

Accuracy of genomic selection to improve litter traits in the French Landrace pig population

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Objectives

- To assess gains in accuracy due to integration of genomic information in genomic evaluations of pigs,
- Focus on litter traits and on the French Landrace dam line.

Material and methods

Phenotypic data

- Four litter traits considered:
 - Number born alive (NBA),
 - Number of weaned piglets (NW),
 - Mean Birth Weight of piglets (MBW),
 - Within-litter standard deviation of birth weights (SDBW).
- 95 000 litter performances since 01/01/2003 up to 30/09/2015.

Genotypic data

- 579 boars born > 2002 + 504 sows born > 2009,
- Genotyped on the Illumina 60KSNP panel,
- 42 166 SNPs after quality controls.

Genomic evaluation models

- Use of a single-step genomic BLUP approach (ssGBLUP),
- Genomic relationship matrix built following VanRaden (2008),
- Use of the BLUPF90 program suite (Miszta *et al.*),
- Genetic parameters of routine genetic evaluations.

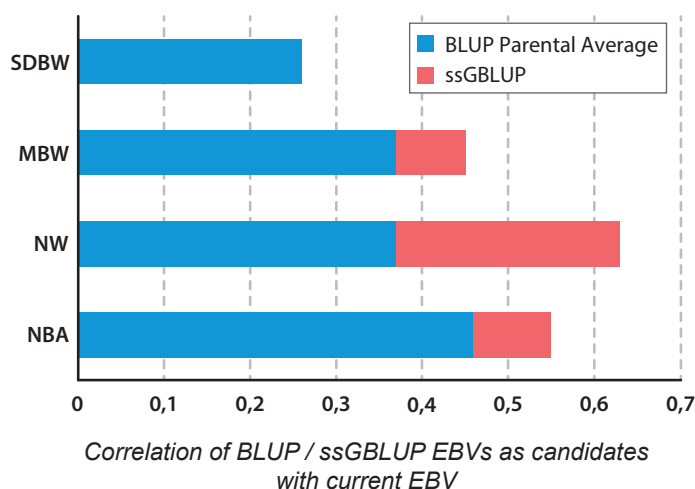
Cross-validation study

- BLUP / GBLUP performed with all the data,
- 2nd dataset : all performance truncated after 01/01/2014:
 - Reference population = 491 boars + 355 sows,
 - 46 validation boars born in 2013 with >15 daughters in 09/2015.
- Predictive ability : for validation boars, correlation between BLUP and GBLUP EBVs without progeny data and BLUP EBVs with progeny data.

Results

Predictive ability of (G)BLUP models

- Moderate to large gains in predicting future breeding value for NBA, NW and MBW due to inclusion of genomic data,
- No gain observed for SDBW in this cross-validation study,
- Results are consistent with gains in the theoretical reliability (CD) obtained from Prediction Error Variances.



Conclusion

- Genomic evaluation has an increased predictive ability for choosing the candidates on litter traits
- Genomic evaluation is now applied in routine in the French Landrace pig population

