Milk molecular species of triacylglycerols characterized by lipidomic approach in cows and goats fed diets supplemented with various lipid sources

Hélène Fougere, Carole Delavaud, Sylvain Emery, J. Bertrand-Michel, Laurence Bernard

Milk molecular species of triacylglycerols characterized by lipidomic approach in cows and goats fed diets supplemented with various lipid sources

H. Fougère[1], C. Delavaud[1], S. Emery[1], J. Bertrand-Michel[2], L. Bernard[1]
[1]Université d'Auvergne, INRA, Vetagro Sup, UMR12133 Herbivores, 63122 St-Genes-Champanelle, France; [2]Institut des Maladies Métaboliques et Cardiovasculaires (I2MC), Inserm/Université Paul Sabatier UMR1048, 1 Avenue Jean Poulhes F-31432 Toulouse

Lipid fraction is a major determinant of milk nutritional quality and efficiency of production that can be modulated by nutritional factors such as lipid supplementation.

In a comparative study between dairy cows and goats fed similar diets supplemented with various lipids, we characterized the milk composition regarding molecular species of triacylglycerols (TAG) by a lipidomic approach. This study was part of a trial aiming at characterizing animal performances and milk lipid responses to diets inducing either milk fat depression (MFD) or increase in milk fat secretion, with species-specific responses (Fougère *et al.*, 2018). The effects of diets containing no additional lipids (CTL) or supplemented with corn oil (5% dry matter intake (DMI)) and wheat starch (COS), marine algae powder (MAP) (1.5% DMI), or hydrogenated palm oil (HPO) (3% DMI), on milk fat content and composition were studied in cows and goats (n=12 per species). Animals of each species were conducted simultaneously in a replicated 4x4 Latin square design. Milk samples were collected over 2 consecutive milkings on d24 of each experimental period. Individual samples were pooled by period and diet (4 x 4 = 16 subsamples by species) and lipid extracted (Bligh & Dyer, 1959) before TAG determination by LC-HR/MS. Data were subjected to ANOVA using dedicated R software. Animal performances and milk FA composition were reported elsewhere (Fougère *et al.*, 2018); in cows, milk fat content was significantly lowered by COS (-45%) and MAP (-22%) and increased by HPO (+13%) compared with CTL, whereas in goats, only MAP decreased milk fat content (-15%) compared to CTL. Lipidomic analysis revealed 48 molecular species of TAG from TAG (18:0) to TAG (64:3) with differences among the 2 species: 1/irrespective of diets, 16 were more abundant in cows (TAG (48:0) to (64:3)) and 23 in goats (TAG (18:0) to (46:3)); 2/on COS, 28 were modulated in cows compared to CTL, but not in goats and 3/on MAP, 13 were modulated in cows and 8 in goats, compared to CTL. Principal component analysis (PCA) performed with milk TAG molecular species and individual FA strongly suggests that the main FA candidates for MFD (*trans*-10 18:1, *trans*-10,*cis*-12 CLA and *trans*-10,*trans*-12 CLA; Shingfield *et al*., 2010) are carried by specific TAG molecular species that differ between cows (TAG (52:3), (54:3), (54:4)) and goats (TAG (60:4)). These new data demonstrate the species specificities of molecular species of milk TAG in cows and goats and their nutritional regulation.

Fougère H, Delavaud C. and Bernard L. 2018. J. Dairy Sci. 101:8429-8445.

Bligh E.G and Dyer W.J. Can. J. 1959. Biochem. Physiol. Vol. 37.

Shingfield, K.J, Bernard L, Leroux C, and Chilliard Y. 2010. Animal 4(7):1140-1166.