Use of mate allocation in pig crossbreeding schemes: a simulation study

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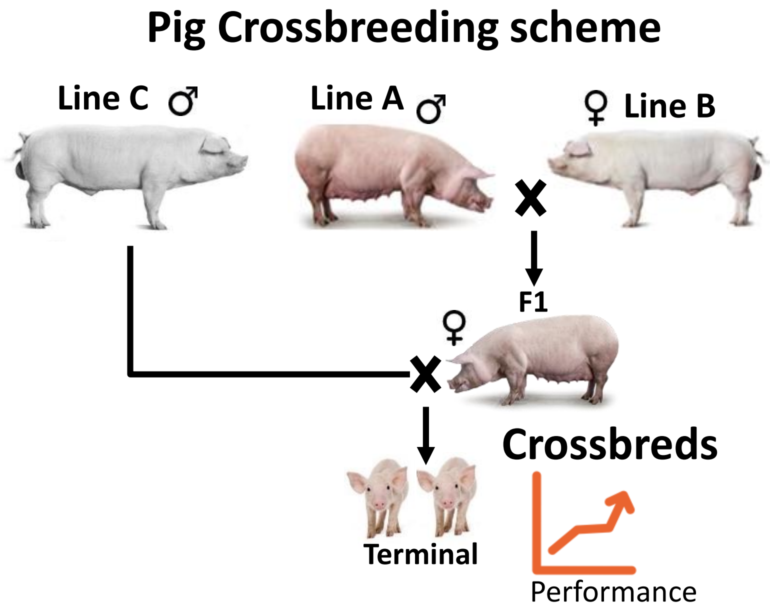
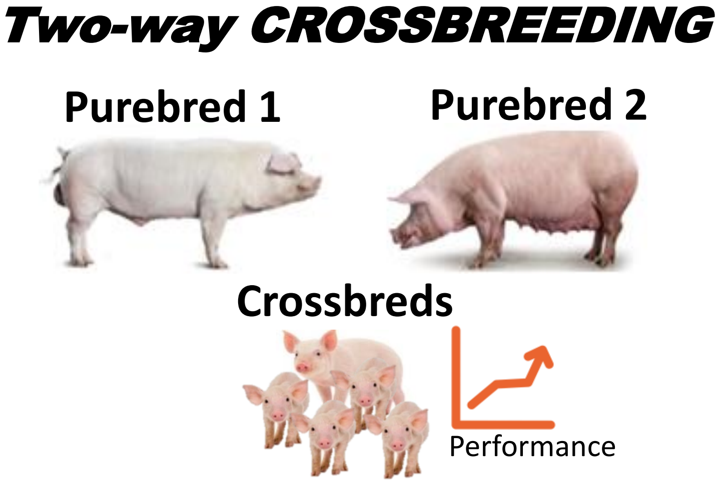
INTRODUCTION

- Crossbreeding schemes are widely used in animal breeding for the purpose of exploiting the heterosis effect and breed complementarity.
- The main goal of crossbreeding is to improve the performance of crossbred animals.
- Mate allocation strategies that account for non-additive genetic effects could be of interest to improve the crossbred performance.



OBJECTIVE

- To simulate a two-way pig crossbreeding scheme and evaluate four scenarios that combine genetic evaluation models and mate allocation strategies in order to improve the performance of crossbred animals.



MATERIALS AND METHODS

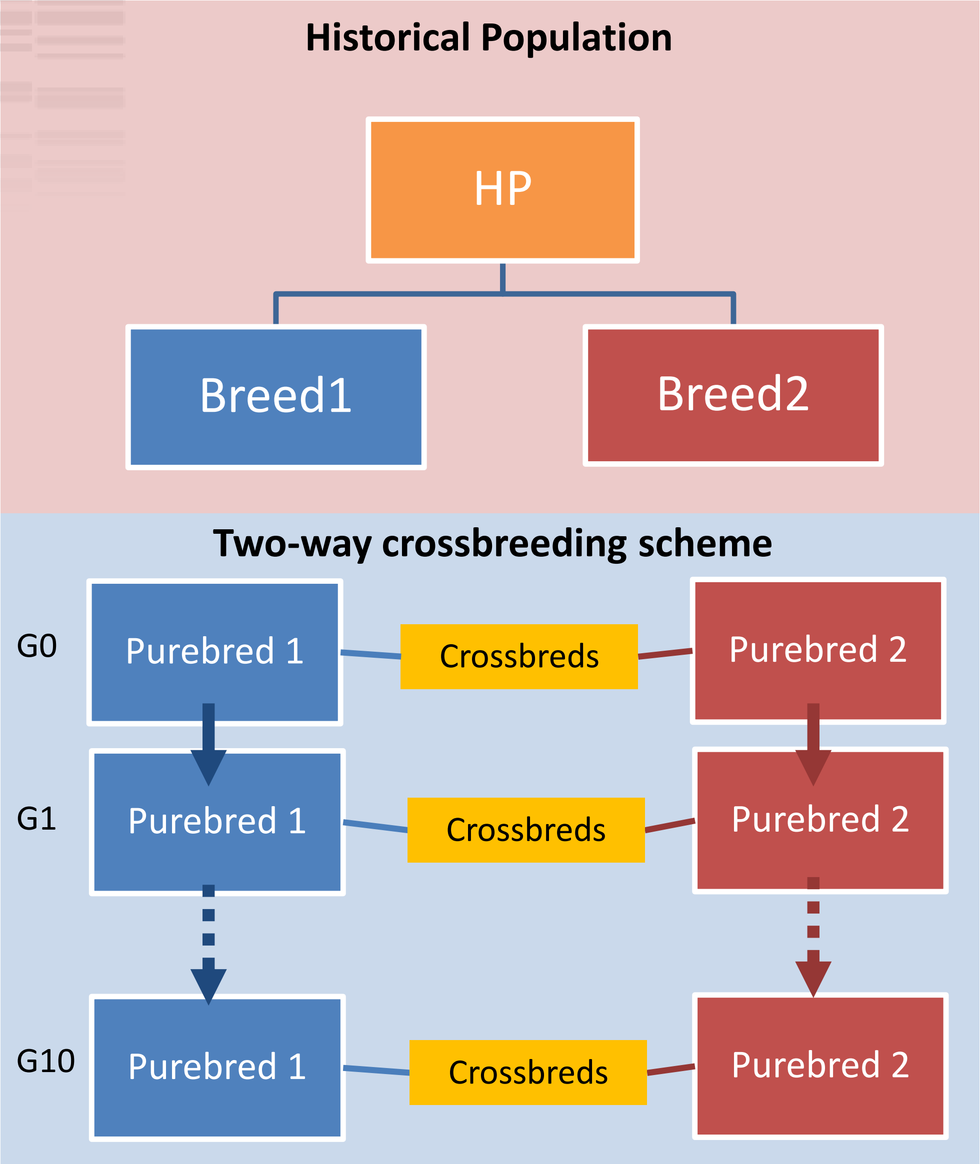
SIMULATION

10 replicates

QMSim*

Fortran

10 generations



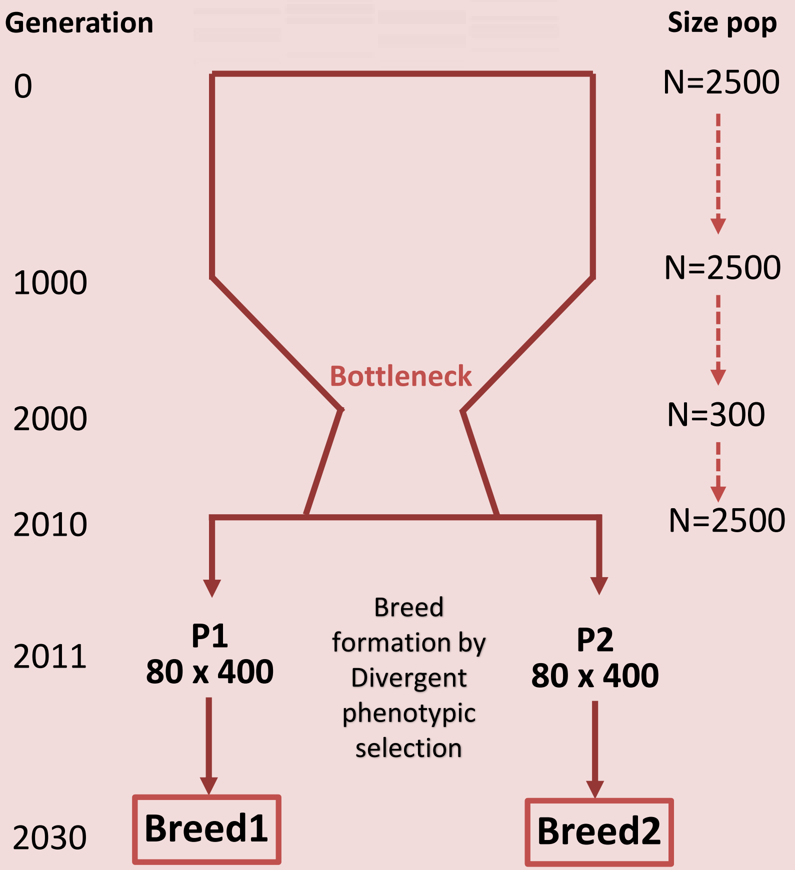
QMSim software was used to create historical populations (HP) and form two divergent breeds.

A program in Fortran was developed to simulate a two-way crossbreeding scheme across 10 generations.

**(Sargolzaei and Schenkel, 2009)*

HISTORICAL POPULATIONS

Simulation parameters



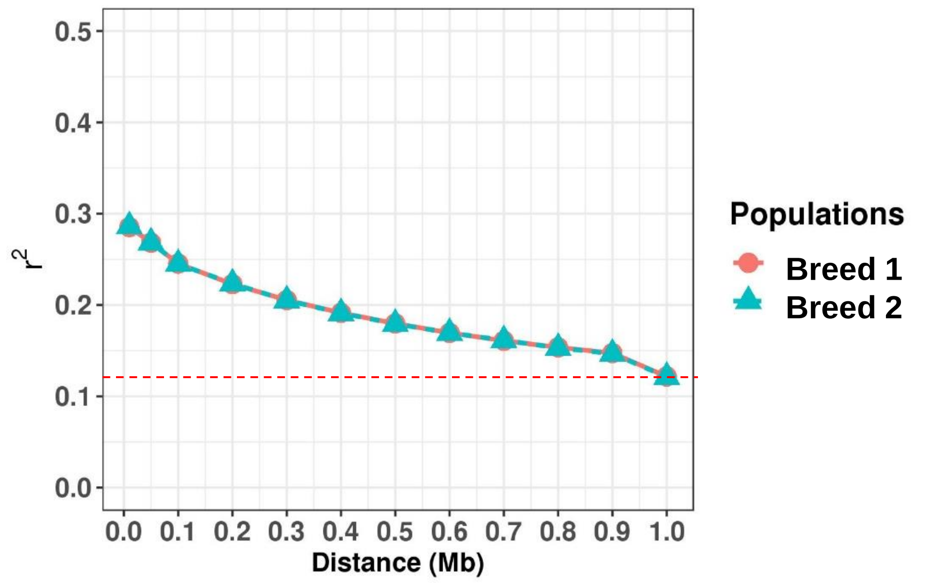
Genome: 18 pairs of chrs. of 120 cM

QMSim

Breeds

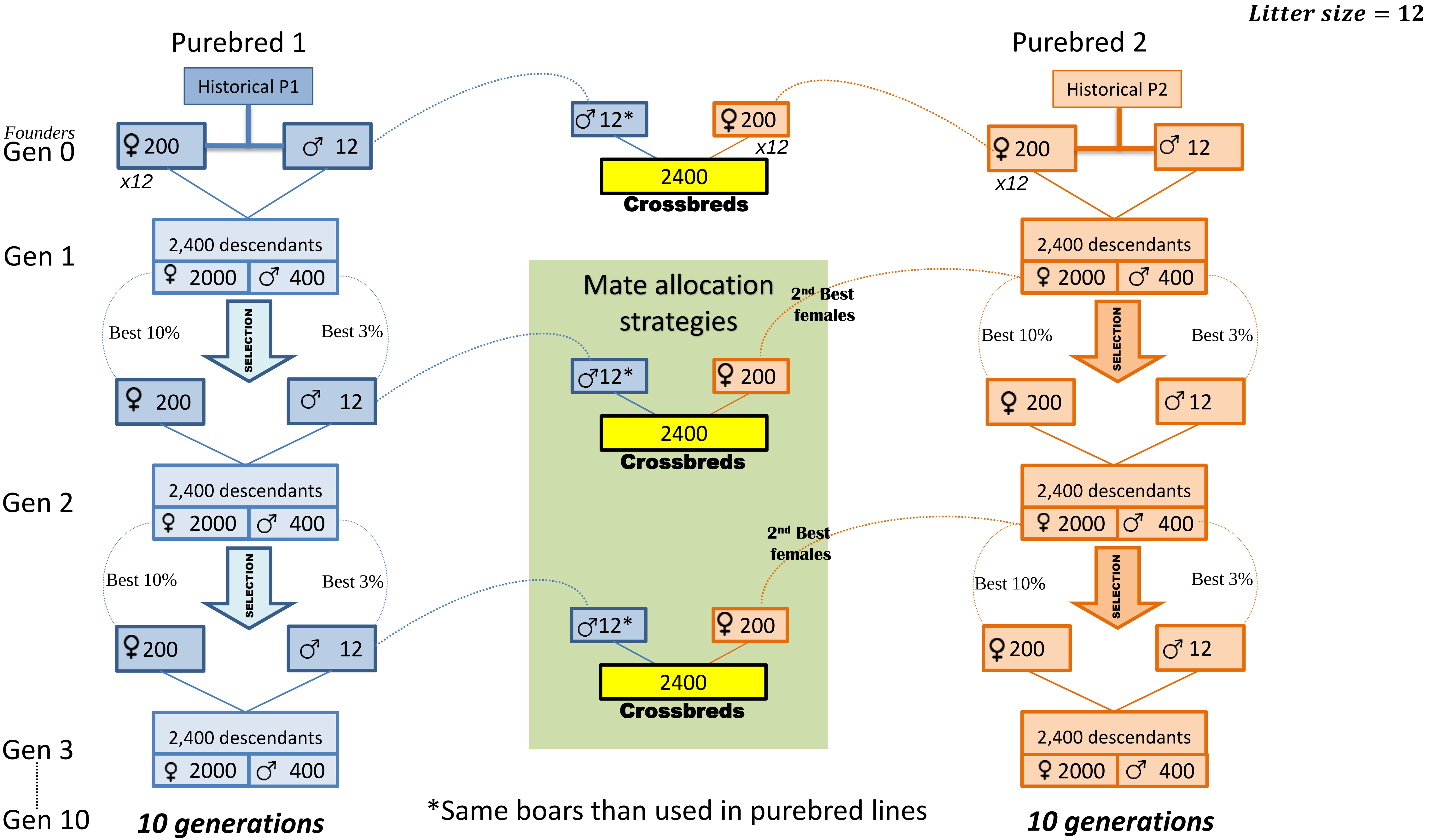
- Polymorphic SNPs in common (MAF>0.05): ~50 k
- $8*\mathrm{cov}(f_{breed1}, f_{breed2}) = 0.23$ → Similar to the relatedness observed across Landrace and Yorkshire base populations in Xiang et al., (2018)

LD decay in breed populations



The decay of LD was similar to those observed in Landrace and Yorkshire breeds at 1 Mb (Boré et al., 2017).

TWO-WAY CROSSBREEDING SCHEME



$Litter\ size = 12$

Purebred 1

Historical P1

Founders
Gen 0

♀200 x12
♂ 12

Gen 1

2,400 descendants
♀ 2000 ♂ 400

Best 10%
SELECTION
Best 3%

♀ 200
♂ 12

Gen 2

2,400 descendants
♀ 2000 ♂ 400

Best 10%
SELECTION
Best 3%

♀200
♂ 12

Gen 3

2,400 descendants
♀ 2000 ♂ 400

Gen 10

10 generations

♂12*
♀200 x12

2400
Crossbreds

Mate allocation strategies

2nd Best females

♂12*
♀ 200

2400
Crossbreds

2nd Best females

♂12*
♀ 200

2400
Crossbreds

Purebred 2

Historical P2

♀ 200 x12
♂ 12

2,400 descendants
♀ 2000 ♂ 400

Best 10%
SELECTION
Best 3%

♀ 200
♂12

2,400 descendants
♀ 2000 ♂ 400

Best 10%
SELECTION
Best 3%

♀200
♂ 12

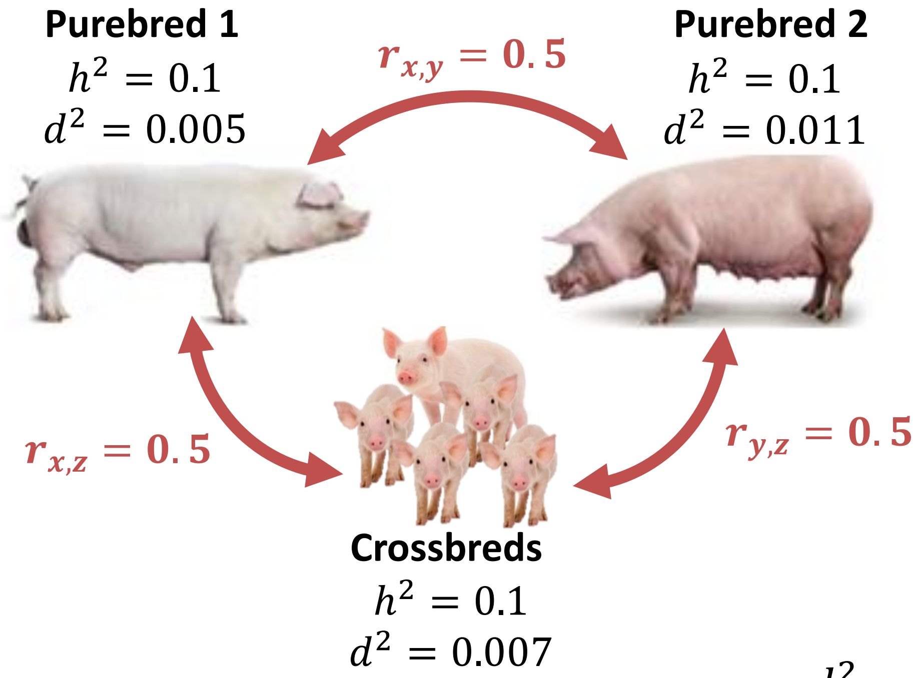
2,400 descendants
♀ 2000 ♂ 400

10 generations

*Same boars than used in purebred lines

PARAMETERS FOR CROSSBREEDING SCHEME

- Maternal trait: “e.g. Litter size”
- 2500 SNPs were randomly selected to be QTL.
- Inbreeding depression was assumed to be -1 piglet per 10% increase in genomic inbreeding.
- Breed specific QTL effects were sampled from a MVN distribution with correlation between the three populations: Additive and dominant genetic variance from Xiang et al. (2016).



Purebred 1
$h^2 = 0.1$
$d^2 = 0.005$

$r_{x,y} = 0.5$

Purebred 2
$h^2 = 0.1$
$d^2 = 0.011$

$r_{x,z} = 0.5$

$r_{y,z} = 0.5$

Crossbreds
$h^2 = 0.1$
$d^2 = 0.007$

Genetic correlation between the purebred and crossbred populations was assumed to be $r_{x,y} = r_{x,z} = r_{y,z} = 0.5$.

d^2*: ratio dominance variance to phenotypic variance.*

GENOMIC EVALUATIONS

Two evaluation models were implemented:

☐ **Univariate model:**
- Only purebred information (genotypes and phenotypes)
- Each purebred population was evaluated independently
- Additive effects ($\boldsymbol{GEBV}$) + genomic inbreeding
- Implemented with *Blupf90* software (Misztal et al. 2012).

☐ **Tri-variate model:**
- Purebred and crossbred information (genotypes and phenotypes)
- Performances of purebreds and crossbreds were considered as three different traits.
- Estimation of additive and dominance SNP effects (correlated across populations) and genomic inbreeding
- $\boldsymbol{GEBV}$ on the purebred scale and $\boldsymbol{GEBV_{cp}}$ for crossbred performance were calculated from SNP effects.
- Implemented with a home made software.

SCENARIOS

Traditional scheme

SCENARIO 1: ● GEBV

- **Evaluation:** Univariate model
- **Selection within purebred:** $GEBV$
- **Creation of crossbreds:** No mate allocation (MA) strategy.

SCENARIO 2: ▲ GEBV + MA(F_{min})

- **Evaluation:** Univariate model
- **Selection within purebred:** $GEBV$
- **Creation of crossbreds:** Mate allocation (MA) strategy to **minimize expected future inbreeding**.

Univariate model

SCENARIO 3: ■ GEBV_{cp}

- **Evaluation:** Tri-variate model
- **Selection within purebred:** $GEBV_{cp}$
- **Creation of crossbreds:** No mate allocation (MA) strategy.

SCENARIO 4: + GEBV_{cp} + MA(TGV_{max})

- **Evaluation:** Tri-variate model
- **Selection within purebred:** $GEBV_{cp}$
- **Creation of crossbreds:** Mate allocation (MA) strategy to **maximize expected total genetic value.**

Tri-variate model

COMPARISON OF SCENARIOS

☐ **Within-purebred:**

- Genetic response based on **TBV**

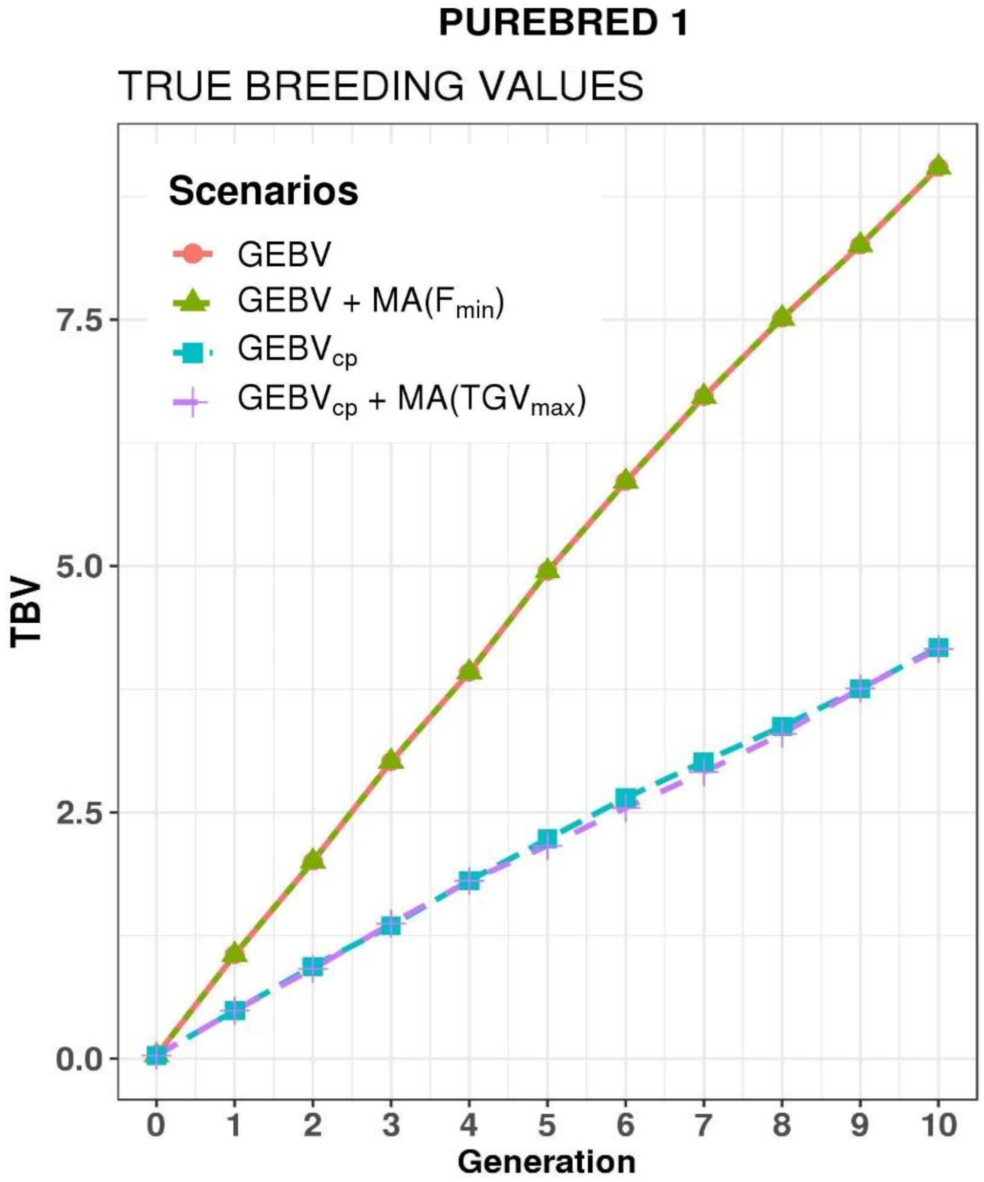
☐ **Crossbreds**:

- Genetic merit based on true total genetic values (**True TGV**).

RESULTS

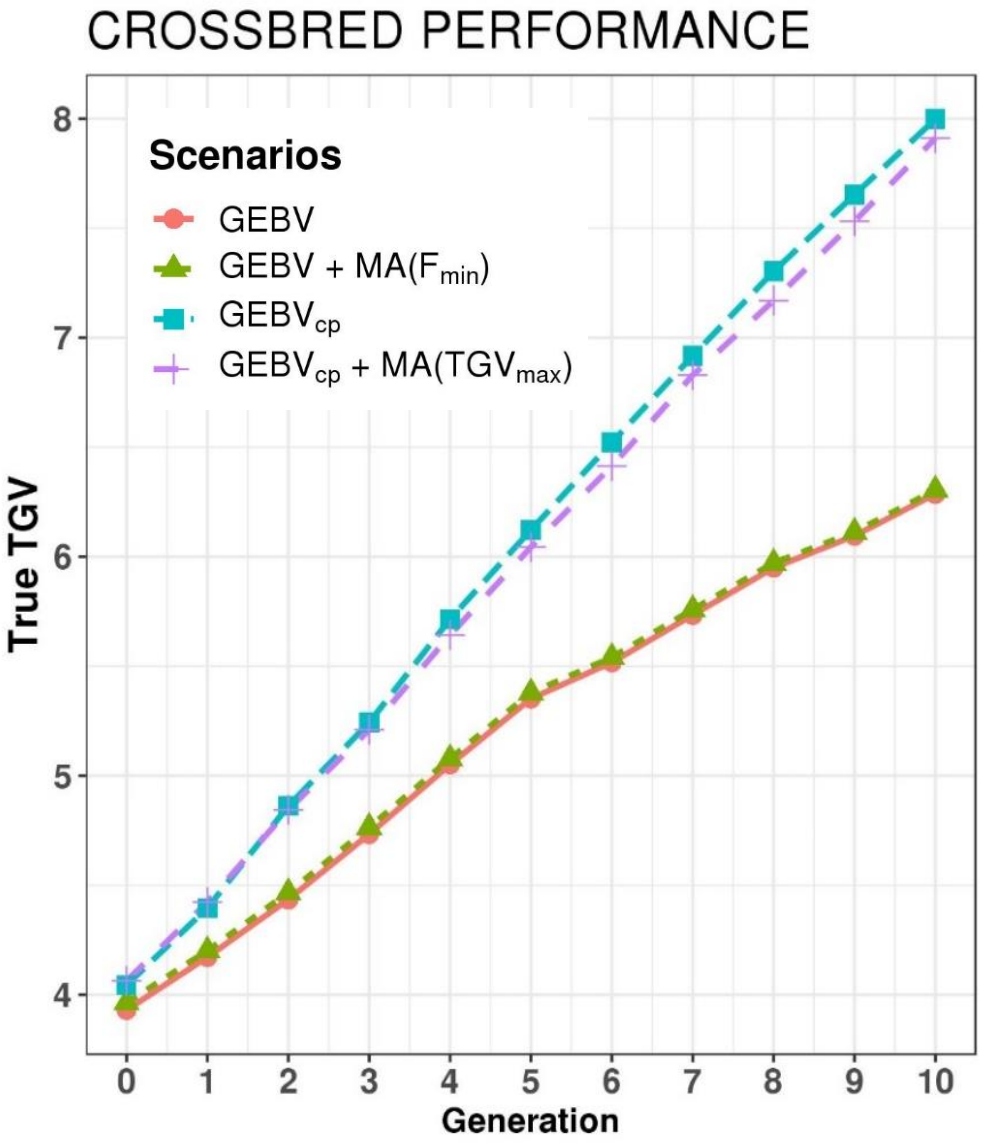
PUREBREDS

- Selecting purebred animals by their $GEBV$ produced the highest genetic response compared to selection on $GEBV_{cp}$.



CROSSBREDS

- Selecting purebred animals by crossbred performance ($GEBV_{cp}$) produced the highest gain in true total genetic value on crossbreds.
- The use of mate allocation by minimizing inbreeding or maximizing expected TGV did not improved the crossbred performance in this simulation study.



CONCLUSIONS

- Selecting purebred animals for crossbred performance ($GEBV_{cp}$) produced the highest gain in crossbred performance, however, the genetic response within purebred populations is reduced compared to selection on $GEBV$.

- The use of mate allocation strategies did not improve the crossbred performance in this simulation study.

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Thanks for your attention!!