

production and fertility EBVs (bull's and cow's calving easiness, body condition score, calving interval, combined longevity, days at first service, somatic cells count, milk, protein and lipid yield, protein and lipid content). Delta ROH (ΔH) scores for each SNP between plus- and minus-variant groups for each EBV were calculated to detect regions with the highest variation. Genes with the highest differences in allele frequencies between minus and plus variant groups and with the highest ΔH were identified. About 500 genes on nine chromosomes (BTA 1, 2, 4, 5, 7, 9, 20, 26 and 29) were detected of which 39 showed signals of selection both for dairy and reproductive traits. These signals were classified as discordant ($N=12$) or concordant ($N=27$) effects on productive and reproductive traits. In addition, these genes are located into QTLs for both dairy and reproduction traits.

This approach seems promising for the identification of genomic regions containing genes that show recent selection both for dairy and reproductive traits. In the genomic evaluation of the animals, the SNPs associated with these genes deserve to be weighted for their peculiar effect on EBVs.

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The CA.RA.VA.N project: toward implementation of a modern dromedary selection system

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In desert and semi-desert areas, camel farming plays a pivotal role in conservation of rural societies and valorisation of natural resources through multifunctional livestock production systems. Rapid, though fragmentary and disorganized, changes are currently ongoing in the camel sector, with urban growth and changing diets contributing to accelerate the commercialisation of camel products and, consequently, production intensification and radical changes in camel management practices. Dromedary national or local breeder associations have been recently established in some Maghreb countries, however animal identification and

phenotype recording are still in an early stage. A recent project named Camel tRAnsnational Value chain (CA.RA.VA.N) has been financed by EU-Arimnet2 through a common pot instrument, involving partners from Spain, Algeria, Morocco, Tunisia, Italy and France, aiming to transfer and apply modern technologies to the various field of the dromedary sector, in order to generate sustainable development opportunities. A specific task will be the implementation of a modern organization system for animal identification, genealogy and phenotypic recording, linear assessment of morpho-functional traits, DNA banking and genotyping, adopting an integrated transnational participatory approach. During the first stage, analysis and standardization of guidelines and practices for work, milk, meat, and reproductive phenotyping in dromedaries and for their individual identification and genealogical recording will be carried out. Later on, a transnational pilot project for the implementation of the above standardized practices, the development of linear assessment protocols and the initial utilization of new-generation genotyping technologies in Southern Mediterranean countries (Morocco, Algeria, Tunisia) will be launched, in collaboration with several breeder associations. An additional pilot project for the development of linear assessment protocols to evaluate the work aptitude of the dromedaries through body and functional (gait, trot and canter) characteristics related to work performance will take place in Canary Islands in collaboration with the Asociación de Criadores de Camellos Canarios. The project will also provide a valuable opportunity for scientific exchange and networking in the dromedary sector, and to increase visibility of a still generally neglected livestock species.

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Whole genome analysis of the Lupo Italiano

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The Lupo Italiano (Italian Wolfdog) is a domestic dog (*Canis lupus familiaris*) breed created in 1966 by crossing of Apennine grey wolves (*Canis lupus italicus*) to German

Shepherd dogs (GSD). The breed has an official studbook with management protocols, under the control of the Ministry of Agriculture. The breed is characterized by strength, resistance, and strong capabilities in learning, as well as participation in search and rescue activities. Considering the depth and completeness of genealogical information, the high levels of inbreeding, and the presence of the wolf as a recent ancestor, the Lupo Italiano can be used as a model to investigate the effects of population structure and selection on wolf-dog hybridization. The aim of this work is to compare the genetic background of the Italian Wolfdog with that of the GSD, village dogs, grey wolves from the Apennines, and other dog populations, with a specific goal of detailing introgression between the Lupo Italiano, wolf and GSD.

Three hundred and seventy-seven individuals were genotyped using a high density chip containing more than 170K SNPs. Genotypes for Lupo Italiano were provided by University of Milano and National Institutes of Health in Bethesda, MD. Those for the Apennine wolves were produced by ISPRA, and those for GSD, village dogs and grey wolves were publicly available (Dryad, Shannon et al. 2015). Samples and loci were quality checked, and then analyzed using Multi-Dimensional Scaling (MDS). The relationship matrix based on pedigrees was compared with the genomic relationship matrix (GRM), calculated using GCTA64 software. In addition, the genomic heterozygosity-based inbreeding coefficient has been estimated using PLINK v1.9 software. Reynolds distances were computed to define the relationships among the five populations. In addition, the Lupo Italiano, wolves and GSD were studied at the chromosomal level. As expected, the closest population to the Lupo Italiano is the German Shepherd dog (Reynold genetic distance 0.25), whereas the farthest is the Apennine Wolf (0.40).

Results are expected to provide a clear picture of the genomic structure of the Lupo Italiano and its hybridization history. Beside scientific interest, these findings will allow the breeder association (AAALI) to better manage their animals and conserve breed genetic variation.

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Polymorphisms in genomic region of *PTX3* gene and their association with somatic cell score breeding value in Italian Holstein

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Using a target re-sequencing approach, we identified SNPs in a region of 20kb of BTA1 containing the Pentraxin3 (*PTX3*) gene, a candidate gene for mastitis resistance in Holstein cattle breed. *PTX3* plays a role in the regulation of innate resistance to pathogens and the consequent inflammatory reactions. *PTX3* is a secreted prototype protein of the long pentraxin group synthesized by a variety of tissues and cells and in particular by innate immunity cells in response to proinflammatory signals and Toll-like receptor (TLR) engagement. A TruSeq Custom Amplicon Assay was designed to resequence the region including *PTX3*: 12 kb upstream of the promoter and 1 kb downstream of the 3'-UTR (Miseq NGS technology). The DNA of 95 Holstein bulls chosen using a selective genotyping approach according to their somatic cell score breeding value (SCS-EBV), was extracted, amplified with the custom assay and sequenced. An individual average coverage threshold of 20X was considered, resulting in 55 high and 35 low SCS-EBV individuals retained. All data analyses were carried out in R environment. On a total of 66 identified SNPs, only 20 with minor allele frequency (MAF) higher than 0.05 were considered: four were in exon 3 and 16 in intron 2. All these SNPs were already recorded in the NCBI database. Allele and genotype frequencies were calculated in the two groups (high and low SCS-EBV) and a Mann-Whitney test was used to detect frequency difference between groups, while the genotype-EBV association was assessed with Kruskal-Wallis Test. The SNP effect was estimated using the heteroscedastic effects model (HEM) (Shen et al. 2013) using the package bigRR (Shen et al., 2013). The genotype distribution of eight SNPs was different between groups and was significantly associated with SCS-EBV ($p < .05$) with a mean HEM effect of 0.032 (0.015-0.037); remarkably, only one of these eight SNPs maps in exon 3 (rs136063049 G/T). An additional SNP in exon 3 (rs378618076) gave a different genotypes distribution but the association genotype/EBV was not significant ($p = .055$) even though its HEM value (0.97) was the highest. In conclusion, nine SNPs were identified as candidate markers for genetic resistance to mastitis in Italian Holstein. Further investigations could be useful to understand the role of intronic