



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

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<p>Abstract:</p>	<p>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.</p> <p>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.</p>

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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.

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