On the added value of genomics for accurate prediction in pig breeding:
LEARNING FROM HISTORICAL DATA

Marcos Lopes
Egiel Hanenberg, Jenelle Dunkelberger, Barbara Harlizius, Egbert Knol

Topigs Norsvin
PROGRESS IN PIGS

Topigs Norsvin
PROGRESS IN PIGS

Does GENOMIC SELECTION work?

Aim

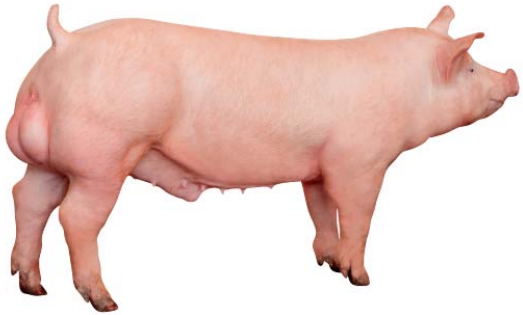
To use **Historical EBV**, recorded via routine breeding program procedure, to evaluate the added value of genomics for accurate prediction of EBVs for selection candidates that lack own or progeny performance records

Data

Historical EBVs
No own or progeny performance
Estimated up to ~3 years ago
Before and after genotyping

Today's EBVs
Own and progeny performance
Estimated recently
After genotyping

TNB: Total Number Born
ADG: Average Daily Gain (~25 to 120 Kg)



Sire Line (N=2,153)

Dam Line (N=935)

Breeding value estimation

Routine breeding value estimation: **multi-breed** and **multi-trait**

- 11 runs
- 106 traits
- > 200,000 animals genotyped
- > 40 million animals in the pedigree
- > 20,000,000,000 EBV's / week

- APY
- Calc_grm + MiXBLUP

Data

Description of the evaluated data

Line	Trait	N	Average reliability of Today's EBV
Dam	TNB	619	58%
	ADG	935	58%
Sire	TNB	360	57%
	ADG	2,153	58%

N: number of animals
Reliability: Tier and Meyer (2004)
Threshold for Todays' EBV reliability: 50%

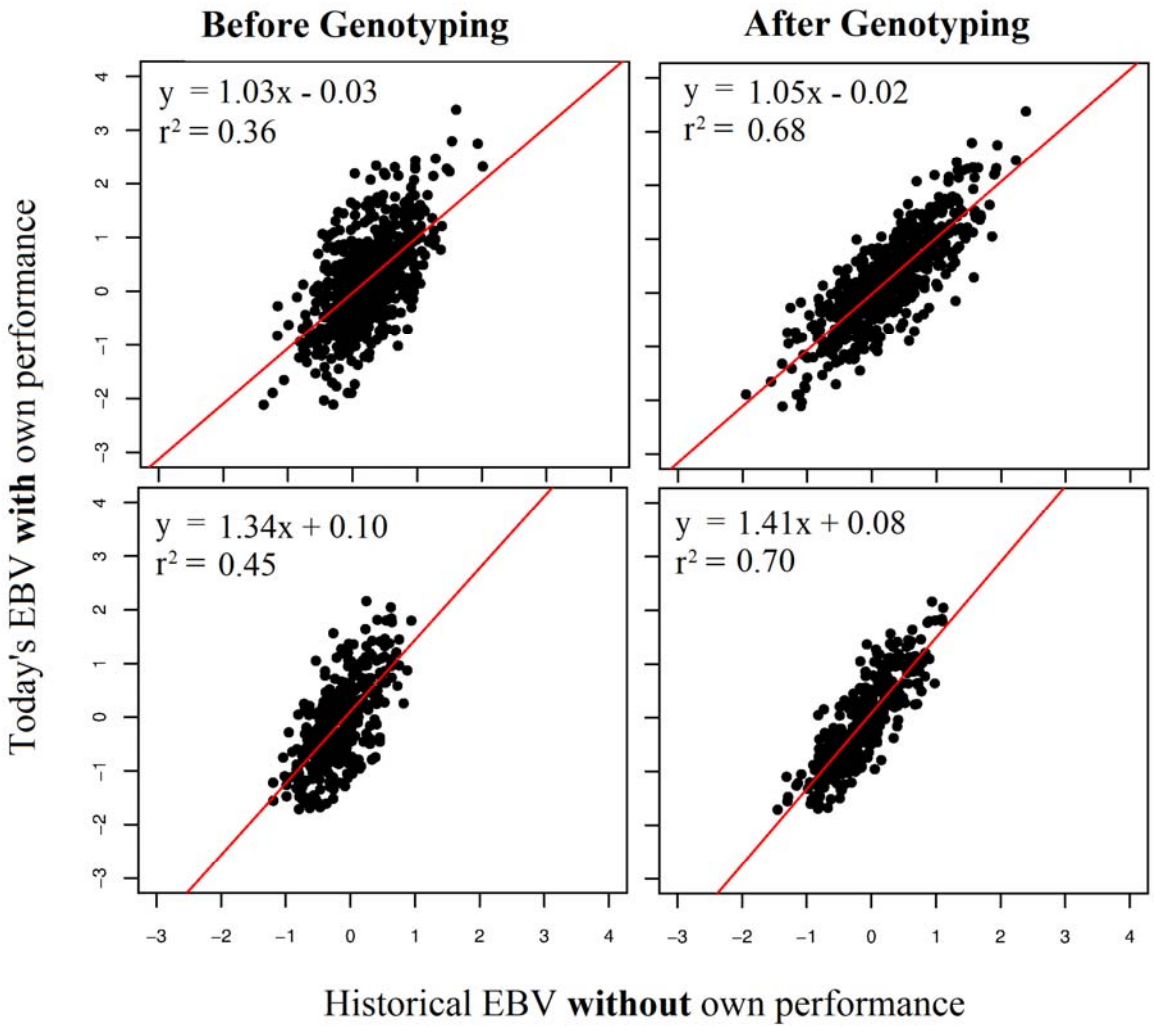
Results

Variation in breeding value before and after genotyping

Line	Trait	Genotyping status	Average ± SD	Minimum	Maximum
Dam	TNB	Before	0.26 ± **0.49**	-1.38	2.02
		After	0.24 ± **0.66**	-1.95	2.38
	ADG	Before	11 ± **26**	-79	76
		After	10 ± **36**	-115	106
Sire	TNB	Before	-0.16 ± **0.40**	-1.20	0.94
		After	-0.14 ± **0.47**	-1.45	1.11
	ADG	Before	35 ± **27**	-43	110
		After	31 ± **33**	-82	129

Variation of EBVs (**SD**) increased up to:
35% - Dam Line | 22% Sire Line

Results - TNB



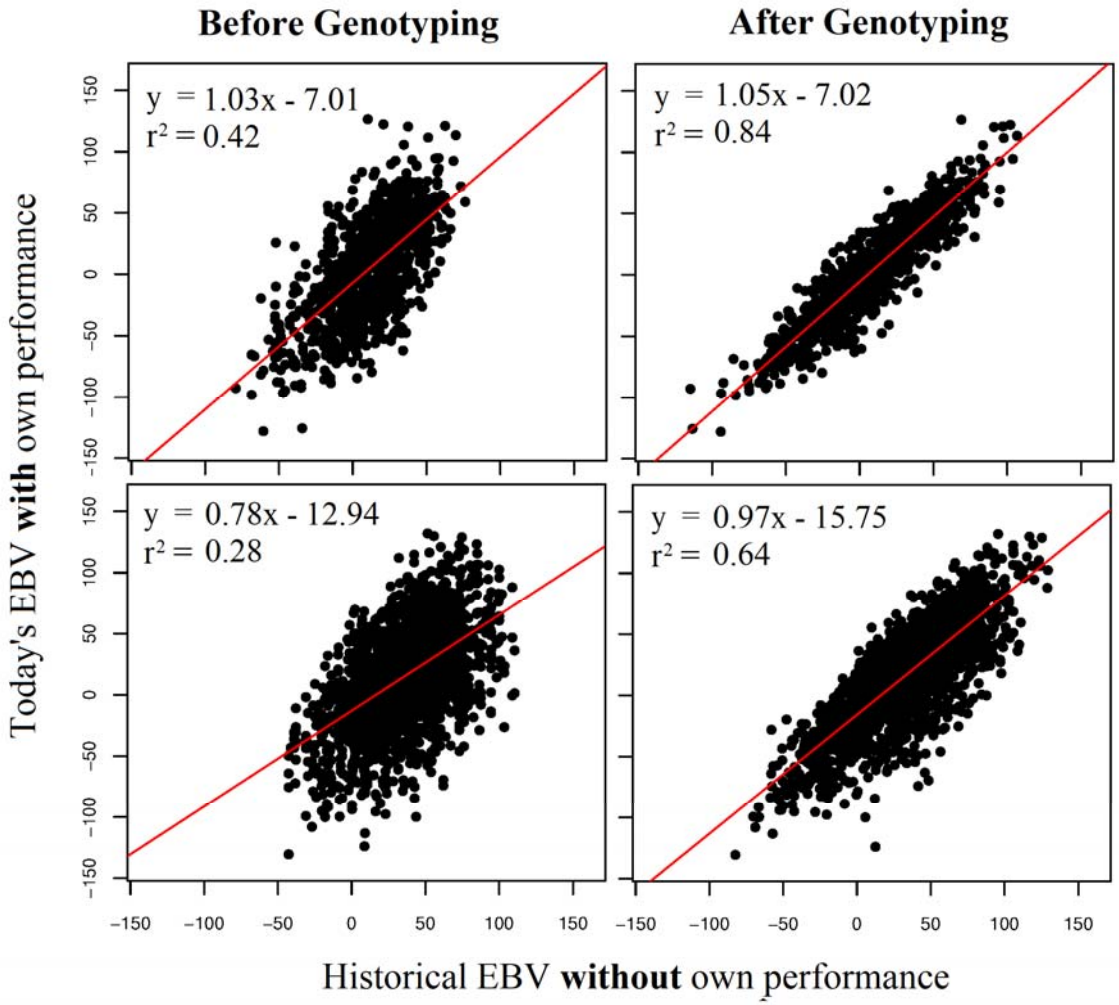
TNB - Dam Line

Correlations:
0.60 – 0.82 (+37%)

TNB - Sire Line

Correlations:
0.67 – 0.84 (+25%)

Results - ADG



ADG - Dam Line

Correlations:
0.65 – 0.91 (+40%)

ADG - Sire Line

Correlations:
0.53 – 0.80 (+51%)

Discussion

- GS in pigs - increase in prediction accuracy: **20 to 50%**
  Real and simulated data (Lillehammer et al., 2013; Hidalgo et al., 2015; Knol et al., 2016)

- Our results - increase in prediction accuracy: **25 to 51%**

- Repeat analyses when more data become available
  3 years ago: beginning of GS in our populations
  Threshold for Todays' EBV reliability > 90% instead of >50%

- Todays' EBV is also using genomics

Discussion

Example (Dam Line)

- Selection of 10% best animals for TNB **before genotyping**
  Their average Today's EBV (with own performance) = **1.23 piglets**

- Selection of 10% best animals for TNB **after genotyping**
  Their average Today's EBV (with own performance) = **1.55 piglets**

For this example, selection **after genotyping**, rather than **before genotyping**, increased the average EBV by **0.32 piglets**

Conclusions

Genomic selection works

- Historical data can be used to indicate the added value of genomics
- Genomics increase the variability of EBVs and the prediction accuracy
- Our results are in line with those demonstrated by previous studies based on real and simulated data