

Management) program. Areas evaluated relate to the proof of training of personnel, availability of clear standard operating procedures, and specific areas of management and animal condition. Literature exists that demonstrates the association of welfare responses such as passive transfer of immunity (colostrum feeding), stocking density and availability of resources, hygiene score, body condition score, and locomotion score and survival, production, and reproduction of dairy cattle. In short, animal welfare standards may be perceived as an unnecessary burden by dairy producers, but economic gains are realized when welfare standards are met by improving animal comfort, longevity and performance, which are generally easily justifiable and support sustainability.

O377

How to combine microsatellite and SNP for parentage verification in sheep?

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Microsatellite markers (MS) have been widely used for parentage verification in most of the livestock species mainly due to their high polymorphic information content. In the genomic era, the spread of genotype information as Single Nucleotide Polymorphism (SNP) has raised the question to eventually use SNPs also for parentage testing. Despite the clear advantages of SNP panels in terms of cost, accuracy, and automation, the transition from MS to SNP markers for parentage verification is still very slow and, so far, only routinely applied in cattle. A major drawback is the need for the same genotyping technology for parents and offspring which results in additional costs. To overcome this issue, in this study, we aimed to assess the feasibility of developing an MS imputation pipeline from SNPs in two Italian local sheep breeds: Comisana ($N = 331$) and Massese ($N = 210$). Those animals were genotyped for eleven MS which are part of the standard ISAG panel and with the Ovine SNP50 Bead Chip. Prior to imputation, a quality control (QC) was performed, and SNPs located within a window of 2 Mb from each MS were selected. The core of the developed pipeline was made up of three steps: (a) storing both MS and SNP data in a Variant Call Format file, (b) masking MS information in a random sample of individuals (10%), (c) imputing masked MS based on non-missing individuals (90%) using an imputation program. The procedure was repeated 100 times randomly selecting a balanced number of animals per breed. The accuracy of the MS imputation was assessed on the genotype concordance which was defined as 0 if none of the imputed alleles matched the true allele, 0.5 if only one of them matched, and 1 if both alleles matched the true alleles. A total of eight MS passed the QC, and 505 SNPs were located within the ± 2 Mb window from each MS, with an average of 63 SNPs per MS. The overall imputation accuracy was 92.84% and 94.10% in the Comisana and Massese, respectively. The MS that performed best was the MAF214 in the Comisana with an accuracy of 99.0% and the FCB304 in the Massese (97.8%). Our findings suggest that the proposed imputation approach can reach high accuracies which is a prerequisite for parentage verification based on imputed MS

genotypes. Additional studies are needed to test if MS imputation in other more distantly related breeds could also be performed.

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O436

MBL2 gene polymorphisms in Mediterranean Italian River Buffalo (*Bubalus bubalis*) in relation to milk production traits

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Mediterranean Italian River Buffalo (MIRB) is mainly reared for milk production intended for mozzarella cheese production. Thus, the selection is focused on the improvement of milk yield and its quality, as well as on the management of technopathies like mastitis. Recent studies have shown that milk somatic cell count (SCC) combined with differential somatic cell count (DSCC) could be used as an indicator of udder inflammatory reactions. The mannose binding lectin 2 (*MBL2*) gene encodes protein involved in innate immune system and several studies demonstrated that some haplotypes of this gene are associated with *Brucella Abortus* infection in MIRB. The aim of this study was the identification of DNA variants in the *MBL2* and the analysis of their association with milk quality traits. Blood and milk samples were collected from 121 female buffaloes: 82 healthy and 39 affected with mastitis. The *MBL2* (NC_059179) was sequenced using the Sanger method. Altogether 33 SNPs were identified: 12 in exons (including 7 missense ones), 8 in promoter region, 8 in 3'UTR or 3'flanking region, and 5 in introns. Distribution of DNA variants in healthy and affected females have been studied using the odd ratio statistical test to check for any correlation. Finally, an association study was performed between all the SNPs found and different milk parameters: 3 SNPs located in non-coding sequences (2 in introns and 1 in 3'UTR), were significantly associated with SCC ($p < 0.05$). This study showed that *MBL2* is a highly polymorphic gene, however, association of its variants with resistance to mastitis and milk production traits needs further studies on larger cohorts of healthy and affected females.

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O173

Perosomus elumbis in a family of Casertana pigs: case description and identification of candidate genes

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Genetic selection relies on the screening of candidate breeders and on the exclusion from the selection schemes of males carrying negative traits. This objective becomes a priority in schemes applied to autochthonous breeds, where high inbreeding rates may cause the accumulation of harmful alleles leading to the emergence of severe abnormalities. Casertana pig is an autochthonous breed reared in Southern Italy particularly appreciated for its rusticity, frugality and muscularity. Currently, the herdbook comprises 1280 Casertana pigs (47 boars, 262 sows, and 961 piglets). A Caserta pig farm recently reported the born of piglets affected by a rare anomaly incompatible with life. The aim of this study was to characterize the congenital abnormality and find possible associations with candidate genes. The eight affected piglets belonged to 2 different litters; in the first litter, 3 out of eight newborn piglets showed dysplasia of the caudal part of the spine and spinal cord, and of the hind limbs; in the second litter, all piglets were born dead or died soon afterward, and 5 of them were malformed. The agenesis or malformation of the caudal spine and the observed macroscopic lesions led to a diagnosis of *Perosomus elumbis* (PE), which is a rare, lethal, congenital disorder characterized by agenesis or malformation of the caudal spine (lumbar, sacral and coccygeal vertebrae), often associated with musculoskeletal alterations of the pelvic bones and hind limbs. Malformations affecting other organs or systems have been described over time in various animal species.