Genomic selection in maternal pig breeds

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Maternal traits

- Considerable weight in the breeding goal

- Low heritability

- Measured only in females, and after selection

Aim of the study

Design genomic selection schemes for maternal traits in pigs

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Methods

- Stochastic simulation
- Population of 2,775 sows
- 18 pairs of chromosomes
- 100 QTL per chromosome
- 500 SNP markers per chromosome
- 10 years (20 rounds) of selection
- Selection based on a maternal trait

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Selection

- 600 dams selected to produce selected litters
- 2 females from each litter used for replacement
- 1-3 males from each litter selection candidates
- 25 males selected as new sires
- Truncated selection

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Breeding values

- Conventional BLUP breeding values (Henderson, 1984)

- Genomic breeding values
  - Marker effects estimated by BLUP method
    (Meuwissen et al, 2001)
  - Genomic EBV estimated as sum of marker effects

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Reference population

- 450 genotyped animals with 40 progeny with records each at start of selection

- Added during selection
  - Genotyped females (added when they got a record, at 1 year of age)

  - Genotyped males with progeny (added when their progeny got records, at 2.5 years of age)

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Schemes to compare

- **CONV** – all selection based on conventional EBVs

- **GS-1m2f** – 1 male and 2 females from each litter genotyped

- **GS-2m1f** – 2 males and 1 female from each litter genotyped

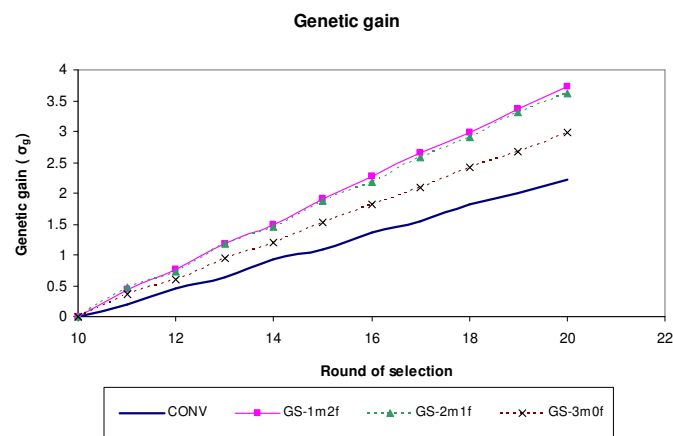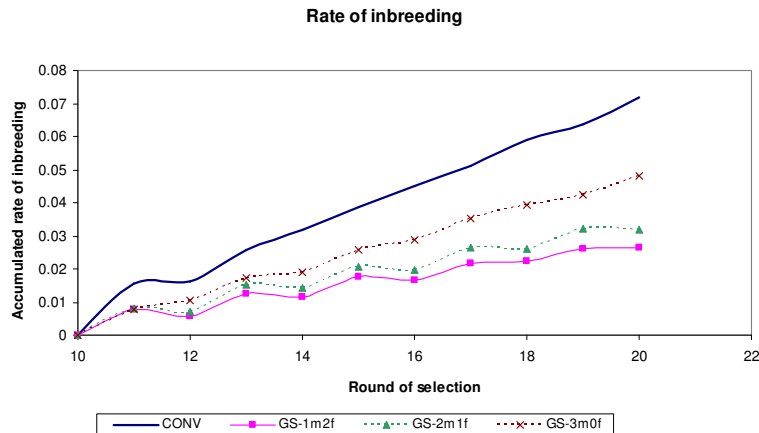- **GS-3m0f** – 3 males from each litter genotyped

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Accuracy of selection

Scheme	Accuracy male selection	Accuracy female selection
CONV	0.21	0.50
GS-3m0f	0.34	0.56
GS-2m1f	0.51	0.61
GS-1m2f	0.55	0.69

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Genetic gain

Genetic gain

Legend: CONV, GS-1m2f, GS-2m1f, GS-3m0f

x-axis: Round of selection

y-axis: Genetic gain (σ_g)

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Rate of inbreeding

Rate of inbreeding

Conclusions

- Genomic selection can increase genetic gain for maternal traits by 35-69 %

- Rate of inbreeding could be reduced by 34-64 %

- Genotyping females gave higher genetic gain and lower rate of inbreeding than genotyping more males when comparing schemes with the same number of genotyped animals.

Full paper:

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