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Book of Abstracts

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particular, the CAN1 (60% of variability) discriminated the strong alleles, CAN2 (22% of variability) discriminated the weak alleles and CAN3 separated the animals carrying the null alleles. The most discriminant SNPs for the three CANs have been found to be located in the casein cluster. In particular two SNPs mapped in the *CSN1S1* chromosomal position and the breeds carrying the null alleles shown opposite allelic frequencies in relation to the other breeds as results of selective selection pressure. Mahalanobis distance, based on the group centroid position in the three-dimensional space, returns a trend of variation from the strong to null alleles classes. Moreover, the CDA analysis allowed to identify associations of *CSN1S1* alleles with other clustered casein genes. This result could help in the developing of a panel of SNPs useful for selection plans aimed to improve milk technological properties for cheese making or, conversely, to modify milk nutraceutical characteristics for goat's milk intolerance.

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P043

Re-sequencing of genes related to mastitis resistance in dairy cows

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Selection for mastitis resistance should be one of the first aims in dairy farms, since mastitis is a major cause of economic loss. Resistance to mastitis is a complex trait and expression profiles of mammary gland infected with different pathogens were conducted for a better understanding of the mechanism underlying this disease. Many different genes were found to be involved with mastitis, but only the identification of causative mutations could be useful for selection of resistant cows. Wide regions of six genes involved in immune response were re-sequenced to look for causative mutation of mastitis resistance: the pentraxin3 (*PTX3*), the chemokine C-X-C motif receptors (*CXCR1* and *CXCR2*), the toll-like receptor 4 (*TLR4*), the mannose-binding lectin 1 (*MBL1*), and serum amyloid A3 (*SAA3*) genes, respectively on BTA1, BTA2, BTA8, BTA28 and BTA29. DNA was extracted from semen of bulls in the positive (58 bulls) and negative (37 bulls) tails of the distributions of estimated breeding values for somatic cell score. Using a target re-sequencing approach by NGS technique on the MiSeq Illumina platform, we identified a total of 1535 polymorphisms (including SNPs and small indels). Excluding mutations, with a minor allele frequency lower than 0.05 only 384 polymorphisms remained. The original phenotypes were adjusted for population structure using the genomic relationship matrix calculated using this dataset and 4 individuals having an identity by state (IBS) > 0.95 were excluded from the following analysis. To test for associations, mutations with a correlation higher than 0.80 with any others were further excluded, together with polymorphisms deviating from Hardy-Weinberg equilibrium. Finally, 101 polymorphisms were tested for associations. A total of 7 SNPs resulted significantly associated with SCS ($p <= .05$): one on PTX3 (rs208223246, missense variant responsible for the amino acid exchange Glu347Lys), one on *CXCR1* (rs109694601, intron variant), one on *TLR4* (rs134052737, intergenic variant), one on *MBL1* (rs208247354 and rs208491630, respectively intron and upstream gene variant), and two on *SAA3* (rs137746604 and rs210417381, both upstream gene variants). These findings represent the first step toward the use of causative mutations in genetic selection for mastitis resistance in dairy cows.

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P044

Genetic diversity, productive and reproductive performance in Italian chicken breed Bianca di Saluzzo

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Bianca di Saluzzo (BS) is a chicken breed reared in Piedmont region and its substitution with commercial lines caused a reduction in size, associated with a progressive decline due to inbreeding. In this study, genetic diversity, productive and reproductive performance were examined. Birds were kept in standard environmental conditions. At hatching, 177 chicks were weighed and at six weeks of age were separated by sex and transferred to growing pens with free-access to water and were fed with a standard commercial starter diet *ad libitum* followed by a growing diet. All birds were genotyped by a set of 14 microsatellite markers chosen by their high polymorphism. Body weight (BW) was