

loci for tick burden and *T. parva parva* infection, respectively. By exploring a region of 25 kbp around the significant loci, two genes were identified as putatively involved into local adaptation for ECF: PRKG1 (Protein kinase, cGMP-dependent, type I) and SLA2 (Src-like-adaptor 2). PRKG1 is an inflammatory response-related gene already described as associated with tick resistance in indigenous South African cattle. SLA2 is involved with lymphocyte proliferation regulatory pathways, which are known to be modified by *T. parva parva* infection. Additionally, a preliminary ancestry analysis of the highlighted candidate regions showed a mixed sanga (African taurine \times zebu) and zebuine origin for PRKG1 region, and a prevalent sanga origin for SLA2 region.

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O018

Variation of Madura cattle in Madura Island, Indonesia

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Madura cattle are between the most important local cattle in Indonesia: they are probably a crossing of Bali (a domesticated form of the Banteng, *Bos javanicus*), *Bos indicus* and *Bos taurus* breeds. The uniformity of this hybrid was achieved after hundreds years of selection in the island of Madura. Madura cattle are embedded in many cultural aspects of local people. Two famous traditional festivals involving Madura cattle are Karapan (a bull racing) and Sonok (a cow/heifer beauty contest); animals from different areas are bred specifically for each event, and also the management practices are differently focused: as a result, there are visible phenotypic differences between the Karapan and Sonok sub-populations. The aim of this study was to prove scientifically the existing phenotypic variation between these two sub-populations. Phenotypic traits were collected from 38 and 86 cows used for Karapan and Sonok breeding respectively, obtained data were analyzed using “R” programme. T-test was used to analyze

body measurements data and showed that Sonok is significantly larger than Karapan ($p < .05$) in all dimensions. Exterior traits like body color patterns, dewlap, hump or back-line were analyzed using χ^2 which also showed significant differences ($p < .05$) between the two sub-populations. Principal Component Analysis was used to visualize the underlying pattern of body measurements data. We could see separate clusters between the Sonok and the Karapan where the first two PC explained 67% and 16% of the total variance. These results allow discriminating the Sonok from the Karapan by means of body measurements and exterior traits.

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O019

BOVITA: a first overview on genome-wide genetic diversity of Italian autochthonous cattle breeds

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Analysis of genomic data is increasingly becoming part of the livestock industry and is an invaluable resource for effective management of breeding programs in small populations. The recent availability of genome-wide SNP panels allows providing background information concerning genome structure in domestic animals, opening new perspectives to livestock genetics. BOVITA was established to join local efforts and resources for the genomic characterization of Italian local cattle breeds. Despite the growing diffusion of some cosmopolite specialized breeds, several autochthonous breeds are still bred in Italy. The main aim of the BOVITA is to investigate

the genomic structure of Italian local cattle breeds, to provide information on their genetic status that will be useful for the management of the genetic variability, as a contribution to biodiversity conservation and prioritization actions.

A total of about 800 animals (20-32 per breed) belonging to thirty Italian cattle breeds (Agerolese, Barà-Pustertaler, Burlina, Cabannina, Calvana, Chianina, Cinisara, Garfagnina, Italian Brown, Italian Holstein, Italian Simmental, Marchigiana, Maremmana, Modenese, Modicana, Mucca Pisana, Pezzata Rossa d'Oropa, Piemontese, Pinzgau, Podolica, Pontremolese, Pustertaler, Reggiana, Rendena, Romagnola, Rossa Siciliana, Sarda, Sardo-Bruna, Sardo-Modicana and Ottonese-Varzese) and two cosmopolitan breeds (Charolaise and Limousine) genotyped with the Illumina BovineSNP50 v2 BeadChip array were collected for the analysis. The genotypes of several breeds were detected in the frame of the project, whereas for some breeds these data are derived by previous studies. The dataset will be analyzed to study several aspects of population genetic diversity, multi-dimensional scaling plot, population structure, linkage disequilibrium, and runs of homozygosity. In addition, comparative analysis of conserved haplotypes will be conducted to identify genomic segments under selection pressure. Such information also provides important insights into the mechanisms of evolution and is useful for the annotation of significant functional genomics regions. Data analysis will also be useful to select SNPs suitable for parentage test and breed genetic traceability. The analysis of the data will pinpoint the genetic distinctiveness of Italian breeds. Moreover, the obtained results contribute to a better characterization of history and genetic structure of Italian cattle breeds.