Genetic Evaluation of Pre-weaning Mortality in Large White Yorkshire Pigs Using Threshold and Linear Models in Hot and Humid Conditions of South India

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ABSTRACT

Background: Large White Yorkshire (LWY) breed has been extensively used for crossbreeding in India. Genetic evaluation of pre-weaning mortality (PWM) in LWY pigs maintained at Kancheepuram district of Tamil Nadu was done to understand adaptability of the breed to tropical conditions.

Methodology: Pre-weaning mortality was recorded as a binomial trait, for which threshold models have been found to be appropriate. (Co)Variance components for random sources of variation including direct genetic, maternal genetic, maternal permanent environmental and common litter were estimated using linear and threshold models. Factors including inbreeding of the individual animal affecting the trait were included as fixed effects in the mixed models used.

Conclusion: The pre-weaning mortality of LWY pigs was comparatively lower indicating better adaptability of the breed. Inbreeding levels above 6 per cent were found to increase PWM. Common litter had significant influence on the genetic parameter estimates. Estimates obtained using threshold model were higher than those obtained by linear models. Threshold models provided solutions for complex models, which had convergence problems with the linear, REML method of estimation. Heritability estimates for PWM obtained through this study could be useful in formulation of breeding plan for LWY pigs in the country.

Key words: Adaptation, Common litter, Heritability, Swine mortality, Tropical conditions.

INTRODUCTION

Large White Yorkshire (LWY) has been predominantly used for crossbreedingin India. Being an exotic breed, genetic evaluation, especially for adaptability under various tropical conditions is essential. Pre-weaning mortality (PWM) is an important fitness attribute, measured as a binomial categorical trait and is a good indicator of adaptability. Studies on genetic parameters for PWM indicate that threshold models (Gianola and Foulley, 1983) are more suitable for the trait as the assumptions of normality and homogenous residual error, required for linear models is not met with in the case of categorical traits (Arango *et al.*, 2005; Arango *et al.*, 2006; Dufrasne *et al.*, 2014). Very few studies on variance components for the trait were available for LWY pigs from the tropics. Meta-analysis of Akanno *et al.* (2013) indicated only three papers for exotic pigs in the whole of tropics. Studies from other parts of the world, using linear models report very low heritability for PWM (Lund *et al.*, 2002; Grandinson *et al.,* 2002), while a few studies based on threshold models show slightly higher estimates (Arango *et al.*, 2006; Dufrasne *et al.*, 2014). Previous studies on genetic evaluation of LWY pigs for PWM using threshold models were not available from India. The objective of this study was to compare estimates of heritability for PWM by linear and non-linear threshold models in LWY pigs rearedin the tropics.

MATERIALS AND METHODS

Data on mortality of 6935 LWY pigs maintained from 1990

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to 2015 were collected from the pig unit of Postgraduate Research Institute in Animal Sciences, TANUVAS. New born piglets were housed with the sows up to weaning. The climate in the region is hot and humid. The mean minimum temperature varies from 19.69°C in January to 28.14°C in May. The mean maximum temperature varies from 27.27°C in January to 37.53°C in May. The relative humidity ranges from 51.19 to 66.65 per cent and is highest during the months of December. Males and females were selected based on litter size at birth (9 and above), litter size at weaning (8 and above), number of teats (minimum six pairs), weaning weight and five-month body weight. Animals were protected against various diseases epidemic to the region. On the first day of

birth, needle teeth cutting was carried out and iron supplement, iron dextron @100-200 mg per piglet was given intramuscularly. Weaning was done at the age of 42 days. Pre-weaning mortality (PWM) was studied as a binary trait and effect of various fixed factors on the trait were studied by using a general linear model.

$$Y_{ijklmno} = \mu + P_i + Q_j + R_k + S_l + T_m + F_n + e_{ijklmno}$$

$Y_{ijklmno}$ is the PWM of the oth animal belonging to i^{th} period of birth, j^{th} season of birth, k^{th} sex of birth, l^{th} parity of birth, m^{th} litter size at birth and n^{th} inbreeding class. P, Q, R, S, T and F are effects of period, season, sex, parity, litter size and inbreeding class, respectively and $e_{ijklmno}$ the random error associated with each observation

(Co)Variance components for PWM were estimated by linear and threshold mixed models. The estimation for linear mixed models were done by Restricted Maximum Likelihood Method (REML) using WOMBAT program of Meyer (2007).

The threshold models were analysed by Gibb's sampling using THRGIBBSF90 (Misztal *et al.*, 2002) and post Gibbs analyses were done using POSTGIBBSF90, a program developed by S. Tsuruta (Misztal *et al.*, 2002). A single chain of 200000 cycles with an initial burn-in of 20000 cycles was run and every 20th sample was stored to obtain a total of 9,000 samples to compute posterior means, standard deviations and confidence interval. Starting values for (co) variance components were obtained from preliminary analysis using linear models implemented with restricted maximum likelihood (Kass *et al.*, 1998).The efficiency of gibbs sampling was inferred based on Monte Carlo error, Geweke's statistic, effective sample size and autocorrelations. Point estimates of parameters were calculated as the posterior modes of the respective variance components. The following models were run with various combinations of random effects.

$Y = Xb + Z_a a + e$	....	Model 1
$Y = Xb + Z_a a + Z_m m + e$	....	Model 2
$Y = Xb + Z_a a + Z_{mp} mp + e$	....	Model 3
$Y = Xb + Z_a a + Z_c c + e$	....	Model 4
$Y = Xb + Z_a a + Z_m m + Z_{mp} mp + e$	....	Model 5
$Y = Xb + Z_a a + Z_m m + Z_c c + e$	....	Model 6
$Y = Xb + Z_a a + Z_{mp} mp + Z_c c + e$	....	Model 7
$Y = Xb + Z_a a + Z_m m + Z_p mp + Z_c c + e$	....	Model 8

Where,

'Y' is a N x 1 vector of records, 'b' denotes the fixed effects in the model with association matrix X, 'a' is the vector of direct genetic effects with the association matrix Z_a, 'm' is the vector of maternal genetic effects with the association matrix Z_m, 'mp' is the vector of maternal permanent environmental effects with the association matrix Z_{mp}, 'c' is the vector of common litter environmental effects with the association matrix Z_c and 'e' denotes the vector of residual (temporary environment) effect.

The assumed variance and covariance structure was as follows:

$$V\begin{bmatrix} a \\ m \\ mp \\ c \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2_a & 0 & 0 & 0 & 0 \\ 0 & A\sigma^2_m & 0 & 0 & 0 \\ 0 & 0 & I\sigma^2_{mp} & 0 & 0 \\ 0 & 0 & 0 & I\sigma^2_c & 0 \\ 0 & 0 & 0 & 0 & I\sigma^2_e \end{bmatrix}$$

RESULTS AND DISCUSSION

The pedigree file had 7069 animals of which mortality records were available for 6935 LWY piglets. The descriptives including frequency and proportion for PWM is presented in Table 1. The mortality per cent in the population studied was 4.0 per cent. The least squares means for PWM and effect of various non-genetic factors on the trait are listed in Table 2. The overall PWM was 4.80 per cent.

The overall least squares mean PWM observed in this study was low (4.80 %) compared to other studies [Singh *et al.*, 1990 (25.71%); Gopinathan, 2001 (26.63%); Gupta *et al.*, 2001; Nuntapaitoon and Tummarak, 2015 (14.5%)]. This value of 4.80 per cent was low even when compared to mortality of LWY pigs in Netherlands, where the conditions are similar to the place of origin of LWY (Knol *et al.*, 2002). Very low PWM for LWY in the region is indicative of better adaptability to the region.

Period, season, sex, parity and level of inbreeding was found to affect PWM. The PWM was higher in piglets born during south-west monsoon. Increase in bacterial load during rainy season, overlay of piglets during rainy days and higher humidity could be the possible reasons for this observation. The mortality gradually reduced up to third parity after which it increased.

Significant effect of level of inbreeding on PWM was observed in the present study. The fourth class with 6.126

Table 1: Frequencies and proportions for Pre-weaning Mortality in LWY pigs.

No. of records	6935
No. of animals in pedigree	7069
No. of sires	130
No. of dams	360
Mean	4.80%
SD	0.035%
CV (%)	0.80
Variance	0.002
Range	0-1

to 12.5 per cent F was found to have maximum PWM, which was significantly different from other classes (Gowrimanokari *et al.,* 2019). Rothschild(1996) reported that about 10% of inbreeding in both litter and dam accounted for reductions in embryo survival and number born alive.

The estimates of variance components and heritability estimated using linear models are presented in Table 3. The best fit noticed was for Model 4 which included direct genetic and common litter effect and the estimate of heritability from this model was very low (0.02).

The results of threshold model with direct additive and common litter as effect is presented in Table 4.The time series trace of direct genetic and common litter components of variance are presented in Fig 1, which showed straightening of the chain, indicative of convergence.The MCMC parameters *viz*., Monte Carlo error and Geweke's

statistic also were low and indicated good convergence. The estimate of heritability for PWM obtained through threshold model, including common liter effect was much higher (0.15), almost seven times that of the linear model.

Several studies have proven that ignoring maternal effects can lead to biased estimates (Satoh *et al.*, 2002; Chimonyo *et al.*, 2006; Ilatsia *et al.*, 2008; Akanno *et al.*, 2013). Litter-bearing species usually have a large number of non-additive relationships (Norris *et al.*, 2007) and common litter effects should be accounted for in the model for analysis of traits (Satoh *et al.*, 2002; Chimonyo *et al.*, 2006; Chimonyo and Dzama, 2007; Ilatsia*et al.*, 2008; Akanno *et al.*, 2013). In the present study, maternal genetic, maternal permanent environmental and common litter effects were included in addition to the individual animal as random effect. Model 4 with direct additive and common

Table 2: Least squares means for pre-weaning mortality in LWY pigs.

Effects	N	Mean (%)	Effects	N	Mean (%)
Overall mean	6935	4.80 ± 0.50			
Period	**		**Sex**	*	
1990-1995	638	6.40[a] ± 0.90	Male	3526	5.30 ± 0.50
1996-2000	675	3.20[c] ± 0.90	Female	3409	4.30 ± 0.50
2001-2005	1741	4.90[bc] ± 0.60	**Inbreeding levels**	*	
2006-2010	1741	5.50[ab] ± 0.60	0	4937	3.80[b] ± 0.40
2011-2015	2140	3.70[c] ± 0.50	>0 - 3.125%	738	3.50[b] ± 0.80
Season of birth	**	3.126 - 6.125%	193	4.90[b] ± 1.40	
Summer	1625	4.20[b] ± 0.60	6.126 - 12.5%	517	7.30[a] ± 0.90
South west monsoon	1859	6.10[a] ± 0.60	12.6 % and above	550	4.30[ab] ± 0.80
North east monsoon	1813	4.20[b] ± 0.60	**Litter size at birth**	NS	
Winter	1638	4.50[b] ± 0.60	<7	469	5.50 ± 0.10
Parity	**	7	699	4.80 ± 0.80	
1	2665	4.50[abc] ± 0.50	8	1004	5.00 ± 0.70
2	1545	3.40[bc] ± 0.60	9	1466	4.80 ± 0.70
3	1064	2.90[c] ± 0.70	10	1468	4.50 ± 0.60
4	735	5.10[ab] ± 0.80	11	811	4.10 ± 0.80
5	446	6.00[a] ± 1.00	12	592	5.40 ± 0.80
6	480	6.80[a] ± 1.00	13 and above	426	4.20 ± 0.10

- Highly significant (p < 0.01); * - Significant (p < 0.05); NS - Non significant. Means carrying same superscript within effect did not havesignificant difference. N - Number of observations. Dashes indicate that the effect was not included in the model.

Table 3: Estimates of (co) variance components and heritability for pre-weaning mortality in Large White Yorkshire pigs obtained through linear mixed models.

Model	σ^2_e	σ^2_a	σ^2_m	σ^2_{pe}	σ^2_c	h^2 ± S.E.	h^2_m ± S.E.	log L
1	0.031	0.005	-	-	-	0.13 ± 0.03	-	8182.496
2	0.031	0.003	0.0009	-	-	0.09 ± 0.03	0.03 ± 0.01	8175.910
3	0.031	0.003	-	0.0009	-	0.08 ± 0.02	-	8177.327
4	0.030	0.001	-	-	0.004	0.02 ± 0.01	-	8253.122
5	0.031	0.003	0.00014	0.0008	-	0.07 ± 0.03	0.004 ± 0.01	8177.377
6	0.030	0.0005	0.00005	-	0.004	0.02 ± 0.02	0.001 ± 0.01	8243.060

σ^2_e - Error variance; σ^2_p - Phenotypic variance; σ^2_a- Direct additive genetic variance; σ^2_m - Maternal genetic variance; σ^2_{mp} - Maternal permanent environmental variance; σ^2_c - Common litter environmental variance; h^2 - Direct heritability; h^2_m - Maternal heritability; log L - Log likelihood; S.E. - Standard error. Best fit model is shown in bold letters. The dashes indicate that the effect was not included in the model. Models 7 and 8 did not converge with REML.

Table 4: MCMC parameters obtained from posterior distribution and heritability estimate for pre-weaning mortality estimated through threshold model.

Random effect	MCE	Mean	Median	Mode	Eff. sample size	Geweke's diagnostic	Autocorrelations			Heritability
							Lag 1	Lag 10	Lag 50	
Direct additive	0.047	0.46	0.40	0.31	40.3	0.30	0.982	0.841	0. 464	0.15 ± 0.001
Common litter	0.007	0.62	0.60	0.57	457.9	0.23	0.703	0.148	0.050	
Residual	0.0003	1.00	1.00	1.00	8000	0.15	-0.011	0.008	0.003	

MCE- Monte Carlo error.
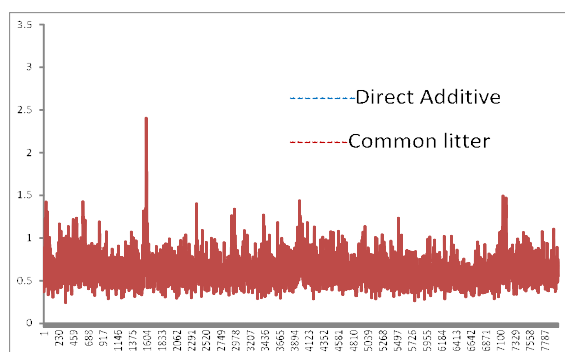
Fig 1: Iteration wise time-series trace for direct additive and common litter variance obtained through gibbs sampling.

litter effect was found to be the best model in the linear mixed model analysis. However, convergence could not be reached for the more complex models (7 and 8). Knol *et al.*, 2002 also encountered problems of non-convergence with linear estimation for complex models. The threshold models had the advantage that estimates could be obtained irrespective of the complexity of models. Though convergence was obtained for complex models (7 and 8), the DIC values were larger.The same factors as in model 4 were used for the threshold models.

Comparison of estimates of heritability for traits like PWM is complex; as the model used, method of estimation and type of random effects included will influence the magnitude of estimates (Arango *et al.*, 2006; Dufrasne *et al.*, 2014). Meta-analysis of Akanno *et al.* (2013) reported a comparatively large heritability estimate of 0.2 for PWM, which was based on three studies on pig mortality from the tropics. The large estimate was attributed to the method of half sib correlation used in the base studies. Similarly using the full sib correlation, Mesa *et al.*, 2006 observed heritability of 0.18 for weaning survival. However, these studies did not consider important random sources of variation such as maternal and common litter effects and method of estimation was linear.

Earlier studies using linear models reported very low heritability values of 0.00 to 0.01 (Lund *et al.*, 2002; Grandinson *et al.*, 2005; van Arendonk *et al.*, 1996; Knol *et al.*, 2002). These studies included other sources of maternal variation as done in the present study.

Earlier studies on piglet mortality based on the threshold model reported values of heritability ranging from 0.02 to 0.05. The estimates obtained through threshold models were

usually higher than those from linear models (Arango *et al.*, 2006; Roehe *et al.*, 2010; Dufrasne *et al.*, 2014). Linear models ignore the categorical nature of binary traits like PWM. PWM is a categorical trait and assumptions for the linear model such as normality and homoscedasticity of error are not completely met. Threshold models have been found to be most suitable for such traits and as observed in earlier studies estimates obtained by threshold model in this study were higher than thoseestimated by linear models. Studies with estimates of heritability for PWM for LWY pigs were not available from India for comparison.

CONCLUSION

The pre-weaning mortality of LWY pigs was comparatively lower indicating better adaptability of the breed. Inbreeding levels above 6 per cent were found to increase PWM. Common litter had significant influence on the estimates. Estimates obtained using threshold model were higher than those obtained by linear models. Threshold models provided solutions for complex models, which had convergence problems with the linear, REML method of estimation. Heritability estimates for PWM obtained through this study could be useful as reference values for formulation of breeding plan for LWY pigs.

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