



Pedigree and genomic-based inbreeding in Italian Holstein dairy cows

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Inbreeding in Holstein cattle

Publed

<u>Key words:</u> Inbreeding Holstein Cattle Genomic

162 Publications83 Publications



Inbreeding in Italian Holstein cattle

animal



Results: 3 Publications



VM

A. 12:12, pp 2480.

Genume-whe menuncation of runs of nomozy associated genes in local dairy cattle breeds

Genome-wide identification of runs of homozygosity islands and

animal

2

S. Mastrangelo '' and B. Portolano [†] M. T. Sardina[†], M. Tolone[†], R. Di Gerlando[†], A. M. Sutera[†], L. Fontanesi²

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SECTIONS



Research questions

- 1) Inbreeding based on Pedigree (F_{PED}) and Runs of homozygosity (F_{ROH}) data
- 2) Correlation between inbreeding measured based on F_{PED} and F_{ROH}
- 3) Inbreeding trend throughout a period of 14 years

Material and methods

- 40,921 Italian Holstein dairy cows with imputed SNPs data
- 245,600 Italian Holstein animals in the pedigree
- F_{PED} and complete generation equivalent (CGE) calculated in ENDOG 4.8

8000

7000

6000

1000

COWS

F_{ROH} calculated using *DetectRUNS* in R (*Biscarini et al., 2019*)
 following *Doekes et al.,* 2019 (Criteria: Length > 1Mbp, minimum 10
 SNPs, minimum density of 1 SNP per 100 kb, a maximum of one
 heterozygous call with a ROH)



Results

ROH counts and average length per chromosome



Results

Inbreeding from F_{ROH} and F_{PED}





Results

Inbreeding trend per year based on F_{ROH} and F_{PED}

- Mean difference among the two methods:
 ~ 0.04 [0.044, 0.045]
- ΔF calculation:

 $\Delta F_{y} = 1 - e^{(slope)}$ ROH ΔF_{y} per year: <u>+ 0.37%</u> *** Pedigree ΔF_{y} per year: <u>+ 0.28%</u> ***





Conclusion

- F_{ROH} higher than F_{PED}
- Moderate correlation (0.60) between F_{ROH} and F_{PED}
- Lower CGE, lower correlation between F_{ROH} and **F**_{PED}
- ΔF per year showed an increasing trend
- Acceleration in ΔF comparing progeny test selection only to the current scenario

What to do next?

- Different methodologies and define best one to be used as routine measurement
 - Threshold to define highly inbred animals?
 - The effect of targeted selection on specific chromosomes
 - Further understand the role of genomic selection



Thank you for listening!

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Picture from: https://www.depoda.it/animali/frisona/



Supplementary

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Mean=10.2

Frequency o – corr.3\$J_GenEqu

Histogram of corr.3\$J_GenEqu

group 븑 PTS 븑 GS



17