
SLU
SCIENCE AND EDUCATION FOR SUSTAINABLE LIFE

Single-step GWAS of factors for young horse test traits in Swedish Warmblood horses

Anahit Nazari-Ghadikolaei[1], Freddy Fikse[2], Åsa Gelinder Viklund [1], Sofia Mikko[1]
Susanne Eriksson[1]

[1]Swedish University of Agricultural Sciences. Dept. of Animal Biosciences,
[2]Växa, Research and Development

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Aims

Investigate possible candidate genes and regions of importance for evaluated and linearly scored young horse test traits in Swedish Warmblood horses (SWB).

Photo: Julio Gonzalez, SLU

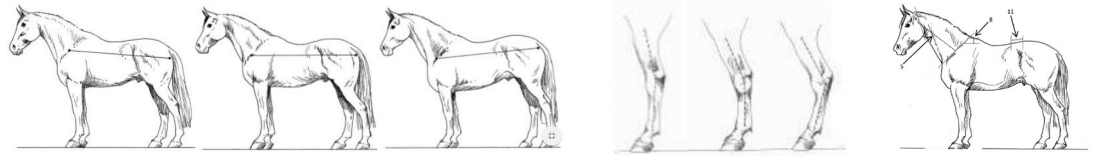
Traits

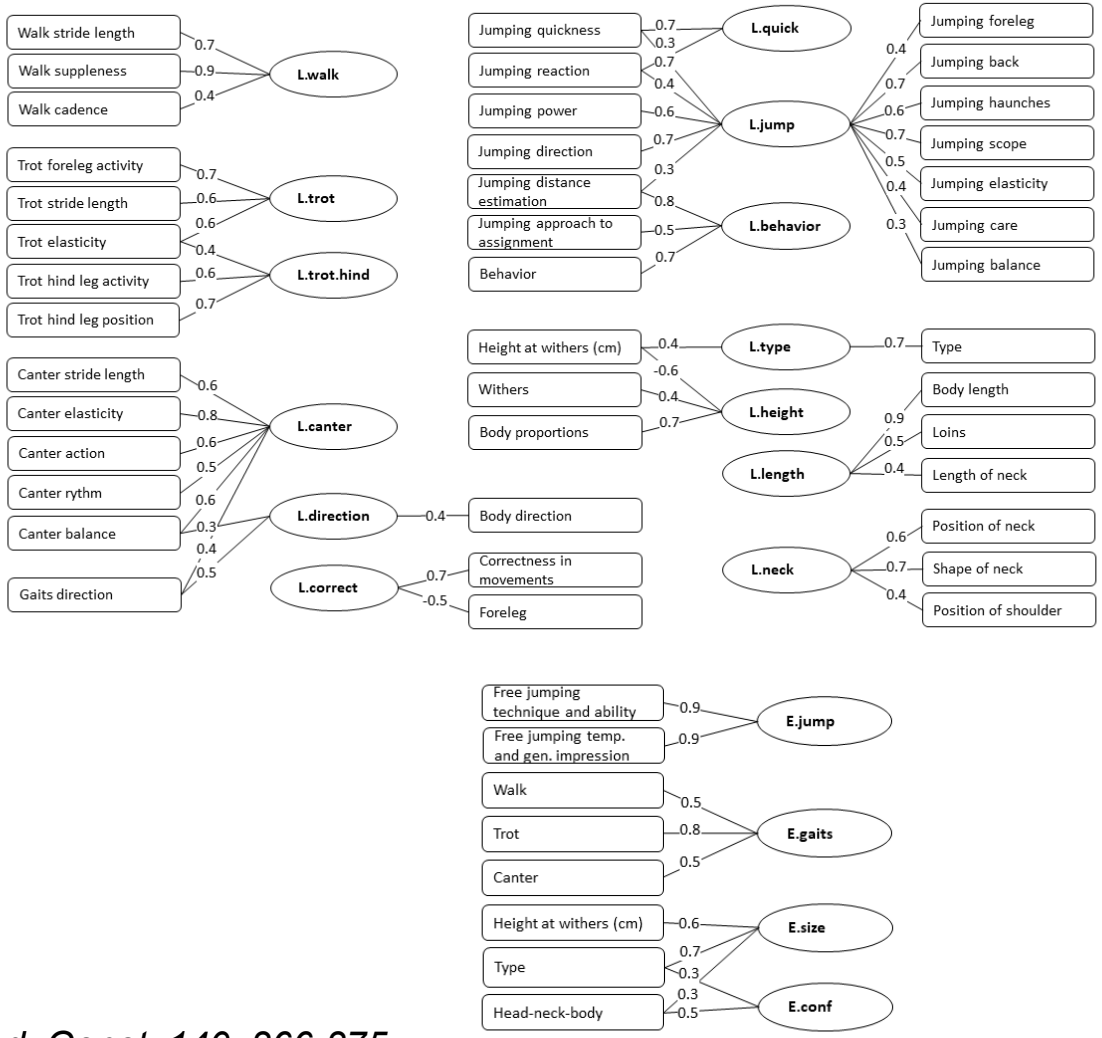
- Young horse tests in 3-year-old SWB:
  - 8 evaluated traits (scale 1-10)
  - height at withers (cm)
  - 50 linearly scored traits (scale A-I ->1-9)

  - Phenotypes from 20,935 assessed SWB, whereof 6,436 with linearly scored traits

- Factor analysis -> reduction of traits based on correlations.

- Further analysed:
  - 13 factors for linearly scored traits (L.)
  - 4 factors for evaluated traits (E.)





Nazari-Ghadikolaei et al. 2023. J. Anim. Breed. Genet. 140, 366-375

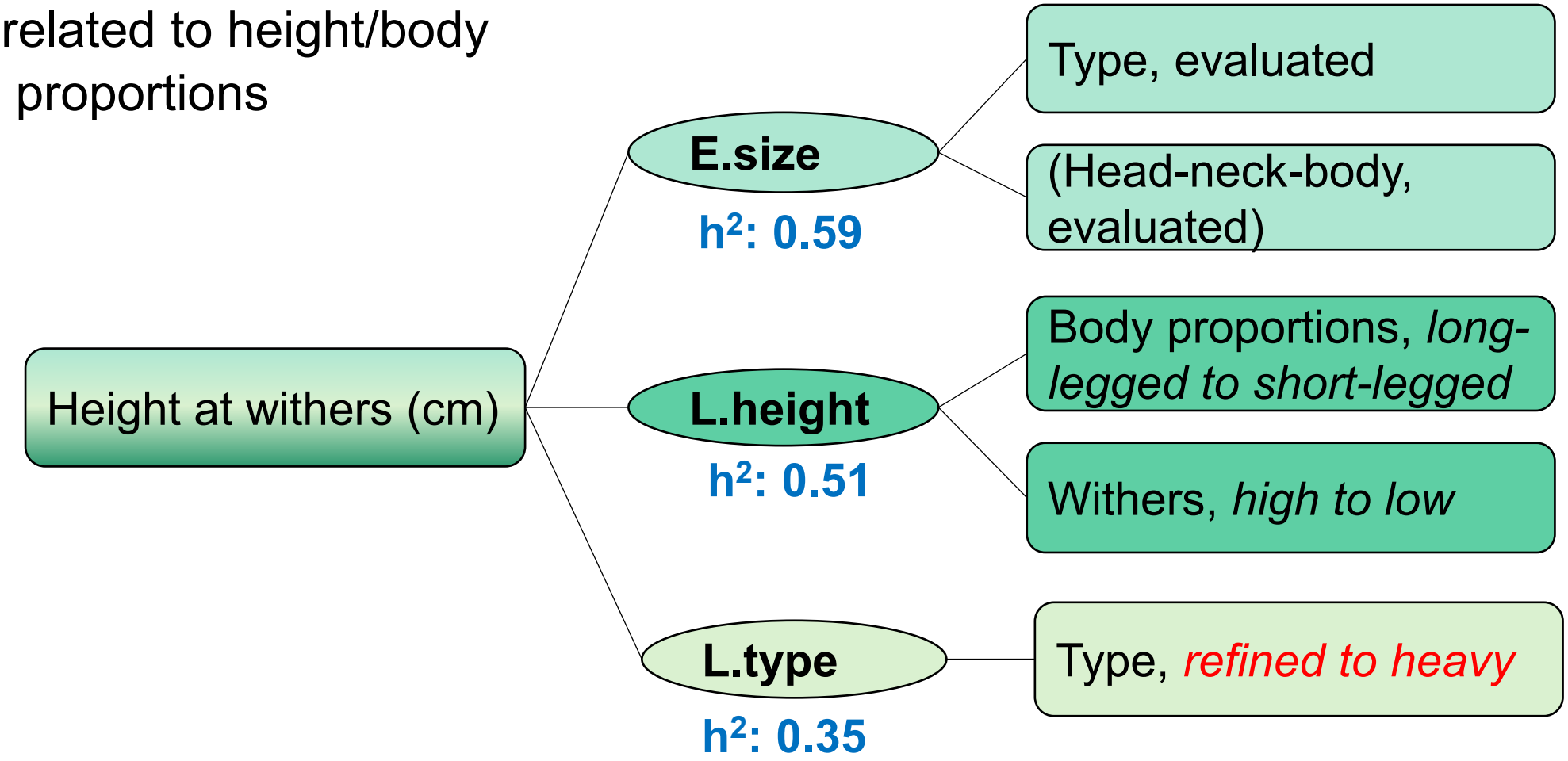
Single-step genome wide association study

- 380 assessed genotyped individuals (389,997 SNPs after QC)
- BLUPf90-suite of software
  - Combination of pedigree- and genomic relationships
- SNP-effects and P-values derived from predicted GEBVs, correction for lambda-values >1
- Regions further studied ± 500kb around top SNPs passing Bonferroni correction, or to be more inclusive FDR ≤0.3

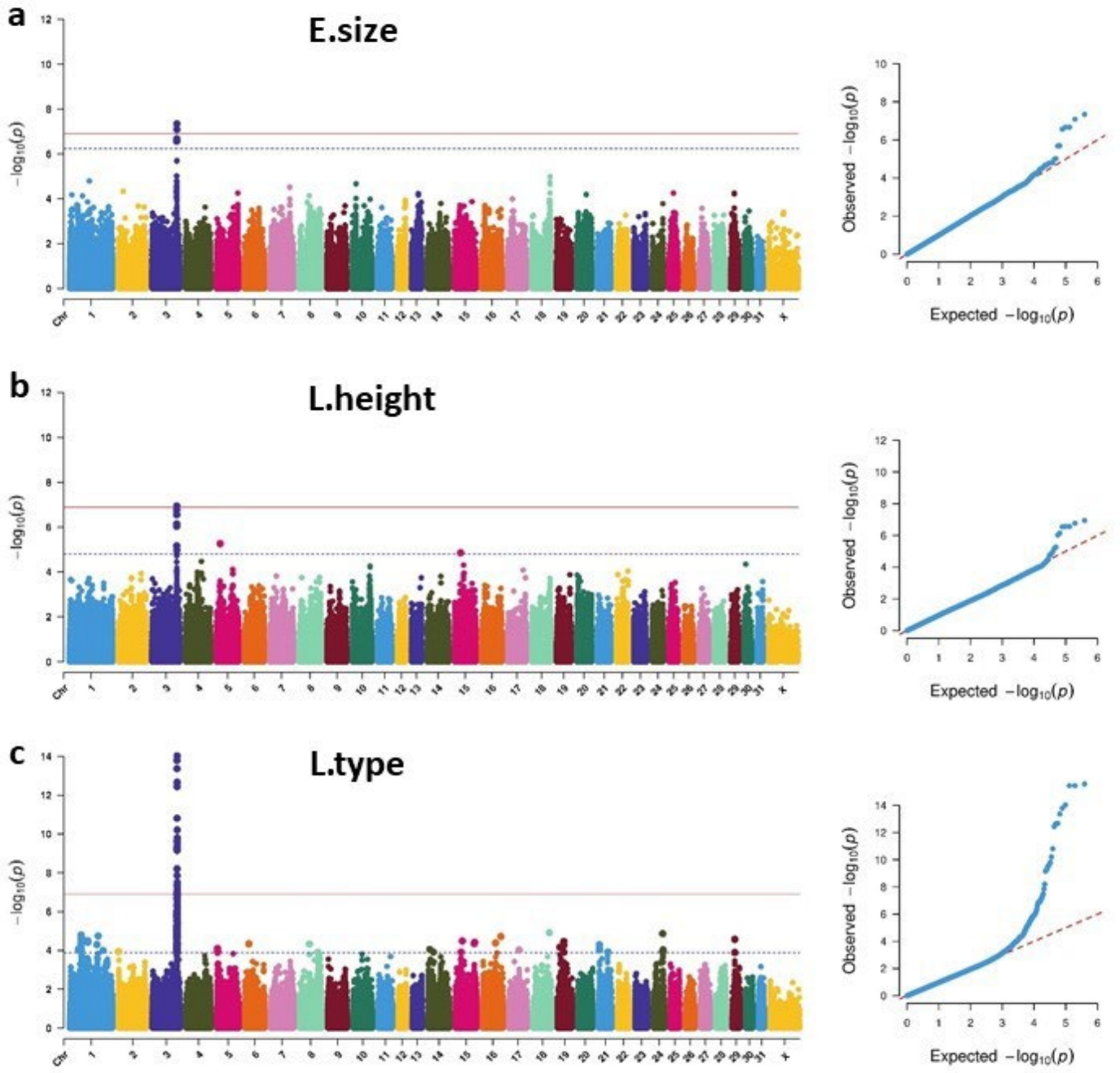
$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & \mathbf{G}^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

Well-known region for height/size/type

Three factors related to height/body size/type, and proportions



- ECA3 region with *LCORL/NCAPG genes*
- Significant SNPs found within the genes *LCORL, DCAF16*, and *FAM184B*



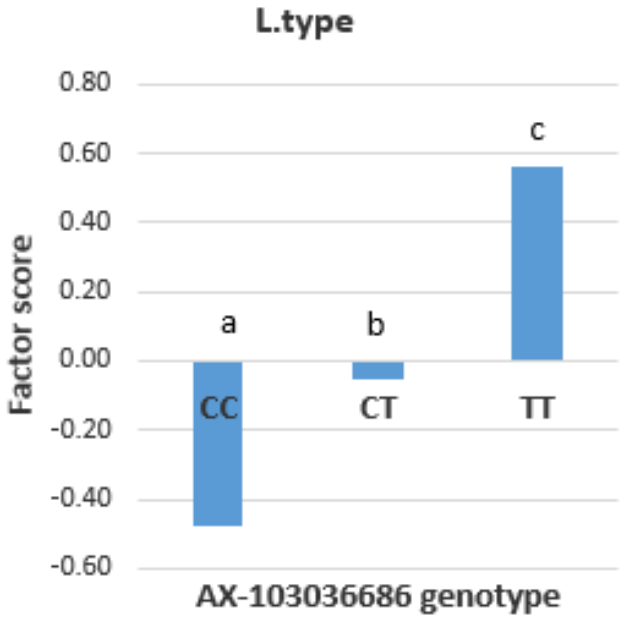
Red line: Bonferroni significance threshold

Blue dotted line: FDR ≤0.3

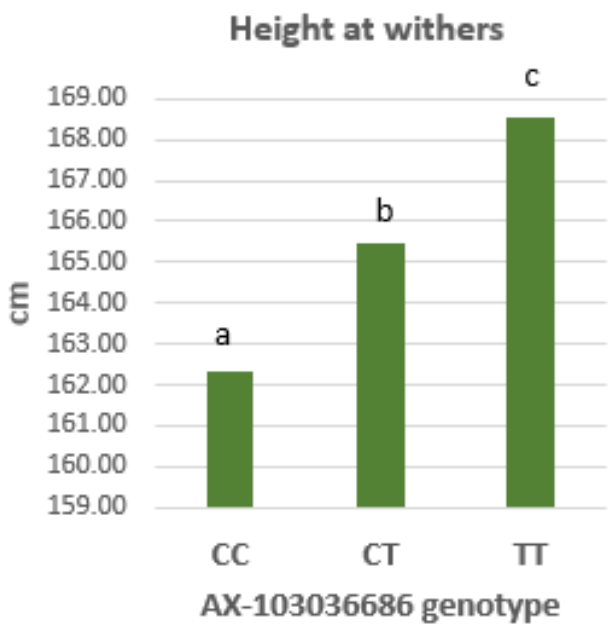
Well-known region for height/size/type

Example: LSMEANS for L.type corrected for sex and event

(L.type standard deviation 0.7)



Higher values -> Taller and heavier body type



Height at withers in cm

Potential region of importance for jumping

One factor related to evaluated (free) jumping ability

Photo: Sofie Sköld

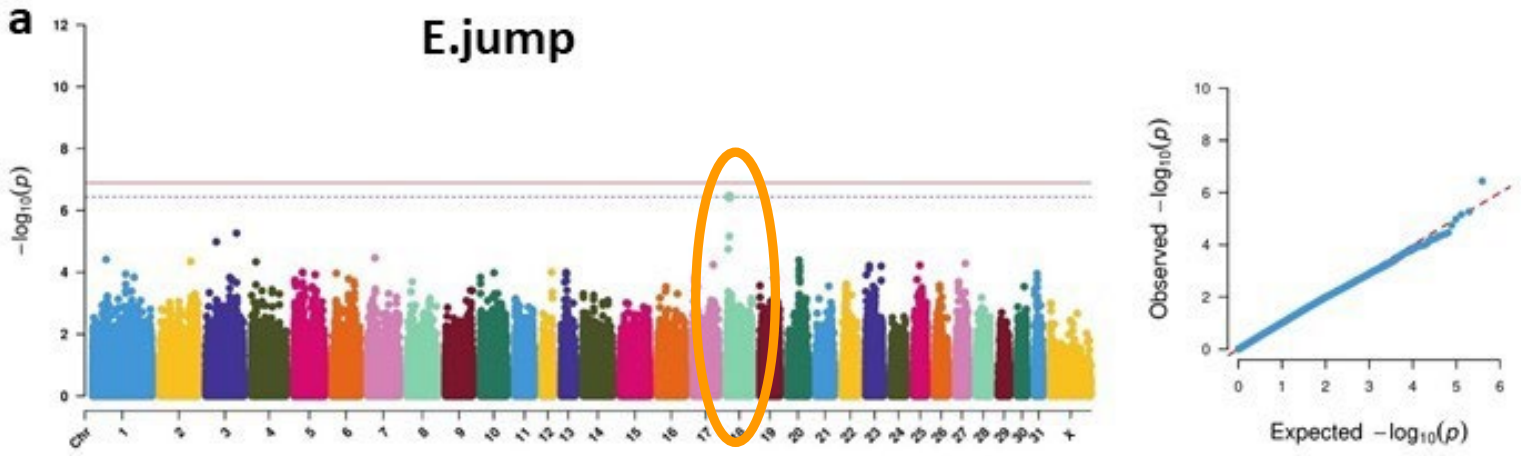
Free jumping technique & ability, evaluated

Free jumping temperament & impression, evaluated

E.jump

h^2: 0.32

- ECA18 region
- Top SNPs within the gene *GLI2 (GLI Family Zinc Finger 2)*
- *GLI2* involved in development of head and eyes among other functions



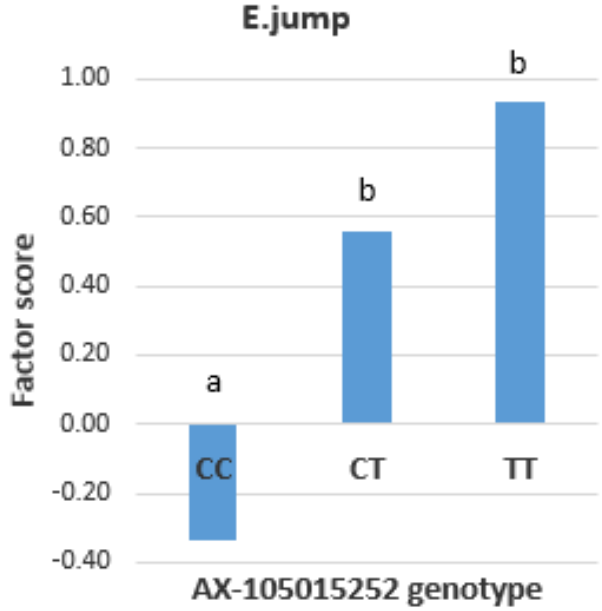
Red line: Bonferroni significance threshold

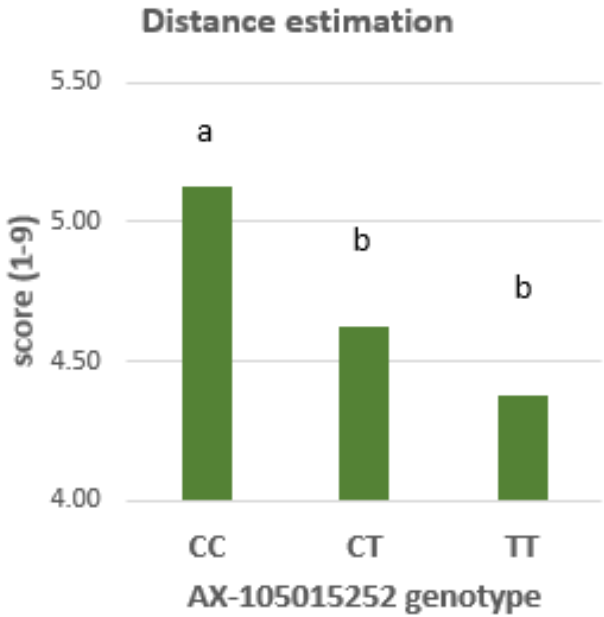
Blue dotted line: FDR ≤0.3

Potential region of importance for jumping

Example: LSMEANS for E.jump corrected for sex and event

(E.jump standard deviation 0.9)





Note: LSMEANS here not corrected for population stratification

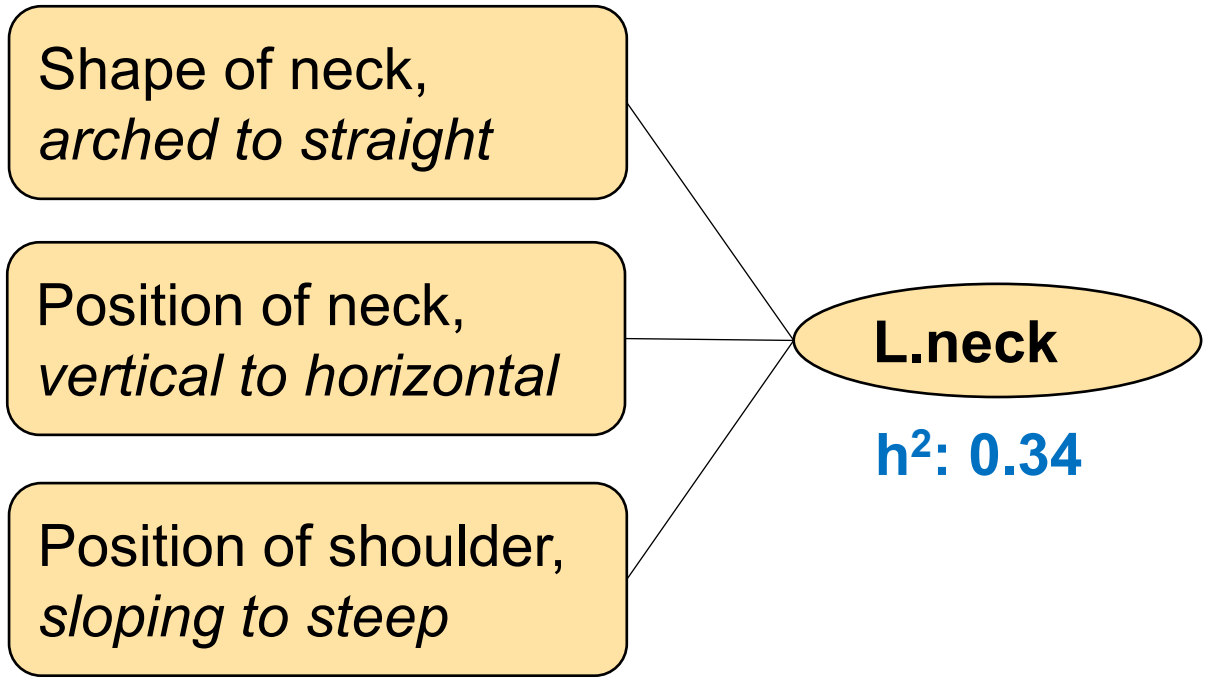
Higher values -> better technique and ability, and approach to jumping assignment

Higher values -> more insecure distance estimation

Potential regions of interest for neck & shoulder conformation

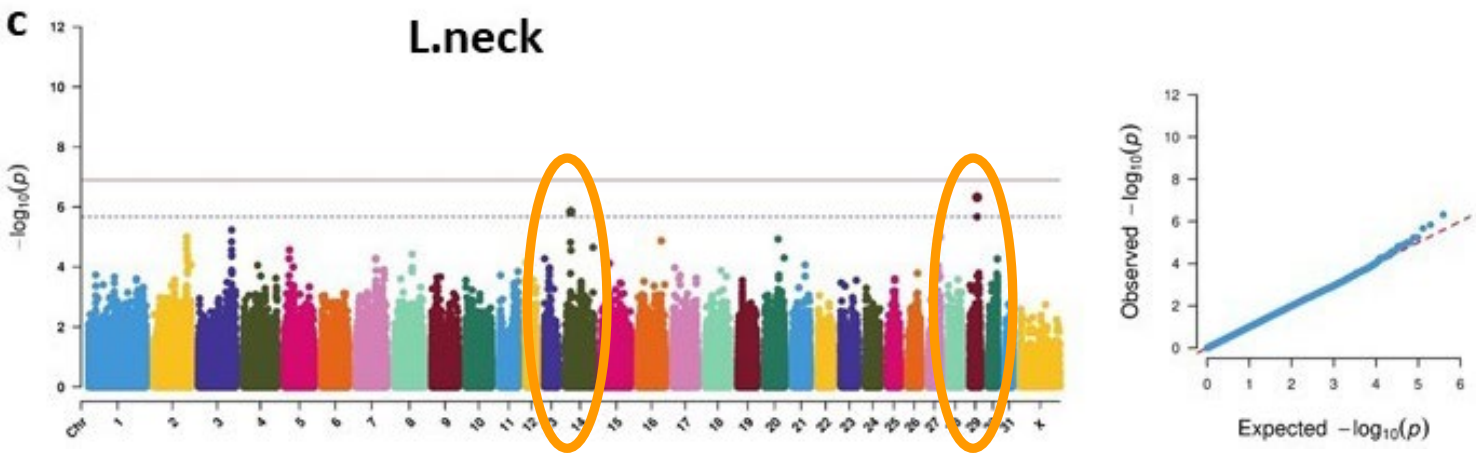
One factor related to linearly scored traits for shape and position of neck and shoulders.


Photo: Sofie Sköld



- Top SNP ECA14 upstream *GABRB2* gene (also nearby *GABRA1* and *GABRA6* genes). These genes have previously been found to be associated with osteochondrosis in horses.

- Top SNPs ECA29 within the gene *CAMK1D,* known for influence on fat deposition, insulin resistance etc.



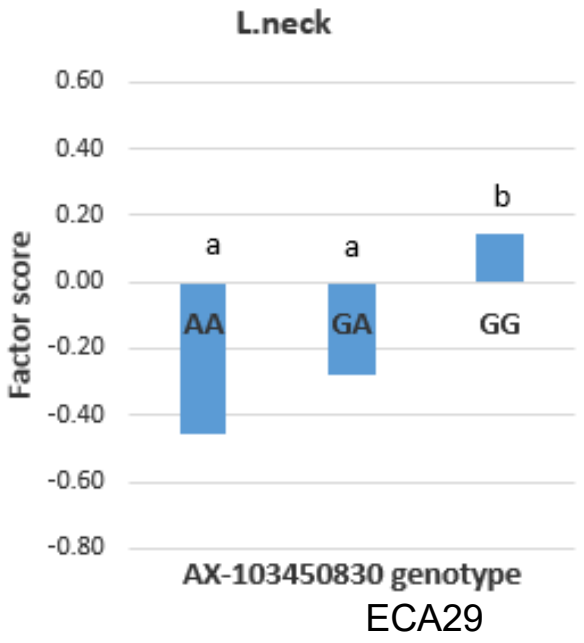
Red line: Bonferroni significance threshold

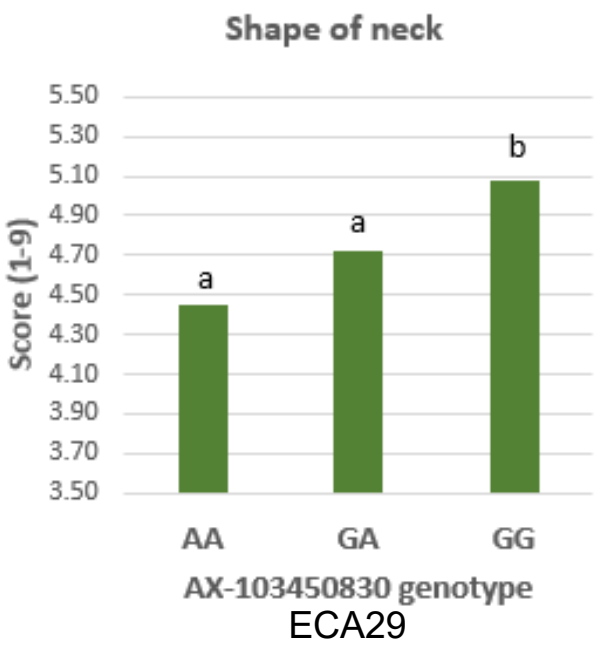
Blue dotted line: FDR ≤0.3

Potential regions of interest for neck & shoulder conformation

Example: LSMEANS for L.neck corrected for sex and event

(L.neck standard deviation 0.8)





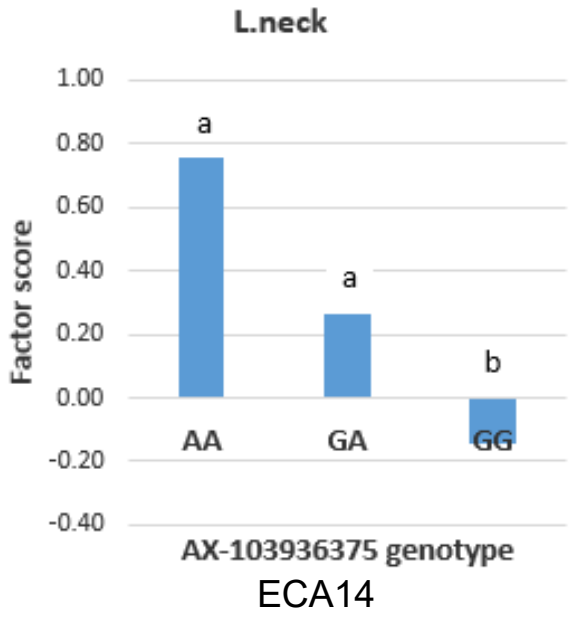
Higher values -> straighter shape and more horizontal position of neck and steeper shoulders

Higher values -> straighter neck shape

Potential regions of interest for neck & shoulder conformation

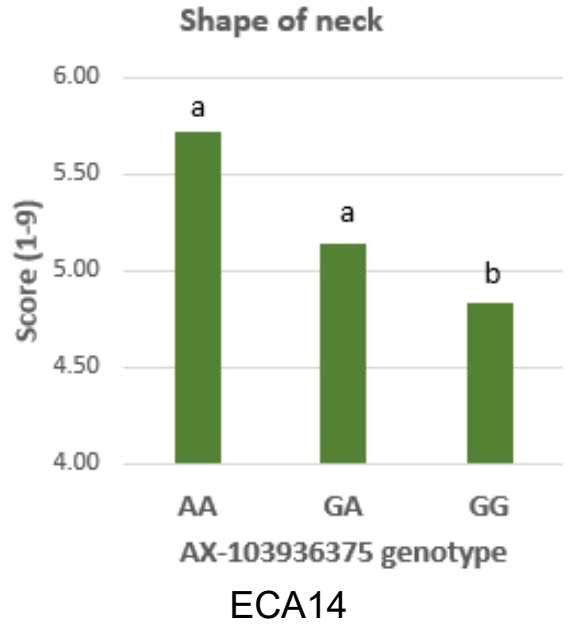
Example: LSMEANS for L.neck corrected for sex and event

(L.neck standard deviation 0.8)



ECA14

Higher values -> straighter shape and more horizontal position of neck and steeper shoulders

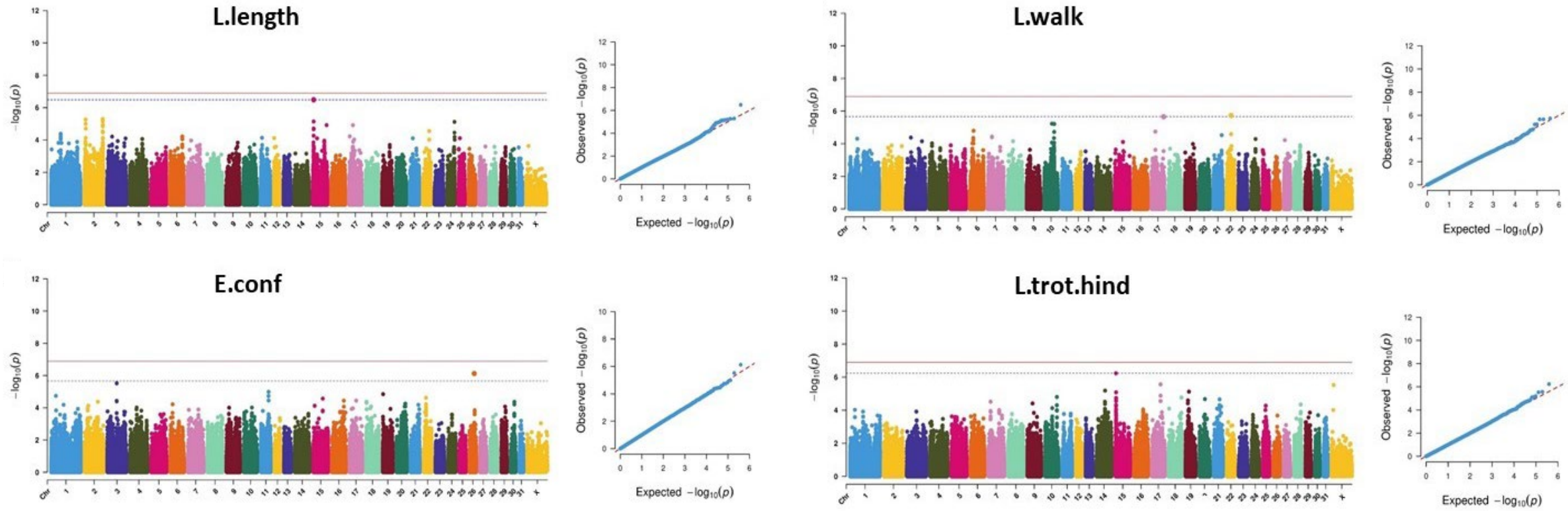


ECA14

Higher values -> straighter neck shape

Additional potential regions to study further…

Potential regions for body length (ECA15), walk (ECA17 & ECA22), trot hind legs (ECA15), and other evaluated conformation traits (ECA26)



Conclusions

- Factor analysis and ssGWAS useful for finding genomic regions of potential importance for young horse traits
- Well-known region for height/size/type detected at ECA3
- Novel regions of interest to study further in larger data sets for jumping and conformation

Thank you for your attention!
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