GENETIC PARAMETERS AND TRENDS FOR WEANING-TO-FIRST SERVICE INTERVAL AND LITTER TRAITS IN A SWINE POPULATION COMPOSED OF LANDRACE, LARGE WHITE, AND THEIR CROSSES IN NORTHERN THAILAND

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SUMMARY

Commercial swine producers in Thailand use production and reproduction phenotypic records to choose replacement animals. However, estimates of genetic parameters for weaning-to-estrous interval (WSI) and litter traits are lacking in commercial populations composed of purebred and crossbred animals under Thai tropical conditions. The objective was to estimate genetic parameters and trends for WSI and litter traits. Direct and maternal heritabilities for all traits were low (0.03 ± 0.02 to 0.06 ± 0.02). Significant boar and sow genetic trends were low and negative suggesting that phenotypic selection was ineffective to identify the best genotypes. Selection based on predicted genetic values would be advantageous to identify the best genotypes and improve genetic trends.

INTRODUCTION

Commercial swine producers in Thailand consider both production and reproduction traits in their genetic improvement programs. Litter traits such as number born alive (NBA), number of piglets at weaning (NPW), litter birth weight (LBW), and litter weaning weight (LWW) are normally used in swine selection programs. In recent years, commercial producers have begun to use weaning-to-first service interval (WSI) to cull and select dams in commercial swine operations. This trait is economically relevant for the efficiency of commercial operations because it represents a non-productive period for sows. Thus, swine commercial producers in Thailand need reliable estimates of genetic variability for WSI and litter traits as well as genetic correlations among these traits to carry out effective genetic improvement programs. Reported estimates of heritability in the hot and humid environmental conditions of Thailand were low for WSI and litter traits (0.17 ± 0.03 for WSI, 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). The only available genetic correlations in Thailand were the near zero values between WSI and total number of piglets born in Landrace (-0.07 ± 0.34 to 0.05 ± 0.23; Imboonta et al., 2007). In addition to genetic parameters, estimation of genetic and phenotypic trends for WSI and litter traits would give information to Thai swine producers on the effectiveness of their genetic improvement and management programs. Published genetic trends in Thailand were for WSI (0.01 ± 0.01 d/yr) and for total number of piglets born (-0.02 ± 0.02 piglets/yr) in Landrace (Imboonta et al., 2007). Estimation of genetic and phenotypic correlations between WSI and litter traits, and genetic trends for these traits have not been done in Thai swine populations composed of purebred and crossbred animals. Thus, the objectives of this study were to estimate genetic parameters and trends for WSI and litter traits in a commercial swine population composed of purebred Landrace, Large White, and reciprocal Landrace x Large White crossbreds in the province of Chiang Mai, northern Thailand.

MATERIAL AND METHODS

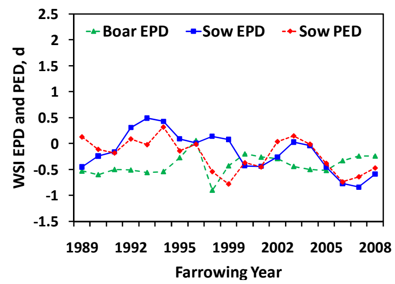
Animals, dataset, and traits. Data were collected from 1989 to 2008 in a commercial Landrace-Large White swine population composed of purebred and crossbred animals in Chiang Mai, northern Thailand. The original dataset of 12,974 records was edited for erroneous and incomplete information. All identified cross-fostered records were eliminated. The edited dataset contained 4,399 records of each of the five traits of interest: WSI, NBA, LBW, NPW, and LWW. Breeds represented in the dataset were Landrace (L) and Large White (T). Breeds groups of boars were L and T. Breed groups of sows were L, T, and reciprocal crossbred groups LT and TL. There were 356 boars and 1,852 sows represented in the dataset. The pedigree file contained 3,081 animals (660 boars and 2421 sows).

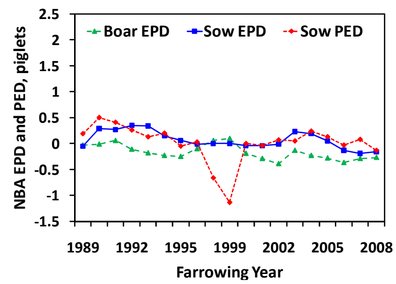
Climate, feeding, and management. Mean temperature in Northern Thailand from 1989 to 2008 was 26.2ºC and mean humidity was 71.6%; Thai Meteorological Department, 2009). Seasons were winter (November to February), summer (March to June), and rainy (July to October). Mean season temperature and humidity were 23.2ºC and 68.7% in winter, 28.3ºC and 65.0% in summer, and 27.1ºC and 81.2% in the rainy season. Gilts and sows were housed in open barns with foggers (gilts and non-lactating sows) or dippers (nursing sows) activated when the ambient temperature surpassed 33ºC. Boars were kept in closed barns with evaporative cooling. Boars, non-lactating sows, and gilts received 2.5kg of concentrate twice a day (16% crude protein and 3,200 to 3,500 kcal/kg). Nursing sows were fed 5 to 6 kg of concentrate (17 to 18% crude protein and 4,060 kcal/kg) 4 times a day. Replacement gilts were inseminated for the first time at 8 to 9 months of age or 140 kg of body weight. Pregnant sows were kept in a breeder cage until approximately 7 days before parturition, and then taken to a farrowing barn with dippers. Piglets were weaned at roughly 7 kg (26 to 30 d of age). Estrus of gilts and weaned sows was detected by daily boar exposure. Gilts and sows were inseminated twice with the same boar (12 hours after detection of estrus and 12 hours after the first insemination).

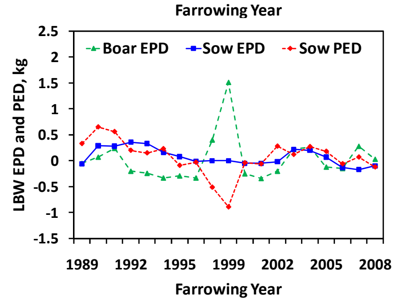
Genetic parameters and trends. Variance and covariance components were estimated using restricted maximum likelihood procedures using an average information algorithm. Data allowed estimation of variance components for pairs of traits only. Ten pairwise analyses were conducted: WSI-NBA, WSI-LBW, WSI-NPW, WSI-LWW, NBA-LBW, NBA-NPW, NBA-LWW, LBW-NPW, LBW-LWW, and NPW-LWW. Models differed by trait. Fixed effects were farrowing year-season, breed group of sow, breed group of boar (litter traits), parity, heterosis (litter traits), sow age, and lactation length (NPW and LWW). Random effects were boar (litter traits), sow, permanent environment, and residual. Boar-sow covariances were assumed to be zero for computational reasons. Relationships among animals were accounted for. Heritabilities, repeatabilities, and genetic, permanent environment, environmental, and phenotypic correlations were computed for all traits. Computations were performed with ASREML (Gilmour et al., 2006). Weighted yearly means of boar and sow expected progeny differences, sow permanent environment deviations, and farrowing year least squares means were used to evaluate genetic, permanent environmental, and environmental trends, respectively.

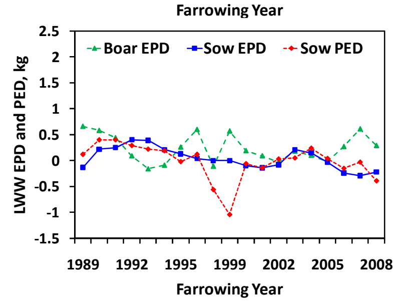
RESULTS AND DISCUSSION

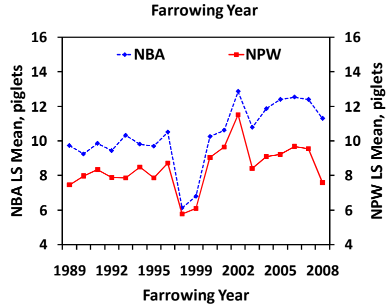
Heritabilities for direct genetic effects were low for WSI (0.04 ± 0.02) and litter traits (0.05 ± 0.02 to 0.06 ± 0.02). Most heritabilities for maternal litter trait effects were from 20% to 50% lower than their direct counterparts. Repeatability for WSI was similar to its heritability whereas repeatabilities for litter traits ranged from 0.15 ± 0.02 to 0.18 ± 0.02. Direct genetic, permanent environment, and phenotypic correlations between WSI and litter traits were near zero. Direct genetic correlations among litter traits ranged from 0.56 ± 0.20 to 0.95 ± 0.05, except for near zero estimates between NBA and LWW, and LBW and LWW. Maternal, permanent environment, and phenotypic correlations among litter traits had similar patterns of values to direct genetic correlations. Genetic and permanent environmental trends are shown in Figure 1, and environmental trends in Figure 2. Boar genetic trends were small and significant only for NBA (-0.015 ± 0.005 piglets/yr, P < 0.004). Sow genetic trends were small, negative, and significant (-0.036 ± 0.013 d/yr, P < 0.01 for WSI; -0.017 ± 0.005 piglets/yr, P < 0.007, for NBA; -0.015 ± 0.005 kg/yr, P < 0.01, for LBW; -0.019 ± 0.008 piglets/yr, P < 0.02, for NPW; and -0.022 ± 0.006 kg/yr, P < 0.003, for LWW). The low significant negative values for boar NBA genetic trend and for sow genetic trends for all litter traits suggest that the phenotypic information used to choose replacements was insufficient to successfully identify the best boars and sows for litter traits in this herd. Permanent environmental trends were small, negative, and significant only for WSI (-0.028 ± 0.011 d/yr, P < 0.02). Environmental trends were positive and significant only for litter traits (P < 0.01 to P < 0.0003). The positive environmental trends for litter trait means between 1989 and 2008 suggest that the level of nutrition, management, and health care of animals in this swine herd improved over time. However, the larger environmental than genetic trends for litter traits suggest that the phenotypic information used for selection primarily reflected environmental rather than genetic effects.

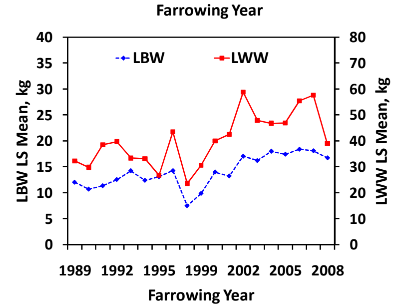












CONCLUSIONS

Although estimates of genetic parameters estimated here for WSI and litter traits were low, they were similar to values found in other swine populations in Thailand and in other countries. However, genetic trends were also low. Thus, the current phenotypic evaluation and selection program would need to be replaced with one based on genetic predictions. One alternative would be to implement a multiple-trait system for litter traits and single-trait system for WSI. It would also be desirable if several farms joined forces to create a larger breeding population in the region. This would increase the likelihood of identifying outstanding animals, and consequently improving genetic trends in the extended population. The proposed system could also serve as a model for future regional and national swine genetic improvement programs in Thailand.

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