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First results on genomic selection in French show-jumping horses

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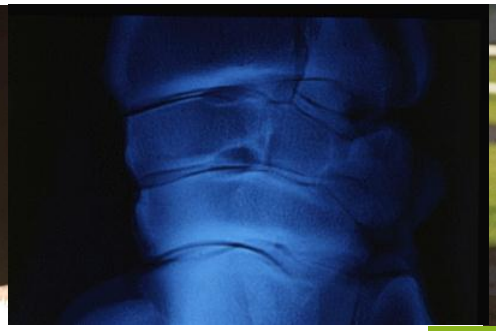

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Objective

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

Material

- 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

Material

- Illumina Equine BeadChip
  - 54,602 SNP
  - 44,444 retained
    - Call frequency > 80%
    - Minimum Allele Frequency >=5%;
    - Hardy Weinberg test with p-value > 10^{-8}

Models used

- For genomic selection, 2 models were tested and compared
  - G-BLUP (Van Raden, 2008)
  - BayesC π (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

Pseudo-Performance

Which performances were used in this models ?

- The whole system for EBV is very large and with non linear traits

➔ it was not possible to manage it for testing only a thousand of genotyped horses

- 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.

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

Cross Validation

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

	All Breed	SF + FH
N training	805	713
N validation	103	84
BLUP (pedigree)	0.36	0.28
GBLUP (genomic)		
Bayes Cπ (genomic)		

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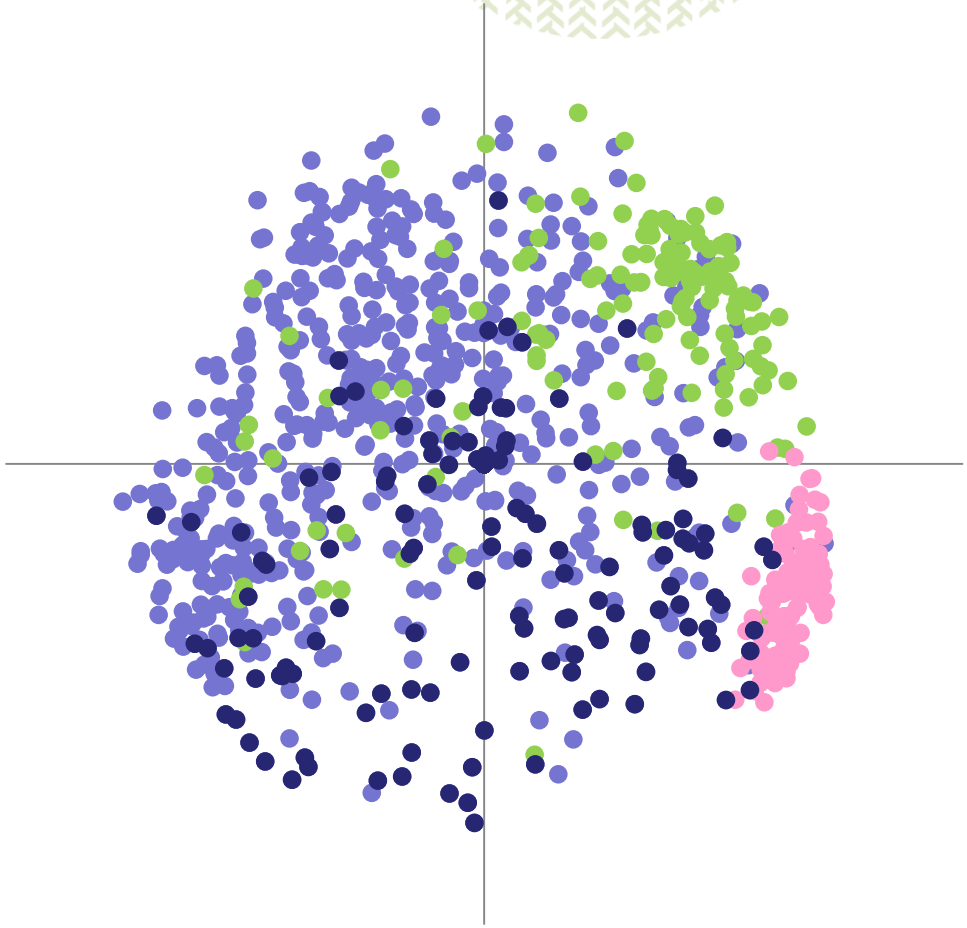
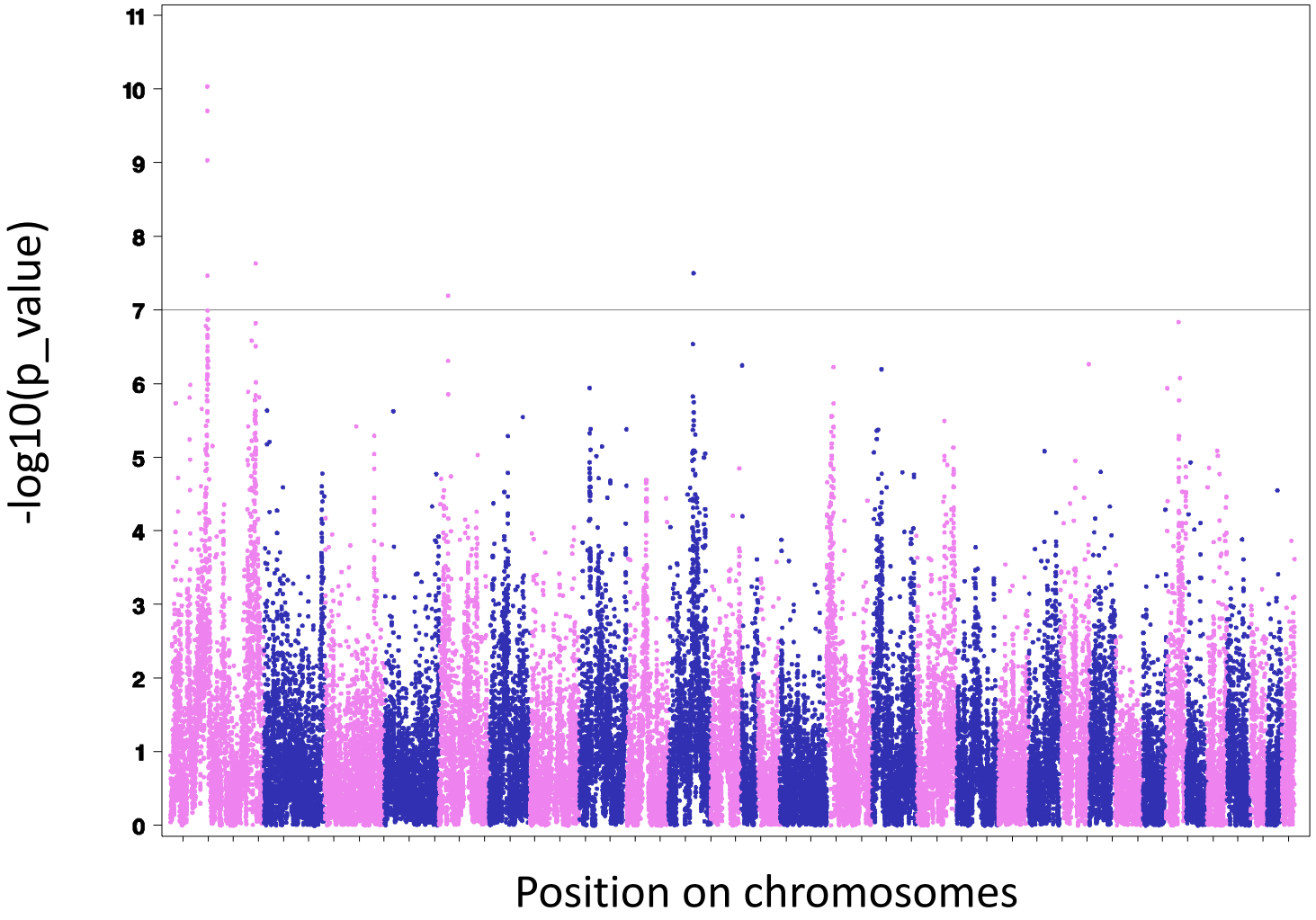
Bayes Cπ (genomic)	0.39	0.29

PCA Genomic relationships between the 908 stallions



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

Results : QTL (hidden states) SF+FH



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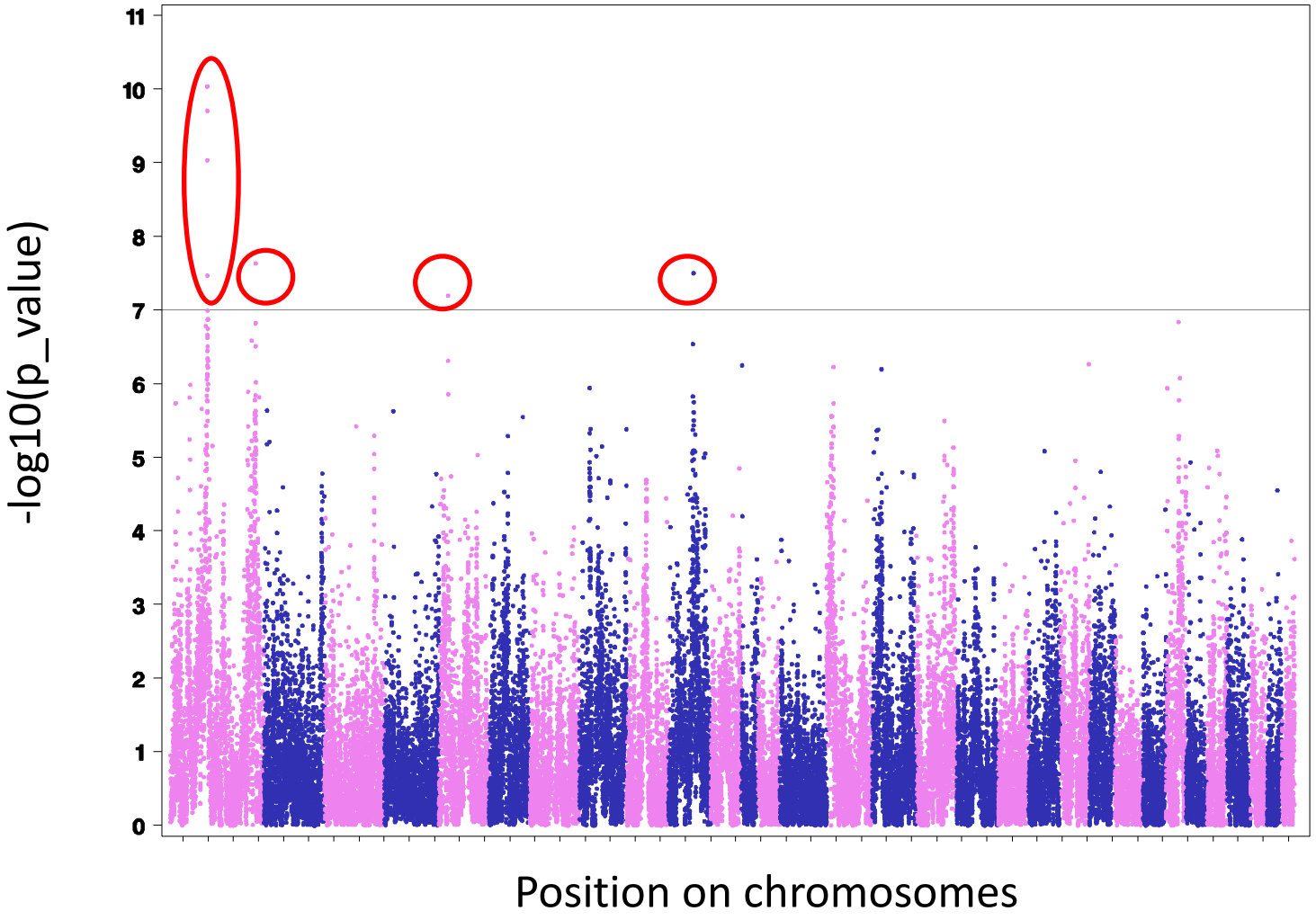
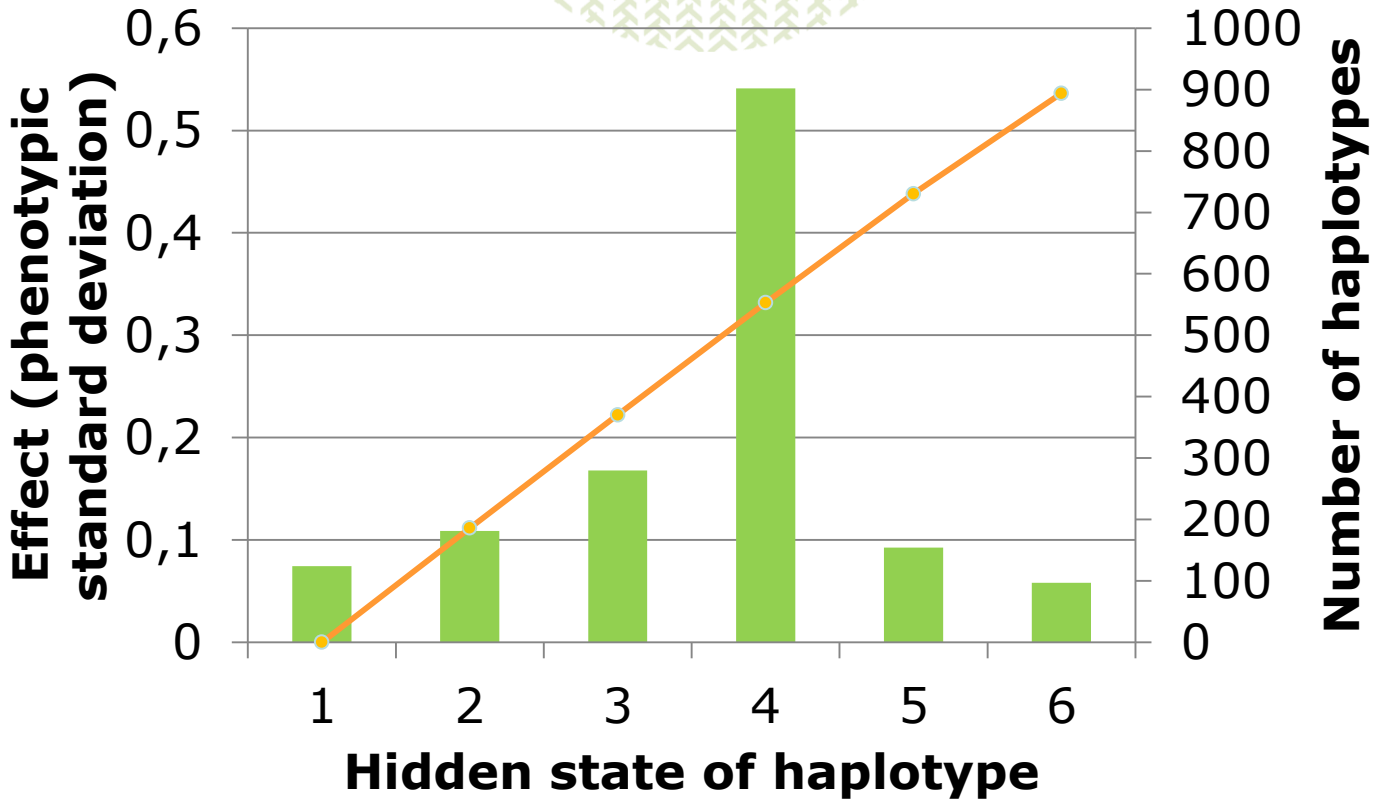
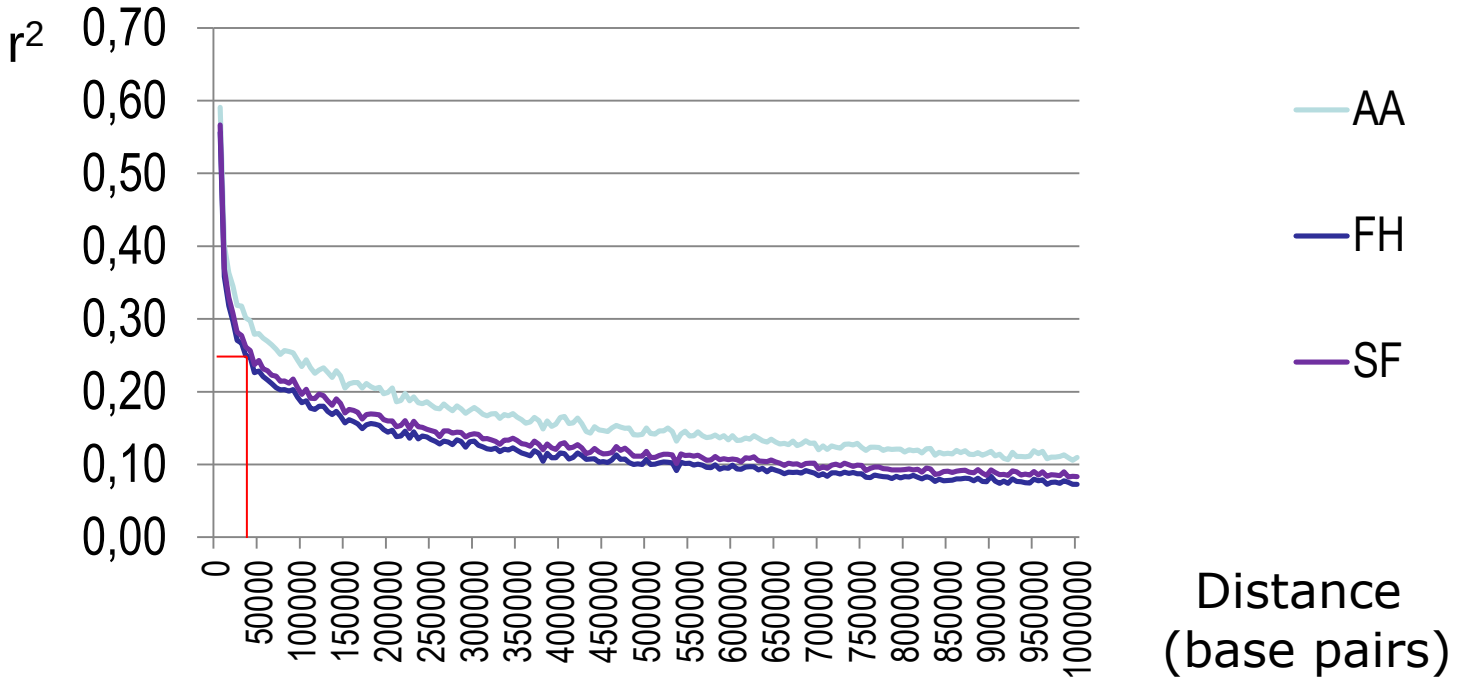


Results : QTL SNP BIEC2-31630



Conclusion

Accuracy of genomic evaluation was obtained in a large and rather exhaustive sample with favorable **linkage disequilibrium**



Conclusion

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 informations about the difference between tested and proven sires is included in the datahere, 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

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Selle Français

anaa ANGLO - ARABE - FRANCE

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