



ASPA 24th Congress Book of Abstract

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ASPA 24th Congress

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metabolism and energy homeostasis in response to nutrient availability. Dietary OMWW phenolics can mitigate negative effects exerted by oxidative stress and contribute to reduce the environmental impact of olive oil industry by-products.

P144

Influence of green forage on metabolomic characteristics of buffalo milk

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The aim of this study was to compare, with a metabolomic approach, different feeding strategies in lactating water buffaloes. The study was carried out on 32 milking buffaloes that were randomly divided into two groups: Group D ($n = 16$) that were fed a total mixed ratio (TMR) and Group F ($n = 16$) that had a isoenergetic and isoproteic diet as Group D, but with the inclusion of the 30% of alfalfa green forage. Milk samples were collected individually, once a month, for four months, from June to September and analysed by LC-MS. Statistical analysis was carried out by using Mass Profile Professional, version 13.1.1 (Agilent Technologies). Metabolomic analysis revealed the presence of several metabolites differentially expressed between Group D and Group F. Among these, a total of five metabolites were identified by comparison with an online database and a standard compound as L-Carnitine, Acetylcarnitine, Propionylcarnitine, Butyrylcarnitine and 2-Methylbutyrylcarnitine. Distinct separation between these two groups was evident in principal components (PC1 – PC2) of the variance in the LC-MS dataset. Moreover, hierarchical clustering analysis also showed a clear separation of Group D and Group F in all months taken into account. In the first month, we only detected three metabolites out of five and we founded an up-regulation ($p < .05$) of Acetylcarnitine, Butyrylcarnitine and 2-Methylbutyrylcarnitine in Group D compared to Group F. In the other three months L-Carnitine, Acetylcarnitine, Propionylcarnitine were always down-regulated ($p < .05$) in Group F compared to Group D. Butyrylcarnitine and 2-Methylbutyrylcarnitine were down-regulated during the second month and up-regulated the third and the fourth months in Group D compared to Group F ($p < .05$). In conclusion, the inclusion of green forage in buffalo diet enhances the presence of functional molecules in milk with important antioxidant and

anti-inflammatory activities. The presence of these molecules should induce consumers to consider milk as a highly important source of specific nutrients with health-promoting properties.

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Insect meal and poultry by-products as innovative ingredients for rainbow trout feed: impact on intestinal microbiota and gut health

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Fish consumption and fishing levels rose sharply in the last decades leading to dramatic consequences on marine habitats. Aquaculture represents the fastest growing food production sector although its sustainability is strictly linked to provenance of feed ingredients. In the search for fish meal (FM) and fish oil (FO)-free formulations, insect meal (IM) and poultry by-product meal (PBMs) ingredients have been proposed as candidate protein sources. The aim of this study was to evaluate the effect of partial replacement of vegetable meal (VM) with IM and PBM in rainbow trout (*Oncorhynchus mykiss*) on gut health, by focusing on microbiota composition, markers of inflammation and gut barrier integrity. Animals were fed eight dietary treatments with different percentages of *Hermetia illucens*-IM or PBM to replace FM and VM. Test diets showed comparable growth performances to FM and VM. Microbial 16S rRNA analysis revealed that IM increased microbiota alpha diversity and led to a significant increase of chitin degraders *Actinomyces* and *Bacillus* genera. Analysis of feed microbiota revealed shared OTUs between IM feed and intestinal microbiota of IM fed fish supporting connectivity between food-chain microbiomes. IL-1 β , IL-10, TGF- β , COX-2 and TCR- β gene expression in midgut and head kidney, together with plasma LPS as biomarker of gut permeability,

revealed that the experimental diets were well tolerated and did not compromise gut barrier function or induce inflammation. Both IM and PBM singly or in combination could be considered as valid alternatives to VM and FM in the aquaculture practice.

P146

Erythrocyte membrane lipidome profile of heifers during the transition period: a preliminary study

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The analysis of red blood cells (RBC) membrane lipidome is a powerful tool to assess the quantity and quality of fatty acid composition and for the follow-up of the membrane remodeling under physiological and pathological conditions. In dairy cows, the transition period is marked by nutritional, metabolic, hormonal and immunological changes that have an impact on the incidence of infections and metabolic diseases. The aim of this study was to evaluate RBC membrane lipidome profiles in healthy heifers 30 days before calving (T0) and at 7 (T1) and 30 days (T2) post calving. RBC membranes were isolated from EDTA blood of 13 Friesian heifers and a cluster of 10 saturated [SFA (palmitic; stearic)], monounsaturated [MUFA (palmitoleic; oleic; vaccenic)] and polyunsaturated [PUFA (linoleic; dihomo-gamma-linolenic (DGLA); arachidonic; EPA; DHA)] fatty acids was quantitatively evaluated by Gas-Chromatography. Relevant lipid parameters [SFA/MUFA, SFA/PUFA, n6/n3, PUFA balance, Peroxidation (PI) and Unsaturation (UI) indexes] were calculated. We observed an increase in the biosynthesis of SFA with higher value of Palmitic acid ($p < .0001$) at T1 and Stearic acid at T2 ($p < .001$) compared to T0. The n6, PUFA, DGLA and arachidonic acids ($p < .0001$), decreased at T1 compared to T0 and DGLA decrease also at T2 compared to T1 ($p < .001$). EPA levels were decreased at T2 ($p < .0001$) while we register an increase in the n6/n3 ratio ($p < .001$) at the same time. Also, UI and PI were significantly decreased after calving ($p < .0001$). The increase in SFA could be due to an energetic role of SFA during post-partum period even if the increase in SFA should be avoided to the insulin resistance. The UI decrease at T1 ($p < .0001$) underlines a change of the membrane properties, with increased rigidity and reduced permeability. The level of DGLA decreased at T1 ($p < .001$) compared to T0 and was also lower at T2 compared to T1 ($p < .001$). This result could be due to a reduction of anti-inflammatory defenses with possible onset of inflammatory

diseases during the post-partum. Moreover, we observed a significant decrease in the n6/n3 ratio after calving, that could be considered as valid indicators to monitor and predict inflammatory conditions in cattle during this critical period. In conclusion, an early knowledge on lipid membrane changes allows personalized nutritional intervention in order to promote a healthy status reducing metabolic stress and promoting anti-inflammatory activity.

P147

Effects of the MTNR1A gene polymorphism and month of ram introduction on reproductive recovery in Sarda sheep

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Small ruminants in the Mediterranean latitudes show a marked reproductive seasonality which, hence determines the seasonality of production, resulting in problems for marketing of these products. The photoperiod is the factor mainly involved in the regulation of reproductive seasonality through the secretion of melatonin by the epiphysis. Melatonin is secreted during the hours of darkness and acts through its binding to specific receptors involved in regulating reproductive seasonality in sheep. In particular, in different sheep breeds, the polymorphism g.17355452C > T of the melatonin receptor 1A (MTNR1A) gene is associated with an early reproductive recovery in spring. The aim of this study was to highlight the influence of this polymorphism on the reproductive recovery of Sarda sheep after the ram introduction into the flock in the months of March, April, May and June. In a farm that raised about 1000 animals, we genotyped 600 ewes. Among the genotyped animals, 60 animals were selected for each genotype. The selected animals were 3–6 years old, and had a body condition score (BCS) between 2.0 and 4.0. The animals were divided into four groups (A, B, C and D) of 60 sheep each, based on age, BCS and genotype. In group A rams were introduced on March 1, in group B on April 1, in group C on May 1 and in group D on June 1. In all groups, the lambing and the number of lambs born from 150 to 220 days after the ram introduction were recorded. In all the groups, the genotypes C/C and C/T of the polymorphism in position g.17355452 showed the greatest fertility ($p < .01$) and the shortest distance between ram introduction to lambing ($p < .01$), compared with the T/T genotype. In addition, sheep in groups A and B, carrying C/C or T/C genotype, showed higher fertility than those in group C and D. Sheep in group A and B, carrying A/A genotype showed the lambing peak 10 days later than those in groups C and D. We concluded that the polymorphism in position g.17355452C > T influences