Genotypic Polymorphisms for Adiponectin and Follicle Stimulating Hormone Receptor Genes Related to Weaning-to-First Service Interval and Litter Traits in a Swine Population in Northern Thailand

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Abstract

The objectives of this research were to estimate the allele frequencies of previously identified polymorphism in the ADIPOQ and FSHR genes and to evaluate their association with weaning-to-first service interval (WSI), number of piglets born alive (NBA), total litter birth weight (LBW), number of piglets at weaning (NPW) and total litter weaning weight (LWW) in a commercial swine population consisted of Landrace (L), Large White (W), L × W and W × L sows in northern Thailand. The dataset consisted of 470 records for WSI, NBA, and LBW, and 330 records for NPW and LWW from 363 sows. Blood samples were also collected from these 363 sows. One SNP and 2 alleles were studied for the ADIPOQ (G and A) and FSHR (C and T) genes. The SNP for ADIPOQ was AJ849536: g.1716G>A and the SNP for FSHR was SNP as AF025377: g.1166C>T. Associations between traits and alleles and genotypes were performed using linear models. Allele substitution effects were modeled as regressions of traits on numbers of G alleles for ADIPOQ and numbers of T alleles for FSHR. The allelic model included year-season, parity of sow, breed group of sow, number of G alleles, number of T alleles, age of sow at farrowing , lactation length, number of piglets weaned, and residual. The genotypic model substituted genotype of the sow at the ADIPOQ locus and genotype of the sow at the FSHR locus for numbers of G and T alleles. Neither allelic nor genotypic effects were significant for either the ADIPOQ or the FSHR gene. Small numbers of animals, tropical environmental conditions and genetic similarity among animals due to intra-herd replacement of boars and gilts during the period of the study may have contributed to the lack of significant differences among allelic and genotypic effects in this population. Thus, the ADIPOQ and FSHR genes will be of little help for selecting pigs in this population.

Keywords: adiponectin, follicle stimulating hormone receptor, litter traits, polymorphism, service interval, swine, tropical

Introduction

Sow efficiency can be improved by decreasing the period of weaning-to-first service interval (WSI) and increasing litter trait performance (number of piglets at birth and at weaning). Previous studies have found low values of heritability for WSI and litter traits suggesting that these traits are influenced by environmental effects (Holm et al., 2005; Imboonta et al., 2007). Consequently, genetic improvement for WSI and litter traits based on quantitative selection is expected to be slow. However, if genes with known effects on WSI and litter traits were used to

predict the genetic value of animals for these traits, then the accuracy of prediction and the rate of genetic progress for these traits would increase.

Studies dealing with associations between specific alleles of candidate genes and WSI are lacking. However, there are some swine association studies between genes and weaning-to-estrus interval (WEI) and litter traits in temperate regions. Houde et al. (2008) found shorter WEI, but similar number of piglets born alive (NBA) in Landrace sows with the GA genotype than in sows with the GG genotype in both the adiponectin (c.178G>A) and the adiponectin receptor (c.*112G>A; $P < 0.01$) genes. Adiponectin (ADIPOQ) and its receptors are important factors for fatty-acid oxidation and glucose metabolism to regulate energy homeostasis in mice (Yamauchi et al., 2002; Kadowaki and Yamauchi, 2005) and decrease fat deposition in the pig carcass (Dai et al., 2006). Reduction of fat deposition directly affected energy reserves that were relevant negative effects for reproduction of sows (Barb et al., 2008). Substitution of A for G at position 178 of the coding region of ADIPOQ (SNP c.178G>A) contributed to a higher fat deposition in the pig carcass (Dai et al., 2006). Interestingly, higher fat deposition is also known to be associated with the higher energy reserves needed for re-establishment of estrus and ovulation (Barb et al., 2008; Quesnel et al., 2007). In addition, Li et al. (2008) reported different WEI according to the follicle stimulating hormone β subunit (FSHB) microsatellite polymorphism present in a crossbred Large White × Meishan population in China. Follicle stimulating hormone (FSH) is known to stimulate the proliferation and differentiation of granulosa cells in antral follicles and the production of estrogen regulated by FSH receptor (FSHR) in the ovary (Ulloa-Aguirre et al., 2007). The WSI depends on the expression of estrus, which in turn depends on estrogen activity. Polymorphisms in the FSHR gene may affect FSH signal transduction, the production of estrogen and, indirectly, the length of WSI. Association studies between FSHR gene polymorphisms and WSI are lacking in the literature. However, association between FSHR polymorphisms in exon 10 and litter size was reported in German Landrace sows (T/C genotype had larger litter sizes than C/C and T/T genotypes) and Chinese Erhualian sows (larger litter sizes in sows with the TT genotype; Jiang et al., 2002).

Thus, the objectives of this research were to estimate the allele frequencies of previously identified polymorphisms in the ADIPOQ and FSHR genes and to evaluate the association between specific genotypes and reproductive traits in a commercial swine population composed of Landrace (L), Large White (W), L × W and W × L sows in northern Thailand.

Materials and Methods

Animals, Traits and Data

Sows in this study (n = 363) were from a commercial Landrace – Large White population in the province of Chiang Mai (18° 28' 30" N, 98° 47' 59" E; elev. 288 m), northern Thailand. All sows were kept in an open-house system. Sows belonged to 4 breed groups: Landrace (L; n = 120), Large White (W; n = 120), L × W (LW; n = 26), and W × L (WL; n = 97) and all of them were related through their sires. Purebred boars (L or W) were used to mate to sows in different breed groups (L or W). Thus, all breed groups of sows were connected. This commercial herd has been maintained as a closed population since 2002.

The initial dataset contained reproductive records (n = 619) from 363 sows collected from 2006 to 2009. Records contained information on weaning-to-first service interval (WSI), number of piglets born alive (NBA), total litter birth weight (LBW), number of piglets at weaning (NPW) and total litter weaning weight (LWW). The initial 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 contained 470 records for WSI and litter traits at birth (NBA and LBW) and 330 records for litter traits at weaning (NPW and LWW). Table 1 contains means, standard deviations, minima, and maxima for WSI and litter traits at birth and weaning.

Parities of sows were classified in 4 groups (1, 2, 3, and ≥ 4 parities). Seasons were classified as winter (November to February; cool [13°C to 29°C] and dry [70% RH]), summer (March to June; hot [20°C to 34°C] and dry [68% RH]), and rainy season

Table 1 Descriptive statistics for weaning-to-first service interval, number of piglets born alive, litter birth weight, number of piglets at weaning and litter weaning weight.

Trait[1/]	Number of record	Mean	Standard deviation	Min	Max
WSI (d)	470	7.23	4.54	1.0	30.0
NBA (piglet)	470	10.18	2.89	1.0	18.0
LBW (kg)	470	16.94	4.89	1.5	29.6
NPW (piglet)	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 birth weight, NPW = number of piglets at weaning, and LWW = litter weaning weight.

(July to October; hot [23°C to 31°C] and humid [83% RH]). From 2006-winter to 2009-summer, 11 categories for farrowing year-season combinations were created. Age at farrowing of sow ranged from 10 to 37 mo (mean = 16.59 mo, SD = 5.19 mo). Lactation length ranged from 20 to 31 d (mean = 24.83 d, SD = 2.16 d).

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 kept 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.

DNA Amplification and Fragmentation

The porcine adiponectin gene (ADIPOQ; GenBank accession No. AJ849536) was amplified by using the following forward: 5'-TCAGGATGCTGTTGTTGGGA-3' and reverse: 5'-CCCTGTGAATAGGCCTTTGG-3' primers (Table 2; Houde et al., 2008). The total volume of the PCR mixture was 12.6 μL and included 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: 1) An initial denaturation at 94°C for 5 min, 2) 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 3) a final elongation period of 5 min at 72°C. 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 nt by using the *Bsa*HI restriction enzyme (Houde et al., 2008).

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'-GCAACAAATCTATTTTAAGGCAAGA-3', and the reverse primer (outer primer) was 5'-GATGCTCACCTTCATGTAGCTG-3'. 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 (GenBank accession no. AF025377). These inner primers were: forward primer 5'-ATGGTTTATTAGTATCCTTGCCAC-3' (positions 1143 nt to 1166 nt) and reverse primer 5'-AGCACTATGATGTTCCCAGTGA-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 fragment 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 fragment 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 2) and it had a total volume of 10.07 μL. In the second step, 1.0 μL of genomic DNA was added to the PCR mixture. The PCR amplification protocol had the following steps: 1) an initial denaturation period of 5 min at 94°C, 2) 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 3) an additional elongation period of 5 min at 72°C.

Genotyping

Separation of the products of the digestion process for the SNP of the ADIPOQ gene (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 UV light after being stained with ethidium bromide (Fermentas, USA). The ADIPOQ gene 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 181 and 145 bp, whereas those having the GA genotype show 3 bands of 326 bp (for the uncut portion), 181 and 145 bp (Houde et al., 2008).

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 (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 674 and 442 bp was associated with the CC genotype, whereas in CT animals, 3 fragments of 674, 442 and 277 bp were observed. Finally, the TT genotype was identified with the presence of 2 fragments of 674 and 277 bp.

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, 2003). In addition, allele and genotype frequencies for ADIPOQ and FSHR among breed groups were compared using Chi-square tests. The 4 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 gene and number of T alleles for the FSHR gene in a linear model that accounted for fixed genetic and environmental effects. The linear model included farrowing year-season (11 year-season combinations), parity of sow (1, 2, 3, and ≥ 4 parities), and breed group of sow (L, W, LW and WL) as fixed subclass effects, age of sow at farrowing, lactation length, number of piglets weaned, number of G alleles in the ADIPOQ locus, and 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, 2003).

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 of year-season, parity of sow, breed group of sow, genotype of the sow at the ADIPOQ locus, genotype of the sow at the FSHR locus, the covariate effects of age of sow at farrowing , lactation length, and number of piglets weaned, and random residual effects.

Results and Discussion

Allele and Genotype Frequencies

Allele and genotype frequencies for the ADIPOQ and FSHR genes are shown in Table 3. All breed groups and the whole population (all groups) 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).

Table 2 Primer sequences used to amplify PCR product for swine adeponectin (ADIPOQ) and follicle stimulating hormone receptor (FSHR) genes.

Gene	Primer sequence (5'to 3')	bp[1/]	Position (nt)	GenBank Acc No.
ADIPOQ	F: TCA GGA TGC TGT TGT TGG GA	20	1537 - 1557	AJ849536
	R: CCC TGT GAA TAG GCC TTT GG	20	1842 - 1862	
FSHR (outer)	F: GCA ACA AAT CTA TTT TAA GGC AAG A	25	911 - 935	AF025377
	R: GAT GCT CAC CTT CAT GTA GCT G	22	1562 - 1584	
FSHR (inner)	F: ATG GTT TAT TAG TAT CCT TGC CAC[2/]	24	1143 - 1166	AF025377
	R: AGC ACT ATG ATG TTC CCA GTG A	22	1166 - 1187	

[1/] Number of base pairs in each strand primer.
[2/] Underlined letter = C/T nucleotide substitution at position 1166.

Table 3 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 group
Adiponectin (ADIPOQ)					
Number of pig	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)					
Number of pig	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

[1/] numbers in parenthesis () correspond to percentages.
[2/] L = Landrace, W = Large White, LW = Landrace × Large White, and WL = Large White × Landrace.
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 ($P < 0.05$).

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 L and W population in China (100%; Dai et al., 2006) and a purebred L population in Canada (88%; Houde et al., 2008). Among breed groups, W sows had the lowest proportion of GA genotypes (1.7%; $P < 0.01$; Table 3). The other 3 breed groups (L, LW, and WL) had similar frequencies of GA sows (11.6 to 12.9 %; Table 3). 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 3). 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 3). 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. In contrast, the frequency of TT genotypes was higher in L sows (15.3%; $P < 0.05$; Table 3) than in sows from the other 3 breed groups (4.9% for W, 5.3% for LW, and 5.6% for WL).

Frequencies for the C and T alleles in Chinese Erhualian pigs (Jiang et al., 2002) were the opposite of those found here. Jiang et al. (2002) reported frequencies of 0.39 for allele C and of 0.61 for allele T. 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 here 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 here.

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 4). 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 4). 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. No literature values were available for comparison with allelic effects here for either ADIPOQ or FSHR.

Genotypic Effects

The difference between ADIPOQ genotypes GA and GG was non-significant for WSI and all studied litter traits (Table 5) 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 L 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) were in agreement with the non-significant estimates of the difference between GA and GG sows obtained here for the NBA trait (Table 5). Studies dealing with the association between SNP (AJ849536: g.1716G>A) and LBW, NPW and LWW were not available in the literature.

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 be associated with weaning to estrus interval and still born piglets in a Landrace sow population by Houde et al. (2008). Association studies relating swine prenatal and pre-weaning growth and ADIPOQ were unavailable. However, Dall'Olio et al. (2009) reported that GA Duroc pigs had higher postweaning average daily gain ($P = 0.003$) and lower feed:gain 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 5). No association studies between FSHR gene and WSI or litter traits were available in Thailand. However, Jiang et al. (2002) found that CC and CT sows had larger ($P = 0.0499$) total piglets born than TT sows in German L.

Table 4 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
WSI (d)	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 birth weight, NPW = number of piglets at weaning, and LWW = litter weaning weight.

Table 5 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 (d)	-0.90 ± 0.73	-0.59 ± 0.72	-0.24 ± 0.72
	(P < 0.2173)	(P < 0.4109)	(P < 0.7424)
NBA (piglets)	0.08 ± 0.45	0.23 ± 0.45	0.34 ± 0.45
	(P < 0.8617)	(P < 0.6082)	(P < 0.4532)
LBW (kg)	0.42 ± 0.73	0.00 ± 0.73	0.33 ± 0.73
	(P < 0.5709)	(P < 0.6082)	(P < 0.4532)
NPW (piglets)	-0.23 ± 0.35	-0.25 ± 0.35	-0.20 ± 0.35
	(P < 0.5106)	(P < 0.4737)	(P < 0.5709)
LWW (kg)	0.90 ± 3.10	-3.67 ± 3.08	-1.96 ± 3.09
	(P < 0.7728)	(P < 0.2337)	(P < 0.5266)

[1/] WSI = weaning-to-first service interval, NBA = number of piglets born alive, LBW = litter birth weight, NPW = number of piglets at weaning, and LWW = litter weaning weight.

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 here. 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 in position 1166 of 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) in the transmembrane-region of the FSHR protein (Ulloa-Aguirre et al., 2007). 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 here may have been influenced by genetic similarity among animals because this population has remained closed since 2002, thus all replacement boars and sows were produced within the herd.

Conclusions

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. 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. This suggests that the ADIPOQ and FSHR genes will be of 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 gilts 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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