

Characterising the genetic diversity of German and Irish Beef cattle breeds

Project motivation / Introduction

- Relative to conventional breeding value estimation, genomic selection (GS) increases the rate of genetic gain.
- The increase in genetic gain is usually associated with a loss of genetic diversity.
- With the recent introduction of GS in German beef cattle populations
 - **Aim:** Characterize the genomic similarity between Irish and German beef cattle sub-populations.
 - **Goal:** Provide reference values for monitoring genetic progress and diversity in beef cattle populations

Conclusions

- Compared to the German sub-populations, we found higher levels of recent inbreeding in Irish cattle sub-populations.
- Relative to other breeds, Aberdeen Angus populations showed the highest level of ancient and recent inbreeding.
- High level of similarity between German and Irish beef cattle populations.

Potential for genotype exchange and increased collaboration between Irish and German beef cattle breeders

Data and Methods

A sample of 100 animals across five beef cattle populations and two countries was used to calculate the ROHs.

ROHs were calculated using the **PLINK** software.

ROHs defined as homozygous sequences of 4MB or longer.

Genotype data merged to retain the common SNPs between the two countries.

Retained **37,294** SNPs and **186,509** animals.

Principal Component Analysis calculated from genetic relationship matrix.

Results

Figure 1: The distribution of the total number of ROH across breeds and sub-populations

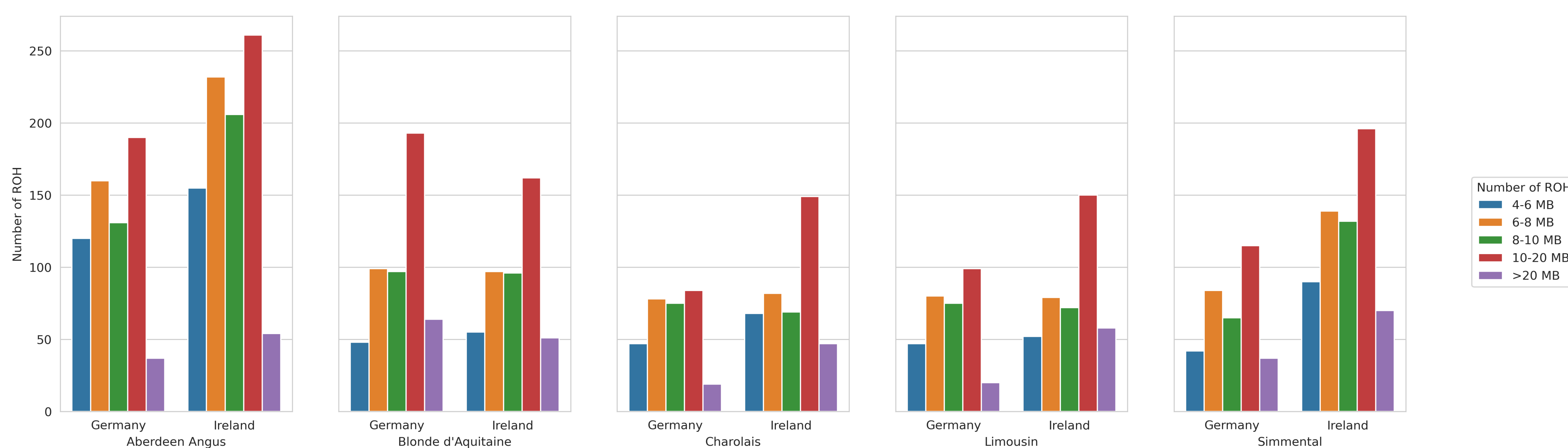


Figure 2-3: Genetic relatedness among the cattle breeds from Germany and Ireland using principal component analysis

