

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

Federica Mannelli<sup>a</sup>, Matteo Daghio<sup>a</sup>, Roberta Pastorelli<sup>b</sup>, Carlo Viti<sup>a</sup>, Maria Alexandra Cucu<sup>b</sup>, Luca Turini<sup>c</sup>, Federica Scicutella<sup>a</sup>, Arianna Buccioni<sup>a</sup>

<sup>a</sup>*Dipartimento di Scienze e Tecnologie Agrarie, Alimentari, Ambientali e Forestali (DAGRI), University of Florence, Firenze, Italy*

<sup>b</sup>*Centro di ricerca Agricoltura e Ambiente, Consiglio per la Ricerca in Agricoltura e l'analisi dell'Economia Agraria, CREA-AA, Florence, Italy*

<sup>c</sup>*Dipartimento di Scienze Veterinarie, Istituto Zooprofilattico Sperimentale del Lazio e della Toscana 'M. Aleandri', Pisa, Italy*  
Contact [federica.mannelli@unifi.it](mailto:federica.mannelli@unifi.it)

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

Giorgia Secchi<sup>a</sup>, Nicolò Amalfitano<sup>a</sup>, Ilaria Carafa<sup>b</sup>, Kieran Michael Tuohy<sup>c</sup>, Elena Franciosi<sup>c</sup>, Giovanni Bittante<sup>a</sup>

<sup>a</sup>*Dipartimento di Agronomia, Animali, Alimenti, Risorse naturali e Ambiente, University of Padova, Padova, Italy*

<sup>b</sup>*Facoltà di Scienze e Tecnologie, University of Bolzano, Bolzano, Italy*

<sup>c</sup>*Dipartimento di Qualità alimentare e nutrizione, Centro Ricerca e Innovazione (CRI), Fondazione Edmund Mach (FEM), San Michele all'Adige, Italy*

Contact [giorgia.secchi@phd.unipd.it](mailto:giorgia.secchi@phd.unipd.it)

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

for the environment, society, tourism, animal health and welfare. The aim of this study was to analyze the evolution of the milk microbiota before, during, and after summer transhumance to highland pasture in relation to possible effects on animal/human health and cheese-making properties. The study involved 12 healthy, multiparous, mid-lactation Brown Swiss cows reared in a farm located in the Trento province (Northern East Italy). The cows were monitored from June to October and divided into two groups: six cows were used as a control group and kept in the lowland permanent farm (PF); the other six cows were moved to a temporary alpine farm (ALP) from July to September. From each milk, samples were collected every four weeks for genomic DNA extraction and microbiota characterization using community 16S rRNA amplicon (V3–V4 region) based Illumina Miseq sequencing and QIIME2 (2018.2 version). The relative abundance was analyzed after a  $\log_{10}$  transformation and identified species were classified into two unfavorable categories: Spoilage and Pathogenic species, and two favorable categories: Probiotics and Dairy species. For the statistical analysis, we used a linear mixed model, where the combined Month  $\times$  Group (MG) effect was used as fixed and the cow effect as random. The results revealed a different behavior in the ALP group compared to the PF group during the 3 months of summer transhumance. The Spoilage bacteria tended to decrease in the alpine pasture (MG effect:  $p < .001$ ), with significant differences in terms of *Pseudomonas*, *Alicyclobacillus*, and *Clostridiales* ( $p < .001$ ,  $p < .001$ ,  $p < .05$  respectively). Pathogenic did not show large differences between the two groups; instead, the Probiotic category, which includes *Propionibacterium* and *Bifidobacterium*, showed a gradual increase in the ALP group ( $p < .001$ ). Dairy species also had a significant increase in the ALP group ( $p < .001$ ), especially *Lactococcus* and *Lactobacillus* (both  $p < .001$ ). All the microbiological changes disappeared when cows were moved back from alpine pasture to the permanent indoor farm. Summer transhumance to alpine pasture, therefore, has a favorable effect on the milk microbiota, with positive implications for both the cheese-making attitude of milk produced and its possible effect on human health.

## O123

### Dehydrated sulla forage in dairy ewes feeding: effects on cheese properties

Antonino Di Grigoli<sup>a</sup>, Marialetizia Ponte<sup>a</sup>, Riccardo Gannuscio<sup>a</sup>, Margherita Addis<sup>b</sup>, Marco Alabiso<sup>a</sup>, Giuseppe Maniaci<sup>a</sup>, Monica Bacchi<sup>c</sup>, Massimo Todaro<sup>a</sup>, Adriana Bonanno<sup>a</sup>

<sup>a</sup>Dipartimento Scienze Agrarie, Alimentari e Forestali, Università degli Studi di Palermo (UNIPA), Palermo, Italy

<sup>b</sup>Azienda AGRIS Sardegna, Olmedo, Sassari, Italy

<sup>c</sup>Dipartimento AGRARIA, Università Mediterranea di Reggio Calabria (UNIRC), Reggio Calabria, Italy

Contact [adriana.bonanno@unipa.it](mailto:adriana.bonanno@unipa.it)

Feeding green sulla forage (GSF) (*Sulla Coronarium* L.), a short-lived perennial legume containing phenolic compounds, especially condensed tannins, showed to increase intake, milk yield and casein level in ruminants, and enhance fatty acid (FA) profile and antioxidant activity of dairy products. To obtain analogous favourable effects using conserved sulla forage, dehydration could be a valid alternative to the haymaking process which causes greater losses of biomass and its nutritional and bioactive compounds. The aim of this research was to evaluate the dairy products from ewes fed with pelleted dehydrated sulla forage (PDSF) in the diet by comparisons with those obtained using sulla hay (SH) and GSF based diets. Twenty primiparous (PR) and pluriparous (PL) milking Valle del Belice ewes were allocated homogeneously into 5 groups and fed 5 diets in a partial  $5 \times 2$  Latin square design with 2 periods. The diets differed for the forage component: SH ad libitum (SHL); 2 kg/d per ewe of PDSF and SH ad libitum (DSF); 2 kg/d of GSF and SH ad libitum (2GSF); 4 kg/d of GSF and SH ad libitum (4GSF); GSF ad libitum (GSFL). Concentrate feed was supplied to PR (0.8 kg/d) and PL (1.2 kg/d) ewes in the function of their different production needs. The results confirmed the superiority of diet in which GSF was the only forage source offered ad libitum, as occurs with grazing; in fact, the GSFL diet resulted in higher milk yield and casein content and enhanced in cheese the number of polyphenols and antioxidant vitamins A and E, the oxidative stability, and the level of health polyunsaturated FA (PUFA) such as rumenic, the main of conjugated linoleic acids (C18:2c9t11), and  $\alpha$ -linolenic (ALA, C18:3n-3). On the whole, the DSF diet showed better results than SHL and was comparable to the 4GSF diet for milk yield and casein level and, in cheese, for external colour and vitamin A and total PUFA contents; moreover, ALA was detected at the same high level in DSF and GSFL cheeses. Thus, dehydration seems to represent a valid opportunity to exploit the considerable potential of sulla forage, and maintain adequate production levels and nutritional and health properties of milk and cheese in periods of insufficient grazed green resources.

#### Acknowledgements

Work supported by AGER 2 Project, grant 2017-1144.

## O124

### Use of different levels of hemp meal supplementation in diets of veal calves: effects on *in vivo* performances and metabolic profile

Elisabetta Bacchin, Nadia Guzzo, Lucia Bailoni

Dipartimento di Biomedicina Comparata e Alimentazione, University of Padova, Padova, Italy

Contact [elisabetta.bacchin.1@studenti.unipd.it](mailto:elisabetta.bacchin.1@studenti.unipd.it)