Effects of two different high-fat diets on the gut microbiota of adult mice

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Introduction
Growing evidence supports the role of gut microbiota in the regulation of host energy homeostasis and its interaction with hyper-caloric diets to influence the development of metabolic disorders and obesity. However, little is known about how high-fat diets induce changes in the intestinal bacterial community and how this reshaped gut microbiota mediates the development of metabolic diseases. Recently, we reported that a soy oil-based high-fat diet can markedly affect cecal microbiota of weaning mice even over short periods of time (2). We suggested that the observed shifts of specific bacterial populations within the gut may represent an early consequence of increased dietary fat with potential implications for host disease. Here, we extend our previous research by investigating the effects of high-fat diets differing in their fatty acid composition on mouse physiology and gut ecology over a prolonged period of time.

Purpose
The aim of the present study was to characterize and compare alterations induced by two diets enriched with either soy oil (high in polyunsaturated fat) or coconut oil (high in saturated fat) with respect to gut microbiota and intestinal morphology, as well as growth, fat deposition and metabolic status of adult mice.

Methods
• Female C57BL/6 mice were fed either a low-fat, control diet (LFD, n=12), or a high-fat diet containing 30% soy oil (HFSD, n=12), or a high-fat diet containing 30% coconut oil (HFCD, n=12).
• Six mice from each group were sacrificed after 2 (W2) and 8 weeks (W8) of dietary exposure.
• Body weight and abdominal fat mass were measured.
• Total plasma cholesterol, triglycerides and haptoglobin were determined using commercial assays.
• Cecum tissues were subjected to histological examination (1).
• DNA was extracted from cecal content and used for PCR-DGGE analysis using universal 16S rRNA gene primers (2).
• Sequence analysis was performed on bands of interest for identification.
• DGGE results were checked by real-time quantitative PCR assays (3, this study).
• Volatile fatty acids (VFA) and lactate were determined by HPLC (4).
• Statistical analysis was performed using the PROC GLM of SAS version 9.2 software.

Results
HFSD and HFCD mice showed a higher daily weight gain both at W2 and W8, and an increased body fat storage at W8 as compared to LFD mice (Figure 1).

Plasma total cholesterol levels were higher in the HFSD and HFCD groups than LFD group at W2, but only in the HFCD group at W8 (Figure 2).

Conclusions
These results corroborate and extend our previous findings on the impact of dietary fat on the gut microbial ecosystem and the physiology of the host. Our findings suggest that high-fat diets affect the composition of the cecal microbiota of mice by modulating the relative abundances of individual species/phylotypes rather than total community structure. The effect of HFCD on lipid metabolism persisted through time whereas a prolonged administration of HFSD seemed to result in metabolic adaptation to fat feeding. The soy oil-based diet appeared to trigger the onset of cecum inflammation inducing tissue alterations which were not observed with the HFCD. Further investigation is needed to gain insight into the relationship between gut bacterial community shifts and metabolic and physiological disturbances in mice.

Literature cited

INRA-Rowett Symposium on Gut Microbiology. Gut microbiota: friend or foe?, 17-20 June 2012, Clermont-Ferrand, France