Application of genomic evaluation for Canadian Yorkshire pigs
A preliminary study

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Introduction:

- Simulation and empirical studies have shown the potential of genomic information for increasing the reliability of the Estimated Breeding Values (EBV).
- High-density Single Nucleotide Polymorphism (SNP) chips can be used for predicting genomic EBV (GEBV) to preselect breeding animals for meat quality .
- For maternal traits such as litter size, GEBV can be used to increase accuracy and decrease the generation interval.

Objective:

- Investigate the impact of using genomic information on the reliabilities of backfat thickness EBV as a preliminary step in application for other traits. Backfat was chosen for having more reliable EBVs.

Materials & Methods:

Animals

- 744 purebred Yorkshire pigs from herds across Canada were genotyped.
- From a total of 744 pigs , 619 which had a backfat thickness EBV reliability greater than 60% were included in the analyses.
- Animals were divided in two sets:
  - Training set: 546 pigs born in 2009 and before, used to estimate SNP effects (with an average EBV accuracy of 78.4%).
  - Validation set: 73 pigs born after 2009, which had their GEBV predicted based on animals in the training set (with an average EBV accuracy of 64.8% in 2011).

Backfat EBVs

- Estimated Breeding Values for backfat thickness were obtained from the Canadian national genetic evaluation released on February 17, 2011.
- Parental Average (PA) EBVs adjusted to a common base were obtained from the first national genetic evaluation after the birth of each pig in the validation set.

Genotyping

- Illumina PorcineSNP60 BeadChip.

SNPs filtration

- 38,275 out of the 64,232 SNPs were included in the analyses:
  - 17,382 SNPs were excluded because they were either located on the sex chromosomes or not yet mapped to a specific chromosome.
  - 8,575 of SNPs which had minor allele frequency<0.05 were excluded.

	Number of animals	r^2 (PA or GEBV, EBV[1])	
		PA	GEBV
Training set	546	33.0	98.7
Validation set	73	33.0	35.0

[1] Backfat thickness EBV in 2011

Genomic EBV (GEBV)

- gebv software (Sargolzaei et al, 2009) was used to estimate genomic EBVs, using VanRaden (2008) equivalent model.

Validation of GEBV

- The square correlation between the PA or GEBV and EBV in 2011 was calculated for training and validation animals.

Results & Discussions:

- GEBV was not a better predictor of EBV in 2011 compared to PA prior to the performance test of pigs in the validation group.
- Possible reasons for this result are the relatively low reliability of EBVs and lower numbers of animals in both the prediction and validation groups compared to studies reported in other species.
- In practice there is a limit to increase the reliability of EBV for pigs due to rapid turnover of nucleus animals.
- Options for increasing the number of animals for both training and validation include collaboration with other groups to pool datasets and development of lower cost SNP panels, associated with imputation to the 60k SNP panel.

Conclusions & Recommendations:

- Higher number of animals and/or possibly higher accuracy of EBV may be required for effective implementation of genomic evaluations in pigs.
- This preliminary study was done using a trait with high heritability where phenotypes are readily available on most animals. Potential benefits from GEBV for traits with lower EBV accuracy or without available phenotypic observation is expected to be greater than for backfat thickness .
- Unmapped SNPs will be included in a future research to assess how much they would contribute to the accuracy of the genomic predictions.

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