



SCIENCE AND  
EDUCATION **FOR**  
**SUSTAINABLE**  
**LIFE**

# Genomic inbreeding over time for Swedish Red and Swedish Holstein-Friesian cattle

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- We studied changes over time in homozygosity and inbreeding in Swedish Red and Swedish Holstein-Friesian cattle (old samples more Friesian, new samples Holstein)
- We used 50k SNP data for AI bulls used in Sweden provided by the Nordic genetic cattle evaluation (NAV) and Viking Genetics
  - 3032 HOL
  - 5545 RDC

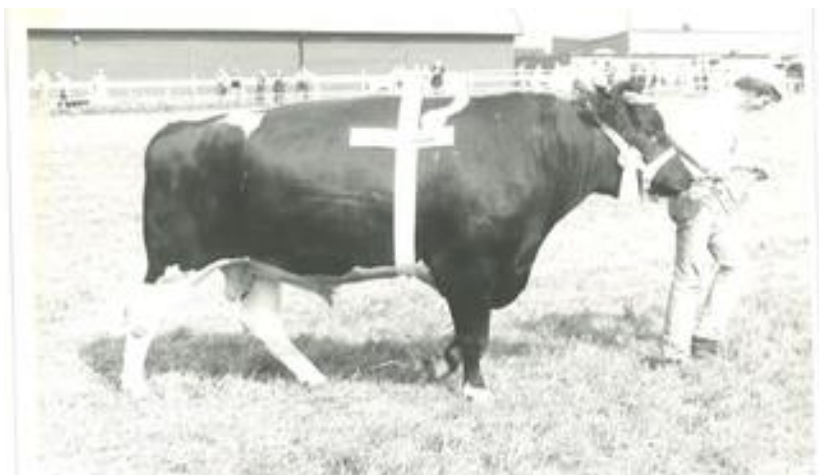


# **New techniques and breeding regimes have been implemented for Swedish dairy cattle over the years**

- BLUP evaluation in 1984
- Joint Nordic evaluation in 2005
- Genomic selection from around 2010
- Can these developments be detected as changes in homozygosity and inbreeding in these breeds?



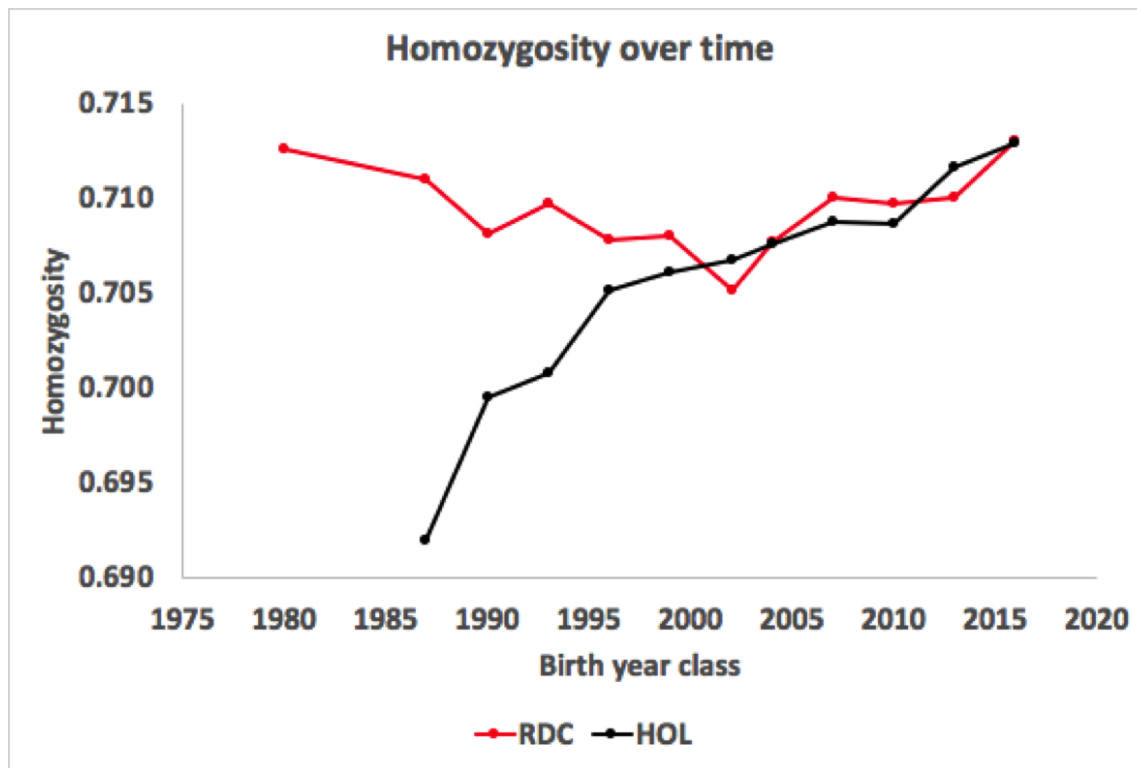
# Old bulls



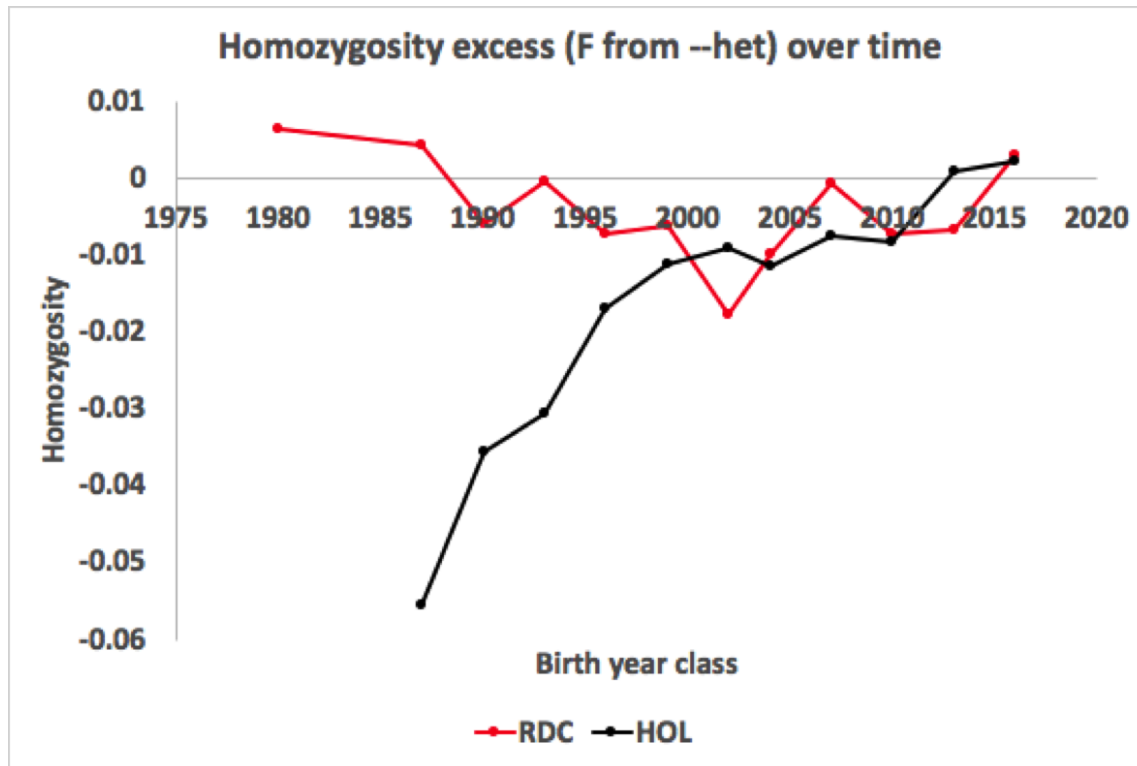
# Modern bulls



## Different pattern of homozygosity change in the two breeds

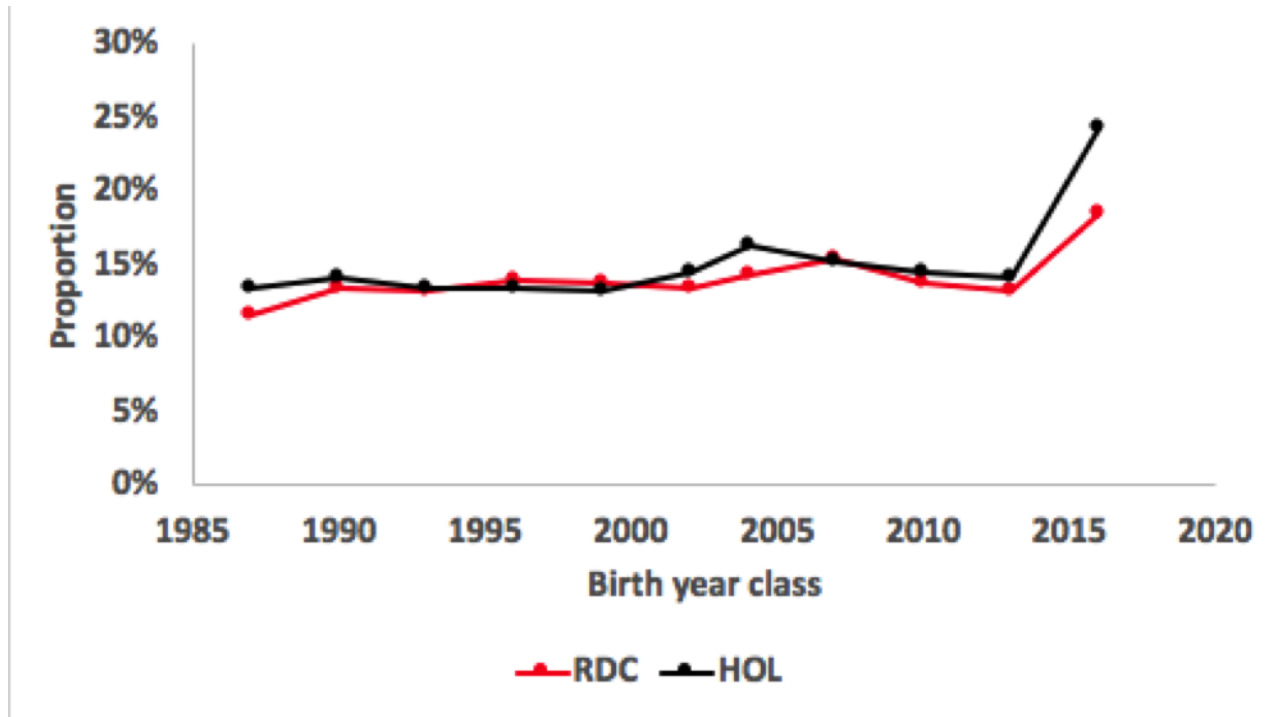


# Pattern of change in homozygosity excess similar to pattern of homozygosity





## Proportion of fixed SNPs



## Runs of homozygosity

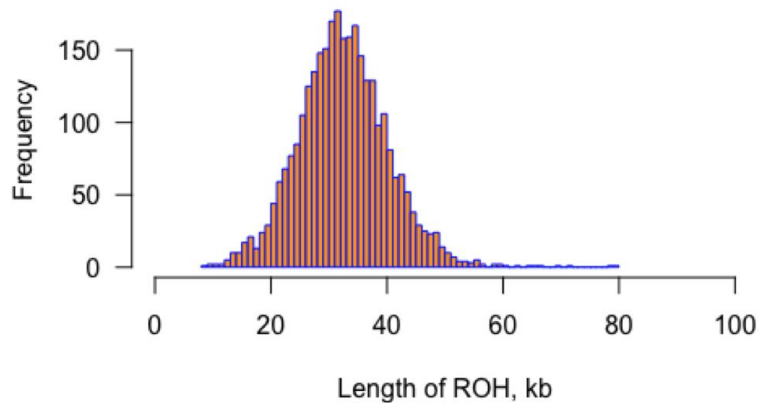
The analyses of ROH were made in plink with the following settings:

```
--homozyg-density 1000 --homozyg-kb 1000 --homozyg-snp 20 --  
homozyg-window-snp 20 --homozyg-window-het 1
```

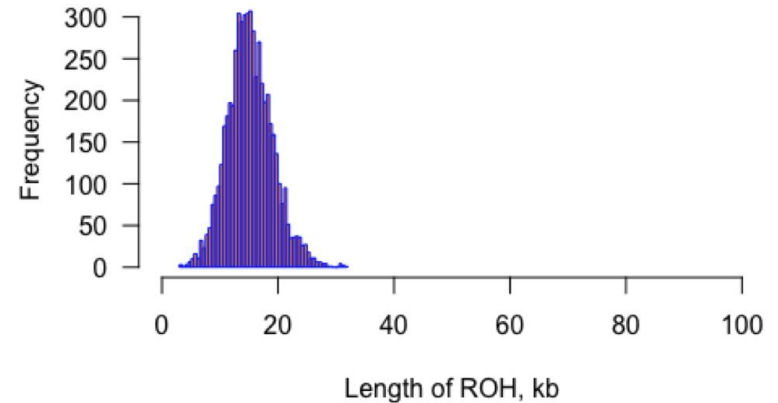


# Holstein has on average twice as long ROH as RDC

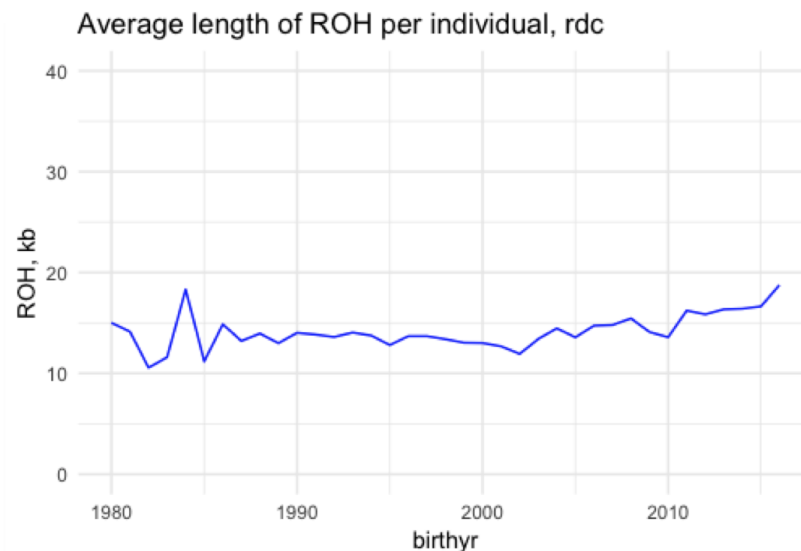
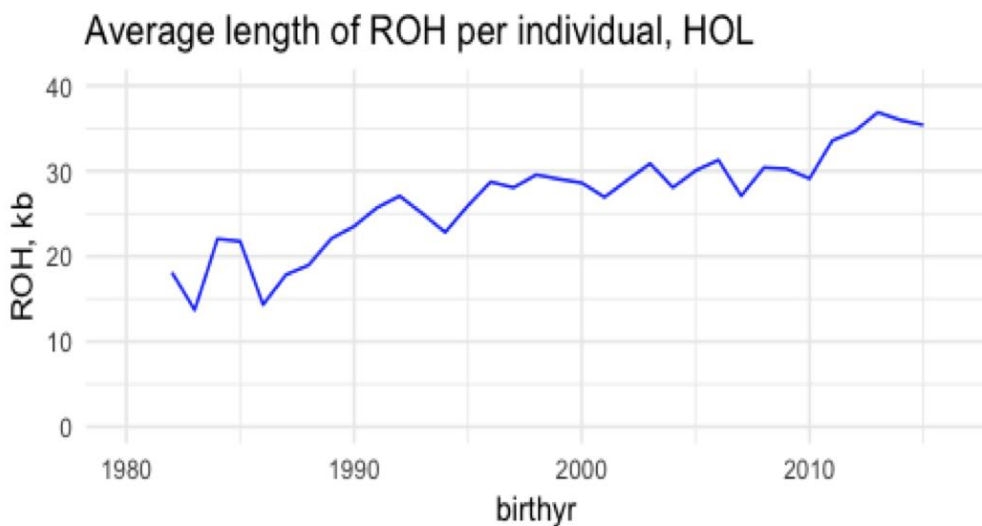
Average length of ROH per individual, HOL



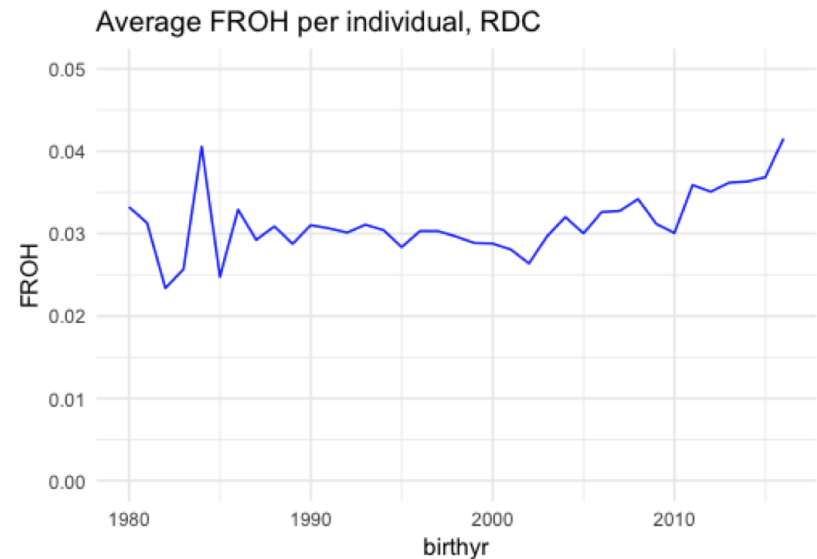
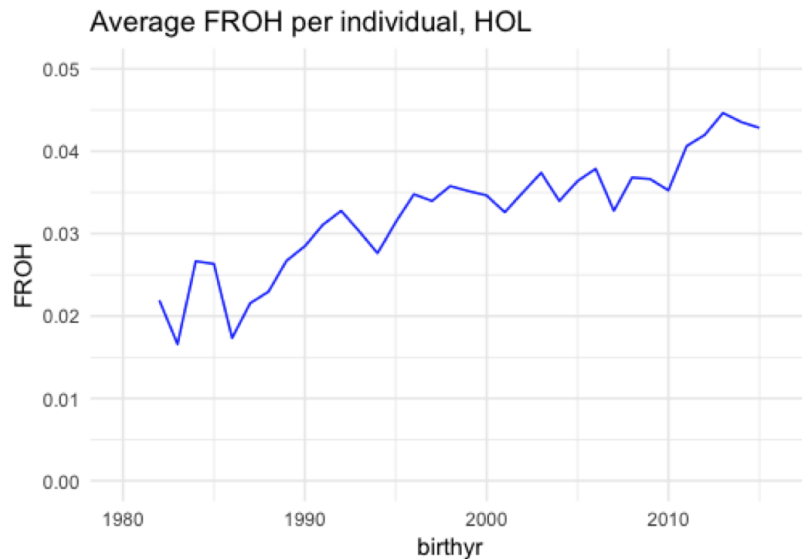
Average length of ROH per individual, rdc



# Steady increase in ROH length in HOL, recent increase in RDC



# Increase in inbreeding in HOL, stable inbreeding in RDC until recently when it started increasing



## Conclusion

- The homozygosity and inbreeding has increased in recent years. This coincides with the introduction of genomic selection.



## Future research

- We have genotyped additional old semen samples from Viking Genetics to be able to compare further back in time, oldest genotyped bulls born in 1950ies
- We will add this new data to the data presented here and re-run the analyses.





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