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Agaro-oligosaccharides prevent high-fat diet-induced gut dysbiosis in mice with regard to the correlation between gut microbiota and bile acid profile

(アガフィトースTMは高脂肪食によるマウスの腸内細菌叢や二次胆汁酸産生の悪化を抑制する)

Introduction:

Alterations in the composition of gut microbiota, known as dysbiosis, are increasingly recognized as a major risk factor for various diseases. Agarose is hydrolyzed to yield oligosaccharides, designated as agaro-oligosaccharides (AGOs) (AgaphytoseTM). In this study, we investigated the effect of AGOs on high-fat diet (HFD)-induced gut dysbiosis in mice, particularly in correlation between microbiota and bile acid profile.

Methods:

Mice were fed standard diet (SD) with 4.6% of calories from fat, HFD with 32% of calories from fat for 8 weeks. AGOs was supplemented in the drinking water as a concentration of 3.0% (w/w). To analyze the fecal microbiota profiles, we performed terminal restriction fragment length polymorphism (T-RFLP) approach. The profiles of cecal organic acids and serum bile acids were determined using HPLC and LC-MS/MS systems, respectively.

Results:

T-RFLP analyses showed that the order Lactobacillales was decreased in HFD-treated mice. However, the HFD-induced down-regulation of the order Lactobacillales was cancelled by AGOs supplementation, thereby increasing in the cecal concentration of lactic acid. Meanwhile, Clostridium subcluster XIVa was increased in HFD-treated mice, and the increase was suppressed in AGOs supplementation. The data from serum bile acid profile showed that the level of deoxycholic acid (DCA), a carcinogenic secondary bile acid produced by gut bacteria such as strains belonging to Clostridium subcluster XIVa, was increased in HFD-treated mice. The up-regulation of DCA level generated by HFD treatment was suppressed by AGOs supplementation.

Conclusion: With regard to the correlation between gut microbiota and bile acid profile, AGOs supplementation prevents HFD-induced gut dysbiosis.