First results on genomic selection in French show-jumping horses

A. Ricard¹,³, S. Danvy³, A. Legarra²
¹Biologie Intégrative et Génétique Equine, UMR 1313 GABI, INRA
²Station d’amélioration génétique des animaux, UR 631, INRA
³Institut français du cheval et de l’équitation, recherche et développement
Genomic radically changed selection schemes in dairy cattle

⇒ Because reliability for genetic evaluation for milk traits obtained with genotypes reached 0.50, similar to the one obtained with performances of 20 progeny and then sufficient to select before progeny test

1. Is it possible to obtain such reliability in Jumping Horses?

2. In addition, genome-wide association study was performed in order to find quantitative trait loci (QTL) and to explain more accurately the biology of jumping ability
- 908 stallions genotyped
  - 71% Selle Français (SF),
  - 17% Foreign Sport horses (FS),
  - 13% Anglo-Arabian (AA)

- 336 stallions with own sire genotyped
- 82 families with 3 half sibs and more

- Estimated Breeding Values (EBV) for jumping
  - Performance criteria based on ranking and points attributed to ranking in official competition
  - Mean reliability 0.67
- Illumina Equine BeadChip
  - 54,602 SNP
  - 44,444 retained
    - Call frequency > 80%
    - Minimum Allele Frequency >=5%;
    - Hardy Weinberg test with p-value > $10^{-8}$
For genomic selection, 2 models were tested and compared

- G-BLUP (Van Raden, 2008)
- BayesC $\pi$ (Habier et al., 2011)

For the research of QTL, 2 models have been studied

- GWAS with mixed model and SNP genotype
- GWAS with mixed model and hidden states used to build haplotypes
  for this part of the study, only the results of the second model will be presented
The whole system for EBV is very large and with non linear traits. Therefore, an “Equivalent Performance” was calculated from official EBV’s and their reliabilities. It summarizes own performance, performances of progeny and performances of all relatives outside the genotyped data. These pseudo-performances should contain all the information that was outside the genotyped sample.

Which performances were used in this models?
Cross Validation

The sample was divided in 2 parts:

- a **training** data set
- a **validation** data set

1. Genetic values are estimated in the **training** data set from pseudo performances and genealogical/genomic relationships

2. Genetic values are calculated in the **validation** data set from genetic evaluations of the training population only, so without pseudo performances but only genealogical/genomic relationships between the two samples

Results are the comparison between genetic values and pseudo performances in validation data set
Genetic values were:

- Classical genetic evaluation from pedigree information
- Genomic evaluation from GBLUP model and BayesCπ

Different validation data set were used, following recommendation of literature (Hayes and Goddard, 2008, Goddard, 2009 and Habier et al., 2010)

- have the Sires of the stallions in the training data set
- have a minimum reliability of EBV of stallion and sire of stallion
- have families for stallions to highlight differences between sibs
Results: genomic evaluation

Correlation between pseudo-phenotypes and genetic evaluation
In validation data set

Validation data set: Sire genotyped, Half sibs families ≥3, EBV reliability >0.52

<table>
<thead>
<tr>
<th></th>
<th>All Breed</th>
<th>SF + FH</th>
</tr>
</thead>
<tbody>
<tr>
<td>N training</td>
<td>805</td>
<td>713</td>
</tr>
<tr>
<td>N validation</td>
<td>103</td>
<td>84</td>
</tr>
<tr>
<td>BLUP (pedigree)</td>
<td>0.36</td>
<td>0.28</td>
</tr>
<tr>
<td>GBLUP (genomic)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bayes $C_\pi$ (genomic)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Results: genomic evaluation

Correlation between pseudo-phenotypes and genetic evaluation
In validation data set

Validation data set: Sire genotyped, Half sibs families ≥3, EBV reliability >0.52

<table>
<thead>
<tr>
<th></th>
<th>All Breed</th>
<th>SF + FH</th>
</tr>
</thead>
<tbody>
<tr>
<td>N training</td>
<td>805</td>
<td>713</td>
</tr>
<tr>
<td>N validation</td>
<td>103</td>
<td>84</td>
</tr>
<tr>
<td>BLUP (pedigree)</td>
<td>0.36</td>
<td>0.28</td>
</tr>
<tr>
<td>GBLUP (genomic)</td>
<td>0.39</td>
<td>0.30</td>
</tr>
<tr>
<td>Bayes $C_\pi$ (genomic)</td>
<td>0.39</td>
<td>0.29</td>
</tr>
</tbody>
</table>
PCA Genomic relationships between the 908 stallions

- SF
- FH
- AA
- SF, >55% thoroughbred

A L I M E N T A T I O N
A G R I C U L T U R E
E N V I R O N NEMENT
Results: QTL (hidden states) SF+FH

-log10(p value)

Position on chromosomes
Results: QTL (hidden states) SF+FH
Results: QTL SNP BIEC2-31630

Effect (phenotypic standard deviation) vs. Hidden state of haplotype

<table>
<thead>
<tr>
<th>Hidden state of haplotype</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.1</td>
</tr>
<tr>
<td>2</td>
<td>0.2</td>
</tr>
<tr>
<td>3</td>
<td>0.3</td>
</tr>
<tr>
<td>4</td>
<td>0.5</td>
</tr>
<tr>
<td>5</td>
<td>0.4</td>
</tr>
<tr>
<td>6</td>
<td>0.6</td>
</tr>
</tbody>
</table>

Number of haplotypes

0 100 200 300 400 500 600 700 800 900 1000
Accuracy of genomic evaluation was obtained in a large and rather exhaustive sample with favorable linkage disequilibrium.
Unfortunately the accuracy was not sufficiently higher than the one of classical genetic evaluation to propose an application.

why?
Conclusion

Why?

- Sample size
  
  *compared to dairy cattle with tens thousands of sires*

- Lack of sire/progeny couples between validation and training data set
  
  *in dairy cattle, for each generation of young tested bulls, all sires are genotyped*

- Small accuracy of pseudo-performances
  
  *in dairy cattle, reliability of EBVs is always more than 0.90*

- Selection of data (selected stallions)
  
  *in dairy cattle, sires are selected but the information about the difference between tested and proven sires is included in the data here, the difference between good and bad performances stallions before selection was not included*

- Multi breed sample (AA/SF)
  
  *always difficult to manage*
Conclusion

- The GWAS is promising but not in accordance with Schröder and al. results (Animal Genetics, 2011).

- The research will be pursued to improve this result.

→ It is our intention to extend this line of research:

1. to estimate whether our results make sense or not,
2. under which conditions would genomic selection be promising.
Acknowledgment

The national associations and

The breeders

Funders of research

Fonds Éperon

Institut National de la Recherche Agronomique

Ecole Nationale d'Équitation

Les Haras nationaux

Institut français du cheval et de l'équitation