



Investigating pig survival in different productive stages using genomic models

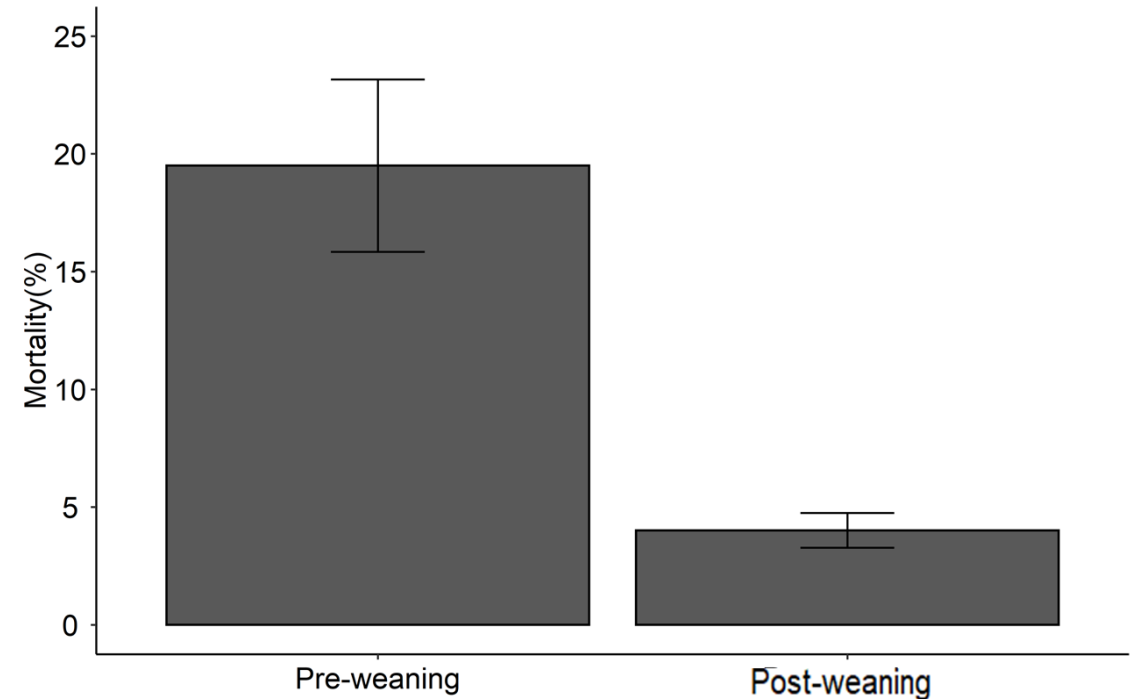
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Introduction

Economic and animal welfare concern

~20% pre-weaning

~4% post-weaning



Agostini et al., 2014; Hellbrügge et al., 2008; Arango et al., 2006; Grandinson et al., 2005; Maes et al, 2004; Grandinson et al., 2002; Knol et al., 2002; Maes et al., 2001

Introduction

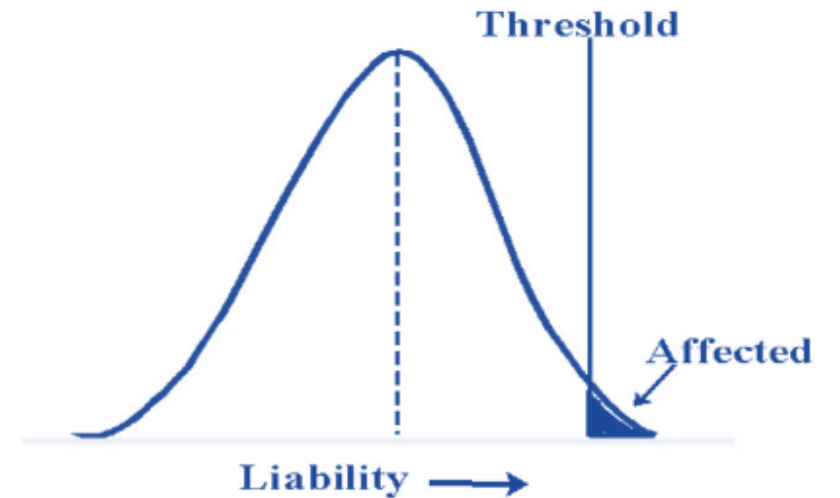
Genetic basis

Pre-weaning

Hellbrügge et al., 2008; Arango et al., 2006; Grandinson et al., 2005; Grandinson et al., 2002; Leenhouders et al., 2003, Su et al., 2004; Knol et al., 2002; Lund et al., 2002; Mesa et al., 2002; Tuchscherer et al 2000; Arendonk et al., 1996; Blasco et al., 1995

Post-weaning

Dufresne et al., 2014



Introduction

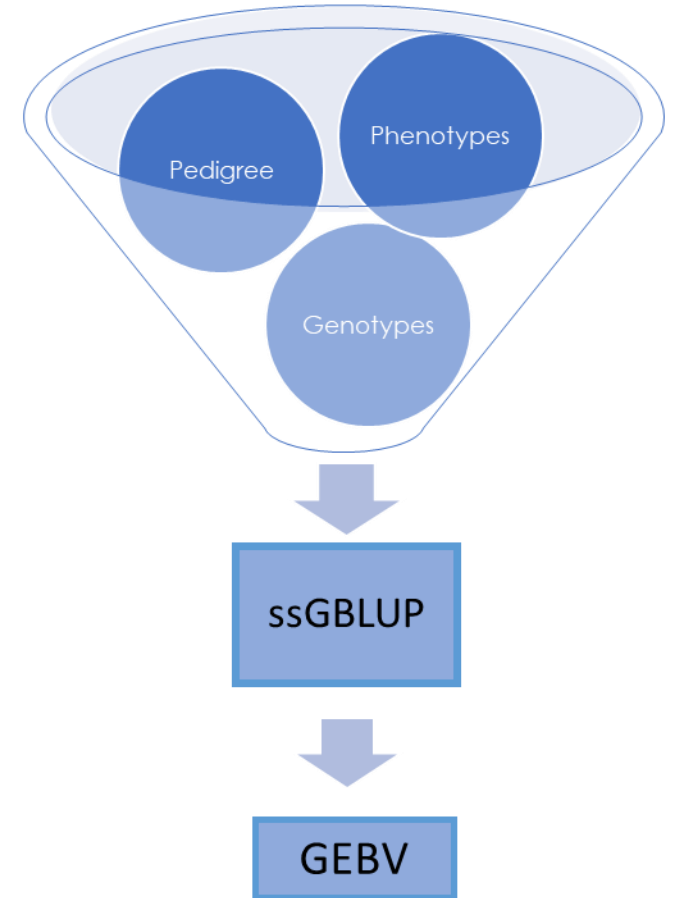
Genomic information from high density SNP panels

Single-step genomic BLUP

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + H^{-1}\lambda \end{bmatrix} \begin{bmatrix} \beta \\ u \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$



$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$



Legarra et al., 2009

Objectives

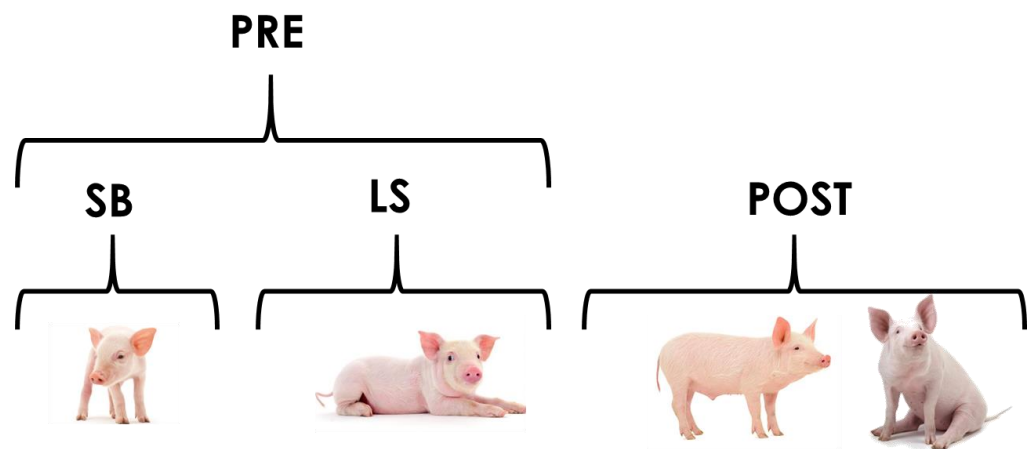
- 1) to estimate genetic parameters for survival in different productive stages using threshold models
- 2) to compare traditional pedigree-based BLUP and single-step GBLUP evaluations

Materials and Methods - Data

64,962 crossbred records

4,237 litters (1,250 sows and 590 boars)

9,916 genotyped 50K SNP chip - Illumina



Stage	Survival(%)
Stillborn	0.94
Lactation	0.89
Pre-weaning	0.83
Post-weaning	0.96

Materials and Methods - Models

(1) SB: $\mathbf{l} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_{\text{hys}} + \mathbf{Z}_3\mathbf{u}_{\text{li}} + \mathbf{e},$

LS: $+ \mathbf{Z}_4\mathbf{u}_m$

POST: $+ \mathbf{Z}_5\mathbf{u}_{\text{gr}}$

(2) PRE: $+ \mathbf{Z}_4\mathbf{u}_m$

POST: $+ \mathbf{Z}_5\mathbf{u}_{\text{gr}}$

Parents bought

Records on piglets

Finished pigs sold

Materials and Methods – Validation

LR Validation

Corrected phenotype (binary)

Validation on the youngest piglets with genotype and phenotype

Prediction accuracy:

$$\hat{\rho} = \sqrt{\frac{\text{cov}((G)EBV_W, (G)EBV_P)}{(1 + \bar{F} - 2\bar{f})\sigma_u^2}}$$

Trait	Phenotypes	Validation
Stillborn	1,249	789
Lactation	52,529	5,613
Pre-weaning	56,264	5,656
Post-weaning	32,595	4,771

Results – Genetic parameters

Model	Trait	%VE *				
		h_a^2	h_m^2	σ_{hys}^2	σ_{li}^2	σ_{gr}^2
1	SB	0.09 ^(0.01)	-	0.01 ^(0.00)	0.16 ^(0.01)	-
	LS	0.07 ^(0.01)	0.05 ^(0.01)	0.06 ^(0.02)	0.09 ^(0.01)	-
	POST	0.06 ^(0.02)	-	0.26 ^(0.04)	0.10 ^(0.01)	0.17 ^(0.02)

* Proportion of total phenotypic variance explained

SB: $\mathbf{l} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_{hys} + \mathbf{Z}_3\mathbf{u}_{li} + \mathbf{e},$

LS: $+ \mathbf{Z}_4\mathbf{u}_m$

POST: $+ \mathbf{Z}_5\mathbf{u}_{gr}$

Results – Genetic parameters

		%VE *				
Model	Trait	h_a^2	h_m^2	σ_{hys}^2	σ_{li}^2	σ_{gr}^2
2	PRE	0.06 ^(0.02)	0.06 ^(0.01)	0.06 ^(0.01)	0.09 ^(0.01)	-
	POST	0.06 ^(0.02)	-	0.26 ^(0.04)	0.10 ^(0.01)	0.17 ^(0.02)

* Proportion of total phenotypic variance explained

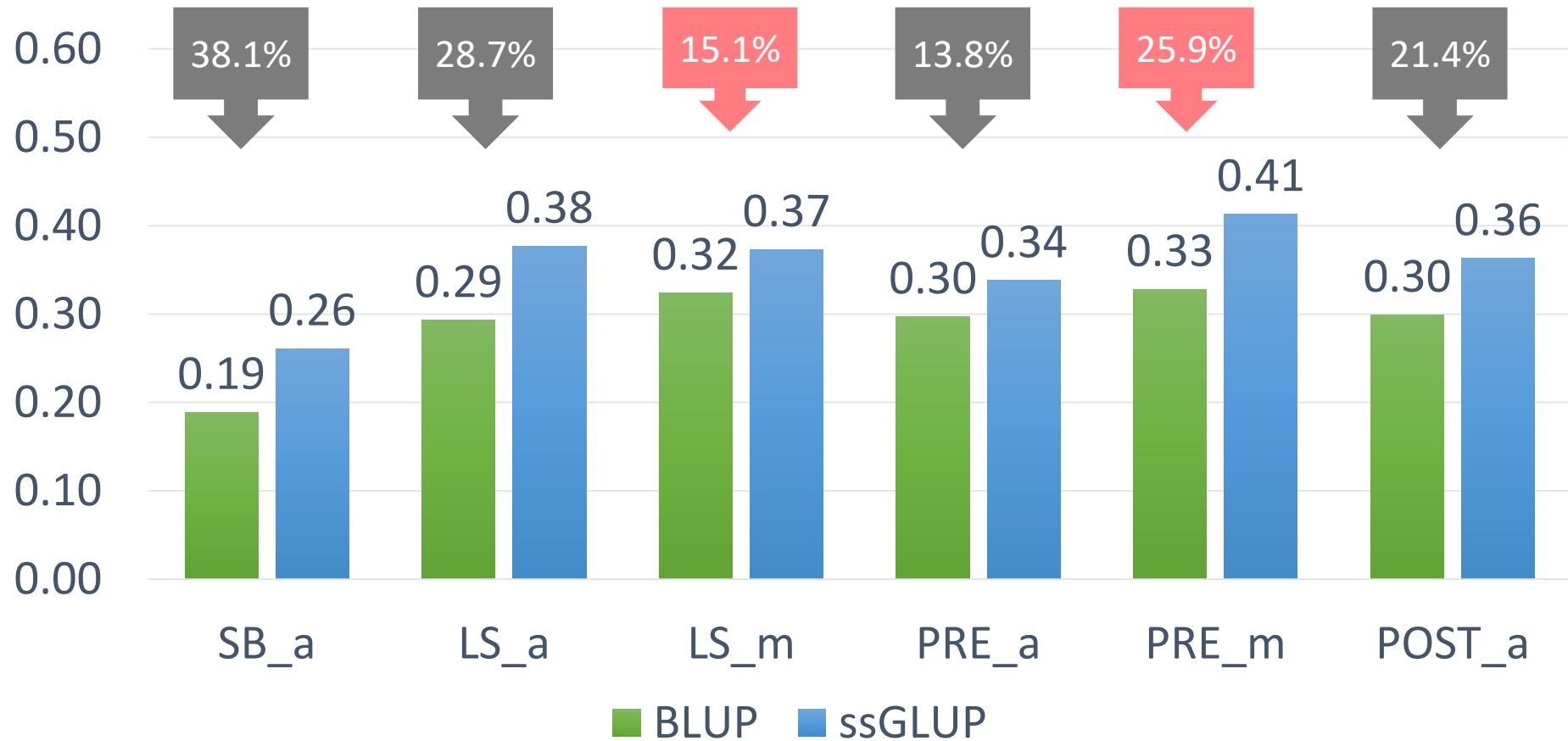
PRE: $\mathbf{l} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_2\mathbf{u}_m + \mathbf{Z}_3\mathbf{u}_{hys} + \mathbf{Z}_4\mathbf{u}_{li} + \mathbf{e},$

POST: $\mathbf{l} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{u}_a + \mathbf{Z}_3\mathbf{u}_{li} + \mathbf{Z}_4\mathbf{u}_{hys} + \mathbf{Z}_5\mathbf{u}_{gr} + \mathbf{e}.$

Results – Genetic parameters

Model	Traits	$r_{a1,a2}$
1	SB-LS	0.90 ^(0.06)
	SB-POST	0.14 ^(0.14)
	LS-POST	0.43 ^(0.14)
2	PRE-POST	0.19 ^(0.17)

Results – Accuracy



Conclusions

- There is significant evidence of exploitable genetic variance
- SB and LS are highly correlated (0.90) and can be considered the same trait
- All pre-weaning stages are weakly positive or non-correlated with post-weaning survival
- Genomic information through single-step increased the accuracy of survival in up to 38.1%

Acknowledgements

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