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present differences in both morphology and production traits. In the Principal Component Analysis, the first dimension (C1) well-separated BAR from other dairy sheep breeds. As expected, relatively close relationships were observed among the dairy Sicilian sheep (COM, PIN, and VDB). A long genetic distance was found with the SAR breed. The average transitions to transversions ratio was 2.55 for all sheep breeds and similar to the values observed in other mammalian genomes, indicating relatively low potential random sequencing errors. We observed the largest number of single-nucleotide polymorphisms (SNPs) in SAR (9,434,843) and BAR (8,943,103), reflecting their genetic differentiation. In contrast, the COM showed the lowest number of SNPs (4,351,307). All breeds showed that about 9% of these SNPs were novel. There was approximately one variant every 260 base pairs (bp) for BAR, PIN, SAR and VDB, and one variant every 521 bp in COM. A total of 5,799,001 unique SNPs were identified among the five breeds, ranging from 419,211 (COM) to 1,817,926 (SAR). All the sheep breeds showed 4% of insertion and deletion compared to all variants discovered. SnpEff was used for functional annotation of identified autosomal SNPs based on the Ensemble sheep genome assembly Oar_v3.1.99. Most SNPs were intergenic or intronic, with approximately 1% located in the remaining genic regions. These markers represent the most important subset of SNPs as probably associated with changes in protein sequences, structures and functions. An advantage of genotyping by sequencing with respect to medium or high-density SNPs arrays is that it allows detecting selection signatures over relatively short distances. The results provide an improved understanding of genetic diversity for these sheep and will facilitate the identification of genomic regions involved in the phenotypic variation among breeds.

SESSION 24 – FEED EFFECTS ON NUTRITIONAL PROFILE OF ANIMAL PRODUCTS – II

O121

Milk nutritional quality and rumen microbial community of Holstein-Friesian cows fed a diet supplemented with olive oil pomace

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Olive oil pomace (OOP) is a by-product derived from the olive milling process. Its disposal in the environment is complex and onerous but, in animal feeding, it may represent an interesting source of bioactive compounds for its chemical composition. Pomaces are rich in soluble polyphenols and functional fatty acids (FAs) as oleic acid. In literature, several authors reported positive effects of polyphenols in modulating rumen microbiota lowering methanogenesis and enriching milk with unsaturated FAs. Thus, 40 lactating Holstein-Friesian cows were randomly allotted in two groups (20 cows *per group*) and fed a basal diet (control, C) or the same diet supplemented with OOP (8 g/100g dry matter head and day, T). After two weeks of dietary adaptation, milk yield was daily recorded during the next 30 days. Milk samples were individually collected weekly (4 times of sampling: T7 d, T14 d, T21 d, T28 d) and analyzed for clotting parameters, chemical and nutritional characteristics, and FA profile. At the end of the trial, rumen liquor was collected for rumen microbial community analysis. No differences were found for milk chemical and nutritional parameters and ruminal bacterial taxonomic composition. Anyway, the difference in the relative abundance of specific bacterial taxa was observed and a significant delay was evaluated for the milk clotting time in the T group with respect to C. Concerning the fatty acid profile, saturated fatty acid concentration was lower in the milk from the T group than in C, while functional fatty acid, such as vaccenic (0.622a vs. 0.401b; $p < .0001$), oleic (9.819a vs. 8.055b; $p = .0043$), and conjugated linoleic acids were more concentrated in the milk from T group with respect to the one from C (0.226a vs. 0.116b $p < .0001$). These findings highlight the effect of OOP on rumen microbiota metabolism.

O122

Metagenomics of milk before, during and after summer transhumance to highland pasture in relation to human health and cheese making properties

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Summer transhumance is a traditional form of pastoralism to highland pasture in the dairy system of alpine regions and it is practiced all over the world. Positive influences can be obtained