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Preferred fruit and vegetable consumption and colonic microbiota in young residents of Arkhangelsk

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ABSTRACT

BACKGROUND: The composition of colonic microbiota is influenced by environmental factors, including dietary habits. Several studies on dietary habits and nutrition of Arctic residents have been published, but the information on the associations between fruit and vegetable consumption and gut microbiota is scarce.

AIM: This study aimed to evaluate the impact of preferred fruit and vegetable consumption on colonic microbiota in young residents of Arkhangelsk, using a sample of students and staff from a medical university.

MATERIAL AND METHODS: The study included 90 healthy volunteers (23 men and 67 women) from Northern State Medical University in Arkhangelsk aged 18–45 years with a normal body mass index. Fruit and vegetable consumption was assessed using a questionnaire. Stool samples were collected for molecular genetic analysis of colonic microbiota. Associations between fruit and vegetable consumption and concentrations of 33 microbiota indicators were examined using multivariable median regression, with adjustments made for age, gender, and place of origin.

RESULTS: Vegetables and fruits were consumed daily by 43.33% and 15.56% of respondents, respectively. The most frequently consumed vegetables were tomatoes (77.78%) and cucumbers (80.0%), while only 25.00% consumed potatoes and carrots. Among fruits, apples were consumed most frequently (74.44%), followed by bananas (57.78%) and citrus fruits (41.11%). Significant associations were found between *Methanobrevibacter smithii* and tomatoes (p=0.008) and carrots (p=0.006), between *Prevotella* spp. and cucumbers (p=0.032), *Blautia* spp. and carrots (p=0.002) and bananas (p=0.020). Additionally, association was found for *Acinetobacter* spp. with tomatoes (p=0.036), potatoes (p=0.028) and citrus fruits (p=0.019), *Bifidobacterium* spp. with potatoes (p=0.039) and citrus fruits (p=0.002). Direct association was found between *Bacteroides* spp. and cucumbers (p=0.023).

CONCLUSION: Our findings on the associations between selected fruits and vegetables and microbial concentrations may contribute to the development of personalized and balanced diet to enrich microbiota biodiversity and improve the quality of life of the residents of the North.

Keywords: microbiota; colon; vegetables; fruits; Arctic.

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Потребление предпочитаемых овощей и фруктов и микробиота толстой кишки у молодых жителей Архангельска

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АННОТАЦИЯ

Обоснование. Состав микробиоты подвержен воздействиям окружающей среды, в том числе пищевого поведения. Имеется достаточное количество исследований по изучению характера и особенностей питания у жителей Севера, однако информации о влиянии овощей и фруктов на микробиоту северян крайне мало.

Цель. Изучить влияние потребления предпочитаемых овощей и фруктов на микробиоту толстой кишки у молодых жителей Архангельска на примере студентов и сотрудников медицинского вуза.

Материал и методы. В исследовании приняли участие 90 человек (23 мужчины и 67 женщин) из числа сотрудников и студентов СГМУ. Критерии включения: возраст от 18 до 45 лет, практически здоровые лица, индекс массы тела в пределах нормы, без острых и хронических воспалительных заболеваний на момент исследования. Употребление овощей и фруктов оценивали по данным анкетирования. Материалом для молекулярно-генетического исследования представителей микробиоты толстой кишки являлись фекалии. Оценку связи между употреблением овощей и фруктов и микробиотой проводили с помощью многомерных медианных регрессионных моделей с коррекцией на пол, возраст и регион постоянного проживания для каждого из 33 показателей микробиоты.

Результаты. Ежедневно овощи употребляли 43,33% респондентов, фрукты — 15,56%. Чаще всего участники потребляли томаты (77,78%) и огурцы (80,00%), лишь 25,00% употребляли картофель и морковь. Среди фруктов чаще всего потребляли яблоки (74,44%), далее бананы (57,78%) и цитрусовые (41,11%). Значимые связи обнаружены между *Methanobrevibacter smithii* и томатами (p=0,008), а также морковью (p=0,006), между *Prevotella* spp. и огурцами (p=0,032), между *Blautia* spp. и морковью (p=0,002), бананами (p=0,020). Концентрация *Acinetobacter* spp. была связана с томатами (p=0,036), картофелем (p=0,028) и цитрусовыми (p=0,019), а *Bifidobacterium* spp. — с картофелем (p=0,039) и цитрусовыми (p=0,002). Прямая связь выявлена между *Bacteroides* spp. и огурцами (p=0,023).

Заключение. Выявлены значимые связи между употреблением ряда овощей и фруктов и численностью отдельных микроорганизмов. Знания об алиментарных факторах, влияющих на микробиоту, позволяют составлять персонифицированный и сбалансированный рацион для обогащения биоразнообразия микробиоты и улучшения качества жизни северян.

Ключевые слова: микробиота; толстая кишка; овощи; фрукты; Арктика.

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年轻阿尔汉格尔斯克居民偏好蔬菜水果的摄入与结肠微生物群的关系

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摘要

背景。微生物群的组成受多种环境因素的影响，其中饮食行为是关键因素之一。尽管北方居民饮食特点的研究已有较多文献支持，但有关蔬菜和水果摄入对北方居民微生物群影响的研究仍极其有限。

研究目的。分析阿尔汉格尔斯克年轻居民（以医科大学的学生和工作人员为例）对蔬菜和水果的偏好及其与结肠微生物群组成之间的关系。

材料与方法。研究纳入90名参与者（23名男性和67名女性），均为北方国立医科大学的学生或工作人员。入选标准包括：18至45岁之间、身体健康、体重指数正常，以及在研究期间无急性或慢性炎症性疾病。通过问卷调查评估蔬菜和水果的摄入情况，并通过粪便样本进行结肠微生物群的分子遗传学分析。利用多变量中位数回归模型评估33种微生物群指标与蔬菜和水果摄入的关系，调整因素包括性别、年龄和常住地区。

结果。每日食用蔬菜的参与者占43.33%，每日食用水果的参与者占15.56%。最常食用的蔬菜是番茄（77.78%）和黄瓜（80.00%），土豆和胡萝卜的摄入率相对较低（25.00%）。最常见的水果包括苹果（74.44%）、香蕉（57.78%）和柑橘类水果（41.11%）。显著关联如下：Methanobrevibacter smithii 与番茄（p=0.008）和胡萝卜（p=0.006）显著相关；Prevotella spp. 与黄瓜（p=0.032）显著相关；Blautia spp. 与胡萝卜（p=0.002）和香蕉（p=0.020）显著相关；Acinetobacter spp. 与番茄（p=0.036）、土豆（p=0.028）和柑橘类水果（p=0.019）显著相关；Bifidobacterium spp. 与土豆（p=0.039）和柑橘类水果（p=0.002）显著相关； Bacteroides spp. 与黄瓜（p=0.023）显著相关。

结论。研究表明，特定蔬菜和水果的摄入显著影响某些微生物的数量和分布。更深入地研究饮食因素对微生物群的影响，有助于为北方居民制定个性化饮食方案，从而改善微生物群的多样性与整体生活质量。

关键词：微生物群；结肠；蔬菜；水果；北极地区。

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BACKGROUND

Colonic microbiota is the most abundant microbial community in the human body. It consists of over 700 genera and 2500 species of microorganisms [1]. Its composition is host-specific and evolves throughout life subject to both endogenous and exogenous influences. This evolutionarily developed system with balanced microbial ecology exists in dynamic equilibrium with symbiotic microflora creating microbial associations that occupy a certain ecological niche [2].

Taxonomic variations in the gut microbiome, including microbial types and biodiversity, facilitate the evaluation of the overall microbial population in a host's gastrointestinal (GI) tract in relation to its food requirements at various life stages. However, as most studies suggest, the finer-level composition of genera and species remains understudied in the average healthy population. This complicates the assessment of how exogenous and endogenous factors, including diet, influence the microbiome [3].

Socioeconomic factors, including the residence, family income, share of food expenditures, family composition, and education, are the most important factors influencing food patterns and diet [4]. In recent years, there has been a trend in Russia toward decreased consumption of milk and dairy products, fish and seafood, meat and meat products, eggs, fruit, and vegetables [5]. A study of 38 participants showed significant nutritional deficiencies in children, including decreased consumption of fresh fruit and vegetables and increased consumption of pastry [6]. The World Health Organization recommends consuming at least 400 g of fruit and vegetables daily to prevent chronic diseases of the circulatory system, neoplasms, diabetes, and obesity [7]. Fruit and vegetables are rich in important nutrients, such as vitamins, minerals, dietary fiber, and phytochemicals. The consumption of these substances contributes to cardiovascular health. Increased amount of fruit and vegetables in one's diet may help reduce blood pressure [8]. Plant foods are a source of dietary fiber that promotes earlier satiety and a longer feeling of fullness, while reducing food intake. This prevents excessive weight gain and severe obesity accompanied by various clinical complications [9].

The parameters and biodiversity of the microbiota are defined by environmental factors. Therefore, it is important to study these factors in individuals living in different climatic and geographical regions. Human activity in the North is associated with unfavorable factors, such as low temperatures, sudden changes in atmospheric pressure, unstable magnetosphere, and irregular photoperiods. Adapting to these conditions leads to significant morphofunctional stress. In harsh climates, health preservation is only possible with adequate and balanced diet. However, today, the indigenous and immigrant populations of the North have mostly carbohydrate and fat food patterns with less vitamins, minerals, dietary fiber, and other essential nutrients [10]. The inhabitants of Russia's Arctic zone have a high carbohydrate load with their sugar intake exceeding the recommended level by 44% [11]. However, despite the numerous studies of food patterns and peculiarities of the population's diet in the North, peer-reviewed scientific data does not provide data on the relationship between diet and microbiota biodiversity.

The **study aims** to examine how mostly fruit- and vegetable-based diet affects the colonic microbiota of young Arkhangelsk residents with a focus on students and employees of the medical university.

MATERIALS AND METHODS

The study was conducted from March 2023 to February 2024. The sample included 90 students and employees of Northern State Medical University in Arkhangelsk. Due to its natural conditions and climate, Arkhangelsk is considered part of the Far North and the Arctic zone of the Russian Federation.

Inclusion criteria are age (18 and up to 45); body mass index (BMI) within normal limits; no acute and chronic inflammatory diseases, autoimmune diseases, allergies, endocrine disorders, and malignant neoplasms.

Exclusion criteria include use of antibacterial drugs or probiotics within three months prior to the collection of specimens; no voluntary informed consent and participant questionnaire.

The specimens used for the study were feces. The colonic microbiota was studied using the molecular genetic method of real-time polymerase chain reaction (PCR). Desoxynucleic acid (DNA) was extracted from the feces using a reagent kit (DNA-Sorb-B, AmpliSens, Russia) as directed. Samples of purified DNA were stored frozen at –20 °C for one month. Real-time PCR was performed using the Colonolor-16 Premium (AlfaLab, Russia) reagent kit. This kit analyzes 33 parameters (total bacterial mass, *Lactobacillus* spp., *Bifidobacterium* spp., *Escherichia coli, Bacteroides* spp., *Faecalibacterium prausnitzii*, the ratio of *Bacteroides* spp., *Faecalibacterium prausnitzii, Bacteroides thetaiotaomicron, Akkermansia muciniphila, Enterococcus* spp., *Escherichia coli enteropathogenic, Klebsiella pneumoniae, Klebsiella oxytoca, Candida* spp., *Staphylococcus aureus, Clostridioides difficile, Clostridium perfringens, Proteus vulgaris/mirabilis, Citrobacter* spp., *Enterobacter* spp., *Fusobacterium nucleatum, Parvimonas micra, Salmonella* spp., *Shigella* spp., *Blautia* spp., *Acinetobacter* spp., *Agathobacter rectalis, Streptococcus* spp., *Roseburia inulinivorans, Prevotella* spp., *Methanobrevibacter smithii, Methanosphaera stadmanae,* and *Ruminococcus* spp.). The number of microorganisms was expressed as decimal logarithms of colony-forming units per gram (lg CFU/g).

The participants filled a questionnaire developed by the Department of Clinical Biochemistry, Microbiology, and Testing of Northern State Medical University. The questionnaire was based on nutritional factors that may influence the biodiversity of colonic microbiota, according to foreign and Russian data. The personal section of the questionnaire included gender, age, weight, and height. These data were used to calculate BMI and exclude participants with abnormal BMI values. The respondents were further asked about chronic diseases or the use of antibiotics or probiotics. If antibiotics were used, the participants were prompted to specify the antibiotic class. In this case, the use of any antibiotics was an exclusion criterion. The next section included dietary habits, including the consumption of fruit, vegetables, dairy products, meat, seafood, tea, coffee, and alcohol. This article focused on the influence of plant foods, particularly fruits and vegetables, on the colonic microbiota. It was assumed that the respondents answered based on their taste preferences and dietary habits when they resided in Arkhangelsk, excluding the summer break.

The respondents were asked how often they consumed fruits and vegetables. The frequency was documented as daily; one or two times a week; three or four times a week; five or six times a week; several times a month, or not at all. They were also asked about their preferred types of fruit and vegetables. Based on the provided data, four types of vegetables (cucumbers, tomatoes, carrots, and potatoes) and three types of fruit (bananas, apples, and citrus fruits) were selected. The development of greenhouse vegetable growing and fruit imports from southern countries allow to purchase these products all year, regardless of the season.

The sample was not divided into groups as this would have reduced its statistical power.

The relationship between the consumption of each type of vegetables and fruit and each microorganism was studied using multivariate median regression models. These models included the main factor as well as the participant's sex, age, and residence (local or non-local). The regression coefficients, both crude and adjusted, were calculated. The results were presented as adjusted coefficients and standard errors. The data were analyzed using Stata 18 (Stata Corp., TX, USA) software. The median regression method was chosen due to the significant asymmetry observed in the concentrations of the studied microorganisms. As the regression analysis was performed on log-transformed data, a coefficient of 1 indicates a one-order-of-magnitude change in microorganism concentration when the predictor value increases by 1.

The study was conducted in accordance with the World Medical Association's Declaration of Helsinki of 1964 and its subsequent revisions. All participants provided a voluntary written informed consent. The study was approved by the Ethics Committee of Northern State Medical University (Arkhangelsk), Ministry of Health of the Russian Federation (Minutes No. 07/09-22, September 28, 2022).

RESULTS

The study examined 67 women and 23 men who were students or employees of Northern State Medical University. The mean age of the participants was 21.5.

Fig. 1 shows the frequency of fruit and vegetable consumption. Fruit and vegetables were consumed daily by 15.56% and 43.33% of respondents, respectively. One participant (1.11%) reported not consuming any fruits. Vegetables included tomatoes, cucumbers, carrots, and potatoes; fruits included bananas, citrus fruits, and apples. Fig. 2 shows the frequency of consumption of preferred types of vegetables and fruit. More than 77% respondents reported consuming tomatoes and cucumbers, while approximately 25% reported consuming carrots and potatoes. The most frequently consumed fruit was apples (74.44%) followed by bananas (57.78%) and citrus fruits (41.11%).

The relationships of colonic microbiota and consumption of vegetables (see Table 1) and fruit (see Table 2) were evaluated. Regression models were built for 14 microbiota members. The remaining microorganisms showed insufficient variability for modeling.

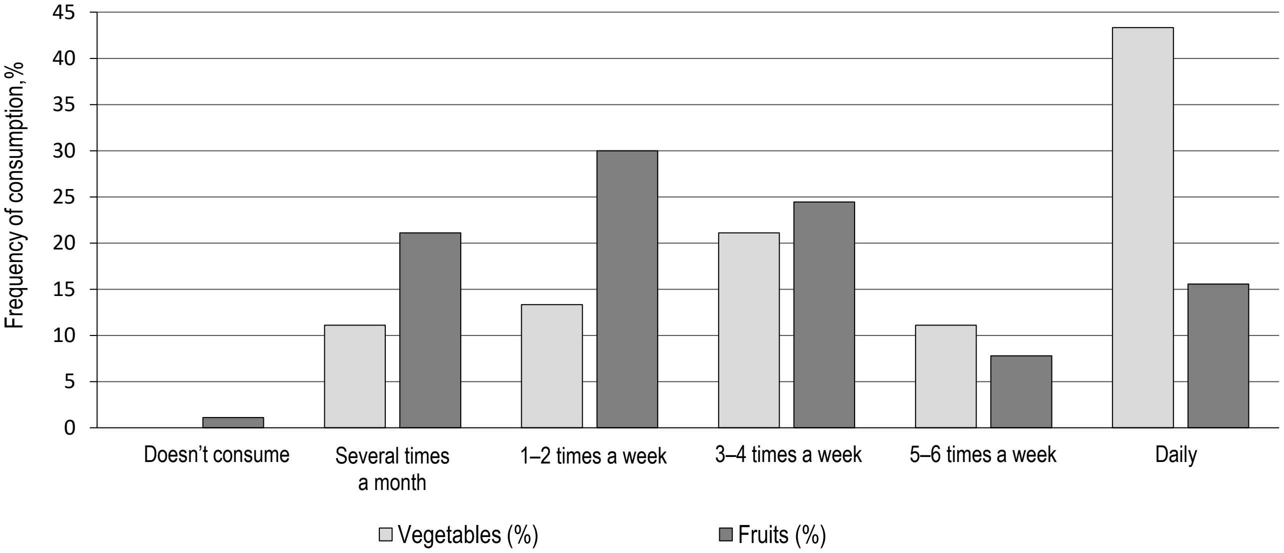

Fig. 1. Frequency of fruits and vegetables consumption in the study sample.

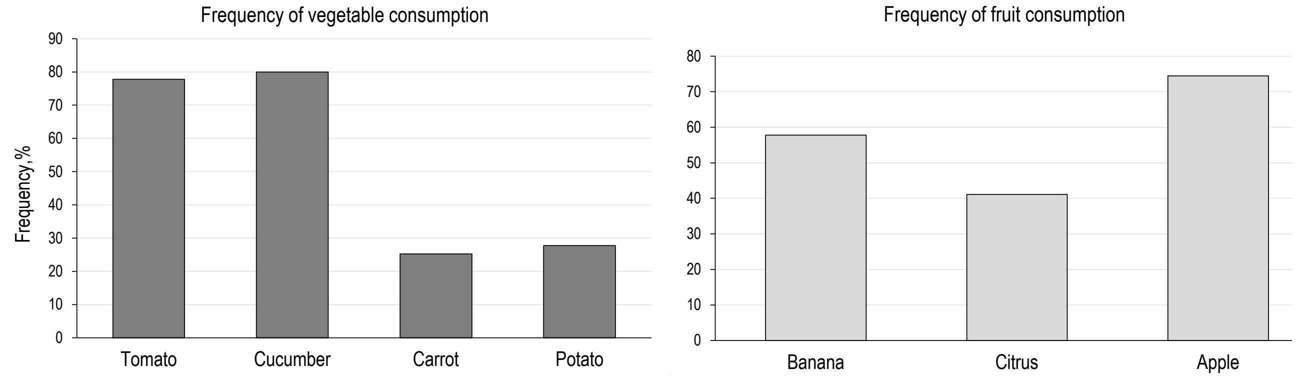

Fig. 2. Frequency of preferred fruits and vegetables consumption in the study sample.

Significant relationships were found when evaluating the relationship between vegetable consumption (see Table 1) and gut microflora members. These relationships included *Acinetobacter* spp. and tomato and potato consumption (p=0.036 and p=0.028, respectively); *Bacteroides* spp. and cucumber consumption (p=0.023); *Bifidobacterium* spp. and potato consumption (p=0.039), and *Faecalibacterium prausnitzii* and cucumber consumption (p=0.005). The regression coefficients were > 1 for *Methanobrevibacter smithii* and tomatoes (p=0.008) and carrots (p=0.006), *Prevotella* spp. and cucumbers (p=0.0032), and *Blautia* spp. and carrots (p=0.002).

When evaluating the relationship of fruit consumption and colonic microbiota (see Table 2), significant results were obtained in three cases. The first was citrus fruits and *Acinetobacter* spp. (p=0.019) followed by *Bifidobacterium* spp. (p=0.002). However, the most significant relationship was found between *Blautia* spp. and banana consumption (p = 0.020).

DISCUSSION

The study supports the hypothesis that fruit and vegetables influence the composition of the colonic microbiota. Notably, medical university students and staff consumed insufficient amount of fruit and vegetables. The survey showed that, despite the low frequency of fruit and vegetable consumption, dietary habits significantly influenced the number of individual colonic microbiota members.

Table 1. Regression coefficients and their standard errors for assessing the relationship between preferred vegetable consumption and the abundance of gut microbiota (lg CFU/g)

Genus/species of gut microbiota	Regression coefficients and their standard errors			
	Tomatoes	Cucumbers	Carrots	Potatoes
Acinetobacter spp.	0.18 (0.08)*	0.18 (0.09)	—	–0.18 (0.08)*
Agathobacter rectalis	–0.05 (0.37)	–0.36 (0.40)	0.08 (0.36)	0.03 (0.32)
Akkermansia muciniphila	0.00 (0.80)	1.63 (2.76)	0.00 (2.69)	–3.00 (2.49)
Bacteroides spp.	–0.18 (0.26)	0.65 (0.28)*	0.07 (0.25)	0.07 (0.24)
Bacteroides thethaiotaomicron	–0.17 (1.01)	0.47 (0.88)	–0.10 (0.89)	–0.68 (0.83)
Bifidobacterium spp.	0.46 (0.38)	0.13 (0.37)	0.16 (0.33)	0.65 (0.31)*
Blautia spp.	–0.52 (2.23)	–0.52 (2.31)	6.85 (2.12)*	0.21 (2.08)
Escherichia coli	0.12 (0.44)	0.14 (0.45)	0.52 (0.42)	0.11 (0.39)
Faecalibacterium prausnitzii	0.00 (0.23)	0.55 (0.19)*	–0.08 (0.21)	–0.18 (0.23)
Methanobrevibacter smithii	5.63 (2.06)*	1.10 (2.12)	–5.54 (1.97)*	–0.52 (1.88)
Prevotella spp.	0.89 (0.96)	–2.00 (0.92)*	–0.56 (0.97)	0.14 (0.89)
Roseburia inulinivorans	0.15 (0.34)	0.01 (0.37)	–0.07 (0.32)	–0.10 (0.31)
Ruminococcus spp.	–1.00 (1.71)	0.00 (2.20)	0.00 (2.04)	0.57 (1.97)
Streptococcus spp.	0.04 (0.44)	0.78 (0.47)	0.25 (0.46)	0.23 (0.42)

* The significance value is $p < 0.05$.

Table 2. Regression coefficients and their standard errors for assessing the relationship between preferred fruit consumption and the abundance of gut microbiota (lg CFU/g)

Genus/species of gut microbiota	Regression coefficients and their standard errors		
	Bananas	Citrus fruits	Apples
Acinetobacter spp.	0.00 (1.00)	0.15 (0.06)*	0.00 (1.00)
Agathobacter rectalis	–0.12 (0.34)	0.09 (0.31)	–0.60 (0.32)
Akkermansia muciniphila	0.00 (1.00)	–0.21 (2.34)	–3.09 (2.74)
Bacteroides spp.	–0.13 (0.91)	–0.17 (0.77)	0.34 (0.88)
Bacteroides thethaiotaomicron	–0.12 (0.24)	0.05 (0.22)	0.15 (0.25)
Bifidobacterium spp.	–0.17 (0.33)	–0.70 (0.22)*	–0.59 (0.32)
Blautia spp.	4.77 (2.01)*	0.00 (1.00)	0.00 (1.00)
Escherichia coli	–0.14 (0.36)	–0.44 (0.35)	–0.30 (0.44)
Faecalibacterium prausnitzii	–0.15 (0.18)	–0.22 (0.16)	0.00 (1.00)
Methanobrevibacter smithii	–0.24 (1.81)	0.10 (1.70)	–0.97 (2.04)
Prevotella spp.	–0.23 (0.84)	–1.30 (0.87)	–0.79 (1.04)
Roseburia inulinivorans	0.05 (0.30)	0.15 (0.29)	–0.36 (0.38)
Ruminococcus spp.	–0.30 (1.90)	–0.49 (1.81)	0.48 (2.07)
Streptococcus spp.	–0.13 (0.44)	–0.30 (0.35)	0.02 (0.81)

* The significance value is $p < 0.05$.

The study focused on the four all-season vegetables that are most common for the diet of northern residents, i.e. tomatoes, cucumbers, carrots, and potatoes. Thanks to greenhouse growing and international trade, the domestic market offers fresh fruit and vegetables all year, ensuring that the population's food requirements are met during the off-season [12]. According to publications, consuming 150 mg of tomato extract twice daily for four weeks leads to significant changes in colonic microbiota. This is evidenced by study, which showed a decreased number of *Bacteroides* spp. and *Ruminococcus* spp. [13]*double-blind, placebo-controlled cross-over study in overweight and obese adults»,»title-short»:»A water-soluble tomato extract rich in secondary plant metabolites lowers trimethylamine-n-oxide and modulates gut microbiota»,»volume»:»153»,»author»:[{«family»:»Rehman»,»given»:»Ateequr»},{«family»:»Tyree»,»given»:»Susan M.»},{«family»:»Fehlbaum»,»given»:»Sophie»},{«family»:»DunnGalvin»,»given»:»Gillian»},{«family»:»Panagos»,»given»:»Charalampos G.»},{«family»:»Guy»,»given»:»Bertrand»},{«family»:»Patel»,»given»:»Shriram»},{«family»:»Dinan»,»given»:»Timothy G.»},{«family»:»Duttaroy»,»given»:»Asim K.»},{«family»:»Duss»,»given»:»Ruedi»},{«family»:»Steinert»,»given»:»Robert E.»}],»issued»:{«date-parts»:[[«2023»,1]]}}}],»schema»:»https://github.com/citation-style-language/schema/raw/master/csl-citation.json»}* . Moreover, the study shows that the amount of *Methanobrevibacter smithii* significantly increased when tomatoes were consumed; carrots had the opposite effect. This confirms that this microorganism is present in vegetables [14]. The data on this methanobacterium is limited and now its properties and capacity are being studied. Thus, our findings will help evaluate the influence of vegetables that can modify the abundance of these methanobacteria.

For vegetables, cucumbers is the most common product in the Mediterranean diet. This diet reduces plasma cholesterol level and increases the number of *Faecalibacterium prausnitzii* [15]. In addition, daily consumption of pickled cucumbers increases the number of *Bacteroides* [16]according to the World Health Organization (WHO. Cucumbers also have abundant microbiome, including *Prevotella, Bacteroides, Lactobacillus, Dialister*, and *Faecalibacterium*. These bacteria play an important role in the human colonic microbiota, demonstrating the health benefits of cucumbers as a food product [17]. Our finding of a negative relationship between cucumber consumption and *Prevotella* spp. raises the question of factors preventing gut colonization by certain microbiota members due to the consumption of foods with antagonistic effects.

For root crops, carrots had significant relationship with microbiota. Rhamnogalacturonan-I, a cell wall component isolated from carrots, had prebiotic properties by affecting the growth of butyrate-producing bacteria such as *Blautia faecis*, *Blautia obeum*, and *Blautia massiliensis* [18] which are not only linked to health and disease but also determine the outcome of nutritional interventions. In line with the growing interest for developing targeted gut microbiota modulators, the selectivity of a carrot-derived rhamnogalacturonan I (cRG-I.

The evaluation of the relationship between potato consumption and microorganisms identified insignificant deviations of median; the number of microorganisms changed by less than one order of magnitude. The main substrates available to bifidobacteria are oligosaccharides, non-starch plant cell wall polysaccharides, hemicellulose, pectins as components of dietary fiber, and a starch fraction resistant to enzymatic hydrolysis in the upper GI tract. Starch resistant to amylase has been recognized as an effective fermentation substrate for colonic microbiota. *Bifidobacterium* use indigestible polysaccharides, including resistant starch, as sources of carbon and energy for metabolism [19].

To evaluate fruit popularity, three most frequently purchased all-season fruits were selected, including apples, bananas, and citrus fruits (oranges, lemons, and tangerines). Fruit, including oranges and lemons, are imported from Turkey and Egypt [20]. Due to limited sampling power, less common products could not be considered.

Fruit is another common source of plant fiber. There is evidence that fruit plays an important role in promoting intestinal peristalsis [21]. Some plant compounds found in fruit, vegetables, and herbs are polyphenols, including flavonoids, lignans, isoflavones, and stilbenes. Their low molecular mass allows for rapid diffusion through enterocyte membranes [22]. It is widely accepted that polyphenols in plant-rich diets have prebiotic properties that promote the growth of beneficial bacteria, including *Bifidobacterium* and *Lactobacillus*. These polyphenols may also have antimicrobial properties against various bacterial pathogens and anti-inflammatory properties [23]. The relationship between bananas and *Blautia* may be explained by the presence of inulin, a polysaccharide and D-fructose polymer that increases the number of *Blautia* spp. [24]*SCFA.*

Citrus fruits are associated with changes in bacterial abundance in the residents of the Northern region. Citrus albedo, i.e. loose white layer under the peel, acts as a water reservoir for juices, seeds, and leaves during drought. Previous studies have examined the hypolipidemic effects and bifidogenic potential of dietary fiber prepared from the albedo of Japanese mandarin orange [25]. However, this study showed a slight decrease (less than one order of magnitude) in the number of bifidobacteria in individuals who preferred citrus fruits, possibly due to consuming pulp without the albedo. Clinical studies evaluating the influence of different fiber types on the microbiota have reported an increased number of *Bifidobacterium* spp. with the dietary intake of several fibers, including galactooligosaccharides, inulin-type fructans, xylooligosaccharides, and arabinoxylan-oligosaccharides [26]nondigestible oligosaccharides (NDOs. Like onions and pumpkin, citrus fruits contain high amounts of vitamin C. It has been observed that onions and pumpkin increase *Acinetobacter* abundance by four and two times, respectively [27]and diet is closely related to the high prevalence of BC. The microbiome directly reflects eating habits. In this study, a diagnostic algorithm was developed by analyzing the microbiome patterns of BC. Blood samples were collected from 96 patients with BC and 192 healthy controls. Bacterial extracellular vesicles (EVs.

This study found no significant relationships between apples and colonic microbiota; though the available data indicate this fruit's influence on microbiota biodiversity. For example, a complex pectin found in apples may be digested by *Bacteroides thetaiotaomicron* [28]. The lack of significant relationships may be due to the fact that the respondents consumed apples without the peel, which contains four times more polyphenols. Nevertheless, the level of phenolic compounds differs significantly in different apple varieties (respondents have not been asked about their preferred apple variety). Assuming that the respondents consumed apples with the peel, the stability, release, and bioavailability of polyphenols would be influenced by certain exogenous and endogenous factors. These factors include interactions with other food components (e.g. glycosylation and esterification by dietary fiber); absorption kinetics of the GI tract, and modification of polyphenols in the liver [29]bioactivities (antioxidant activity, α-amylase, and α-glucosidase inhibition. Several compounds may affect the gut. Apples are treated with biphenyls to extend their shelf life. These compounds may disrupt intestinal integrity by affecting tight junction proteins (zonulin and occludin) and increasing epithelial permeability and, apparently, the translocation of colonic microbiota [30].

CONCLUSION

This study presents survey of the frequency of fruit and vegetable consumption by the respondents and their preferences in relation to these foods. Other components of the diet, including meat, dairy products, and beverages, could also have affected the number of the studied microorganisms. This study is based on survey rather than clinical study of the influence of particular foods on humans or animals. Our exploratory, hypothesis-generating study aims to help scientists focus on fruit, vegetables, and microbiota that have significant relationships and are important for human health. In addition, data indicating that young people in Arkhangelsk consume insufficient amount of fruit and vegetables highlight the importance of raising awareness about the role of plant foods in preserving a healthy GI tract and preventing conditions associated with decreased microbiota biodiversity.

The study showed that *Acinetobacter* spp., as well as *Methanobrevibacter smithii*, *Blautia* spp., and *Prevotella* spp., were associated with fruit and vegetable consumption. Thus, the results from a study conducted in an Arctic city in Russia were similar to the studies conducted in other regions. The authors have formulated new hypotheses about the potential influence of several products on the number of colonic microbiota members that require further study. Data on nutritional factors will allow to adjust the diet of residents of Northern regions and improve the gut biodiversity. This approach is expected to ensure colonization resistance, immune function, and metabolic activity of the microbiota in the studied biotope.

ADDITIONAL INFORMATION

Authors' contribution. T.A. Bazhukova — concept and design of the study; N.N. Kukalevskaya, M.A. Sabanaev — data collection and interpretation; A.M. Grjibovski, N.N. Kukalevskaya — data analysis and interpretation of the results; N.N. Kukalevskaya, T.A. Bazhukova, A.M. Grjibovski — writing the first draft; all authors — editing, approval of the final version of the article, responsibility for the integrity of all parts of the article. All authors confirm that their authorship meets the international ICMJE criteria (all authors made a substantial contribution to the conception of the work, acquisition, analysis, interpretation of data for the work, drafting and revising the work, final approval of the version to be published and agree to be accountable for all aspects of the work).

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Patients' consent. Written consent was obtained from all study participants in accordance with the study protocol approved by the local ethic committee (No. 07/09-22 от 28.09.2022).

ДОПОЛНИТЕЛЬНАЯ ИНФОРМАЦИЯ

Вклад авторов. Т.А. Бажукова — концепция и дизайн исследования; Н.Н. Кукалевская, М.А. Сабанаев — сбор и интерпретация данных; А.М. Гржибовский, Н.Н. Кукалевская — статистическая обработка данных и интерпретация; Н.Н. Кукалевская, Т.А. Бажукова, А.М. Гржибовский — написание текста; все авторы — редактирование, утверждение окончательного варианта статьи, ответственность за целостность всех частей статьи. Все авторы подтверждают соответствие своего авторства международным критериям ICMJE (все авторы внесли существенный вклад в разработку концепции, проведение исследования и подготовку статьи, прочли и одобрили финальную версию перед публикацией).

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