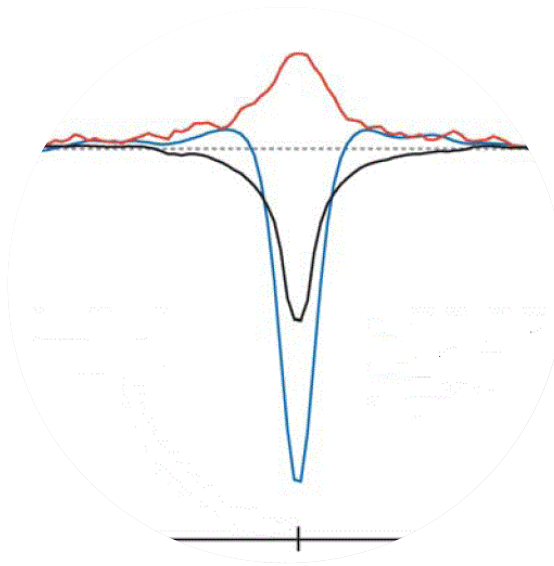


Signatures of selection in Holstein Friesian dairy cattle.

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Introduction

Genotyping individuals for a large number of markers made it possible to detect

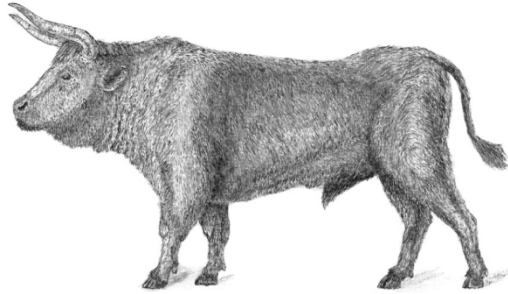
- genomic regions contributing to current genetic variation

- ➔ GWAS

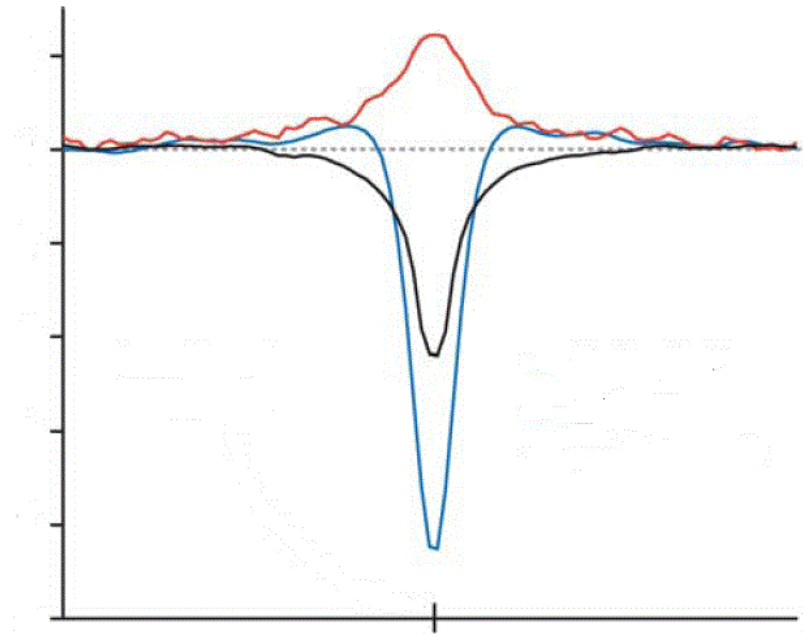
- genomic regions that have been under past selection

- ➔ selective sweeps

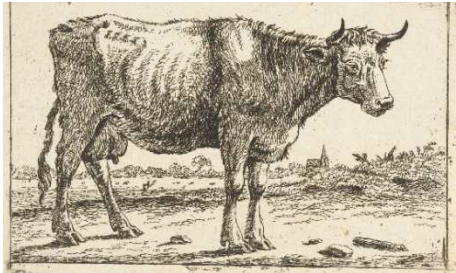
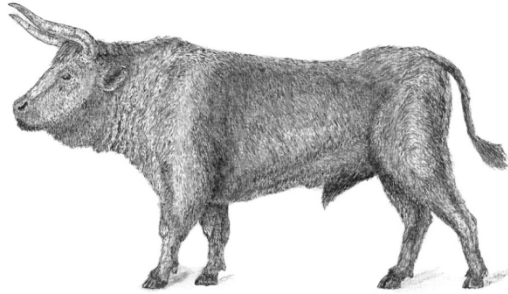
Introduction



Selection will change allele frequencies of advantageous mutation and of linked loci



Introduction



1

Aim

Detect signatures of past and recent selection in the genome of Holstein-Friesian dairy cattle.

2

Material & Methods

- 2,029 Holstein-Friesian cows subdivided in 5 different populations from 4 countries

| Origin | | | Number |
|-------------------|-----------|----------------|--------|
| 1.Ireland | Moorepark | IRL | 504 |
| 2.Sweden | SLU | SWE | 222 |
| 3.The Netherlands | WUR | NLD | 670 |
| Scotland | SAC | | |
| 4 | | SAC1-selection | 301 |
| 5 | | SAC2 - control | 332 |
| Total | | | 2029 |

- Genotypes: Illumina BovineSNP50 BeadChip

Material an Methods

- Haplotype phasing
Fastphase v1.4.0, phasing within each population
- Integrated Haplotype Score (iHs) – Voight et al. 2006
 - ✓ SNPs with unknown derived/ancestral alleles were removed
 - ✓ SNPs with $MAF \leq 5\%$ were removed
- Analysis based on combined data as well as for individual populations

Material & Methods

| | Birth Year | | | | | | | | | | | | | | | | | | | | |
|------|------------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| | 1987 | 1988 | 1989 | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 |
| IRL | | | | | | | | | | 36 | 16 | 13 | 36 | 40 | 17 | 72 | 98 | 54 | 71 | 70 | |
| SWE | 1 | 2 | 4 | 10 | 9 | 9 | 12 | 13 | 15 | 8 | 20 | 12 | 10 | 12 | 3 | | | | | | |
| NLD | | | 7 | 45 | 80 | 77 | 145 | 140 | 77 | 7 | | | | | | | | | | | |
| SAC1 | | | | | 1 | 2 | 5 | 9 | 12 | 15 | 16 | 18 | 19 | 22 | 30 | 29 | 22 | 24 | 35 | 28 | 14 |
| SAC2 | | | | 1 | 1 | 10 | 20 | 12 | 18 | 18 | 23 | 29 | 21 | 17 | 28 | 19 | 25 | 26 | 20 | 33 | 11 |

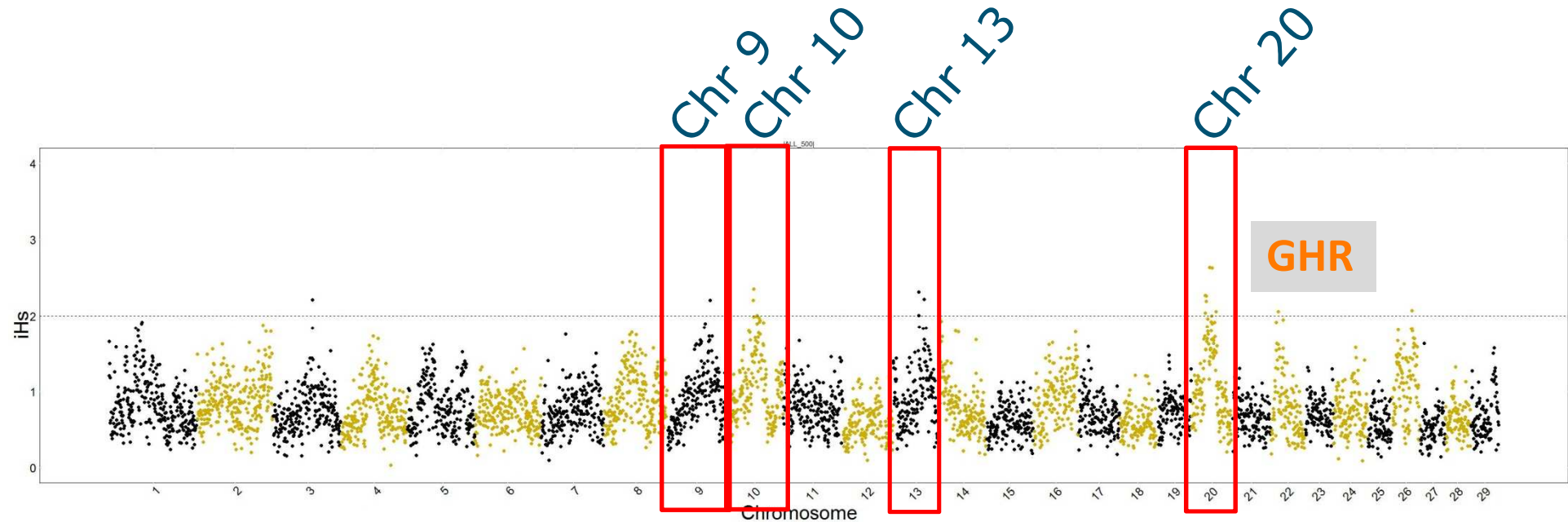
Change in allele frequencies in time?

$$SNP_{ij} = \mu + Country_i + \beta \cdot BirthYear_j + e_{ij}$$

Results - Integrated Haplotype Score (iHs)

- 5 populations separately:
 - 51 chromosomal regions in which at least one population is significant for at least one of the bin within the region.
- Combined data:
 - 9 significant chromosomal regions

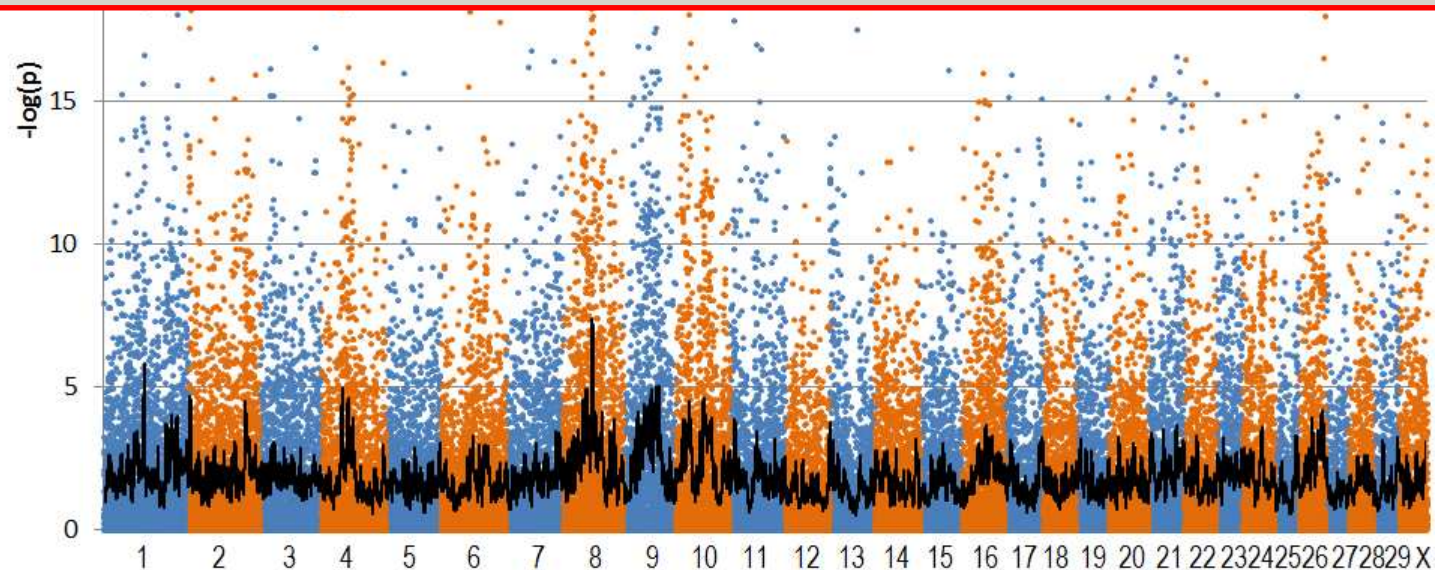
Results - Integrated Haplotype Score (iHs)



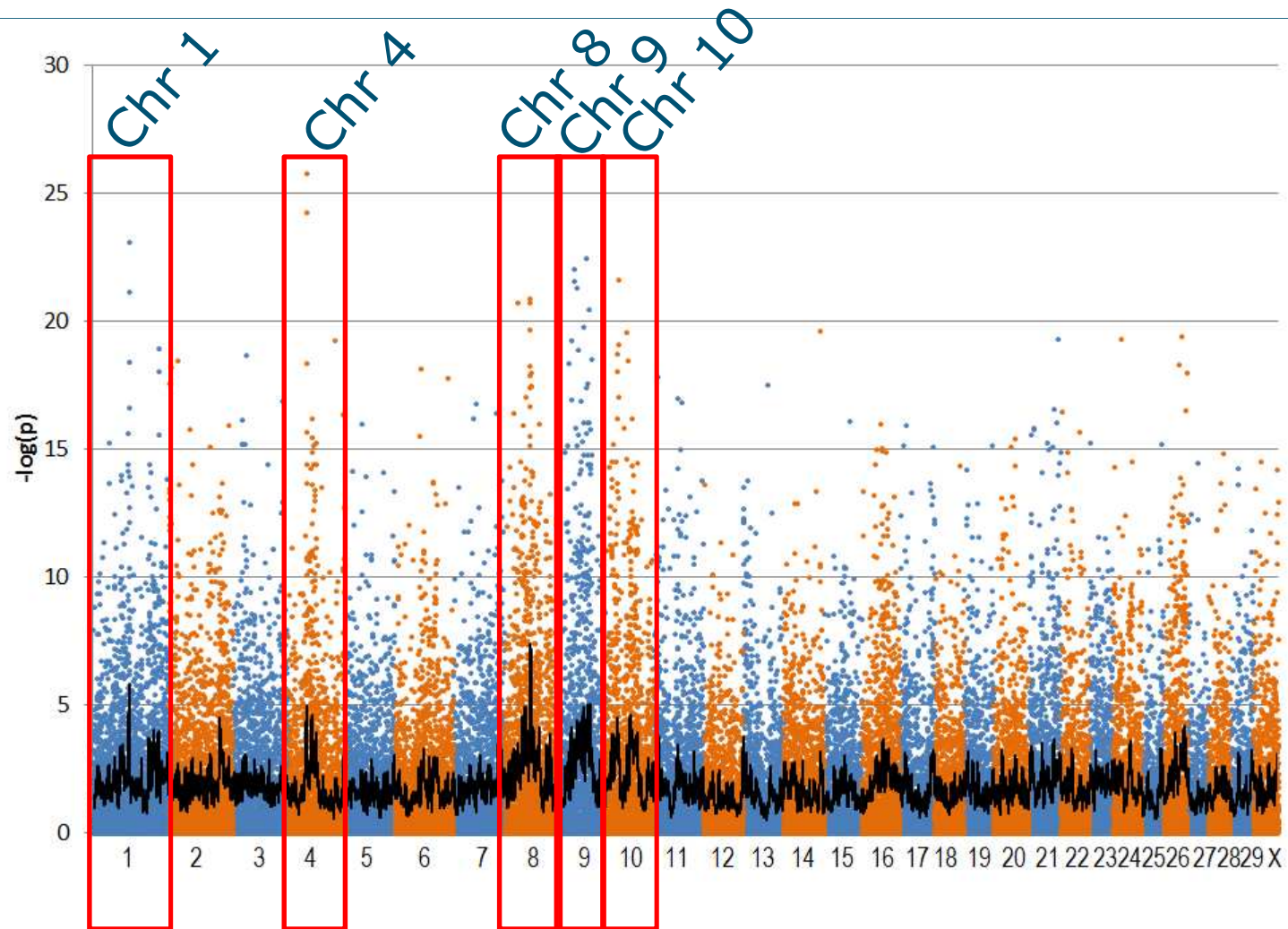
Genome-wide plot of the $|iHs|$ values based on combined data. $|iHs|$ values averaged for 500 kb windows.

Results – Birth Year

Many SNPs:
statistically significant, genetically not relevant



Results – Birth Year



Results

- Highly significant allele frequency changes in time
 - ✓ Estimated effects: change in allele frequency $\sim 0.5 / 20$ years
 - ✓ No evidence for (Country x BirthYear) interaction

- Significant effects "Country"
especially for the X chromosome

Discussion and conclusions

- Standard settings of software (based on human data) were adjusted to account for:
 - ✓ larger extend of LD in cattle
 - ✓ relatively low SNP resolution

- A number of studies reported on signatures of selection in the bovine genome
 - ✓ Chr 20 (GHR) has been reported previously, e.g. Hayes et al. (2008), Flori et al. (2009), Qanbari et al. (2010)
 - ✓ Also differences – what is the extend of underlying assumptions?

Discussion and conclusions

- Recent allele frequency changes
 - ✓ Effect in GWAS?

Discussion – results GWAS



Discussion and conclusions

- Recent allele frequency changes
 - ✓ Effect in GWAS?

Overlap, however.....

regions explain relatively small fraction of the variance.

Are there other traits?

In short

Signatures of past selection:

Chr 9,10,13 & 20

Signatures of more recent of selection:

Chr 1, 4, 8, 9 & 10

