

Abstract

Inflammatory bowel disease is a serious condition with an incomplete etiology and pathogenesis. In this thesis, a mouse model of sodium dextran sulfate-induced inflammation was used to study different changes in the metabolism of germ-free and conventionally raised mice due to the development of the inflammatory process. NMR metabolomics of fecal, urine and serum samples, combined with uni- and multivariate statistical analysis, were used to characterize the changes. It was shown that the metabolic signature differs between germ-free and conventional mice. In germ-free mice, significant amounts of carbohydrates were found in feces. Their levels decreased during inflammation as they were excreted in urine. In contrast to conventional mice, germ-free mice also excreted large amounts of amino acids in feces during the developing inflammation.

Disorders of sugar and protein metabolism found in germ-free mice indicate severe malnutrition caused by inflammation. The results show that the presence of a microbiome represents a protective mechanism against significant disruption in the body.

A stability study of fecal extracts of healthy conventionally colonized mice confirmed that none of the identified and quantified metabolites showed significant systemic changes in several consecutively collected samples in one week or several samples collected from the same mouse in one day. Thus, the fecal metabolome of the control group can be considered sufficiently stable and the differences detected in the thesis can be attributed to the influence of inflammation and / or the absence of the microbiome.

Keywords: DSS-induced inflammation, metabolomics, microbiome, nuclear magnetic resonance spectroscopy, inflammatory bowel disease