



ASPA 24th Congress Book of Abstract

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were housed in pens and they were fed four different diets designed to have different levels of fresh forage (F), hay and mixed grains (HG): 100% F (F); 70% F and 30% HG (7F3HG); 30% F and 70% HG (3F7HG); 100% HG (HG). The experiment lasted 7d for adaptation and 8d for cheese making and sample collection. The raw bulk milk of groups was processed into PFC according to the product specification. Cheeses after 30 days of ripening were analyzed for fatty acid profile, α -tocopherol, cholesterol, polyphenols and antioxidant capacity; cheese indexes DAP (α -tocopherol/cholesterol), HPI ($\omega 3 + \omega 6 + \text{MUFA}$)/C12:0 + (4 \times C14:0) + C16:0 and GHIC (Σ polyphenols, CLA isomers, PUFA, $\omega 3$ and total antioxidant capacity scores) were calculated. Statistical analysis was performed by GLM procedure. The model included feeding treatment as fixed factor, comparisons between means were tested with the Tukey test.

The DAP index was able to discriminate PFC when the percentage of F changed. DAP index decreased from 9.7 (F), 8.6 (7F3HG), 7.8 (3F7HG), to 6.5 (HG) ($p < .01$). No significant differences were found among groups for HPI, values were 0.44, 0.46, 0.47 and 0.45 in F, 7F3HG, 3F7HG and HG groups, respectively. A significant effect of the feeding treatment was detected for GHIC. The higher GHIC was observed in F group (31) compared to HG (14) group ($p < .01$), intermediate values were found in 7F3HG and 3F7HG (20 and 18, respectively). This study has highlighted a relationship between level of F in the diet and DAP and GHIC in PFC. Both indexes are able to discriminate different feeding groups whereas HPI cannot do the same for feeding groups.

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P046

Bovine beta casein polymorphism and environmental sustainability of cheese production

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Beta casein constitutes up to 45% of bovine milk total casein and presents several genetic variants. Bovine beta casein variants may play an important role on milk production and composition; besides their possible influence on milk digestibility and human diseases, beta casein variants can influence cheese yield and quality and, in turn, environmental sustainability of cheese production.

The aim of the study is to investigate a possible effect on the environmental impact of cheese production, related to beta casein polymorphism. A Life Cycle Assessment was performed,

considering Grana Padano PDO (GP) and mozzarella cheese (MOZ) and three different genotypes of beta casein, A1A1, A2A2, A1A2.

Three groups of 10 lactating cows were reared under the same conditions; each group belonged to the three different beta casein genotypes. Separated cheesemaking procedures were performed for the three genotypes' milk. The evaluation of environmental impact of 1 kg of packaged cheese was performed using primary data as much as possible, together with secondary and tertiary data. Following classification, characterization was conducted through Recipe Midpoint (H) V1.10 method. With this approach, normalization was also performed, for identifying the impact categories which are important for this specific sector. Normalized results represent the fractional contribution of GP and MOZ production, to an average European Union citizen's cumulative annual environmental impact.

The results pointed out that cheese produced with A2A2 milk seems to be the most environmentally sustainable, both for GP and MOZ. This is probably due to the higher cheese yield (8.00%) of A2A2 milk, compared with the others, mainly related to the protein content. Carbon footprint (CF) of A2A2 was 16.6 kg CO₂ eq/kg packaged cheese and 10.7 kg CO₂ eq/kg packaged cheese for GP and MOZ, respectively. The main contribution to CF was given by raw milk production at the barn, for all the three genotypes and both for GP and MOZ. Normalization highlights that the first largest impact category was natural land transformation, followed by marine eutrophication and terrestrial acidification. In conclusion, cheese produced from A2A2 milk seems to favour environmental sustainability, mainly because of milk composition, which favours cheese yield.

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P047

Impact on goat milk composition and rumen microbiome of *Camelina sativa* cake and *Cynara cardunculus* supplements

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The study was aimed to evaluate changes in milk composition and rumen microbiome in response to Camelina sativa cake and Cynara cardunculus meal supplementation in dairy goats. Eighteen primiparous and multiparous Alpine lactating goats were divided into three balanced groups according to parity number, milk production and days in milk (1.83, 2.23 kg, 273 DIM), and assigned randomly to 3 treatment groups. The treatment groups were: 200 g/d of camelina cake (CAM; $n = 6$), 200 g/d of cardoon meal (CAR; $n = 6$), and control (CON, $n = 6$) receiving the standard diet without supplementation. The supplementation lasted 21 days. Milk yield and composition were measured weekly. Proximate analysis was performed according to AOAC official methods while milk fatty acid profile was determined by means gas-chromatographic technic. Rumen content samples were collected on a subsample of 7 animals on days 0 and 21. The DNA extraction was performed using the PowerSoil[®] DNA Isolation Kit (MO BIO Laboratories, Carlsbad, USA). The V3-V4 region of the 16S rRNA gene was amplified. Sequencing was performed by MiSeq Illumina (Illumina, San Diego, USA). Bioinformatic elaborations were performed in R 4.0.2 with the package DADA2. A non-metric multidimensional scaling (NMDS) and a permutational multivariate analysis of variance (PERMANOVA) based on Hellinger transformed genera abundance data were performed. The taxa with a different relative abundance between the conditions were identified by a Kruskal–Wallis test. Milk composition data were analyzed by PROC MIXED of SAS for repeated measures. Vaccenic acid was increased both in CAM and CAR (44%, 18%) compared to CON and also C18:1 trans 9, trans 10 and trans 12 ($p < .01$). The alpha-diversity was similar between the tested groups and a tendency to a higher evenness was observed in the rumen of goats fed camelina. The classes Bacteroidia, Clostridia and Negativicutes (~53%, ~19% and ~12%, respectively) accounted for more than 80% of the community, regardless the diet. The relative abundance of the class Desulfovibrionia was higher ($p < .1$) in CAM (~0.9%) compared to CON (~0.3%). Conversely the relative abundance of the class Saccharimonadia was lower ($p < .1$) in CAM (~1.2%) compared to CON (~2.4%). Furthermore, a higher relative abundance ($p < .1$) of the class Vampirivibrionia in the rumen content of CAR (~2.5%) compared to CAM (~0.7%) was observed. The most abundant genus in the rumen content was Prevotella, regardless the diet.

P048

Use of a partial least-squares regression model to estimate intramuscular fatty acid profile in beef from blood analysis

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Fatty acids (FA) contribute importantly to various aspects of meat quality and to its nutritional value. Unfortunately, the evaluation of the meat FA composition requires the sacrifice of the animal. Since drawing blood from cattle is a relatively simple and painless practice, to be able to predict the meat FA composition from that of blood it would be an important advancement. Partial Least Square Regression (PLSR) is a quite recent statistical tool able to handle multivariate regression models characterized by high collinearity among predictors. This study is a first evaluation of the use of PLSR to predict the meat FA composition of cattle from that of blood. Within a framework of a long-term research project (Kent'erbass), 15 calves (429 ± 49 kg live weight) were blood sampled from the tail and subsequently led to slaughter. Blood samples were centrifuged at $1200 \times g$ for 15 min at 10°C , to separate and store plasma at -70°C until FA analysis. At 24 h post mortem, samples of Longissimus thoracis et lumborum (LTL) between sixth and seventh thoracic vertebrae from each left half-carcass of animals blood-sampled were removed and submitted to FA analysis. PLSR was then applied to a dataset consisting of FA composition detected in both meat and plasma. The evaluation of the model in predicting FA was assessed by means of Pearson's correlation coefficient (r), the coefficient of determination R^2 , and root mean square error of prediction (RMSEP). Within the boundary of the ranges of FA values and despite the limited number of data used in the analysis, PLSR procedure was able to provide an estimate with a good degree of precision for many interesting FA, whose values are reported below as predicted and actual value, respectively: CLA, 1.25 ± 0.11 and 1.25 ± 0.12 % total FA, with a $r = 0.91$, $R^2 = 0.80$ ($p < .001$) and RMSEP = 0.16. n-3 fatty acids, 1.86 ± 0.49 and 1.86 ± 0.50 % FA, with a $r = 0.98$, $R^2 = 0.95$ ($p < .001$) and RMSEP = 0.36. n-3/n-6 ratio, 0.22 ± 0.02 and 0.22 ± 0.03 , with a $r = 0.91$, $R^2 = 0.82$ ($p < .001$) and RMSEP = 0.04. C18:3 n-3 (linolenic acid), 1.22 ± 0.29 and 1.22 ± 0.30 % FA, with a $r = 0.98$, $R^2 = 0.96$ ($p < .001$) and RMSEP = 0.18. C22:5 n-3 (docosapentaenoic acid, DPA), 0.50 ± 0.15 and 0.50 ± 0.16 % FA, with a $r = 0.97$, $R^2 = 0.94$ ($p < .001$) and RMSEP = 0.13. This model represents an initial attempt to predict meat FA composition of cattle from blood. A more complete database is needed to increase the robustness of the model.