Potential benefits of distributing males and females among phenotyping candidates in genomic selection

T. O. Okeno¹, M. Henryon²,³ and A. C. Sørensen¹

¹Center for Quantitative Genetics and Genomics, Department of Molecular Biology and Genetics, Aarhus University, Denmark
²Danish Agriculture and Food Council, Pig Research Centre, Copenhagen, Denmark
³School of Animal Biology, University of Western Australia, Crawley, Australia
Previous study - Diminishing marginal returns from genomic selection as more selection candidates are phenotyped - WCGALP

Hypotheses

- There is diminishing marginal return from genomic selection as more candidates are phenotyped

- Phenotyping candidates based on a priori information is beneficial
ΔG, genotypic standard deviation  

Phenotyping proportions (%)  

Rate of inbreeding (%)  

- Estimated breeding value  
- Random selection  
- Genetic gain  
- Rate of inbreeding  

02-09-2014
✓ Diminishing return to genomic selection as more candidates are phenotyped

✓ Use of *a priori* information to select phenotyping candidates is beneficial

❑ Most benefits of genomic selection can be realised by phenotyping only high ranking selection candidates

❖ The effect of phenotyping candidates’ sex ratio on returns to genomic selection was not considered
Objective

- To determine the effect of male-to-female ratio of the phenotyping candidates on returns to genomic selection
Simulation design

- Genetic gain

Phenotyping proportions

- 20-50%

Male:Female sex ratio

- 100:0
- 75:25
- 50:50
- 25:75
- 0:100
- Phenotyping criteria

- Parental information
  - Yes
    - Estimated breeding values
  - No
    - Random Selection

- Phenotyping

- Genotyping

- Selection decisions

[Diagram of phenotyping criteria and decision-making process]
Breeding scheme

Population structure
- Boars = 10
- Sows = 100
- Litter size = 5

Implementation
- 12 discrete generations
- 8-12 - Implementation of genomic selection and phenotyping criteria

Breeding objective - Single trait selection with $h^2 = 0.4$
Simulated genome

- Genetic architecture of the founder population—represent LD in the Danish pigs

- Genome = 18 chromosomes of 167 cM each

- 60,000 markers and 8,000 QTLs

- Haplotypes sampled to initiate breeding schemes
Genetic gain

$\Delta G$, genotypic standard deviation

Phenotyping proportion (%)

- Estimated breeding value
- Random selection
- Sex differentiation
- No sex differentiation
Genetic gain for Males and Females

ΔG, genotypic standard deviation

Number of phenotyped candidates

02-09-2014
- Considering sex ratio among the phenotyping candidates is beneficial.

- Phenotyping sex with high selection intensity is beneficial at low proportions.

- Less intensively selected sex should also be considered at high phenotyping proportions.