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Effect of the dietary supplementation with sunflower oil and incremental levels of marine algae on the rumen bacterial community in dairy sheep

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In lactating ruminants, the dietary supplementation with lipids rich in linoleic acid, such as sunflower oil (SO), and long-chain polyunsaturated fatty acids (PUFA), such as marine algae (MA), has proved to increase the milk concentration of conjugated linoleic acid (CLA), which may exert benefits to human health. Milk fatty acid (FA) profile depends on ruminal FA biohydrogenation, the rumen microbial composition being therefore a key factor in the milk fat composition. In order to study the effect of the dietary supplementation with SO plus incremental levels of MA on the rumen bacterial community in dairy sheep, 25 lactating ewes were allocated to 5 treatments: non-lipid supplementation, or supplementation with 2.5% SO plus 0, 0.8, 1.6, or 2.4% of MA. After 28 days rumen fluid was sampled through a stomach tube and DNA was extracted and analysed by quantitative PCR (qPCR) and terminal restriction fragment length polymorphism (T-RFLP).

According to qPCR, the *Butyrivibrio* strains reported to produce vaccenic or stearic acid (VA- and SA-producing bacteria) were neither abundant (0.23 and 0.29%, respectively) nor significantly affected by treatments ($P>0.10$). However, according to T-RFLP results, MA supplementation altered the rumen bacterial composition, with increases ($P<0.05$) in the relative abundance over the total peak area of fragments compatible with *Quinella*-like microorganisms and of others that match uncultured bacteria of the family Lachnospiraceae (possibly related to biohydrogenation of long-chain PUFA), and with reductions ($P<0.05$) in Firmicutes compatible fragments. These changes suggest that yet uncultivated bacteria may play a key role in the biohydrogenation process of unsaturated FA.

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The composition and metabolic activity of the gut microbiota in young rats is highly impacted by dietary iron concentration

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Iron is a trace element necessary for most organisms including gut bacteria. Since iron deficiency and adequate supplementation is a global health concern, this study investigated the impact of iron deficiency and dietary iron supplementation on the gut microbiota in rats. Four groups of rats (control (n=3); iron depleted (n=8); depleted and repleted with 10 mg (n=8) or 20 mg (n=8) $FeSO_4$) received a diet differing only in iron content. Fecal samples were collected at baseline, after a depletion period of 24 days, after a repletion period of 14 days and at endpoint. Caecal water samples at endpoint were investigated on their microbial metabolites composition by HPLC. DNA of fecal samples was analyzed on the microbial diversity and composition with TGGE and real time PCR. The HPLC analysis revealed a sharp ($P<0.05$) decrease in butyrate and propionate in deficient rats compared to the control rats and to the 20 mg $FeSO_4$ subsequently repleted rats. The TGGE fingerprint analysis of 16S rDNA showed a massive loss of diversity following depletion. Investigation with real time PCR indicated an increase in number of copies of the Lactobacilli group and a massive decrease of the *Roseburia / E. rectale* group after depletion. Our investigation with rats showed the high impact of dietary iron on composition and metabolic activity of the gut microbiota. Iron deficiency seemed to induce major population changes leading especially to a decrease of butyrate-producing bacteria and their metabolite butyrate which is an important energy source for colonocytes and has anti-inflammatory effects.

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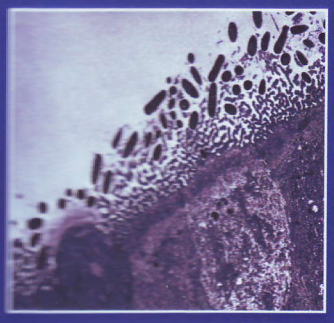

Gut Microbiology:
new insights into gut microbial ecosystems

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