The American Quarter Horse

- Originated in the colonial United States
- Formally recognized as a breed in 1940 (AQHA)
- ⅓ of the US equine population (3 million horses)

The American Quarter Horse

- Moderate to high genetic diversity
  - Large population
  - Diverse founding stock
  - Extensive breed admixture
- Thoroughbred (TB) influence
- Selective breeding for performance types: population stratification (Petersen et al., 2014)
  - Stock
  - Halter/Pleasure
  - Racing

Objectives

1. Identify genomic signatures of selection within or among QH subpopulations;
2. Identify putative functional alleles within genomic regions of interest (ROIs);
3. Potential overlap between the racing QH subpopulation and Thoroughbreds and/or Standardbreds.

Methods

- 144 individuals from 6 QH subpopulations genotyped on the Equine SNP70 bead chip
- $d_i$ statistics calculated for each subpopulation
  - Pairwise $F_{ST}$ statistic (Akey et al., 2010)
  - Nonoverlapping 500kb windows
  - High $d_i$ values: high levels of population structure relative to the genome-at-large
  - Well suited for detecting selection specific to a particular subpopulation
**Genomic Regions of Interest**

- Haplotype structure and frequency within each significant $d_i$ window
- Identification genomic regions of interest (ROIs)

25 ROIs

- 22 shared
- 3 unique

4 Racing QH + TB
1 Racing QH + TB + STDB
2 Western Pleasure
1 Cutting

**ROI Refinement**

- 7 ROIs selected for further analysis
  - 5 shared between racing QH and TB and/or STDB
  - 2 unique to a subpopulation

**ECA1:45Mb**

- $d_i$ Statistics

**ROI Refinement**

- 2M SNP data for a subset of 75 QHs, 28 TBs and 40 STDBs
  (More about it tomorrow at 9:20am – Rob Schaefer)

- Local haplotype sharing (LHS) between groups
  - 2Mb window around each ROI
  - hapQTL (Xu & Guan, 2014):
    - Estimates haplotype associations at windows around a core SNP
    - Significant LHS values ($\log_{10} BF > 5$): similar local ancestral haplotype

- Identification of candidate genes for association

**ECA1:45Mb**

- THSD4: thrombospondin, type I, domain containing 4
- Associated with lung function in humans (Repapi et al., 2010)
Conclusions

→ Selective breeding for unique performance and aesthetic traits: population stratification within the QH (Petersen et al., 2014)
→ ROIs found in QH subpopulations are shared between groups and sometimes with other breeds
→ Identification of putative functional alleles responsible for important phenotypes
  • Biologically and economically important

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