	Lat	bor	ato	ry of microbial chromatograph	Y E-mail V	Phone: +7(812)6002557 E-mail: lab@medbazis.com Website: dysbio.ru		Results of the study of biological material by chromatography mass- spectrometry Human microbiota				
Nº	rmicutes	inobacteria	naerobes	Microorganism	Sample	Normal arithmetical	Permissible deviation range	Occurrence in this biotope		Biotope "Small intestine"		
	Ë	Act	A			incan				MBKc2061 Albana Qemail		
Res	iden	t m.	.0. C	ases > 50% determined	cells/g ×10 ⁵	cells/g ×10 ⁵	cells/g ×10 ⁵	% 71	A	ge at last birthday: 7 Date of completion: 15.09.2021		
2		Ac	An	Actinomyces spp	1567	670	259	97	2			
3				Alcaligenes spp	109	60	40	86	3			
4		Ac	An	Bifidobacterium spp	2259	3824	1511	91	4			
5	F		An	Clostridium coccoides	113	37	28	93	5	J		
6	F		An	Clostridium perfringens	20	71	67 81	99	6	b		
8	F		An	Clostridium ramosum	5751	1721	1033	92	8			
9	F		An	Clostridium tetani	0	438	290	100	9			
10		Ac		Corineform CDC-group XX	0	79	56	99	10			
11		Ac	An	Eggerthella lenta	54	273	221	100	11			
12	F		An	Eubacterium spp	5741	6364	3105	100	12			
13	F		An	Fusobacterium/Haemophylus	0 657	5 2378	4 851	81 97	13			
14	F		An	Lactococcus spp	0	563	498	97	14			
16	-	Ac		Nocardia asteroides	401	1063	872	100	16			
17			An	Prevotella spp	0	28	16	100	17			
18		Ac	An	Propionibacterium acnes	0	24	18	55	18	1		
19		Ac	An	Propionibacterium freudenreichii	478	1868	843	100	19			
20		Ac	An	Propionibacterium jensenii	0	95	69	54	20			
21		Ac		Pseudonocardia spp Rhodococcus spp	59	18	62	100	21			
23	F	710	An	Ruminococcus spp	319	460	264	100	22			
24	F		An	Staphylococcus	356	464	175	100	24	Sample		
25	F		An	Staphylococcus epidermidis	242	72	44	91	25			
26	F		An	Streptococcus mutans (anaerob)	577	182	103	100	26	Norma		
27	F		An	Streptococcus spp	0	144	144	81	27			
28 Tra	nsie	Ac nt m	n o (Streptomyces spp	0	112	67	67 9/	28			
29	F	nt n	II.U. V	Bacillus cereus	$cens/g \times 10^{-1}$	$\frac{\text{cens/g} \times 10^2}{2}$	$\frac{\text{cens/g} \times 10^2}{2}$	%0 15	29			
30			An	Bacteroides fragilis	0	1	1	7	30			
31			An	Bacteroides hypermegas	0	0	0	4	31			
32				Campylobacter mucosalis	0	0	0	1	32			
33	F		An	Clostridium difficile	0	0	0	4	33			
34	F		An	Clostridium hystolyticum	0	7	5	17	34			
36	Г			Elavobacterium spp	0	4	0	2	35			
37				Helicobacter pylori	0	3	1	19	37			
38				Kingella spp	0	0	0	1	38			
39				Acinetobacter spp	0	0	0	1	39			
40	F		An	Peptostreptococcus anaerobius 17642	0	0	0	4	40			
41	F		An	Peptostreptococcus anaerobius 18623	0	14	0	11	41			
42			۸	I OLDHVIOHIOHAS SDD					42			
			An An	Prevotella ruminicola	0	1	1	9	43			
44			An An	Prevotella ruminicola Pseudomonas aeruginosa	0	1 0	1 0	9 1	43 44			
44 45			An An An	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe	0 0 0	1 0 0	1 0 0	9 1 1	43 44 45			
44 45 Mic	crose	copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi	0 0 0 cells/g ×10 ⁵	1 0 0 cells/g ×10 ⁵	1 0 0 cells/g ×10 ⁵	9 1 1 %	43 44 45			
44 45 Mic 46	crosc	copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa сем. Enterobacteriaceae (E.coli and othe gi Candida spp	0 0 0 cells/g ×10 ⁵ 1031	1 0 0 cells/g ×10 ⁵ 493	1 0 cells/g ×10 ⁵ 324	9 1 1 % 100	43 44 45 46			
44 45 Mic 46 47	crosc	copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Camportarel)	0 0 cells/g ×10⁵ 1031 193	1 0 cells/g×10 ⁵ 493 188 705	1 0 cells/g ×10 ⁵ 324 125 554	9 1 1 % 100 100	43 44 45 46 47			
44 45 46 46 47 48 49	crosc	copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gei Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spn (Sitosterol)	0 0 cells/g ×10⁵ 1031 193 1802 1833	1 0 cells/g ×10⁵ 493 188 795 857	1 0 cells/g ×10⁵ 324 125 554 517	9 1 1 100 100 99 99	43 44 45 46 47 48 49			
44 45 46 47 48 49 Virt		copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol)	0 0 cells/g ×10⁵ 1031 193 1802 1833	1 0 cells/g ×10⁵ 493 188 795 857	1 0 cells/g×10 ⁵ 324 125 554 517	9 1 1 100 100 99 99 99	43 44 45 46 47 48 49			
44 45 46 47 48 49 Vir 50	uses	copic	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa сем. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex	0 0 0 cells/g ×10⁵ 1031 193 1802 1833 1857	1 0 cells/g ×10⁵ 493 188 795 857 800	1 0 0 cells/g×10 ⁵ 324 125 554 517 498	9 1 1 100 100 99 99 99 % 100	43 44 45 46 47 48 49 50			
44 45 46 47 48 49 Vir 50 51		copid	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa сем. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0	1 0 cells/g ×10 ⁵ 493 188 795 857 800 260	1 0 0 cells/g×10 ⁵ 324 125 554 517 498 80	9 1 1 100 100 99 99 99 % 100 53	43 44 45 46 47 48 49 50 51			
44 45 46 47 48 49 Vir 50 51 52		copid	An An An C fun	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0	1 0 cells/g ×10 ⁵ 493 188 795 857 800 260 384	1 0 cells/g×10 ⁵ 324 125 554 517 498 80 142	9 1 1 9% 100 100 99 99 99 99 99 99 100 53 41	43 44 45 46 47 48 49 50 51 52			
44 45 46 47 48 49 Vir 50 51 52 Not 52		copid	An An An c fur	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus e normal condition Bacillus condition	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0 0 cells/g ×10 ⁵	1 0 cells/g ×10 ⁵ 493 188 795 857 857 800 260 384 cells/g ×10 ⁵	1 0 0 cells/g ×10 ⁵ 324 125 554 517 498 80 142 cells/g ×10 ⁵	9 1 1 % 100 100 99 99 % 100 53 41 % 0	43 44 45 46 47 48 49 50 51 52			
44 45 Mic 46 47 48 49 Virr 50 51 52 Not 53 54	uses F		An An An c fur n the	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus e normal condition Bacillus megaterium Chlamidia trachomatis	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0 0 cells/g ×10 ⁵ 0 0	1 0 cells/g ×10 ⁵ 493 188 795 857 800 260 384 cells/g ×10 ⁵ 0 0	1 0 0 cells/g ×10 ⁵ 324 125 554 517 554 517 498 80 142 cells/g ×10 ⁵ 0	9 1 1 % 100 100 99 99 % 100 53 41 % 0 0	43 44 45 46 47 48 49 50 51 52 53 53 54	Resident microorganisms are highlighted in red		
Image: Notes 44 45 Mixed 46 47 48 49 Vir 50 51 52 Not 53 54 55	uses F	**	An An An c fur C fur n the	Prevotella ruminicola Pseudomonas aeruginosa сем. Enterobacteriaceae (E.coli and othe ogi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus e normal condition Bacillus megaterium Chlamidia trachomatis Mycobacterium spp	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0 0 cells/g ×10 ⁵ 0 0 0 0	1 0 cells/g ×10 ⁵ 493 188 795 857 800 260 384 cells/g ×10 ⁵ 0 0	1 0 0 cells/g ×10 ⁵ 324 125 554 517 498 80 142 cells/g ×10 ⁵ 0 0	9 1 1 100 100 99 99 99 % 100 53 41 % 0 0 0 0	43 44 45 46 47 48 49 50 51 52 51 52 53 53 54 55	Resident microorganisms are highlighted in red Transient microorganisms are highlighted in blue		
10 44 45 Mic 46 47 48 49 Virt 50 51 52 Not 53 54 55 56	uses four	copid ***	An An An c fur n the An	Prevotella ruminicola Pseudomonas aeruginosa сем. Enterobacteriaceae (E.coli and othe gi Candida spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus e normal condition Bacillus megaterium Chlamidia trachomatis Mycobacterium spp Propionibacterium spp	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0 0 cells/g ×10 ⁵ 0 0 0 cells/g ×10 ⁵	1 0 cells/g ×10 ⁵ 493 188 795 857 800 260 384 cells/g ×10 ⁵ 0 0 0	1 0 0 cells/g ×10 ⁵ 324 125 554 517 498 80 142 cells/g ×10 ⁵ 0 0 0 0	9 1 1 100 100 99 99 99 99 99 99 99 99 99	43 44 45 46 47 48 49 50 51 52 53 52 53 54 55 56	Resident microorganisms are highlighted in red Transient microorganisms are highlighted in blue A value of " 0 " indicates that the quantity of this m.o. ≤10 ⁴ cells/g		
12 44 45 Mice 46 47 48 49 Vir 50 51 52 Not 53 54 55 56 57	uses F	**	An An An c fur c fur n the An	Prevotella ruminicola Pseudomonas aeruginosa cem. Enterobacteriaceae (E.coli and othe gi Candida spp Aspergillus spp Micromycetes spp (Campesterol) Micromycetes spp (Sitosterol) Herpes simplex Epstein-Barr virus Cytomegalovirus e normal condition Bacillus megaterium Chlamidia trachomatis Mycobacterium spp Propionibacterium spp Stenotrophomonas maltophilia	0 0 0 cells/g ×10 ⁵ 1031 193 1802 1833 1857 0 0 0 cells/g ×10 ⁵ 0 0 0 cells/g ×10 ⁵ 0 0 0 0 0 0 0 0 0 0 0	1 0 cells/g ×10 ⁵ 493 188 795 857 857 800 260 384 cells/g ×10 ⁵ 0 0 0 0	1 0 0 cells/g ×10 ⁵ 324 125 554 517 498 80 142 cells/g ×10 ⁵ 0 0 0 0 0	9 1 1 % 100 100 99 99 % 100 53 41 % 0 0 0 0 0 0 0	43 44 45 46 47 48 49 50 51 52 53 54 55 55 56 57	Resident microorganisms are highlighted in red Transient microorganisms are highlighted in blue A value of " 0 " indicates that the quantity of this m.o. ≤10 ⁴ cells/g		

Ratios of results by groups m.o.						
Microorganis	sm	load	norma	of TBL		
Resident		19041	21225	100%		
Transient		0	33	0%		
None in the r	normal condition	0	0	0%		
Including	Anaerobic bacteria	18386	19844	97%		
	Firmicutes	13893	13041	73%		
	Actinobacteria	5039	8118	26%		
	Bacteroidia, Flavobacteriia	0	35	0%		
	Proteobacteria	109	63	1%		
Total bacteria	al load (TBL)	19041	21257			
Total fungal	load (TFL)	4860	2332			
Viral activity		1857	1444			
	Plasmalogen	19	50	mkg/ml		
	Endotoxin (total)	0.36	0.5	nanomole/ml		

	Performed by					
Laborato	Laboratory of microbial chromatography					
Operator:	Kondrashkova					

Human microbiota is a complex of microorganisms colonizing human internal organs, mucous membranes and skin, including not only bacteria, but also microscopic fungi and viruses.

Reference values are determined by statistical analysis on the basis of mass screening in accordance with the patent for invention RU2715223, 02.12.2019.

* Permissible deviation range - is the limits of permissible deviations of the arithmetic mean, i.e. normal interval. Excess or shortage of microorganisms are outside of the confidence interval.

** The report on the viral load is made in conventional computer units for convenience of assessment and means not the number of viral bodies, but the marker (chemical) load.

Information about consultations based on the results of the analysis http://dysbio.ru/research/consultations/.

lab.medbazis

Annex. Reference information about the results of analysis.

General components of bacterial origin. Assess yourself.

Plasmalogen. Plasmalogens (aldehydogenic lipids) — phospholipids. Common in nature; found in all animal cells (sometimes up to 22 % by weight of the total content of phospholipids) and in some species of plants. Contained in large quantities in the spinal cord and brain, cardiac muscle and blood plasma. They can accumulate in tissues in case of some pathological conditions, for example, ischemia of the cardiac muscle. The biological role of plasmalogens has not been fully established. It has been found that a genetic defect in their synthesis leads to cerebral disorders (Zellweger syndrome). Plasmalogens participate in the cellular metabolism of polyunsaturated fatty acids, arachidonic in the first place, performing functions of intermediate depots for transportation of acids to the membrane diacyl phospholipids.

Endotoxin. Endotoxin or, to be more precise, bacterial lipopolysaccharide (LPS) is considered to be the strongest mediator of microbial origin, which participates in the pathogenesis of sepsis and septic shock. Small doses of LPS in a limited tissue space help the host organism to organize effective antimicrobial defense and elimination of pathogens to the external environment. At the same time, a sudden release of a large quantity of LPS, on the contrary, has a negative impact on the host organism, because in this case it launches an uncontrolled and life-threatening release of numerous mediators of inflammation and procoagulants to the systemic circulation.

The recovery of lactic and bifidobacteria in case of their deficiency is long - at least 1.5 months.

Firmicutes – phyllum of gram-positive bacteria with a low content of nucleotide pairs G-C (Guanine- Cytosine). Many of these from endospores that are very resistant to drying and can withstand extreme conditions found in various environments.

Actinobacteria - phylum of gram-positive bacteria with a high (over 55%) the content of guanine and cytosine in DNA, have a mycelial structure. These are active antibiotic producers. They are considered antiparasites

Bacteroidia - phylum of gram-negative non-spore-forming anaerobic rod-shaped bacteria. Widespread in the environment, including soil, sediment and sea water, sewage treatment plants, as well as in the intestines and on the skin of animals and human.

Proteobacteria - gram-negative phylum of bacteria that includes large amount of pathogens. They are distinguished by a wide variety of biochemical, physiological and morphological properties. As with other bacteria, this group stands out via a certain ribosomal RNA sequence (16S rRNA).

Note the microorganisms that are in excess compared to the normal range in this analysis!

1,2. Actinomycetes are common inhabitants of the gastrointestinal tract and the oral cavity; however, they may acquire aggressive properties in certain conditions. They are often included in concurrent infection in combination with coccal bacteria (staphylococci, anaerobic streptococcus mutans and Peptostreptococcus anaerobius) and lead to a resistant synergistic infection. Actinomycetes can result in development of a rare disease - actinomycosis. When it affects the abdominal cavity organs and the lungs, actinomycosis is manifested by disorders of these organs.

3. Alcaligenes is a genus of eubacteria in the group of Gram-negative non-fermenting bacteria. They inhabit the human intestine. They are found in water, food, and soil. There is information about their role in the development of diseases of the urogenital tract. They cause diseases in people with compromised immunity, who are unable to defend themselves against weakly virulent bacteria, as well as when the pathogen gets into the organism in very large quantities.

5,6,7,8,9. Clostridia are common in nature. Their source is – soil, water bodies and many species of animals. They are normally found in humans in the intestine, on the skin, oral mucous membrane, genital system, and respiratory tract. Many clostridia are pathogens of dangerous diseases (C. botulinum, C. tetani, C. perfringens), but it should be understood that clostridia of the microbiome do not cause these diseases thanks to the regulating effect of microbial biofilm and functioning of the immune system, because they require a traumatic way of infection! A special feature of the negative effect of clostridia in case of their excessive growth is the production of strong bacterial exotoxins, as well as a number of proteolytic enzymes, which causes local damage to the tissues.

21. Pseudonocardia is a little-studied Gram-positive bacterium, belonging to the biocenosis of actinomycetes. It is well adapted to the formation of symbiosis with microorganisms. These microorganisms were isolated for the first time from animals, in particular, from fungus-growing ants from the surface of their chelicerae. According to the available studies, it is a promising source of new antibiotics.

25. Staphylococcus epidermidis - this type of staphylococcus is not as dangerous pathogen as Staphylococcus aureus, because it is a part of the microbiome of a healthy human being. It is dangerous for people with compromised immunity. The risk group includes pregnant women, patients in the postoperative period, patients in the intensive care unit, people with dysbiosis. Possible symptoms are carbuncles and boils on the skin, nausea, vomit, acne, spots, bowel disorders, moderate body temperature rise to subfebrile values, fatigue, weakness.

26. Streptococcus mutans are Gram-positive, anaerobic bacteria, inhabitants of the oral cavity. Since they need oxygen-free conditions, they are present in the gaps between adjacent teeth and deep cracks. They cause offensive breath and caries as a result of the impact of lactic acid (product of fermentation with participation of Streptococcus mutans) on the enamel.

46. Candida is an opportunistic microorganism that inhabits mucous membranes. There are around 140 known different varieties of Candida (most of them are pathogenic), which lead to candidiasis in certain conditions. Candida produces toxins that weaken the immune system. According to the literature, the frequency of carrier status of Candida fungi in healthy people reaches up to 65–80 % in the intestine (Shevyakov M.A.), and according to the statistics of gas chromatography-mass spectrometry - 100%. Colonization of the gastrointestinal tract by Candida fungi is asymptomatic.

48,49. Micromycetes spp. Gas chromatography-mass spectrometry often reveals other micromycetes (not Candida or Aspergilus). Clinically significant micromycetes include species pathogenic for humans, causing penicilliosis, yeast lesions; imperfect fungi – dermatomycetes - cause skin, hair and nail diseases. They are present in the intestine as permanent representatives of the microbiome. In case of dysbiosis, they have an adverse effect on the intestinal wall as a part of associations of fungi, viruses and bacteria.

50. Herpes. Herpes simplex virus type 1 and 2 is permanent participant of the human microbiome. It acts as a part of microbial and viral associations.