(2n=50) is characterized by the presence of all four casein fractions (αS1, β, αS2, and κ) encoded by the four linked autosomal genes (CSN1S1,CSN2,CSN1S2 and CSN3, respectively) mapped on chromosome 7. In particular, the CSN1S1 gene is characterized by an extremely split architecture with 19 exons, many of which of small size (24 bp). It encodes for a precursor of 214 amino acids with a signal peptide of 15 amino acid residues.In recent years, several polymorphisms at milk protein loci associated with traits of economic interest like milk coagulation properties or milk composition have been intensified.Despite that, so far, not any SNP within the milk protein loci was found to be associated with an important trait like milk yield.The aim of this study was to evaluate possible effects of the SNP c.628C>T, identified at position 89 of 17th exon of the CSN1S1 gene and responsible for the amino acid change p.Ser178Leu (A and B allele, respectively) (EMBL n° HE573919-20), on milk yield in Italian Mediterranean river buffaloes. A total of 7547 records for milk yield measured monthly on 1096 lactations of 552 buffaloes belonging to different farms located in Salerno and Caserta province (Southern Italy) were analyzed. Sampling and phenotypic collection data were carried out in collaboration with the Italian National Association of Buffalo Breeders (ANASB).The genotyping of examined animals was carried out by a method based on MboI-ACRS.The major allele (B) had a relative frequency of about 0.6 and χ^2 values showed that there was no evidence of departure from the Hardy-Weinberg equilibrium (P≤0.05). Association between CSN1S1 polymorphism and milk yield was investigated with a mixed linear model that included effects of parity, calving season and month of production. A significant association between the SNP c.628C>T and milk yield was found (P<0.05).In particular, the BB genotype showed an average daily milk yield approximately 0.61 kg higher than AA buffaloes.The results reported in the present work represent the first example of association between a genetic marker in a milk protein encoding gene and milk yield for the Mediterranean river buffalo.Such association, if confirmed on larger population, should be evaluated in order to supply useful indications for the application of marker-assisted selection programs in river buffaloes.

Acknowledgements

The research was founded by Ministry of Agricultural, Food and Forestry Policies (MiPAAF), INNOVAGEN project.

P-040

Imputation of microsatellite from dense SNP in the Valdostana Red Pied cattle – A Master thesis in Animal Production

Cristina Costa[1], Erika Frigo[1], Maria Cristina Cozzi[1], Maria Giuseppina Strillacci[1], Fausta Schiavini[1], Raphaelle Teresa Matilde Maria Prinsen[1], Mario Vevey[2], Alessandro Bagnato[1]

[1]*Dipartimento di Scienze Veterinarie per la Salute, la Produzione Animale e la Sicurezza Alimentare, Università degli Studi di Milano, Italy*

[2]*Associazione Nazionale Allevatori Bovini di Razza Valdostana, Gressan (AO), Italy*

Corresponding author: erika.frigo@unimi.it

Microsatellite markers (MS) have been used efficiently for parentage verification in various livestock species and their impact on the industry to certify exact pedigree information has been massive for long time. In cattle, the International Society of Animal Genetics (ISAG) recommended a panel of 12 bovine MS markers for the individual parentage verification testing and a large MS database contains the historical data of populations. Recently, there is an increasing interest from the stakeholders in agriculture and the research community to use Single Nucleotide Polymorphism (SNP) for parental verification due to their higher genotyping accuracies, speed of genotyping, lower overall cost per genotype, and simplicity of automation. Thus, ISAG opened the parentage testing in cattle to SNP chips methodology. A tool to link the MS database to SNP markers tool have been developed in USA for main populations such as the Holstein and Brown Swiss cattle. The objective of the thesis is to develop a SNP-MS haplotype reference panel set in the Valdostana Red Pied cattle (the most common autochthonous dual purpose breed in the region Valle d'Aosta in Italy). The information on MS alleles recognized from ISAG are available from the National Association of Valdostana Breeders (A.N.A.Bo.Ra.Va.) and the genotypes obtained from the Illumina BovineHD BeadChip (777,962 SNPs) array for 143 bulls are already accessible at UNIMI. Specific imputation software (*e.g.*: Beagle) and pipelines will be used for the haplotype estimation. This strategy may be employed in any species that has dense SNP genotypes and MS alleles information on a subset of the population large enough to define phase associations among MS alleles and SNP haplotypes. Moreover, this methodology will validate the parentage among individuals when different genotyping platforms have been used through the generations and will assess the sensitivity of such a conversion system using HD SNP data.

Acknowledgments

This study was funded by EC-FP7/2007-2013, agreement n°222664, "Quantomics".