APPLICATION OF GENOMIC SELECTION IN THE SPANISH ARAB HORSE BREEDING PROGRAM

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Introduction

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

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

1º FOALING → STUDBOOK
   Parentage test
   Identification and official description

2º GENETIC VARIABILITY MANAGEMENT
   Inbreeding, gene flow, genetic lines

3º INDIVIDUAL GENETIC EVALUATION
   YOUNG RECOMMENDED HORSE FOR BREEDING
   Young Horse Competitions (Endurance, Eventing, etc.) and Conformation. 4-7 years old

4º PROGENY TEST
   PROVEN STALLIONS AND MARES
   (own performance and progeny test >7 years old)

5º STALLIONS AND MARES BOOK
### Genetic evaluation in 2014, Endurance races

<table>
<thead>
<tr>
<th>Trait</th>
<th>Heritability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ranking</td>
<td>0.10</td>
</tr>
<tr>
<td>Total time</td>
<td>0.10</td>
</tr>
<tr>
<td>Race time</td>
<td>0.11</td>
</tr>
<tr>
<td>Recovery time</td>
<td>0.15</td>
</tr>
</tbody>
</table>
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 ≥ 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.

<table>
<thead>
<tr>
<th></th>
<th>F</th>
<th>AR</th>
<th>g_e</th>
</tr>
</thead>
<tbody>
<tr>
<td>F</td>
<td>6.1%</td>
<td>8.5%</td>
<td>5.1</td>
</tr>
</tbody>
</table>

- 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 Relatednes, $g_e$: 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 (Misztal, 1999)
Methods

- **BLUP-SNP evaluation**
  - The training set included 2000 animals.
  - The validation set included 613 animals.

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

- The validation set included 613 animals.

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

- **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

<table>
<thead>
<tr>
<th>$h^2=0.1$</th>
<th>BLUP-SNP</th>
<th>BLUP-pedigree</th>
<th>Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training</td>
<td>0.54±0.01</td>
<td>0.49±0.01</td>
<td>0.05</td>
</tr>
<tr>
<td>Validation</td>
<td>0.44±0.02</td>
<td>0.36±0.02</td>
<td>0.08</td>
</tr>
</tbody>
</table>
Results and Discussion

Accuracies between true and predicted breeding values

<table>
<thead>
<tr>
<th>h^2=0.2</th>
<th>BLUP-SNP</th>
<th>BLUP-pedigree</th>
<th>Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training</td>
<td>0.66±0.01</td>
<td>0.60±0.01</td>
<td>0.06</td>
</tr>
<tr>
<td>Validation</td>
<td>0.54±0.01</td>
<td>0.43±0.02</td>
<td>0.10</td>
</tr>
</tbody>
</table>
## Results and Discussion

Accuracies between true and predicted breeding values

<table>
<thead>
<tr>
<th>h²=0.3</th>
<th>BLUP-SNP</th>
<th>BLUP-pedigree</th>
<th>Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training</td>
<td>0.73±0.01</td>
<td>0.68±0.01</td>
<td>0.05</td>
</tr>
<tr>
<td>Validation</td>
<td>0.60±0.01</td>
<td>0.48±0.01</td>
<td>0.11</td>
</tr>
</tbody>
</table>
Results and Discussion

Increase in accuracy using genomic selection

![Bar chart showing increase in accuracy using genomic selection for different heritability levels.](chart.png)

- **0.1** heritability level shows an increase of **10%**.
- **0.2** heritability level shows an increase of **8%**.
- **0.3** heritability level shows an increase of **6%**.

*Note: The chart illustrates the training accuracy improvements for different heritability levels.*
Results and Discussion

Increase in accuracy using genomic selection

Testing

Increase in percentage

<table>
<thead>
<tr>
<th>Heritability</th>
<th>Increase in percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.1</td>
<td>25%</td>
</tr>
<tr>
<td>0.2</td>
<td>25%</td>
</tr>
<tr>
<td>0.3</td>
<td>25%</td>
</tr>
</tbody>
</table>
Conclusions

- 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

Acknowledgements
This work has been made within a collaboration agreement between the Spanish Arab horse breeders association (AECCA). We acknowledge the simulation program by Robin Wellman. This work was partially supported by UCM- EAA and NMBU grants.