The gastrointestinal microbiome - Intestinal check

With modern high-throughput molecular genetic sequencing, the entire microbial intestinal flora is revealed from a stabilised stool sample. A healthy colonization can be differentiated from a dysbiotic one. Publications are constantly finding new connections between the gastrointestinal microbiome and clinical pictures. In the context of a comprehensive investigation of inflammatory bowel disease, food intolerance, diabetes mellitus, autoimmune diseases and intestinal dysbiosis, the additional determination of biochemical parameters may be useful.

General bacteriology distinguishes between gram-positive and gram-negative as well as aerobic and anaerobic bacteria. The cultural method presupposes that the sampling and the transport take place optimally, so that living bacteria germs can grow in the dispatch laboratory. Despite the use of special transport media, this is only possible to a limited extent with anaerobic bacteria. Many anaerobes are therefore not detected or have even never been described. Molecular genetic methods reveal the abundance and diversity of these bacteria and their importance is becoming increasingly clear.

The intestinal flora: *Bacteroidetes* & *Firmicutes*

Most anaerobic bacteria of a stool sample can be assigned to ***Bacteroidetes*** and ***Firmicutes***. These large families are significantly involved in the digestive process. In an oxygen-free environment this takes place through fermentation. Secondary degradation products are formed, which reach the cells of the colon as food and messenger substances. The ***short-chain fatty acid butyrate***, which is supposed to counteract immunomodulating latent inflammations, is considered essential. The bacterium ***Faecalibacterium prausnitzii*** is particularly highlighted as a producer of butyrate. In addition, acetate, L-lactate, propionate, succinate and other short-chain fatty acids are produced and converted. These are used, for example, as food for other bacterial species. A deficiency of a fatty acid can trigger a negative trend, resulting in the loss of important bacterial species.

Lactic acid bacteria and the pH value

The colon environment should be slightly acidic for an optimal fermentation process. Ideal pH values are between 6 and 7. Although digestive gases (e.g. H_2, CO_2) are produced, they do not cause bloating. Lactic acid bacteria can make a decisive contribution to this. Typically, neither lactobacilli nor enterococci or other lactic acid bacteria colonize the large intestine in large numbers, but they have a very positive transient effect. This is why, being L-lactate producers, they are often used as ***probiotics*** .

Diversity, enterotype and dysbiosis

The intestinal flora is based on the principle that "the more types of bacteria, the better". These should come from the large families *Bacteroidetes* and *Firmicutes* as well as the Actinobacteria. To monitor this diversity, the ***Shannon index*** and the ***Firmicutes to Bacteroidetes* ratio** have prevailed. These two indices provide a good overview of the health status of the intestinal flora. The diversity should be "diverse" or even "very diverse" and *Firmicutes* and *Bacteroidetes* must be in balance. The overgrowth of one or the other large family can be evaluated as dysbiosis (pathological composition). Dysbiosis is also described as the loss of obligate anaerobic bacteria (e.g. *Bacteroides*, *Ruminococcus*) in favour of facultatively anaerobic bacteria, especially *proteobacteria*. The consequence is the reduced metabolic performance of the intestinal flora (= missing short-chain fatty acids). If the energy carriers for the intestinal cells are missing, the mucous layer barrier is broken down and the intestinal wall is attacked (= leaky gut). The cells experience oxidative stress and thus intestinal inflammation is favoured. Without a healthy amount of bacteria in the area of the mucus barrier, the immune system will also suffer. ***Akkermansia muciniphila*** is an essential bacterium for the mucus layer household, as it breaks down mucin and regulates the tight junctions of the intestinal wall.

In a healthy intestine, a digestive machinery, referred to as enterotype, is formed. The strictly anaerobic genera Bacteroides and Prevotella vie for access to complex, long-chain carbohydrates from the large Bacteroidetes family. The first studies describing the enterotypes assumed that "Western" food typically formed ***enterotype 1 dominated by Bacteroides*** and the ***more "original" Prevotella dominated enterotype 2*** by frequent consumption of raw food. However, it is likely that the interplay of genes with a person's dietary behaviour is decisive.

Intestinal microbiome and chronic diseases

Studies on the mouse model and with patient cohorts have shown that in overweight and diabetes mellitus type 2, in particular bacterial species of *Bacteroidetes*

are lost. A low bacterial diversity was clearly associated with overweight, low grade inflammation and metabolic derailment. Conversely, the results also indicate that a (very) diverse intestinal flora can be regarded as an indicator of metabolic homeostasis and possibly even as a protective factor against metabolic derailment.

Inflammatory intestinal diseases (IBD) are also associated with intestinal microbiome dysbiosis. The following mechanisms play a role in this context: the distribution of the beneficial intestinal bacteria is out of balance (cf. *Firmicutes* to *Bacteroidetes* ratio), potentially pathogenic bacterial species settle (γ-Proteobacteria: especially *Enterobacteriaceae* *Citrobacter*, *Enterobacter, Escherichia, Klebsiella, Morganella*) and the loss of bacteria (especially *Firmicutes* species), which produce short-chain fatty acids, leads to a disturbed immune system regulation. In the context of a comprehensive investigation of inflammatory bowel disease, food intolerance, diabetes mellitus, autoimmune diseases and intestinal dysbiosis, the additional determination of biochemical parameters may be useful: increased zonulin levels may correlate with a disturbed intestinal barrier and increased intestinal permeability (leaky gut), the calprotectin indicates inflammatory processes , the pancreatic elastase is decreased in the case of pancreatic insufficiency.

Requirement profile: Profile 7588 Intestinal check with microbiome

Molecular genetic microbiome analysis by sequencing:
Aerobic and anaerobic microorganisms (putrefactive and acidifying flora, fatty acid producers, butyrate, lactic acid and equole formers), biodiversity index, classification of the enterotype, ratio Firmicutes/Bacteroidetes

Cultural analysis: yeast-like and mold fungi

Biochemical parameters: calprotectin, zonulin, pancreatic elastase, pH

Material: Stool set for microbiome analysis M900567 (stool nativ and stool in DNA/RNA stabilization solution)

Price: CHF 281.10 (CHF 100.00 not covered by health insurance)

References:

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- MIKROBIOM Wissensstand und Perspektiven. Stallmach A. und Vehreschild M. J. G. T. (Hrsg.). Walter de Gruyter GmbH, Berlin/Boston. 2016.
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Further literature recommendations are available on request in the laboratory.