GENETIC AND PHENOTYPIC PARAMETERS OF ON-FARM PERFORMANCE TESTING OF LANDRACE AND LARGE WHITE PIGS FROM A LOCAL BREEDING FARM IN THE PHILIPPINES

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ABSTRACT

Restricted maximum likelihood (REML) was used to analyze 6500 on-farm performance test records obtained from a local swine breeding farm from 2014 and 2016, consisting of 2651 Landrace (759 boars; 1912 gilts) and 3829 Large White (1145 boars; 2684 gilts). The high heritability estimates based on paternal half sib correlation for average daily gain, ADG (0.65-0.85 in boars, 0.26-0.37 in gilts), feed conversion ratio, FCR (0.26-0.28), weight at end of test, WtEOT (0.60-0.87 in boars, 0.35-0.43 in gilts), backfat thickness - from shoulder, BFT1 (0.52-0.58 in boars, 0.30-0.51 in gilts), midback, BFT2 (0.45-0.76 in boars, 0.14-0.38 in gilts), ham, BFT3 (0.32-0.61 in boars, 0.36 for gilts), and their average, AveBFT (0.62-0.77 for boars, 0.36-0.42 for gilts) suggest that local selection for performance test traits in Landrace and Large White pigs may lead to substantial response to selection while the significant genetic correlations among them is expected to bring correlated responses in the other traits. Significant phenotypic correlations among performance test traits (except FCR) were positively correlated with each other, ranging from 0.39 to 0.96. FCR was negatively correlated to other boar performance test traits, ranging from -0.32 to -0.83. Significant genetic correlations varied considerably among performance test traits.

Keywords: Genetic and phenotypic correlations, heritabilities, Landrace, Large White, on-farm performance test

INTRODUCTION

The design of swine breeding programs for the tropics requires knowledge of genetic parameters for economically important traits determined under tropical conditions (Akanno et al., 2013). These are needed for accurate and unbiased prediction of genetic values, to predict direct and correlated selection responses, and to develop economic multi-trait selection indices (Van Vleck, 1993; Hofer, 1998).

In the Philippines, local swine farmer-breeders rely on imported purebred boars and gilts for local multiplication and sale as breeding stocks that are required in the subsequent production of commercial hybrids (Bondoc, 2008). However, studies on genetic parameter

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estimation in on-farm performance test traits in a few local breeding farms are very scarce (e.g., Lambio *et al.*, 1991).

In this regard, the aim of the study was to estimate heritabilities, genetic and phenotypic correlations for average daily gain, feed conversion ratio, and backfat measurements at shoulder, mid-back and ham area of Landrace and Large White boars and gilts from a local breeding farm in the Philippines. Such information derived from the application of proper statistical methodology will be especially useful for the National Swine Performance Testing Program established since 1989 (Bondoc and Chua, 2017) as it requires the development of its own selection index to assist our local swine raisers towards an impartial assessment of the genetic values for young boars belonging to different breeds.

MATERIALS AND METHODS

Data for this study were collected from 6500 performance-tested purebred pigs consisting of 2651 Landrace (759 boars and 1912 gilts) and 3829 Large White (1145 boars and 2684 gilts) at the International Farm Corporation (INFARMCO) swine nucleus breeding farm in Barangay San Isidro, Cabuyao, Laguna (approx. 14° 14' 49.69" N, 121° 8' 34.41" E) from 2014 to 2016. The number and distribution of performance-tested animals, sires and dams, by breed, sex and year of birth are shown in Table 1.

The initial weight on performance testing for both breeds and sex was at least 30 kg at 77 days old. Test animals were chosen on the basis of their physical conformation including body length, soundness of feet, and muscle development. Boars were penned in groups of 2 to 3. Gilts were tested in groups of 8 to 10 pigs per pen. Boars and gilts were fed customized starter feeds for 21 days. Boars were then given performance test ration until the end of test. Gilts, on the other hand, were given grower ration and gilt developer ration for 35 days and 49 days, respectively.

Test animals were measured at the start of the test (i.e. 77 ± 3 days old) and at the end of test - 66 days later for boars (i.e. 143 ± 3 days old) or 73 days later for gilts (i.e. 150 ± 3 days old). The performance test traits for boars included average daily gain (ADG, kg/day) and feed conversion ratio (FCR, g/g) covering the test period. In contrast, gilts were

Table 1. Number and distribution of performance-tested animals, sires, and dams, by breed, sex and year of birth.

| | Landrace | | | Large White | | |
	Boars	**Gilts**	**Total**	**Boars**	**Gilts**	**Total**
Total no. of performance tested pigs	759	1912	2671	1145	2684	3829
No. of sires	62	99	161	89	113	202
No. of dams	294	414	708	453	595	1048
Year of birth						
2013	83	379	462	121	404	525
2014	151	298	449	372	631	1003
2015	301	845	1146	429	1177	1606
2016	224	390	614	223	472	695

measured for total ADG, covering the period from birth until the end of test. Gilts were not measured for FCR. Backfat thickness was measured for each boar and gilt using the RENCO© ultrasound backfat probe at shoulder, mid-back and ham. Backfat thicknesses at shoulder (BFT1, mm), mid-back (BFT2, mm) and ham (BFT3, mm) were measured at a position directly above the point of the elbow, last rib and last lumbar vertebra locations, taken 5 cm off the midline on one side of the pig. The average of the three backfat measures (AveBFT, mm) was derived as another trait. Individual age at end of test (AgeEOT, days) and weight at end of test (WtEOT, kg) were also recorded. In this study, performance test traits were analyzed separately for boars and gilts.

The general least squares procedures for unbalanced data were used to examine the principal sources of variation affecting ADG, FCR, BFT1, BFT2, BFT3, AveBFT, AgeEOT and WtEOT of the Landrace and Large White breeds. The following linear "fixed effects" model was used to determine, using an F-test, the appropriate model that would best describe each trait:

$$\mathbf{y}_{ijklmn} = \boldsymbol{\mu} + \mathbf{Sex}_i + \mathbf{YBorn}_{ij} + (\mathbf{Sex \ x \ YBorn})_{ij} + \mathbf{MBorn}_k + \boldsymbol{\beta}_n\mathbf{Covariates}_l + \mathbf{e}_{ijklmn}$$

where
- $\mathbf{y}_{ijklmn}$ is the dependent variable (i.e. performance test trait for each animal),
- $\boldsymbol{\mu}$ is the overall mean,
- $\mathbf{Sex}_i$ is the fixed effect of ith sex (i.e. boar or gilt),
- $\mathbf{YBorn}_{ij}$, $(\mathbf{Sex \ x \ YBorn})_{ik}$, and $\mathbf{MBorn}_l$ are fixed effects for the jth year of birth, interaction effect of ith sex and j^{th} year of birth, k^{th} month of birth, respectively,
- $\boldsymbol{\beta}_n$ is the regression coefficient for $\mathbf{Covariates}_n$ which are random covariate effects of lth age at end of test and/or m^{th} weight at end of test, and
- $\mathbf{e}_{ijklmn}$ is the error term assumed to be normally distributed with variance of errors as constant across observations.

Only those significant (P<0.05) fixed effects and covariates were included in the final linear models. The list of linear models, regression coefficient (no intercept model), and their coefficients of variation (CV) are presented in Table 2.

Variance component estimates for each trait in a breed and sex were estimated using the Restricted Maximum Likelihood Method (REML) option of SAS-VARCOMP (SAS, 2009) fitting the model:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\mu} + \mathbf{e}$$

where,
- $\mathbf{y}$ is a vector of observations,
- $\boldsymbol{\beta}$ is a vector of fixed effects (sex, year and month of birth),
- $\boldsymbol{\mu}$ is a vector of random additive genetic effects,
- $\mathbf{X}$ and $\mathbf{Z}$ are known incidence matrices relating observations to the respective fixed and random effects (sire and dam) and
- $\mathbf{e}$ is a vector of random residual effects.

The procedure uses a Newton-Raphson algorithm, iterating until convergence is reached for the log-likelihood objective function of the portion of the likelihood that does not contain the fixed effects.

Table 2. Mean square F tests for the fixed effects of sex, year of birth, sex x year of birth interaction, month of birth, covariate effects of age and weight at end of test.

	Sex	Year born	Sex x Year born	Month born	Age EOT	Wt EOT	CV (%)
Landrace							
ADG, kg/day	**	**	**	**	** b=-0.004	** b=+0.008	4.97
Feed efficiency, g/g	-	*	**	**	** b=-0.019	** b= -0.038	7.49
BFT1, mm	**	**	**	**	ns	** b=+0.148	16.46
BFT2, mm	**	**	**	**	ns	** b=+0.097	16.65
BFT3, mm	**	**	**	ns	ns	** b=+0.141	16.00
Ave. BFT, mm	**	**	**	**	ns	** b=+0.129	12.64
Age EOT, days	**	**	**	**	-	-	2.36
Wt EOT, kg	**	**	**	**	-	-	10.17
Large White							
ADG, kg/day	**	**	**	**	** b=-0.004	** b= 0.008	5.69
Feed efficiency, g/g	-	*	**	**	** b= 0.013	** b=-0.038	8.08
BFT1, mm	**	**	**	**	ns	** b= 0.148	16.36
BFT2, mm	**	*	**	**	ns	** b= 0.106	15.58
BFT3, mm	**	*	**	**	** b=-0.032	** b= 0.154	14.83
Ave. BFT, mm	**	**	**	**	* b=-0.019	** b= 0.136	11.97
Age EOT, days	**	**	**	**	-	-	2.40
Wt EOT, kg	**	**	**	**	-	-	10.87

Note:　b is regression coefficient using no intercept model
　　　　ns - no significant differences (P>0.05)
　　　　* - significant differences (P<0.05)
　　　　** - highly significant differences (P<0.01)

Heritability values were then computed from the estimates of variance of the random variables, i.e. sire variance (σ^2_{sire}) or covariance of half sibs, dam variance (σ^2_{dam}) or differences between dam groups, and residual variance ($\sigma^2_{residual}$), using the following formulas (Becker, 1984):

Based on paternal half sib correlation: $h^2 = (4\sigma^2_{sire}) / (\sigma^2_{sire} + \sigma^2_{dam} + \sigma^2_{residual})$
Based on maternal half sib correlation: $h^2 = (4\sigma^2_{dam}) / (\sigma^2_{sire} + \sigma^2_{dam} + \sigma^2_{residual})$
Based on full sib correlation: $h^2 = (2 \times (\sigma^2_{sire} + \sigma^2_{dam}) / (\sigma^2_{sire} + \sigma^2_{dam} + \sigma^2_{residual})$

The approximate reliability (standard errors) of the heritability estimates were: for h^2 based on half sib correlation, $SE(h^2) \cong (32h^2)/T$ and for h^2 based on full sib correlation, $SE(h^2) \cong (16h^2)/T$ where T (or total number of individuals measured) = n (or number of individuals per family) x N (or number of families).

The Pearson product-moment correlation coefficients were then computed to measure linear relationships among the performance test traits (i.e. phenotypic correlations) in a particular breed and sex using the CORR procedure of SAS (2009). Genetic correlations among performance test traits in a particular breed and sex were calculated using multivariate Restricted Maximum Likelihood (REML) estimation through the MIXED procedure of SAS (Holland, 2006).

Table 3. Least square means (and standard errors) of performance test traits for different sex and breeds.

	Boars		Gilts	
	Landrace	Large White	Landrace	Large White
ADG, kg/day	0.789 ± 0.002	0.786 ± 0.001	0.587 ± 0.001	0.587 ± 0.001
FCR, g/g	2.64 ± 0.01	2.64 ± 0.01	-	-
BFT1, mm	14.71 ± 0.13	14.14 ± 0.10	15.84 ± 0.07	15.50 ± 0.06
BFT2, mm	11.52 ± 0.10	10.84 ± 0.07	12.15 ± 0.05	11.78 ± 0.04
BFT3, mm	13.22 ± 0.12	12.39 ± 0.08	14.88 ± 0.06	14.73 ± 0.05
Ave BFT, mm	13.15 ± 0.09	12.46 ± 0.06	14.29 ± 0.05	14.00 ± 0.04
AgeEOT, days	144.84 ± 0.14	145.36 ± 0.12	150.01 ± 0.09	150.38 ± 0.08
WtEOT, kg	93.05 ± 0.36	92.30 ± 0.32	84.47 ± 0.22	85.03 ± 0.20

RESULTS AND DISCUSSION

Least square means and standard errors of the performance test traits for breed and sex are given in Table 3.

Boars had higher ADG during the test period than gilts' ADG covering birth to end of test. Boars also had lower backfat thickness measurements but were heavier at the end of test. This could mainly be attributed to younger age of boars at end of test than gilts.

Among boars, Landrace had slightly higher ADG, similar FCR, higher backfat thickness and were heavier at the end of test than Large Whites. Landrace gilts also had slightly higher backfat but slightly lower weight at end of test than Large White gilts. Landrace and Large White gilts had the same total ADG from birth to end of test.

Heritability estimates and standard errors based on paternal half sib (PHS), maternal half sib (MHS), and full sib (FS) correlations are shown in Table 4 and 5. Figure 1 shows heritability estimates by breed x sex for ADG, FE and WtEOT (A) and BFT1, BFT2, BFT3, and AveBFT (B).

Heritability estimates for ADG and WtEOT, BFT1, BFT2, BFT3 and AveBFT were higher in boars than in gilts. Heritability based on PHS correlations were higher than those based on MHS and FS correlations for ADG, WtEOT, BFT1, BFT2 and AveBFT in boars, but the reverse is true for gilts.
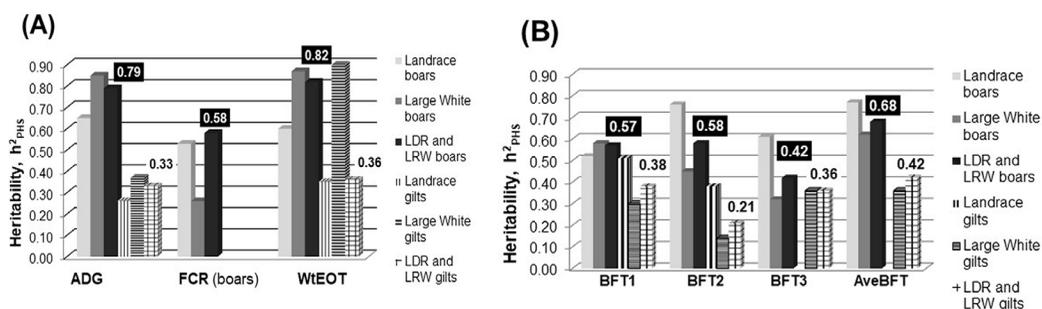

Figure 1. Heritability estimates based on paternal half sib correlation for (A) ADG, FCR (boars) and WtEOT and (B) BFT1, BFT2, BFT3, and AveBFT.

Table 4. Heritability estimates and standard errors ($h^2 \pm SE$) for ADG, FCR, and WtEOT in Landrace and Large White pigs.

	ADG	FCR	Wt EOT
Landrace boars			
- h^2, paternal half sibs	0.65 ± 0.03	0.53 ± 0.02	0.60 ± 0.03
- h^2, maternal half sibs	0.65 ± 0.03	0.55 ± 0.02	0.89 ± 0.04
- h^2, full sibs	0.65 ± 0.01	0.54 ± 0.01	0.74 ± 0.02
Large White boars			
- h^2, paternal half sibs	0.85 ± 0.02	0.26 ± 0.01	0.87 ± 0.02
- h^2, maternal half sibs	0.39 ± 0.01	0.29 ± 0.01	NA
- h^2, full sibs	0.62 ± 0.01	0.01 ± 0.00	NA
LDR and LRW boars			
- h^2, paternal half sibs	0.79 ± 0.01	0.58 ± 0.01	0.82 ± 0.01
- h^2, maternal half sibs	0.47 ± 0.01	0.34 ± 0.01	0.58 ± 0.01
- h^2, full sibs	0.63 ± 0.01	0.46 ± 0.00	0.70 ± 0.01
Landrace gilts			
- h^2, paternal half sibs	0.26 ± 0.00	-	0.35 ± 0.01
- h^2, maternal half sibs	0.60 ± 0.01	-	0.71 ± 0.01
- h^2, full sibs	0.43 ± 0.00	-	0.53 ± 0.00
Large White gilts			
- h^2, paternal half sibs	0.37 ± 0.00	-	0.43 ± 0.01
- h^2, maternal half sibs	0.54 ± 0.01	-	0.64 ± 0.01
- h^2, full sibs	0.46 ± 0.00	-	0.54 ± 0.00
LDR and LRW gilts			
- h^2, paternal half sibs	0.33 ± 0.01	-	0.36 ± 0.00
- h^2, maternal half sibs	0.55 ± 0.00	-	0.65 ± 0.00
- h^2, full sibs	0.44 ± 0.00	-	0.51 ± 0.00

Estimated heritability based on PHS correlations for boar ADG, FCR and WtEOT, BFT1, BFT2, BFT3 and AveBFT were 0.65, 0.53, 0.60, 0.52, 0.76, 0.61 and 0.77 respectively for Landrace and 0.85, 0.26, 0.87, 0.58, 0.45, 0.32, and 0.62 respectively for Large White. PHS heritability estimates for gilt ADG, WtEOT, BFT1, BFT2, BFT3 and AveBFT were 0.26, 0.35, 0.51., 0.38, NA and NA respectively for Landrace and 0.37, 0.43, 0.30, 0.14, 0.36 and 0.36 respectively for Large White.

Nevertheless, high levels of PHS heritability estimates were estimated for ADG (0.65 - 0.85 in boars and 0.26 - 0.37 in gilts), FCR (0.26 - 0.28), WtEOT (0.60 - 0.87 in boars and 0.35 - 0.43 in gilts), BFT1 (0.52 - 0.58 in in boars and 0.30 - 0.51 in gilts), BFT2 (0.45 - 0.76 in boars and 0.14 - 0.38 in gilts), BFT3 (0.32 - 0.61 in boars and 0.36 in gilts), and AveBFT (0.62 - 0.77 in boars and 0.36 - 0.42 in gilts).

Phenotypic measures of performance test traits (except FCR) were significantly (P<0.05) and positively correlated with each other, ranging from 0.42 - 0.83 and 0.39 - 0.95 in Landrace boars and gilts, respectively; and 0.50 - 0.86 and 0.47 - 0.96 in Large White boars

Table 5. Heritability estimates and standard errors (h² ± SE) for BFT1, BFT2, BFT3, and
AveBFT in Landrace and Large White pigs.

	BFT1	BFT2	BFT3	AveBFT
Landrace boars				
- h², paternal half sibs	0.52 ± 0.02	0.76 ± 0.03	0.61 ± 0.03	0.77 ± 0.03
- h², maternal half sibs	0.60 ± 0.03	0.27 ± 0.01	0.58 ± 0.02	0.66 ± 0.03
- h², full sibs	0.56 ± 0.01	0.52 ± 0.01	0.56 ± 0.01	0.71 ± 0.02
Large White boars				
- h², paternal half sibs	0.58 ± 0.02	0.45 ± 0.01	0.32 ± 0.01	0.62 ± 0.02
- h², maternal half sibs	0.35 ± 0.01	0.32 ± 0.01	0.72 ± 0.02	0.48 ± 0.01
- h², full sibs	0.47 ± 0.01	0.62 ± 0.02	0.52 ± 0.01	0.55 ± 0.01
LDR and LRW boars				
- h², paternal half sibs	0.57 ± 0.01	0.58 ± 0.01	0.42 ± 0.01	0.68 ± 0.01
- h², maternal half sibs	0.44 ± 0.01	0.20 ± 0.00	0.67 ± 0.01	0.54 ± 0.00
- h², full sibs	0.51 ± 0.01	0.39 ± 0.00	0.55 ± 0.00	0.61 ± 0.01
Landrace gilts				
- h², paternal half sibs	0.51 ± 0.01	0.38 ± 0.01	NA	NA
- h², maternal half sibs	0.39 ± 0.01	0.19 ± 0.01	0.05 ± 0.00	NA
- h², full sibs	0.45 ± 0.00	0.28 ± 0.00	NA	NA
Large White gilts				
- h², paternal half sibs	0.30 ± 0.00	0.14 ± 0.00	0.36 ± 0.00	0.36 ± 0.00
- h², maternal half sibs	0.36 ± 0.00	0.32 ± 0.00	0.46 ± 0.01	0.46 ± 0.01
- h², full sibs	0.33 ± 0.00	0.23 ± 0.00	0.41 ± 0.00	0.41 ± 0.00
LDR and LRW gilts				
- h², paternal half sibs	0.38 ± 0.00	0.21 ± 0.00	0.36 ± 0.00	0.42 ± 0.00
- h², maternal half sibs	0.55 ± 0.00	0.27 ± 0.00	0.47 ± 0.00	0.45 ± 0.00
- h², full sibs	0.44 ± 0.01	0.24 ± 0.00	0.41 ± 0.00	0.43 ± 0.00

NA means not estimable.

and gilts, respectively. FCR was negatively correlated to other boar performance test traits,
ranging from -0.32 to -0.82 and -0.42 to -0.83 in Landrace and Large White, respectively.

Significant genetic correlations among performance tested traits ranged from -0.08 to
1.00 and -0.01 to 1.00 in Landrace boars and gilts, respectively; -0.50 to 1.00 and -0.08
to -0.57 for Large White boars and gilts, respectively. Some genetic correlations were not
estimated due to the following reasons: did not converge, infinite likelihood, G matrix is not
positive definite, too many likelihood evaluations, and when convergence criteria were met
but final hessian is not positive definite.

The high PHS heritability estimates for ADG, FCR, WtEOT, BFT1, BFT2, BFT3, and
AveBFT suggest that selection for on-farm performance test traits in Landrace and Large
White pigs may lead to significant (direct) response to selection to improve them separately
for Landrace and Large White and for boars and gilts. The significant genetic correlations
among them is expected to bring the correlated responses in the other traits. However,
development and updating the local selection index would be required to maximize the

selection responses for the local markets. While the least square means and estimates of heritability, phenotypic and genetic correlations in this study may correspond with published reports (e.g., Kim *et al.*, 2004; Akanno *et al.*, 2013), differences in the on-farm performance testing protocols should not be overlooked.

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