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Study on the worldwide genetic structure of Holstein-Friesian cattle

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SAB Scientific Advisory Board

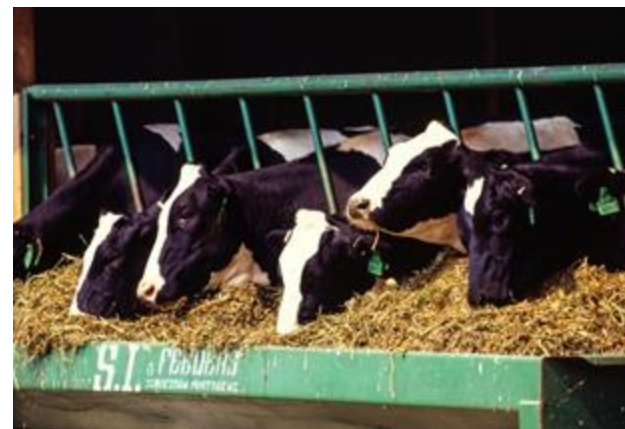
- ITALY – Cassandro and Pilla and Persichilli,
 - NLD - Gerben de Jong
 - HUN - Laszlo Bognar (absent)
 - FRA - Tiphaine MACE,
 - DEU – Herman Swalve (absent)
 - POL - Magdalena Graczyk-Bogdanowicz
-
- other countries and names are welcome



Introduction



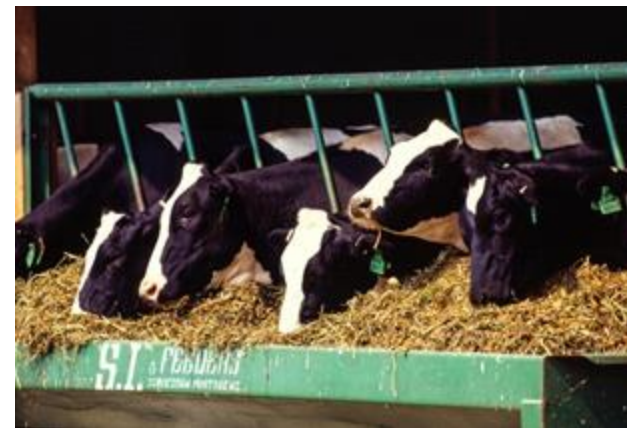
- **Global Prevalence:** Holstein cattle, with a global population exceeding 65 million, are the most widespread dairy breed internationally .
- **Genetic Concerns:** Recent genetic studies have raised concerns about a significant reduction in the genetic diversity of traditional Holstein populations due to intense directional selection.
- **Challenge of Genetic Diversity:** Maintaining a robust level of genetic diversity remains a crucial challenge, especially in high-yield production systems, given the constantly evolving market demands.



Aim



The primary objective of this study is to examine the genotypes of Holstein cattle worldwide in order to evaluate the variability that may have arisen due to distinct selective pressures from country-specific factors, including different selection goals, breeding programmes and farming systems.



TIMETABLE of the Projects

Items	15 th apr-21	last sem. '21	first sem. '22	last sem. '22	first sem. '23	last sem. '23	first sem. '24	last sem. '24
Proposed the Idea								
Discussion & Agreement definition								
Recording agreements with signatures								
Kick-off technical meeting								
Presentation at WHFF conference								
Deadline to receive data by countries						31 th dec '23		
Analyse of data								
Discussion at SAB-Scientific Advisory Board								
Presentation final results at WHFF council								dec '24



History of the Proposal and Participants

- **History of the proposal**

- 44° WHFF council of 15th April 2021: The idea was proposed the first time by Italy
- 45° WHFF council of 29th June 2021: The idea was discussed and Martino prepared a survey's draft
- 46° WHFF council of 20st October 2021: A draft's agreement was discussed and proposed
- 47° WHFF council of 16th Febraury 2022: The draft's agreement and appendix on M&M were discussed
- 48° WHFF council of 12 May 2022: Discusson on final paper go out to members from WHFF.

- **Answers received at the present:**

- Following 19 countries signed the agreement: FRA, LATVIA, DFS, POR, BEL, SPA, BRA, ITA, CAN, POL, HUN, NLD, UK, IRL, CZE, COL, DEU, CHE1,CHE2



Materials (19 countries +2[DFS])



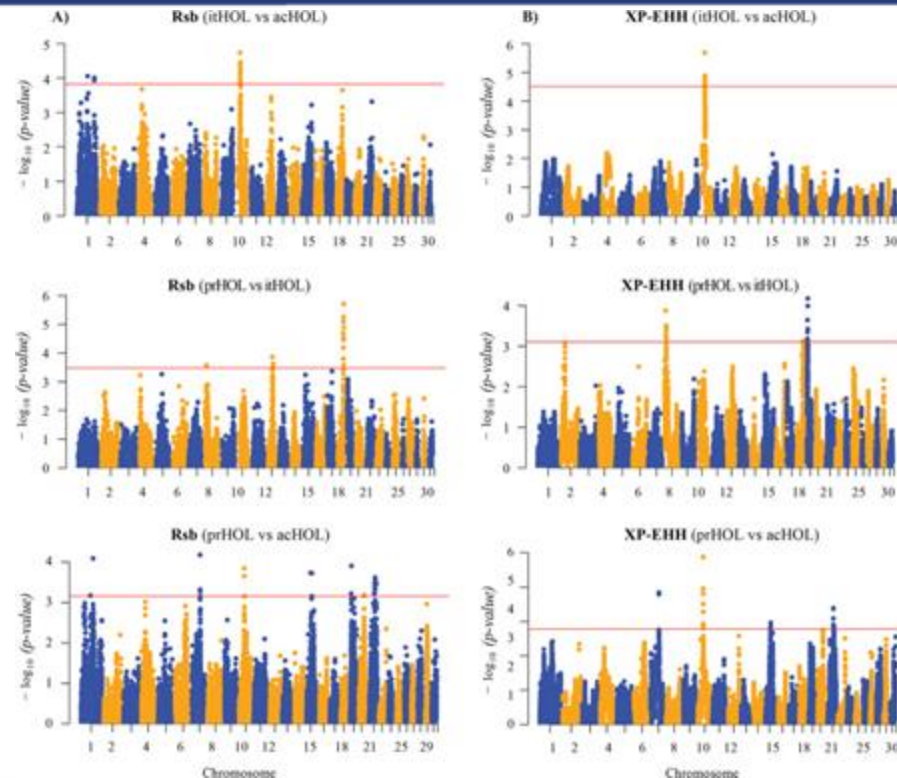
Country	N. Samples
Belgium	256
Netherlands	300
Colombia	71
Czech Republic	292 Holstein + 151 Red Holstein
Denmark-Nordic (genotypes from DK, SW & FIN)	915
France	300
North America	101 (From Previous article)
Italia	179 (from previous article)

Country	N. Samples
United Kingdom	299
Portugal	300
Hungary	30
Latvia	200
Poland	300
Switzerland (Qualitas)	250
Spain	600 Holstein + 297 Red Holstein

We are waiting: IRL, BRA, CAN, DEU, SWI2

Table 1: Number of Genotypes currently part of the dataset

- Dataset Almost complete: 4,841 genotypes from 15 countries.
- Additional data from 6 countries will be added to the dataset.
- The merged dataset we now have contains over 30k SNPs after quality control filtering of the genotypes.



MDS Analysis of a Sample dataset derived from the dataset of the first work + Genotypes from Hungary demonstrates that samples tend to cluster based on the country

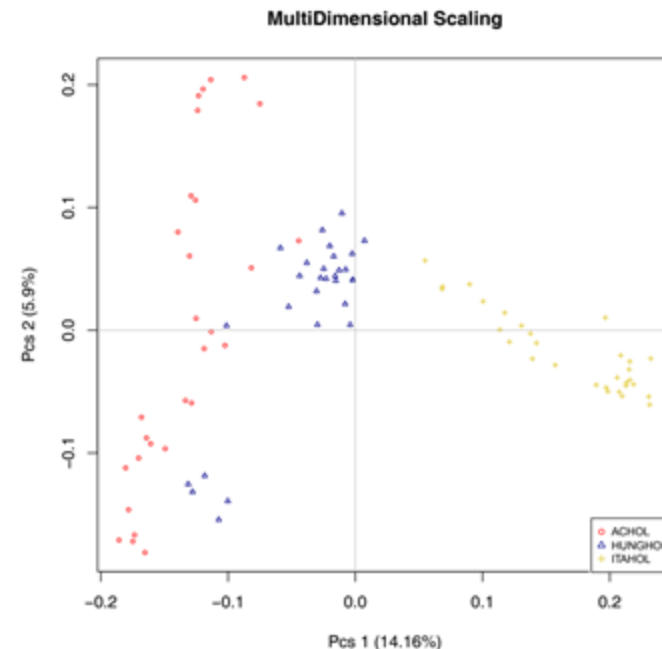


Fig. 1: MDS comparing American Friesian (red), Hungarian Friesian (blue) and Italian Friesian (yellow)

- The result is confirmed by ADMIXTURE Analysis
- We will also calculate indexes of genetic diversity like average inbreeding indexes (F_{ROH}), effective population size (N_e), and Heterozygosity.
- Signatures of selection between the mostly diverging populations will be detected

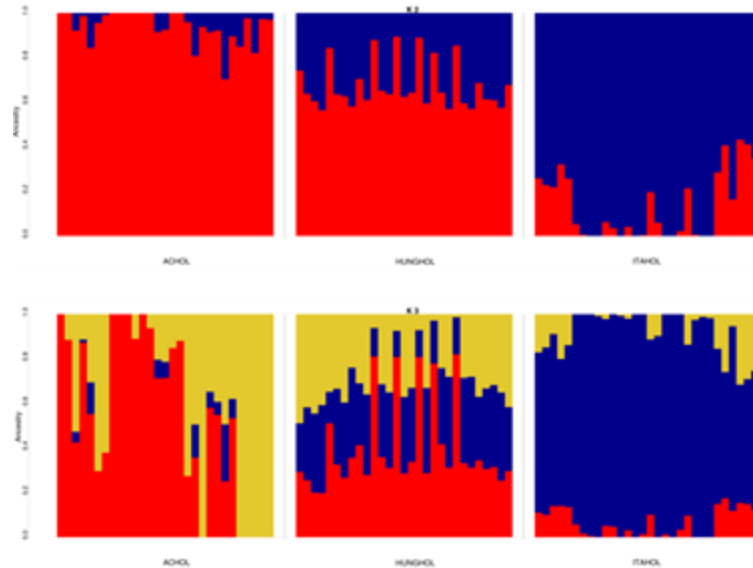


Fig. 2: Admixture analysis comparing American Holstein (left), Hungarian Holstein (middle) and Italian Holstein (right)

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Thank you for your kind
attention

- We investigated the genetic structure and signatures of selection by comparing two groups of Italian Holsteins selected for two different genetic indexes and a dataset of North American Holstein.
- We found that different indexes can influence the structure of the populations
- We inspected signatures of selection, some suggesting adaptation to diverging rearing conditions



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Exploring genome-wide differentiation and signatures of selection in Italian and North American Holstein populations

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