

produced per sample, with varying mapping efficiency (18.0–33.6%). The two groups showed similar proportion of methylation at CpG sites, while they differed at non-CpG sites.

Significant methylation changes were observed in 360 regions and 95 genes. KEGG pathway analyses indicated that these genes were mainly involved in glucocorticoids metabolism, stress responses, cellular defense and calcium signaling pathways.

These preliminary results suggest that stress response in livestock is mediated by epigenetic regulation, provide target biomarkers to assess the effect of stress-mitigation management procedures and candidate genes for the selection of stress-tolerant animals.

P035

A GWAS in the autochthonous Italian Valdostana Red Pied cattle population based on a high resolution Copy Number Variant (CNV) scan

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CNVs are an important source of genomic structural variation, recognized to affect phenotypic variation in many mammalian species especially related to regulation of complex disease. Recently CNVs have been mapped in several cattle populations and they have been shown to be located also in relevant gene families affecting productive, functional and health traits. Valdostana Red-Pied, an autochthonous Italian dual purpose cattle population, did not undergo strong selection for production traits as compared to Holstein or Brown Swiss and can thus deliver valuable information on structural variation and its association with complex traits in an Italian local cattle breed. CNVs have been mapped from the log R ratio (LRR) and B allele frequency obtained genotyping 143 bulls with the Illumina BovineHD bead chip. After PennCNV-CNVruler analysis, a total of 368 CNVRs were found with a MAF threshold above 0.05 (165 gains and 204 losses). Official EBVs for cheese yield (IRC) and cheese yield + muscularity (IRCM) were

provided by A.N.A.Bo.Ra.Va. In addition, the traits milk yield (MILK), fat yield (FAT), fat % (FAT%), protein yield (PROT), protein % (PROT%), muscularity (MUSC) and udder (UD) were analyzed. After PennCNV-CNVruler analysis, a total of 368 CNVRs were found with a MAF threshold above 0.05 (165 gains and 204 losses). Our results indicate that the 27% of the CNVRs here identified resulted to be significantly associated with functional and productive traits on several chromosomes. Some of these regions overlap known chromosome regions previously identified in other breeds using different experimental designs for the same traits on BTAs 2, 5, 9, 18, 23 and 29. Data were generated as part of the FP7 project QUANTOMICS contract n. 2226642.

P036

Identification of genomic regions of recent selection for productive and reproductive traits in Italian Holstein bulls

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The impressive genetic improvement of milk production obtained in cosmopolitan dairy breeds during the last 65 years has been accompanied by a reduction in fertility, due to negative genetic correlation between those traits. Aim of this work is to identify genomic regions recently selected for dairy and reproductive traits in ~3000 Italian Holstein Bulls born between 1987 and 2007.

Illumina BovineSNP50 and BovineHD SNP chip genotype data from SELMOL, PROZOO and INNOVAGEN projects were used. Estimated Breeding Values (EBVs) of the genotyped animals were provided by the Italian Holstein association (ANAFI) for 32 productive, morphological and reproductive traits. Genotypes were quality-checked and medium-density data were imputed to high density using BEAGLE (v.3). The working dataset comprised 2,918 animals and 613,956 SNPs. Contrasting groups of bulls, identified as minus- or plus-variant for each EBV over the 20-year span were previously analyzed to find chromosomes containing genomic regions with the highest differences in allele frequency between groups, and thus supposed to be under strong directional selection. On these chromosomes, runs of homozygosity (ROHs) were investigated on plus- and minus-variant bulls for 13

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.

P037

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.

P038

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