

Relevance of purebred information for predicting genetic merit of survival at farrowing of crossbred piglets



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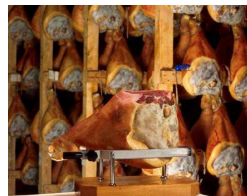
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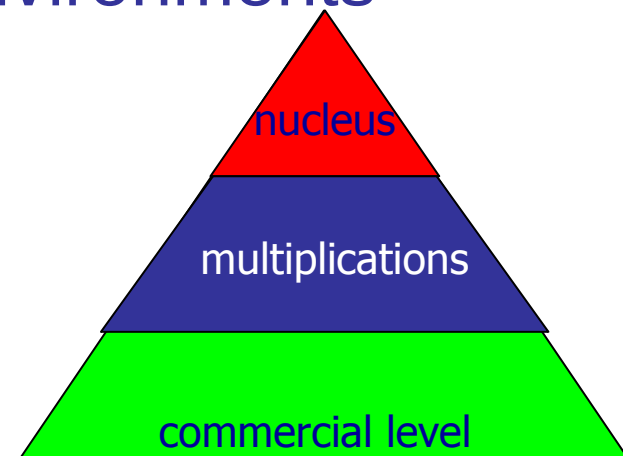
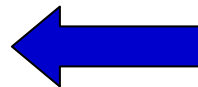
Introduction

In a commercial pig-breeding program:

- Economic importance is focused on crossbred performance
- Selection is largely carried out in nuclei of purebreds
- Animals are raised in different environments



trasformation





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Introduction

Genotype x environment interaction (**G x E**):

- Measured by the genetic correlation between phenotypes for the same genotype in different environments (Falconer, 1952)
- Reciprocal recurrent selection (**RRS**)
- Combined purebred and crossbred selection (**CCPS**)
- Use of data recorded only in crossbreds for evaluation of purebreds





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Introduction

- Piglet farrowing survival is relevant
 -  **economical:** estimated loss for each piglet dead ~ 15\$ USA (NSIF, 2000) and 14 € Italy (C.R.P.A., 2006)
 -  **animal welfare:** acceptability of the production system by the consumer
- Additive genetic variation is large enough to be exploited in breeding programs (Grandison et al., 2002; Knol et al., 2002; Lund et al., 2008)
- Does purebred performance (in nucleus) predict accurately outcomes in crossbreds (commercial tier) ?





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Aim

- Infer (co)variance components for farrowing survival in purebred sire line and crossbred pigs



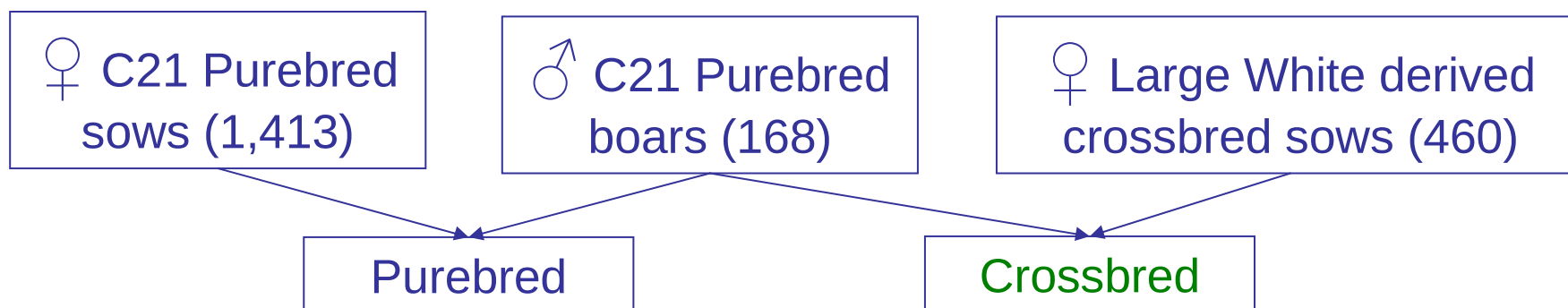


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Data

- 30,919 purebreds (3,162 litters)
- 13,643 **crossbreds** (1,213 litters)
- born from 2000 to 2006
- originated by mating:



- ***data recorded (nucleus and commercial farm)***



routine data (identity, sex, litter, etc.)



piglet mortality (dead or alive at birth)





Statistical analysis

Bayesian bivariate threshold model

$$\begin{pmatrix} \tilde{y}_1 \\ \tilde{y}_2 \end{pmatrix} = \begin{pmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{pmatrix} \begin{pmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{1s} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{2s} \end{pmatrix} \begin{pmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{1d} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{2d} \end{pmatrix} \begin{pmatrix} \mathbf{d}_1 \\ \mathbf{d}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{1l} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{2l} \end{pmatrix} \begin{pmatrix} \mathbf{l}_1 \\ \mathbf{l}_2 \end{pmatrix} + \begin{pmatrix} \boldsymbol{\varepsilon}_1 \\ \boldsymbol{\varepsilon}_2 \end{pmatrix}$$

where:

$\tilde{y}_1 \quad \tilde{y}_2$ is a vector to liability to survival for pure and crossbred

$\boldsymbol{\beta}_1 \quad \boldsymbol{\beta}_2$ vector of non genetic effects (sex, litter size, parity of the dam, year-month of birth)

$\mathbf{s}_1 \quad \mathbf{s}_2$ vector of sire effects

$\mathbf{d}_1 \quad \mathbf{d}_2$ vector of dam effects

$\mathbf{l}_1 \quad \mathbf{l}_2$ vector of litter effects

$\boldsymbol{\varepsilon}_1 \quad \boldsymbol{\varepsilon}_2$ vector of residual effects





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Statistical analysis

$$p(s_1, s_2, d_1, d_2, l_1, l_2, \beta_1, \beta_2, G_{0sd}, \sigma_{d2}^2, \sigma_{l1}^2, \sigma_{l2}^2) =$$

$$p(\beta_1, \beta_2) p(s_1, s_2, d_1 | G_0) p(d_2 | \sigma_{d2}^2) p(l_1 | \sigma_{l1}^2) p(l_2 | \sigma_{l2}^2)$$

$$\times p(G_0) p(\sigma_{d2}^2) p(\sigma_{l1}^2) p(\sigma_{l2}^2) p(\sigma_{\varepsilon1}^2) p(\sigma_{\varepsilon2}^2)$$

$$G_0 = \begin{pmatrix} \sigma_{s1}^2 & \text{Symm} & & \\ \sigma_{s1,s2} & \sigma_{s2}^2 & & \\ \sigma_{d1,s1} & \sigma_{d1,s2} & \sigma_{d1}^2 & \\ & & & \end{pmatrix}$$

- LW-derived dams (dams of crossed animals) are unrelated to individuals in the sire nucleus





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Statistical analysis

$$\begin{pmatrix} \mathbf{l}_1 \\ \mathbf{l}_2 \\ \mathbf{d}_2 \\ \mathbf{s}_1 \\ \mathbf{s}_2 \\ \mathbf{d}_1 \end{pmatrix} \sim N \left[\mathbf{0}, \begin{pmatrix} \mathbf{I}\sigma_{l1}^2 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_{l2}^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{A}_{LW}\sigma_{d2}^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{G}_0 \otimes \mathbf{A}_{C21} \end{pmatrix} \right]$$

$\mathbf{A}_{LW}$ is the matrix of additive relationships among LW-derived dams

$\mathbf{A}_{C21}$ is the numerator relationship among sires and dams of the nucleus





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Model comparison

- Four models evaluated using the Bayesian information criterion (**BIC**, Schwartz, 1978):
 - M1 litter
 - M2 litter + dam
 - M3 litter + sire
 - M4 litter + dam + sire
- Convergence assessed by inspection of trace plots
- After burn-in (20,000) the number of samples were 600,000 for M1 to M4 respectively



Results





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Descriptive statistics of farrowing survival in purebred and crossbred line

Characteristics	Number or value	
	Purebred	Crossbred
Total number of piglets born	39,919	13,643
Survival at birth (%)	89.41	92.79
Number of litters	3,162	1,213
Number of sows	1,413	460
Number of boars	168	168





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Log-Likelihood value and BIC

Model (random effects)	N. of variance and covariance	Log-Likelihood	BIC ¹		
			M2	M3	M4
M1 (Litter)	4	-11,470	0		
M2 (Litter+Dam)	6	-11,467	15.83		
M3 (Litter+Sire)	7	-11,472	36.73	20.90	
M4 (Litter+Dam+Sire)	10	-11,468	60.61	44.78	23.87

$$^1BIC_{r,s} = -2 (\log Lik r - \log Lik s) - (Pr - Ps) \log(N)$$



Posterior means (SD) for (co)variance components of farrowing survival by model and trait (pure/crossbred)

Model	Component	Purebred	Crossbred
M1	σ^2_{litter}	0.407 (0.025)	0.295 (0.035)
M2	σ^2_{litter}	0.357 (0.024)	0.214 (0.032)
	σ^2_{dam}	0.077 (0.023)	0.112 (0.034)
M3	σ^2_{litter}	0.393 (0.024)	0.268 (0.035)
	σ^2_{sire}	0.021 (0.009)	0.033 (0.021)
	$\sigma_{\text{sire (pure-cross)}}$		0.0015 (0.011)
M4	σ^2_{litter}	0.347 (0.025)	0.189 (0.032)
	σ^2_{dam}	0.078 (0.020)	0.121 (0.034)
	σ^2_{sire}	0.018 (0.008)	0.031 (0.018)
	$\sigma_{\text{sire (pure-cross)}}$		0.006 (0.008)
	$\sigma_{\text{dam pure – sire pure}}$		0.005 (0.011)
	$\sigma_{\text{dam pure – sire cross}}$		0.002 (0.016)

Posterior means, SD, Monte Carlo standard error of heritability and genetic correlation for farrowing survival (M 4)



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Component	Mean	SD	Monte Carlo Standard Error	HPD-95%	
				Lower bound	Upper bound
h^2_{purebred}	0.05	0.02	0.002	0.01	0.09
$h^2_{\text{crossbred}}$	0.09	0.05	0.006	0.01	0.19
$r_{\text{sire pure-cross}}$	0.24	0.33	0.037	-0.38	0.82
$r_{\text{dam pure - sire pure}}$	0.17	0.28	0.024	-0.42	0.68
$r_{\text{dam pure - sire cross}}$	0.03	0.32	0.033	-0.56	0.63





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Conclusions

- Genetic variance (sire effects) on piglet survival is large enough to be exploited
- Genetic correlation is moderate, and a 95% Bayesian confidence region included zero
- Traits measured (mortality in pure and cross) are different
- Results suggest that genetic progress expected in crossbred when selection is based on purebred may be nil
- Breeding goal should be at the commercial level

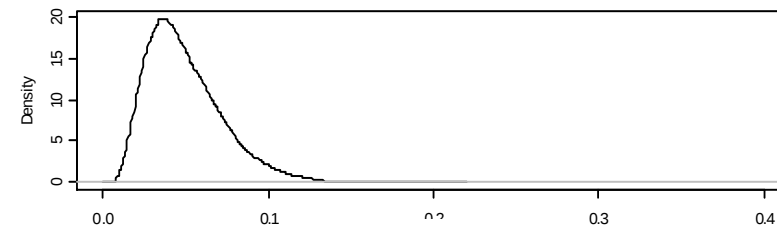
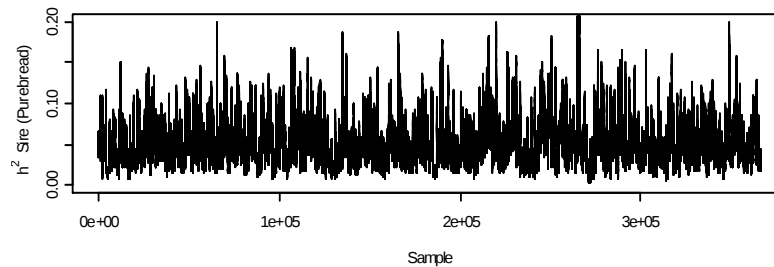




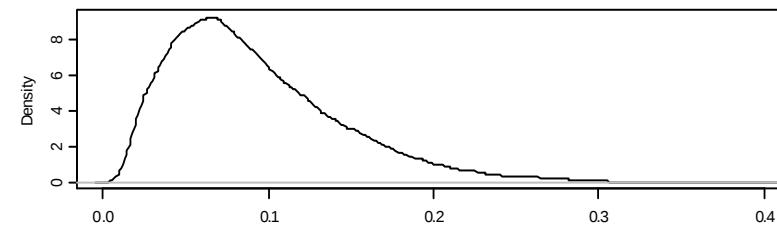
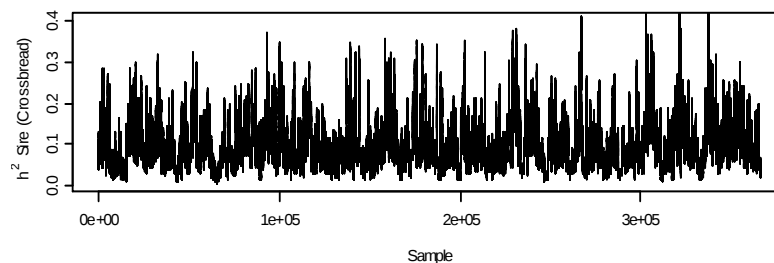
Thanks for your attention!

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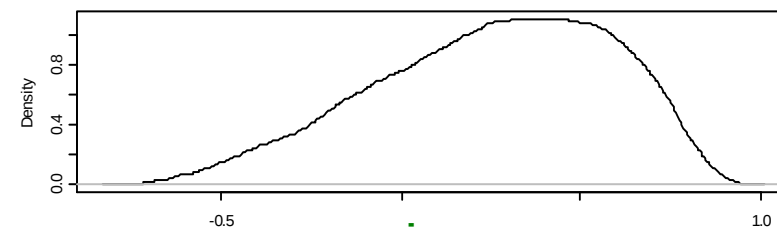
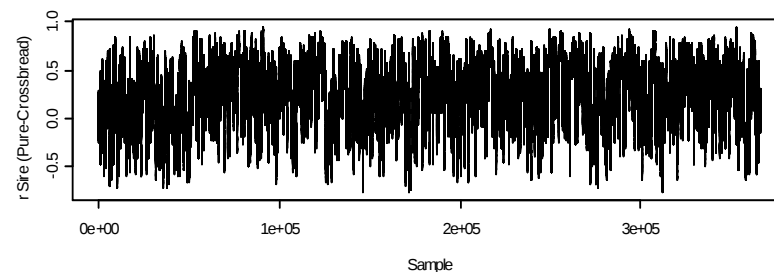
Marginal posterior densities and trace plots of heritability of sire variances and of the correlation between the sire effects on pure and crossbred animals (M 4)



h^2 purebred



h^2 crossbred



rg sire pure - cross

Posterior means, SD, Monte Carlo standard error of heritability and genetic correlation for farrowing survival (M 4^a)



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Component	Mean	SD	Monte Carlo Standard Error	HPD-95%	
				Lower bound	Upper bound
h^2_{purbred}	0.05	0.02	0.002	0.01	0.09
$h^2_{\text{crossbred}}$	0.09	0.05	0.006	0.01	0.19
$r_{\text{sire pure-cross}}$	0.25	0.33	0.037	-0.38	0.82
$r_{\text{dam pure - sire pure}}$	0.18	0.28	0.024	-0.42	0.68
$r_{\text{dam pure - sire cross}}$	0.04	0.32	0.033	-0.56	0.63

^a model without the litter effect

