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

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Summary

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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).

<table>
<thead>
<tr>
<th>Trait</th>
<th>Boars</th>
<th>Sows</th>
<th>Genotyped animals</th>
<th>Number of records</th>
<th>Mean (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGE (days)</td>
<td>789</td>
<td>2179</td>
<td>2968</td>
<td>2968</td>
<td>149.03 (9.36)</td>
</tr>
<tr>
<td>BD (mm)</td>
<td>1007</td>
<td>2675</td>
<td>3682</td>
<td>3682</td>
<td>11.20 (1.68)</td>
</tr>
<tr>
<td>APWL (g)</td>
<td>-</td>
<td>1226</td>
<td>1226</td>
<td>3297</td>
<td>1321.73 (213)</td>
</tr>
</tbody>
</table>

*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: $\sigma_A^2$ $\sigma_D^2$

- 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:

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

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

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

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

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

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

Toro and Varona (2010)
**Allocation of matings**

Top$_{\text{GEBV}}$ 40 males

* i-th boar

* j-th sow

e.g. AGE

2,179 females

Possible matings

87,180

**Mate allocation strategies**

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

Mate allocation strategies

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

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

**Optimization by linear programming**

R package *lpsolve* (Berkelaar et al., 2004)
Expected genetic gain

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

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

selected matings = 600
RESULTS
Genetic variance components

**AGE**

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

**BD**

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

**APWL**

- $h^2 = 0.36$
- $d^2 = 0.04$
Expected genetic gain

Increase in $\Delta G$: 51%

No differences were observed in $\Delta U$ 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 ...