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Dysbiosis in the Gut Microbiota of Adolescents with Obesity

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Motivation

The obesity problem is genuinely alarming. In recent decades the obesity prevalence has increased dramatically and has nearly tripled since 1975. Development of obesity depends on genetic, psychological causes, obesogenic lifestyle, excess caloric intake and differences in gut microbial ecology. Changes in the intestinal microbial composition may be in phyla level as well as at phylotypes level (genera).

Aim

Checking a gut microbiota composition at adolescents with obesity and normal weight.

Materials and Methods

Totally we examined 40 adolescents who were grouped according to their Body Mass Index (BMI): the obese group (OB) consisting of 18 adolescences with SDS BMI \ge 2.0; the control group (CO) composed of 22 adolescences with SDS BMI < 1.0. OB group was comparable to CO at the ethnicity, gender and age.

Materials and Methods

Faecal sampling and sample preparation before amplicon sequencing was done according to SOP recommended by International Human Microbiome Standards. Metagenome sequencing of V3-V4 variable regions of 16S rDNA was done by Novogene Company (China). Bioinformatic analysis was performed using software packages FLASH, version 1.2.7, QIIME, version 1.7.0, UPARSE, version 7.0.1001. Sequences were grouped into OTUs based on \geq 97% similarity. Data were analyzed using the StatSoft STATISTICA 6.0 software package. Total read number in the gut microbiomes were normalized according to minimum value. Statistical significance was accepted at the p<0.05 level. The research study of the human microbiome in obese adolescents was approved by the Ethical Committee of the Scientific Centre of Family Health and Human Reproduction Problems, Irkutsk, Russia.

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Results

Microbial richness and biodiversity indices were similar in the groups with obesity and normal weight. No difference was found between two groups in the phyla Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, and in the genera Bacteroides, Alistipes, Subdoligranulum, Megasphaera, Blautia, Akkermansia, Odoribacter. Faecalibacterium, Lactobacillus, Bifidobacterium, and Streptococcus. On the other hand the obese participants had a 2-fold decrease in Enterobacter (42 (13-61) in OB, 167 (42-371) in CO, p=0.02), and an increase – in the Anaerotruncus phylotypes (326 (215-732) in OB, 226 (165-320) in CO, p=0.04).

Indices / phylum / phylotype	OB group (n=18)	CO group (n=22)	р
ΟΤυ	465±56	486±61	0.27
Shannon	5.89±0.57	5.94±0.52	0.79
Simpson	0.95±0.04	0.95±0.04	0.80
Chao1	502.65±59.01	526.22±65.26	0.24
ACE	508.90±58.95	531.99±62,79	0.24
Bacteroidetes/ Firmicutes	0.93 (0.67-1.34)	1.18 (0.74-1.65)	0.47
Proteobacteria/Actino bacteria	4.05 (3.02-8.04)	4.01 (2.33-7.58)	0.56

Firmicutes	22407	21334	0.55
T II TIIICULES	(18131-27155)	(17194-26040)	0.55
Bacteroidetes	21734	23723	0.48
	(18863-27120)	(19813- 27388)	
Proteobacteria	3337	2618	0.95
	(1433-5372)	(1867-4329)	
Actinobacteria	682	563	0.76
	(311-932)	(403-935)	
Bacteroides	8490.50	9993	0.88
	(6662-15519)	(8106-14328)	
Alistipes	2613	2661	0.59
	(1158-4021)	(1496- 4257)	
Subdoligranulum	1441	1775	0.71
	(775-2257)	(829-2389)	
Megasphaera	84	144	0.30
	(43-195)	(67-395)	
Blautia	411	364	0.95
	(103-1028)	(195-786)	
Akkermansia	189	226	0.94
	(66-521)	(57-445)	
Enterobacter	42	167	0.02*
	(13-61)	(42-371)	
Anaerotruncus	326	226	0.04*
	(215-732)	(165-320)	
Odoribacter	66	75	0.91
	(51-112)	(35-127)	
Faecalibacterium	1218	1119	0.71
	(819-2241)	(776-1778)	
Lactobacillus	11	16	0.58
	(7-23)	(6-62)	0.00
Bifidobacterium	226	300	0.15
	(113-359)	(214-489)	
Streptococcus	55	52	0.97
	(16-117)	(19-109)	

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Conclusion

There were no significant differences in microbial richness and the biodiversity in obese and normal weight adolescences. The main phyla Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria of human microbiome were comparable at adolescents with obesity and normal weight.

At the lower taxonomic levels, our data shows that gut microbiota of adolescences with obesity have a prevalence of *Anaerotruncus* (the phylum Firmicutes) and decreased number of *Enterobacter* phylotypes (the phylum Proteobacteria).

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Declaration of interest

No conflicts of interest were disclosed.