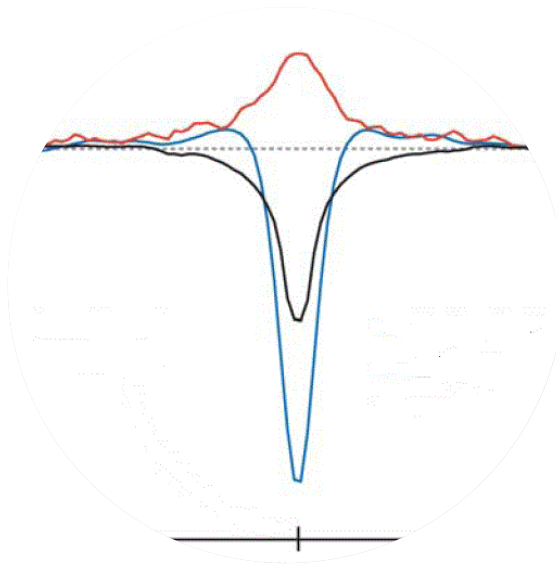


Signatures of selection in Holstein Friesian dairy cattle.

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Introduction

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

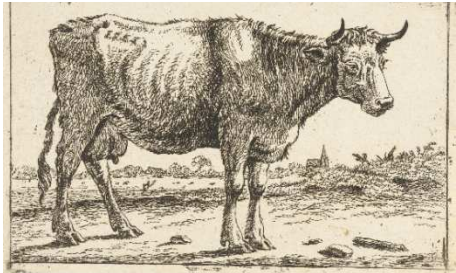
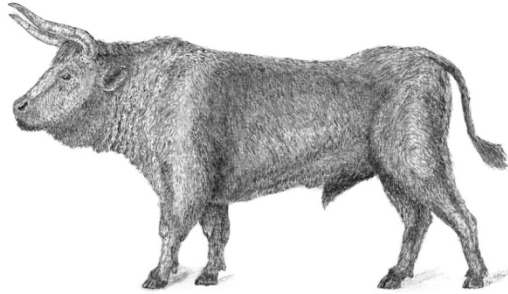
- genomic regions contributing to current genetic variation

- GWAS

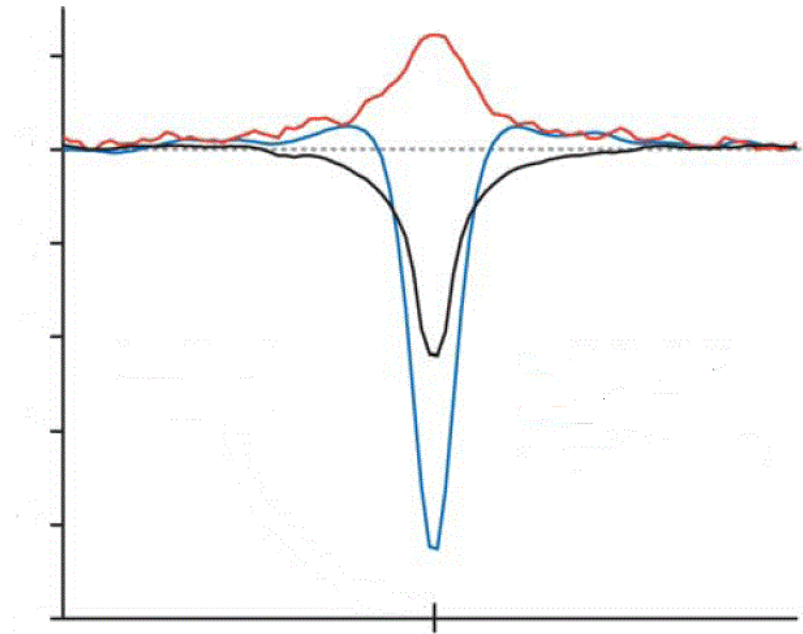
- genomic regions that have been under past selection

- selective sweeps

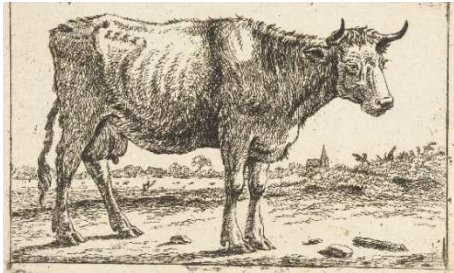
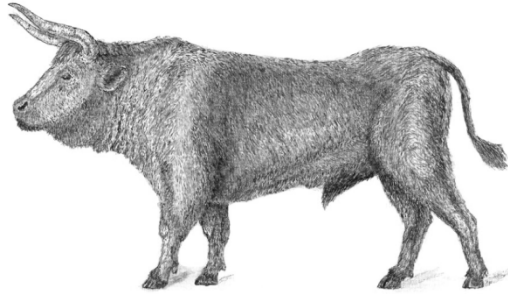
Introduction



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

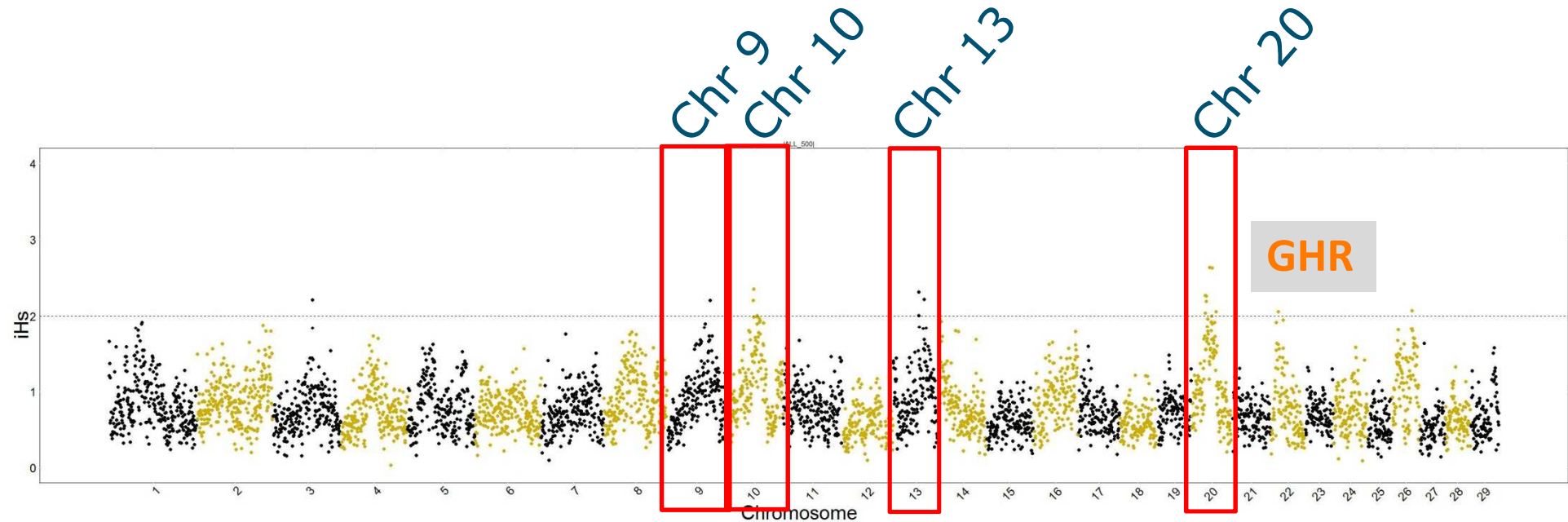
Change in allele frequencies in time?

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

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

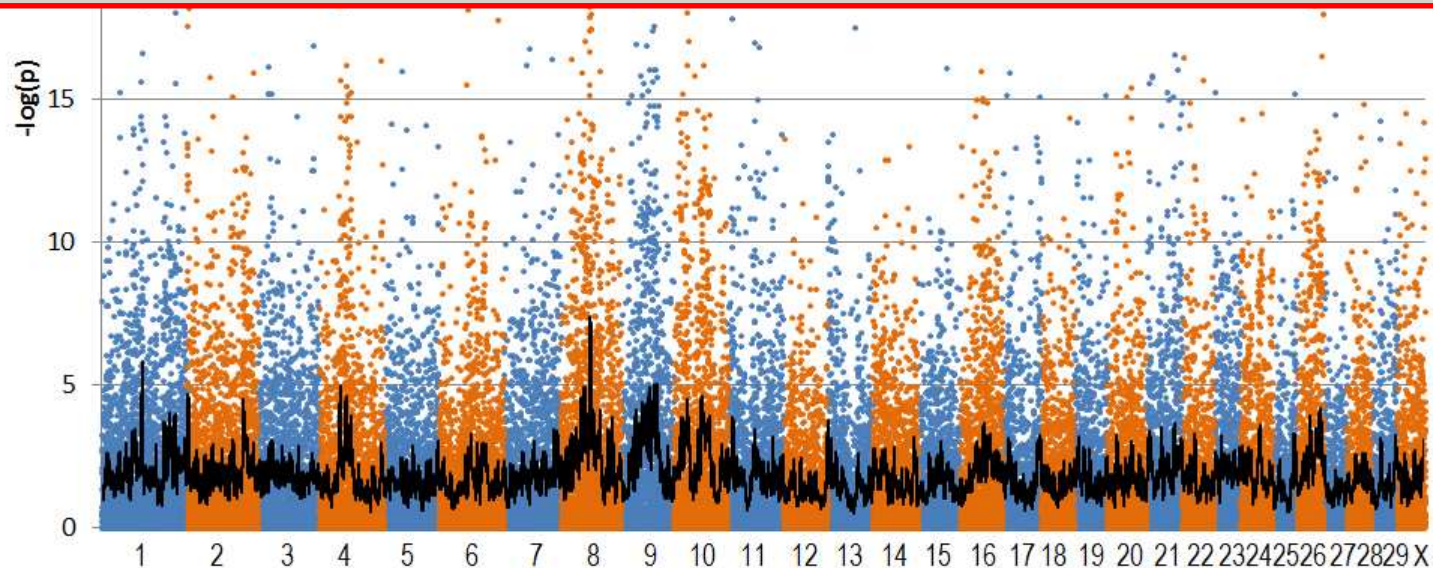
Results - Integrated Haplotype Score (iHs)



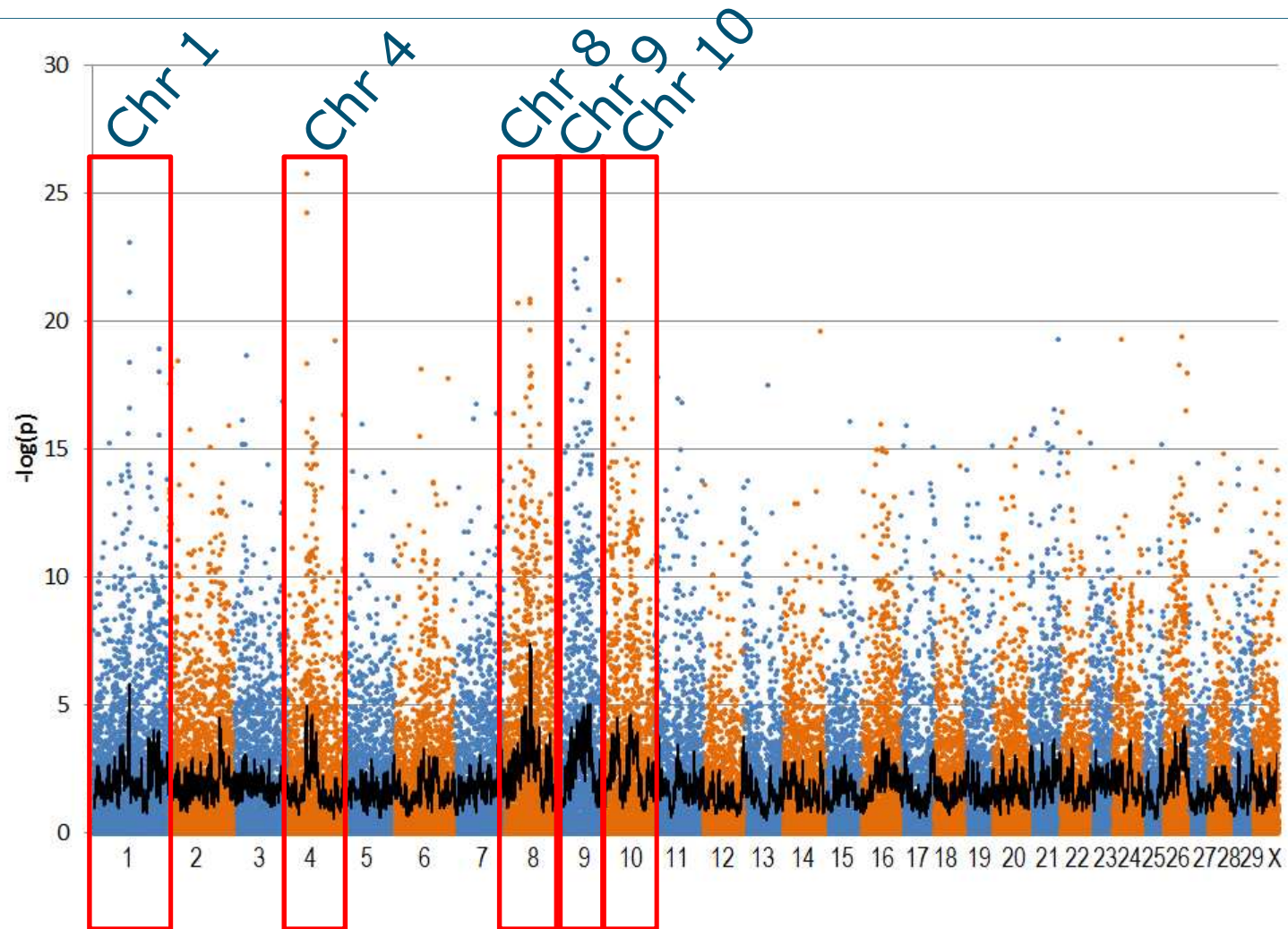
Genome-wide plot of the $|iHs|$ values based on combined data. $|iHs|$ values averaged for 500 kb windows.

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

