University of Milan in the 'step by step' project development. During the first year of the project 2183 Holstein females of five farms were sampled using Flexoplus Geno biopsy ear tags and genotyped by the Neogen laboratory (UK) with the DNA chip GeneSeek Genomic Profiler (GGP) Bovine 100K. A principal component analysis (PCA) based on genotypes was performed using the SVS 8.9 software of Golden Helix to assess the genetic diversity within and among farms. For all bovine of each farm two genomic inbreeding coefficients were estimated based on the difference between the observed and expected numbers of homozygous genotypes (FHOM) and based on the Runs of Homozygosity (FROH), respectively. The FHOM values show that farmers pay attention in controlling inbreeding in their farms: the average values obtained in the first five farms were slightly negative in four of them (−0.01/−0.02) and zero in the fifth one. The FROH represents the proportion of genome tracts of minimum length equal to 1 Mb with all markers in homozygous state over the total length of the genome. The average value of FROH is similar in all the farms, ranging from 0.11 to 0.13. This shows the homogeneity in the selection process of males and females in the Holstein breed across all farms. The PCA showed the existence of genomic variability in each of the farms and clusters of females clearly separating.

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Genomic analyses for adaptation of Italian cattle breeds: preliminary results. The BOVITA Project

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Climate change will impact diverse geographic areas, including the Mediterranean region. Understanding the adaptive ability of livestock to climate variations has become a crucial focus in biodiversity conservation and management. Cattle breeds are valuable genetic resources to understand and study the molecular mechanisms of adaptation to their specific environments. Several landscape genomics approaches have been proposed to detect adaptation to different environmental pressures including correlative genotype-environment associations. The BOVITA project aims at characterizing the genetic basis of adaptation for 755 individuals from 30 Italian local cattle breeds. Here we present the first results of a joint analysis of genetic and climatic data. By considering Bovine 50K SNP genotyping data and four climate variables data from Climond database (i.e. annual temperature, annual precipitation, annual mean radiation, and annual mean moisture index). To identify genomic regions harboring footprints of selection, a whole-genome scan for adaptive differentiation was performed using genotyping data with the XtX model implemented in the BAYPASS software. In addition, whole-genome scans for association with the population-specific climatic variables were performed using the AUX model. Footprints of selection were detected on BTA1, BTA4, BTA5, BTA6, BTA7, BTA12, BTA13, BTA14, BTA16, BTA20 pointing out several candidate genes (e.g. ST3GAL6, NUDCD3, CCND2, ABCG2, LCORL, VDAC1, MIR466B-2, CTNNBL1, XKR4, CDC42BPA, SLC45A2, RXFP3); moreover, different genomic regions (on BTA7, BTA19, and BTA20) were associated with the annual mean moisture index. Ongoing analyses will specify candidate regions and genes involved in local adaptation.

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Type trait evolution of the Italian Mediterranean Buffalo: preliminary results of the last 15-year selection

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The linear type trait evaluation for the Italian Mediterranean buffalo (IMB) was introduced by the Italian National Association of Buffalo Breeders (ANASB) at the beginning of the 2000s. The proposed chart contains 23 traits, and it has been used for the admission to the herd book of both buffalo cows and bulls. Despite this, the morphology was captured in the selective process only in 2018, with the new aggregate index IBMI which include udder