

Taxonomic composition of cultivable stool microbiota in residents of Karachay-Cherchessia province, Russia

Катчиева П.Х.¹, Соколова С.Р.²

1 - Северо-Кавказская государственная гуманитарно-технологическая академия, Черкесск, Россия, *E-mail: polya.ya.91@mail.ru*; 2 - Российский национальный исследовательский медицинский университет имени Н.И. Пирогова, Москва, Россия, *E-mail: dima-usagychan@yandex.ru*

Backgrounds. At present, comparative studies of microbiota, depending on ethnicity, on the environmental conditions in which the macroorganism developed [1,2]. Karachay-Cherkessia is a province located in the mountainous North Caucasus area of southern European Russia. The province is populated by a diverse multicultural society of over 80 different ethnic groups. Over 50% of population are indigenous Karachays and Cherkess people who largely continue to maintain traditional rural lifestyle and dietary habits.

Objectives. To assess taxonomic composition of cultivable faecal microbiota in Karachay-Cherkessian residents in comparison with earlier obtained data on faecal microbiota of westernised population in European Russia.

microbiota composition was studied in 5 pairs of healthy adult siblings using a combination of aerobic and anaerobic bacterial culture techniques with species- and strain-level identification based on whole cell MALDI-TOF mass-spectrometry and 16S rRNA gene sequencing.

Conclusions. A total of 856 bacterial strains belonging to 78 bacterial and fungal species were isolated of which 733 strains could be identified using MALDI-TOF mass-spectrometry and 123 by 16S rRNA gene sequencing. The most commonly found bacterial genera included *Bacteroides*, *Alist*, *Prevotella*, *Bifidobacterium*, and *Collinsella*, which were typically present in concentrations exceeding 10⁹ cfu/g of faeces. The genera *Lactobacillus*, *Streptococcus*, *Enterococcus*, and *Escherichia* were detected equally often but were present in significantly lower titers. Seven bacterial strains represented novel species within the genera *Dialister*, *Butyricimonas*, *Collinsella*, *Prevotella*, and *Ruminococcus*. Significant differences in species level composition of microbiota was observed Karachay-Cherkessian residents compared to residents of European Russia. In particular, elevated levels of *Butyricimonas*, as well as presence of certain rare species of *Lactobacillus* and *Prevotella* were observed.

Источники и литература

- 1) Zakharevich N.V., Averina O. V., Klimina K. M., Kudryavtseva A. V., Kasianov A. S., Makeev V. J., Danilenkova V. N.. Complete Genome Sequence of *Bifidobacterium longum* GT15: Unique Genes for Russian Strains// Genome Announc.2014. №2 (6). e01348. DOI: 10.1128 / genomeA.01348-14.
- 2) Yatsunenکو T, Rey F.E, Manary M.J, et al. Human gut microbiome viewed across age and geography// Nature. 2012. № 486(7402).P.222-227.