66th EAAP Annual Meeting
Warsaw, Poland

Pedigree and genomic evaluation of pigs using a terminal cross model

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Project funded by:
ANR-10-GENOM_BTV-015 UtOpIGe
Bioporc; IFIP
SelDir SelGen Metaprogramme

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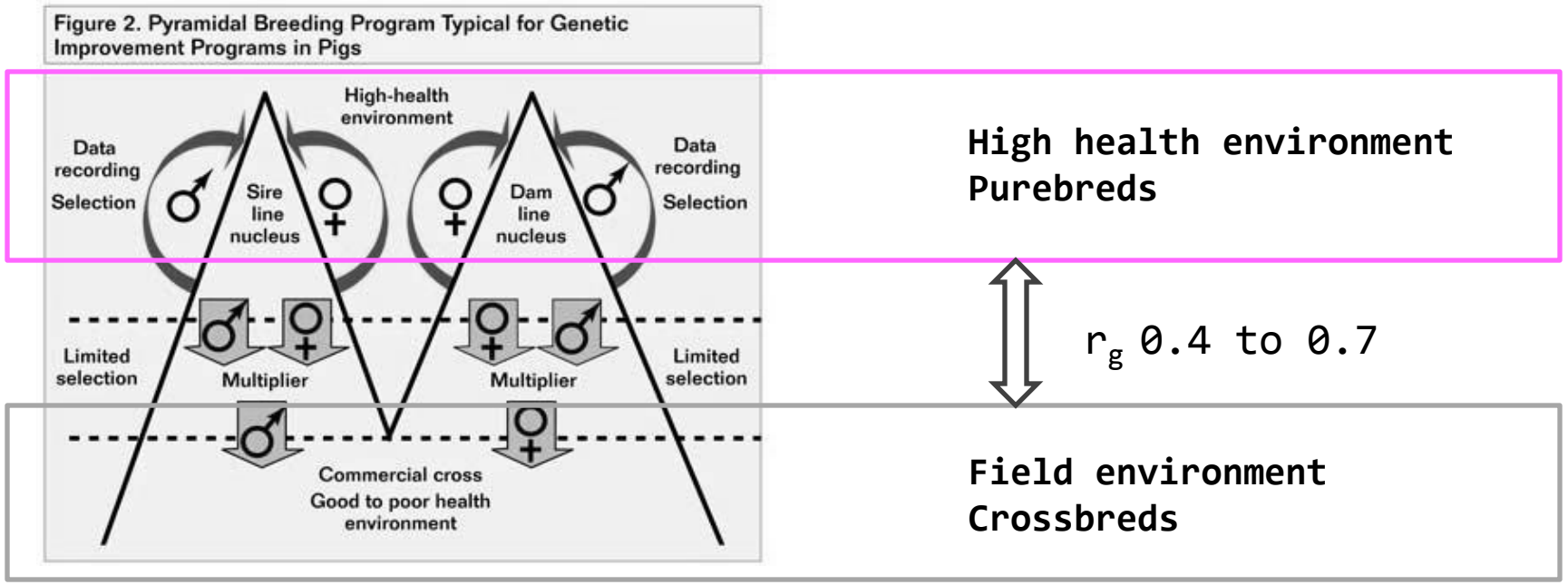
SCIENCE & IMPACT

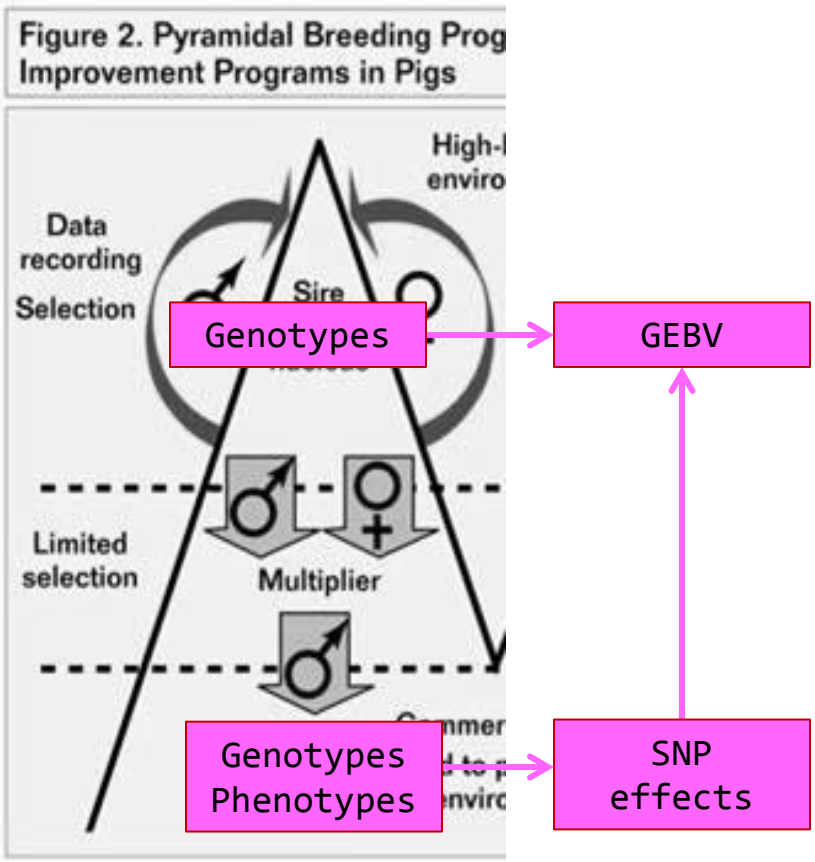
Introduction

Selection in pig breeding programs is entirely performed in the purebred nucleus, aiming to improve crossbred performance



Introduction

Can we expect a change with the use of genomic information?



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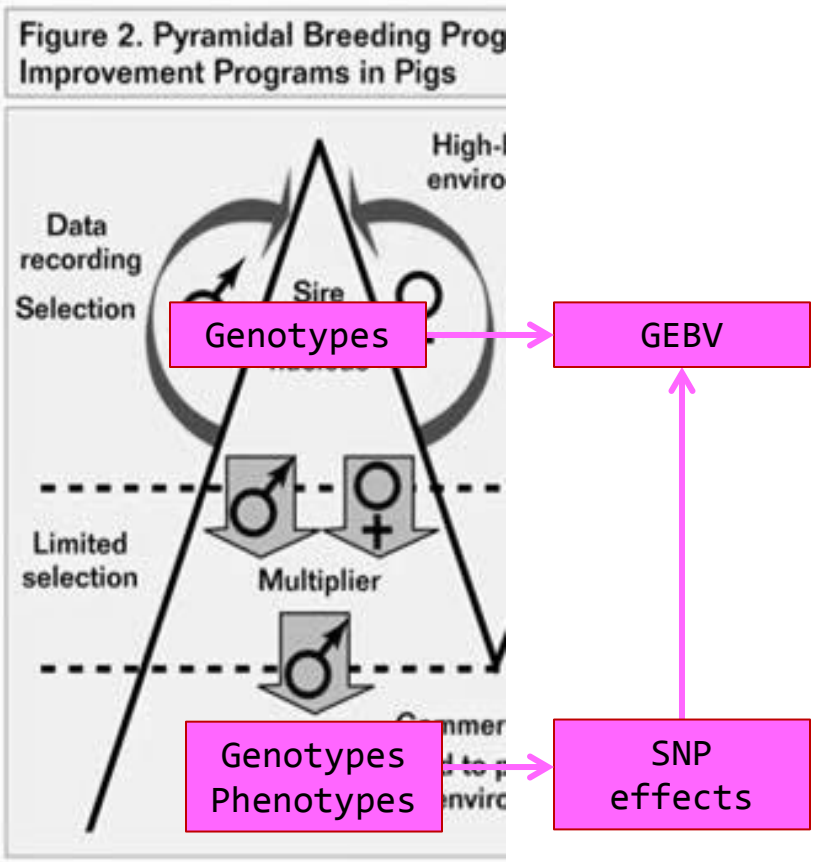

Genomic selection approaches:

Estimate marker effects on crossbred performance in field to obtain EBV of purebreds

Combine both genomic and pedigree information to get the EBV

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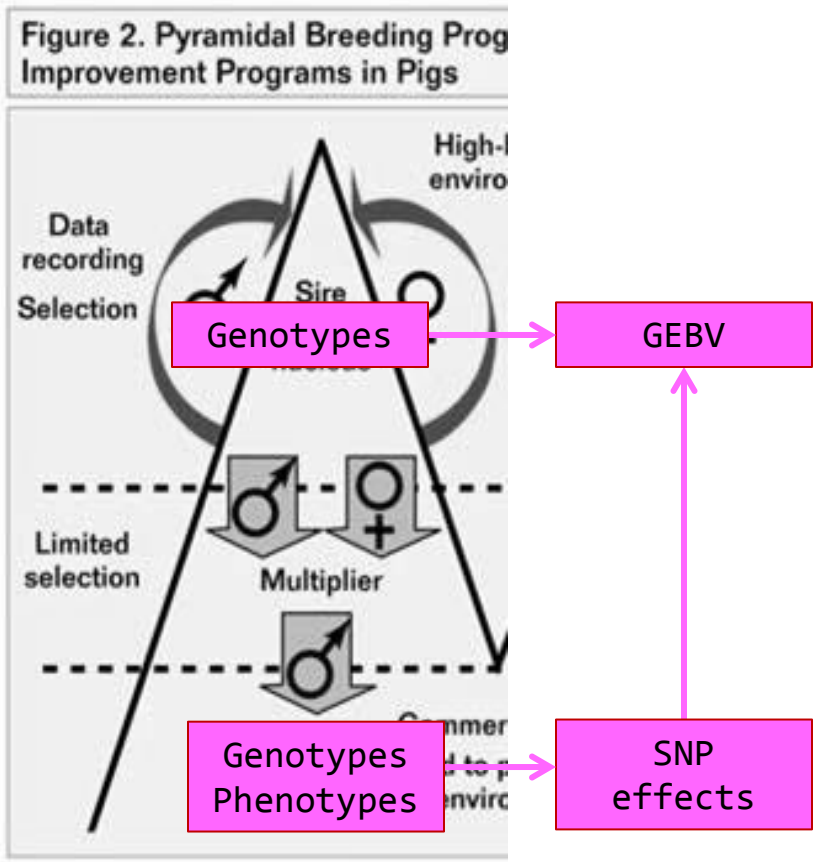


Genomic selection approaches:

Estimate marker effects on crossbred performance in field to obtain EBV of purebreds

Combine both genomic and pedigree information to get the EBV

✓Increased EBV accuracy

✓ Greater response to selection

✓ Lower rate of inbreeding

✓ No pedigree connecting PB with CB needed (not always)

✓ SNP effect estimates can be used for several generations

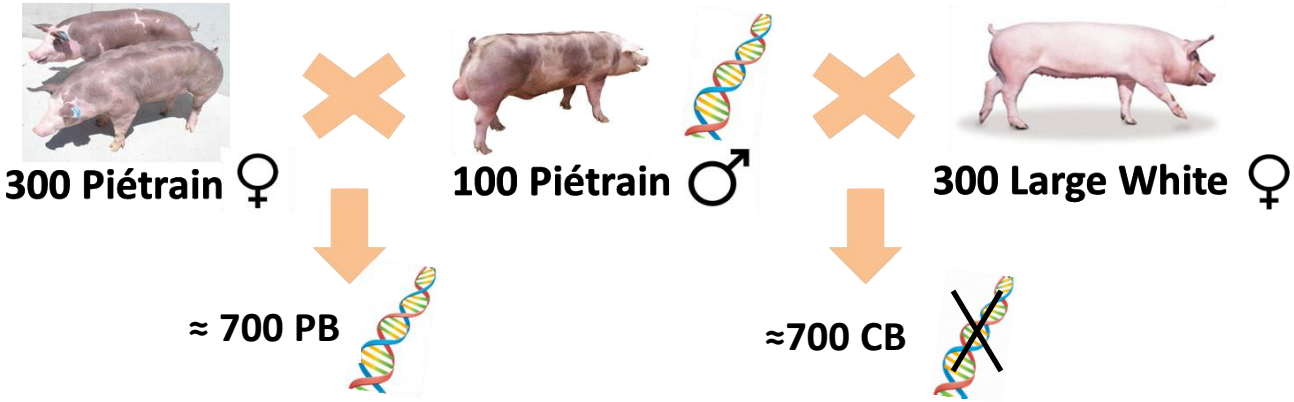
OBJECTIVE

To present a **single-step terminal-cross model** for the estimation of genetic parameters of several production traits in a terminal cross population of pigs.

Compare the obtained **genetic parameter estimates** and **breeding value accuracies** with:

- a pedigree-based terminal-cross model
- 2 univariate single-step models for PB and CB performance.

Experimental design



PEDIGREE AND GENOMIC INFORMATION

- 2 pedigrees: 3,084 Piétrain and 2,686 Large White animals
- Illumina 60K SNP-bead chip genotypes 39,650 SNPs kept for the analyses

ANALYZED TRAIT

- Growth rate between 35Kg and slaugther (110kg)
- ...

SINGLE-STEP TERMINAL-CROSS MODEL (GEN)

We have adapted the terminal-cross model proposed by **Wei and Van der Werf (1994)** to combine both genomic and pedigree information

$$\begin{bmatrix}\mathbf{y}_A\\ \mathbf{y}_C\end{bmatrix} = \begin{bmatrix}\mathbf{X}_A & 0\\ 0 & \mathbf{X}_C\end{bmatrix}\begin{bmatrix}\mathbf{b}_A\\ \mathbf{b}_C\end{bmatrix} + \begin{bmatrix}\mathbf{W}_A & 0\\ 0 & \mathbf{W}_C\end{bmatrix}\begin{bmatrix}\mathbf{p}_A\\ \mathbf{p}_C\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_A & 0 & 0\\ 0 & \mathbf{Z}_{AC} & \mathbf{Z}_{BC}\end{bmatrix}\begin{bmatrix}\mathbf{u}_{AA}\\ \mathbf{u}_{AC}\\ \mathbf{u}_{BC}\end{bmatrix} + \begin{bmatrix}\mathbf{e}_A\\ \mathbf{e}_C\end{bmatrix}$$

Systematic effects — Pen nested within batch effects — Additive genetic effects

- The purebred model includes an animal additive genetic effect: $\boldsymbol{u}_{AA}$.
- The additive genetic effect in the crossbred model is decomposed into Piétrain sire and Large White dam additive genetic allelic effects for crossbred performance:

$$\boldsymbol{u}_{CC} = \boldsymbol{u}_{AC} + \boldsymbol{u}_{BC} + \boldsymbol{\phi}_A + \boldsymbol{\phi}_B$$

$$\boldsymbol{e}_C = \boldsymbol{\phi}_A + \boldsymbol{\phi}_B + \boldsymbol{e}_C^*$$

SINGLE-STEP TERMINAL-CROSS MODEL (GEN)

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Genetic (co)variance matrix

$$var\begin{bmatrix}\boldsymbol{u}_{AA}\\ \boldsymbol{u}_{AC}\\ \boldsymbol{u}_{BC}\end{bmatrix}=\begin{bmatrix}\mathbf{H}\sigma_A^2 & \mathbf{H}\sigma_{A(AC)} & 0\\ \mathbf{H}\sigma_{(AC)A} & \mathbf{H}\sigma_{AC}^2 & 0\\ 0 & 0 & \boldsymbol{A}_{(B)}\sigma_{BC}^2\end{bmatrix}$$

$$\mathbf{H}^{-1}=\mathbf{A}_{(A)}^{-1}+\begin{bmatrix}0 & 0\\ 0 & \tau\mathbf{G}^{-1}-\omega\mathbf{A}_{(A)22}^{-1}\end{bmatrix}$$

Legarra et al. 2009

- A **genetic covariance** between Piétrain genetic effect ($\boldsymbol{u}_{AA}$) and sire Piétrain additive genetic effect for CB performance

SINGLE-STEP TERMINAL-CROSS MODEL (GEN)

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Legarra et al. 2009

- A **genetic covariance** between Piétrain genetic effect ($\boldsymbol{u}_{AA}$) and sire Piétrain additive genetic effect for CB performance
- The **dam genetic effect** ($\boldsymbol{u}_{BC}$) is included as another random effect not correlated with the other two genetic effects.

BENCHMARK MODELS

PEDIGREE-BASED TERMINAL-CROSS MODEL (PED)

$$\begin{bmatrix}\mathbf{y}_A\\ \mathbf{y}_C\end{bmatrix}=\begin{bmatrix}\mathbf{X}_A & 0\\ 0 & \mathbf{X}_C\end{bmatrix}\begin{bmatrix}\mathbf{b}_A\\ \mathbf{b}_C\end{bmatrix}+\begin{bmatrix}\mathbf{W}_A & 0\\ 0 & \mathbf{W}_C\end{bmatrix}\begin{bmatrix}\mathbf{p}_A\\ \mathbf{p}_C\end{bmatrix}+\begin{bmatrix}\mathbf{Z}_A & 0 & 0\\ 0 & \mathbf{Z}_{AC} & \mathbf{Z}_{BC}\end{bmatrix}\begin{bmatrix}\mathbf{u}_{AA}\\ \mathbf{u}_{AC}\\ \mathbf{u}_{BC}\end{bmatrix}+\begin{bmatrix}\mathbf{e}_A\\ \mathbf{e}_C\end{bmatrix}$$

$$var\begin{bmatrix}\boldsymbol{u}_{AA}\\ \boldsymbol{u}_{AC}\\ \boldsymbol{u}_{BC}\end{bmatrix}=\begin{bmatrix}\boldsymbol{A}_{(A)}\sigma_A^2 & \boldsymbol{A}_{(A)}\sigma_{A(AC)} & 0\\ \boldsymbol{A}_{(A)}\sigma_{(AC)A} & \boldsymbol{A}_{(A)}\sigma_{AC}^2 & 0\\ 0 & 0 & \boldsymbol{A}_{(B)}\sigma_{BC}^2\end{bmatrix}$$

TWO UNIVARIATE SINGLE-STEP MODELS (GEN_UNIC)

$$\mathbf{y}_A=\mathbf{X}_A\mathbf{b}_A+\mathbf{W}_A\mathbf{p}_A+\mathbf{Z}_A\mathbf{u}_{AA}+\mathbf{e}_A$$

$$\mathbf{y}_C=\mathbf{X}_C\mathbf{b}_C+\mathbf{W}_C\mathbf{p}_C+\mathbf{Z}_{AC}\mathbf{u}_{AC}+\mathbf{Z}_{BC}\mathbf{u}_{BC}+\mathbf{e}_C$$

GIBBS1f90 Misztal et al. 1999

COMPARISON - Breeding value accuracies

$$R_{i,j} = \sqrt{1 - \frac{PEV_{i,j}}{(1 + F_i)\sigma^2_{k,j}}}$$

i = 1,…,individuals
k = A, AC
j = pedigree model, single-step model
PEV = prediction error variance
F = inbreeding coefficient

RESULTS - Genetic parameter estimates

POSTERIOR MEAN [HPD at 95%]

Model	$rg_{A,AC}$	h^2_A	u^2_{AC}	u^2_{BC}
PED	**0.79** [0.37,1.00]	**0.33** [0.08,0.57]	**0.24** [0.11,0.40]	**0.29** [0.12,0.44]
GEN	**0.84** [0.45,1.00]	**0.22** [0.05,0.37]	**0.25** [0.03,0.45]	**0.28** [0.12,0.44]

$\uparrow rg_{A,AC}$

In the same environment, PB selection is already successful to indirectly improve CB performance

RESULTS - Genetic parameter estimates

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Model	$rg_{A,AC}$	h_A^2	u_{AC}^2	u_{BC}^2
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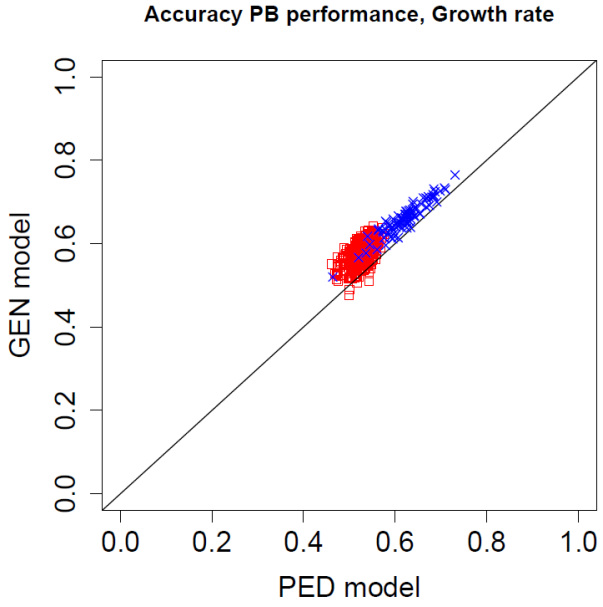
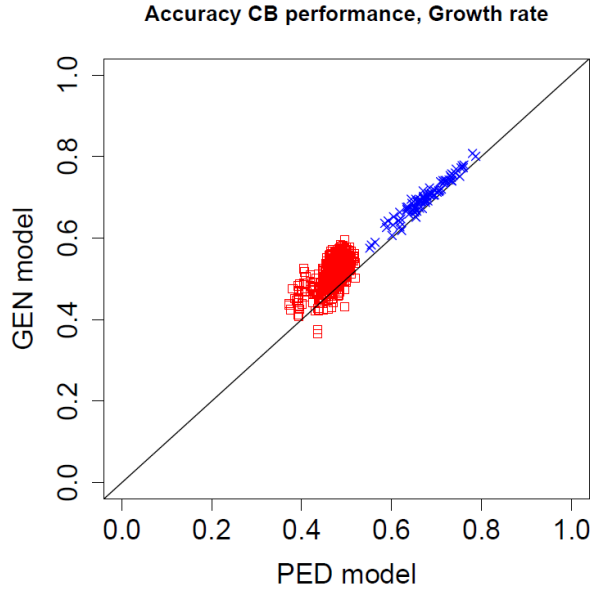
HPD95% are narrower in the GEN model, possibly because of the higher amount of information used.

Posterior mean estimate of the h2 is higher with the PED than with the GEN model but posterior modes are similar.

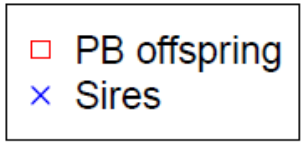
RESULTS – Breeding value accuracies





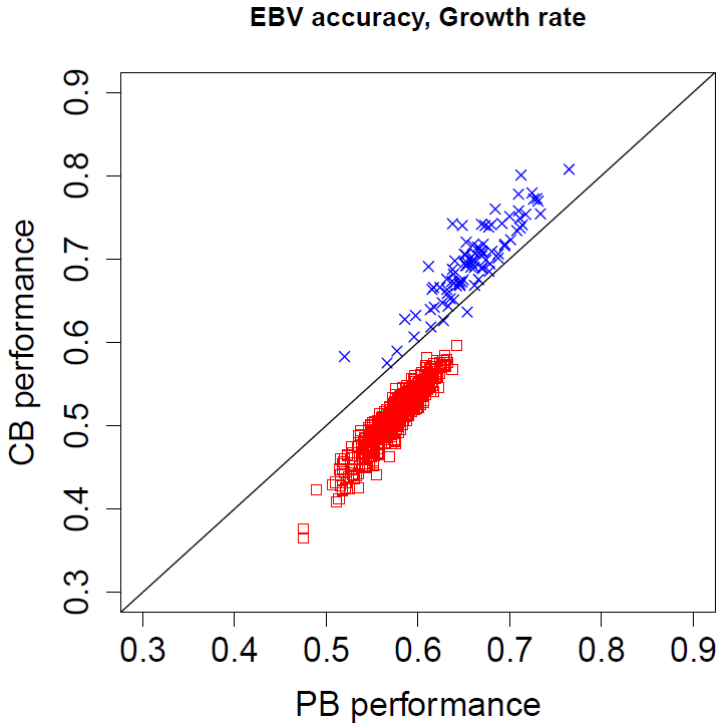
PED model *vs* GEN model

Genotyped animals obtained higher EBV accuracies with the single-step than with the pedigree-based model.



RESULTS - Breeding value accuracies

PB *vs* CB performance – GEN model



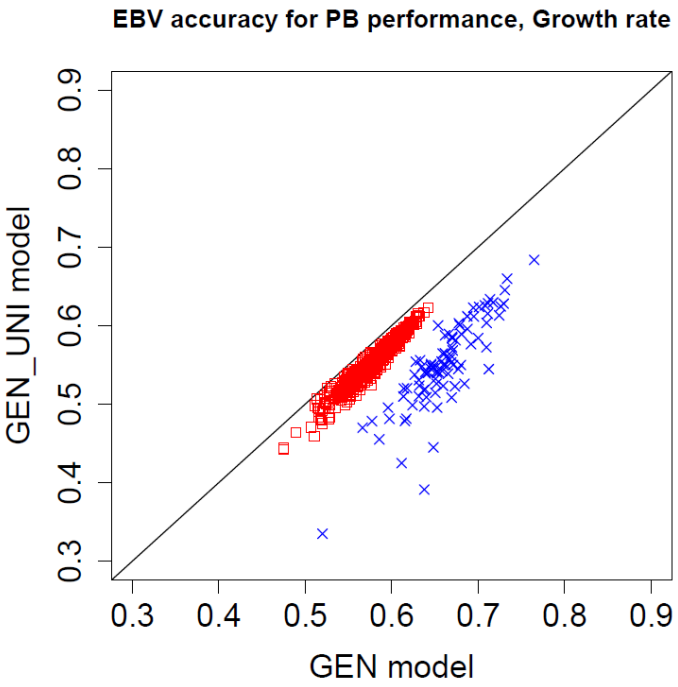
× Sires

Sire accuracy was higher than PB offspring accuracy
The EBV accuracies were higher when sires were evaluated for CB than for PB performance.

□ PB offspring

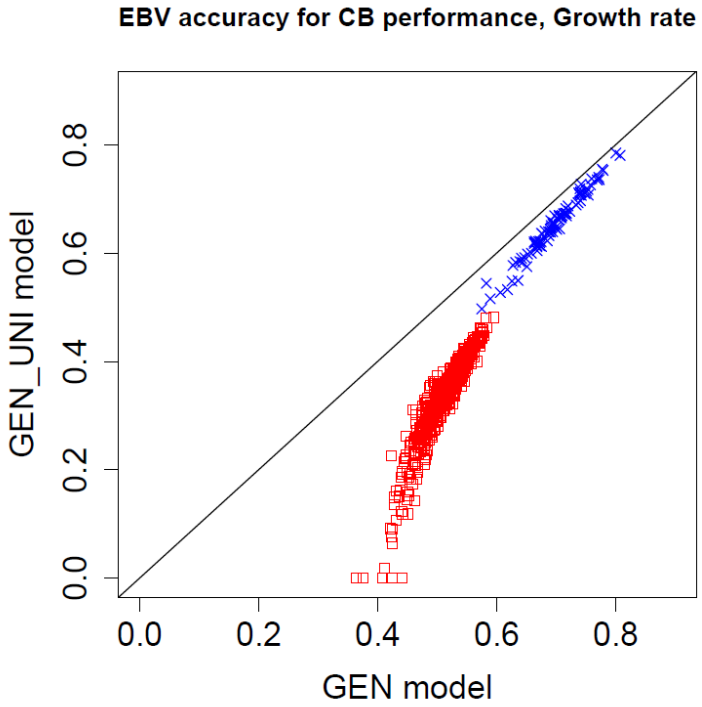
The EBV accuracies were higher when PB offspring were evaluated for PB than for CB performance.

RESULTS – Breeding value accuracies



GEN model *vs* GEN_UNIC models

The EBV accuracies were always higher using a 2 trait model (GEN) than using an univariate model (GEN_UNIC) for both PB and CB performances.



Conclusions

We have developed and empirically used a single-step terminal-cross model that uses the sire genotype to model crossbred performance.

Need to be compared with a more complex single-step method for genomic evaluation making full use of PB and CB genotypes.

Given the high genetic correlations, within line selection in purebreds is already successful to indirectly improve crossbred performance (in the same environment).

This improvement can be higher when accounting for crossbred performance together with genomic information because precision of the genetic parameter estimates and the accuracy of the EBV increase.

Thank you