

Genomic prediction of growth in pigs based on additive and dominance effects

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Acknowledgement



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Recent developments



Focus: additive effects (EBV)

Performance? Dominance effects?

Recent developments

Pedigree-based

☹️ difficult to accurately estimate dominance effects

de Boer et al. (1993); Misztal (1997)

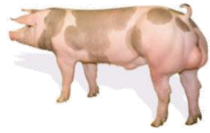
Genomic-based

😊 Dominance variance and dominance effects in genomic evaluations

Toro and Varona (2010); Su et al. (2012); Vitezica et al. (2013); Zeng et al. (2013); Da et al. (2014); etc.

Do dominance effects contribute to the phenotypic variance of growth in purebred pig populations?

Material and methods



Pietrain (1,424)



Landrace (2,023)



Large White (2,157)

- Genotyped 60K chip
- Growth: from birth to ~120Kg (pre-corrected)

Within line (>30,000 animals) pedigree-based linear model in ASReml v3 (Gilmour et al., 2009)

$$y \sim \text{sex} + \text{HYW} + \text{BW} + \text{litter} + \text{pen} + \text{animal} + e$$

$$y_c = y - \text{sex} - \text{HYW} - \text{BW} - \text{pen}$$

Material and methods

Random regression on SNP genotypes: BayZ (<http://www.bayz.biz/>)

$$\mathbf{y}_c = \mathbf{1}\mu + \mathbf{Lb} + \mathbf{Aa} + \mathbf{e} \quad (\text{MA})$$

$$\mathbf{y}_c = \mathbf{1}\mu + \mathbf{Lb} + \mathbf{Aa} + \mathbf{Dd} + \mathbf{e} \quad (\text{MAD})$$

Vitezica et al. (2013); Nishio and Satoh (2014)

$$\mathbf{A}_{i,j} = \begin{cases} 0 - 2p_j \\ 1 - 2p_j \\ 2 - 2p_j \end{cases} \quad \text{and} \quad \mathbf{D}_{i,j} = \begin{cases} -2p_j^2 \\ 2p_jq_j \\ -2q_j^2 \end{cases} \quad \text{for genotypes} \begin{cases} \text{GG} \\ \text{GC} \\ \text{CC} \end{cases}$$

$a \sim N(0, \sigma_a^2)$ and $d \sim N(0, \sigma_d^2)$

$\sigma_{\mathbf{Aa}}^2$ and $\sigma_{\mathbf{Dd}}^2$ each MCMC cycle

MCMC: 350,000

burn-in 50,000

each 100

Variance explained



Population*	Model	σ_{Aa}^2/σ_p^2	σ_{Dd}^2/σ_p^2	σ_{Dd}^2/σ_g^2
Pietrain	MA	0.26 (0.04)	0.11 (0.05)	0.30
	MAD	0.26 (0.04)		
Landrace	MA	0.28 (0.03)	0.06 (0.04)	0.18
	MAD	0.27 (0.03)		
Large White	MA	0.26 (0.03)	0.04 (0.02)	0.13
	MAD	0.26 (0.03)		



*80% oldest animals were used for estimating variance components

$$\sigma_p^2 = \sigma_{Aa}^2 + \sigma_{Dd}^2 + \sigma_L^2 + \sigma_e^2$$

$$\sigma_g^2 = \sigma_{Aa}^2 + \sigma_{Dd}^2$$

Can we predict phenotypes more accurately
using **MAD** instead of **MA**?

Accuracy of prediction



Population*	Model	\hat{u}	\hat{g}
Pietrain	MA	0.195	0.222
	MAD	0.190	
Landrace	MA	0.277	0.284
	MAD	0.277	
Large White	MA	0.354	0.359
	MAD	0.354	

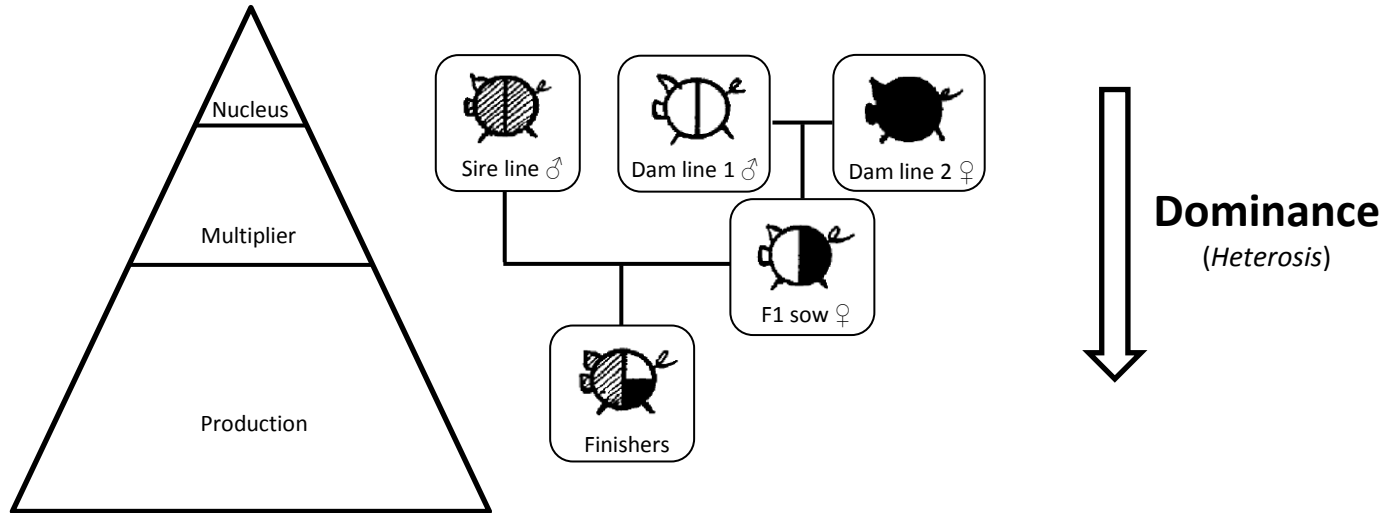
$$\hat{u} = A\hat{a}$$

$$\hat{g} = A\hat{a} + D\hat{d}$$

*20% youngest animals were used for validation

Correlation(\hat{u} or \hat{g} , y_c)

Do dominance effects contribute to the phenotypic variance of growth in **CROSSBRED** pig populations?



Final considerations

- σ_{Dd}^2 accounts for 13-30% of σ_g^2
- σ_{Aa}^2/σ_p^2 was similar across lines (0.26-0.28)
- σ_{Dd}^2/σ_p^2 varied considerably across populations (0.04-0.11)

- $\uparrow \sigma_{Dd}^2/\sigma_g^2$, \uparrow added value for predicting phenotypes (growth)

- Larger datasets