

Alfalfa Saponins Prevents High Fat Diet Induced Lipid Metabolism Disorder by Regulating the Gut Microbiota - Bile Acid -Liver Axis In Rabbit

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In animal husbandry production, the occurrence of animal fatty liver syndrome (LMD) is becoming more common. The occurrence of LMD poses a major threat to the development of animal husbandry. This study aims to provide a theoretical basis for the rational use of Alfalfa Saponins (AS) to prevent LMD in rabbits caused by a high-fat diet through the activity and mechanism of AS based on gut microbiota bile acid liver metabolic axis. Five treatment groups were set up in this study: CON, HFD, HFD_AS1, HFD_AS2, and HFD_AS3. At the end of the experiment, for growth performance: Compared with the CON group, the average body weight and average daily gain of the HFD, HFD_AS1, HFD_AS2 and HFD_AS3 groups were significantly increased ($P < 0.05$), compared with the HFD group, the average body weight and average daily gain of the HFD_AS2 and HFD_AS3 groups were significantly lower ($P < 0.05$); for the pathological sections of the liver and abdominal aorta, compared with the HFD group, it was found that the HFD_AS2 and HFD_AS3 groups were significantly improved ($P < 0.05$); for lipid metabolism in the liver: Compared with the HFD group, the PPAR- α mRNA expression in the HFD_AS2 and HFD_AS3 groups were significantly increased ($P < 0.05$), LXR- α , SREBP-1 mRNA expression were significantly decreased ($P < 0.05$), but still did not reach the level of CON group. Further quantitative determination of bile acid content in ileal contents using targeted metabolomics. In ileum, the levels of LCA_3S in HDF group were significantly higher than those in CON group ($P < 0.05$). In HDF-AS2 group, the levels of UDCA, TCDC, GUDCA, and isoLCA were significantly increased ($P < 0.05$). Compared with HDF group, the levels of UDCA, TCDC, and GUDCA in HDF-AS2 group were significantly increased ($P < 0.05$). The expression of *ASBT*, *CYP7A1*, *CYP8B1*, and *CYP2A1* mRNA was significantly increased in HDF and HFD_AS2 groups compared with CON group ($P < 0.05$). Compared with HDF group, the expression of FXR was decreased significantly in HDF_AS2 group, while the expressions of *ASBT* and *BSEP* mRNA were increased significantly ($P < 0.05$). It is suggested that AS can exert its biological activity of preventing LMD through gut flora bile acid liver metabolic axis, and its specific mechanism still needs to be further studied. In conclusion, an appropriate amount of AS can prevent LMD by regulating the gut microbiota bile acid liver metabolic axis.

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