Worldwide Holstein-Friesian Biodiversity Project

Sampling guideline proposal

SAB Scientific Advisory Board of WHFF

Introduction

Holstein cattle, with a global population exceeding 65 million, stand as the most prevalent dairy breed internationally (FAO, 2018). Originating from the Dutch regions of North Holland and Friesland, as well as Schleswig-Holstein in Northern Germany, Holsteins boast a rich history of dual-purpose breeding. In the 1870s and 1880s, they made their way to the United States, where they underwent rigorous selection to enhance milk production (Theunissen, 2012). Subsequently, as the demand for milk surged throughout the twentieth century, North American Holsteins were reintroduced into many European countries to augment milk output (Cassandro, 2014; Hulsegge et al., 2022). While this contributed significantly to global milk productivity, recent genetic investigations have raised concerns about a substantial reduction in the genetic diversity of traditional Holstein populations due to intense directional selection (Doekes et al., 2018; Makanjuola et al., 2020). Conversely, maintaining a robust level of genetic diversity remains a pivotal challenge, particularly within high-yield production systems, given the constantly evolving market demands.

The primary objective of this study is to examine the genotypes of Holstein-Friesian cattle worldwide, aiming to evaluate the variability that may have arisen due to distinct selective pressures stemming from country-specific factors, such as varying selection objectives, diverse breeding programs, and distinct rearing systems.

Materials

The study involves Holstein herd-books from 14 different countries (France, Latvia, Germany, Portugal, Belgium, Spain, Brazil, Italy, Canada, Poland, Hungary, the Netherlands, United Kingdom, and Ireland). We aim to obtain an ideal sample size of 250 to 300 random cow samples from each country's population, around 25 to 30 samples per year, in the last decade, from each specific Holstein population. These samples will be drawn from existing genotypes, ensuring a minimum set of 54,000 chip SNPs.

The animals sampled will be conducted in a randomized manner, with the following criteria:

1. Only the female population will be taken into account.
2. The sampled animals must have been born in the respective country within the last 10 years, if possible spread over years (preferable in the last 5 years, respect to first 5-years) in the last decade.
3. They should have a lineage traceable to at least three generations on the maternal side born in the same country, and a maximum of five generations with documented registration. This ensures that the sampled animals are representative of the selective breeding applied within their country's population.
4. We will require the birth date for each cow with a 54,000 chip SNP profile, in plink format, if possible.
5. To verify the representativeness of the sampled animals within their respective countries, we will collect some phenotypic measurements, specifically milk yield-305, protein yield-305, and fat yield-305, all measured during the first lactation.
6. To each country, will be requested the official breeding goal used in the last 15 years, to understand eventual differences among the population. Breeding goal request will be provided in term of kind of traits and weights in % over total (e.g. in Italy we used from 2009 to 2019 the old PFT with these traits and weights: 8% Fat kg, 36% Prt kg, 2% Fat percentage, 3% Protein percentage, 4% type, 14% udder index, 6% Feet&Legs, 8% longevity, 10% somatic cells count, 10% Fertility. From 2019 until today the new PFT is equal to: 8% Fat kg, 33% Prt kg, 3% Fat percentage, 3% Protein percentage, 4% type, 9% udder index, 4% Feet&Legs, 5% longevity, 5% somatic cells count, 6% mastitis, 20% Fertility.)
7. Additional notes that every country can provide to understand the countries-circumstances.

Subsequently, we will carry out genotypes quality control filtering for MInimum Allele Frequency, missingness per marker and missingness per individual.
In order to evaluate genetic diversity, indexes such as effective population size (Ne), expected (He) and observed (Ho) heterozygosis, will be assessed. Furthermore runs of homozygosity will be inspected both to calculate the inbreeding coefficient (F_{ROH}) and assess Signatures of selection. To analyze population structure and admixture a Multidimensional-Scaling plot and an ADMIXTURE analysis will be done. Finally, Signatures of Selection will be inspected with a variety of methods based on both F_{ST} and haplotypic approaches and the enrichment of the divergently selected regions eventually found will be done both to inspect QTLs and functional pathways involved in the selective sweeps. All the analyses will be done in the fashion of our previous study on Italian Holstein (Persichilli et al., 2023) and additional analyses will be taken into consideration.

References

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