Linear profiling in SWB – new breeding values and genetic background

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Swedish Warmblood

“Internationally competitive horses in dressage, show jumping or eventing”

65,000 horses
4,400 covered mares (2017)
Introduction of linear profiling

2013
Young horse test for 3-year-olds (≈40%)

2014
Young horse test for 4- and 5-year-olds
Foal inspections
Stallion performance test
Mares for conformation grading

Scientific background

Scientific results published in November 2017
**Scientific results in short**

**Heritabilities**

Conformation (21 traits)
- 0.10 hock joint from behind - 0.52 for shape of the neck

Movements (21 traits)
- 0.08 energy in walk - 0.54 elasticity in trot

Jumping (14 traits)
- 0.05 ability to focus on the assignment - 0.57 scope

**Genetic correlations**

very strong between corresponding traits

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**Correlation between EBVs**

- **Jumping technique** (evaluating score)
- **Scope (linear)**

Much

Little
**Scientific results in short**

**Heritabilities**
- Conformation (21 traits)
  - 0.10 hock joint from behind
  - 0.52 for shape of the neck
- Movements (21 traits)
  - 0.08 energy in walk
  - 0.54 elasticity in trot
- Jumping (14 traits)
  - 0.05 ability to focus on the assignment
  - 0.57 scope

**Genetic correlations**
- Very strong between corresponding traits

**Conclusion:**
Linear information suitable for genetic evaluation and can be a useful tool for breeders.
New breeding values

2017 March
- Stallions - minimum 10 offspring with linear assessment (but at least 15 offspring at young horse test)

2018 January
- Stallions - minimum 10 offspring with linear assessment
- Mares – with own linear assessment

**BLUP Animal Model**

\[ y_{ijk} = \text{sex}_i + \text{event}_j + \text{horse}_k + \text{residual}_{ijk} \]

New breeding values

- Based on young horse test for 3-year-olds (4,000 horses)
- 50 traits (conformation, movements, jumping)
- 100 = average of all assessed horses
- Genetic standard deviation of 4 units
- Same direction of scale as protocol
- Accuracy – low, moderate and high

[www.blup.se](http://www.blup.se)
On-going activities

Add information in breeding value estimations from:

- Young horse test for 4- and 5-year-old horses
- Performance test for stallions

Genome-wide Association Study (GWAS) of Young Horse Test Traits in SWB Horses

Aim

To find genomic regions associated with conformation and performance traits in Swedish Warmblood (SWB)
Background

- SWB selected for show jumping and dressage traits.
- Weak positive genetic correlations previously estimated between jumping and dressage traits.
- Breeders focus increasingly on one discipline rather than both.
- Still, some stallions have high EBVs for both disciplines.

SWB stallions by dressage EBVs

- Stallions with ≥10 offspring born 2006-2009
Material and methods

- 380 horses tested as 3-year-olds 2013-2014, hair samples
- Total of 97 young horse test traits
  - Height at withers
  - 8 traditional evaluating scores
  - 2 summarized traits: show jumping and dressage talent
  - 57 linearly scored traits
  - 29 deviations scored as 0/1
- Genotyped using the equine 670K SNP-chip (Affymetrix)

Two main clusters

EBV (dressage) = 97
EBV (show jumping) = 123
EBV (dressage) = 117
EBV (show jumping) = 84
Height at withers

Confirmed published region on ECA3 highly significant for height at withers ($p=3.4 \times 10^{-21}$).

Conformation

Significant peak in linear conformation trait ($p = 2.6 \times 10^{-9}$) on ECA3.

Potentially interesting regions for deviation traits (0/1). Generally few individuals in one of the categories.
**Movements**

Only few suggestive associations for movement traits in spite of high heritabilities ($p = 1.3 \times 10^{-6}$).

**Jumping technique**

No significant association found in full data set (N=378) or in dressage cluster.

But potentially interesting association(s) in show jumping cluster only for linear jumping trait (N=189, $p = 6.4 \times 10^{-8}$).
Conclusions

- Increasing focus towards either show jumping or dressage among SWB-breeder.
- With 380 horses and 670K SNP-chip genome-wide assoc. for 'normally distributed' traits could be detected.
- A highly significant genome-wide association was confirmed for height at ECA3.
- Significant SNP associations were found for conformation traits.
- Within one of two clusters, significant association was found for linear jumping traits.

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