

climatic variable and for THI_adj were estimated for each ADG. Multiple trait models (MTM) were performed to investigate possible GxE interactions, and ADGs within each dataset were partitioned based on the median values of the climatic variables and treated as two traits to correlate. The presence of GxE interactions was assessed using the 90% posterior maximum density interval for a right tail (HDP90) of the genetic correlation. In addition to genetic effects, the fixed effect of test group was included in the models. The average ADG values were 1.33, 1.50, and 1.43 kg/day for the P1, P2, and TOTAL datasets, respectively. MTM revealed HDP90 values below 0.8, indicating GxE interactions, for P1 with THI_adj (0.60) and WIND (0.79), and for TOTAL with HUM (0.78) and RAD (0.64). In contrast, no significant values were found for P2. The results for P1 suggest a better genotype expression in environments with higher THI values, while higher WIND limits expression. For the TOTAL dataset, higher HUM positively affects genotype expression, while higher RAD negatively impacts it. In conclusion, the study highlights GxE interactions for ADG in different environments. The availability of genomic data opens the way for further investigations into specific environmental variables of interest for Maremmana, such as solar radiation.

Research supported by PNRR project DM118/2023 grant.

O316

Describing Reggiana cattle farms using genomic information from the breed population

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Reggiana is an autochthonous cattle breed mainly raised in the province of Reggio Emilia, located in the Emilia-Romagna region, in the North of Italy. Reggiana cattle are closely associated with the production of the unique mono-breed branded Parmigiano-Reggiano cheese, which provides the economic support that is needed for the sustainable conservation of this animal genetic resource. The breed population consists of approximately 4500 cattle registered in the herd book, distributed in 60 farms. This study investigated the breed structure by combining genomic data obtained from high-throughput genotyping arrays (GGP Bovine 150k single nucleotide polymorphism chip) and whole genome sequencing, which provided genomic information for

4026 animals of this breed from 45 farms, including 280 sires. Pedigree information available in the herd book was corrected using these genomic datasets. Population genomic structures were investigated using admixture analysis and multi-dimensional scaling plots. Some differences in farm clustering profiles were observed suggesting varying degrees of genetic stratification between farms. The mean Fst value, when comparing a single farm with the global population, ranged from 0.00076 to 0.006. However, the Fst values calculated for specific genomic regions had a higher average of 0.018 ± 0.043 , with some comparisons between individual farms reaching a maximum value of 0.648. Genomic inbreeding patterns were determined using runs of homozygosity (ROH). The average inbreeding level, based on Runs of Homozygosity, was 0.066 ± 0.038 , ranging from 0.003 to 0.128 when considering specific farms. Farm-specific information was gathered and used to monitor breeding practices and suggest corrections in the genetic management of the herds. The results of this study will be useful in designing more effective genetic improvement and conservation programs for the Reggiana breed, enhancing the sustainability of this animal genetic resource.

Research funded by the European Union – NextGenerationEU under the National Recovery and Resilience Plan (PNRR) – Mission 4 Education and research – Component 2 From research to business – Investment 1.1 Notice PRIN 2022 PNRR (DD N. 1409 del 14/09/2022), proposal code P2022ALHF4 – CUP J53D23018270001.

O114

Genomic basis of Bovine Respiratory Disease resistance in preweaned dairy calves

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Bovine Respiratory Disease (BRD) is a leading cause of illness and death in preweaned dairy calves, representing a major concern for cattle farming. As a multifactorial disease caused by various pathogens, BRD affects both animal health and farm productivity, prompting research into strategies for enhancing disease resistance. Despite its importance, genome-wide association studies (GWAS) targeting genetic resistance to BRD in preweaned calves remain scarce. This study combined two diagnostic methods—thoracic ultrasonography (TUS) and the Wisconsin respiratory score (WISC)—to improve the accuracy of BRD phenotyping and classify calves as either resistant or susceptible. A cohort of 240 calves was evaluated, resulting in 47