

First results on genomic selection in French show-jumping horses



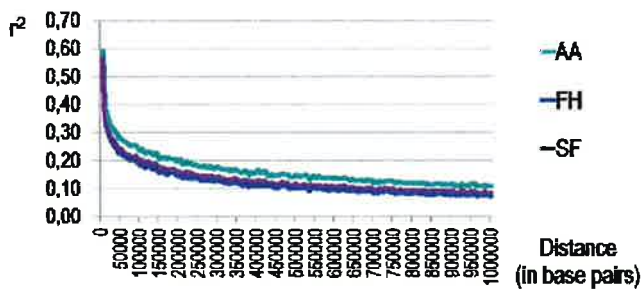
A. Ricard¹, S. Danvy², A. Legarra³. ¹INRA, UMR 1313, 78350 Jouy-en-Josas, ²IFCE, Service recherche et développement, Jumenterie du Pin, 61310 Exmes, ³INRA, UR 631, 31326 Castanet-Tolosan.

Objective

To measure reliability of genomic evaluation for jumping horses in France.

Materials

- 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 based on ranking and annual sum of points allowed to ranking in official competition
 - Mean reliability 0,67
- Illumina Equine BeadChip
 - 54,062 SNP; 44,444 retained (MAF≥5%; Hardy Weinberg test with p_value<10⁻⁸, call freq>80%)
 - Linkage disequilibrium:



Models

■ Gblup

$$y^{(eq)} = \mathbf{1}\mu + \mathbf{u} + \mathbf{e}$$

$$V(\mathbf{u}) = \mathbf{G}\sigma_u^2$$

$$\mathbf{G} = \frac{\mathbf{X}'\mathbf{X}}{2 \sum_{j=1}^{44444} p_j(1-p_j)}$$

Centered incidence matrix of marker effects

Allelic frequency

■ BayesCπ

$$y^{(eq)} = \mathbf{1}\mu + \sum_{j=1}^{44444} \mathbf{z}_j \sigma_a^2 \delta_j + \mathbf{e}$$

SNP effect

Indicator variable Bernoulli

$$\Pr(\delta_j = 1 | \pi) = \pi$$

$y^{(eq)}$: pseudo-performance = deregressed EBV
Composite performance including all information of all relatives (performances of progeny, sibs, parents...) excepted the one of genotyped relatives (special procedure developed)

Cross Validation

- Genetic value estimated in training data set with genealogic relationships or genomic models from pseudo performances
- Genetic value estimated in validation data set with genealogic relationships or genomic models from genetic evaluation of the training population only
- Comparison between genetic values and pseudo performances in validation data set

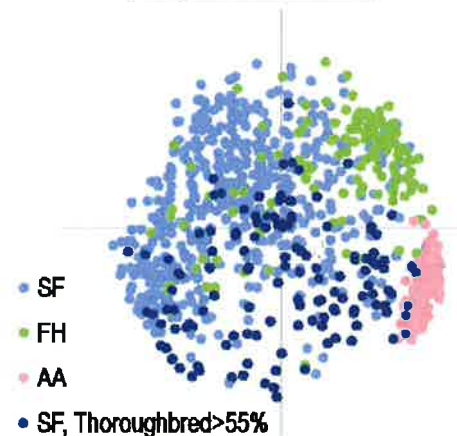
Results

Correlation between pseudo-phenotypes and genetic evaluation based on pedigree or SNP relationships (GBLUP and Bayes C pi)

	Validation data set 1		Validation data set 2	
	All Breed	SF + FH	All breed	SF + FH
N	103	84	98	89
BLUP (pedigree)	0.36	0.28	0.33	0.30
GBLUP (genomic)	0.39	0.30	0.37	0.34
Bayes Cpi (genomic)	0.39	0.29	0.37	0.33

Validation data set 1: -Sire genotyped, -Half sibs families ≥3, -EBV reliability >0.52
Validation data set 2: -Sire genotyped with EBV reliability >0.97, -EBV reliability >0.52

Principal component analysis of genomic matrix



- Accuracy of genomic evaluation was obtained in a large (for horses) and rather exhaustive (for active stallions) sample
- Unfortunately the accuracy was not sufficiently higher than the one of classical genetic evaluation to propose an application, why?
 - Sample size (compared to dairy cattle), lack of sire/progeny couples between validation and training data set, small accuracy of pseudo-performances (reliability<0,90), selection of data (selected stallions), multi breed sample (AA/SF)
- The research will be pursued to improve this result