ROH as hint of selection in the genome of a modern sport horse breed

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Selection for sport performance
Intensive use of phenotypic recording systems to estimate genetic parameters and breeding values for sport traits.
Aim of the study

Detect genomic signatures of selection for sport performance in horses
Materials and Methods

380 SWB horses genotyped with high-density SNP chip (670K)

Runs of homozygosity were detected by using a sliding windows approach in PLINK v1.90
In addition...

285 Exmoor ponies were genotyped with 670K SNP chip from a previous study (Velie et al., 2016)
ROH:

- Runs of homozygosity are stretches of homozygous sites
- ROH can be useful to highlight signatures of strong selection

**ROH criteria:**
- Length
- Number of SNP
- Density & Max gap

**Sliding window criteria:**
- Size
- Heterozygous SNP
- Missing SNP
» Short ROH were five times more abundant in Exmoor ponies

» Short ROH were in both breeds spread across the genome

Mean number per Exmoor: 3,553

Mean number per SWB: 688
Mean number per SWB: 1,001

Mean number per Exmoor: 1,155

» Mean number per individual was similar in the two breeds

» In SWB medium ROH covered on average more genome than in Exmoor
Long ROH were the rarest, although they covered the largest proportion of the genome in both breeds.

Long ROH were spread along the genome in Exmoor ponies, rather than in few chromosomes only in SWB.
We filtered homozygous regions from the **LONG ROH** analysis shared among more than 85% of SWB horses.
GENES were biologically interrelated

Learning ability
Memory

Muscle contraction & synapses response
Causative function in sport horses?
Our findings help to unravel the complex nature of performance traits in horses.

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