

## Popular science summary

Several epidemiological studies have shown that the development of metabolic diseases such as obesity, type II diabetes and insulin resistance can be related to lifestyle factors such as low physical activity and an unhealthy diet with low amounts of dietary fibre and high amounts of saturated fat. Dietary fibre, quantitatively the most important substrate for the colon microbiota, can change and shape the microbiota composition, as shown by the microbial metabolites (short-chain fatty acids) formed from these prebiotic components in the diet.

Bile acids (BAs), mostly known to play a role in bile formation and fat absorption, can also act as signalling molecules and are involved in several metabolic activities such as glucose regulation and lipid and energy metabolism. It is often claimed that the BA profile is a measure of the body's physiological balance. The BA profile is very dependent on the microbiota composition. However, the microbiota and BAs have a complex mutual relation, and the BAs may also alter gut microbiota composition, which in turn is dependent on the diet consumed. Primary BAs are synthesized from cholesterol in the liver, stored in gallbladder to be secreted into the systemic circulation. In the fasting state, the extraction rate of BAs is constant but after a meal a significant amount of BA is secreted into the small intestine to facilitate fat digestion.

A number of interesting physiological effects have been associated with BAs. Some BAs, referred to as beneficial BAs, have been reported to prevent diet-induced obesity and insulin resistance as well as being capable of reducing weight gain. Many of these BAs have been widely used as therapeutic drugs to treat liver dysfunction, type II diabetes, cholesterol gallstones and even neurological diseases. However, other types of BAs have been linked to metabolic diseases such as liver disease, intestinal inflammation and colonic cancers. Due to the important health effects of BAs in the body and to their close connection to microbiota composition, it is important to study how diets can modulate the composition of BAs in blood and colon and relate these changes to alterations in metabolic markers.

In this thesis, new extraction and analytical techniques for analyses of BAs in samples from caecum, faeces and blood were developed. Prebiotic dietary fibre, i.e. highly degraded by the colon microbiota, was included in the diets of rats and mice. Examples of products included were pectin, guar gum and a mixture of the two, products with specific chemical properties (guar gum with different viscosities and pectin with different degrees of methoxylation) and barley varieties containing different contents of  $\beta$ -glucan, all for studies of BAs in the caecum of rats. In the mouse study, the concentration of serum BAs was investigated after consumption of whole lingonberries and two lingonberry fractions. The last study was on humans, where postprandial serum concentration of BAs was measured after intake of

turmeric drink, a product containing polyphenols and other components with prebiotic potential, prior to a breakfast meal. The effects of fat content in the diet was also evaluated. An evaluation was also made of BAs in caecum of rats and serum samples from mice and how the BAs related to gut microbiota composition.

The compositions of BAs in caecum and blood were very much dependent on the types of diet and dietary fibre. To have an effect, the dietary fibre had to be highly degraded by the microbiota, i.e. be prebiotic. The amounts of beneficial BAs generally increased, while the amounts of non-beneficial/unhealthy BAs decreased along with dietary fibre in the diet. In this respect, guar gum and the mixture of guar gum and pectin were the most effective diets for altering BA compositions. Among guar gums with different viscosities, the one of medium viscosity was the most effective for changing BA composition to a healthier profile. Among the different barley varieties, the variety with highest  $\beta$ -glucan content showed the highest amounts of beneficial BAs, at least in the low-fat setting, while in the high-fat groups, the highest amounts could be seen in the diet with highest amounts of arabinoxylan. Also, the non-beneficial BAs were most affected, i.e. were reduced by the diet containing the highest amounts of arabinoxylan. In blood, the diet containing whole lingonberries, which have high amounts of dietary fibre as well as polyphenols, gave a healthier BA profile in mice with high amounts of beneficial BAs and low amounts of non-beneficial BAs. The other fractions of lingonberries, especially the soluble fraction, had also positive effects. The serum BA profile in human subjects was also improved after intake of a drink containing turmeric prior to the breakfast meal, proving the beneficial health effects of this spice that is particularly rich in polyphenolic compounds. When the fat content increased in the diets, the total amounts of BAs increased supporting the main role of BAs to digest fat.

Regarding the gut microbiota composition, the consumption of dietary fibre increased the abundance of *Bifidobacterium*, *Lactobacillus* and *Prevotella*, which are known for their probiotic effects, and these bacteria were also connected to beneficial BAs. However, diets with a low dietary fibre content and high amounts of saturated fat showed a higher abundance of bacteria often linked to diseases such as obesity, colon cancer and Alzheimer's disease.

In conclusion, consumption of dietary fibre changed the BA profile in caecum of rats and serum of mice and humans to a healthier composition by altering the gut microbiota composition. The fat level of the diets also affected the BA composition. The molecular properties of the dietary fibre were also important to modulate caecal BA formation. Results from this thesis can be expected to be used in the development of food products for improving metabolic health and decreasing disorders associated with the liver.