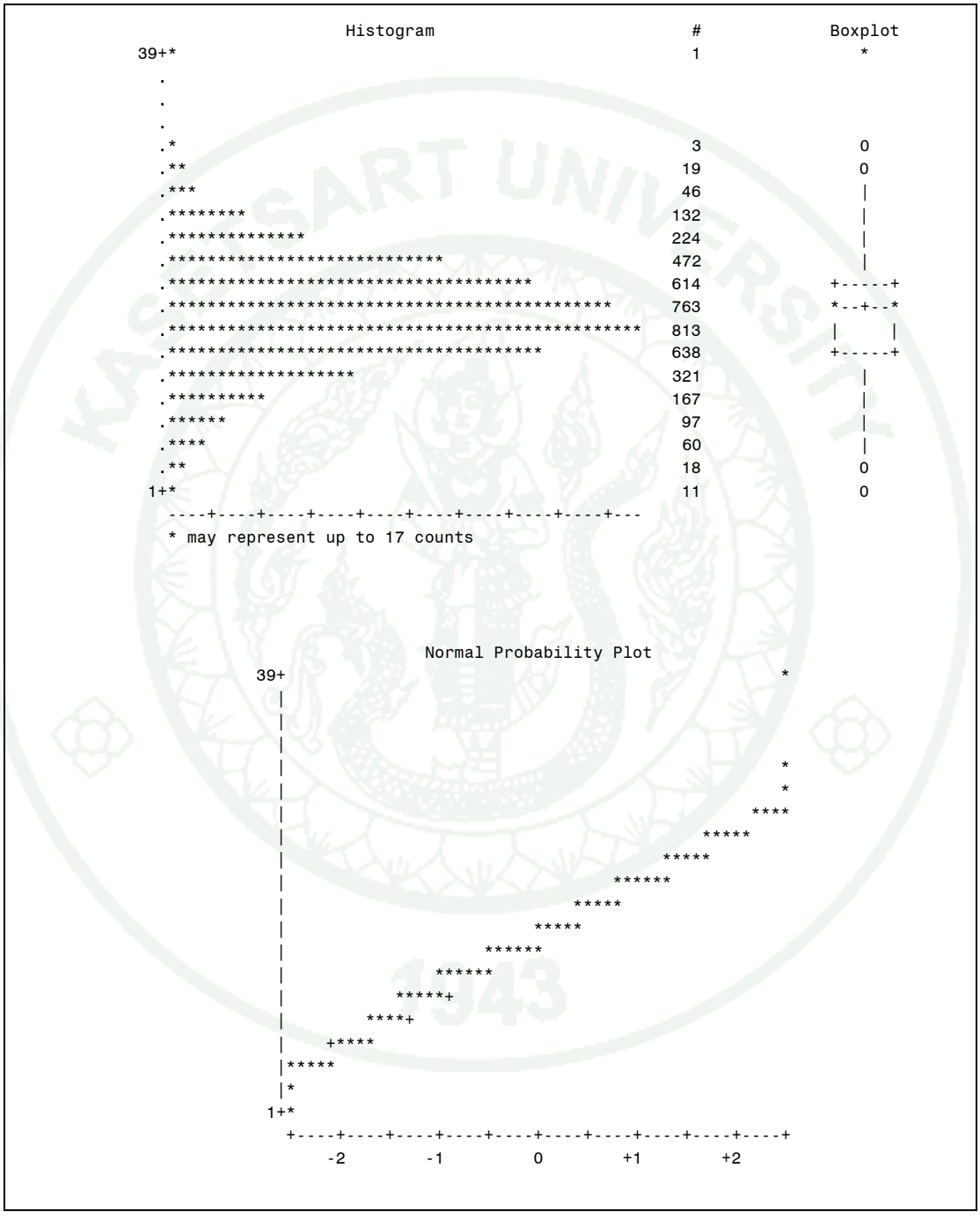
Appendix Figure A2 Histogram, box plot and normal probability plot for number of piglets born alive (NBA) range from 1 to 21 piglets

Appendix Table A2 Basic and descriptive statistical values for number of piglets born alive (NBA) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (piglets)	10.49
Median (piglets)	11.00
Mode (piglets)	10.00
Std Deviation (piglets)	2.76
Variance (piglets^2)	7.63
Range (piglets)	20.00
Distribution parameters	
Number of observations	4,399.00
Mean (piglets)	10.49
Std Deviation (piglets)	2.76
Variance (piglets^2)	7.63
Sum Weights (piglets)	4,399.00
Sum Observations (piglets)	46,128.00
Skewness	-0.41
Kurtosis	0.73
Uncorrected SS (piglets^2)	517,238.00
Corrected SS (piglets^2)	33,538.89
Coefficient of Variation (%)	26.34
Std Error Mean (piglets)	0.04

The UNIVARIATE Procedure for Genetic Analysis

Variable: LBW



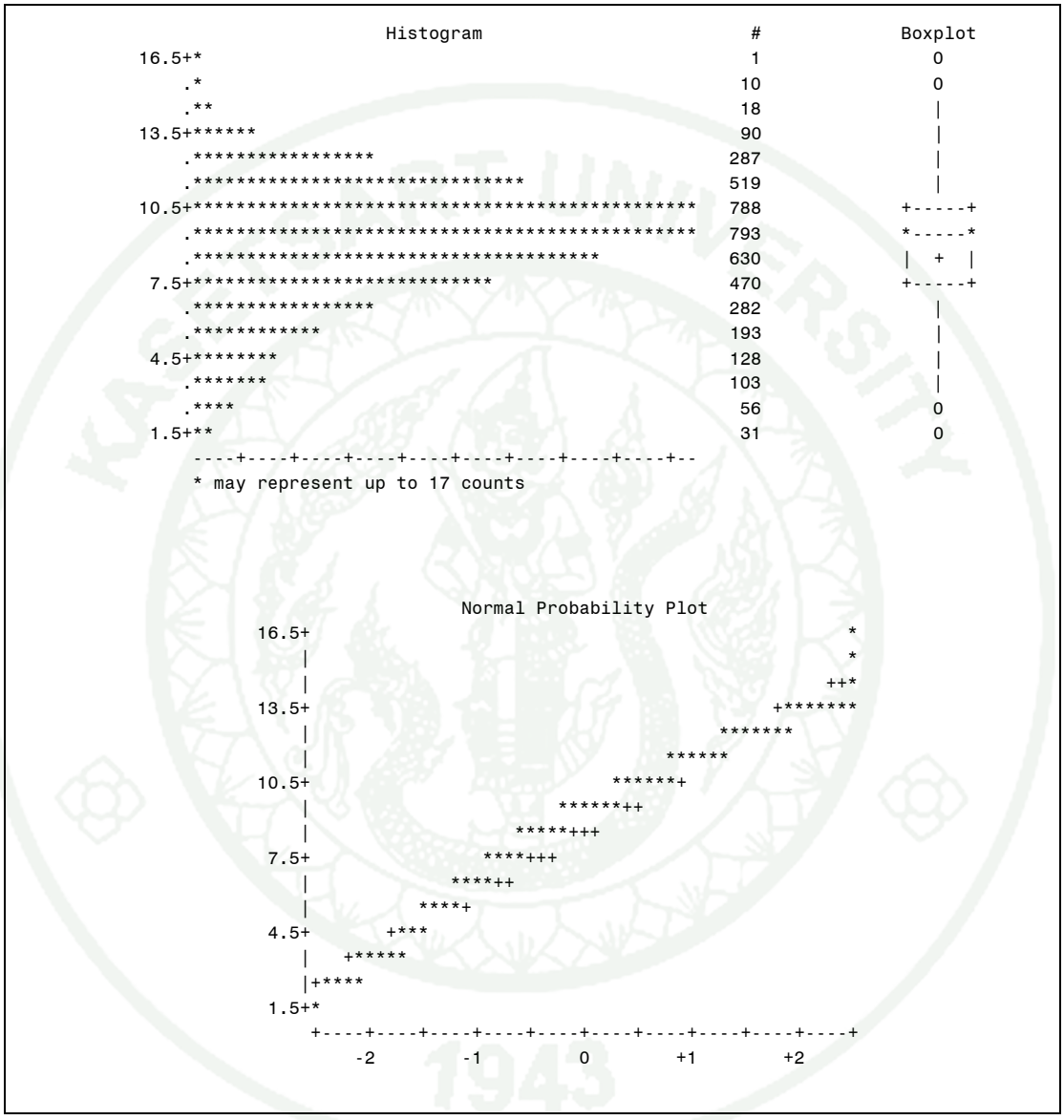
Appendix Figure A3 Histogram, box plot and normal probability plot for litter weight of live piglets at birth (LBW) range from 0.6 to 39.7 kg

Appendix Table A3 Basic and descriptive statistical values for litter weight of live piglets at birth (LBW) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (kg)	16.05
Median (kg)	16.00
Mode (kg)	13.00
Std Deviation (kg)	4.66
Variance (kg^2)	21.71
Range (kg)	39.10
Distribution parameters	
Number of observations	4,399.00
Mean (kg)	16.05
Std Deviation (kg)	4.66
Variance (kg^2)	21.71
Sum Weights (kg)	4,399.00
Sum Observations (kg)	70,612.00
Skewness	-0.08
Kurtosis	0.29
Uncorrected SS (kg^2)	12,28917.70
Corrected SS (kg^2)	95,465.88
Coefficient of Variation (%)	29.03
Std Error Mean (kg)	0.07

The UNIVARIATE Procedure for Genetic Analysis

Variable: NPW



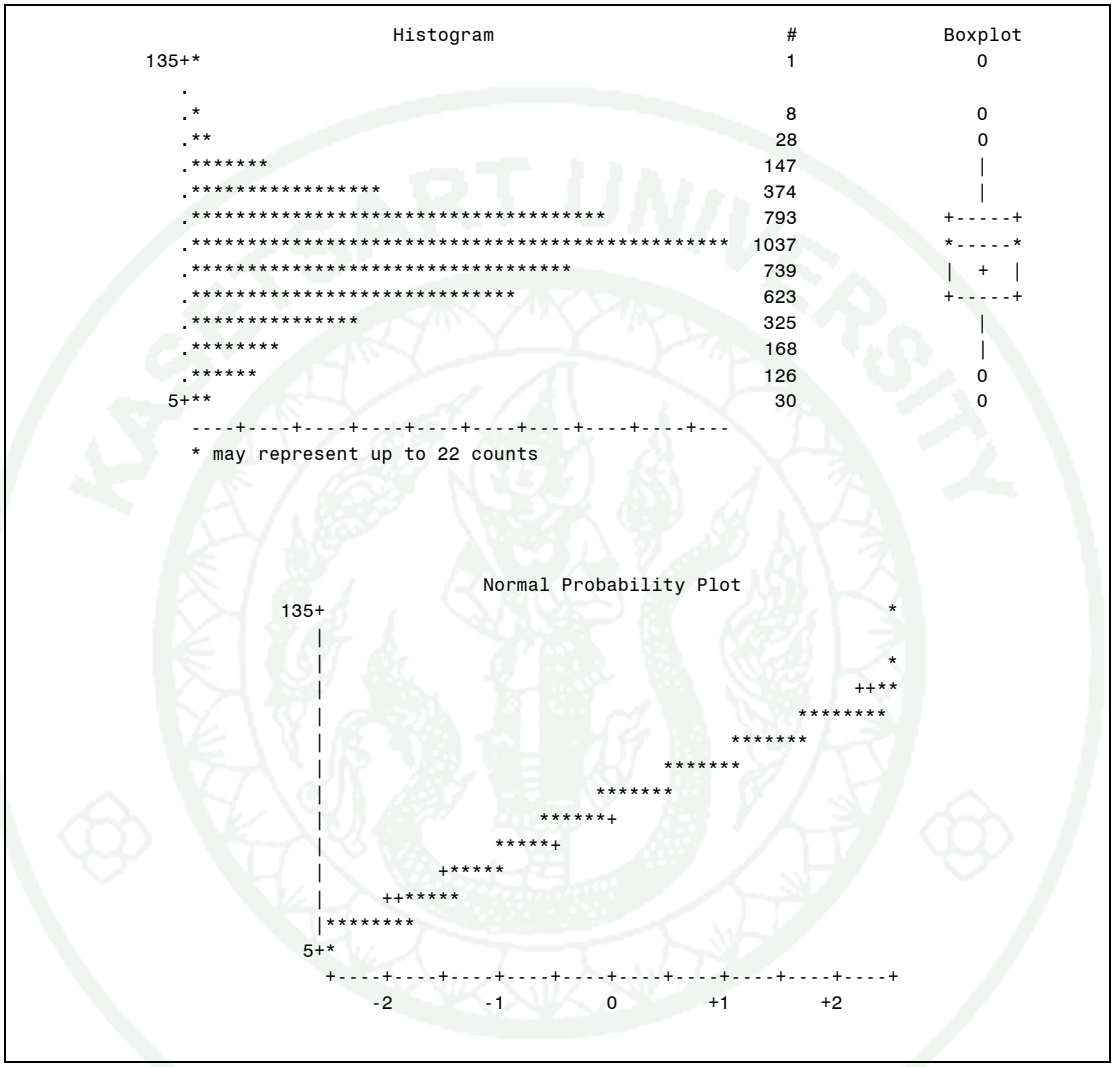
Appendix Figure A4 Histogram, box plot and normal probability plot for number of piglets at weaning (NPW) range from 1 to 16 piglets

Appendix Table A4 Basic and descriptive statistical values for number of piglets at weaning (NPW) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (piglets)	8.57
Median (piglets)	9.00
Mode (piglets)	9.00
Std Deviation (piglets)	2.47
Variance (piglets^2)	6.07
Range (piglets)	15.00
Distribution parameters	
Number of observations	4,399.00
Mean (piglets)	8.57
Std Deviation (piglets)	2.47
Variance (piglets^2)	6.07
Sum Weights (piglets)	4,399.00
Sum Observations (piglets)	37,709.00
Skewness	-0.61
Kurtosis	0.33
Uncorrected SS (piglets^2)	349,961.00
Corrected SS (piglets^2)	26,712.83
Coefficient of Variation (%)	28.75
Std Error Mean (piglets)	0.04

The UNIVARIATE Procedure for Genetic Analysis

Variable: LWW



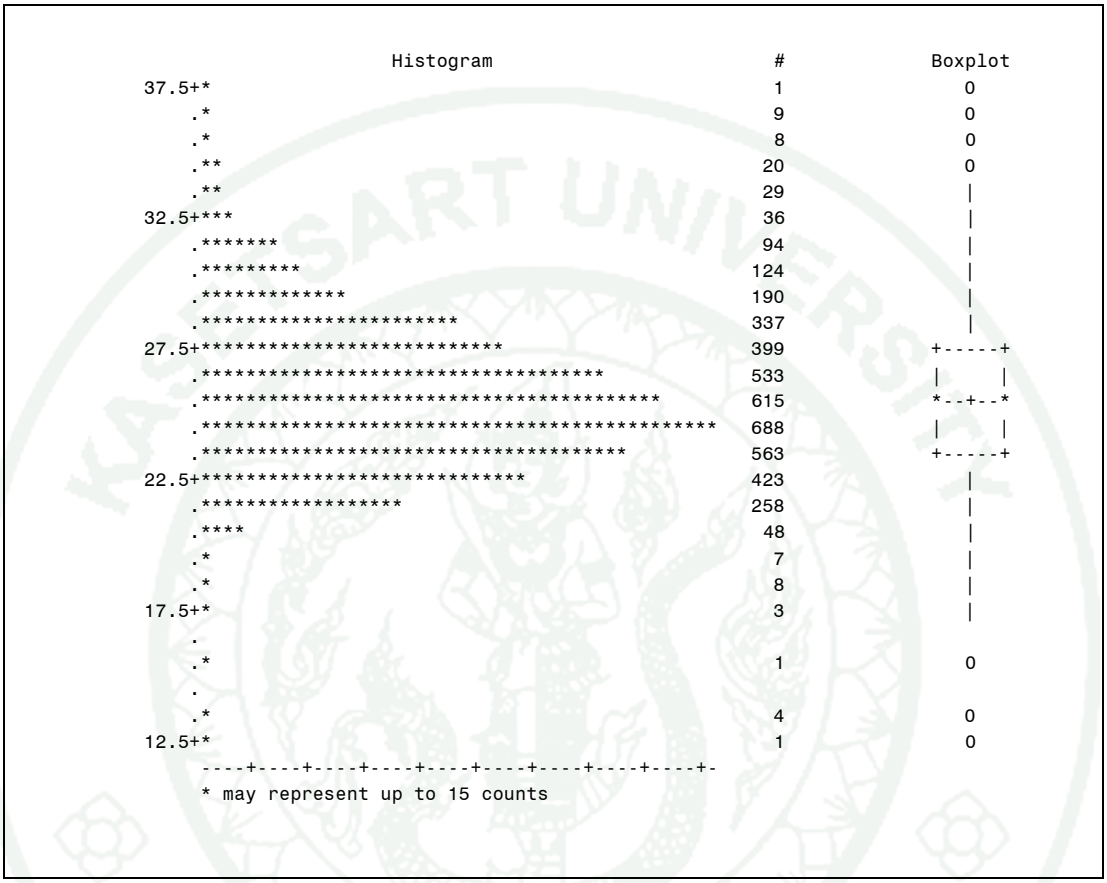
Appendix Figure A5 Histogram, box plot and normal probability plot for litter weight at weaning (LWW) range from 3.5 to 138.6 kg

Appendix Table A5 Basic and descriptive statistical values for litter weaning weight (LWW) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (kg)	59.39
Median (kg)	60.60
Mode (kg)	60.00
Std Deviation (kg)	19.12
Variance (kg^2)	365.47
Range (kg)	135.10
Distribution parameters	
Number of observations	4,399.00
Mean (kg)	59.39
Std Deviation (kg)	19.12
Variance (kg^2)	365.47
Sum Weights (kg)	4,399.00
Sum Observations (kg)	261,241.30
Skewness	-0.33
Kurtosis	0.05
Uncorrected SS (kg^2)	17,121,539.20
Corrected SS (kg^2)	1,607,327.63
Coefficient of Variation (%)	32.19
Std Error Mean (kg)	0.29

The UNIVARIATE Procedure for Genetic Analysis

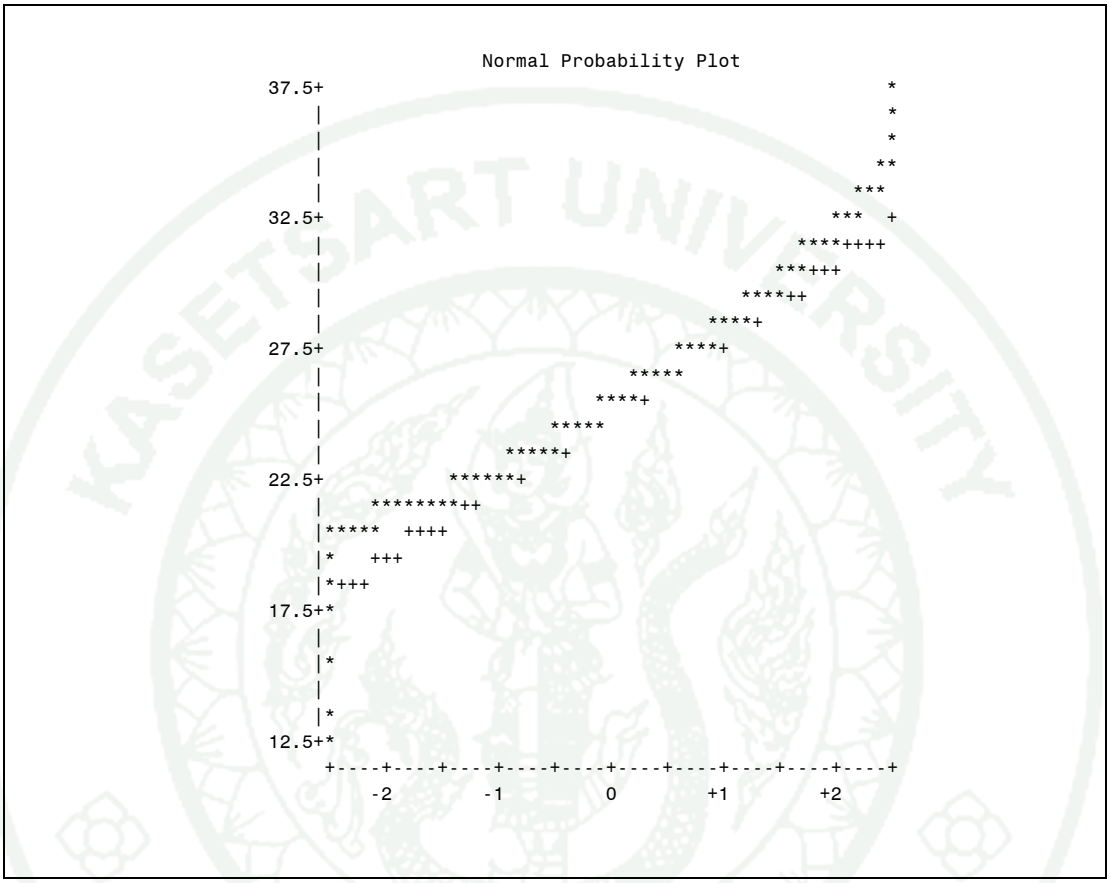
Variable: LL



Appendix Figure A6 Histogram and box plot for lactation length (LL) range from 12 to 37 days

The UNIVARIATE Procedure for Genetic Analysis

Variable: LL



Appendix Figure A7 Normal probability plot for lactation length range (LL) from 12 to 37 days

Appendix Table A6 Basic and descriptive statistical values for lactation length (LL) by UNIVARIATE procedure

Descriptive statistic	Value
Basic statistical measures	
Mean (days)	25.14
Median (days)	25.00
Mode (days)	24.00
Std Deviation (days)	2.85
Variance (days^2)	8.10
Range (days)	25.00
Distribution parameters	
Number of observations	4,399.00
Mean (days)	25.14
Std Deviation (days)	2.85
Variance (days^2)	8.10
Sum Weights (days)	4,399.00
Sum Observations (days)	110,568.00
Skewness	0.54
Kurtosis	0.88
Uncorrected SS (days^2)	2,814,740.00
Corrected SS (days^2)	35,635.06
Coefficient of Variation (%)	11.32
Std Error Mean (days)	0.04

The SAS program for descriptive statistic and test fixed effects

```
*VARIABLES DESCRIPTION;
/*
Litt  = Virtual piglets (records)
Sire  = Boar that mating with Sow
Dam   = Sow
Mgs   = Sire of the sow
Mgrd  = Dam of the sow
BgS   = Breed Group of Sire (Y=Large White; L=Landrace; LY=Landrace
        x Large White; YL=Large White x Landrace)
BgD   = Breed Group of Dam (Y=Large White; L=Landrace; LY=Landrace x
        Large White; YL=Large White x Landrace)
Het   = Heterosis proportion [0 = same breed(L×L,Y×Y); 0.5 =
        Crossbred(L×LY,Y×YL,…); 1 = different breed(L×Y,Y×L)]
Par   = Parity [1,2,3,4,5,6,7 and more than 7]
FYr   = Farrowing year
FMo   = Farrowing month
FSn   = Farrowing season
FYS   = Farrowing year-seaaon
Age   = Age at farrowing (month)
TPB   = Total Piglet Born (piglets)
NBA   = Number Born Alive (piglets)
LBW   = Litter Birth Weight (kg)
WYr   = Weaning year
WMo   = Weaning month
LL    = Lactation Lenght
NPW   = Number of Pig Weaned (pigs
WSI   = Weaning to First Service Interval
LWW   = Weaning weight
LL2   = Square of LL
NPD   = Number of piglets dead from NBA
npd2  = Number of piglets dead from TPB
*/
OPTION Nodate;

DATA WSIFourT;
INFILE D:\-SAS_TempDir-\ DataSAS20090619.txt ' DLM = '09'x;
INPUT Litt Sire Dam MgS MgD BgS BgD Het BgP Par FYr FMn FSn FYS Age
      TPB NBA LBW WYr WMn LL NPW LWW WSI LL2 NPD WST;
*ABW = LBW/NBA;
*AWW = LWW/NPW;

/* Run Univaritate Analyses */

PROC Univariate plots;
  Var WSI NBA LBW NPW LWW LL;
  Histogram WSI NBA LBW LWW NPW LL;

/* Test fixed effects for all studies traits */

PROC Mixed;       * For WSI
    Class FYS Sire Dam BgS BgD Het Par Age;
    Model WSI = FYS BgD Par Age LL /solution;
/*  Random Dam;    Repeated Dam;    */
    LSMeans FYS /adjust=bon;
    LSMeans BgD Par /adjust=bon;
```

```
PROC Mixed;       * For NBA
    Class FYS Sire Dam BgS BgD Het Par Age ;
    Model NBA = FYS BgS BgD Het Par Age /solution;
/*  Random Dam;    Repeated Dam;    */
    LSMeans FYS /adjust=bon;
    LSMeans BgS BgD Het Par /adjust=bon;

PROC Mixed;       * For LBW
    Class FYS Sire Dam BgS BgD Het Par Age;
    Model LBW = FYS BgS BgD Het Par Age /solution;
/*  Random Dam;    Repeated Dam;    */
    LSMeans FYS /adjust=bon;
    LSMeans BgS BgD Het Par /adjust=bon;

PROC Mixed;       * For NPW
    Class FYS Sire Dam BgS BgD Het Par Age;
    Model NPW = FYS BgS BgD Het Par Age LL /solution;
/*  Random Dam;    Repeated Dam;    */
    LSMeans FYS /adjust=bon;
    LSMeans BgS BgD Het Par /adjust=bon;

PROC Mixed;       * For LWW
    Class FYS Sire Dam BgS BgD Het Par Age;
    Model LWW = FYS BgS BgD Het Par Age LL /solution;
/*  Random Dam;    Repeated Dam;    */
    LSMeans FYS /adjust=bon;
    LSMeans BgS BgD Het Par /adjust=bon;

/* Contrast comparison between BGr in PROC Mixed */
    Estimate 'crossbred - purebred' BGr -1 1 -1 1;
    Estimate 'L - Y' BGr 1 0 -1 0;
    Estimate 'LY - YL' BGr 0 1 0 -1;
    Estimate 'YL - All' BGr 1 1 1 -3;
    Estimate 'Gilt VS Sow' Par 6 -1 -1 -1 -1 -1 -1;

/* Contrast comparison for Heterosis effects in PROC Mixed */
    Estimate 'Heterosis' BGr -0.5 0.5 -0.5 0.5;
    Estimate 'LY - purebred' BGr -0.5 1 -0.5 0;
    Estimate 'YL - purebred' BGr -0.5 0 -0.5 1;

RUN;
```

The ASReml programs for genetic evaluation

ASReml-Univariate analysis program :

```
Genetic Parameters Evaluation
 Litt              # Virtual piglets
 Sire !P           # Boar of VP
 Dam  !P           # Dam of VP, Sow with record
 Mgs               # Sire of sow
 Mgd               # Dam of sow
 BgS  !I 2         # Breed group of Boar that mating with Sow
 BgD  !I 4         # Breed group of sow : L = 1; Y = 2; LY = 3; YL = 4
 Het               # Heterosis group(regression) : 0 = same breed; 1 =
                   different breed; 0.5 = crossbred
 BgP  !I 4         # Breed of Virtual Piglets : L = 1; Y = 2; LY = 3;
                   YL = 4
 Par  7            # Parity 1 to 7 (7 and more)
 FYr  2008         # Farrowing year
 FMo  12           # Farrowing month
 FSn  3            # Farrowing season: 1 = Wither (Nov - Feb); 2 =
                   Summer (Mar to Jun); 3 = Rainny (Jul to Oct)
 FYS  56           # Contemporary Group (year-season; 56 categories)
 Age               # Farrowing Age of the sow
 TPB               # Total Piglet Born (piglet)
 NBA  !*5          # Number Born Alive (piglet)
 LBW  !*5          # Litter Birth Weight (kg)
 WYr  2008         # Weaning Year
 WMo  12           # Weaning Month
 LL                # Lactation Length (days)
 NPW  !*10         # Number of Pig Weaned (pig)
 LWW               # Weaning Weight
 WSI  !*5          # Weanining to First Service Interval (day)
 LL2               # Square of Lactation Length
 Npd               # Number Piglets death
 WST  !*5

Ped.csv     !skip 1 !csv !repeat !make
Data.csv    !skip 1 !csv !maxit 100 !asuv !mvremove !dopart 1

!part 1
 WSI ~ FYS BgD Par Age LL !r Dam ide(Dam)

!part 2
 NBA ~ FYS BgS BgD Het Par Age !r Sire Dam ide(Dam)

!part 3
 LBW ~ FYS BgS BgD Het Par Age !r Sire Dam ide(Dam)

!part 4
 NPW ~ FYS BgS BgD Het Par Age LL !r Sire Dam ide(Dam)

!part 5
 LWW ~ FYS BgS BgD Het Par Age LL !r Sire Dam ide(Dam)
```

ASReml-Multivariate analysis program :

```
Genetic Parameters Evaluation
 Litt              # Virtual piglets
 Sire !P           # Boar of VP
 Dam  !P           # Dam of VP, Sow with record
 Mgs               # Sire of sow
 Mgd               # Dam of sow
 BgS  !I 2         # Breed group of Boar that mating with Sow
 BgD  !I 4         # Breed group of sow : L = 1; Y = 2; LY = 3; YL = 4
 Het               # Heterosis group(regression) : 0 = same breed; 1 =
                   different breed; 0.5 = crossbred
 BgP  !I 4         # Breed of Virtual Piglets : L=1; Y=2; LY=3; YL=4
 Par  7            # Parity 1 to 7 (7 and more)
 FYr  2008         # Farrowing year
 FMo  12           # Farrowing month
 FSn  3            # Farrowing season: 1 = Wither (Nov - Feb); 2 =
                   Summer (Mar to Jun); 3 = Rainny (Jul to Oct)
 FYS  56           # Contemporary Group (year-season; 56 categories)
 Age               # Farrowing Age of the sow
 TPB               # Total Piglet Born (piglet)
 NBA  !*5          # Number Born Alive (piglet)
 LBW  !*5          # Litter Birth Weight (kg)
 WYr  2008         # Weaning Year
 WMo  12           # Weaning Month
 LL                # Lactation Length (days)
 NPW  !*10         # Number of Pig Weaned (pig)
 LWW               # Weaning Weight
 WSI  !*5          # Weanining to First Service Interval (day)
 LL2               # Square of Lactation Length
 Npd               # Number Piglets death

Ped.csv     !skip 1 !csv !repeat !make
Data2.csv   !skip 1 !csv !maxit 100 !asmv 2 !mvremove !dopart 1

!part 1     #= Multi-source of G structure ====================

 WSI NBA ~ Trait Tr.FYS at(Tr,2).BgS Tr.BgD at(Tr,2).Het Tr.Par ,
           Tr.Age at(Tr,1).LL !r !{ Tr.Dam at(Tr,2).Sire !} ,
           Tr.ide(Dam)

 1 2 2               # 1 R structure, 2 dimensions and 2 G structure
 0 0 0               # Independent across animals
 Trait 0 US !GP !+3  # General structure across traits
 535.536
 0 126.217
 Tr.Dam              # Effects of additive genetic
 3 0 US !GP !+6      # General structure across traits
 23.2550             # Dam effects for trait1(WSI); Tr1 direct
 0 7.02377           # Dam effects for trait2(NBA); Tr2 maternal
 0 0 1.97845         # Dam effects for trait2(NBA); Tr2 direct
 Dam
 Tr.ide(Dam)         # Effects of maternal permanent environment
 Trait 0 US !GP !+3  # General structure across traits
 18.7221
 0 18.0906
 ide(Dam)
```

```
!part 2     #= Multi-source of G structure ====================

 WSI LBW ~ Trait Tr.FYS at(Tr,2).BgS Tr.BgD at(Tr,2).Het Tr.Par ,
           Tr.Age at(Tr,1).LL !r !{ Tr.Dam at(Tr,2).Sire !} ,
           Tr.ide(Dam)

 1 2 2                # 1 R structure, 2 dimensions and 2 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 691.149
 0 281.002
 Tr.Dam               # Effects of additive genetic
 3 0 US !GP !+6       # General structure across traits
 10.1005              # Dam effects for trait1(WSI); Tr1 direct
 0 16.5899            # Dam effects for trait2(LBW); Tr2 maternal
 Dam
 at(Tr,2).Sire        # Effects of additive genetic for Trait2
 1 0 US !GP !+1       # General structure across traits
 5.25966              # Litt effects for trait2(LBW); Tr2 direct
 Sire
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 76.0055
 0 41.5922
 ide(Dam)



!part 3     #= Multi-source of G structure ====================

 WSI NPW ~ Trait Tr.FYS at(Tr,2).BgS Tr.BgD at(Tr,2).Het Tr.Par ,
           Tr.Age Tr.LL !r !{ Tr.Dam at(Tr,2).Sire !} Tr.ide(Dam)


 1 2 2                # 1 R structure, 2 dimensions and 2 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 691.149
 0 126.255
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 10.1005              # Dam effects for trait1(WSI); Tr1 direct
 0 7.54355            # Dam effects for trait2(NPW); Tr2 maternal
 Dam
 at(Tr,2).Sire
 1 0 US !GP !+1       # General structure across traits
 2.17475              # Litt effects for trait2(NPW); Tr2 direct
 Sire
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 112.141
 0 18.0906
 ide(Dam)
```

```
!part 4     #= Multi-source of G structure =====================

 WSI LWW ~ Trait Tr.FYS at(Tr,2).BgS Tr.BgD at(Tr,2).Het Tr.Par ,
           Tr.Age Tr.LL !r !{ Tr.Dam at(Tr,2).Sire !} Tr.ide(Dam)


 1 2 2                # 1 R structure, 2 dimensions and 2 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 702.170
 0 212.640
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 15.9827              # Dam effects for trait1(WSI); Tr1 direct
 0 7.55781            # Dam effects for trait2(LWW); Tr2 maternal
 Dam
 at(Tr,2).Sire        # Effects of additive genetic for trait 2
 1 0 US !GP !+1       # General structure across traits
 13.2197              # Litt effects for trait2(LWW); Tr2 direct
 Sire
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 56.2445
 0 16.8175
 ide(Dam)



!part 5     #= Separated G structure ============================

 NBA LBW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age ,
           !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 161.891
 0 324.374
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 5.67276              # Sire effects for trait1(NBA); Tr1 direct
 0 14.4398            # Sire effects for trait2(LBW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 7.64661              # Dam effects for trait1(NBA); direct+maternal
 0 17.0292            # Dam effects for trait2(NBA); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 18.7092
 0 35.6901
 ide(Dam)
```

```
!part 6     #= Separated G structure ============================

 NBA NPW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age ,
           at(Tr,2).LL !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 111.110
 0 212.640
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 6.16320              # Sire effects for trait1(NBA); Tr1 direct
 0 13.2197            # Sire effects for trait2(NPW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 5.50623              # Dam effects for trait1(NBA); direct+maternal
 0 7.55781            # Dam effects for trait2(NPW); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 8.06601
 0 16.8175
 ide(Dam)



!part 7     #= Separated G structure ============================

 NBA LWW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age ,
           at(Tr,2).LL !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 212.640
 0 161.891
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 13.2197              # Sire effects for trait1(NBA); Tr1 direct
 0 5.67276            # Sire effects for trait2(LWW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 7.55781              # Dam effects for trait1(NBA); direct+maternal
 0 7.64661            # Dam effects for trait2(LWW); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 16.8175
 0 18.7092
 ide(Dam)
```

```
!part 8     #= Separated G structure ============================

 LBW NPW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age ,
           at(Tr,2).LL !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 459.990
 0 281.002
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 7.32849              # Sire effects for trait1(LBW); Tr1 direct
 0 5.25966            # Sire effects for trait2(NPW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 30.7043              # Dam effects for trait1(LBW); direct+maternal
 0 16.5899            # Dam effects for trait2(NPW); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 45.1349
 0 40.6529
 ide(Dam)



!part 9     #= Separated G structure ============================

 LBW LWW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age ,
           at(Tr,2).LL !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 212.640
 0 324.374
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 13.2197              # Sire effects for trait1(LBW); Tr1 direct
 0 14.4398            # Sire effects for trait2(LWW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 7.55781              # Dam effects for trait1(LBW); direct+maternal
 0 17.0292            # Dam effects for trait2(LWW); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 16.8175
 0 35.6901
 ide(Dam)
```

```
!part 10    #= Separated G structure ============================

 NPW LWW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age Tr.LL ,
           !r Tr.Sire Tr.Dam Tr.ide(Dam)

 1 2 3                # 1 R structure, 2 dimensions and 3 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 111.110
 0 212.640
 Tr.Sire              # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 6.16320              # Sire effects for trait1(NPW); Tr1 direct
 0 13.2197            # Sire effects for trait2(LWW); Tr2 direct
 Sire
 Tr.Dam               # Effects of additive genetic
 Trait 0 US !GP !+3   # General structure across traits
 5.50623              # Dam effects for trait1(NPW); direct+maternal
 0 7.55781            # Dam effects for trait2(LWW); direct+maternal
 Dam
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 8.06601
 0 16.8175
 ide(Dam)



!part 11    #= Multi-source of G structure =====================

 NPW LWW ~ Trait Tr.FYS Tr.BgS Tr.BgD Tr.Het Tr.Par Tr.Age Tr.LL ,
           !r !{ Tr.Sire Tr.Dam !} Tr.ide(Dam)

 1 2 2                # 1 R structure, 2 dimensions and 2 G structure
 0 0 0                # Independent across animals
 Trait 0 US !GP !+3   # General structure across traits
 111.110
 0 161.891
 Tr.Sire              # Effects and co-effects of additive genetic
 4 0 US !GP !+10      # General structure across traits
 5.50623              # Sire effects for trait1(NPW); Tr1 direct
 0 7.64661            # Sire effects for trait2(NBA); Tr2 direct
 0 0 6.16320          # Dam effects for trait1(NPW); direct+maternal
 0 0 0 5.67276        # Dam effects for trait2(NBA); direct+maternal
 Sire
 Tr.ide(Dam)          # Effects of maternal permanent environment
 Trait 0 US !GP !+3   # General structure across traits
 8.06601
 0 16.817518.7092
 ide(Dam)
```

ASReml : Pin-file for pair-wise analysis between WSI and litter traits at birth.

```
F  Env11     1 * 0.04              # 13
F  Env21     2 * 0.04              # 14
F  Env22     3 * 0.04              # 15
F  Gen11     4 * 0.04              # 16 COV(D1,D1) ; DamTr1 and DamTr1
F  Gen31     7 * 0.04              # 17 COV(D1,S2) ; DamTr1 and SireTr2
F  Gen33     9 * 0.04              # 18 COV(S2,S2) ; SireTr2 and SireTr2
F  Gen21     5 * 0.04              # 19 COV(D1,D2) ; DamTr1 and DamTr2
F  Gen32     8 * 0.04              # 20 COV(S2,D2) ; SireTr2 and DamTr2
F  Gen22     6 * 0.04              # 21 COV(D2,D2) ; DamTr2 and DamTr2
F  EnvP11    8 * 0.04              # 22
F  EnvP21    9 * 0.04              # 23
F  EnvP22    10 * 0.04             # 24

F  Gen11     16                    # 25 COV direct Tr1 direct Tr1
F  Gen31     17 * 2                # 26 COV direct Tr1 direct Tr2
F  Gen33     18 * 4                # 27 COV direct Tr2 direct Tr2
F  Mat11     16 * 0                # 28 COV maternal Tr1 maternal Tr1
F  Mat21     19 - 17               # 29 COV direct Tr1 maternal Tr2
F  Mat32/2   20 - 18               # 30 COV direct Tr2 maternal Tr2
F  Mat32     30 * 2                # 31
F  Mat22     21 - 18 - 26 - 26     # 32 COV maternal Tr2 maternal Tr2

F  GPe11     16 + 22               # 33 Gen + Permanent Env Tr1 Tr1
F  GPe21     17 + 19 + 23          # 34 Gen + Permanent Env Tr2 Tr1
F  GPe22     18 + 24               # 35 Gen + Permanent Env Tr2 Tr2

F  Phe11     16 + 22 + 13          # 36 Phenotypic Tr1 Tr1
F  Phe21     17 + 19 + 23 + 14     # 37 Phenotypic Tr2 Tr1
F  Phe22     18 + 24 + 15          # 38 Phenotypic Tr2 Tr2

H  H2d11     25 36                 # 39 Heritability direct Tr1
H  H2d22     27 38                 # 40 Heritability direct Tr2
H  H2m22     32 38                 # 41 Heritability maternal Tr2

H  t11       33 36                 # 42 repeatability Tr1
H  t22       35 38                 # 43 repeatability Tr2

R  DirGenCor21     25 26 27        # 44
R  MatGenCor21     25 29 32        # 45
R  MatGenCor32     27 31 32        # 46

R  PeCor21         22 23 24        # 47 Permanent Env Correlation
R  PheCor21        36 37 38        # 48 Phenotypic Correlation
```

ASReml : Pin-file for pair-wise analysis between NBA and LBW.

```
F  Phe11     1 * 0.04              # 13
F  Phe21     2 * 0.04              # 14
F  Phe22     3 * 0.04              # 15
F  Gen11     4 * 0.04              # 16
F  Gen21     5 * 0.04              # 17
F  Gen22     6 * 0.04              # 18
F  Dam11     7 * 0.04              # 19
F  Dam21     8 * 0.04              # 20
F  Dam22     9 * 0.04              # 21
F  Pe11      10 * 0.04             # 22
F  Pe21      11 * 0.04             # 23
F  Pe22      12 * 0.04             # 24

F  Phe11     13 + 16 + 19 + 22     # 25
F  Phe21     14 + 17 + 20 + 23     # 26
F  Phe22     15 + 18 + 21 + 24     # 27

F  Gen11     16 * 4                # 28 Direct variance 1
F  Gen21     17 * 4                # 29 Direct covariance 12
F  Gen22     18 * 4                # 30 Direct variance 2

F  Mat11     19 - 16               # 31 Maternal variance 1
F  Mat21     20 - 17               # 32 Maternal covariance 12
F  Mat22     21 - 18               # 33 Maternal variance 2

F  Pe11      22                 # 34 Permanent environment variance 1
F  Pe21      23                 # 35 Permanent environment covariance 12
F  Pe22      24                 # 36 Permanent environment variance 2

F  GPe11     16 + 19 + 22          # 37
F  GPe21     17 + 20 + 23          # 38
F  GPe22     18 + 21 + 24          # 39

H  H2D11     28 25                 # 40 Direct heritability 1
H  H2D22     30 27                 # 41 Direct heritability 2
H  H2M11     31 25                 # 42 Maternal heritability 1
H  H2M22     33 27                 # 43 Maternal heritability 2

H  t11       37 25                 # 44 Repeatability 1
H  t22       39 27                 # 45 Repeatability 2

R  DirGenCor12     28 29 30        # 46 Direct genetic correlation 12
R  MatGenCor12     31 32 33        # 47 Maternal genetic correlation 12

R  PeCor12         34 35 36        # 48 Permanent Env correlation 12

R  PhenCor12       13 14 15        # 49 Phenotypic correlation 12
```

ASReml : Pin-file for pair-wise analysis between NPW and LWW .

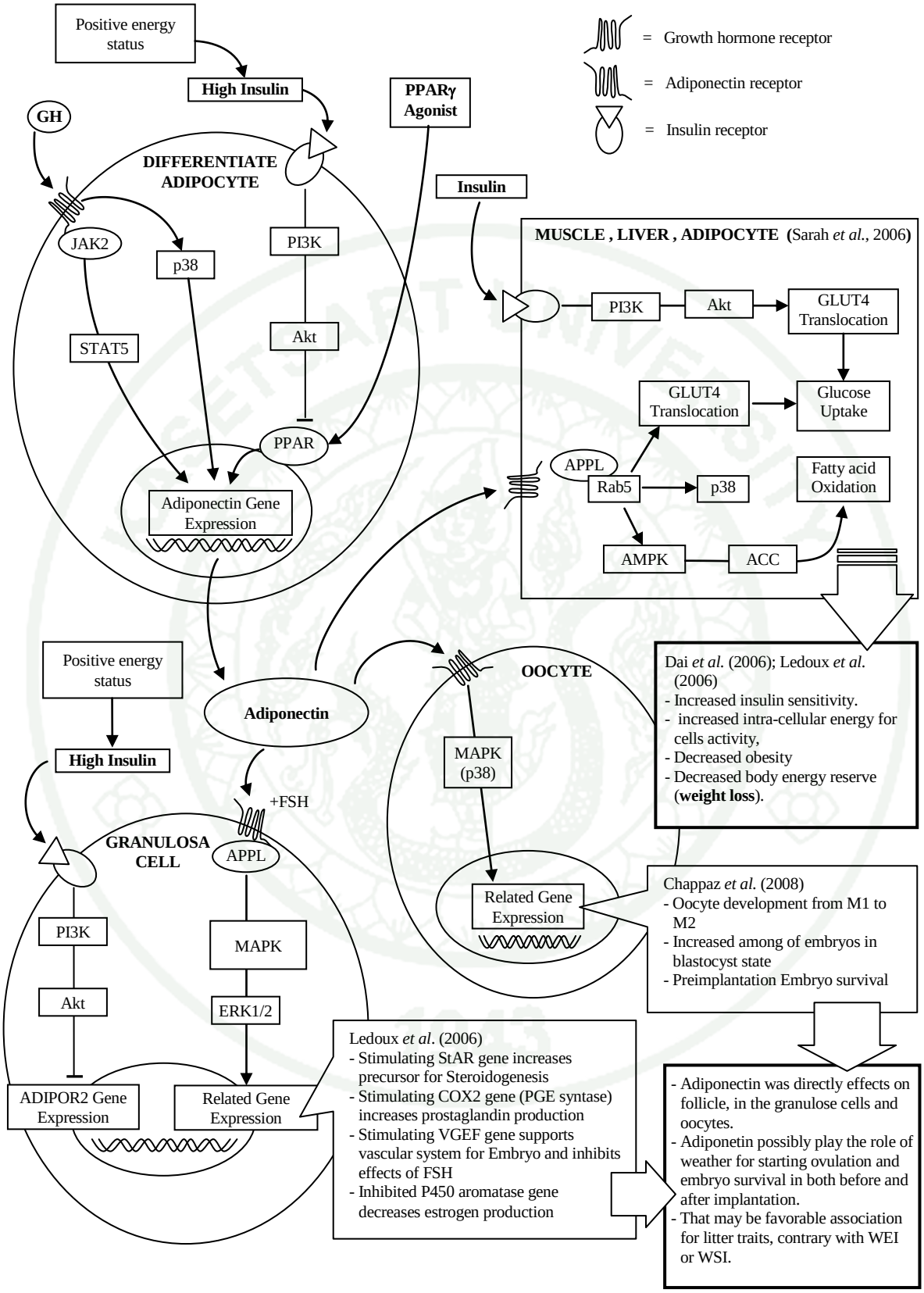
```
F  Phe11     1 * 0.01              # 13
F  Phe21     2 * 0.1               # 14
F  Phe22     3                     # 15
F  Gen11     4 * 0.01              # 16
F  Gen21     5 * 0.1               # 17
F  Gen22     6                     # 18
F  Dam11     7 * 0.01              # 19
F  Dam21     8 * 0.1               # 20
F  Dam22     9                     # 21
F  Pe11      10 * 0.01             # 22
F  Pe21      11 * 0.1              # 23
F  Pe22      12                    # 24

F  Phe11     13 + 16 + 19 + 22     # 25
F  Phe21     14 + 17 + 20 + 23     # 26
F  Phe22     15 + 18 + 21 + 24     # 27

F  Gen11     16 * 4                # 28 Direct variance 1
F  Gen21     17 * 4                # 29 Direct covariance 12
F  Gen22     18 * 4                # 30 Direct variance 2

F  Mat11     19 - 16               # 31 Maternal variance 1
F  Mat21     20 - 17               # 32 Maternal covariance 12
F  Mat22     21 - 18               # 33 Maternal variance 2

F  Pe11      22                 # 34 Permanent environment variance 1
F  Pe21      23                 # 35 Permanent environment covariance 12
F  Pe22      24                 # 36 Permanent environment variance 2

F  GPe11     16 + 19 + 22          # 37
F  GPe21     17 + 20 + 23          # 38
F  GPe22     18 + 21 + 24          # 39

H  H2D11     28 25                 # 40 Direct heritability 1
H  H2D22     30 27                 # 41 Direct heritability 2
H  H2M11     31 25                 # 42 Maternal heritability 1
H  H2M22     33 27                 # 43 Maternal heritability 2

H  t11       37 25                 # 44 Repeatability 1
H  t22       39 27                 # 45 Repeatability 2

R  DirGenCor12     28 29 30        # 46 Direct genetic correlation 12
R  MatGenCor12     31 32 33        # 47 Maternal genetic correlation 12

R  PeCor12         34 35 36        # 48 Permanent Env correlation 12

R  PhenCor12       13 14 15        # 49 Phenotypic correlation 12
```

ASReml : Pin-file for pair-wise analysis between litter trait at birth and weaning.

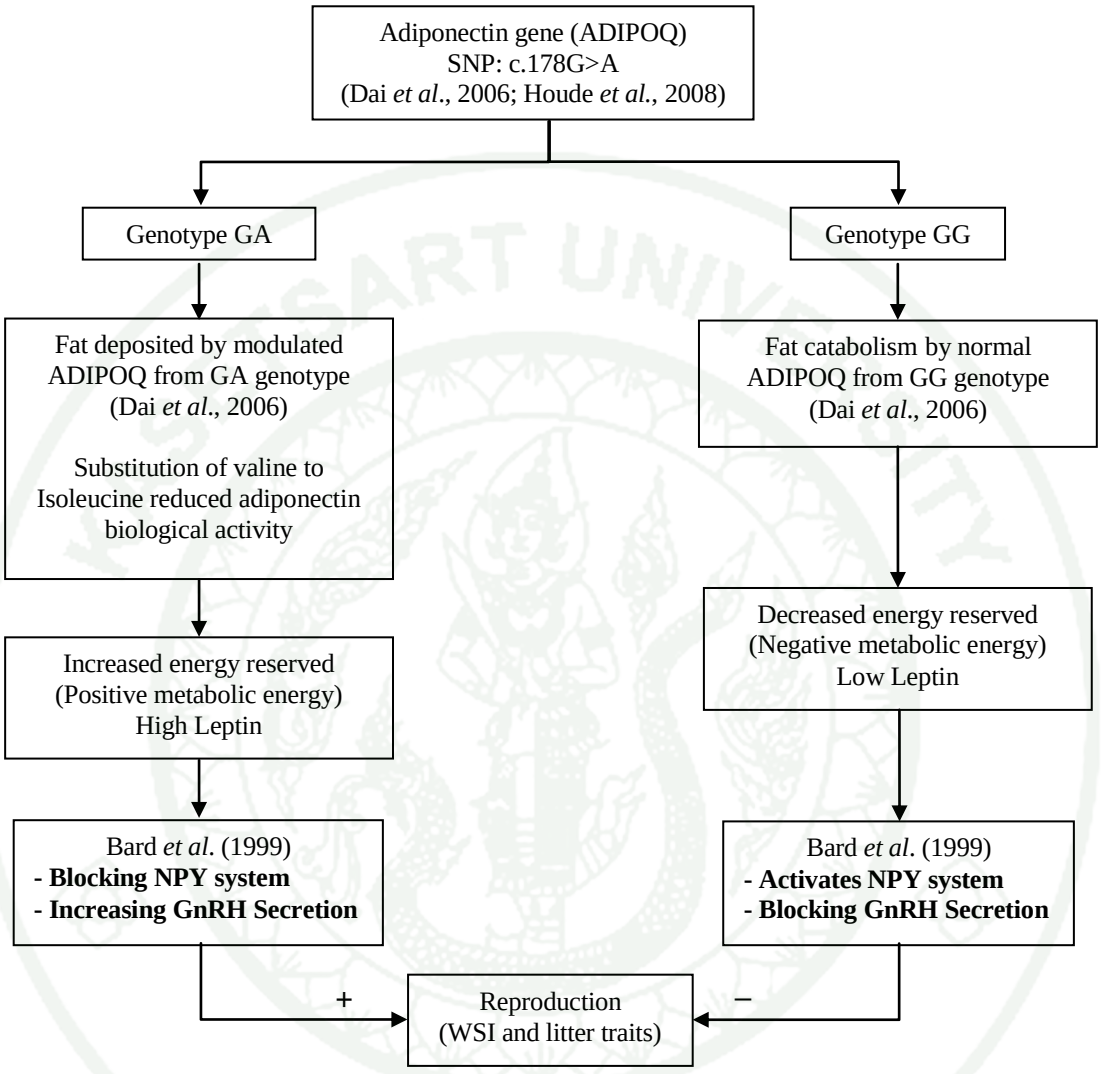
```
F  Phe11     1 * 0.01              # 13
F  Phe21     2 * 0.02              # 14
F  Phe22     3 * 0.04              # 15
F  Gen11     4 * 0.01              # 16
F  Gen21     5 * 0.02              # 17
F  Gen22     6 * 0.04              # 18
F  Dam11     7 * 0.01              # 19
F  Dam21     8 * 0.02              # 20
F  Dam22     9 * 0.04              # 21
F  Pe11      10 * 0.01             # 22
F  Pe21      11 * 0.02             # 23
F  Pe22      12 * 0.04             # 24

F  Phe11     13 + 16 + 19 + 22     # 25
F  Phe21     14 + 17 + 20 + 23     # 26
F  Phe22     15 + 18 + 21 + 24     # 27

F  Gen11     16 * 4                # 28 Direct variance 1
F  Gen21     17 * 4                # 29 Direct covariance 12
F  Gen22     18 * 4                # 30 Direct variance 2

F  Mat11     19 - 16               # 31 Maternal variance 1
F  Mat21     20 - 17               # 32 Maternal covariance 12
F  Mat22     21 - 18               # 33 Maternal variance 2

F  Pe11      22                 # 34 Permanent environment variance 1
F  Pe21      23                 # 35 Permanent environment covariance 12
F  Pe22      24                 # 36 Permanent environment variance 2

F  GPe11     16 + 19 + 22          # 37
F  GPe21     17 + 20 + 23          # 38
F  GPe22     18 + 21 + 24          # 39

H  H2D11     28 25                 # 40 Direct heritability 1
H  H2D22     30 27                 # 41 Direct heritability 2
H  H2M11     31 25                 # 42 Maternal heritability 1
H  H2M22     33 27                 # 43 Maternal heritability 2

H  t11       37 25                 # 44 Repeatability 1
H  t22       39 27                 # 45 Repeatability 2

R  DirGenCor12     28 29 30        # 46 Direct genetic correlation 12
R  MatGenCor12     31 32 33        # 47 Maternal genetic correlation 12

R  PeCor12         34 35 36        # 48 Permanent Env correlation 12

R  PhenCor12       13 14 15        # 49 Phenotypic correlation 12
```

Appendix B

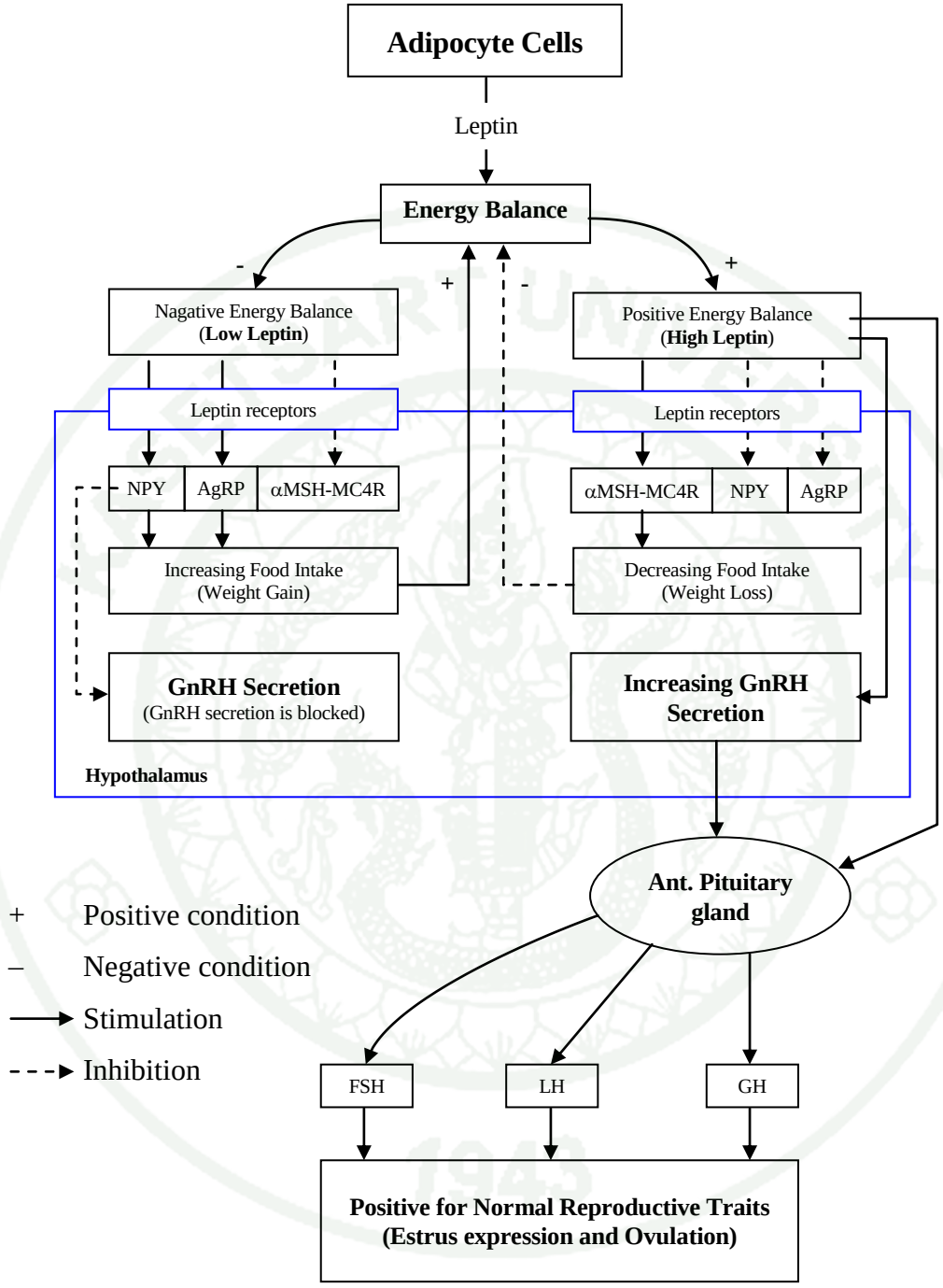
Regulation pathways for ADIPOQ and FSHR genes related to reproductive traits



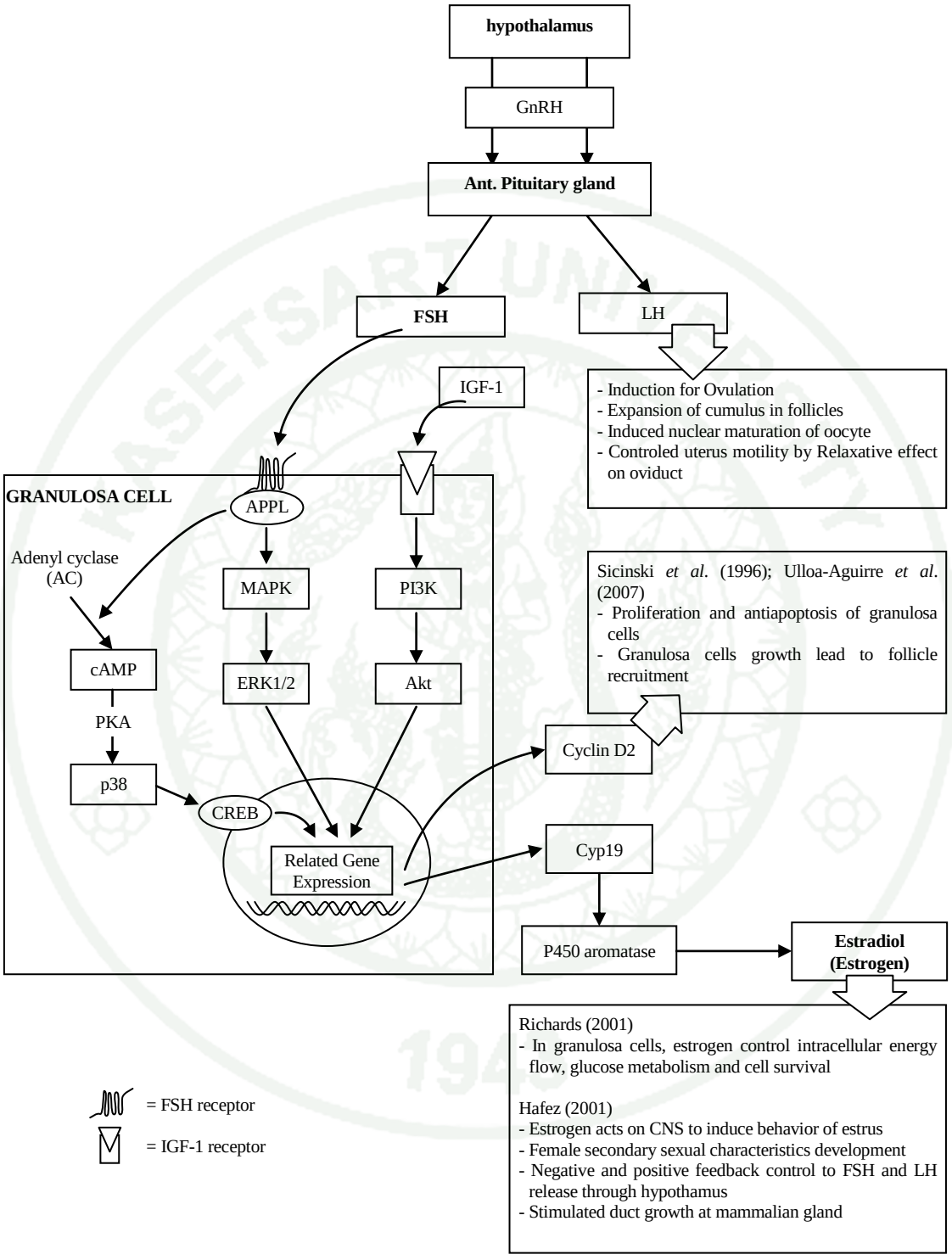
Appendix Figure B1 Regulation pathways of adiponectin relating to reproductive and productive traits



Appendix Figure B2 Association diagram and regulating mechanisms for reproduction of swine (WSI and litter traits) by adiponectin polymorphisms (GG and GA genotypes)



Appendix Figure B3 Mechanisms of body weight loss regulating GnRH secretion affects to swine reproduction (NPY = Neuropeptide Y, AgRP = Agouti-related protein, αMSH = α Melatonin stimulating hormone and MC4R = Melanocortin receptor type 4)



Appendix Figure B4 Association diagram and mechanism pathways of FSH and FSHR controling the expression of reproductive traits

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PUBLICATIONS

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