A genome-wide association study of young horse test traits in Swedish Warmblood

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EAAP Annual Meeting 2016, Belfast, UK, Session 63, Abstract 23528
Aim of study

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

- “A ...horse, which by its good temperament, rideability, good movements and/or jumping ability is internationally competitive”

Photo: Maria Håkansson.
- 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 index

Stallions with ≥10 offspring born 2006-2009
Test for 3-year-old SWB

- ~40% of all 3-year-olds are tested for conformation, movements, and jumping.
- Traditional evaluating traits according to breeding goal (scale 1-10), $h^2$ 0.09 - 0.85.
- Linear profiling protocol (scale 1-9) introduced 2013, $h^2$ 0.05 - 0.70. Certain deviations marked (0/1).

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Material & Methods

- 380 horses tested as 3-year-olds 2013-2014, hair-samples.
- Total of 97 young horse test traits
  - Height at withers (cm)
  - 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).
Material & Methods

- Quality control and analyses in GenABEL, R.
- After QC 379 horses and 467,606 SNPs remained.
- Fast score test for association, with genomic control.
- $\lambda$-values generally highest for jumping traits.
- Model included effects of
  - sex (male/female)
  - event (year x location).
- (Analyses taking relationships into account on to-do-list.)
Two main clusters

Cluster 1:
\[ \bar{x} \text{ EBV (dressage)} = 117 \]
\[ \bar{x} \text{ EBV (show jumping)} = 84 \]

Cluster 2:
\[ \bar{x} \text{ EBV (dressage)} = 97 \]
\[ \bar{x} \text{ EBV (show jumping)} = 123 \]

Genotyped horses, born 2010-2011
Confirmed published region on ECA3 highly significant for height at withers \((p=3.4 \times 10^{-21})\).

LCORL/NCAPG associated with growth and height in horses and other species.

Proof of concept.
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.
• Only few suggestive associations for movement traits in spite of high heritabilities ($p=1.3 \times 10^{-6}$)
• No significant association found in full data set (N=378) or in cluster 1.
• But potentially interesting association(s) in cluster 2 only for linear jumping trait (N=189, p = 6.4 x 10^{-8})
Affymetrix raw data files from 670k-SNP genotyping.

Prel. analysis using BioDiscovery’s SNP-FASST2 Segmentation Algorithm. Significance testing for aberrant copy number.

Gene families known for high CNVs are clearly visible, other chromosomal regions are under investigation.

### Copy Number Variations in SWB

- All horses
- Cluster 1: T-cell receptors, MHC
- Cluster 2: Olfactory receptors
Conclusions

• Increasing focus towards *either* show jumping *or* dressage among SWB-breeders.

• With 380 horses and 670K SNP-chip genome-wide assoc. for ‘normally distributed’ traits could be detected.

• A highly significant genome-wide association was found for height at ECA3.

• SNP-associations significant after Bonferroni correction was found for conformation traits.

• Within one of two clusters, significant association was found for a linear jumping trait.
Thank you for listening!

And thanks for contributions from:

- Hanna Göransson-Kultimaa & Anders Isaksson at SciLifeLab
- Swedish Warmblood Association 🏆
- Swedish-Norwegian Foundation for Equine Research 🐎