Genomic mate allocation strategies with dominance to maximize overall genetic merit in pigs

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Introduction

Mate allocation

Mate allocation has been used in animal breeding schemes mainly to:

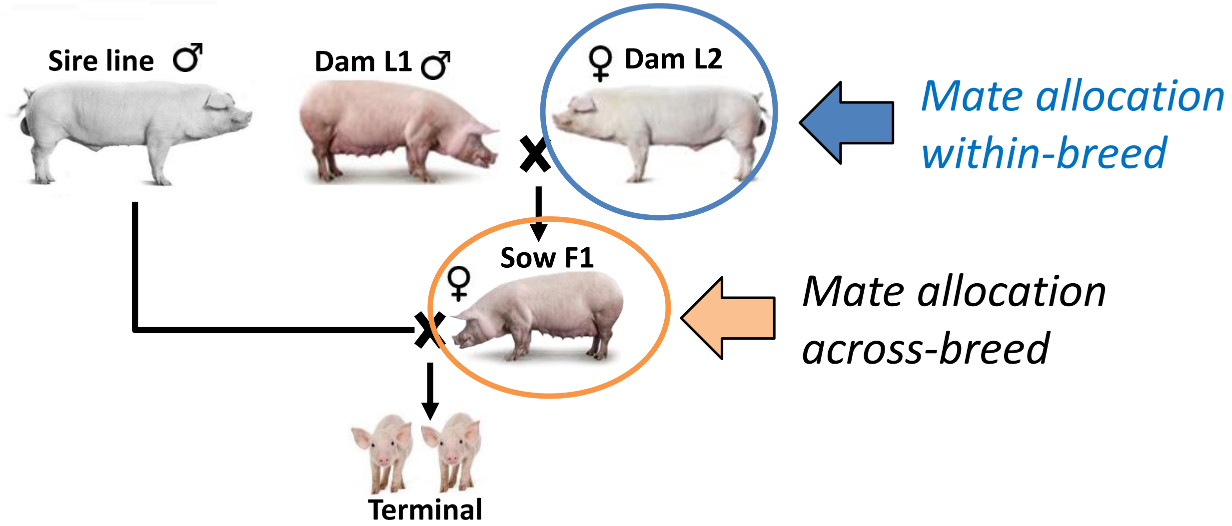
- Control inbreeding
- Increase connection among herds
- Preserve genetic diversity
- exploit dominance

We can exploit dominance by selecting specific matings (specific combining ability) that maximize the total genetic merit of future progeny.

(DeStefano and Hoeschele, 1992; Hayes and Miller, 2000).

Pig breeding scheme

- Traditional pig breeding scheme: three-way cross



- Pig breeding schemes could take benefits from mate allocation strategies across and within-breed.

- Dominance variation in pigs, expressed as percentage of phenotypic variance, varies from 2% to 10% on pedigree-based estimations (Culbertson et al., 1998).

Objective

Evaluate the efficiency of mate allocation strategies in a pig population:

- Can we have the same additive genetic gain with higher total genetic value in the offspring?

Materials and methods

Phenotypes and genotypes

- Age at 100 kg (AGE),
- Backfat depth (BD) and
- Average piglet weight at birth within litter (APWL).

Trait	Boars	Sows	Genotyped animals	Number of records	Mean (SD)
AGE (days)	789	2179	2968	2968	149.03 (9.36)
BD (mm)	1007	2675	3682	3682	11.20 (1.68)
APWL (g)	-	1226	1226	3297	1321.73 (213)

From a sample of a French Landrace pig population.

All animals with records had genotype.
39,353 SNPs retained after quality control

Estimation of variance components: $\sigma_A^2 \quad \sigma_D^2$

- G Model: only additive genetic effects
- GD Model: both additive and dominance genetic effects and inbreeding depression.

EM-REML with *remlf90* software (Misztal et al. 2012).

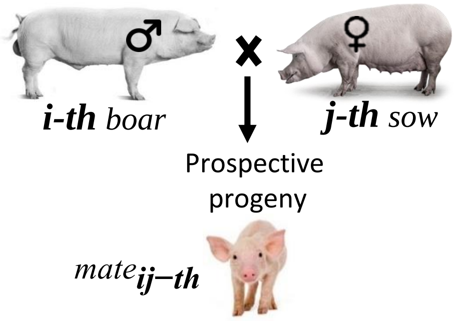
Estimation of additive and dominant SNP effects: $\hat{a}$ and $\hat{d}$

- BLUP-SNP model including additive, dominant and inbreeding depression effects, assuming variance component known.

Using GS3 software (Legarra et al. 2014).

Prediction of expected progeny values

- g_{ij} and u_{ij} of the offspring of the *i-th* boar and *j-th* sow were computed for each potential mating using estimated SNP effects as:



Prediction of the total genetic values (g_{ij}) of the mating

$$\hat{g}_{ij} = \sum_k \left[P_{ijk}(AA)\hat{a}_k + P_{ijk}(Aa)\hat{d}_k + P_{ijk}(aa)(-\hat{a}_k)\right]$$

Prediction of the breeding values (u_{ij}) of the progeny

$$\hat{u}_{ij} = \sum_k \left[P_{ijk}(AA)(2-2p_k)\hat{\alpha}_k + P_{ijk}(Aa)(1-2p_k)\hat{\alpha}_k + P_{ijk}(aa)(-2p_k)\hat{\alpha}_k\right]$$

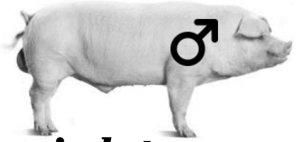
$$\hat{\alpha}_k = \hat{a}_k + \hat{d}_k(q_k - p_k)$$

Toro and Varona (2010)

Allocation of matings

Top$_{GEBV}$ 40 males

e.g. AGE
2,179 females



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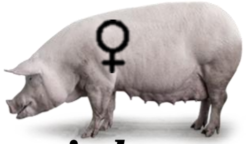


i-th *boar*

j-th *sow*

Prospective
progeny

$mate_{ij-th}$

$\hat{g}_{ij}, \hat{u}_{ij}$

possible matings

87,180

Mate allocation strategies

Selection + mate allocation of females based on $\hat{u}_{ij}$ or $\hat{g}_{ij}$

600 matings → $f_{optim}(\hat{u}_{ij})$

600 matings → $f_{optim}(\hat{g}_{ij})$

Optimization by linear programming
R package *lpsolve* (Berkelaar et al., 2004)

Expected genetic gain

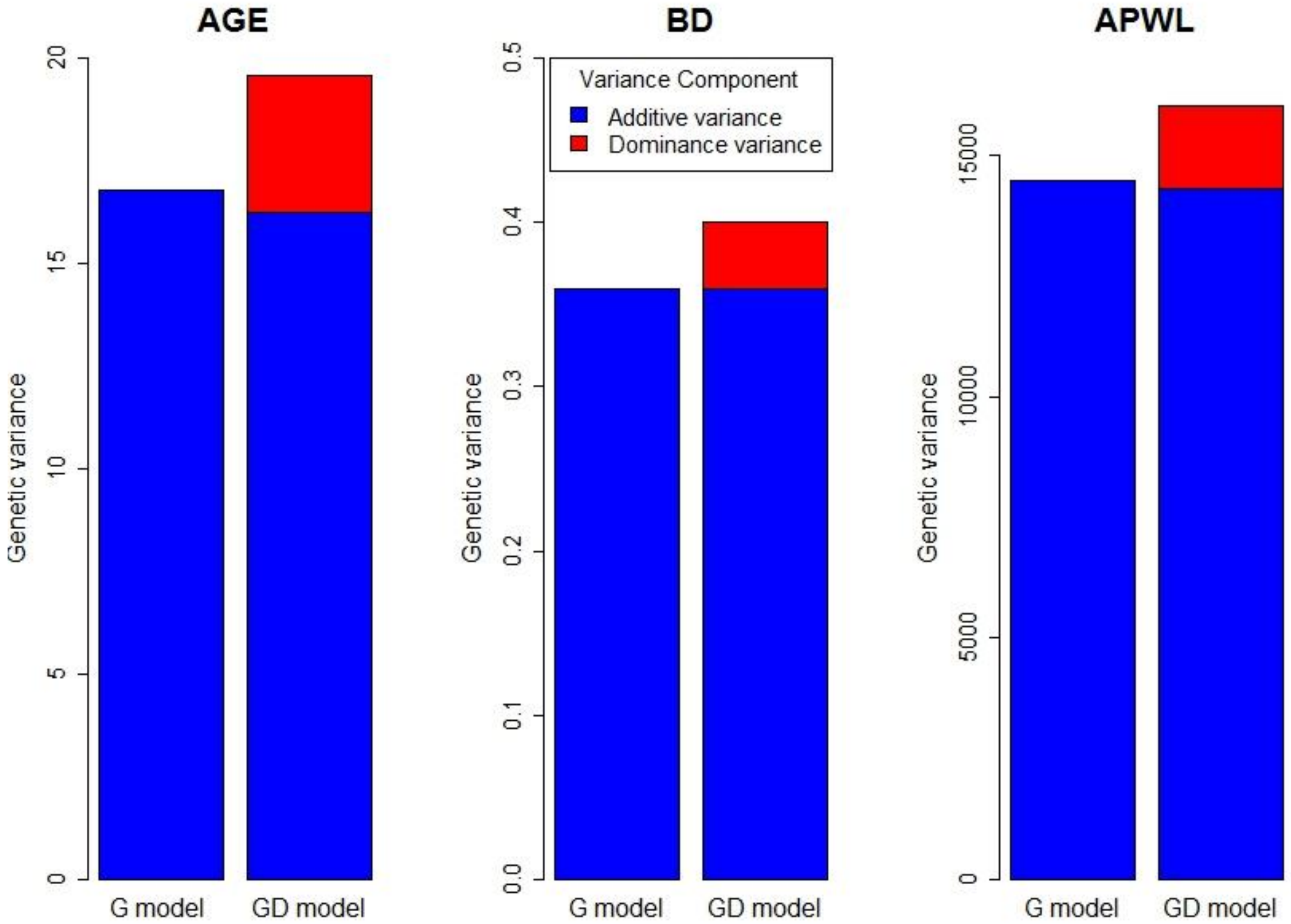
- Expected additive genetic gain (ΔU)
  - $\Delta U = mean(\hat{u}_{selected\_matings}) - mean(\hat{u}_{all\_matings})$

- Expected total genetic superiority (ΔG)
  - $\Delta G = mean(\hat{g}_{selected\_matings}) - mean(\hat{g}_{all\_matings})$

$selected\ matings = 600$

RESULTS

Genetic variance components

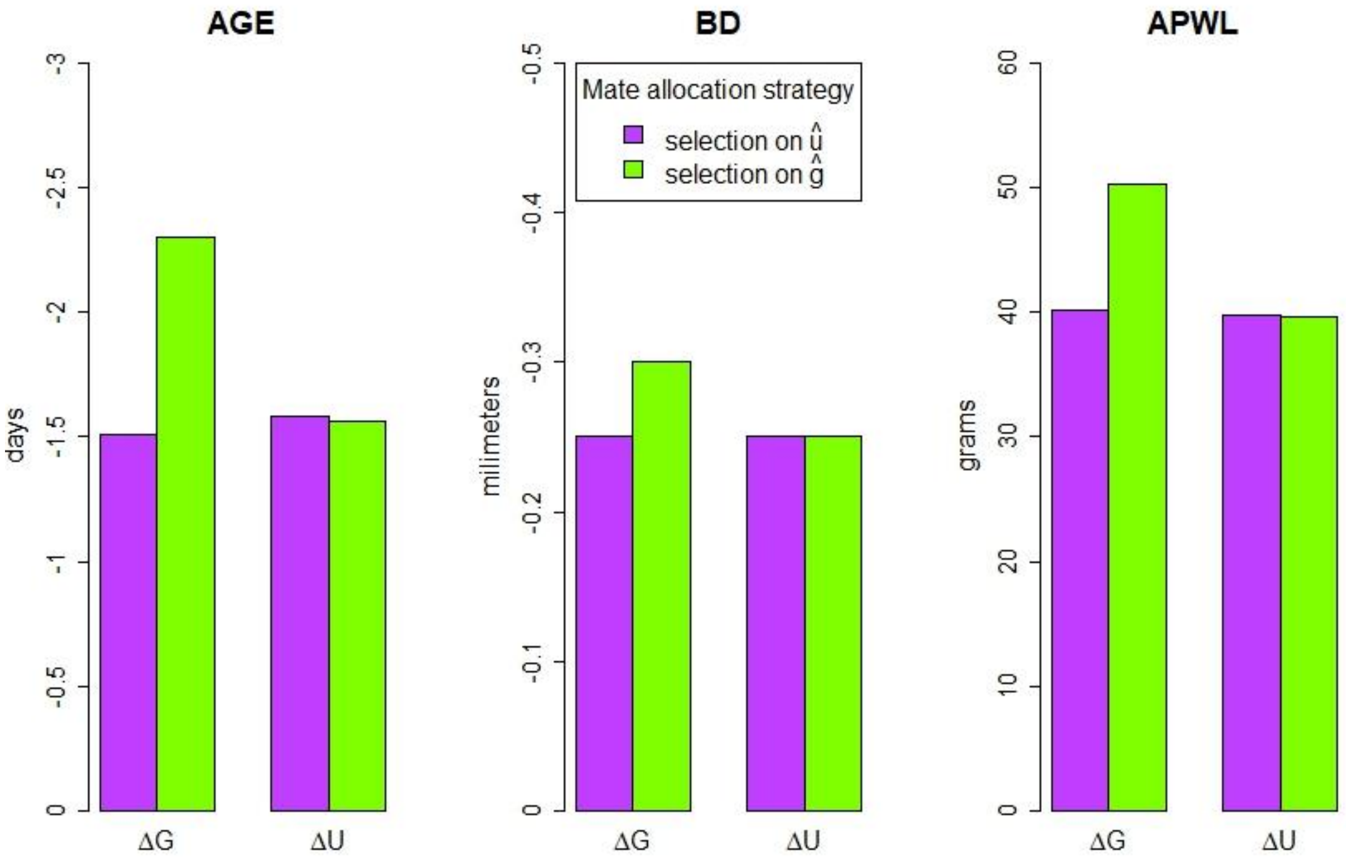


$h^2 = 0.27$
$d^2 = 0.05$

$h^2 = 0.20$
$d^2 = 0.02$

$h^2 = 0.36$
$d^2 = 0.04$

Expected genetic gain



Increase in ΔG: 51% 17% 27%

No differences were observed in ΔU regardless selection was based on $\hat{g}$ or $\hat{u}$.

Conclusions

- Genomic mate allocation, accounting for non-additive genetic effects, is a feasible and a promising strategy.
- It improves the performance of future offspring without losing additive genetic gain in this pig dataset.

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Thank you for your attention ...