Screening for selection signatures in Norwegian Red

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Motivation

• Genomic inbreeding using runs of homozygosity (ROH):
  – Rate of inbreeding (ΔF)
  – Effective population size (Ne)
Runs of homozygosity (ROH)

Chromosome

Ancient inbreeding

Recent inbreeding

\[ F_{ROH} = \frac{\sum L_{ROH}}{\sum L_{AUTO}} \]
What if….

We could narrow this down?

1. Segmental level
2. SNP level
So what?

• Trace the cause
  – Define individuals that had a great impact on important traits
  – Detect strategic fortunate or unfortunate genetic moves
• Control for inbreeding
Is it possible?

• Trace selection over time
• Detect selective sweeps
  – Ongoing
  – Historical
Expectations

• ROH could give us an illustrative pattern on the genome showing:
  – Segments with an excess of homozygosity
  – Segments reaching towards homozygosity at different rates

• ROH could be able to map SNP specific
  – Inbreeding
  – Rate of inbreeding
  – Selection signatures
Objective

1. Locate segments and markers exposed to inbreeding
2. Map the rate of change over time on a segmental level
3. Search for selection signatures, both historical and ongoing
Animals and genotyping

• 381 Norwegian Red bulls (1971-2004)

• Illumina HD-panel (708K):
  – Individual call rate > 95 %
  – SNP call rate > 90 %
  – Autosomal SNP only
  – Hardy-Weinberg deviation $p < 10^{-6}$
Positional inbreeding from ROH

\[ F_j = \frac{\sum_{i=1}^{N} s_{ij}}{N} \]

* Where \( s_{ij} \) is the status of the locus, whether it is within a ROH or not (1 or 0) and \( N \) is the total number of animals in the dataset
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F_j BTA 6
Positional rate of change

\[ L(\beta_j) = \prod_{i=1}^{N} \text{Bernoulli}(p_{ij}) \]

\[ p_{ij} = \frac{\exp(\eta_{ij})}{1 - \exp(\eta_{ij})} \]

\[ \eta_{ij} = [\eta_1 \ldots \eta_{N_j}]' \]

\[ \log it(p_{ij}) = \eta_{ij} = \mu_j + \beta_j t_i \]

* Where \( \mu \) is the intercept and \( \beta \) is slope of the regression, while \( t \) is CGE of individual \( i \)
The slope of change at BTA 14

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$F_j$ BTA 6
The slope of change BTA 6
Take home messages

• ROH located segments and markers exposed to inbreeding

• ROH mapped the rate of change over time both over segments and markers

• ROH did also make it possible to search for selection signatures
  – Ongoing
  – Historical