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DAkkS Deutsche Akkreditierungsstelle D-ML-13188-01-00

External ID 101299915900

Name	**Angelov**	Date of Birth	**05.01.2011**	Order ID	**13580425**
First Name	**Alexandar**	Sex	Male	Order Date	11.04.2024
Sampling Date	09.04.2024 11:00	Validation by	Dr. med. univ. Vilmos Fux	Findings Status	**Final Report**
Sample Material	FE	Validation Date	22.04.2024	Findings Date	22.04.2024

Test	Result	Unit	Standard Range	Previous Result (Date/Material/Method)
Stool Diagnostics				
Molekulargenetische Mikrobiomanalyse Maxi NEU				
Molecular genetic microbiome analysis 3.0				
Stool Properties				
Colour	brown			FE NA) VISU
Consistency	mushy			FE NA) VISU
pH	6,0		5,8 - 6,5	FE NA) TESTS
Biodiversity				
Diversity	**3,95**		> 5,5	FE NA) MGSEQ

The bacterial diversity in the intestinal tract may vary considerably from person to person. Antibiotic therapies, infections, increasing age, unbalanced diets or smoking are causes of declining diversity.

Grad **1**

Enterotype				
Enterotyp	1=2			FE NA) MGSEQ

Human intestinal microbiomes can be differentiated into three Enterotypes. Enterotypes are defined by dominant bacterial clusters with distinct metabolic properties.

Enterotyp

Dysbiosis index				

The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.

FE NA) RECHN

0 5 10 15 20 25 30

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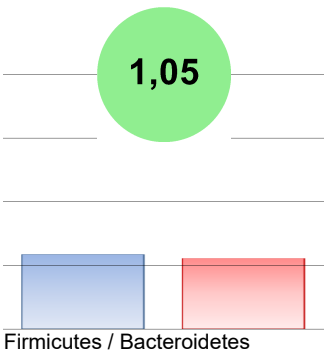
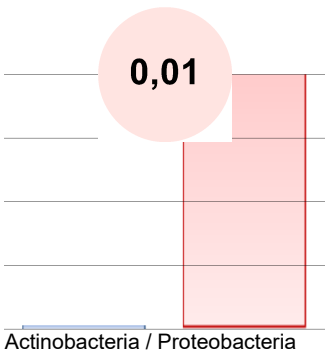
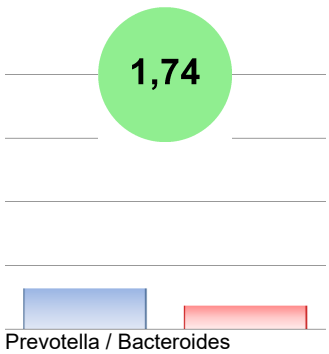
Ratio



Firmicutes / Bacteroidetes
Standard Range: < 3,0



Actinobacteria / Proteobacteria
Standard Range: > 1,0



Prevotella / Bacteroides
Standard Range: > 0,1

FE=stool

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Test	Result	Unit	Standard Range	Previous Result
Phyla				
Actinobacteria	0,3	%	1,5 - 7	FE NA) MGSEQ
Bacteroidetes	27,8	%	20 - 45	FE NA) MGSEQ
Firmicutes	29,3	%	50 - 75	FE NA) MGSEQ
Fusobacteria	0,0	%	0,0 - 1,0	FE NA) MGSEQ
Proteobacteria	42,5	%	1,0 - 3,5	FE NA) MGSEQ
Verrucomicrobia	0,0	%	1,5 - 5,0	FE NA) MGSEQ
Other	0,1	%		FE NA) MGSEQ
Metabolome (functional groups)				
Secondary bile acids	-27,2	%		
TMA / TMAO	72,5	%		
Indoxyl sulfate	-50,0	%		
Phenols	1112,1	%		
Ammonia	26,8	%		
Histamine	-50,0	%		
Equol	15,0	%		
Beta glucuronidases	1947,6	%		
Bacteria Phyla - most important genera and species				
Actinobacteria				
Bifidobacterium	6,2 x 10^8	CFU/g faeces	> 1,0 x 10^10	FE NA) MGSEQ
Bacteroidetes				
Bacteroides	9,2 x 10^10	CFU/g faeces	> 5,0 x10^10	FE NA) MGSEQ
Prevotella	1,6 x 10^11	CFU/g faeces	> 1,0 x 10^10	FE NA) MGSEQ
Prevotella copri	16	%		FE NA) MGSEQ
Firmicutes				
Butyrate producing bacteria				
Total bacteria count	1,3 x 10^11	CFU/g faeces	> 2,4 x 10^11	FE NA) MGSEQ
Faecalibacterium prausnitzii	1,2 x 10^11	CFU/g faeces	>1,0 x10^11	FE NA) MGSEQ
Eubacterium rectale	3,8 x 10^9	CFU/g faeces	> 2,0 x 10^10	FE NA) MGSEQ
Eubacterium hallii	6,2 x 10^8	CFU/g faeces	> 1,5 x 10^10	FE NA) MGSEQ
Roseburia spp.	4,0 x 10^9	CFU/g faeces	> 3,0 x10^10	FE NA) MGSEQ
Ruminococcus spp.	1,9 x 10^9	CFU/g faeces	> 5,0 x 10^10	FE NA) MGSEQ
Coprococcus spp.	1,9 x 10^9	CFU/g faeces	> 5,0 x 10^10	FE NA) MGSEQ
Butyrivibrio spp.	2,4 x 10^9	CFU/g faeces	>1,5 x 10^10	FE NA) MGSEQ
Clostridia				
Clostridia total bacteria count	2,1 x 10^9	CFU/g faeces	< 4,0 x 10^9	FE NA) MGSEQ
Clostridia Cluster I	1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9	FE NA) MGSEQ
Clostridium histolyticum	< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9	FE NA) MGSEQ
Clostridium perfringens	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8	FE NA) MGSEQ
Clostridium sporogenes	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^8	FE NA) MGSEQ
Other Firmicutes				
Christensenellaceae	1,5 x 10^8	CFU/g faeces	> 5,0 x 10^9	FE NA) MGSEQ
Dialister spp.	< 1,0 x 10^5	CFU/g faeces	< 4,0 x 10^10	FE NA) MGSEQ
Cl. butyricum	< 1,0 x 10^5	CFU/g faeces	> 1,0 x 10^8	FE NA) MGSEQ

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Test	Result	Unit	Standard Range	Previous Result
Fusobacteria				
Fusobacterium	2,6 x 10^7	CFU/g faeces	< 1,0 x 10^7	FE NA) MGSEQ
Verrucomicrobia				
Akkermansia muciniphila	1,0 x 10^7	CFU/g faeces	> 5,0 x 10^9	FE NA) MGSEQ
Proteobacteria				
Pathogenic or potentially pathogenic bacteria				
Haemophilus spp.	2,2 x 10^8	CFU/g faeces	< 5,0 x 10^8	FE NA) MGSEQ
Acinetobacter spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6	FE NA) MGSEQ
Proteus spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6	FE NA) MGSEQ
Klebsiella spp.	1,5 x 10^9	CFU/g faeces	< 1,0 x 10^7	FE NA) MGSEQ
Enterobacter spp.	6,6 x 10^6	CFU/g faeces	< 1,0 x 10^6	FE NA) MGSEQ
Serratia spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^7	FE NA) MGSEQ
Hafnia spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6	FE NA) MGSEQ
Morganella spp.	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^6	FE NA) MGSEQ
Citrobacter spp.	4,2 x 10^8	CFU/g faeces	< 5,0 x 10^8	FE NA) MGSEQ
Pseudomonas spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^7	FE NA) MGSEQ
Providencia spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^7	FE NA) MGSEQ
H2S production				
Sulphate reducing bacteria	2,1 x 10^9	CFU/g faeces	< 2,5 x 10^9	FE NA) MGSEQ
Desulfovibrio piger	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^9	FE NA) MGSEQ
Desulfomonas pigra	< 1,0 x 10^5	CFU/g faeces	< 1,0 x 10^9	FE NA) MGSEQ
Bilophila wadsworthii	< 1,0 x 10^5	CFU/g faeces	< 2,0 x 10^9	FE NA) MGSEQ
Oxalate degrading bacteria				
Oxalobacter formigenes	5,3 x 10^8	CFU/g faeces	> 1,0 x 10^8	FE NA) MGSEQ
Immunogenicity / Mucus production				
Immunogenically effective bacteria				
Escherichia coli	3,5 x 10^9	CFU/g faeces	10^6 - 10^7	FE NA) MGSEQ
Enterococcus spp.	1,32 x 10^6	CFU/g faeces	10^6 - 10^7	FE NA) MGSEQ
Lactobacillus spp.	4,4 x 10^7	CFU/g faeces	10^5 - 10^7	FE NA) MGSEQ
Mucin production / Mucosal barrier				
Akkermansia muciniphila	1,0 x 10^7	CFU/g faeces	> 5,0 x 10^9	FE NA) MGSEQ
Faecalibacterium prausnitzii	1,2 x 10^11	CFU/g faeces	>1,0 x10^11	FE NA) MGSEQ
Archaea				
Methanogens				
Methanobrevibacter spp.	< 1,0 x 10^5	CFU/g faeces	< 5,0 x 10^8	FE NA) MGSEQ

ATTENTION: The new OmicSnap tube and the matrix enable even more effective sample disruption, especially with gram-positive bacteria. This results in slight shifts in the standard ranges. We ask you to take this into account.

Mycobiome: relevant yeasts				
Candida albicans (CA)	<1,0 x 10^3	CFU/g faeces	<1,0 x 10^3	FE NA) QPCR
Candida krusei (CK)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	FE NA) QPCR
Candida glabrata (CG)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	FE NA) QPCR
Candida dubliniensis (CD)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	FE NA) QPCR
Candida parapsilosis (CP)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	FE NA) QPCR
Candida tropicalis (CTp)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3	FE NA) QPCR

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Candida lusitaniae (CL)	<1,0 x 10^3	CFU/g faeces	< 1,0 x 10^3		FE NA) QPCR
Parasites					
Pathobionts					
Blastocystis hominis	negative		negative		FE A) MOLEK
Dientamoeba fragilis	negative		negative		FE A) MOLEK
Pathogenic intestinal protozoa					
Giardia lamblia	negative		negative		FE A) MOLEK
Entamoeba histolytica	negative		negative		FE A) MOLEK
Cryptosporidium species	negative		negative		FE A) MOLEK
Cyclospora cayetanensis	negative		negative		FE A) MOLEK

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Overview - Results and Therapy Options

Dysbiose-Index 34

pH		
Enterotype		
Biodiversitiy	↓	balanced diets, do without non-essential antibiosis
Ratio Firmicutes/Bacteroidetes		
Butyrate producing bacteria	↓	prebiotics on the basis of resistant starch* or scFOS/scGOS*
Mucus production	↓	prebiotics (scFOS/scGOS)*
Mucosa integrity		
Milieu stabilising bacteria	↓	milieu stabilizing probiotics*, prebiotics (scFOS/scGOS)*
Immunogenic bacteria	↑	immunogenic effective probiotics*
Clostridia - total bacteria count		
Clostridia cluster I		
Fusobacteria	↑	
H2S producing bacteria (SRB)		
Potentially pathogenic bacteria	↑	immunogenic effective / toxin inhibiting probiotics*
Candida (facultive pathogenic)		
Oxalate degrading bacteria		

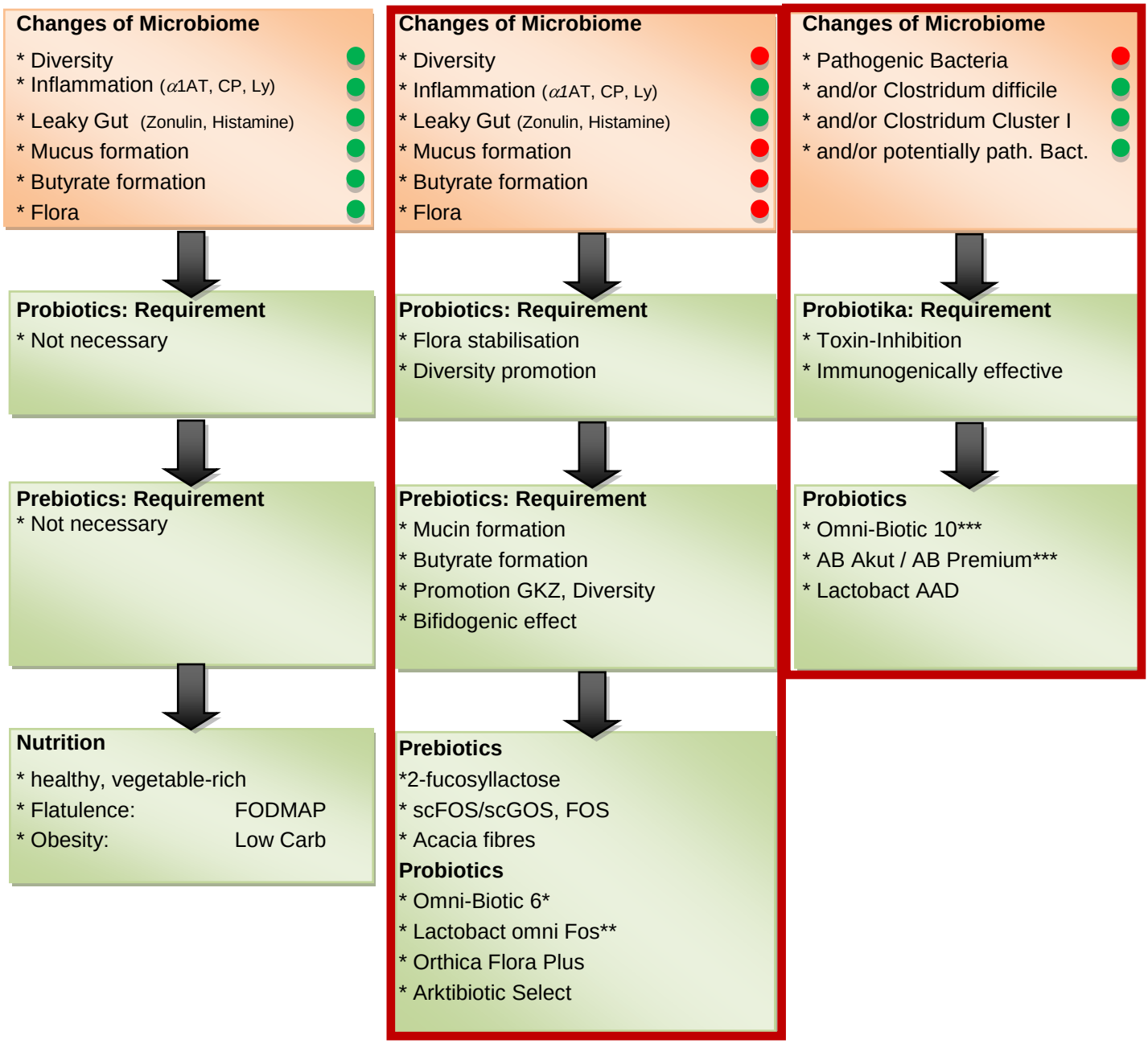
Metabolome (functional groups)

Secondary bile acids		
TMA / TMAO	↑	
Beta glucuronidases	↑	
Indoxyl sulfate		
Phenols	↑	
Ammonia	↑	
Histamine		

13580425	**Alexandar**	**Angelov**	**05.01.2011**

Equol

Therapy options with prebiotics and probiotics in overview (13580425)



* age related: Omni-Biotic Active

*** in combination with other probiotics

** age adapted: Lactobact 60plus

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Introduction

The **intestinal microbiome** (entirety of all bacteria living in the intestinal tract) has considerable influence on health or illness of humans. It modulates the immune defence, supplies the organism with vitamins (vitamin B1, B2, B6, B12, and K), participates in the digestion of food components, supplies intestinal epithelia with energy via developing short-chain fatty acids and stimulates intestinal peristalsis. The microbiome also plays an important role in the scope of xenobiotic detoxification. Shifts within the microbiome are causally relevant factors for diseases like adiposity, non-alcoholic fatty liver disease, diabetes, coronary heart disease or cancer. After the composition of the human intestinal microbiome was studied in more detail, alterations can be detected and counteracted with well-aimed measures.

The microbiome analysis shows a uncommon unilateral distribution of the bacterial phyla. This may indicate an impairment of the intestinal microbiome e. g. attributed to drug therapies (antibiotics, cortisone, chemotherapy, etc.), inflammatory bowel diseases (Crohn's disease, Ulcerative colitis) or postoperative conditions.

Result Evaluation
With the help of the **molecular-genetic stool analysis,** the intestinal microbiome was analysed in order to assess the composition and to determine possible shifts. The evaluation yielded the following **results**:

Evaluation of Stool Consistency, Color and pH-Value

General viewing of the stool sample showed **mushy consistency**. Healthy stool should be mushy and formed. Liquid or slurry stool indicates accelerated, doughy or solid stool samples delayed intestinal passage.

The color of the analysed stool sample was brown. The **pH-value** was **within normal range** at 6.

Evaluation of the Intestinal Diversity

More important than individual bacteria species or types is the interaction of the bacteria present in the microbiome. Manifold tasks of the intestinal flora require adequate **diversity**. The intestinal diversity of humans may vary considerably.

In the microbiome of healthy people one finds **300 to 500 bacteria species**, in sick persons there are often a lot less. Causes for reduced diversity are manifold. They are for example repeated **antibiotic therapies, infections,** increasing **age, unbalanced diet** or **smoking**.

Research revealed that numerous diseases come along with reduced diversity and thus presumably promote disease manifestation. Very often reduced diversity is found in patients suffering from **adiposity, fatty liver** (NAF), **diabetes type 2, Alzheimer disease, chronic inflammatory bowel disease, intestinal cancer** or **irritable colon syndrome**. Due to decreasing diversity the intestinal microbiome no longer grants adequate protection against endogenic infections. Obese patients with reduced diversity tend to gain more weight, respond worse to diets and there are often already indications of fat metabolism disorders or insulin resistance. In patients suffering from chronic inflammatory bowel disease (CIBD) reduced diversity promotes recurrence and chronicity. Research data are also available for the irritable bowel syndrome, the manifestation of which is promoted by reduced diversity.

Results

The **diversity** analysis indicated **reduced biodiversity**.

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Determination of the Enterotype

Recent research showed that the human microbiome can be assigned to **three main groups-** so-called enterotypes. Intestinal bacteria develop – depending on the enterotype – stable, clearly different clusters with typical metabolic properties (9). **Enterotype 1** is characterized by high **bacteroides counts** and **enterotype 2** by strong **Prevotella** population. **Enterotype 3** is only found rarely – in hardly more than 5 % of the analysis. This type shows strong **Ruminococcus** flora.

The described enterotypes show significantly differing **metabolic performance.** The bacteroides dominated flora (enterotype 1) is optimally adjusted to the utilisation of **fat, fatty acids, protein and amino acids**. **Carbohydrates**, however, are metabolized significantly worse than by Prevotella dominated flora (enterotype 2), which in turn cannot metabolize fat and protein adequately.

The enterotypes also influence the absorption of minerals like **sodium, potassium, calcium** (11) or **iron.** Enterotypes are independent of sex or age and remain stable for years. Via **long-term change of diet** and taking **prebiotics** they can be influenced (12, 13 and positively effects human sustenance and health.

Result

The microbiome analysis showed **no clear assignment** to one of the three enterotypes. There are two almost equally strong populations of **bacteroides** and the bacteria species assigned to enterotype 2 and the main bacteria species **Prevotella**. The present distribution presumably indicates that Alexandar keeps a **balanced mix diet** with comparably high share of vegetables and fruits.

Determination of relevant ratios

Firmicutes-Bacteroidetes ratio

Patients suffering from **irritable bowel syndrome** or **obesity** often show a high share of Firmicutes.

Obesity increases the risk of diseases like e.g. diabetes, coronary heart disease and cancer. It influences life expectancy and quality of life. In studies, the influence of the microbiome on the development of overweight was evaluated. **Firmicutes** have been shown to be capable of fermenting **complex, indigestible carbohydrates** to produce short-chain fatty acids (SCFA) which are absorbed through the intestinal mucosa and serve as additional energy sourced to the host (19, 20). Due to the fermentation of carbohydrates by firmicutes **10 – 12 %** more **energy** is available (21).

Bacteroidetes are not able to utilize complex carbohydrates. If firmicutes dominate bacteroides in the microbiome one speaks of an increased **firmicutes-bacteroidetes-ratio** which may promote gaining weight.

In case of patients suffering from irritable colon syndrome increased firmicutes-bacteroidetes-ratios often come along with meteorism or flatulence.

Result

The microbiome analysis shows a balanced ratio of Firmicutes to Bacteroidetes. The Firmicutes-Bacteroidetes ratio is normal.

Actinobacteria-Proteobacteria ratio

Actinobacteria and Proteobacteria make up around 5 – 10 % of the total intestinal microbiota. The proportion of Proteobacteria should not exceed 5 % in healthy adults. Numerous bacterial species from this phylum have **facultative pathogenic properties** and produce metabolites such as histamine, indoles, phenols, TMA and hydrogen sulfide, which are directly or indirectly harmful to the intestinal mucosa or other organs.

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Decreased Actinobacteria-Proteobacteria ratios have been demonstrated in numerous intestinal and extraintestinal diseases, most of which have an **inflammatory component**. For example, a greater proportion of Proteobacteria was found in Crohn's disease patients with a severe course than a mild course.
An decreased ratio can also occur as a result of antibiotic therapies and intestinal symptoms such as severe flatulence and constipation can be increasingly evident.

Result

The microbiome analysis shows a **clear predominance** of Proteobacteria over Actinobacteria. The **Actinobacteria-Proteobacteria ratio** is **decreased**.

Prevotella-Bacteroides ratio

Prevotella and Bacteroides are the two most prevalent genera of bacteria in the intestine. Their share in the microbiome is the basis for the assignment to the enterotypes 1 (Bacteroides) and 2 (Prevotella). Furthermore the Prevotella-Bacteroides ratio is associated with development of metabolic disease and weight changes.

Result

The microbiome analysis shows a balanced ratio of Prevotella to Bacteroides. The **Prevotella-Bacteroides ratio** is **normal**.

Frequency Scale of the Most Important Bacteria Phyla

The colon is populated by bacteria, which reach a total density of approximately $10^{11} – 10^{12}$ bacterial cells/ml colon content. This dense community of bacteria consists mainly of three or four large bacteria phyla: **Bacteroidetes, Firmicutes, Actinobacteria** and **Proteobacteria**. Other phyla (Verrucomicrobia, Fusobacteria) show smaller shares.

In most cases 30 – 60 % of the microbiota are Bacteroidetes. The Firmicutes have the same share and mainly consist of Lachnospiraceae and Ruminococcaceae families. Actinobacteria have significantly lower bacteria counts. Mainly Bifidobacteria make up the Actinobacteria phylum. In the microbiome of healthy people Proteobacteria have a share of 1.5 – 5 %, which can, however, after repeated antibiotic therapies or in case of inflammatory bowel diseases, increase significantly.

Result

The distribution of the bacteria-phyla shows an increase of:

- Proteobacteria

The distribution of the bacteria-phyla shows a reduction of:

- Actinobacteria
- Firmicutes
- Verrucomicrobia

Metabolome (functional groups)

Formation of secondary bile acids

The number of bacteria that can produce secondary bile acids is normal.
In the intestine, bile acids are in part deconjugated by bacteria and the resulting free bile acids are mostly converted to secondary bile acids (e.g. deoxycholic acid DCA, litocholic acid LCA) by clostridia and eubacteria. These can be toxic and cause DNA damage. The chemical conversion of bile acids caused by intestinal bacteria influences their effect in the organism to a large extent. Bile acids influence the mucosal immune system through interactions with receptors such as the farsenoid X receptor (FXR), Takeda G protein recep-

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tor 5 (TGR5) or the vitamin D receptor (VDR). By activating the bile acid receptors, they also regulate glucose and lipid metabolism.

A decrease in bile acid metabolizing bacteria therefore not only has consequences for the bile acid metabolism, but also for the glucose and cholesterol balance, the immune system and several others aspects of the hosts health.

TMA formation

The present findings indicate an **increased number of TMA-producing bacteria**.
A direct TMAO analysis in urine (A675) is recommended to quantify the actual exposure to potentially harmful TMAO.

The bacterial metabolite trimethylamine (TMA) can form bacterial genera from choline, but also from betaine or L-carnitine. TMA is the precursor of TMAO (trimethyl-N-oxide) formed in the liver. TMAO is a key molecule in the pathogenesis of cardiovascular diseases. It influences cholesterol and bile acid metabolism and promotes inflammation of the vascular walls.

In the case of increased TMAO exposure, it may be advisable to adequately reduce the intake of meat, eggs or other foods containing choline, betaine or L-carnitine. It is also possible to administer **resveratrol** or **curcumin** at the same time. In both cases, the TMAO level drops significantly.

Indoxyl sulfate

Indoxyl sulfate is inconspicuous in the actual analysis.
Indoxyl sulfate is classified as an indolic substance of uremic toxins and is a product of bacterial tryptophan metabolism.
In elevated concentrations, indoxyl sulfate has marked pro-oxidative effects via activation of NADPH oxidase and thus enhances inflammatory processes in the vascular system. These favor the progressive course of cardio-vascular risk events.
Furthermore, negative influences on bone density, kidney function or an anemic situation, among others, can be confirmed.

Phenol Formation

The findings indicate an **increased** number of **phenol-producing bacteria**.
To clarify if the bacteria do not only carry corresponding genes but also actually produce phenols, quantification and specification of the individual phenolic substances in an analysis of uremic toxins in urine (A681) are recommended.
Phenols or phenolic substances belong to the group of uremic toxins and are degradation products of bacterial amino acid metabolism. Phenolic substances have negative effects in the body under increased concentration. P-cresol sulphate, for example, has a pro-oxidative effect and may promote endothelial dysfunction and thus cardiovascular events. In addition, the substance may inhibit cytochrome P450 enzymes and impair cellular detoxification. Increased levels of phenylacetylglutamine, a compound of phenyl acetate and glutamine, are detectable in urine with increasing nitrogen load and can promote cardiovascular events.
Use of multi strain probiotics is recommended to regulate dysbiosis and as an antagonistic therapy to reduce exposure to uremic toxins. The administration of oligosaccharide-based prebiotics has proven to be effective in reducing p-cresol sulphate. Alternatively, acacia fibre has proven to be highly effective with significantly better tolerability.

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Ammonia formation

The present finding shows an increased number of ammonia-producing bacteria.
Ammonia is produced by the breakdown of amino acids. The anaerobic flora is also an important producer of ammonia. In the case of dysbiosis and an alkaline intestinal environment ammonia is increasingly absorbed through the intestinal wall.
Ammonia is a cytotoxin and can negatively affect both nerve cells and mitochondrial function.

Histamin producing bacteria

The present findings show a normal number of histamine-forming bacteria.
Histamine plays a central role as a messenger substance in the human immune system and in the allergic reaction. It is a biogenic amine and is formed from the amino acid histidine. This conversion can also take place in the intestine by certain bacteria.

Elevated levels are mainly found in type I allergies or pseudoallergies.

Causes for an increased histamine load can be a food allergy, pseudoallergy or chronic stress, which lead to increased mucosal permeability via a degranulation of mast cells, among other things.

Equol

The current findings indicate a **sufficient number of equol-forming bacteria**.

To clarify whether the existing bacteria really produce equol, a quantitative equol diagnostic is recommended.

As a bacterial metabolic product, equol is mainly synthesized upon consumption of soy products.

Its binding affinity to oestrogen receptors has been associated with beneficial effects in menopausal disorders and may protect against artherosclerosis, osteoporosis or neuroinflammatory diseases.

Mainly species such as Adlercreutzia, Eggerthella and Slackia are able to form equol. The bacterial formation, however, varies greatly between individuals. While in Europe, only about 20 – 30 % of the population is able to form equol, in Asia it is 50 – 60 %.

β-Glucuronidase formation

The present findings indicate an increased number of β-glucuronidase-bearing bacteria.
Further confirmatory diagnostic testings are recommended for quantification of the actual β glucuronidase activity.
β-glucuronidases are enzymes formed in the course of human metabolism, as well as by various bacterial genera. The microbial β-glucuronidase activity in the intestine ensures that inactivated hormones, active ingredients or toxins are released again as conjugate.
Depending on the intensity of the activity, this has a physiologically important effect, but may also promote a wide range of diseases.

In case of high activity, calcium D-glucarate can be given to reduce the activity. Milk thistle also inhibits the enzyme. Calcium D-glucarate promotes the glucuronidation of toxins, drugs or steroid hormones. By converting into a water-soluble form, excretion is made easier.

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Actinobacteria

Bifido bacteria are the most important genre in the scope of actinobacteria. They are gram-positive anaerobic rod-shaped bacteria, which utilize starch, but mainly oligosaccharides. Mostly acetic and lactic acid are developed. Common representatives are *B. adolescentis, B. breve* and *B. longum*.

Reduced bifido bacteria are often found after repeatedly applied antibiotic therapies, in case of irritable colon syndromes, chronic-inflammatory intestinal diseases or colorectal carcinoma. They mainly come along with reduced diversity in the intestines. By developing short-chained fatty acids and related pH-value reduction in the intestinal lumen bifido bacteria do not only counteract proliferation of pathogenic bacteria (**colonisation resistance**), they also have **anti-inflammatory effects.**

Result

In case of Alexandar the **bifido bacteria count is below the norm.** Reduced bifido bacteria promote endogenic infections. Inflammation inhibiting properties are not at all or only little effective.

Bacteroidetes

Bacteroides and **Prevotella** are particularly common genera in the microbiome of many people and regularly reach > 40 % of the total intestinal microbiota. As distinct biomarkers for nutrition they define enterotypes 1 and 2.

Results

Bacteroides are the most common species in the microbiome of many people. In case of Alexandar 9,2 % are of these species, which equals a bacteria count of 9,2 x 10^10 CFU / g Stool.

Also high **prevotella** bacteria counts can be reached (=> enterotype 2). Here it is with 1,6 x 10^11 CFU / g stool within normal range.

Firmicutes

Development of Butyrate and Short-Chain Fatty Acids by Firmicutes

Carbohydrate fermentation in the colon leads to the development of short-chain fatty acids (SCFA) (37) and gases (H_2, CO_2, methane). SFCA detectable in stool samples are mainly **formic acid, acetic acid, propionic acid** and **butyric acid**. Dietary changes lead to altered production rates of short-chain fatty acids. **Low-carb diets** lead to butyrate development reduction to one quarter (38) while **prebiotic agents** or **increased fibre consumption** lead to butyrate and propionate increases (39), the acetate levels decrease.

Short-chain fatty acids have positive influence on health. They stimulate intestinal motility and reduce inflammatory reactions by binding with GPR receptors (GPR 41 / GPR 43).
Butyrate is the most important **energy source** for colonocytes; it has an anti-inflammatory effect (40, 41, 42), protects against cell degeneration and also has **preventive influence** in regard to colorectal carcinoma.

Propionate
is metabolized in the liver, **acetate** in peripheral tissue. It is a precursor of cholesterol metabolism and lipid development. By giving prebiotics a shift of the fermentation products – from acetate to butyrate - may therefore be an advantage and lead to reduction of the **cholesterol level** (43).

Higher **SFCA concentrations** in the intestinal tract may increase mineral consumption like for example calcium (44). Therefore alterations of the intestinal microbiota after giving **FOS** come along with an increase of calcium absorption and improvement of the bone situation.

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Mainly **firmicutes** develop butyrate. Among firmicutes mostly ***Eubacterium rectale***, ***Roseburia species*** and ***Ruminococcus sp.*** are potent butyrate developers. The strongest butyrate developer, however, is ***Faecalibacterium prausnitzii* –** also a firmicute **–** which in contrast to the other listed butyrate developers cannot utilize starch. As butyrate is quickly absorbed via the intestinal mucosa, measurements in stool only provide unreliable results. Important information about butyrate development can be obtained with the aid of quantitative analyses of butyrate developing bacteria.

Result

The molecular-genetic microbiome analysis on butyrate-forming bacteria showed **deficits in several important butyrate formers**.

The **total bacteria count** of the butyrate formers was also **reduced**.

Deficits in several important butyrate formers and a reduced total bacteria count indicate an **insufficient butyrate formation**.

E. hallii is a bacterium that can convert acetate to butyrate. The butyrate source is not available, or only to a limited extent, when the number of microorganisms is low. A butyrate deficiency can result.

Evaluation of the Clostridia Flora (Total Bacteria Count, Toxin Development)

Clostridia belong to the group of firmicutes. They are obligatory anaerobic bacteria and develop spores. Pathogens belong to the clostridia species, but also apathogenic, useful bacteria, which have an immune modulating effect and lead to an increase of IL-10. Mainly *Clostridium botulinum, Clostridium tetani or Clostridium difficile* belong to the group of pathogenic representatives. In regard to their favoured energy sources clostridia can be assigned to two groups: **proteolytic** and **saccharolytic species**.

Proteolytic clostridia utilize protein and amino acids. Saccharolytic species on the other hand ferment carbohydrates, starch or fibres. During this process butyrate, acetone, butanol, CO_2 and hydrogen are developed. Dominance of proteolytic species often indicates so-called **"putrescence dyspepsia",** which frequently comes along with increased pH-values in stool. If the pH-value is – in spite of high counts of proteolytic species – within the norm or reduced, this is most often caused by accelerated intestinal passage. High clostridia counts may also come along with "**fermentative dyspepsia**". In this case, however, they are saccharolytic species.

Some clostridia groups – so-called **Cluster I-Clostridia** contain **toxin developing species**, like for *example C. perfringens, C. sporogenes* or *C. histolyticum*. Cluster I clostridia are often found in diseases of the autistic spectrum disorders and are not rarely the cause of **autism associated intestinal** and frequently also **extra-intestinal complaints.**

Result

The microbiome analysis of Alexandar showed **inconspicuous clostridia counts**.

Toxin developing clostridia (Cluster I) could also not be detected during sequencing. But only the most important representatives C. perfringens, C. sporogenes und C. histolyticum are considered.

Additional Relevant Firmicutes

Christensenella

The genus Christensenella, which was recently discovered in 2012, contains gram-negative, obligate anaerobic bacteria, which can be isolated from human feces. As extensive investigations on twins showed, the occurrence of Christensenella is to a large extent inherited. Especially twins with a **low BMI** showed high bacterial counts (Goodrich et al., 2014, Hamazelou, 2016). Animal experiments suggest that Christensenella

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is **counteracting obesity** (Waters et al., 2016). Christsensenella is often found in feces of very old people (Kong et al., 2016).

Result

In the case of Alexandar Christensenella are not present or only present in low bacterial counts.

Dialister invisus

The Dialister species are part of the Firmicutes. Their share of the total microbiome is about **1-1.5%** (Van Zanten et al., 2014). 5 species belong to this generic group of which 3 can be determined in stool. Before all Dialister invisus is of importance – a gram-negative, obligate anaerobic bacterium – which may be involved in **oral cavity infections** (periodontitis, gingivitis) (Morio et al., 2007). Only little is known so far about the function of Dialister invisus in the intestines. They are not of physiological significance. High bacteria counts should be regarded as in indication of dysbiosis.

Result

In case of Alexandar the bacteria count of Dialister invisus is within normal range.

Fusobacterium spp.

In humans Fusobacteria occur as part of the physiological microbiota of the oral cavity and are regularly detected in small amounts in the intestinal microbiotia. Fusobacteria are obligatory anaerobic growing, spindle-shaped bacilli. Especially Fusobacterium nucleatum and Fusobacterium necrophorum have a pathological potential in the infectiology and in the oral cavity they are associated with caries and periodontitis.

Already in 2012, in metagenomic analysis an accumulation of Fusobacterium nucleatum in **colorectal carcinoma (CRC)** has been detected. If Fusobacteria are actually able to cause a tumour or if they use the decayed tumour tissue as “food source”, has not been clarified yet. However, an etiological relevance does not seem unlikely.

In this case we found **Fusobacteria spp.** According to the results of the studies available to date, this may be a risk factor. Age-dependent and with simultaneous increased **calprotectin or conspicuous hemoglobin-haptoglobin complex test**, a precautionary endoscopic clarification seems sensible.

Proteobacteria

Like microbiome analyses show there is decreasing digestive performance in older age, which often leads to an increase of *Enterobacteriaceae* (***Escherichia coli, Klebsiella, Enterobacter, Proteus*)** or *pasteurellaceae* (e.g. ***haemophilus***). There are also alterations of the obligatory anaerobic flora. Increases of **clostridia** are suspicious. **Bifido bacteria** and **lactobacilli** on the other hand reduce.

The described alterations can also be caused by other factors. Reapplied **antibiotic therapies** lead to increasing enterobacteria, enterococci and clostridia counts as well as to significantly decreasing bifido bacteria. (62). Similar can be observed in case of **chronic inflammatory bowel diseases or irritable colon syndromes** (63, 64).

Determination of Pathogenic or Potentially Pathogenic Bacteria

Result

The following pathogens were found in the microbiome:

- Enterobacter spp.
- Klebsiella spp.

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The presence of multiple **potentially pathogenic Enterobacteriaceae (Enterobacter spp., Klebsiella spp.)** may indicate inflammatory mucosal changes, especially if they are detectable in high bacterial counts.

Archea

Methanobrevibacter spp.

Methanogens such as Methanobrevibacter spp. belong to the domain of the archaea and are not bacteria. In humans, a stable colonization is found in the gastrointestinal tract and oral cavity, in the vagina and on the skin. There, methanogens form a syntropic community with other microorganisms. The most common representative in the gastrointestinal tract with >90% is Methanobrevibacter smithii.

Methanogens are able to reduce CO2 under H2 consumption, as well as secondary bacterial metabolites like acetate to methane. The frequency of methanogens is related to various diseases. Increased methanogenesis can reduce intestinal motility and promote constipation-type irritable bowel syndrome. Increased methanogenesis is also reported for Diverticulosis patients. However, by consuming H2, methanogens also favor the growth of fiber-fermenting bacteria and thus SCFA production.

In the present case, **Methanobrevibacter spp. were found only in minor bacterial counts or not at all.**

Mucosa-relevant bacterial groups

Damage of the Intestinal Mucosa due to Hydrogen Sulphide Development (H_2S)

Hydrogen sulphide is a toxic metabolic product, which – in case of higher concentrations – leads to damage of intestinal epithelia and such promotes the occurrence of cellular atypia. H_2S is produced in the colon by **sulphate reducing bacteria** – especially by **Bilophila wadsworthii**, **Desulfomonas pigra** and **Desulfovibrio piger**. Meat is an important source of sulphur, which promotes the growth of sulphate reducing bacteria. The **cancer promoting potential** of hydrogen sulphide is based on the formation of **free radicals** (oxidative stress) and up-regulation of **cyclooxygenase-2** activity in the epithelia cells.

Gut bacteria can also produce N-nitroso compounds. Their quantity increases in case of high-protein diets, especially if a lot a meat is consumed. Cooking meat produces heterocyclic amines, which can be transformed to cancer promoting intermediate products.

Result

In the scope of sequencing no increased Bilophila wadsworthia, Desulfomonas pigra or Desulfovibrio piger counts could be determined. This indicates **minor H_2S production**.

Oxalobacter formigenes

Oxalobacter formigenes is an oxalate decomposing anaerobic bacterium, which is often found in the colon flora. *Oxalobacter formigenes* lives in symbiosis with humans. If this bacterium is not or only available in insufficient counts, the primary energy source for the enzyme oxalyl-CoA-decarboxylase is missing. This enzyme decomposes **calcium oxalate**. Oxalyl-CoA-carbolase deficiency promotes the development **calcium oxalate containing kidney stones**.

Result

In case of Alexandar the adequate bacteria count of Oxalobacter formigenes argues **against** increased risk of developing **calcium oxalate containing kidney stones**

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Escherichia coli, Enterococci and Mucosa Immune System

Microbiome alterations may under certain circumstances also allow conclusions about the mucosa immune system (MIS) activity level.

Result

Increased *E.coli* bacteria counts may – aside from above described causes – also be due to **deficient mucosa immunity.**

Mucin Development and Mucosa Barrier

In the healthy large intenstine a layer of mucosa mucus (**mucin layer**) protects the epithelial cells. If the mucin layer is damaged or insufficient mucin is formed, pathogens, pollutants or allergens can come into direct contact with the mucosa and lead to inflammation. Mucin formation and mucosal barrier are therefore closely connected. The maintenance of an intact mucosal barrier protects against bacterial translocation (LPS) and thus against inflammation. Bacteria such as **A. muciniphila** are significantly involved in maintaining the mucin layer. They emit mediator substances that stimulate the goblet cells to form mucosal mucus.

Result

Reduced Akkermansia muciniphila counts in the microbiome of Alexandar indicate **insufficient mucin** formation.

The **Faecalibacterium prausnitzii count** in stool was **normal**.

Mycological Stool Analysis

No yeasts could be found in the stool sample of Alexandar.

Determination of Parasites or Parasitic Enteritis Pathogens

There was no indication of Blastocystis hominis, Cryptosporidium species, Cyclospora cayetanensis, Dientamoeba fragilis, Entamoeba histolytica, Giardia lamblia in stool.

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Therapeutic Approaches

The results of the microbiome analysis require therapeutic approaches, which protect the microflora against negative consequences or ease existing complaints by supporting the microflora.

Successful therapies, however, also take basics into consideration, which practicably apply for everyone and often already lead to significant improvement of ailments. These basic therapies are based on decade-long experiences. They are listed in short form below and can be found under www.biovis.de.

Basics for healthy intestines:

Diet Healthy diets consist of a plentiful breakfast, a main meal at lunch and a modest dinner. It should be varied and diverse.

Giving Psyllium seed husks (dosage 1 tablespoons) should lead to 1 – 2 formed stools per day. They are tolerated well and may also be given in case of obstipation or diarrhoea.

Wheat Avoid or significantly reduce wheat. Wheat is often not tolerated well, even if there is no evidence of intolerance. This is caused by amylase-trypsin inhibitors (ATI), which inhibit digestive enzymes and promote mucosa irritations.

Sugar Radical reduction of sugar consumption (maximum 1 g / day)

Chewing Thoroughly chewing and salivating of food is the first step to healthy digestion and nutrient absorption.

Exercise Adequate moderate exercise

Relaxation Keep adequate resting phases

Detoxification Drink enough (water / unsweetened herbal teas) – this provides for improved intestinal passage and excretion of foreign matters. Possibly drainage of toxic substances via zeolite and/ or humic acids may be sensible.

Substitution Consumption high-value herbal oils (e.g. linseed oil) and/or fish, possibly curcumin or aloe vera, which have an anti-inflammatory effect respectively promote butyrate development.

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Diversity

The microbiome analysis indicates reduced **diversity**. Only adequate biodiversity provides protection against endogenic infections. If the diversity is adequate, the intestinal microbiota can fully unfold their immune modulating and anti-inflammatory activities and only then they can fulfil their function as important supporter of the mucosa barrier.

Biodiversity can be influenced by **prebiotics** and **probiotics** but also by **dietary factors**. The treatment should be based on the type of determined alterations. Well aimed measures based on findings and medical history are described below.

Please make sure to keep a **balanced diet** to provide for the maintenance of the microbiome diversity. An antibiotic therapy should always be accompanied by taking **probiotics.** They not only counteract proliferation of resistant pathogens, but also further reduction of bacteria diversity. Please keep in mind that also **smoking, aging, imbalanced high-fat diets** ("Western Diet") or diseases coming along with inflammatory mucosa irritations ("**low grade inflammation**") or medication (NSAR) lead to biodiversity decline. Therefore therapies should always start here and fight against the causal factors.

Individual prebiotic or probiotic therapies

Prebiotics

Prebiotics can promote diversity and achieve targeted changes in the composition and metabolism of the gut microbiota. Prebiotics consist of hard-to-digest carbohydrates, such as **resistant starches**, which lead to the proliferation of firmicutes and some bifidobacteria. **Oligosaccharides** such as XOS, AXOS, FOS, GOS or acacia fibers also show a bifidogenic effect. They too lead to an increase in butyrate formers. In addition, Faecalibacterium prausnitzii or Akkermansia muciniphila can be propagated via FOS / GOS or acacia fibers, resulting in a stabilization of the mucus layer and the membrane barrier. Recently, 2-fucosyllactose has also become available, an oligosaccharide that leads to a particularly strong proliferation of bifidobacteria and can also noticeably enrich Akkermansia muciniphila.

Probiotics

Probiotics are selected, living microorganisms that positively affect the environment in the intestine. Above all, strains of bifidobacteria and lactobacilli, but also E. coli, and enterococci are used. Whereas in the past it used to work predominantly with **individual strains**, it is now known that combinations of several potentiating probiotic strains can achieve significantly stronger effects. **Modern multispecies probiotics** can stimulate the mucosal immune system or have an immunomodulating effect. Depending on the selection and composition of the strains used, probiotics can stabilize the mucosal barrier in the intestine by stabilizing mast cell membranes and counteract a leaky gut. Modern multispecies probiotics have an anti-inflammatory effect and lead to a significant reduction of proinflammatory cytokines.

Pre- and probiotics should be used as specifically as possible in order to achieve an optimal effect. The selection is based on the following criteria:

- Patient age
- Complaint image
- Diversity
- Mikrobiota changes
- Butyrate and mucin formation
- Existing pathogenic / potential-pathogenic germs
- Existing facultatively pathogenic yeasts
- Inflammatory mucosal changes
- Leaky Gut (disturbed mucous membrane barrier)
- Mucosal immune system
- Incompatibilities / intolerances

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• Overweight or underweight

Nutritional forms, such as **FODMAP** or **low carb** have an impact on diversity and microbiota composition. Therefore, they are also taken into account in the following compilations.

Pre- and probiotics should be used as **specifically** as possible in order to achieve an **optimal effect**. The following tables allow you to determine suitable pre- and probiotics according to fixed criteria. If prebiotics can easily be restricted to the naming of active substances, this is practically impossible with probiotics, since even the same named bacterial species can vary greatly in their abilities. Even if products are named for these reasons, a claim for completeness cannot be guaranteed due to the large number of products offered. However, attempts were made above all to include probiotics which can substantiate the indication and efficacy with studies. If the listing is based only on similar parent compositions or indications by the manufacturer, this is marked in color. For further explanations, please refer to the tables.

Microbiological Therapy
Increased counts of **potentially pathogenic Enterobacteriaceae** are often caused by inadequate mucosa immune system activity. With the aid of **microbiological therapies** applying preparations with viable (Symbioflor I, II, Mutaflor) or inactivated bacteria (ProSymbioflor) the MIS can be activated. Preparations with viable bacteria principally have a stronger immune stimulating effect than those with inactivated bacteria.

Therapy uremic toxins

An increased occurrence of bacteria that can produce toxic metabolites from their amino acid metabolism is shown. Further diagnosis of bacterial uraemic metabolites (A681) is recommended.

Uremic toxins are products of the bacterial metabolism of amino acids – in this case especially of tryptophan, tyrosine and phenylalanine. In addition, there are substances that originate from the conversion of phenolic substances.

An increased number of uremic toxins is usually due to dysbiosis – in the sense of an increase in certain bacterial species that carry the corresponding enzymes for the synthesis of uremic toxins. These include primarily proteobacteria and clostridia.

Prebiotic therapy
In addition to a change to a **plant-based diet**, (vegetarians show a reduced occurrence of uremic toxins by up to 60 %) and a shift in the ratio of protein to dietary fibre, the administration of oligosaccharide-based prebiotics has proven to be effective in reducing **indoxyl sulfate** and **phenols**. These include **oligofructose** and **galacto-oligosaccharides**. The daily dose should be **15 g**, but should not be less than 10 g (divided into 3 single doses). In case of intolerance please start with 5 g per day and then slowly increase the dose. The use of acacia fiber can also support the growth of toxin-lowering bacteria strains.

Probiotic therapy
Recommended for **all uremic toxins** is the additional use of a multi-strain probiotic to regulate dysbiosis and as an antagonistic therapy aiming at the reduction of the toxin load.
In the literature, the following strains have proven to be particularly effective: Lb. casei, B. longum, B. infantis, Lb. acidophilus, Lb. gasseri, Lb. rhamnosus, saccharomyces boulardii and Enterococcus faecalis.

Dietetic Treatment

The microbiome composition is significantly influenced by the diet. Long-term change of diets alter the bacteria-phyla distribution (e. g. of firmicutes or bacteroidetes) as well as the bacteria count of those bacteria species, which are important for intestinal health.

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Please note:
The recommended dietetic treatment may lead to flatulence in the beginning. If this is the case starch or oligo-saccharide containing foods have to be increased gradually.

Certain carbohydrates – so-called oligo-saccharides – promote the growth of *F. prausnitzii* and *A. muciniphila*. *F. prausnitzii* is a butyrate developer, has an anti-inflammatory effect and together with *A. muciniphila* stabilizes the mucosa. Also bifido bacteria are promoted.

Oligosaccharides are for example contained in chicory, black salsify, radicchio, endive, asparagus, broccoli, sugar peas and sugar beet syrup. Also onion and garlic plants are good suppliers. Respective fruits are water melons and white peaches. In individual cases flatulence may occur. For this reason the individual tolerance should be tested with small amounts of the respective foods.

With kind regards

Your Biovis-Diagnostik

Prebiotics	Butyrate formation	Anti-inflammatory	Fp and/or Am	Bifidogenic effects	F/B-Ratio	LI	FM	Flatulence*	Diversity
RS	**+**	(+)	**-**	(+)[1)]	**+**	yes	yes	**40**	**+**
PPb	**+**	**+**	**+**	**+**	**+**	yes	yes	**60**	**+**
scFOS/scGOS	**+**	**+**	**+**	**+ +**	(+)	**no**	**no**	**100**	**+**
FOS	**+**	**+**	**+**	**+**	(+)	yes	**no**	**100**	**+**
Inulin	**+**	**+**	**+**	(+)[2)]	(+)	yes	**no**	**100**	**+**
Acacia fibres	**+**	**+**	**+**	**+**	**- -**	yes	yes	**20**	**+**
XOS / AXOS	**+**	**+**	**-**	**+**	?	yes	yes	**50**	**+**
Butyrate	**+**	**+**	**-**	**-**	+/-	yes	yes	**10**	+/-
FODMAP	**-**	-	**- -**	**- -**	**- -**	yes	yes	**- -**	**- -**
Low Carb	**-**	-	+/- [3)]	+/- [3)]	**- -** [3)]	yes	yes	**- -**	**- -**

Note:

***** Relative occurrence of flatulence compared to FOS/GOS (100 %)

+ Promoting effect | **-** no detectable or only very little effect | **+/-** no influence | **- -** reduction | **yes** compatible | **not** necessarily compatible, gradually increase dosage (start: 1 g / day)

[1)] Decomposition of RS by B. breve and B. adolescentis (Aliment Pharmacol Ther 2015; 42:158-179); [2)] depending on phenotype, incomplete decomposition of inulin (Appl Environ Microbiol 2009; 75:454-461); [3)] Decreasing numbers of bacteria such as A. muciniphila (Clin Nutr Experiment 2016; 6: 39-58), F. prausnitzii- and Bifidobacteria are described with a protein- and fat-rich low-carb-diet. (Proc Nutr Soc 2015; 74: 23 – 36). Low Carb diets can contain between 25 and 250 g carbohydrates per day.

RS: Resistant Starch
PPb: „Pro Prebioma“ (combination of several prebiotic substances)
FOS/GOS: **F**ructo-/**G**alacto**o**ligo**s**accharides: short chain variants (**sc**FOS / **sc**GOS) show significantly better compatibility
XOS/AXOS: **X**ylo-, **A**rabino**x**yl**o**ligo**s**accharides: Butyrate formation mainly through bifidogenic effect („Cross-Feeding“)
FODMAP: **F**ermentable **O**ligo-, **D**i-, **M**onosaccharides and **P**olyols“ (Polyols: polyvalent alcohols)
Fp / Am: Reproduction of Faecalibacterium prausnitzii / Akkermansia muciniphila
F/B-Ratio: Firmicutes-Bacteroidetes-Ratio
LI: Compatibility for people with lactose intolerance
FM: Compatibility for people with fructose malabsorption
Diversity: Diversity promoting effect

Probiotics Indications	OB Panda Ec. Panda OF Start Lb.Junior[2)] AB Start	OB 6[4)] AB Select Lb. omni Fos OF Plus pb pur	OB Active Lb. 60 plus OF Senior AB Compens	Lactobact AAD Ec. AAD[4)] AB Akut	Lactobact Forte[1)] AB Compens Ec. 825	OB Power Ec. Perform. AB Compens	OB Hetox Ec. Barrier[5)]	OB Hetox light Ec. Barrier Ec. Sense	OB Flora plus+ OF Fem
Babies	+ + +			week 1 - 4	week 5 - 12				
Children	+ + +[2)]	*/+ +[4]				*	*	*	
Adults		+ + +	+	+ +	+ +	+ +	+ +	+ +	+ +
Seniors		+	+ + +	+ +	+ +	+ +	+ +	+ +	+ +
Antibiotics				+ + +					
Lack of Butyrate					+ + +	+ +			
C. albicans	+	+ +		+ +					+ +
C. krusei /glabrata		+		+					+ + +
Diversity low	+ +[3)]				+ +		+ +	+	
Inflammation					+ + + +[1)]	+ +	+ +	+ +	
Flora (pH +)		+ + +	+ + +		+	+			
MIS-Activity - [6)]	+ +	+ + +	+ +	+ +	+	+ + +	+ +	+	
Lack of Mucin									+ +
Leaky Gut	+ +[3)]				+ + +	+ + +		+ + + +	
PO / PPO		+		+ + + +	+ +			+	
SRB		+ + +	+ +		+				

Notes:

+ + + / + + + + Method of choice | + + appropriate | + slight effect detectable | * from 8 years on

[1)] Lb. Forte: Indication: inflammatory mucosa reactions, CED (Interval); [2)] from 2nd year of life on; [3)] detected for OB Panda and Ec. Panda;
[4)] OB 6, OB 10 AAD, Ec. AAD also for children from 2nd year of life on, until 3 years half of dosage; [5)] Ec. Barrier double dosage; [6)] see introductory paragraph

OB: Omni-Biotic | Ec.: Ecologic | Lb.: Lactobact | OF: Orthica Flora / Orthiflor | pb: Probiotik | AB: Arktibiotic

MIS: Mucosal immune system | PO / PPO: pathogens / potentially pathogenic bacteria | SRB: sulfate-reducing bacteria

Important:

Information based on scientific studies or on indication statements of manufacturers. Due to the large quantity of probiotics available, there is no claim for completeness.
Black: based on study | **Violet**: manufacturer's specification