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FRENCH GENOMIC EVALUATION OF SHOW JUMPING IN SPORT HORSES

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In France, Estimated Breeding Value (EBV) of show jumping horses are based on performance in official competitions and has been calculated every year since 1986 with BLUP animal model.

Thanks to the GenoSport project, genomic data were used for the first time in 2023 and Genomic Estimated Breeding Value (GEBV) were published.

MATERIALS & METHODS

DATA – 2023

347,137 horses with performances.

Matrix relationship included 617,903 horses.

3,658 genotypes from 3 different beadchips (54,602 to 670,806 SNPs) imputed to 375,687 SNPs.



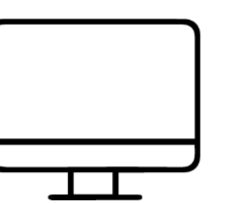
2 CORRELATED TRAITS

- **POINT** = annual sum of points earned in each event according to rank and technical difficulty.
- **RANK** = ranking considered as the result of expression of an underlying unobservable performance.

SINGLE STEP MODEL

MODEL EFFECTS

- Fixed effect : Age x Year of performance x Sex
- Permanent environment effect inside one year for RANK
- Permanent environment effect between years for RANK and POINT
- Random effect : genetic additive value



Single Step GBLUP multitrait model (BLUPf90 software).

EBV and GEBV are expressed in points and standardised using : 10 points = 1 genetic standard deviation, and 0 = mean of the population born 5 years before.

RESULTS AND DISCUSSION

GENETIC PARAMETERS

	POINT	RANK
Heritability	0.31	0.13
Repeatability	0.42	0.23

Genetic correlation between RANK and POINT = 0.90

CORRELATIONS EBV/GEBV

57,921 horses with performances in 2023

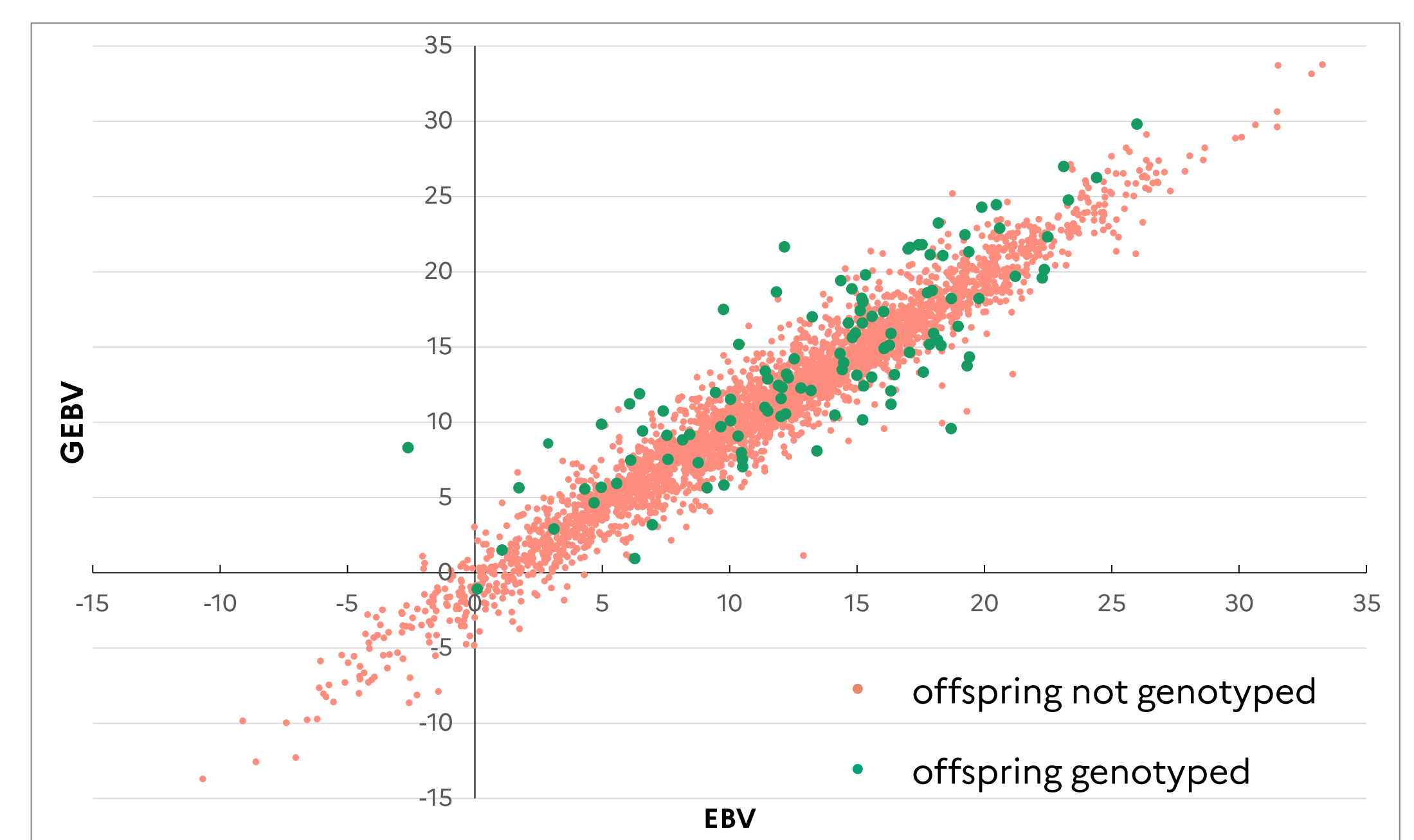
Horses	N	Mean GEBV	Mean EBV	Corr EBV/GEBV
Not genotyped	56,846	0.52 ± 12.06	0.07 ± 12.58	0.992
Genotyped	1,075	7.38 ± 7.92	6.59 ± 8.12	0.934

361 stallions > 6 years old, min 10 progeny with performances

Horses	N	Mean GEBV	Mean EBV	Corr EBV/GEBV
Not genotyped	231	3.01 ± 14.06	2.33 ± 14.5	0.995
Genotyped	130	8.33 ± 8.10	7.41 ± 8.94	0.985

- ▶ Horse ranking mostly respected and reliability improved by integrating genomic information.
- ▶ Horses with genotype are here a specific population (stallions or horses specialised for jumping) => explain higher average GEBV.
- ▶ Horses well known for performances or offspring => less genomic information impact.
- ▶ Expected impact of genomic information on reliability for non-performing horses (to be confirmed).

DIAMANT DE SÉMILLY OFFSPRING



3,286 progeny from Diamant de Sémilly have been evaluated. 114 of them were genotyped. The genomic information allowed a better discrimination of the genetic values, thanks to a better estimation of the allele transmission between halfsib.

CONCLUSION

The introduction of genomic information into the evaluation process will increase the reliability of the EBVs. However, horse classifications are mostly respected.

To complete this first step in genomic field, the French equine industry is working on a project based on a 60,000 SNPs array developed by the French Research to be used routinely for parentage control and breeding evaluation.