the activity of transposable elements contained in Bovidae genomes explained the variability and speciation of this taxon and provide helpful information about the activity of new TE families of *Bos taurus indicus*.

PO32

Cabannina: genomic characterisation of a local Italian Breed

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Cabannina is a small dual-purpose cattle breed, reared almost exclusively in Liguria. Other local cattle breeds in the area might have experienced a genetic introgression with Cabannina. Moreover, a 1938 law stipulated the use of Bruna Italiana bulls to improve the productivity of local breed population. As a result, the Cabannina breed may have interbred with Bruna Italiana and/or other local breeds. This work aimed to disentangle the genomic background of Cabannina with respect to local/cosmopolitan breeds and to identify the effects of recent selection in this breed. Consequently, a subset of 170 individuals, belonging to 7 Italian cattle breeds and genotyped with BovineSNP50 BeadChip within the BOVITA project were used. As the first step, after an initial quality check that reduced the number of SNPs to 36,202, phylogenetic analysis was performed in order to determine the genetic background of Cabannina. Our results highlighted the uniqueness of the Cabannina breed, which is clearly distinguishable from the other breeds in MDS plots. Furthermore, Reynolds distances indicated the genetic proximity of Cabannina to Bruna Italiana. Haplotype analysis revealed that Cabannina shares the longest median with Bruna Italiana (5.13 Mb) and that 73% (of the cows) of these two breeds display haplotypes in common. Subsequently, we investigated the signatures of recent selection on the genome of Cabannina breed respect to Bruna Italiana breed, using Integrated Haplotype Score and the Wright's Fixation Index (F_{ST}). The results from these two approaches enabled us to identify 3 different genomic regions, harbouring 3 genes (*SLC8A1*, *ARNT2*, *PRKCB*) that can be considered under selection in Cabannina but not in Bruna Italiana.

These genes are associated with QTLs related to milk production, fertility and morphological traits connected to grazing in mountainous and hilly areas.

In conclusion, this study allowed us to determine the genomic uniqueness of the Cabannina breed, despite its eventful history, which differentiates it from the other bovine populations studied.

Finally, the genomic regions we identified are linked to selection in response to Cabannina's adaptation to the local environment.

PO33

Metagenomic analysis of water bacteria communities in South Adriatic Sea (Kornati islands, Croatia)

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Isolation of environmental DNA (eDNA) is a new and promising method for analysing bacteria and aquatic species. In the present research, a variety of bacteria communities were analysed in the South Adriatic Sea (Kornati islands, Croatia) in three locations (Kurba, Klobucar, Silo Vela) and at two sea depths (5 and 20 m). The water was collected and filtered using a peristaltic pump and 0.22 µm, 50 mm diameter, cellulose filters (Millipore, USA). After filtration, filters were stored in liquid nitrogen for six days, and subsequently at −80 °C. eDNA was extracted from the filters using the PowerWater DNA Isolation kit (MoBio Laboratories Inc., Carlsbad, CA). DNA extracted from filters was sequenced by means of a Illumina Sequencer (HiSeq 2500), using a 16S rRNA profiling method. All trimmed and filtered data were processed using a custom script based on the QIIME software suite. All reads were classified to the lowest possible taxonomic rank using a reference dataset from the SILVA database. Biodiversity of the samples (alpha-diversity) was calculated with Chao1 and Shannon indexes. Similarities between samples (beta-diversity) were calculated by unweighted uniFrac. Overall, results showed the presence of a large variety of bacteria among four phyla. The most abundant phylum was the *Proteobacteria*, followed by *Actinobacteria*, *Bacteroidetes* and *Firmicutes*. Phyla *Proteobacteria* and *Bacteroidetes* were the most present at the Kurba location while phylum *Actinobacteria* was present at the Velo Silo. Phylum *Firmicutes* was more present at Klobucar. Regarding depths, phylum *Proteobacteria* showed the same abundance at the two depths while phylum *Firmicutes* showed a major presence at 5 m and phylum *Actinobacteria* at 20 m. The study identified the presence