

# APPLICATION OF GENOMIC SELECTION IN THE SPANISH ARAB HORSE BREEDING PROGRAM

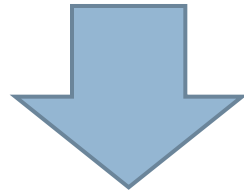
Cervantes, I.<sup>1</sup>; Meuwissen T.H.E.<sup>2</sup>

<sup>1</sup>Department of Animal Production. Complutense University of Madrid, Spain. <sup>2</sup>Department of Animal and Aquacultural Sciences, Norwegian University of Life Sciences, Ås, Norway.



# Introduction

- Long generation interval.
- Suboptimal selection intensities.
- Low heritable functional traits.



- Genomic Selection could be an advantage in horse breeding programs.



# Arab Breeding Program

1<sup>o</sup>

FOALING

*Parentage test*  
→ **STUDBOOK**  
*Identification and official description*

2<sup>o</sup>

**GENETIC VARIABILITY MANAGEMENT**

Inbreeding, gene flow, genetic lines

3<sup>o</sup>

**INDIVIDUAL GENETIC EVALUATION**

YOUNG RECOMMENDED HORSE FOR BREEDING  
Young Horse Competitions (Endurance, Eventing, etc.) and  
Conformation . 4-7 years old

4<sup>o</sup>

**PROGENY TEST**

PROVEN STALLIONS AND MARES  
(own performance and progeny test >7 years old)

5<sup>o</sup>

**STALLIONS AND MARES BOOK**

# Genetic evaluation in 2014, Endurance races

Trait	Heritability
Ranking	0.10
Total time	0.10
Race time	0.11
Recovery time	0.15

# Genetic evaluation in 2014, Endurance races

- **Young Horses:** After genetic evaluation 80% of males that could obtain the young genetic category were castrated animals.
- **Horses >7 years old:** After genetic evaluation 70% of males with genetic index >100 and accuracy  $\geq 0.6$  were castrated animals.

# Objective

- The objective of this study was to compare the genomic selection tools with traditional BLUP by simulation in Arab horse breeding program in Spain.



# Material and Methods

- Simulated marker data
  - ▣ Thirty-two chromosomes.
  - ▣ Mutation rate=  $2 \times 10^{-9}$ .
  - ▣ An average of 83000 SNPs markers, MAF=0.03.
  - ▣ Probability to become a QTL =3.7%.
  - ▣ Historical population:  $N_e=200$  and 2000 generations.
  - ▣ Founders of a subset of the Real pedigree of Arab Horse.
  - ▣ A simulated genotype for each animal included in the pedigree.

# Material and Methods

- The real pedigree contained 3613 Arab horses.

F	AR	$g_e$
6.1%	8.5%	5.1

- Simulated breeding values and phenotypes:
  - ▣  $h^2=0.1, 0.2$  and  $0.3$ .
  - ▣ Twenty replicates of each scenario were used.

F: Average Inbreeding, AR: Average Relatedness,  $g_e$ : Average Equivalent Complete generations



# Material and Methods

- A traditional BLUP genetic evaluation (BLUP-pedigree):
  - 3613 animals in the pedigree.
  - 2000 with phenotypes.
  - 613 young animals without phenotype. Relatives from the previous set of animals.
- BLUPF90 (Miształ, 1999)

# Methods

- BLUP-SNP evaluation

- ▣ The training set included 2000 animals.

$$y_i = \mu + \sum_{j=1}^n x_{ij} \cdot \text{SNP}_j + e_i \quad \sigma_a^2 = \frac{\sigma_u^2}{2 \sum p_i q_i}$$

- ▣ The validation set included 613 animals.

$$\text{GEBV}_i = \hat{\mu} + \sum_{j=1}^n x_{ij} \cdot \widehat{\text{SNP}}_j$$

- GS3 (Legarra et al., 2014)
- Both methods were compared by accuracies between predicted and true breeding values.

# Results and Discussion

Accuracies between true and predicted breeding values

<b><math>h^2=0.1</math></b>	<b>BLUP-SNP</b>	<b>BLUP-pedigree</b>	<b>Difference</b>
<b>Training</b>	0.54±0.01	0.49±0.01	0.05
<b>Validation</b>	0.44±0.02	0.36±0.02	0.08

# Results and Discussion

Accuracies between true and predicted breeding values

<b><math>h^2=0.2</math></b>	<b>BLUP-SNP</b>	<b>BLUP-pedigree</b>	<b>Difference</b>
<b>Training</b>	0.66±0.01	0.60±0.01	0.06
<b>Validation</b>	0.54±0.01	0.43±0.02	0.10

# Results and Discussion

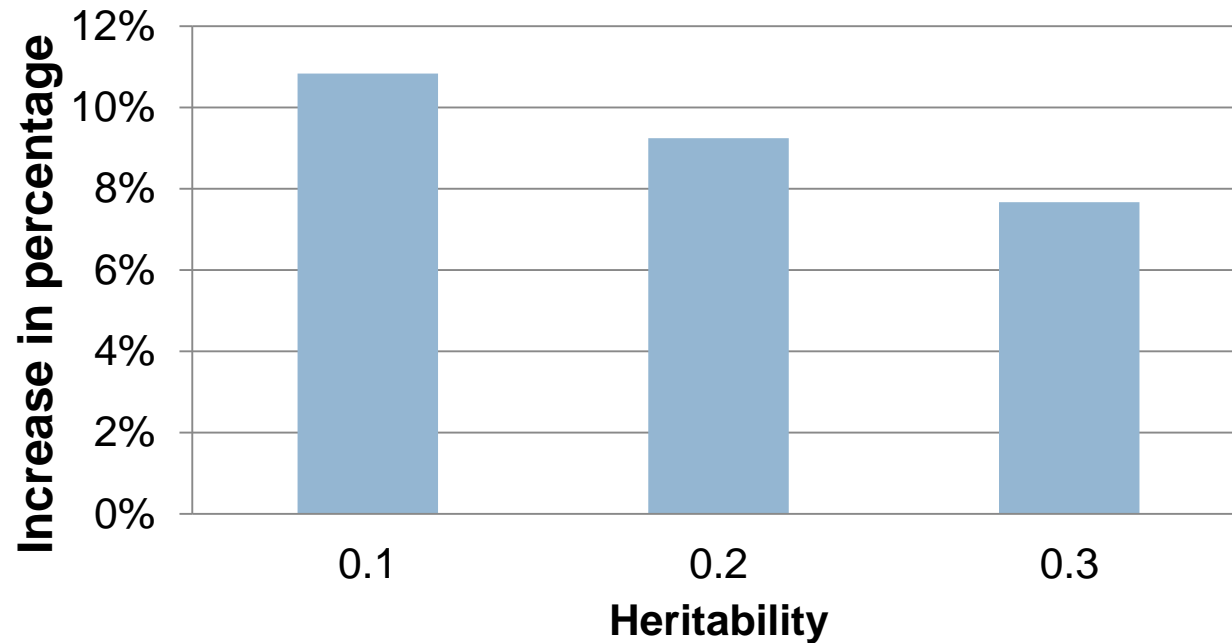
Accuracies between true and predicted breeding values

$h^2=0.3$	<b>BLUP-SNP</b>	<b>BLUP-pedigree</b>	<b>Difference</b>
<b>Training</b>	0.73±0.01	0.68±0.01	0.05
<b>Validation</b>	0.60±0.01	0.48±0.01	0.11

# Results and Discussion

Increase in accuracy using genomic selection

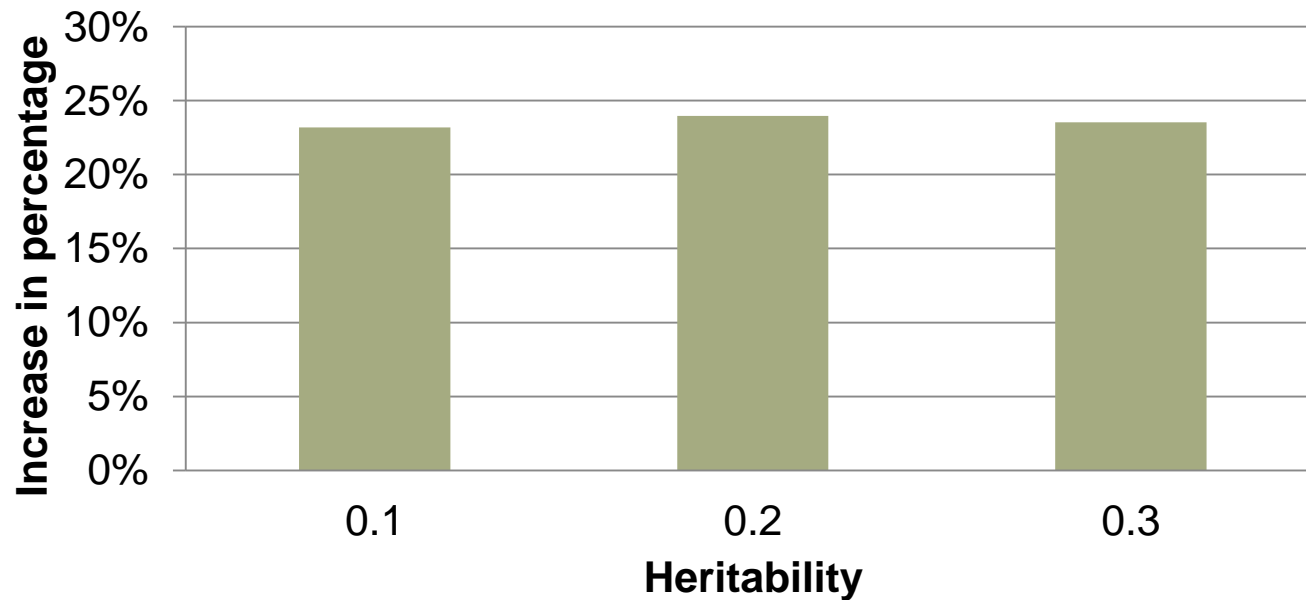
## Training



# Results and Discussion

Increase in accuracy using genomic selection

## Testing



# Conclusions

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- The structure in Spanish Arab Horse population is appropriate to attain reliable breeding values using genomic data.
- The application of genomic selection could help preselecting young males before being castrated increasing the selection intensity and therefore the genetic response.





Thank  
you



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