COMPARATIVE CHARACTERISTICS OF INTESTINE MICROBIOME OF REPUBLIC OF GUINEA AND RUSSIAN FEDERATION RESIDENTS

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Abstract. The gut microbiota of healthy people, living in different regions, may vary considerably. The article presents the results of comparative qualitative and quantitative study of the intestine aerobic and anaerobic microbiota of residents of the Republic of Guinea (46) and Russia (60). The content of microorganisms (*Enterobacteriaceae, Enterococcus* spp., *Lactobacillus* spp., *Bifidobacterium* spp., *Staphylococcus* spp., *Candida* spp., non-fermentative gram-negative bacteria and others) in 1.0 gram of faeces was determined by bacteriological methods. Generic and species identification was performed using Vitek 2 Compact (bioMerieux, France), tube biochemical tests and MALDI-TOF mass spectrometry (Bruker Daltonics, Germany). Pearson χ^2 criterion, $p < 0.05$ and Fisher's exact test (medstatistica.ru) were used to assess the differences in the compared groups. 95% confidence intervals were calculated by the method of Wilson. Microbiological disorders were characterized by a decrease in the number of obligate microorganisms, an increase in the number of facultative (opportunistic) microorganisms (above 10^6 CFU/g) and the emergence of their associations. Dysbiotic disorders were identified in both compared groups: in 100% patients from Republic of Guinea (95% CI:92.3–100) and in 86.7% patients from St. Petersburg (95% CI:75.8–93.1). Severe degree of microbiota disorders in the residents of the Republic of Guinea was revealed at 19.6% (95% CI:10.7–33.2), in group of residents of St. Petersburg in 9.6% (95% CI:4.2–20.6). In both groups the microbiota disorders of third degree were detected less frequently, compared with the microbiota disorders of second degree. The study has found no significant differences in the content of obligate bacteria (*Bifidobacterium* spp. and *Lactobacillus* spp.), however, significant differences in the species composition of the facultative part of the microbiota were revealed. The residents of the Republic of Guinea had "atypical" *E. coli* (lactosonegative and hemolytic) and non-fermenting gram-negative bacteria *Comamonas kerstersii* more frequently. Opportunistic microorganism associations have been found in 30.4% of the residents of the Republic of Guinea (95% CI:19.1–44.8) and 18.3% of residents of St. Petersburg (95% CI:10.6–29.9). Opportunistic microorganism associations from the residents of the Republic of Guinea always contained *Staphylococcus aureus*. It is necessary to conduct further research on a bigger population to access the differences in the compared groups in *Staphylococcus aureus* and *Hafnia alvei*.

Key words: intestine microbiome, Republic of Guinea, Enterobacteriaceae, Hafnia alvei, Comamonas kerstersii, Staphylococcus aureus, Escherichia coli, Enterococcus spp.

СРАВНИТЕЛЬНАЯ ХАРАКТЕРИСТИКА ОСОБЕННОСТЕЙ МИКРОБИОТЫ КИШЕЧНИКА ЖИТЕЛЕЙ ГВИНЕЙСКОЙ РЕСПУБЛИКИ И РОССИИ

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Резюме. Известно, что микробиота кишечника у клинически здоровых людей, проживающих в разных регионах, может значительно различаться. Цель исследования — сравнительное изучение качественного и количественного состава аэробной и анаэробной микробиоты кишечника на случайной малой выборке проб испражнений жителей Гвинейской Республики (46 человек) и России (60 человек). Содержание микроорганизмов (*Enterobacteriaceae, Enterococcus* spp., *Lactobacillus* spp., *Bifidobacterium* spp., *Staphylococcus* spp., дрожжеподобные грибы рода *Candida*, неферментирующие грамотрицательные бактерии и др.) в 1,0 грамме фекалий определяли бактериологическим методом. Родовую и видовую идентификацию проводили с использованием бактериологического анализатора Vitek 2 Compact (bioMerieux, Франция), рутинных биохимических тестов, а также MALDI-TOF масс-спектрометрии (Bruker Daltonics, Германия). Для оценки различий результатов в сравниваемых группах применяли критерий χ^2 Пирсона, $p < 0,05$ и точный критерий Фишера, вычисленные с использованием он-лайн калькулятора medstatistica.ru. 95% доверительные интервалы рассчитывали по методу Уилсона. Микробиологические нарушения характеризовались снижением количества облигатных, повышением количества факультативных (условно-патогенных) микроорганизмов (в количестве 10^6 и выше КОЕ/г.) и появлением их ассоциаций. Дисбиотические нарушения были выявлены в обеих сравниваемых группах: у 100% обследованных из Гвинейской Республики (95% ДИ:92,3—100) и у 86,7% обследованных из Санкт-Петербурга (95% ДИ:75,8—93,1). Выраженная степень нарушений микробиоциноза в группе жителей Гвинейской Республики встречалась в 19,6% (95% ДИ:10,7—33,2), в группе жителей Санкт-Петербурга в 9,6% (95% ДИ:4,2—20,6). Как у жителей Гвинейской Республики, так и у жителей Санкт-Петербурга нарушения третьей степени выявлялись реже, по сравнению с нарушениями второй степени. Исследование не выявило значимых различий в содержании облигатных бактерий (*Bifidobacterium* spp. и *Lactobacillus* spp.), однако, выявлены достоверные различия в видовом составе факультативной части микробиоты. У жителей Гвинейской Республики чаще обнаруживали «атипичные» *Escherichia coli* (гемолитические и лактозонегативные) и неферментирующие грамотрицательные бактерии *Comamonas kerstersii*. Ассоциации условно-патогенных микроорганизмов в разных по составу сочетаниях обнаружены в составе микробиоты у 30,4% обследованных жителей Гвинейской Республики (95% ДИ:19,1—44,8) и у 18,3% жителей Санкт-Петербурга (95% ДИ:10,6—29,9). Ассоциации микроорганизмов у жителей Гвинейской Республики всегда содержали *Staphylococcus aureus*. Выявлены отличия в сравниваемых группах в отношении *Staphylococcus aureus* и *Hafnia alvei,* однако необходимо проведение дальнейших исследований на большей выборке.

Ключевые слова: *микробиота кишечника, Гвинейская Республика, Enterobacteriaceae, Hafnia alvei, Comamonas kerstersii, Staphylococcus aureus, Escherichia coli, Enterococcus spp.*

Introduction

At present, the importance of bacteria for life, normal development and full functioning of the human body is beyond doubt. It has been proved by numerous studies of both Russian and foreign authors [2, 3, 10, 17, 19]. In the gastrointestinal tract (GIT) of a healthy person, as a result of a long joint evolution, a complex multicomponent ecological system that contains a large number of various types of bacteria and is called a "microbiome" was formed [2]. Its functional state, species composition, quantitative characteristics are influenced by various biotic and abiotic factors: climatic, ecological, social, etc. Being an open system, a microbiome, on the one hand, has a certain stability, and on the other hand it is capable of changing under the influence of the above factors [7, 12]. The adaptive possibilities of microbiome depend not only on external influences, but also are closely related to the individual genetic characteristics of the macroorganism, the state of its immune system. At present, it has been shown that disruption of the well-functioning of intestinal microbiocenosis plays a leading role in the emergence and development of many pathological processes, both infectious and non-infectious [1, 9, 10, 23, 27].

The composition of the intestinal microbiome is formed from the first days of a newborn's life, varies depending on the age and nature of nutrition [1, 4]. As the development of age processes in humans, the composition of microorganism associations in the intestine changes (the content of *Bifidobacterium* spp., *Lactobacillus* spp., etc. decreases) [8].

Dysbiosis, the quantitative and qualitative disturbance of homeostasis of the intestinal microbiome, as already mentioned above, plays an important role in the pathogenesis of various diseases [13]. In this case, the dysbiotic states, depending on the degree

of disturbances in the composition of the microbiome, and the intensity and duration of the reasons that cause them, can either disappear due to the inclusion of compensatory mechanisms, or grow to a pathological stage requiring specific therapy.

A lot of work has been devoted to the study of the microbiome of the intestine, both in children and in adults. Thanks to the research conducted within the framework of the Human Microbiome Project, the participants were able to compile a comprehensive understanding of the diversity of microorganisms inhabiting the biotopes of the human body. The results of genetic analysis showed that in the human body there are over 10 thousand species of various microorganisms, and the most colonized organ is the intestine: the number of bacteria varies from $10-10^3$ cells in 1.0 gram in the small intestine to 10^{12} in the large intestine [5].

It is noted that the microbiome of the intestine in clinically healthy people living in different regions and countries can vary significantly. For example, the distinctive features of the microbiome of children living in Mongolia, whose diet was dominated by meat products, was an excessive amount of *Clostridium* spp. against a pronounced deficiency of *Lactobacillus* spp., *Bifidobacterium* spp. and other anaerobic non-spore-forming bacteria. In children who lived in Russia and were on a mixed diet, the intestinal microbiome also showed a deficiency of *Bifidobacterium* spp. and *Lactobacillus* spp. However, in general, the content of these microorganisms was significantly higher than that of children living in Mongolia. At the same time, various species of *Enterobacteriaceae, Staphylococcus* spp., yeast-like fungi of the *Candida* genus were present in abundant quantities in children living in Russia. One third of the children living in Switzerland had an increase in *Enterobacteriaceae,* and 16.7% had no *Enterococcus* spp. and in 50% had a reduced amount of *Bifidobacterium* spp. [7].

In a study of healthy residents of Vietnam and Russia, it was found that Vietnamese residents' fecal samples contained more *Enterobacteriaceae* and less *Lactobacillus* spp. than Russians, apart from the differences in the species belonging to *Enterococcus* spp. [6]. The residents of Uganda, Japan, India had a lower number of bacteroides than those living in Europe and America [21]. The peculiarities of microbiome in the residents of the highland and lowland regions of China, various regions of India, Indonesia, Japan, Mongolia and Hong Kong have been revealed [16, 18, 24, 25, 27].

The aim of the study was to carry out a comparative study of the qualitative and quantitative composition of the aerobic and anaerobic microbiome of the intestine in a random batch of feces samples from the residents of the Republic of Guinea (Conakry) and Russia (St. Petersburg).

Materials and methods

Laboratory studies were conducted in the laboratory of enteric infections of the St. Petersburg Pasteur Institute. 106 samples of feces were obtained from 46 residents of the Republic of Guinea (Conakry) aged 24−64 and from 60 residents of St. Petersburg aged 19−63. The qualitative and quantitative composition of microbial communities of the intestine was determined in the autumn-winter periods (December 2015, October 2016). The persons were clinically healthy and did not have a history of somatic and infectious diseases of the digestive tract during the 12 months preceding the study. A survey of food characteristics showed that the diet of the surveyed group of residents of the Republic of Guinea included a large number of local vegetables, fruits, cereals and a limited number of meat and, especially, natural dairy products. The surveyed group of residents of St. Petersburg followed a typical diet for our country with sufficient consumption of meat, dairy and plant products.

The content of microorganisms (bacteria of the *Enterobacteriaceae* family, *Enterococcus* spp., *Lactobacillus* spp., *Bifidobacterium* spp., *Staphylococcus* spp., yeast-like fungi of the *Candida* genus, non-fermenting gram-negative bacteria, etc.) in 1.0 gram of feces was determined by the bacteriological method. Russian selective and differential-diagnostic nutrient media were used to isolate and identify bacteria, according to the current regulatory documents. Generic and species identification was carried out using a bacteriological analyzer Vitek 2 Compact, routine bio-

Table 1. The degree of microbiota disorders of the gastrointestinal tract in the residents of the Republic of Guinea and Saint Petersburg

Comparable groups	Number of samples, in which abnormalities were detected		Degree of severity of microbiota disorders		
			1	2	3
Residents of St. Petersburg	52	abs.	17	30	5
		%	32.7	57.7	9.6
		95%CI	21.5–46.2	44.2–70.1	4.2–20.6
Residents of Guinea	46	abs.	9	28	9
		%	19.6	60.8	19.6
		95%CI	10.7–33.2	46.5–73.6	10.7–33.2
The value of χ^2 ($d_f = 1$)			2.158	0.102	1.973
Level of significance (P)			> 0.05	> 0.05	> 0.05

Table 2. Contents of obligatory and facultative microorganisms in fecal samples of residents of the Republic of Guinea and Saint Petersburg

Comparable groups	Number of samples		Obligatory microorganisms corresponding to the norm					Facultative microorganisms exceeding the norm			
			Bifidobacterium spp.	Lactobacillus spp.	Enterococcus spp.	Typical E. coli	Atypical E. coli	Clostridium spp.	Opportunistic pathogen enterobacteria	S. aureus	Candida spp.
Residents of St. Petersburg	60	abs.	50	43	49	39	10	15	21	10	9
		%	83.3	71.6	81.6	65.0	16.7	25	35.0	16.7	15.0
		95% CI	72.0–90.7	59.2–81.5	70.1–89.4	52.4–75.8	9.3–28.0	15.8–37.2	24.2–47.6	9.3–28.0	8.1–26.1
Residents of the Republic of Guinea	46	abs.	31	37	26	28	20	9	27	16	7
		%	67.4	80.4	56.5	60.8	43.5	19.6	58.7	34.8	15.2
		95% CI	53.0–79.1	66.8–89.3	42.2–69.8	46.5–73.6	30.2–57.8	10.7–33.2	44.3–71.7	22.7–49.2	7.6–28.2
The value of χ^2 (d$_f$ = 1)			3.672	1.081	7.956	0.191	9.224	0.439	5.9	4.616	0.001
Level of significance (P)			> 0.05	> 0.05	< 0.05	> 0.05	< 0.05	> 0.05	< 0.05	< 0.05	> 0.05

chemical tests, and MALDI-TOF mass spectrometry. For MALDI-TOF mass spectrometry, the bacterial cells from isolated colonies grown on differential diagnostic solid media for 18–24 hours of incubation were applied in a thin layer on the MALDI target wells, followed by lamination of 1 μl of the matrix, which is a saturated solution of α-cyano-4-hydroxycinnamic acid (Bruker Daltonics, Germany) in an aqueous solution of 50% acetonitrile and 2.5% trifluoroacetic acid (Sigma-Aldrich). Spectra of the samples were obtained in the linear positive mode of operation of the MALDI-TOF mass spectrometer "Microflex LRF" (Bruker Daltonics, Germany) using the "FlexControl" 3.3 software (Bruker Daltonics, Germany). Prior to measurement, the instrument was calibrated using a bacterial test standard (Bruker Daltonics, Germany). The spectral profiles of the samples were the sum of ions obtained from 240 laser flares at different locations in each MALDI target well, performed automatically in the mass/charge range (m/c) from 2000 to 20 000 Da. Identification of the microorganisms was carried out using the "MALDI Biotyper RTC" software (Bruker Daltonics, Germany) by comparing the mass spectra of each test sample with the reference spectra data from the taxonomic base and calculating the coincidence coefficients represented as scores.

The degrees of microbiological disturbances were assessed according to the Industry Standard OST No. 91500.11.004-2003 "Protocol of patient management. Dysbacteriosis of the Intestine", Federal Clinical Recommendations "Determination of Dysbiotic Changes in the Gastrointestinal Tract by Markers of the Intestinal Content", 2015. In order to evaluate the differences in the results in the compared groups, the χ^2 Pearson criterion, $p < 0.05$ and Fisher's exact test, calculated using the on-line calculator medstatistica.ru, were used. 95% confidence intervals were calculated using the Wilson method.

Findings

According to OST No. 91500.11.004-2003 and FCG (Federal clinical guidelines) of 2015, the degree of microbiological disturbances is characterized by a decrease in the number of obligatory ones, an increase in the number of facultative (opportunistic pathogens) microorganisms (OPM) and the appearance of their associations. Using these criteria, dysbiotic disorders were detected in both compared groups: 100% (95% CI: 92.3–100) surveyed from the Republic of Guinea and 86.7% (95% CI: 75.8–93.1) surveyed from St. Petersburg (Table 1).

Minor deviations from the norm (the first degree of microbiological disorders) occurred in the group of St. Petersburg residents in 32.7% (95% CI: 21.5–46.2), in the group of residents of the Republic of Guinea in 19.6% (95% CI: 10.7–33.2). The changes revealed were characterized by a decrease in the amount of *Bifidobacterium* spp. (up to 10^8–10^7 CFU/g), *Lactobacillus* spp. (up to 10^6 CFU/g), "typical" *Escherichia coli* (up to 10^6 CFU/g).

Microbiota disorders corresponding to the second degree occurred in 60.8% (95% CI: 46.5–73.6) in the group of surveyed residents of the Republic of Guinea and in 57.7% (95% CI: 44.2–70.1) of the surveyed residents of St. Petersburg. Deviations from the norm were characterized by a decrease in the content of *Bifidobacterium* spp. (up to 10^7 CFU/g) and *Lactobacillus* spp. (up to 10^5 CFU/g), an imbalance in the quantitative and qualitative composition of *Escherichia coli* (the presence of "atypical" strains with hemolytic activity and not able to ferment lactose), as well as the appearance in the microbiome of OPM and their associations in an amount exceeding 10^5 CFU/g.

The third degree of microbiota disorders in the group of residents of the Republic of Guinea was found in 19.6% (95% CI: 10.7–33.2), in the St. Petersburg group in 9.6% (95% CI: 4.2–20.6).

The disorders were characterized by a pronounced decrease in the number of obligate bacteria (*Bifidobacterium* spp. — less than 10^7 CFU/g, *Lactobacillus* spp. — less than 10^5 CFU/g), an increase in the content of OPM and their associations in an amount of 10^6 CFU/g and higher. When comparing the prevalence of each of the three degrees of microbiota disorders between the population of the Republic of Guinea and the population of St. Petersburg, no differences were found, however, statistically significant differences in the distribution of the proportion of microbiota disorders of various degrees were found within each population. Second degree disorders prevailed in the residents of the Republic of Guinea, the differences between the prevalence of disorders of the first and third degrees were not identified. In St. Petersburg residents, the prevalence of microbiota disorders of the third degree is significantly lower than the first and second degree, however, there is no difference between the prevalence of disorders of the first and second degree. At the same time, both in the residents of the Republic of Guinea and in St. Petersburg residents, the proportion of disorders of the third degree is significantly lower than the second degree.

Associations of OPM in different combinations were found in microbiome in 30.4% of the surveyed residents of the Republic of Guinea (95% CI: 19.1–44.8) and 18.3% of St. Petersburg residents (95% CI: 10.6–29.9). At the same time, OPM associations in the surveyed residents of the Republic of Guinea always contained *Staphylococcus aureus*.

Table 2 represents data on the number of samples corresponding to norm for the content of obligatory and facultative microorganisms, significant for determining the severity of dysbiotic conditions. In the compared groups, the proportion of samples corresponding to norm by the number of *Bifidobacterium* spp., *Lactobacillus* spp. and "typical" *Escherichia coli*, did not differ statistically significantly.

Statistically significant differences were detected in the number of samples corresponding to the norm for the content of *Enterococcus* spp.: in St. Petersburg residents — 81.6% (95% CI: 70.1–89.4), in the Republic of Guinea residents — 56.5% (95% CI: 42.2–69.8). Species composition of *Enterococcus* spp. was identical in both groups. Proportions of *E. faecium* and *E. faecalis* were practically the same and amounted to 38.7% and 32.3%, respectively in the group of residents of St. Petersburg and 38.9% and 33.3% in the group of residents of the Republic of Guinea. In both groups there were isolated findings of other species *(E. avium, E. durans, E. galinarum, E. hirae, E. casseliflavus)*.

Analysis of the content of facultative microorganisms revealed statistically significant differences in relation to some bacteria. In the group of surveyed residents of the Republic of Guinea, samples with "atypical" (hemolytic and lactose-negative) *Escherichia coli* exceeding the norm were more common: 43.5% (95% CI: 30.2–57.8) compared to 16.7% (95% CI: 9.3–28.0) in the group of residents of St. Petersburg. The nonfermentative gram-negative bacteria *Comamonas kerster-*

Table 3. The frequency of opportunistic pathogens detection in the feces of the residents of the Republic of Guinea and Saint Petersburg

Comparable groups of residents:	Total samples		Number of samples containing opportunistic pathogens							
			Klebsiella spp.	*Citrobacter* spp.	*Enterobacter* spp.	*Proteus* spp.	*H. alvei*	*Comamonas kerstersii*	*S. aureus*	*Candida* spp.
St. Petersburg	60	abs.	12	3	5	0	1	1	10	9
		%	20.0	5.0	8.3	0	1.7	1.7	16.7	15.0
		95% CI	11.8–31.8	1.7–13.7	3.6–18.1	0.0–6.0	0.3–8.9	0.3–8.9	9.3–28.0	8.1–26.1
The Republic of Guinea	46	abs.	12	4	4	1	6	8	16	7
		%	26.1	8.7	8.7	2.2	13.0	17.4	34.8	15.2
		95% CI	15.6–40.3	3.4–20.3	3.4–20.3	0.4–11.3	6.1–25.7	9.1–30.7	22.7–49.2	7.6–28.2
Fisher's exact test			0.48992	0.46430	1.00	0.43396	0.04111	0.0096	0.04096	1.00

sii were detected in 17.4% (95% CI: 9.1–30.7) of residents from the Guinean Republic and 1.7% (95% CI: 0.3–8.9) of residents from St. Petersburg (Table 3).

There were no statistically significant differences in the prevalence of facultative opportunistic pathogenic *Enterobacter*ia among residents of St. Petersburg and the Republic of Guinea: *Klebsiella* spp. — 20.0% (95% CI: 11.8–31.8) and 26.1% (95% CI: 15.6–40.3), *Citrobacter* spp. — 5.0% (95% CI: 1.7–13.7) and 8.7% (95% CI: 3.4–20.3), *Enterobacter* spp. — 8.3% (95% CI: 3.6–18.1) and 8.7% (95% CI: 3.4–20.3), *Proteus* spp. — 0% (95% CI: 0.0–6.0) and 2.2% (95% CI: 0.4–11.3), *Clostridium* spp. — 25.0% (95% CI: 15.8–37.2) and 19.6% (95% CI: 10.7–33.2), *Candida* spp. — 15.0% (95% CI: 8.1–26.1) and 15.2% (95% CI: 7.6–28.2), respectively.

It was found that *Staphylococcus aureus* and *Hafnia alvei* were more common in the group of residents of the Republic of Guinea, but when the results were projected for the population, the differences were statistically insignificant: *Staphylococcus aureus* 34.8% (95% CI: 22.7–49.2) and 16.7% (95% CI: 9.3–28.0); *Hafnia alvei* — 13.0% (95% CI: 6.1–25.7) and 1.7% (95% CI: 0.3–8.9).

Discussion

The human society is constantly confronted with various new problems, despite progress in many areas of medical science and health. One of such problems at present is the violation of the microbial balance of the gastrointestinal tract, leading to the dysbiotic states of the human body. Analysis of the microbiome of the gastrointestinal tract in healthy people living in different regions of the world, presented in the works of many researchers, have shown significant variations in its quantitative and qualitative composition [11, 14, 15, 16, 17, 18, 20, 24, 25, 26, 27].

The results of our pilot project showed that in compared groups of practically healthy people in St. Petersburg, who had a relatively balanced diet with a predominance of animal proteins, and residents of the Republic of Guinea, who had a predominant prevalence of vegetables and cereals in the diet, significant differences in the content of obligate bacteria (*Bifidobacterium* spp. and *Lactobacillus* spp.), responsible for colonization resistance (one of the most important factors of the anti-infection protection system), have not been identified. According to our data, the prevalence of microbiota disorders of varying severity was noted with equal frequency among residents of the

Republic of Guinea and among residents of St. Petersburg. Moreover, within each population, statistically significant differences in the distribution of the proportion of microbiota disorders of various degrees were found. Both in the residents of the Republic of Guinea and the residents of St. Petersburg, the proportion of disorders of the third degree was detected less frequently, compared with the proportion of disorders of the second degree.

Reliable differences in the species composition of the facultative part of the microbiome are revealed. "Atypical" *Escherichia coli* (hemolytic and lactose-negative) and non-fermenting gram-negative bacteria *Comamonas kerstersii* are more often found in the residents of the Republic of Guinea.

We obtained differences in the compared groups for *Staphylococcus aureus* and *Hafnia alvei* (Fisher's exact test of 0.04096 and 0.04111, respectively), however, when projecting the results to population, the differences were statistically insignificant, further research on a larger population is necessary. It should be noted that these bacteria belong to the OPM and sanitary indicator microorganisms. Under certain conditions, any OPM can cause human diseases, especially in people with weakened immunity (purulent-septic infections, food poisoning, etc.) On the other hand, the presence of these bacteria in the digestive tract may reflect the characteristics of the macroorganism's habitat. This is confirmed by the example of our data on the content of *Comamonas kerstersii* in the digestive tract in a group of surveyed residents of the Republic of Guinea. For these microorganisms, the ecological niche is the environment: according to the literature sources, strains of *Comamonas* spp. were often identified in the study of samples of swampy soil and water environment, washings from fruit and vegetables, plankton, termites gut, etc. *Comamonas kerstersii* is often present in microbial communities associated with natural biocenoses and biodegradation processes [28]. More frequent findings of *Comamonas kerstersii* and "atypical" *Escherichia coli* characterize the microbiome of the gastrointestinal tract of the residents of the Republic of Guinea. It can be assumed that this is due to the humid tropical climate, low socio-economic level, and also the predominance of local vegetables and fruits in the diet.

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