Book of Abstracts

of the 3rd Mountain Livestock Farming Systems Meeting of the European Federation of Animal Science

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Scientific programme

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Effects of grassland biodiversity on digestive process, milk composition, and microbiota of dairy cows

M. Musati[1,2], M. Coppa[3], C. Delbes[4], I. Verdier-Metz[4], M. Popova[1], V. Niderkorn[1], M. Bouchon[5], Y. Farizon[6], F. Enjalbert[6], M. Renna[7], C. Lussiana[3], A. Natalello[2], B. Martin[1], A. Ferlay[1]

[1] Université Clermont Auvergne INRAE, VetAgro Sup, UMR Herbivores, Route de Theix, 63122 Saint-Genès-Champanelle, France, [2] University of Catania, Dept. of Agriculture, Food and Environment, Via Santa Sofia 100, 95123 Catania, Italy, [3] University of Turin, Dept. Agricultural, Forest and Food Sciences, Largo Paolo Braccini 2, 10095 Grugliasco (TO), Italy, [4] Université Clermont Auvergne, INRAE, VetAgro Sup, UMR Fromage, 20 Côte de Reyne, 15000 Aurillac, France, [5] INRAE, Herbipôle, Laborie, 15190 Marcenat, France, [6] GenPhySE, Université de Toulouse, INRAE, ENVT, INPT, 24 Chem. de Borde Rouge, 31320 Auzeville-Tolosane, France, [7] University of Turin, Dept. Veterinary Sciences, Largo Paolo Braccini 2, 10095 Grugliasco (TO), Italy

The effects of pasture botanical biodiversity on rumen and faecal microbiota composition and milk fatty acids profile was studied in an in vivo and in vitro experiment carried out with 2 groups of 7 dairy cows. Cows were led for 4 weeks on 2 plots with high (HD) and low (LD) levels of plant biodiversity. The herbage from HD was more fibrous and had a higher total tannin content, but lower total fatty acids and C18:3 n-3 contents than LD. Samples of simulated bites, rumen fluid, faeces, and milk were collected at the end of week 4. Though species richness of bacterial and fungal communities were similar, their composition differed and discriminative species have been pointed out for each level of biodiversity. Total gas production and CH4 proportion during in vitro ruminal fermentation of HD herbage was lower than LD, probably because of the partial inhibition of bacterial activity by tannins. Remarkable was the comparable proportion of C18:3 n-3 in milk, despite the lower total fatty acids and C18:3 n-3 content of HD herbage. Plant metabolites could have partially inhibited the activity of ruminal bacteria responsible for lipid biohydrogenation.

Session 3 Theatre 5

A new look at the microbial diversity of indigenous ferments in Beaufort technology and their influence on the organoleptic qualities of cheeses

B. Polturat[1], C. Lecaude[1], V. Flammier[2], N. Bel[3], S. Chuzeville[4], A. Bertry[3]

[1] CERAQ, 40 Rue du terraillet, 73190 Saint-Baldoph, France, [2] UPB, 228 Chemin de Californie, 73200 Albertville, France, [3] ACTALIA, Unité produits laitiers, pôle technologie fromagère, 419 route des Champs Laitiers, 74800 Eteaux, France, [4] ACTALIA, Unité expertise analytique laitière-Cécalait, département microbiologie laitière, 419 route des Champs Laitiers, 74800 Eteaux, France

The starters used in Beaufort cheese production are derived from traditional microbial cultures. The preparation of these cultures can vary from one dairy plants to another, and can have an impact on their microbial composition. The aim of this trial was to gain a new, more complete picture of the diversity and richness of starters, and to determine whether certain taxon synergies could be linked to organoleptic qualities. To answer those questions, samples of milk, starters and cheeses were taken during 39 production runs in thirteen dairy plants. The samples's microbiota was studied by pasteurian analysis and 16S metabarcoding. This study revealed that 103 bacterial species were present in all the starters, and starters showed only 4 species in common. The starters, which contained an average of 29 bacterial species, could be categorized into six groups, taking into account minority species. Only one ferment group was specific to one dairy plants, while the other groups could be observed in three to five different dairy plants. Links could be established between starters' s group and the organoleptic qualities of the cheeses: the diversity of aromas and the bitterness of the cheeses were not the same according to the groups of starters used. A positive correlation was also detected between the Shannon diversity of the starters and the aromatic diversity of the cheeses.