approach to dairy cattle herds. The GENORIP project collected longitudinal data from AMS and genotyped all females of 7 herds for more than 5000 individuals with the GGP 100K Bovine SNP chip. Genotypes, milk yields and environmental factors were analysed by an AI machine learning model to estimate the lactation curve in a phenomics approach on more than 500 cows from one herd with AMS. A sensitivity analysis including various environmental predictors showed the value of the approach used and the usefulness to fine tuning the prediction including environmental descriptors. The Pearson correlation between estimated and true lactation was, in the best prediction, 0.85.
The results obtained in predicting the lactation curves allow estimating the future production of calves, managing the herd reproduction according to the expected revenues.
Discussion with farmers provided insights to further develop the exploitation of the approach in managing large herds.
The longitudinal data from AMS coupled with genomic information on all females of a herd represents a new frontier in exploiting added values from SNP chip data in addition to the GEBV estimation.

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Genetic evaluation for profitability in Italian Mediterranea Buffalo

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Italian Mediterranean Buffaloes, in Italy, are selected for milk, fat, protein, mozzarella yield, limb conformation, and mammary apparatus. Buffaloes could be registered in one of the official herdbooks, RIS Bufala and ANASB, both focused on selection and genetic improvement of Mediterranean Buffaloes. Ris Bufala introduced the IPday scoring system, which quantifies the profitability of a buffalo per day of life by estimation of incoming money and outgoing expenses, considering average milk market price, feeding costs, and age at first calving, with penalties for intercalving exceeding 450 days and for age at first calving exceeding 37 months. Collaboration between RIS bufala and SYNERGY has led to changes in data collection and management which paves the way for an update of data and for corrections of any inaccuracies at any time. IPday has been developed using a dataset containing 21,873 lactations recorded from 41,687 buffaloes, 611,653 pedigree records, and 40,162 results of parentage verification. A pipeline has been created in R, has been used in order to identify data, that were incomplete or incompatible with the statistical model. BLUP Animal model method was used to estimate genetic breeding values of animals. Genetic additive components and breeding value estimation are performed by Blupf90 software package, using, in the statistical model, a random animal additive effect, a fixed herd effect and a random error component. A total number of 663,228 breeding values have been estimated using a heritability of 0.27. We performed three consecutive runs of genetic evaluation to assess the stability of the system, truncating the data at the end of 2019, 2020, and 2021. Finally, trend comparison and correlation analysis were conducted between different runs. The results of stability analyses demonstrate a correlation of 95% between consecutive yearly runs. The study results show the potential of using IPday for genetic evaluation for profitability in Italian Mediterranea Buffalo.

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Differentially expressed miRNAs in the stool of Bos indicus divergent for feed efficiency

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The fecal microbiota is an emerging field of research in cattle, being an essential component of the gut microbiota and host metabolism. Recent evidence indicates that small RNAs, like microRNAs (miRNAs), may be isolated from feces and can be involved in host-microbial interactions. In this context, transcriptomic analysis of the stool has the potential to reveal the linkages between host-miRNAs and microbiome gene expression, which in turn is expected to influence production traits. For this study, stool samples were collected from the rectal ampulla of 16 Nelore bulls divergent for Residual Feed Intake (RFI) phenotype. Total RNA extraction was performed using Trizol reagent, and sequencing of miRNA was performed using the Illumina Hiseq 2500

platform, with a throughput of 8,000,000 paired-end reads per sample. Reads were trimmed and low-quality sequences were removed. Host reads were mapped to the *Bos taurus* genome (ARS-UCD1.2) with STAR software. Differential expression (DE) analyses were performed using DESeq2 software and analyzed to predict potential regulatory target genes with Targetscan and DIANA miRPath v3.021 softwares. Functional enrichment of target genes was performed with WEB-based Gene seT AnaLysis Toolkit. In total, 163 expressed miRNAs were identified, being seven miRNAs more expressed in the efficient group; bta-miR-126 ($p$adj =0.0019), bta-miR-30a ($p$adj =0.0042), bta-miR-196a ($p$adj =0.0164), bta-miR-205 ($p$adj =0.0401), bta-miR-27b ($p$adj =0.0517), bta-miR-143 ($p$adj =0.0965), and bta-miR-155 ($p$adj =0.0942). Target genes from bta-miR-143 were enriched for PI3K-Akt signaling pathway and target genes from bta-mir-27b were enriched for Type II diabetes mellitus, Insulin resistance, TNF, and Insulin signaling pathway. Previous studies also identified these pathways related to RFI in a Nelore population. Altogether, these results point to miRNAs identified from the stool as potential regulators of feed efficiency, which may provide the knowledge to develop future strategies to manipulate the microbiome.

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Microbial diversity in the stool of Bos indicus divergent for feed efficiency

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Microbiome research is gaining attention in livestock species, as it assists in understanding host biological processes under the prism of symbiotic microorganisms. Feed efficiency is a livestock production trait with economic and environmental impacts, and there is increasing evidence that the gut microbiota plays a vital role in its regulation, suggesting that the modulation of an animal's microbiota composition can promote more sustainable and efficient livestock production. Next generation sequencing studies have used 16S rRNA sequencing to describe the microbiota composition, stating that metabarcoding can offer new opportunities to use microbial composition to assess feed efficiency. For this study, stool samples were collected from the rectal ampulla of 16 Nelore bulls divergent for Residual Feed Intake (RFI) value. DNA extraction was performed using the Quick-DNA™ Fecal/Soil Microbe Miniprep Kit (ZYMO Research Corp), using 150 mg of stool. PCR target amplification for bacterial 16S rRNA was performed using designed primers and amplicons were sequenced in an Illumina Hiseq platform (2 × 250 bp) using the Illumina V3 sequencing kit. After sequencing, raw reads were filtered for quality (>Q25) and trimmed at positions 220 (F) and 175 (R) using QIIME 2 version 2018.8. The filtered data was submitted to the DADA2 package to generate amplicon sequence variants (ASVs) and bacterial sequences were annotated using the SILVA database version 132. The resulting ASV table was used to determine alpha diversity (number of ASVs and the Shannon–Wiener index) with QIIME2. We identified a total of 5006 bacterial ASVs in the Nelore bulls' microbiomes. The most prominent bacterial phyla identified in the both groups were Firmicutes and Proteobacteria. Comparison of samples from different groups using alpha diversity metrics (Chao I index and Shannon index) revealed no significant difference ($p > 0.10$) in the richness of bacteria populations between efficient and inefficient groups. Nonetheless, Pearson correlation analysis between the Shannon index and RFI showed significant association ($p < 0.10$), indicating a relationship between feed efficiency and microbial diversity.

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RNA-seq profiling of milk somatic cells in four cattle breeds reared in different management systems

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The lactation cycle is a continuous process where several developmental and physiological changes occur in the mammary gland in particular changes in its functionality, milk yield and milk composition, and mammary epithelial cells (MECs). MECs are involved in the synthesis and secretion of milk, and in the immune response. The principal aim of the present study was to profile the transcriptome of bovine milk somatic cells (BMSCs) in four cattle breeds, some of which not previously investigated: Holstein (HO), Simmental (SM), and Simmental × Holstein (SM × HO) reared in Monterotondo (Italy) in an intensive production system, under the same management and feeding