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Influence of estrogen receptor 1 (*ESR1*) genotypes on litter size, sow productivity, and performance test traits in a local marker-assisted selection program for Landrace and Large White pigs

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ABSTRACT

Genetic improvement of litter size through marker-assisted selection (MAS) based on the estrogen receptor 1 (*ESR1*) gene is of considerable economic value to local pork producers. This study confirmed the favorable effect of *ESR1* genotypes to improve litter size born alive (LSBA), litter size at weaning (LSW), and sow productivity index (SPI) of Landrace and Large White sows of the progeny generation produced in a MAS program adapted by a local nucleus breeding farm in the Philippines. Analysis of 581 litter records from 163 sows genotyped at the *ESR1* locus showed that Large White sows with BB genotype had 1.56 more LSBA and 1.74 more LSW than those with AA genotype ($P<0.05$), with no significant effect ($P>0.05$) on piglet birth weight (BWT). Sow productivity index (SPI) for BB sows was 3.17 and 3.31 higher SPI for Landrace and Large White, respectively, than those for AA sows ($P<0.05$). Additive and dominance effect for LSBA in Large White sows was +0.78 and – 0.29, respectively. Favorable pleiotropic effects ($P<0.05$) were found in LSW at +0.57 and +0.88 for Landrace and Large White sows, respectively. There was no difference between *ESR1* genotypes ($P>0.05$) in terms of farrowing interval, farrowing index, and teat number. For a local nucleus breeding farm that is constrained to initially determine *ESR1* genotype of its replacement boars only, this study suggests prioritizing the use of replacement boars, sows with "BB" sire, and other high-SPI sows (i.e., SPI ≥ 24) with "AA" or "AB" sire with the favorable BB genotype to improve LSBA, LSW, and SPI.

INTRODUCTION

Marker-assisted selection (MAS) had long been proposed as a complementary tool to enhance the rate of genetic improvement of litter size in pigs, which has a low heritability and sex-limited expression. Using a candidate gene approach for a divergent breed cross involving the Chinese Meishan pig, Rothschild et al. (1996) reported that the recessive B allele of the estrogen receptor gene (*ESR1*), a steroid binding hormone receptor gene found at chromosome 1 in pigs is associated with increased litter

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ESR1 genotypes, Litter size (pigs), Marker-assisted selection, Pleiotropy

size (i.e., BB homozygote females produced 1.5 more pigs per litter than did AA females).

Van Rens et al. (2002) noted that the *Proteus vulgaris* II (*Pvu*II) - restriction enzyme polymorphism of *ESR1* is in an intron, which makes difference in expression or in structure relatively unlikely, and hence the site is more likely a marker rather than a major gene for litter size. Soboleva et al. (2004) suggested that gilts with BB genotype recruited ovarian follicles that varied more in size but had fewer very small follicles, which could have affected the relative estradiol secretion of the ovarian follicles at commitment. The follicle estradiol levels at commitment influence follicle estradiol levels at ovulation, which in turn, may influence the fertilization rate and/or the developmental capacity of the embryos throughout pregnancy after successful fertilization.

The *ESR1* allele associated with higher prolificacy in pigs with Chinese origin and predominant in Meishan was also found in Large White-based commercial lines (Short et al. 1997). Similar results were reported by Chen et al. (2001) in Large Yorkshire, Landrace, Chinese Erhualian, double-muscled Yorkshire, and Chinese Xiangzhu breeds. Some global breeding companies have since incorporated the favorable allele B into conventional dam lines of commercial breeds that do not have the allele by using marker-assisted introgression. Many more researchers eventually screened the distribution and polymorphism of *ESR1 Pvu*II in other breeds (e.g., Snegin et al. 2019) and examined its association with reproductive traits (e.g., Mencik et al. 2019) but sometimes with contrasting results. For example, *ESR1 Pvu*II polymorphisms showed no significant association with litter size in Italian Large White sows (Dall'Olio et al. 2011). Muñoz et al. (2018) reported that the *ESR1* gene was not polymorphic in twenty European local breeds, with the unfavorable allele A in terms of litter size being fixed in all of them. Their genotyping results agreed with previously published reports of the characteristic low prolificacy observed in some autochthonous breeds or local/indigenous unselected breeds. The *ESR1 Pvu*II was also found to be monomorphic for the AA genotype in Benguet native pigs from the Philippines (Tabon et al. 2022). Rahman et al. (2021) and Vashi et al. (2021) both reported no significant association between *ESR1* and litter traits in indigenous breeds from India. The inconsistency of results when tested in various populations of a breed or even on several breeds may be due to different allelic and genotypic frequency and sample size in each breed, and epistatic effects or different linkage phases between marker and causal mutation (Vaishnav et al. 2023).

While the potential use of *ESR1* gene as a marker for litter size had been evaluated based on data from large numbers of pigs especially those supported by global genetic companies, the results of MAS program for the *ESR1* in the long term are rarely (if at all) reported. In the Philippines, a few government-accredited nucleus breeding farms who had shown interest in running a local MAS program for the *ESR1* gene, are constrained by the low initial frequency of the B allele in their small (< 500 sow-level) breeding herd. It was also difficult to identify BB sows because *ESR1* genotyping all performance-tested boars and gilts can be very costly.

In this study, we showed how MAS was adapted in a local swine breeding program. Through a research collaboration with a government-accredited privately owned swine nucleus breeding farm, the *ESR1* genotypes were initially determined for purebred Landrace and Large White pigs but only for young replacement boars that have been performance-tested for production traits. Because of the small number of performance-tested replacement boars with BB genotype, both AB and BB boars were mated to ungenotyped replacement gilts/sows in a circular mating scheme involving five lines per breed. However, to meet the minimum number of boars per line, the boar-based marker-assisted selection program in a few instances was forced to use replacement boars with the AA genotype.

The objective of this study was to examine the effects of the *ESR1* locus on LSBA and to measure pleiotropic effects on farrowing and weaning data, sow productivity, and gilt performance test traits of Landrace and Large White sows of the progeny generation produced in a marker-assisted selection program adapted by a local nucleus breeding farm. *ESR1* genotypes in each breed were also compared between sows with "BB" sire versus sows with "AA" or "AB" sire.

MATERIALS AND METHODS

Data

A total of 581 litter records from 163 sows (i.e., 60 Landrace and 103 Large White) genotyped at the *ESR1* locus were analyzed to determine the influence of *ESR1* genotypes on farrowing and weaning data, sow productivity, and performance test records. Data were obtained from the progeny generation of a marker-assisted selection (MAS) program adapted by a government-accredited International Farm Corporation (INFARMCO) swine nucleus breeding farm in Barangay San Isidro, Cabuyao City, Laguna. The local MAS program initially determined *ESR1* genotypes for replacement boars only, wherein boars with the AB or BB genotype were mated to ungenotyped gilts/sows of the same breed. The genotyping activities were part of the Department of Agriculture Biotechnology Program (DA-BIOTECH) and the Bureau of Agricultural Research (DA-BAR) - funded project approved by the Institutional Animal Care and Use Committee (IACUC) of the College of Veterinary Medicine, University of the Philippines Los Baños, Laguna with approval number 2019-0034.

Traits of interest per farrowing record were litter size born alive (LSBA), litter size at weaning (LSW), piglet birth weight (BWT, in kg) and weaning weight (WWT, in kg), and number of stillbirths (NSB), mummified piglets (NMP), and pre-weaning mortality per litter (MORT).

Individual sow's age at first farrowing (AFF, in days), farrowing interval (F-Interv, in days), farrowing index (F-Index) or the number of litters born by a sow per year, and sow productivity index (SPI) or the number of weaned pigs sow^{-1}year^{-1} were calculated based on the average F-Interv and average LSW of all litters produced by each sow, i.e., "F-Index = 365 ÷ F-Interv" and "SPI = LSW × F-Index".

Total number of teats (TN), body length (BL, in cm), average daily gain (ADG, in kg/day), and real-time ultrasonic backfat thickness (BF, in cm) were measured at the completion of the 84-day performance test for gilts. The average age and weight at the end of test period was 151.8 ± 5.4 days and 97.7 ± 7.3 kg, respectively.

DNA Extraction, Amplification, and Genotyping

Genomic DNA was extracted from hair follicles of replacement boars (parental generation) and sows of the progeny generation using the Vivantis GF-1 Nucleic Acid Extraction Kit following the supplier's protocol with some modifications. About 20 hair follicles (roots) were placed in a 1.5 mL microcentrifuge tube and added with 20 µl Dithiothreitol (DTT) to aid the action of Proteinase K, and then frozen with liquid nitrogen.

Polymerase chain reaction (PCR) was used to amplify DNA in

0.5 mL Eppendorf tubes. Reactions included 14.8 µL water, 2.0 µL 10×PCR buffer, 0.6 µL 50 mM $MgCl_2$, 0.16 µL 25mM dNTP, 0.2 µL forward (F) primer (20 µM), 0.2 µL reverse (R) primer (20 µM), 0.04 µL Taq DNA polymerase (5U/µL), and 2.0 µL DNA lysate. Primer sequences were designated according to Short et al. (1997), namely *forward* 5'-CCTGTTTTTACAGTGACTTTTACAGAG-3' and *reverse* 5'-CACTTCGAGGGTCAGTCCAATTAG-3'.

The reactions were loaded onto a Veriti 96-well thermal cycler under the following conditions: 1 cycle at 94°C for 4 min, 30 cycles of 94°C for 30 sec, 55°C for 30 sec, and 72°C for 30 sec; 1 cycle at 72°C for 8 min; and hold at 4°C. The amplified 120-bp products were digested using the *Pvu*II restriction enzyme with recognition site 5'-CAGCTG-3' corresponding to *ESR1* (exon 17 chromosome 1).

The PCR products from PCR-RFLP were loaded in a 3% agarose gel electrophoresis with a 50bp DNA ladder standard and visualized under UV transillumination (Bio-Rad Gel Doc XR+ Systems). AA genotype appears as a single band on the 120-bp marker, while a BB genotype appears as two bands on the 65-bp and 55-bp marker. AB genotype appears as a combination of both bands produced from homozygous A and B (see Figure 1).

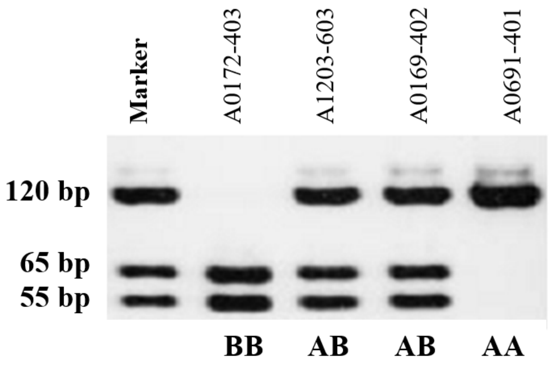

Figure 1: Sample visualization of *ESR1* genotypes (AA, AB, and BB) of four Landrace (lines 401, 402, and 403) and Large White (line 603) sows used in the study after enzymatic digestion by *PvuII* according to the following restriction fragment lengths: AA – 120bp; AB – 120, 65, and 55bp; BB – 65 and 55bp

Statistical Analysis

The effects of *ESR1* genotypes were analyzed separately for three data sets, namely: (1) sows whose sire has the BB genotype, (2) sows whose sire has the AA or AB genotype (with at least 24 weaned pigs sow^{-1} year^{-1}), and (3) combined data sets 1 and 2, using the following linear model (SAS/STAT ® v. 9.2; 2009): $y_{ijklm} = u + \text{Breed}_i + (\text{Breed} \times ESR1)_{ij} + \text{Parity}_k + \text{AFF}_l + e_{ijklm}$ where y_{ijklm} is the dependent variable for farrowing and weaning records, sow productivity, and performance test traits; u is the overall mean; Breed_i is the fixed effect of the ith breed of sow (Landrace and Large White); $(\text{Breed} \times ESR1)_{ij}$ is the interaction effect between the ith breed of sow and jth genotype (AA, AB, and BB), Parity_k is the covariate effect of the kth parity (number of litters produced); AFF_l is the covariate effect of the lth age at first farrowing (days); e_{ijklm} represents the random error $\sim$NID (0, e^2). The effects of the *ESR1* genotype on farrowing and weaning records, sow productivity, and performance test traits were presented as least square means and standard deviations. Differences are considered significant at P value < 0.05.

Allele substitution effects for all traits were estimated using the formula as follows: $\alpha = [a + d\,(q - p)]$ where α is average effect of gene substitution, "a" is genotypic value for the BB genotype equal to the phenotypic value of BB minus the average phenotypic values of AA and BB, "d" is dominance effect estimated as the deviation of heterozygotes from the mean of the homozygous genotypes, and p and q are the gene frequency of allele A and B, respectively.

Least square means and standard deviations for "Breed × *ESR1* genotype" interaction effects were used to compare the effects of *ESR1* genotypes for sows with "BB" sire versus high-SPI sows (i.e., SPI ≥ 24) with "AA" or "AB" sire.

RESULTS AND DISCUSSION

ESR1 Gene and Genotypic Frequencies

A total of 163 sows of the progeny generation were genotyped for the *ESR1* gene. There were 235 litters with 2,537 piglets produced by 60 Landrace sows, and 346 litters with 3,530 piglets produced by 103 Large White sows. Average parity (number of litters produced) for Landrace and Large White sow was 3.93 ± 0.19 and 3.36 ± 0.18, respectively.

Gene frequencies for the favorable B allele in Landrace and Large White sows of the progeny generation were 50.83% and 49.51%, respectively (Table 1). Genotypic frequencies for the favorable genotype BB were higher in Landrace sows (23.33%) than in Large White sows (12.62%). Genotypic frequencies were highest in the heterozygotes (AB) representing 55% and 74% of all Landrace and Large White sows, respectively. The difference in genotypic frequency in the two breeds suggests that it will be more difficult initially to find BB sows in Large White than in Landrace in the local nucleus breeding herd.

Table 1: Gene and genotypic frequencies of *ESR1* polymorphism in Landrace and Large White sows.

	Landrace	Large White
No. of all genotyped sows		
AA	13	14
AB	33	76
BB	14	13
Total	60	103
Gene frequency		
A	49.17	50.49
B	50.83	49.51
Genotypic frequency		
AA	21.67	13.59
AB	55.00	73.79
BB	23.33	12.62
No. of sows with "BB" sire		
AA	0	0
AB	13	43
BB	8	4
Total	21	47
Gene frequency		
A	30.95	45.74
B	69.05	54.26
Genotypic frequency		
AA	0.00	0.00
AB	61.90	91.49
BB	38.10	8.51
No. of sows with "AA" or "AB" sire		
AA	9	10
AB	17	26
BB	5	8
Total	31	44

Gene frequency		
A	56.45	52.27
B	43.55	47.73
Genotypic frequency		
AA	29.03	22.73
AB	54.84	59.09
BB	16.13	18.18

Breed Differences

Table 2 shows that Landrace sows had 0.56 more LSBA, 0.17 kg heavier BWT, 0.6 more LSW and 1.70 cm longer BL than Large White sows ($P<0.05$). However, Landrace sows had 0.18 less NMP and 0.11 cm lower BFT than Large White sows ($P<0.05$). The NSB, WWT, MORT, AFF, F-Interv, F-Index, and SPI, TN, and ADG were not significantly different between Landrace and Large White sows ($P>0.05$).

Table 2: Least square means for farrowing and weaning data, sow productivity and performance test traits in Landrace and Large White pigs.

	Landrace	Large White
Farrowing and weaning data		
LSBA	$10.76^a \pm 0.26$	$10.20^b \pm 0.25$
BWT, kg	1.44 ± 0.02	1.46 ± 0.02
NSB	0.16 ± 0.04	0.15 ± 0.04
NMP	$0.23^b \pm 0.08$	$0.41^a \pm 0.07$
LSW	$9.68^a \pm 0.26$	$9.08^b \pm 0.25$
WWT, kg	8.14 ± 0.14	8.36 ± 0.14
MORT	1.04 ± 0.13	1.24 ± 0.12
Sow productivity traits		
AFF, days	343.8 ± 2.1	344.9 ± 2.0
F-Interv, days	151.9 ± 1.1	151.4 ± 1.1
F-Index	2.41 ± 0.01	2.42 ± 0.01
SPI	25.00 ± 0.68	24.25 ± 0.64
Performance test traits		
TN	13.53 ± 0.14	13.25 ± 0.14
BL, cm	$116.1^a \pm 0.4$	$114.4^b \pm 0.4$
ADG, kg/day	0.655 ± 0.014	0.644 ± 0.013
BF, cm	$1.32^b \pm 0.04$	$1.43^a \pm 0.04$

Note: Least square means with different superscript letters in the same row are significantly different between Landrace and Large White sows ($P<0.05$).

[Abbreviation: LSBA – litter size at birth; BWT – piglet birth weight; NSB – no. of stillbirths; NMP – no. of mummified piglets; LSW – litter size at weaning; WWT – piglet weaning weight; MORT – no. of pre-weaning mortality; AFF – age at first farrowing; F-Interv – farrowing interval; F-Index – farrowing index; SPI – sow productivity index or no. of weaned pigs $sow^{-1}year^{-1}$; TN – no. of teats; BL – body length, ADG – average daily gain, BF – backfat thickness]

Additive and Dominance Effects of *ESR1* Genes

Landrace and Large White sows that were homozygous for the beneficial allele (BB) had 0.75 and 1.56 more LSBA, respectively, than sows homozygous for the undesirable allele (AA), see Table 3. All three *ESR1* genotypes had different LSBA ($P<0.05$). The effect of the favorable B allele on LSBA seems to be additive, with an effect of 0.78 LSBA per copy of the B allele in Large White sows and only 0.35 LSBA for Landrace sows. The allele substitution effects per copy of the B allele for LSW were +0.57 and +0.88 for Landrace and Large White sows, respectively. It represents the increase in additive effects when the B allele replaces the A allele in the heterozygous genotype (AB). The results imply that the additive genetic effects or the sum of additive genetic contributions from each locus, and therefore, genetic improvement of LSBA were higher for Large White sows than Landrace sows.

Dominance effects for LSBA were –0.15 and –0.29 or about 37% and 43% of the magnitude of the additive effect in Landrace and Large White sows, respectively. The overdominance effects for the B allele (i.e., genotypic value of the heterozygotes (AB) is less than the mean of homozygous genotypes AA and BB). This suggests potential genetic improvement in LSBA due to heterosis, when using F_1 Large White × Landrace crossbred sows as a specialized dam line to generate more market hogs.

By comparison, Rothschild et al. (1996) reported additive effects (0.8) and dominance effects (0.6) for LSBA in all parities in Meishan pigs. Short et al. (1997) reported additive effects for LSBA in the first parity (0.39) and later parities (0.31) in Large White pigs but found no dominance effect for LSBA in the first parity, although in later parities a dominance effect of half the magnitude of the additive effect was detected. The discrepancy of the estimated additive and dominance effects of the *ESR1* gene in these reports compared to our study could be due to the different allelic and genotypic frequency, sample size, breeding goals, and genetic background of each breed.

Pleiotropic Effects of the *ESR1* Gene

Favorable pleiotropic effects ($P<0.05$) of *ESR1* genotypes were detected for LSW in both breeds. LSW depends on LSBA, BWT, and the sow's milk production which reflects the maternal instincts and care of the sow (Nowak et al. 2020). In this study, sows with the BB genotype had 1.15 and 1.31 more LSW in the Landrace and Large White breed, respectively, than those with AA genotype ($P<0.05$).

Sows with the BB genotype also had 3.17 and 3.31 higher SPI for Landrace and Large White breeds, respectively, than those with AA genotype ($P<0.05$). As a measure of the sow's milking ability and prolificacy, SPI is influenced by LSW and F-Index. In both breeds, F-Interv was about 152 days corresponding to 2.4 farrows a year. Since F-Interv and F-Index were not significantly different breeds ($P>0.05$), SPI depended largely on LSW in the nucleus breeding farm.

Litter size is widely known to be negatively correlated with birth weight (Kemp et al. 2018) which may indirectly affect the survival of piglet from birth to weaning. Feldpausch et al. (2019) also reported that piglets with high birth weight in a litter are more resistant to the effect of adverse external environment that results in decreasing pre-weaning piglet mortality rate. The present study, however, showed no significant effect of *ESR1* genotypes on BWT in both breeds ($P>0.05$). *ESR1* genotypes even had favorable pleiotropic effects on MORT for Large White sows, which was significantly lower in AB and BB sows compared to AA sows ($P<0.05$). This implies that selection for litter size through MAS based on the *ESR1* gene may not necessarily necessarily decrease BWT nor increase TN, and that the average BWT (1.42 kg) of Large White piglets which when supported by innovative farm (non-genetic) interventions to counteract various environmental stress factors affecting piglet health or maternal ability may be enough to allow them to survive until weaning.

Litter size is also related to the number of stillborn piglets, which has been associated with decreased litter weights, more occurrences of uterine prolapse or abortions at subsequent pregnancy, difficult farrowing, decreased farrowing rate, low prolificacy and longevity due to low fertility (Koketsu and Iida 2020). Around 10% of piglets born are stillbirth at parturition (Langendijk and Plush 2019). In the present study, the favorable pleiotropic (additive) effect of *ESR1* gene was found for NSB (−0.09) for Landrace sows and NMP (−0.18) for Large White

Table 3: Least squares means and allele substitution effects for farrowing and weaning data, sow productivity, and performance test traits in Landrace and Large White sows.

	Landrace					Large White				
	ESR1 genotypes			Genetic effect		*ESR1* genotypes			Genetic effect	
	AA	AB	BB	Additive	Dominance	AA	AB	BB	Additive	Dominance
Farrowing and weaning data										
LSBA	10.46 ± 0.53	10.66 ± 0.30	11.16 ± 0.48	0.35	-0.15	9.51^{b} ± 0.50	10.00^{b} ± 0.21	11.07^{a} ± 0.51	0.78	-0.29
BWT, kg	1.46 ± 0.05	1.44 ± 0.03	1.41 ± 0.05	0.06	0.06	1.49 ± 0.05	1.46 ± 0.02	1.43 ± 0.05	-0.06	-0.08
NSB	0.29^{a} ± 0.09	0.10^{b} ± 0.05	0.10^{b} ± 0.08	-0.09	-0.10	0.17 ± 0.09	0.20 ± 0.04	0.08 ± 0.09	-0.04	0.08
NMP	0.25 ± 0.16^{b}	0.18^{b} ± 0.09	0.26^{b} ± 0.14	0.01	-0.08	0.64^{a} ± 0.15	0.31^{b} ± 0.06	0.29^{b} ± 0.15	-0.18	-0.16
LSW	9.23^{bc} ± 0.54	9.43^{b} ± 0.31	10.38^{a} ± 0.50	0.57	-0.38	8.26^{c} ± 0.51	8.97^{c} ± 0.21	10.00^{a} ± 0.52	0.88	-0.16
WWT, kg	8.48 ± 0.30	7. 94 ± 0.17	7. 99 ± 0.27	-0.24	-0.29	8.30 ± 0.28	8.43 ± 0.12	8.37 ± 0.29	0.04	0.09
MORT	1.16 ± 0.26	1.22 ± 0.15	0.74 ± 0.24	-0.21	-0.27	1.59^{a} ± 0.25	1.03^{b} ± 0.10	1.08^{b} ± 0.25	-0.26	-0.31
Sow productivity traits										
AFF, days	349.6^{a} ± 4.1	343.1^{ab} ± 2.5	338.8^{b} ± 4.0	-5.38	-1.10	345.0 ± 4.1	339.7 ± 1.7	350.2 ± 4.1	2.55	-7.90
F-Interv, days	151.5 ± 2.3	151.2 ± 1.4	153.0 ± 2.1	-0.77	-1.05	149.2 ± 2.2	153.1 ± 0.9	151.8 ± 2.2	1.34	2.60
F-Index	2.41 ± 0.02	2.42 ± 0.02	2.40 ± 0.02	0.01	0.01	2.45 ± 0.02	2.40 ± 0.01	2.40 ± 0.02	-0.03	-0.02
SPI	23.36^{b} ± 1.36	25.07^{a} ± 0.84	26.53^{a} ± 1.25	-1.58	0.13	22.95^{b} ± 1.30	23.55^{b} ± 0.54	26.26^{a} ± 1.32	1.66	-1.06
Performance test traits										
TN	13.53 ± 0.29	13.49 ± 0.17	13.58 ± 0.28	-0.03	-0.06	13.33 ± 0.28	13.18 ± 0.11	13.24 ± 0.28	-0.05	-0.11
BL, cm	116.5 ± 0.8	115.8 ± 0.5	116.1 ± 0.8	0.19	-0.50	113.4^{c} ± 0.8	114.4^{bc} ± 0.3	115.3^{ab} ± 0.8	0.96	0.05
ADG, kg/day	0.672 ± 0.026	0.640 ± 0.016	0.654 ± 0.027	0.009	-0.023	0.634 ± 0.027	0.656 ± 0.010	0.643 ± 0.027	0.005	0.018
BF, cm	1.36 ± 0.08	1.33 ± 0.05	1.25 ± 0.08	0.06	0.02	1.39 ± 0.08	1.44 ± 0.03	1.48 ± 0.08	-0.38	0.36

Note: Least square means with different superscript letters in the same row for Landrace and Large White sows are significantly different ($P<0.05$).

sows. In another study, the highest NSB and NMP were reported in sows with AA genotype and the lowest number of NSB and NMP in sows with BB genotype for Yorkshire and Landrace breeds (Suwanasopee and Koonawootrittriron 2011). In contrast, Mencik et al. (2016) reported that the B allele in “Topigs 20” sows was associated with higher NSB, compared to the A allele, which had a significant impact on NMP in third- and higher parities.

Other breed-specific favorable effects of the B allele in this study include 5.4 days younger AFF in Landrace sows with the BB genotype than those with the AA genotype (P<0.05). Large White sows with the BB genotype had 0.96 cm longer BL at the end of gilt performance test than sows with AA genotype. In both breeds, the F-Interv and F-Index which depends largely on the effective breeding management program (environmental effect) strictly enforced in the local nucleus breeding farm, were not significantly different between *ESR1* genotypes and hence, should not limit selection for the BB genotype. Measurements of ADG and BFT during the gilt performance test were also not significantly different between *ESR1* genotypes (*P*>0.05).

Comparison of Sows with “BB” Sire versus High-SPI Sows with “AA” or “AB” Sire

Table 1 shows that the frequency of the B allele was higher than that of the A allele in the progeny generation, especially for sows with “BB” sire (i.e., 69.05% and 54.26% for Landrace and Large White, respectively) compared to high-SPI sows (i.e., SPI ≥ 24) with the “AA” or “AB” sire (i.e., 43.55% and 47.33% for Landrace and Large White, respectively). The MAS program of a local swine nucleus breeding farm that was restricted initially to determine *ESR1* genotypes of replacement boars only, can be an effective strategy to increase the frequency of B gene in the progeny generation of Landrace and Large White sows. However, lower frequency of the B allele (slightly lower than 50%) was recorded for high-SPI sows with “AA” or “AB” sire.

The frequency of the BB genotype was also higher for Landrace sows with “BB” sire (38.10%) than for high-SPI sows with “AA” or “AB” sire (16.13%). The reverse is true for Large White sows. Nevertheless, additional genotyping services made on high-SPI sows with “AA” or “AB” sire allowed the identification of more BB sows (5 Landrace and 8 Large White) and AB sows (17 Landrace and 26 Large White), which later can be used to accelerate the build-up of the frequency of the favorable B allele and BB genotype in the local nucleus breeding herd.

Table 4 shows that the effects of *ESR1* genotypes on farrowing and weaning records, sow productivity, and performance test traits measured in the progeny generation were different between sows with “BB” sire and high-SPI sows with “AA” or “AB” sire depending on the frequencies of the favorable B allele and BB genotypes specific in each breed.

Table 4: Effects of ESR1 genotypes on farrowing and weaning data, sow productivity and performance test traits for sows with “BB” sire and sows with “AA” or “AB” sire.

	Landrace			Large White		
	AA	AB	BB	AA	AB	BB
Sows with “BB” sire (N=68)						
LSBA	-	10.68^{a} ± 0.54	11.60^{a} ± 0.72	-	$9. 42^{b}$ ± 0.29	10.97^{a} ± 0.94
BWT, kg	-	1.39 ± 0.04	1.42 ± 0.06	-	1.43 ± 0.02	1.36 ± 0.08
NSB	-	0.01^{b} ± 0.09	0.03^{b} ± 0.12	-	0.23^{a} ± 0.05	0.11^{ab} ± 0.15
NMP	-	0.00^{b} ± 0.13	0.14^{ab} ± 0.17	-	0.34^{a} ± 0.07	0.24^{ab} ± 0.22
LSW	-	9.20^{b} ± 0.53	10.94^{a} ± 071	-	$8. 55^{c}$ ± 0.29	9.97^{ab} ± 0.92
WWT, kg	-	$7. 51^{b}$ ± 0.32	8.04^{ab} ± 0.42	-	8.36^{a} ± 0.17	7.66^{ab} ± 0.54
MORT	-	1.48^{a} ± 0.26	0.66^{b} ± 0.34	-	0.87^{b} ± 0.14	1.00^{ab} ± 0.44
AFF, days	-	344.8^{a} ± 3.3	338.9^{ab} ± 4.5	-	338.1^{b} ± 1.8	348.5^{a} ± 6.0
F-Interv, days	-	150.2 ± 1.6	150.0 ± 2.0	-	151.1 ± 0.8	151.3 ± 2.5
F-Index	-	2.43 ± 0.02	2.43 ± 0.03	-	2.42 ± 0.01	2.42 ± 0.04
SPI	-	25.57^{a} ± 1.42	27.90^{a} ± 1.76	-	22.64^{b} ± 0.70	26.11^{a} ± 0.24
TN	-	13.78^{a} ± 0.26	13.60^{a} ± 0.35	-	12.95^{b} ± 0.14	13.23^{ab} ± 0.45
BL, cm	-	115.9^{a} ± 0.9	116.2^{a} ± 1.3	-	114.5^{a} ± 0.4	115.2^{ab} ± 1.2
ADG, kg/day	-	0.639 ± 0.040	0.686 ± 0.056	-	0.669 ± 0.017	0.656 ± 0.055
BF, cm	-	1.34^{c} ± 0.08	1.18^{c} ± 0.11	-	1.44^{b} ± 0.03	1.60^{a} ± 0.11
Sows with “AA” or “AB” sire (N=75)						
LSBA	11.42^{a} ± 0.53	10.81^{a} ± 0.37	11.25^{a} ± 0.69	9.44^{b} ± 0.47	10.69^{a} ± 0.30	11.20^{a} ± 0.54
BWT, kg	1.42 ± 0.06	1.51 ± 0.04	1.42 ± 0.08	1.52 ± 0.05	1.48 ± 0.03	1.46 ± 0.06
NSB	0.35^{a} ± 0.09	0.14^{b} ± 0.06	0.14^{b} ± 0.12	0.02^{b} ± 0.08	0.16^{b} ± 0.05	0.04^{bc} ± 0.10
NMP	0.28 ± 0.22	0.34 ± 0.15	0.46 ± 0.29	0.62 ± 0.20	0.29 ± 0.13	0.28 ± 0.23
LSW	10.39^{a} ± 0.55	9.90^{a} ± 0.38	10.33^{a} ± 0.71	8.39^{b} ± 0.49	9.51^{a} ± 0.31	9.95^{a} ± 0.56
WWT, kg	8.61 ± 0.33	8.26 ± 0.23	8.08 ± 0.43	8.46 ± 0.29	8.40 ± 0.19	8.40 ± 0.34
MORT	0.98^{ab} ± 0.29	0.93^{b} ± 0.20	0.94^{ab} ± 0.38	1.44^{a} ± 0.26	1.17^{a} ± 0.16	1.26^{ab} ± 0.30
AFF, days	350.1^{a} ± 4.7	337.6^{bc} ± 3.4	328.8^{c} ± 6.3	344.0^{b} ± 4.5	341.9^{b} ± 2.8	351.4^{a} ± 5.0
F-Interv, days	152.3 ± 3.4	152.8 ± 2.5	155.7 ± 4.5	148.8 ± 3.0	154.9 ± 1.9	151. ± 3.5
F-Index	2.40^{ab} ± 0.03	2.41^{ab} ± 0.02	2.37^{ab} ± 0.04	2.45^{a} ± 0.03	2.38^{b} ± 0.02	2.40^{ab} ± 0.03
SPI	26.64^{ab} ± 1.19	26.02^{a} ± 0.86	27.17^{a} ± 1.55	23.78^{b} ± 1.06	24.86^{b} ± 0.67	25.30^{ab} ± 1.21

TN	13.43 ± 1.04	13.34 ± 0.71	13.57 ± 1.34	13.51 ± 0.91	13.61 ± 0.60	13.27 ± 1.04
BL, cm	116.1 ± 0.8^{a}	115.3^{a} ± 0.6	115.1^{ab} ± 1.2	113.8^{b} ± 0.8	114.7^{b} ± 0.4	115.9^{ab} ± 0.9
ADG, kg/day	0.675^{a} ± 0.017	0.632^{b} ± 0.011	0.620^{ab}±0.024	0.636^{ab}±0.017	0.635^{b} ± 0.010	0.642^{ab} ± 0.019
BF, cm	1.44 ± 0.10	1.38 ± 0.07	1.36 ± 0.14	1.37 ± 0.10	1.40 ± 0.05	1.34 ± 0.11

Note: Least square means with different superscript letters in the same row for Landrace and Large White sows are significantly different (P<0.05).

[Abbreviation: LSBA – litter size at birth; BWT – piglet birth weight; NSB – no. of stillbirths; NMP – no. of mummified piglets; LSW – litter size at weaning; WWT – piglet weaning weight; MORT – no. of pre-weaning mortality; AFF – age at first farrowing; F-Interv – farrowing interval; F-Index – farrowing index; SPI – sow productivity index or no. of weaned pigs sow^{-1}year^{-1}; TN – no. of teats; BL – body length, ADG – average daily gain, BF – backfat thickness]

For sows with "BB" sire, comparisons of the effects of the *ESR1* marker gene highlighted differences between BB and AB genotypes. (No AA genotype in the progeny generation is produced when a BB boar is mated to AA, AB, or BB sow/gilt.) For high-SPI sows with "AA" or "AB" sire, comparisons showed the advantages of the favorable BB genotype over the undesirable AA genotype.

In Landrace sows with "BB" sire, for example, BB sows had 1.74 more LSW and 0.82 lower MORT than that of AB sows (P<0.05). In high-SPI sows with "AA" or "AB" sire, BB sows had 0.21 lower NSB and were 21.3 days younger AFF than that of AA sows (P<0.05).

In the case of Large White sows with "BB" sire, BB sows had 1.55 more LSBA, 1.42 more LSW, 3.47 higher SPI but were 10.4 days older AFF and 0.16 cm higher BFT than that of AB sows (P<0.05). In high-SPI sows with "AA" or "AB" sire, BB sows had 1.76 more LSBA and 1.56 more LSW but were 7.4 days older AFF than that of AA sows (P<0.05).

The results above emphasize the importance of using BB sires as much as possible or AB sires on sows with high SPI to improve LSBA, LSW, and SPI in the local nucleus breeding farm. In this regard, more government-accredited *ESR1* genotyping laboratories are needed to routinely and inexpensively determine *ESR1* genotypes of all sows with "BB" sire and other high-SPI sows (i.e., SPI ≥ 24) in addition to replacement boars and gilts with the favorable *ESR1* genotype.

CONCLUSION

In this study, we present evidence of increased LSBA in Landrace and Large White sows of the progeny generation produced in a marker-assisted selection program based on the *ESR1* gene adapted by a local nucleus breeding farm. Replacement boars that were performance-tested for production traits with 'BB" or "AB" may be used initially to increase the frequency of the favorable B allele and BB genotypes. Selection of replacement boars, sows with "BB" sire, and other high-SPI sows (i.e., SPI ≥ 24) with "AA" or "AB" sire with the favorable BB genotype should be prioritized to improve LSBA, LSW, and SPI.

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CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

CONTRIBUTIONS OF INDIVIDUAL AUTHORS

Conceptualization and collection of hair follicle samples and animal performance records from replacement boars and sows of the progeny generation, OLB, JFI, and SFDC; genotyping of *ESR1* polymorphism and statistical analysis, PJSD and OLB; writing—original draft preparation, OLB and PJSD; writing—review and editing, OLB and PJSD; project design and coordination, OLB.

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