Original article / Оригинальная статья
УДК 577.1:551.4:551.5:628.1
DOI: 10.18470/1992-1098-2024-4-9

Bacterial Composition of Soils in the Fatala River Basin (Guinea) during the Dry Season: An Examination of its Relationship with Ecological Landscape Characteristics

Darya A. Ignateva[1], Tatiana Yu. Gorbunova[1], Ibrahima Keita[2], Yakov I. Alekseev[3], Roman V. Gorbunov[1], Aleksey A. Shvartsev[3], Aleksandr A. Volkov[3], Yuliya A. Monakhova[3], Vladimir A. Tabunshchik[1], Sory Diakité[2], Abdoulaye M. Baldé[2], Mamadou D. Sow[2] and Alpha I. P. Diallo[2]

[1]A.O. Kovalevsky Institute of Biology of the Southern Seas of RAS, Sevastopol, Russia
[2]Marine and Coastal Research Centre of Guinea (CEREMAC-G), Conakry, Guinea
[3]Syntol LLC, Moscow, Russia

Principal contact
Roman V. Gorbunov, Doctor of Geographical Sciences, A.O. Kovalevsky Institute of Biology of the Southern Seas of RAS; 2 Nakhimov Ave, Sevastopol, Russia 299011.
Tel. +79787294312
Email gorbunov@ibss-ras.ru
ORCID https://orcid.org/0000-0002-8222-3819

How to cite this article
Ignateva D.A., Gorbunova T.Yu., Keita I., Alekseev Ya.I., Gorbunov R.V., Shvartsev A.A., Volkov A.A., Monakhova Yu.A., Tabunshchik V.A., Diakité S., Baldé A.M., Sow M.D., Diallo A.I.P. Bacterial Composition of Soils in the Fatala River Basin (Guinea) during the Dry Season: An Examination of its Relationship with Ecological Landscape Characteristics. *South of Russia: ecology, development.* 2024; 19(4):110-130. DOI: 10.18470/1992-1098-2024-4-9

Received 22 August 2024
Revised 24 September 2024
Accepted 2 October 2024

Abstract
This paper examines the bacterial composition of soils in the Fatala River basin, Republic of Guinea.
This work is based on molecular genetic analysis.
The research findings indicate that the most prevalent phyla are *Proteobacteria*, *Firmicutes*, *Actinobacteria* and *Acidobacteria*. Notable dominant species include *Candidatus Koribacter versatilis* and *Candidatus Solibacter usitatus*. In facies 11, particularly in a bauxite mining zone, there is an increase in cyanobacteria, potentially due to their capacity to enrich soil fertility. Alpha diversity peaks in facies 10, 12, 17 and 18 and bottoms out in facies 7. The decline in alpha diversity in facies 7 might be attributed to the increase in plankomycetes, which produce antimicrobial substances to outcompete other species. When examining beta diversity, facies 10, 12 and 17 show the highest similarity, while facies 3, 5, and 7 exhibit the most significant differences compared to all points analysed.
The identification of the prevailing bacterial phylum and dominant species, along with specific taxa exhibiting increases or decreases in biodiversity, is a crucial first step in characterising the microbial communities found in the natural environments studied. The methodology established can be employed in environmental surveillance and evaluation of the health of diverse soil types.

Key Words
Microbiome, bacterial composition, ecology, species diversity indices, soil, river basin, Fatala River, Republic of Guinea.

Бактериальный состав почв бассейна реки Фатала (Гвинейская Республика) в сухой сезон и его взаимосвязь с экологическими характеристиками ландшафтов

Дарья А. Игнатьева[1], Татьяна Ю. Горбунова[1], Ибрагима Кейта[2], Яков И. Алексеев[3], Роман В. Горбунов[1], Алексей А. Шварцев[3], Александр А. Волков[3], Юлия А. Монахова[3], Владимир А. Табунщик[1], Сори Диаките[2], Абдулайе М. Балде[2], Мамаду Д. Соу[2], Альфа И. П. Диалло[2]

[1]Федеральный исследовательский центр «Институт биологии южных морей имени А.О. Ковалевского РАН», Севастополь, Россия
[2]Морской и прибрежный исследовательский центр Гвинеи (CEREMAC-G), Конакри, Гвинея
[3]ООО «НПФ Синтол», Москва, Россия

Контактное лицо
Роман В. Горбунов, доктор географических наук, Федеральное государственное бюджетное учреждение науки Федеральный исследовательский центр «Институт биологии южных морей имени А. О. Ковалевского РАН»; 299011 Россия, Севастополь, Нахимова 2.
Тел. +79787294312
Email gorbunov@ibss-ras.ru
ORCID https://orcid.org/0000-0002-8222-3819

Формат цитирования
Игнатьева Д.А., Горбунова Т.Ю., Кейта И., Алексеев Я.И., Горбунов Р.В., Шварцев А.А., Волков А.А., Монахова Ю.А., Табунщик В.А., Диаките С., Балде А.М., Соу М.Д., Диалло А.И.П. Бактериальный состав почв бассейна реки Фатала (Гвинейская Республика) в сухой сезон и его взаимосвязь с экологическими характеристиками ландшафтов // Юг России: экология, развитие. 2024. Т.19, N 4. С. 110-130. DOI: 10.18470/1992-1098-2024-4-9

Получена 22 августа 2024 г.
Прошла рецензирование 24 сентября 2024 г.
Принята 2 октября 2024 г.

Резюме
В данной статье рассматривается бактериальный состав почв в бассейне реки Фатала (Гвинейская Республика).
Работа основана на молекулярно-генетическом анализе.
Результаты исследования показывают, что наиболее представленные филумы — это *Proteobacteria*, *Firmicutes*, *Actinobacteria* и *Acidobacteria*. В качестве видов-доминантов наиболее часто отмечены *Candidatus Koribacter versatilis* и *Candidatus Solibacter usitatus*. В фации 11, в районе, специализирующемся на добыче бокситов, наблюдается увеличение цианобактерий, что может быть связано с их способностью восстанавливать плодородие почв. Наиболее высокие показатели альфа-разнообразия фиксируются в фациях 10, 12, 17 и 18, а наименьшие – в фации 7. Снижение альфа-разнообразия в фации 7 может быть связано с увеличением численности планкомицетов, способные вырабатывать антимикробные вещества для устранения видов-конкурентов. При оценке бета-разнообразия выявлено, что наиболее схожими являются фации 10, 12 и 17, а фации 3, 5 и 7 имеют наибольшие отличия в сравнении со всеми проанализированными точками.
Выявление преобладающих бактериальных филумов и видов-доминантов, а также специфических видов с фиксацией повышения или понижения биоразнообразия является важным шагом для оценки характерных для исследуемых природных объектов микроорганизмов. Разработанный подход может быть применен для проведения экологического мониторинга и оценки состояния различных типов почв.

Ключевые слова
Микробиом, бактериальный состав, экология, индексы видового разнообразия, почва, бассейн реки, река Фатала, Гвинейская Республика.

INTRODUCTION

The Republic of Guinea, a West African nation, boasts substantial mineral, hydropower, and agricultural resources, ranking as Africa's top and globally the second-largest bauxite exporter, with reserves also including gold, uranium, iron ore, and diamonds [1]. The Fatala River basin spans Boke and Kindia provinces, home to the majority of Guinea's aluminum ore reserves [2–4]. The rich bauxite deposits of Fouta Djallon province, holding up to a third of Guinea's total aluminum reserves [5; 6], fuel industrial growth and infrastructure development, consequently impacting the environment [7]. Anthropogenic influences on Guinea's landscapes are mainly driven by urban expansion and a lack of active introduction of modern working methods into industrial enterprise activities aimed at reducing negative impact on the environment [8].

To mitigate the adverse, often devastating impacts of mining and safeguard natural landscapes, comprehensive environmental monitoring is essential. This involves periodic assessments of the extent and magnitude of human-induced landscape transformations, followed by the development of strategies for their rehabilitation. A key indicator of soil health is the analysis of its bacterial diversity [8–10]. Moreover, targeted manipulation of soil bacterial composition using both natural and synthetic microbial communities can aid in repairing and protecting healthy soil ecosystems, thereby mitigating or reversing environmental damage [11]. Nevertheless, the relationship between the soil microbiome of Guinea and its ecological and geographical landscape features remains unexplored to this day.

Soil, as a vital living system, underpins Earth's life support functions, with its microbiome serving as the primary driving force [12]. Soil hosts an extraordinary density of microorganisms, up to 10^8 bacterial cells per gram, contributing significantly to its biomass [13]. These microorganisms play a pivotal role in biogeochemical nutrient cycling, mobilising and stabilising nutrients for plants, thereby impacting overall soil fertility and plant health [14]. The soil microbiota mitigates greenhouse gas emissions, sequesters carbon, aids in pollutant degradation and disease suppression and secures nutrients for growth [15].

The soil microbiome is indispensable to the proper functioning of soil ecosystems [16]. Its abundance and diversity are shaped by soil type, climate, edaphic factors, nutrient availability, and oxygen levels [17]. Bacterial composition differs across habitats, from deserts to forests and is heavily influenced by abiotic and biotic factors such as pH, carbon content, soil structure, texture, vegetation and can vary markedly depending on the ecosystem and the corresponding inhabitants [16]. Soil microbiome composition is largely dictated by soil edaphic properties, acting as the primary ecological filter [16]. Surveys of diverse soils reveal that soil bacteria predominantly belong to phyla such as *Verrucomicrobia*, *Acidobacteria*, *Proteobacteria* (*Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, and *Deltaproteobacteria*), *Planctomycetes*, *Bacteroidetes*, and *Actinobacteria* [18]. Soil structure influences mesofauna development, with micropores of clay molecules potentially impeding microbial predation and lighter structures promoting bacterial growth. Moisture content impacts the microbiome, as water availability enables bacterial existence, mobility, nutrient dissolution, and gas diffusion. Different soil microorganisms prefer distinct pH ranges, as seen in correlations with specific microbiome compositions. For instance, liming acidic soil triggers high-frequency changes in bacterial composition and abundance, notably affecting phyla such as *Actinobacteria*, *Gemmatimonadetes*, β and δ*Proteobacteria*, *Chloroflexi*, and *Nitrospirae* [16].

Beyond their direct roles in nutrient cycling and organic matter transformation soil microorganisms can reshape the soil habitat through numerous biochemical and biophysical processes, leading to notable environmental impacts [19]. This becomes increasingly relevant in contemporary times, as global changes like anthropogenic soil threats (e.g., forest conversion to agriculture) and climate change challenge normal soil functioning. To ensure soil health, it is vital to have trustworthy indicators that pinpoint the nature of harmful changes and reflect soil quality [20]. Rapid advancements in molecular (DNA-based) methods now enable deciphering microbiomes and revealing associations between microbial communities and soil ecological states [21].

The objective of this study was to describe the bacterial diversity of soils within the Fatala River basin, which exhibits a range of ecological and geographical features, through molecular genetic analysis.

MATERIALS AND METHODS

The Fatala River serves as a vital waterway for the surrounding region, with its basin encompassing diverse landscape zones, such as plains, hilly terrain and mountain systems. This variability offers an ideal setting for expeditionary research.

The Fatala River is located in the Republic of Guinea, in its western part and belongs to the Atlantic Ocean basin (Fig. 1). The relief of the territory is diverse: the coastal plains give way to the dismembered Fouta Djallon plateau, in the east there is an elevated stratum plain and in the south the North Guinean Upland with low mountains rises. The climate of the Fatala River basin is subequatorial, with pronounced wet and dry seasons. The average annual air temperature range is 24–30 °C. The rainy season lasts from May to October, during which time the bulk of precipitation falls, which maintains a high level of humidity and contributes to the rapid development of vegetation [22]. Soils in the basin are mainly represented by three types: lithic leptosols, ferrallitic soils and thionic fluvisols [23]. The vegetation within the basin comprises tropical forests, savannas, and dense shrubby thickets.

During the expedition studies, 18 facies in various landscape conditions were described. In each, soil profiles were established and horizons identified and described (Fig. 2). Samples from each horizon were collected to ascertain soil bacterial composition. Table 1 offers a concise description of the sampled facies.

METHOD FOR ISOLATING TOTAL DNA FROM SOILS

A detailed soil profile was made at each of the 18 chosen facies, followed by a thorough soil description. Soil samples were collected from each selected horizon, with approximately 15–20 ml of soil placed in a 50 ml tube and preserved with a 95% ethanol solution to maintain the bacterial composition unchanged. Total DNA was extracted from all selected samples, except for facies 14 due to irreparable damage during transportation. Prior to extraction, soil samples were removed from the alcoholic solution into a 1.5 ml tube (700–800 mg), centrifuged at 5000 rpm for three minutes, and the supernatant was discarded. The remaining pellets were heated in an oven at 50°C with open lids until all alcohol had evaporated.

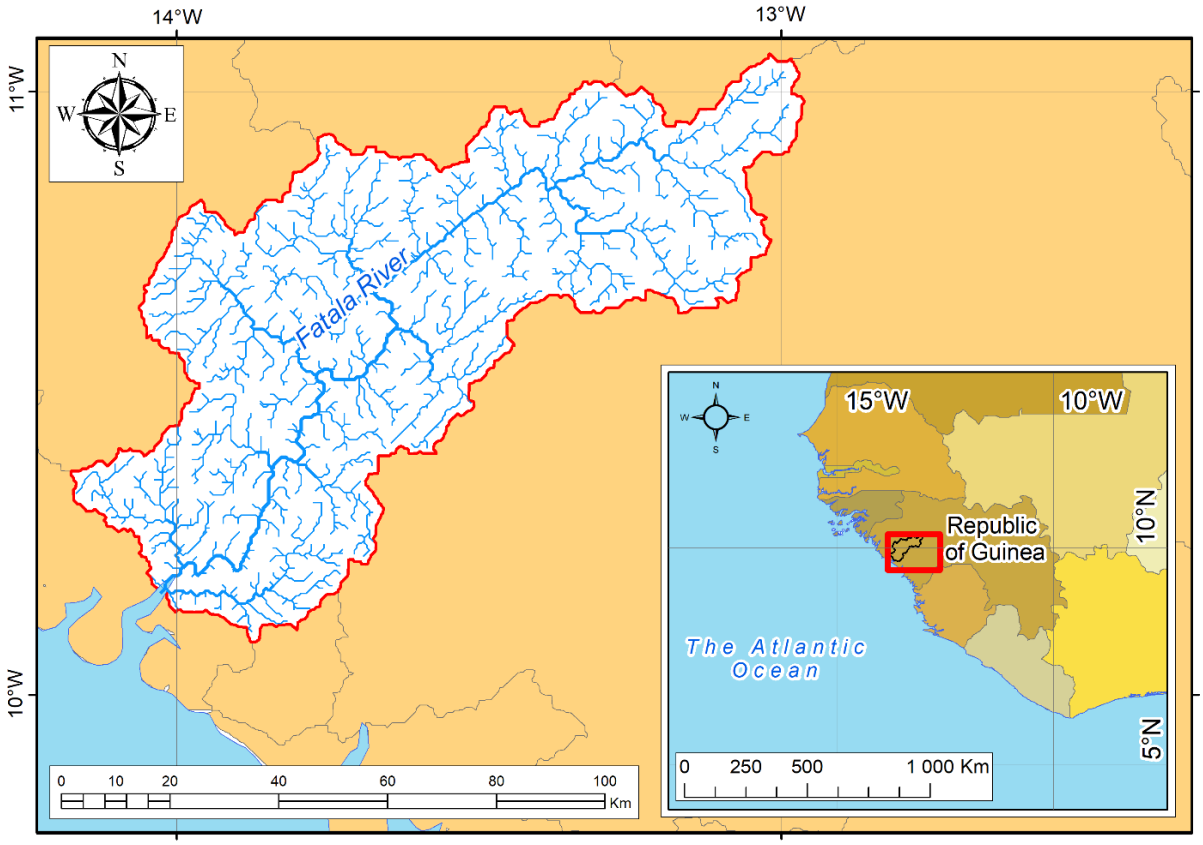

Figure 1. Geographical location of the Fatala River basin
Рисунок 1. Географическое положение бассейна реки Фатала

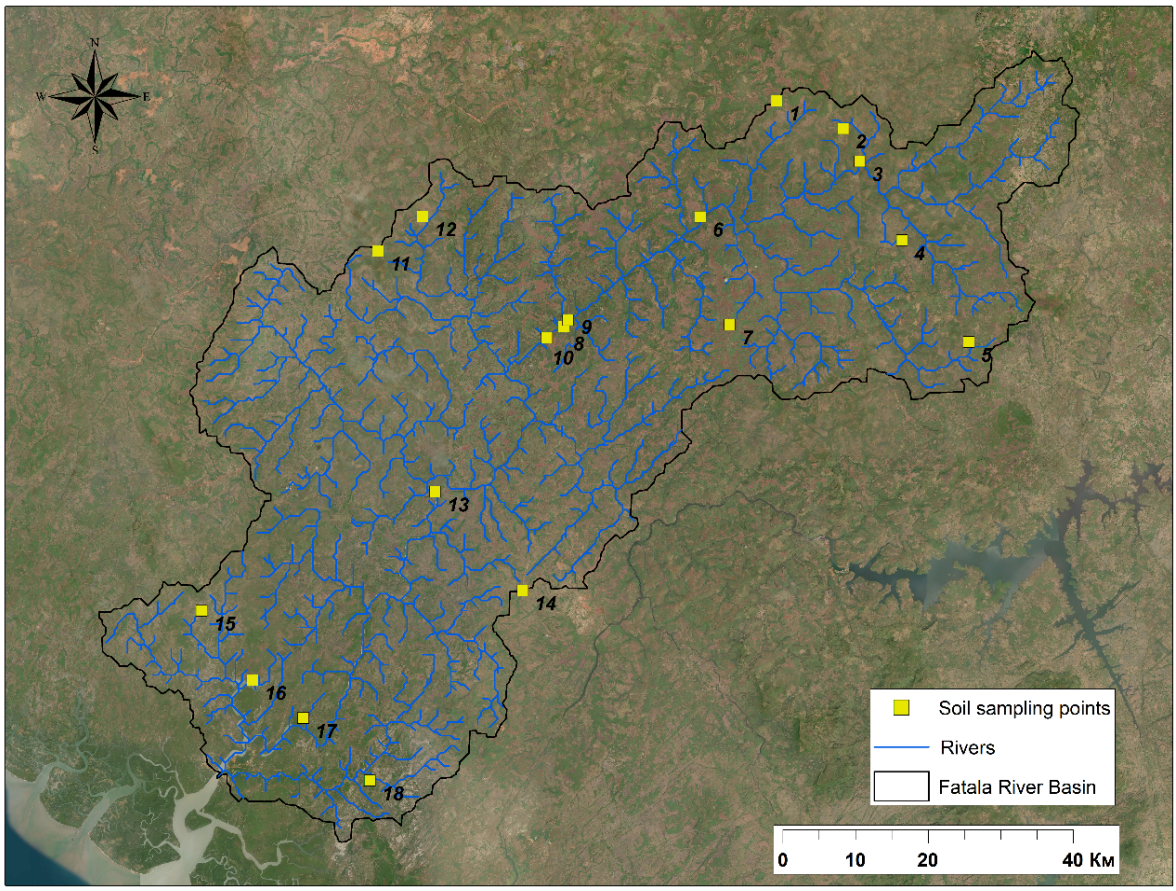

Figure 2. Sampling points in the Fatala River basin
Рисунок 2. Точки отбора проб в бассейне реки Фатала

Table 1. Brief description of the studied facies [22]
Таблица 1. Краткая характеристика исследуемых фаций [22]

Facies Фация	**Description** / Описание
1	Narrow, gently sloping (1–2°) watershed surface of south-southwest exposure, composed of Devonian siltstone-mudstones, mudstones with interlayers of fine-grained sandstones, with a low-growing, single-storied sparse forest on medium-thick, weakly humus-bearing, skeletal sandy loam leptosols on stony-blocky eluvium of Devonian deposits. Поверхность водораздела узкая слабонаклонная (1–2°) юго-юго-западной экспозиции, сложенная девонскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистых песчаников с низкоствольным одноярусным разреженным лесом на литосолях среднемощных слабогумусированных супесчаных сильноскелетных на каменисто-глыбистом элювии девонских отложений.
2	Steep (23°) middle part of the slope of southern exposure, composed of Devonian siltstone-mudstones, mudstones with interlayers of fine-grained sandstones, with a dense, low-growing, single-storied forest on shallow, poorly humus-bearing sandy loam leptosols on the bedrock massif of Devonian deposits. Средняя часть склона крутая (23°), южной экспозиции, сложенная девонскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистых песчаников с густым низкорослым одноярусным лесом на литосолях маломощных слабогумусированных супесчаных на скальном массиве девонских отложений.
3	Gently sloping (1–2°) surface of the Fatala River high floodplain of west-north-western exposure, composed of Devonian coarse-grained quartz sandstones, gritstones and conglomerates, with a dense, tall, two-storied forest on fluvisols, thick, poorly humus-bearing, light loamy soil on alluvium of Devonian deposits. Поверхность высокой поймы реки Фатала слабонаклонная 1–2°, западно-северо-западной экспозиции, сложенная девонскими крупными кварцевыми песчаниками, гравелитами и конгломератами с густым высокорослым двуярусным лесом на аллювиальной мощной слабогумусированной легкосуглинистой почве на аллювии девонских отложений.
4	Gentle (5–10°) upper part of the slope of south-southwestern exposure, composed of Devonian coarse-grained quartz sandstones, gritstones and conglomerates, with a dense, tall, two-storied forest on medium-thick, low-humus, skeletal sandy loam leptosols on the colluvium of Devonian deposits. Верхняя часть склона пологая (5–10°), юго-юго-западной экспозиции, сложенная девонскими крупными кварцевыми песчаниками, гравелитами и конгломератами с густым высокорослым двухъярусным лесом на литосолях среднемощных малогумусных супесчаных сильноскелетных на делювии девонских отложений.
5	Gentle (10–15°) watershed surface of the ridge of southern exposure, composed of Devonian coarse-grained quartz sandstones, gritstones and conglomerates, with a dense, tall, two-storied forest on deep, poorly humus-bearing, skeletal sandy loam ferralitic soils on the eluvium-colluvium of Devonian deposits. Водораздельная поверхность хребта пологая (10–15°), южной экспозиции, сложенная девонскими крупными кварцевыми песчаниками, гравелитами и конгломератами с густым высокорослым двуярусным лесом на желтоземах мощных слабогумусированных супесчаных сильноскелетных на элюво-делювии девонских отложений.
6	Periodically flooded, slightly wavy, gently sloping (1–2°) surface of the Fatala River floodplain of north-northwestern exposure, composed of Devonian dolerites, congadiabases and gabbro-dolerites, with a dense, single-storied floodplain forest on fluvisols soils, thick, poorly humus-bearing, light loamy soil on gravelly alluvium. Поверхность поймы реки Фатала, периодически затопляемая, слабоволнистая, слабонаклонная (1–2°), северо-северо-западной экспозиции сложенная девонскими долеритами, конгадиабазами и габбро-долеритами с пойменным одноярусным густым лесом на аллювиальной мощной слабогумусированной легкосуглинистой почве на галечниковом аллювии.
7	Slightly wavy, gently sloping (1–2°) watershed surface is of south-south-western exposure, composed of Devonian siltstone-mudstones, mudstones with interlayers of fine-grained sandstones, with a grass monodominant community on shallow, low-humus, skeletal sandy loam leptosols on the stony-blocky eluvium of Devonian deposits. Поверхность водораздела слабоволнистая слабонаклонная (1–2°) юго-юго-западной экспозиции сложенная девонскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистых песчаников со злаковым монодоминантным сообществом на литосолях маломощных малогумусных супесчаных сильноскелетных на каменисто-глыбистом элювии девонских отложений.
8	Inclined (5–7°) upper part of the slope of north-eastern exposure, composed of Devonian siltstone-mudstones, fine-grained sandstones and mudstones, with shrub communities and isolated standing trees on deep, poorly humus-bearing, skeletal sandy loam ferralitic soils on the stony-blocky colluvium of Devonian deposits. Верхняя часть склона наклонная (5–7°) северо-восточной экспозиции сложенная девонскими алевро-аргиллитами, мелкозернистыми песчаниками и аргиллитами с кустарниковыми сообществами и единично стоящими деревьями на желтоземах мощных слабогумусированных супесчаных сильноскелетных на каменисто-глыбистом делювии девонских отложений
9	Steep (40–45°) lower part of the slope of the Fatala River valley of north-western exposure, composed of Devonian siltstone-mudstones, mudstones with interlayers of fine-grained sand, with a two-storied broad-leaved forest on deep, poorly humus-bearing, medium loamy skeletal ferralitic soils on the stony-blocky

	colluvium of Devonian deposits. Нижняя часть склона долины реки Фатала, крутая (40–45°) северо-западной экспозиции сложенная девонскими алевро-аргиллитами, аргиллитами с прослоями мелкозернистого песка с двухъярусным широколиственным лесом на желтоземах мощных слабогумусированных среднесуглинистых скелетных на каменисто-глыбистом делювии девонских отложений.
10	Periodically flooded, slightly wavy, gently sloping (5–7°) surface of the first terrace above the floodplain of the Fatala River of south-eastern exposure, composed of Devonian siltstone-mudstones, fine-grained sandstones and mudstones, with a two-storied broad-leaved floodplain forest on fluvisols, deep, poorly humus-bearing, medium-heavy loamy soil on sandy-boulder alluvium. Поверхность первой надпойменной террасы реки Фатала, периодически затопляемая, слабоволнистая, пологонаклонная (5–7°), юго-восточной экспозиции сложенная девонскими алевро-аргиллитами, мелкозернистыми песчаниками и аргиллитами с пойменным двухъярусным широколиственным лесом на аллювиальной мощной слабогумусированной средне-тяжелосуглинистой почве на песчано-валунном аллювии.
11	Wavy, gently sloping (1–2°) surface of the watershed of northeastern exposure, composed of Silurian siltstone-mudstones, mudstones with interlayers of fine-grained sandstones, with a regenerated young forest on medium-depth, poorly humus-bearing, skeletal sandy loam leptosols on the stony-blocky eluvium of Silurian deposits. Поверхность водораздела волнистая слабонаклонная (1–2°), северо-восточной экспозиции, сложенная силурскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистых песчаников с восстановленным молодым лесом на литосолях среднемощных слабогумусированных супесчаных сильноскелетных на каменисто-глыбистом элювии силурских отложений.
12	Gentle (6–7°) middle part of the slope of the watershed ridge of southern exposure, composed of Silurian siltstone-mudstones, mudstones with interlayers of fine-grained sandstones, with a dense regenerated young forest on medium-depth, low-humus, skeletal sandy loam leptosols on the stony-blocky colluvium of Silurian deposits. Средняя часть склона водораздельной гряды пологая (6–7°), южной экспозиции, сложенная силурскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистых песчаников с густым восстановленным молодым лесом на литосолях среднемощных малогумусных супесчаных сильноскелетных на каменисто-глыбистом делювии силурских отложений.
13	Periodically flooded, slightly wavy, gently sloping (5–14°) surface of the first terrace above the floodplain of the Fatala River of south-southwestern exposure, composed of Silurian siltstone-mudstones, fine-grained sandstones and mudstones, with a dense single-storied broad-leaved floodplain forest on fluvisols, gleyed, deep, poorly humus-bearing, medium loamy soil on Silurian alluvial deposits. Поверхность первой надпойменной террасы реки Фатала, периодически затопляемая, слабоволнистая, пологонаклонная (5–14°), юго-юго-западной экспозиции сложенная силурскими алевро-аргиллитами, мелкозернистыми песчаниками и аргиллитами с пойменным одноярусным широколиственным густым лесом на аллювиальной оглеенной мощной слабогумусированной среднесуглинистой почве на аллювии силурских отложений.
14	Wide, slightly wavy, gently sloping (3–4°) surface of the watershed of southern exposure, composed of Silurian siltstone-mudstones, mudstones with interlayers of fine-grained sandstone, with a grass-shrub association on shallow, poorly humus-bearing, skeletal light loamy leptosols on the stony-blocky eluvium of Silurian deposits. Поверхность водораздельная, широкая, слабоволнистая слабонаклонная (3–4°), южной экспозиции, сложенная силурскими алевро-аргиллитами, аргиллитами с прослоями из мелкозернистого песчаника со злаково-кустарниковой ассоциацией на литосолях маломощных слабогумусированных легкосуглинистых скелетных на каменисто-глыбистом элювии силурских отложений.
15	Stepped, gentle (2–7°) middle part of the slope of a low watershed ridge of north-western exposure, composed of Ordovician coarse quartz sandstones, gritstones and conglomerates, with grassy communities in combination with scattered shrubs on deep, poorly humus-bearing sandy loam ferralitic soils on the bedrock massif of Ordovician deposits. Средняя часть склона низкой водораздельной гряды, ступенчатая пологая (2–7°), северо-западной экспозиции, сложенная ордовикскими крупными кварцевыми песчаниками, гравелитами и конгломератами со злаковыми сообществами в комплексе с единично стоящими кустарниками на желтоземах мощных слабогумусированных супесчаных на скальном массиве ордовикских отложений.
16	Periodically flooded, slightly wavy, gently sloping (2–3°) surface of the first terrace above the floodplain of the Fatala River of southern exposure, composed of Ordovician coarse quartz sandstones, gritstones and conglomerates, with a dense two-storied broad-leaved floodplain forest dominated by palm trees, on fluvisols, gleyed, deep, poorly humus-bearing, medium-light loamy soil on Ordovician alluvial deposits. Поверхность первой надпойменной террасы реки Фатала, периодически затопляемая, слабоволнистая, слабонаклонная (2–3°), южной экспозиции сложенная ордовикскими крупными кварцевыми песчаниками, гравелитами и конгломератами с пойменным двухъярусным широколиственным густым лесом с доминированием пальм на аллювиальной оглеенной мощной слабогумусированной средне-легкосуглинистой почве на аллювии ордовикских отложений.
17	Gently sloping (5–7°) lower part of the slope of the hill of south-western exposure, composed of Ordovician coarse quartz sandstones, gritstones and conglomerates, with a single-storied low-growing forest on deep, low-humus, light loamy ferralitic soils on the colluvium of Ordovician deposits.

	Нижняя часть склона холма пологая (5–7°), юго-западной экспозиции, сложенная ордовикскими крупными кварцевыми песчаниками, гравелитами и конгломератами с одноярусным низкорослым лесом на желтоземах мощных малогумусных легкосуглинистых на делювии ордовикских отложений.
18	Gentle (4°) upper part of the slope of a gentle low hill is of western exposure, composed of Ordovician coarse quartz sandstones, gritstones and conglomerates, with a sparse open forests on deep, poorly humus-bearing, medium loamy ferralitic soils on the colluvium of Ordovician deposits. Верхняя часть склона пологого низкого холма пологая (4°), западной экспозиции, сложенная ордовикскими крупными кварцевыми песчаниками, гравелитами и конгломератами с разреженным редколесьем на желтоземах мощных слабогумусированных среднесуглинистых на делювии ордовикских отложений.

Total DNA was isolated from selected soil samples using the protocol developed by the Phylogenomics and Transcriptomics Scientific and Educational Research Equipment Sharing Centre of the A.O. Kovalevsky Institute of Biology of the Southern Seas of the Russian Academy of Sciences (RAS). This process was designed to isolate total bacterial DNA from soil samples for subsequent analysis of soil bacterial composition via mass parallel sequencing [24].

The resulting filler liquid contained a solution of purified total DNA suitable for the preparation of metagenomic libraries. The assessment of the quality and quantity of the isolated DNA was carried out using real-time PCR (PCR-RV). Samples for which the threshold cycle value (Ct) was 30 or less were used for further analysis. Samples with a Ct value of more than 30 were isolated repeatedly.

Preparation of metagenomic libraries with subsequent sequencing for the analysis of the bacterial composition of soils

The bacterial diversity of the selected soil samples was analyzed using the Phylogenomics and Transcriptomics Scientific and Educational Research Equipment Sharing Centre at the A.O. Kovalevsky Institute of Biology of the Southern Seas of the RAS, according to the technology developed by the authors for assessing soil bacterial composition via mass parallel sequencing of V3 and V4 amplicon libraries from the 16S rRNA gene [24].

Raw sequencing data (fastq) was analyzed using FastQC and MultiQC utilities for bioinformatic analysis. Key metrics, including read quality, read length, GC content distribution, and other parameters that allows the evaluation of the quality of sequencing and the efficiency of the device, were presented in a detailed HTML report. This information was used to make decisions about the parameters for further data filtering. At the subsequent stage, we employed the Trimomatic tool to remove subpar data. Throughout this filtration process, we eliminated reads exhibiting an average quality score below Q25, as well as the removal of adapter sequences and nucleotides at read ends with a quality score below Q20. This improved the overall quality of the data before further analysis. For taxonomic classification, we employed the Kraken2 tool, utilizing its proprietary database, Minikraken v2. To visualize the results and generate an HTML report featuring Sankey diagrams, we used the web version of the Pavian utility. Additionally, we created tables and graphs based on Kraken2's output files to facilitate operation. To this end, we developed custom Python scripts that automated data processing and visualization generation.

Methods for identifying dominant species and assessing the alpha and beta diversity of soil bacteria

At each site studied, we identified dominant, subdominant, secondary and rare species based on standard criteria for the distribution of individual numbers in the biocenosis, as presented in Table 2.

Table 2. Criteria for the distribution of the importance of species in the biocenosis
Таблица 2. Критерии распределения значимости видов в биоценозе

Position in the biocenosis Положение в биоценозе	**Relative abundance (%)** Относительное обилие (%)
Dominant species / Виды-доминанты	10–100
Subdominant species / Виды-субдоминанты	1–10
Secondary types / Второстепенные виды	0,1–1
Rare species /Редкие виды	less then 0,1 / менее 0,1

To evaluate the alpha diversity of microbial communities, we computed the Margalef species richness index, the Shannon index, the Simpson index, and the Pielou's evenness index. The Margalef's species richness index (D_{Mg}) gauges biodiversity within a specific area, leveraging absolute values, i.e., abundance, rendering it highly sensitive to sample size. It is calculated using the formula:

$$DMg = (S - 1) / \ln(N), \quad (1)$$

where S represents the total number of species, and N signifies the total number of individuals. A higher index value indicates that the community is richer in species diversity.

The Shannon index (H) is a diversity measure that considers both species richness and evenness. It is calculated using the formula:

$$H = -\Sigma(p_i * \ln(p_i)), \quad (2)$$

where p_i represents the relative abundance of the i-th species. A higher Shannon index value corresponds to greater species diversity.

Simpson's diversity index (D) quantifies species diversity, with heightened sensitivity to dominant species. It is calculated as:

$$D = \Sigma(n_i * (n_i - 1)) / (N * (N - 1)), \quad (3)$$

where n_i is the number of organisms of species i, and N is the total number of organisms. Simpson's diversity index ranges from 0 to 1, with higher values indicating lower diversity. To facilitate comparison with other alpha-diversity indices, the value of (1 - D) was also calculated.

The Pielou's Evenness (E) metric quantifies the uniformity of species distribution within a community. It is

calculated using Shannon's Index and falls within the range of 0 to 1.

$$E = H/ \ln S, \quad (4)$$

where H – the Shannon Index, S – number of identified species. The closer the value is to 1, the more evenly species are distributed within the community.

To analyse the beta-diversity among microbial communities, the Jaccardand Bray-Curtis indices were calculated. The Jaccard similarity index (JI) is a measure of the similarity between two communities, focusing solely on the presence or absence of species and ranging from 0 to 1. A value closer to 1 indicates a higher degree of similarity between the two datasets.

$$JI = C/(A+B-C), \quad (5)$$

where A is the number of species in the first community, B is the number of species in the second community, and C is the number of shared species between the two communities. The Bray-Curtis dissimilarity (BC_{ij}) is used to quantitatively assess the compositional dissimilarity between two different communities based on abundance data, considering both the presence/absence and relative abundance of species. Values closer to 1 indicate a higher degree of dissimilarity between the two datasets.

$$BC_{ij} = 1 – (2*C_{ij}) / (S_i + S_j), \quad (6)$$

where C_{ij} represents the sum of the lesser values among the species found on each plot, S_i is the total number of individuals on plot i, and S_j is the total number of individuals on plot j.

RESULTS AND DISCUSSION

Presence of Bacterial Phylum in Soils

In analysing bacterial diversity among types across 18 sites, it was found that the most prevalent phyla were *Proteobacteria* (ranging from 19.3 % to 46.8 %), *Firmicutes* (ranging from 8.5 % to 5 2%), *Actinobacteria* (ranging from 7.6 % to 30.5 %), and *Acidobacteria* (ranging from 3.6 % to 15.8 %). Based on the data collected, we constructed diagrams illustrating the distribution of phyla in the humic horizon of soils (Fig. 3).

The phylum *Proteobacteria* is dominant in facies 1 (35.9 %), 2 (36.3 %), 7 (46.8 %), 10 (35.2 %), and 12 (36.2 %), while *Firmicutes* dominates in facies 3 (34.5 %), 4 (38.7 %), 5 (52 %), 6 (50.9 %), 9 (50.5 %), 13 (34.6 %), 15 (30.3 %) and 18 (45.6 %). In facies 8, 11, and 17, *Proteobacteria* and *Firmicutes* are equally prevalent (27.3 % and 30 % in facies 8; 33 % and 29.9 % in facies 11; and 31.2 % and 30.2 % in facies 17). In facies 16, *Actinobacteria* and *Firmicutes* are equally dominant (30.5 % and 27.2 %, respectively).

The content of *Proteobacteria* is lowest in facies 5 and 6 (20.5 % and 19.3 %, respectively), and the number of phylum *Firmicutes* decreases sharply in facies 7 (up to 8.5 %), also in this area the lowest content of bacteria of the phylum *Actinobacteria* (7.6 %), but there is an increased content of *Planctomycetes* (14.9 %), *Thermotogae* (2.4 %) and *Verrucomicrobia* (2.7 %). The least *Acidobacteria* was found in facies 4 (3.6 %), and the most in facies 3 (15.8 %). The highest amount of *Cyanobacteria* is observed in facies 7, 11 and 15 (5,1 %, 7,8 % 5,3 %). The phylum *Caldiserica* is specifically present in small numbers in facies 10, 15 and 17, the phylum *Candidatus Cloacimonetes* in facies 2 and 10, *Candidatus gracilibacteria* in facies 5, *Candidatus Micrarchaeota* in facies 3, *Kiritimatiellaeota* in facies 8 and 12. The phylum *Armatimonadetes* is specifically absent in facies 6, *Candidatus Saccharibacteria* and *Euryarchaeota* in facies facies 7, *Chlorobi* in facies 5, 7, 9. *Cyanobacteria* in facies 16, *Deferribacteres* in facies 2 and 9, *Dictyoglomi* in facies 5.

Bacterial Diversity in Soils

Based on the acquired data, we constructed diagrams displaying the distribution of dominant and fluctuating subordinate species (Fig.4).

Upon analysing the bacterial diversity across 18 sites, calculating relative abundances, and identifying dominant, subdominant, secondary, and rare species, it was found that *Acidisphaera* sp. G45-3 is a dominant species in facies 7 (13.3 %) (and also a subdominant species in 6 facies and a secondary species in 9 facies). *Aneurinibacillus soli* is dominant in facies 9 (18.8 %) and absent in facies 3. It is a secondary species in facies 2 and 7, and subdominant in the remaining facies. *Candidatus Koribacter versatilis* is dominant in facies 3 (11.3 %), 5 (10.4 %), 8 (10.3 %), 11 (11.5 %), and 15 (12.1 %). It is a secondary species in facies 7 (0.7 %) and subdominant in the other facies. *Candidatus Solibacter usitatus* is dominant in facies 1 (13.4 %), 2 (10 %), 3 (14.2 %), 7 (15 %), 8 (14.9 %), 10 (12.8 %), 12 (12 %) and 17 (11.1 %), and is subdominant in the remaining facies. *Cutibacterium acnes* is dominant in facies 2 (16.4 %) and is subdominant in facies 6. It is a secondary species in the remaining facies. *Rhodoplanes* sp. Z2-YC6860 is dominant in facies 4 (11.3 %) and is subdominant in the other facies. *Scytonema* sp. HK-05 is dominant in facies 11 (12.1 %), is subdominant in facies 8 and 16 and is absent in facies 3, 5, and 6. *Luteitalea pratensis* is subdominant, except in facies 7 where it is a secondary species (0.2 %). *Mahella australiensis* is subdominant in facies 10 and 16, and is secondary or rare in the other facies. *Methylobacterium* sp. 4-46, *Singulisphaera acidiphila*, and *Planctopirus limnophila* are subdominant in facies 7 and are secondary or rare in the others. *Moraxella osloensis* is subdominant in facies 11, and is rare or secondary in the others. *Mycoplasma wenyonii* is subdominant in facies 2 and17 and is absent in facies 3, being rare or secondary in the others. *Paeniclostridium sordellii* is subdominant in facies 5, 6, and 18 and is absent in facies 3, 7, 9, and 13. *Planctomyces* sp. SH-PL62 is subdominant in facies 7 and absent in facies 3. *Prevotella intermedia* is subdominant in facies 6 and either absent or rare in the others. *Sphaerochaeta globosa* is subdominant in facies 15. *Thermanaeromonas toyohensis* is subdominant in facies 12 and 13. *Jeotgalibacillus malaysiensis* is subdominant in facies 3 (2.6 %) and secondary in facies 5 and has not been found in the other facies. *Lysinibacillus* sp. Marseille-P5727 is subdominant in facies 5 and rare in facies 3 and has not been found in the other facies.

Bacterial community alpha-diversity in soil

According to the Margalef richness index, facies 1 and 16 exhibit the highest species richness (10.6 and 10.51, respectively). The lowest species richness is observed in facies 7 and 11 (both 8.6). The remaining facies show intermediate values ranging from 9.1 to 10.1. The highest Shannon index values are recorded in facies 10 (3.88), 12 (3.86), 17 (3.92), and 18 (3.85), while the lowest value is found in facies 7 (3.13). Simpson's index exhibits its lowest value in facies 7, aligning with Margalef's and Shannon's

indices, while its highest value is seen in facies 18, consistent with the Shannon index. Based on Pielou's evenness, the lowest evenness is found in facies 7, while the highest evenness is observed in facies 10, 12, 17, and 18. Table 3 presents calculated alpha-diversity indices for bacterial communities.

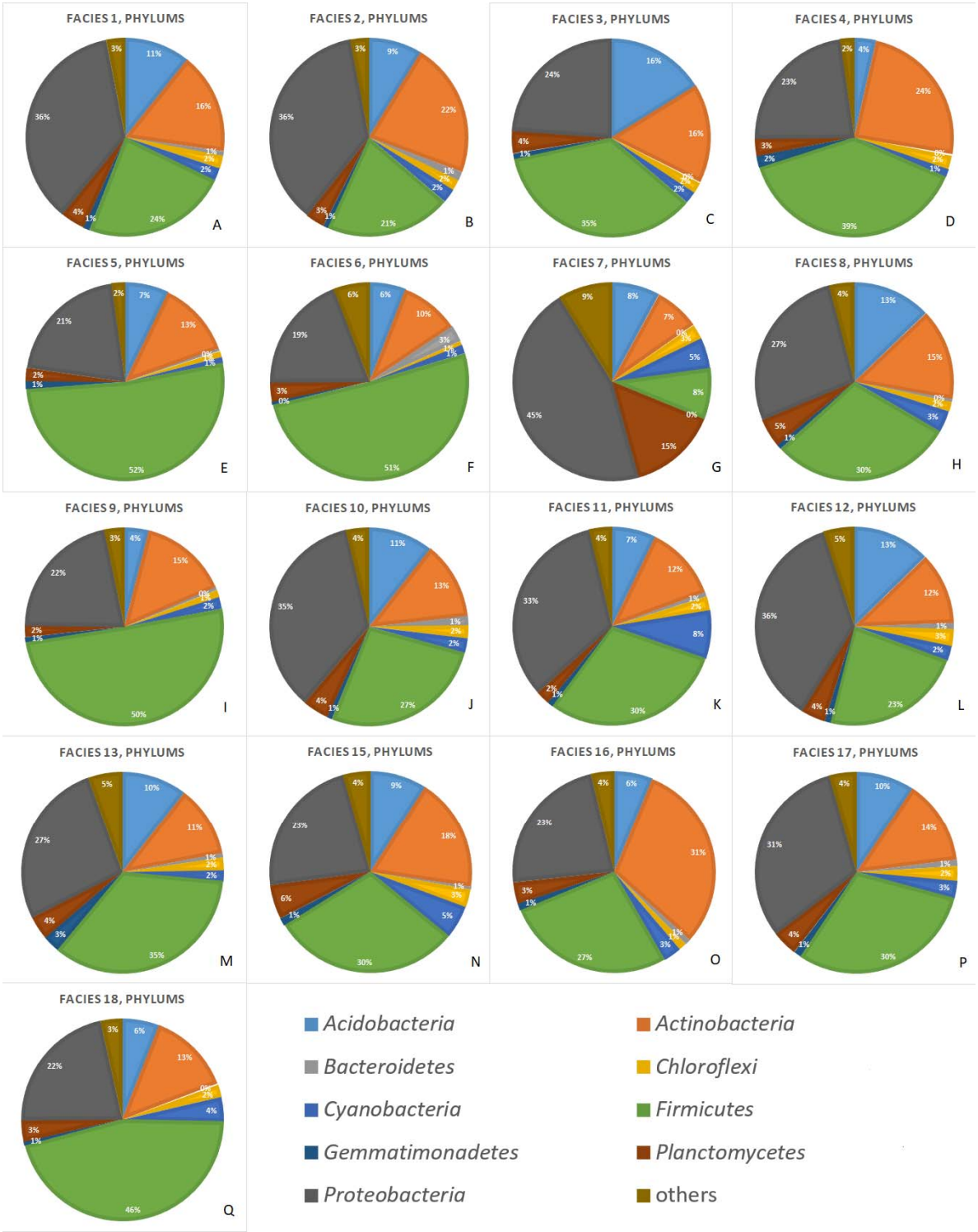

Figure 3. Content of major bacterial phylum in soil
Рисунок 3. Содержание основных филумов бактерий в почве

Bacterial community beta-diversity in soils

Upon calculating the Jaccard similarity index, it was found that the most distinct bacterial communities are those of facies 3 (0.51 ± 0.01) and facies 5 (0.56 ± 0.02). The most similar communities are those of facies 10 and 17 (0.99), as well as facies 2 and 10 and facies 8 and 16 (0.98).

For facies 1, the closest community is that of facies 16 (0.95), for facies 2, it is facies 10 (0.98), 12 (0.96), and 17 (0.95). Considering its significant difference from other points, facies 3 is most similar to facies 5 and 17 (0.53). Facies 4 is most similar to facies 8 (0.96) and 12 (0.95). Both facies 5 and 3 exhibit notable differences in species composition with all studied facies, with facies 7, 9, and 13 (0.58) being the closest among the investigated sites. Facies 6 is most similar to facies 16 (0.91) and 12 (0.9), facies 7 to 2 and 12 (0.91), facies 8 to 16 (0.98),

12 (0.97) and 4 (0.96) and facies 9 to facies 4 and 8 (0.94). Facies 10 exhibits the highest index values among all studied points and is most similar in species composition to facies 17 (0.99) and 2 (0.98). For facies 11, the closest communities are facies 18 (0.9), 4 and 12 (0.88). Facies 12 shows the greatest similarity with facies 8 and 16 (0.97) and also with facies 2 (0.96). Facies 13 is most similar to facies 16 (0.95), 8 and 17 (0.93). Facies 15 is most similar to facies 4, 8, and 17 (0.91). Facies 16 is most similar to facies 8 (0.98), 12 (0.97) and 17 (0.96). Facies 17 has the highest index value of 0.99 with facies 10 and also exhibits high indices with facies 16 (0.96) and 2 (0.95). Facies 18 is similar to facies 8 and 16 (0.95).

Figure 4. Facies distribution of dominant species and a selection of subordinate species with the most variable representation
Рисунок 4. Диаграммы распределения в фациях видов-доминантов и ряда видов-субдоминатов с наиболее изменчивой представленностью

This allows us to identify the most distinct communities in terms of species composition for facies 3 and 5, as well as a similar group of communities comprising facies 2, 4, 8, 10, 12, 16 and 17. Table 4 presents the most similar communities based on species composition.

A statistical inconsistency has been found between the Jacard index and the Brey-Curtis index. While the differences between facies 3, 5 and the rest remain relatively high (0.51±0.08; 0.5±0.07), there are several points where the differences are more pronounced, whereas in previous calculations, the greatest differences were observed when comparing facies 3 and 5 with the overwhelming majority of facies. According to the Brey-Curtis index, the most distinct facies are 7 and 5, 7 and 9 (0.73), 7 and 16 (0.72), as well as there are very high differences between facies 7 and 6, 7 and 11 (0.7), 7 and 2 (0.69). Consequently, the community of facies 7 is the most variable, with an average Brey-Curtis index of 0.65±0.06 ($p<0.05$). The results of the Brey-Curtis index calculation are presented in Table 5.

Table 3. Alpha-diversity indices for bacterial communities
Таблица 3. Индексы альфа-разнообразия бактериальных сообществ

Facies Фация	**Margalef index** Индекс Маргалефа	**Shannon index** Индекс Шеннона	**Simpson index** Индекс Симпсона	**Pielou's evenness** Выравненность Пиелу
1	10.60	3.84	0.96	0.83
2	9.89	3.68	0.95	0.81
3	9.69	3.48	0.94	0.76
4	10.06	3.71	0.96	0.81
5	10.14	3.55	0.95	0.78
6	9.20	3.77	0.96	0.84
7	8.58	3.13	0.93	0.70
8	9.55	3.69	0.95	0.81
9	9.42	3.54	0.94	0.79
10	9.30	3.88	0.96	0.86
11	8.61	3.57	0.95	0.80
12	9.62	3.86	0.96	0.85
13	9.32	3.72	0.96	0.82
15	9.14	3.73	0.96	0.83
16	10.51	3.76	0.96	0.82
17	9.51	3.92	0.97	0.86
18	9.44	3.85	0.97	0.85

Table 4. Similar communities identified through beta-diversity index calculations
Таблица 4. Выявленные при расчете индексов бета-разнообразия схожие сообщества

Facies Фация	**The most similar communities** Наиболее схожие сообщества	**Average similarity** Средняя схожесть
1	16 (0,95)	0,85 ± 0,13
2	10 (0,98), 12 (0,96), 17 (0,95)	0,86 ± 0,14
3	5, 17 (0,53)	0,51 ± 0,01
4	8 (0,96), 12 (0,95)	0,85 ± 0,13
5	7, 9, 13 (0,58)	0,56 ± 0,02
6	16 (0,91) и 12 (0,9)	0,82 ± 0,12
7	2, 12 (0,91)	0,84 ± 0,12
8	16 (0,98), 12 (0,97), 4 (0,96)	0,88 ± 0,14
9	4, 8 (0,94)	0,85 ± 0,12
10	17 (0,99), 2 (0,98)	0,86 ± 0,14
11	18 (0,9), 4, 12 (0,88)	0,82 ± 0,11
12	8, 16 (0,97), 2 (0,96)	0,88 ± 0,14
13	16 (0,95), 8, 17 (0,93)	0,86 ± 0,12
15	4, 8, 17 (0,91)	0,84 ± 0,13
16	8 (0,98), 12 (0,97), 17 (0,96)	0,88 ± 0,14
17	10 (0,99), 16 (0,96), 2 (0,95)	0,87 ± 0,13
18	8, 16 (0,95).	0,86 ± 0,13

DISCUSSION

It has been observed that the phylum *Proteobacteria*, which includes methanotrophic bacteria [25], iron bacteria comprising acidophilic aerobic iron oxidizers, neutralophilic aerobic iron oxidizers, neutralophilic anaerobic iron oxidizers, anaerobic photosynthetic iron oxidizers [26], thiobacteria [27; 28] and denitrifying bacteria [29] dominates in facies 1, 2, 7, 10 and 12 (Fig. 3A, 3B, 3G, 3J, 3L), which are characterized by soils composed of Devonian (with the exception of facies 12, which belongs to Silurian deposits) aleurite-argillites with fine-grained sandstones (Table 1). Members of this phylum are highly adapted to carbon-rich conditions, enabling high metabolic activity, rapid growth, and reproduction and are thus considered copiotrophs or fast-growing microbes [30]. Consequently, their abundance may increase in soil contaminated with petroleum hydrocarbons, as proteobacteria are capable of biodegrading them [31; 32]. Notably, some pathogenic representatives of proteobacteria, such as the genus *Salmonella*, exhibit enhanced survival in clay-rich soils [33; 34]. Moreover, the lowest abundance of *Proteobacteria* was observed in facies 5 (coarse sandy soil)

and 6 (light loamy soil) (Fig. 3E), located in the northeastern part of the study area (Fig. 2) and characterised by the presence of thick weakly humus soils on Devonian deposits (Table 1). Furthermore, the abundance of *Salmonella* in soil can increase with increasing soil moisture and location at the top of the slope [35], but no significant correlations with these factors were found. In facies 6, located on the periodically flooded surface of the Fatala River floodplain, the phylum *Armatimonadetes*, which metabolises various forms of carbon [36], disappears (Fig. 3F). Previously, a decrease in the abundance of this phylum was observed with the transition from leptosols to luvisols, accompanied by an increase in soil carbon content, water-stable aggregates, porosity, moisture and acidity [37].

Table 5. Brey-Curtis index
Таблица 5. Индекс Брея-Кертиса

	2	3	4	5	6	7	8	9	10	11	12	13	15	16	17	18
1	0.24	0.50	0.45	0.44	0.42	0.64	0.31	0.48	0.25	0.43	0.21	0.30	0.37	0.35	0.22	0.38
2		0.52	0.52	0.54	0.47	0.69	0.43	0.52	0.34	0.49	0.31	0.42	0.47	0.43	0.31	0.47
3			0.55	0.55	0.53	0.61	0.31	0.61	0.45	0.50	0.43	0.44	0.50	0.58	0.48	0.55
4				0.43	0.41	0.67	0.46	0.31	0.49	0.39	0.50	0.53	0.46	0.39	0.43	0.36
5					0.49	0.73	0.47	0.52	0.50	0.46	0.49	0.49	0.51	0.40	0.49	0.44
6						0.70	0.41	0.39	0.41	0.42	0.42	0.46	0.45	0.52	0.37	0.35
7							0.54	0.73	0.56	0.70	0.59	0.65	0.60	0.72	0.60	0.64
8								0.51	0.28	0.35	0.27	0.27	0.35	0.42	0.28	0.38
9									0.49	0.47	0.51	0.54	0.50	0.43	0.45	0.40
10										0.42	0.15	0.29	0.40	0.45	0.15	0.42
11											0.41	0.42	0.42	0.46	0.37	0.41
12												0.24	0.39	0.44	0.17	0.41
13													0.39	0.45	0.29	0.44
15														0.47	0.33	0.32
16															0.43	0.45
17																0.35

The *Firmicutes* type, which includes pathogenic and industrially significant bacterial strains [38], dominates in facies 3, 4, 5, 6, 9, 13, 15, 18 (Fig.3C–3F, 3I, 3M, 3N, 3Q). In most of these facies, dense, tall, two-story forests (facies 3, 4, 5, 9) or dense, single-story floodplain forests (facies 6, 13) grow, with exceptions being facies 15, characterised by grass communities with scattered shrubs and facies 18, featuring sparse, open woodlands. These facies are positioned in floodplain (facies 3, 6, 13) and slope (facies 4, 5, 9, 18) areas in the landscape (Table 1). It has been previously established that bacteria of this type can dominate in soils with less favourable ecological conditions, as they help maintain the stability of the soil ecosystem [39]. For instance, a representative of *Paenibacillus polymyxa* enhances plant growth in an unfavorable environment and provides protection against abiotic stresses [38]. It has also been noted earlier that *Firmicutes* are widely distributed in the soils of deciduous forests [40] and meadows [29], which aligns with the findings of this study.

The phyla *Proteobacteria* and *Firmicutes* are equally dominant in facies 8, 11, and 17 (Fig. 3H, 3K, 3P), which are gently sloping (1–2°) and low-angle (5–7°) slope segments containing restored young (facies 11) and low-stature forests (facies 17) or shrub thickets (facies 8) (Table 1). These phyla, along with actinobacteria, share the ability to degrade oxalate to obtain carbon and energy, which is commonly found in natural environments as free acid or in the form of salts [41].

Actinobacteria, on par with *Firmicutes*, dominates in facies 16 (Fig. 3O), located in the southwestern part of the Fatala River basin (Fig. 2) and characterized by medium-light clayey soil with floodplain two-story broad-leaved dense forest dominated by palms (Table 1). The disappearance of the nitrogen-fixing phylum *Cyanobacteria* is noted. The lowest abundance of *Actinobacteria* and *Firmicutes*, with an increase in *Planctomycetes*, *Thermotogae*, *Cyanobacteria*, and *Verrucomicrobia*, and the specific disappearance of the phylum *Candidatus Saccharibacteria* and *Euryarchaeota*, is observed in facies 7 (Fig. 3G), located closer to the central part of the studied territory (Fig. 2) and distinguished by a grass monodominant community on thin, low-humus leptosols (Table 1). Bacteria of the *Planctomycetes* phylum actively interact with phototrophs and utilize carbon but have very slow growth and may be outcompeted in this ecological niche, potentially leading to the production of antimicrobial substances to deter bacterial competitors [42; 43], which may explain the decrease in the abundance of *Actinobacteria* and *Firmicutes*phylum, as well as the disappearance of *Candidatus Saccharibacteria* and *Euryarchaeota*phylum. The increase in *Cyanobacteria* and *Proteobacteria*phylum can be attributed to the absence of competition with planctomycetes due to different ecological niches.

Acidobacteria are least abundant in the soils of facies 4 and most abundant in those of facies 3 (Fig. 3C), both of which are located in the northeastern part of the Fatala River basin (Fig. 2). However, there is a transition from medium-textured, low-humus, sandy-skeletal leptosols on Devonian large quartz sandstone, gravel, and conglomerate alluvium to a thick, weakly humified, sandy-

silt soil on Devonian alluvium (Table 1). Previous studies have shown a decrease in *Acidobacteria* populations when leptosols are replaced by luvisols, accompanied by an increase in porosity, moisture, acidity, and carbon content, as well as water-stable aggregates [37]. Additionally, *Acidobacteria* are known to possess a wide range of transporters for the uptake of multiple substrates and can easily adapt to oligotrophic conditions and complex environments [42].

The highest abundance of *Cyanobacteria*, which are nitrogen-fixing bacteria, is observed in facies 7, 11, and 15 (Fig. 3G, 3K, 3N), located on water divides and mid-slope positions of low water divides with slopes ranging from 1° to 7° with thin, weakly humified sandy soils (Table 1). The presence of Cyanobacteria in facies 11, located in the vicinity of bauxite mining operations, can be explained by their ability to enhance soil fertility and restore soil properties [45,46]. *Caldiserica*, containing acetate-degrading bacteria [47] and serobacteria [48], specifically appears in facies 10, 15 and 17 (Fig. 3N, 3P). *Candidatus Cloacimonetes*, containing a row of syntrophic bacteria specialized in the anaerobic fermentation of propionate [49] and also involved in nitrogen and carbon metabolism cycles [50], arises in facies 2 and 10 (Fig. 3B, 3J). These areas are characterised by the presence of forests on low-humus soils, formed on Devonian aleuroliths and fine-grained sandstones (Table 1). The heat-loving chemoorganotrophic phylum *Dictyoglomi* [51] disappears, while *Candidatus Gracilibacteria*, whose significance for soils is poorly understood, arises in facies 5 (Fig. 3E) on the water divide surface of the ridge (Table 1). Acidophilic archaea *Candidatus Micrarchaeota* [52] arise in facies 3 (Fig. 3C), which is the surface of the high floodplain of the Fatala River (Table 1). It is known that this phylum is widely distributed in thermophilic and mesophilic acidic environments [53].

The phylum *Kiritimatiellaeota*, which includes strains that can break down sulfated polysaccharides under anaerobic conditions [54], has been discovered in facies 8 and 12 (Fig. 3H, 3L). These facies consist of sandy, highly skeletal soils that have formed on rocky debris from aleuritic-argillaceous rocks and fine-grained sandstones (Table 1). *Chlorobi* is absent from facies 5, 7, and 9 (Fig. 3E, 3G, 3I) that contain low- and medium-humus, skeletal, and highly skeletal soils (Table 1). Previous studies have shown a correlation between the presence of this phylum and soil texture, quality and organic carbon content [55]. *Deferribacteres* disappears in facies 2 and 9 (Fig. 3B, 3I), which are located on steep slopes composed of Devonian aleuritic-argillaceous rocks, argillites with interbeds of fine-grained sandstones, and forests on weakly humus soils (Table 1). It has been previously observed that this phylum dominates in forests undergoing restoration, a process that enhances ecosystem stability by increasing the number of nitrogen and phosphorus cycling species. This may indicate the involvement of these bacteria in enhancing soil multifunctionality [56].

Upon analysing facies 7 (Fig. 4G), which is characterised by a grass-dominated community on thin, low-humus leptosols (Table 1), it was found that *Acidisphaera* sp. G45-3 is the dominant species. The genus *Acidisphaera*, belonging to the alpha-proteobacteria phylum, consists of acidophilic chemoautotrophs that thrive in acidic and strongly acidic environments and are capable of photosynthesis [57]. They produce bacteriochlorophyll-a in the presence of zinc sulfate [58]. *Methylobacterium* sp. 4-46, *Singulisphaera acidiphila*, and *Planctopirus limnophila* are subdominants in this facies. *Methylobacterium* sp. 4-46 belongs to the nitrogen-fixing bacteria, but, unlike other members of this genus, it cannot perform methylotrophy. The mechanism of their symbiotic relationship with the host organism is not yet fully understood [59]. *Singulisphaera acidiphila* bacteria are moderately acidophilic, mesophilic planctomycetes that can grow and degrade various biopolymers under acidic, microaerobic and cold conditions [60]. One of their key ecological roles is the ability to utilise chitin as a growth substrate [61]. P*lanctopirus limnophila* are planctomycetes that produce bioactive molecules, form biofilms in water, actively metabolise carbon and, like other *Planctomycetes*, can synthesize their own antibiotics to compete with other species in their niche [42; 62]. *Luteitalea pratensis* is a secondary species in facies 7 (subdominant elsewhere), a slow-growing psychrotroph and a chemoorganotroph [63].

Candidatus Solibacter usitatus is the dominant or subdominant species across all studied sites (Fig. 4A–4Q). It belongs to *Acidobacteria*, which are widely distributed in soils and sediments [64] and play a role in soil organic carbon cycling [65]. The enhanced competitiveness of this bacterium in exploiting environmental resources, coupled with its possession of a vast array of diverse genes that enable a broad spectrum of metabolic and regulatory functions [64], accounts for its dominance and subdominance in virtually all points. Among the acidobacteria is also the species *Candidatus Koribacter versatilis* [66], which dominates in facies 3, 5, 8, 11, 15 (Fig. 4C, 4E, 4H, 4K, 4N), characterised by sandy (except for facies 3) weakly humus soils (Table 1). Its ecological role is to utilize soil carbon [65].

Aneurinibacillus soli dominates at facies 9 (Fig. 4I), found on the steep (40–45°) lower slope of the northwest-facing Fatala River valley, underlain by Devonian aleurolithic-argillites, argillites interbedded with fine-grained sand with a two-story broad-leaved forest on ferralitic soils of thick weakly humus medium-loamy skeletal soils on rocky-blocky colluvium of Devonian deposits (Table 1) and is absent at point 3 (Fig. 4C) – a gently sloping (1–2°) high floodplain surface of the west-northwest-facing Fatala River, underlain by Devonian coarse quartz sandstones, gravels, and conglomerates with a dense tall two-story forest on thick weakly humus light-loamy fluvisols on the alluvium of Devonian deposits (Table 1). This species possesses capabilities for the biosynthesis of streptomycin, taxol, auxin and gibberellin inactivation, which causes plant hormone degradation, suggesting active interactions with plants [67].

The species *Cutibacterium acnes*, which is pathogenic to humans and causes dermatological diseases [68], predominates in facies 2 (Fig. 4B) in the northwest part of the Fatala River basin (Fig. 2). The species *Rhodoplanes* sp. Z2-YC6860, an anaerobic phototrophic bacterium of the alpha-proteobacteria class [69], dominates in the headwaters of the river (Fig. 2) – in facies 4 (Fig. 4D). This genus of bacteria is capable of degrading pollutants such as polyaromatic hydrocarbons and polybrominated diphenyl ethers [70] and is also able to participate in nitrogen fixation [71]. The species *Scytonema* sp. HK-05 is dominant, while *Moraxella osloensis* is subdominant in facies 11 (Fig. 4K), which is located in an area with a high concentration of aluminum ore mining facilities. *Scytonema* sp. has been observed to produce cyanobactins – peptides associated with cytoxicity, antiviral

and antimalarial activity [72], as well as the ability to fix nitrogen [73]. *Moraxella* bacteria produce an enzyme, which degrades non-biodegradable plastics such as polyethylene terephthalate and polyurethane, as well as biodegradable synthetic polyethers such as polycaprolactone, polyhydroxybutyrate, polybutylenesuccinate and polylactic acid [74]. The relationship between the genera *Scytonema* and *Moraxella* and aluminum pollution is not yet studied.

Facies 7 (Table 3) has the lowest alpha-diversity, as indicated by Margalef, Simpson and Shannon indices and the least even species distribution in the bacterial community. This facies is a gently sloping (1–2°) water divide surface with a south-southwest exposure, composed of Devonian aleurite-argillites and argillites with interlayers of fine-grained sandstones, with a monodominant grassland community on thin, low-humus, sandy-skeletal leptosols over rocky-eluvial weathering of Devonian deposits (Table 1). Decreasing alpha-diversity can be linked to an increase in the abundance of planctomycetes (Fig. 3G) on this site, which are capable of producing antibiotics to outcompete other species that actively consume carbon [42].

According to Shannon and Simpson indices, the highest bacterial alpha-diversity is observed in facies 18 (Table 3) on the upper, gentle (4°) slope of a gentle, low hill with a western aspect, composed of Ordovician large quartz sandstones, gravelites and conglomerates with sparse woodland on ferralitic soils, moderately thick, weakly humic, medium-loamy loess on the deluvium of Ordovician deposits (Table 1). The most even species distribution is observed in bacterial communities of facies 10, 12, 17, and 18 (Table 3).

Based on calculations of Jaccard (Table 4) beta-diversity indices, it was found that the most distinct in terms of species composition are the communities of facies 3 and 5 and a group of communities with similar species composition was also identified, including facies 2, 4, 8, 10, 12, 16, and 17. Facies 3 is a high floodplain surface of the Fatala River, covered with a dense, multi-layered, tall forest on powerful, weakly humus, light loamy fluvisols, overlying Devonian large quartz sandstone, gravelite, and conglomerate alluvium (Table 1). Facies 5, on the other hand, is a water divide surface of a ridge with a dense, multi-layered, tall forest on powerful, weakly humus, sandy, strongly skeletal ferralitic soils, developed on the eluvium and colluvium of Devonian large quartz sandstone, gravelite, and conglomerate (Table 1). Facies 2, 4, and 12 are characterized by the presence of forests of different ages on thin to moderately thick leptosols with low to moderate humus content and sandy loam texture. Facies 10 and 16 consist of periodically flooded, gently undulating surfaces of the first floodplains of the Fatala River, supporting a two-story broad-leaved forest in the fluvisol, thick, low-humus soil (Table 1). The Brey-Curtis index distinguishes a narrower group of points with similar species composition – facies 10, 12, and 17 (Table 5). Furthermore, based on the calculations, facies 7 (Table 5) stands out as the most distinct, being a gently sloping water divide surface with a grass-dominated monodominant community (Table 1). On this site, *Planctomycetes* (Fig.3G) dominate, producing antimicrobial substances to compete against other species [42; 43], which likely accounts for the striking differences in bacterial diversity observed.

CONCLUSIONS

Based on the research conducted, several correlations between soil bacterial composition and soil characteristics have been identified. The dominant phyla were *Proteobacteria*, *Firmicutes*, and *Actinobacteria*. Meanwhile, reduced levels of the *Proteobacteria* phylum were observed on areas with thick, low-humus soils (facies 5 and 6), while *Actinobacteria* dominated in the medium-light clay soil (facies 16), with the disappearance of the *Cyanobacteria* phylum. The decrease in *Actinobacteria* and *Firmicutes* and the increase in *Planctomycetes*, *Thermotogae*, and *Verrucomicrobia*, as well as the absence of phyla *Candidatus Saccharibacteria* and *Euryarchaeota* and the dominance of the species *Acidisphaera* sp. G45-3 is likely due to the presence of a grass-dominated monoculture on thin, low-fertility leptosols (facies 7).

The highest abundance of the phylum *Cyanobacteria* was recorded on poorly and weakly humus leptosols on water divide surfaces and yellow earths on interfluve slopes (facies 7, 11, 15). The prevalence of this phylum in an area with a high concentration of bauxite mining enterprises (facies 11) can be preliminarily explained by the ability of cyanobacteria to restore soil fertility and quality. Across a vast number of facies, the species *Candidatus Solibacter usitatus* dominates, owing to its enhanced competitiveness, which is facilitated by its possession of genes that confer an expanded repertoire of metabolic and regulatory functions. In several weakly humified sandy and loamy soils with varying topographic positions (facies 3, 5, 8, 11, and 15), the species *Candidatus Koribacterversatilis* dominates. At the lower slope of the Fatala River valley (facies 9), the dominant species *Aneurinibacillus soli* has been identified, which is completely absent from the high floodplain surface (facies 3). In the northwest-north part of the Fatala River basin (facies 2), *Cutibacterium acnes* is the dominant species. In the headwaters of the Fatala River (facies 4), *Rhodoplanes* sp. Z2-YC6860 is the dominant species. In an aluminum-rich area (facies 11), the species *Scytonema* sp. HK-05 is predominant.

The lowest bacterial diversity and poor species evenness are observed in thin, low-humus sandy, strongly skeletal leptosols with grass monodominant vegetation (facies 7), with the acidophilic species *Acidisphaera* sp. G45-3 being dominant. The decrease in alpha-diversity is presumably associated with an increase in *Planctomycetes*, which are capable of producing antimicrobial compounds to eliminate competitor species that actively consume carbon. The highest bacterial diversity is observed in thick, weakly humified, medium-loamy ferralitic soils with sparse, open forest (facies 18).

Beta-diversity analysis revealed that the most distinct facies are several in the northern part of the basin, namely: facies 3 – high floodplain surface composed of large Devonian quartz sandstones, gravelites and conglomerates with dense, tall two-story forests growing on thick, weakly humified, easily clayey fluvisols over Devonian deposits; facies 5 – water divide surface on the ridge composed of large Devonian quartz sandstones, gravelites and conglomerates with dense, tall two-story forests growing on thick, weakly humified, sandy, strongly skeletal ferralitic soils over Devonian eluvium and colluvium; facies 7 – gently undulating water divide surface composed of Devonian aleurolites and argillites with layers of fine-grained sandstones, featuring a grass-dominant monodominant community on thin, weakly humified,

sandy, strongly skeletal leptosols over Devonian rocky and bouldery eluvium. Despite their differences in vegetation cover and topographic position, several facies (10, 12, 17) exhibit a great similarity in their bacterial composition.

ACKNOWLEDGMENT

This work was supported by a grant from the Russian Federation through the Ministry of Science and Higher Education (Agreement No. 075-15-2023-592, Project No. 13.2251.21.0216) in accordance with Article 78.1, Point 4 of the Russian Federation Budget Code.

БЛАГОДАРНОСТЬ

Работа выполнена при финансовой поддержке Проекта Российской Федерации в лице Минобрнауки России: грант в форме субсидий в соответствии с пунктом 4 статьи 78.1 Бюджетного кодекса Российской Федерации (Соглашение № 075-15-2023-592 по теме № 13.2251.21.0216).

REFERENCES

1. Navarrete A.A., Tsai S.M., Mendes L.W., Faust K., de Hollander M., Cassman N.A., Raes J., van Veen J.A., Kuramae E.E. Soil microbiome responses to the short-term effects of Amazonian deforestation. *Mol Ecol*, 2015, vol.24, no. 10, pp. 2433–2448. https://doi.org/10.1111/mec.13172.
2. Islam W., Noman A., Naveed H., Huang Z., Chen H.Y.H. Role of environmental factors in shaping the soil microbiome. *Environ Sci Pollut Res*, 2020, vol. 27, no. 33, pp. 41225–41247. https://doi.org/10.1007/s11356-020-10471-2.
3. Khan S.T., Adil S.F., Shaik M.R., Alkhathlan H.Z., Khan M., Khan M. Engineered Nanomaterials in Soil: Their Impact on Soil Microbiome and Plant Health. *Plants*, 2022, vol. 11, no. 1, pp. 109. https://doi.org/10.3390/plants11010109.
4. Fierer N. Embracing the unknown: disentangling the complexities of the soil microbiome. *Nat Rev Microbiol.*, 2017, vol. 15, no. 10, pp. 579–590. https://doi.org/10.1038/nrmicro.2017.87.
5. Dubey A., Malla M.A., Khan F., Chowdhary K., Yadav S., Kumar A., Sharma S., Khare P.K., Khan M.L. Soil microbiome: a key player for conservation of soil health under changing climate. *Biodivers Conserv*, 2019, vol. 28, pp. 2405–2429. https://doi.org/10.1007/s10531-019-01760-5.
6. Goss-Souza D., Mendes L.W., Rodrigues J.L.M., Tsai S.M. Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. *Microb Ecol*, 2020, vol. 79, no. 1, pp. 110–122. https://doi.org/10.1007/s00248-019-01401-y.
7. Hermans S.M., Buckley H.L., Case B.S., Curran-Cournane F., Taylor M., Lear G. Bacteria as Emerging Indicators of Soil Condition. *Appl Environ Microbiol*, 2017, vol. 83, pp. e02826-16. https://doi.org/10.1128/AEM.02826-16
8. Ossowicki A., Raaijmakers J.M., Garbeva P. Disentangling soil microbiome functions by perturbation. *Environmental Microbiology Reports*, 2021, vol. 13, no. 5, pp. 582–590. https://doi.org/10.1111/1758-2229.12989.
9. Philippot L., Chenu C., Kappler A., Rillig M.C., Fierer N. The interplay between microbial communities and soil properties. *Nat Rev Microbiol*, 2024, vol. 22, no. 4, pp. 226–239. https://doi.org/10.1038/s41579-023-00980-5.
10. Jansson J.K., McClure R., Egbert R.G. Soil microbiome engineering for sustainability in a changing environment. *Nat Biotechnol*, 2023, vol. 41, no. 12, pp. 1716–1728. https://doi.org/10.1038/s41587-023-01932-3.
11. Mishra A., Singh L., Singh D. Unboxing the black box—one step forward to understand the soil microbiome: A systematic review. *Microb Ecol*, 2023, vol. 85, pp. 669–683. https://doi.org/10.1007/s00248-022-01962-5.
12. Hiraishi A., Matsuzawa Y., Kanbe T., Wakao N. Acidisphaera rubrifaciens gen. nov., sp. nov., an aerobic bacteriochlorophyll-containing bacterium isolated from acidic environments. *International Journal of Systematic and Evolutionary Microbiology*, 2000, vol. 50, pp. 1539–1546. https://doi.org/10.1099/00207713-50-4-1539.
13. Okamura K., Hisada T., Kanbe T., Hiraishi A. Rhodovastum atsumiense gen. nov., sp. nov., a phototrophic alphaproteobacterium isolated from paddy soil. *J Gen Appl Microbiol*, 2009, vol. 55, no. 1, pp. 43–50. https://doi.org/10.2323/jgam.55.43.
14. Ardley J.K., O'Hara G.W., Reeve W.G., Yates R.J., Dilworth M.J., Tiwari R.P., Howieson J.G. Root nodule bacteria isolated from South African Lotononis bainesii, L. listii and L. solitudinis are species of Methylobacterium that are unable to utilize methanol. *Arch Microbiol*, 2009, vol. 191, no. 4, pp. 311–318. https://doi.org/10.1007/s00203-009-0456-0.
15. Kulichevskaya I.S., Ivanova A.O., Baulina O.I., Bodelier P.L., Damsté J.S., Dedysh S.N. Singulisphaera acidiphila gen. nov., sp. nov., a non-filamentous, Isosphaera-like planctomycete from acidic northern wetlands. *Int J Syst Evol Microbiol*, 2008, vol. 58, no. 5, pp. 1186–1193. https://doi.org/10.1099/ijs.0.65593-0
16. Ivanova A.A., Naumoff D.G., Kulichevskaya I.S., Rakitin A.L., Mardanov A.V., Ravin N.V., Dedysh S.N. Planctomycetes of the Genus Singulisphaera Possess Chitinolytic Capabilities. *Microorganisms*, 2024, vol. 12, pp. 1266. https://doi.org/10.3390/microorganisms12071266.
17. Kruppa O., Czermak P. Screening for Biofilm-Stimulating Factors in the Freshwater Planctomycete Planctopirus limnophila to Improve Sessile Growth in a Chemically Defined Medium. *Microorganisms*, 2022, vol. 10, pp. 801. https://doi.org/10.3390/microorganisms10040801.
18. Jeske O., Surup F., Ketteniß M., Rast P, Förster B., Jogler M., Wink J., Jogler C. Developing Techniques for the Utilization of Planctomycetes As Producers of Bioactive Molecules. *Front. Microbiol*, 2016, vol. 7, pp. 1242. https://doi.org/10.3389/fmicb.2016.01242.
19. Pizzetti I., Gobet A., Fuchs B.M., Amann R., Fazi S. Abundance and diversity of Planctomycetesin a Tyrrhenian coastal system of central Italy. *Aquat Microb Ecol*, 2011, vol. 65, pp. 129–141.https://doi.org/10.3354/ame01535.
20. Vieira S., Luckner M., Wanner G., Overmann J. Luteitalea pratensis gen. nov., sp. nov. a new member of subdivision 6 Acidobacteria isolated from temperate grassland soil. *Int J Syst Evol Microbiol*, 2017, vol. 67, no. 5, pp. 1408–1414. https://doi.org/10.1099/ijsem.0.001827.
21. Challacombe J.F., Eichorst S.A., Hauser L., Land M., Xie G., Kuske C.R. Biological consequences of ancient gene acquisition and duplication in the large genome of Candidatus Solibacter usitatus Ellin6076. *PLoS One*, 2011, vol. 6, no. 9, pp. e24882. https://doi.org/10.1371/journal.pone.0024882.
22. Rawat S.R., Männistö M.K., Bromberg Y., Häggblom M.M. Comparative genomic and physiological analysis

provides insights into the role of Acidobacteria in organic carbon utilization in Arctic tundra soils. *FEMS Microbiol Ecol*, 2012, vol. 82, no. 2, pp. 341–355. https://doi.org/10.1111/j.1574-6941.2012.01381.x.
23. Liu Y., Wang L.H., Hao C.B., Li L., Li S.Y., Feng C.P. Microbial diversity and ammonia-oxidizing microorganism of a soil sample near an acid mine drainage lake. *Huan Jing Ke Xue*, 2014, vol. 35, no. 6, pp. 2305–2313. (In Chinese). https://doi.org/10.13227/j.hjkx.2014.06.037.
24. Ignateva D.I., Volkov A.A, Shvartsev A.A., Alekseev Y.I. *Sposob vydeleniya total'noy dna bakteriy iz obrazcov pochvy, sposob otsenki bakterial'nogo sostava pochv posredstvom metagenomnogo sekvenirovaniya i nabory dlya osushchestvleniya sposobov* [Method for isolating total bacterial DNA from soil samples, method for assessing bacterial composition of soils using metagenomic sequencing and kits for implementing the methods]. Patent RF, no. 2829656, 2024.
25. Lee J.S., Lee K.C., Kim K.K., Lee B. Complete genome sequence of the Aneurinibacillus soli CB4(T) from soil of mountain. *J Biotechnol*, 2016, vol. 221, pp. 116–117. https://doi.org/10.1016/j.jbiotec.2016.01.027.
26. De Canha M.N., Komarnytsky S., Langhansova L., Lall N. Exploring the Anti-Acne Potential of Impepho [*Helichrysum odoratissimum* (L.) Sweet] to Combat Cutibacterium acnes Virulence. *Front Pharmacol*, 2020, vol. 10, pp. 1559. https://doi.org/10.3389/fphar.2019.01559.
27. Rayyan A.A., Kyndt J.A. Genome Sequences of Rhodoplanes serenus and Two Thermotolerant Strains, Rhodoplanes tepidamans and "Rhodoplanes cryptolactis," Further Refine the Genus. *Microbiol Resour Announc*, 2023, vol. 12, no. 7, pp. e0009923. https://doi.org/10.1128/mra.00099-23.
28. Wu Y., Song Q., Wu J., Zhou J., Zhou L., Wu W. Field study on the soil bacterial associations to combined contamination with heavy metals and organic contaminants. *Sci Total Environ*, 2021, vol. 778, pp. 146282. https://doi.org/10.1016/j.scitotenv.2021.146282.
29. Too C.C., Keller A., Sickel W., Lee S.M., Yule C.M. Microbial Community Structure in a Malaysian Tropical Peat Swamp Forest: The Influence of Tree Species and Depth. *Front. Microbiol*, 2018, vol. 9, pp. 2859. https://doi.org/10.3389/fmicb.2018.02859.
30. Crnkovic C.M., Braesel J., Krunic A., Eustáquio A.S., Orjala J. Scytodecamide from the Cultured Scytonema sp. UIC 10036 Expands the Chemical and Genetic Diversity of Cyanobactins. *Chembiochem*, 2020, vol. 21, no. 6, pp. 845–852.https://doi.org/10.1002/cbic.201900511.
31. Adelizzi R., O'Brien E.A., Hoellrich M., Rudgers J.A., Mann M., Fernandes V.M.C., Darrouzet-Nardi A., Stricker E. Disturbance to biocrusts decreased cyanobacteria, N-fixer abundance, and grass leaf N but increased fungal abundance. *Ecology*, 2022, vol. 103, no. 4, pp. e3656. https://doi.org/10.1002/ecy.3656.
32. Nikolaivits E., Taxeidis G., Gkountela C., Vouyiouka S., Maslak V., Nikodinovic-Runic J., Topakas E. A polyesterase from the Antarctic bacterium Moraxella sp. degrades highly crystalline synthetic polymers. *J Hazard Mater*, 2022, vol. 434, pp. 128900. https://doi.org/10.1016/j.jhazmat.2022.128900.
33. Hervé V., Junier T., Bindschedler S., Verrecchia E., Junier P. Diversity and ecology of oxalotrophic bacteria. *World J Microbiol Biotechnol*, 2016, vol. 32, no. 2, pp. 28. https://doi.org/10.1007/s11274-015-1982-3.
34. Ling N., Wang T., Kuzyakov Y. Rhizosphere bacteriome structure and functions. *Nat Commun*, 2022, vol. 13, no. 1, pp. 836. https://doi.org/10.1038/s41467-022-28448-9.
35. Gu Z., Feng K., Li Y., Li Q. Microbial characteristics of the leachate contaminated soil of an informal landfill site. *Chemosphere*, 2022, vol. 287, no. 2, pp. 132155. https://doi.org/10.1016/j.chemosphere.2021.132155.
36. Li Y., Zheng B., Yang Y., Chen K., Chen X., Huang X., Wang X. Soil microbial ecological effect of shale gas oil-based drilling cuttings pyrolysis residue used as soil covering material. *J Hazard Mater*, 2022, vol. 436, pp. 129231. https://doi.org/10.1016/j.jhazmat.2022.129231.
37. Gao H., Wu M., Liu H., Xu Y., Liu Z. Effect of petroleum hydrocarbon pollution levels on the soil microecosystem and ecological function. *Environ Pollut*, 2022, vol. 15, no. 293, pp. 118511. https://doi.org/10.1016/j.envpol.2021.118511.
38. Brennan F.P., Moynihan E., Griffiths B.S., Hillier S., Owen J., Pendlowski H., Avery L.M. Clay mineral type effect on bacterial enteropathogen survival in soil. *Sci Total Environ*, 2014, vol. 468–469, pp. 302–305. https://doi.org/10.1016/j.scitotenv.2013.08.037.
39. Callahan M.T., Micallef S.A., Buchanan R.L. Soil Type, Soil Moisture, and Field Slope Influence the Horizontal Movement of Salmonella enterica and Citrobacter freundii from Floodwater through Soil. *J Food Prot*, 2017, vol. 80, no. 1, pp. 189–197. https://doi.org/10.4315/0362-028X.JFP-16-263.
40. Phan-Thien K., Metaferia M.H., Bell T.L., Bradbury M.I., Sassi H.P., van Ogtrop F.F., Suslow T.V., McConchie R. Effect of soil type and temperature on survival of Salmonella enterica in poultry manure-amended soils. *Lett Appl Microbiol*, 2020, vol. 71, no. 2, pp. 210–217. https://doi.org/10.1111/lam.13302.
41. Kuramae E.E., Yergeau E., Wong L.C., Pijl A.S., van Veen J.A., Kowalchuk G.A. Soil characteristics more strongly influence soil bacterial communities than land-use type. *FEMS Microbiol Ecol*, 2012, vol. 79, no. 1, pp. 12–24. https://doi.org/10.1111/j.1574-6941.2011.01192.x.
42. Han X., Huang C., Khan S., Zhang Y., Chen Y., Guo J. nirS-type denitrifying bacterial communities in relation to soil physicochemical conditions and soil depths of two montane riparian meadows in North China. *Environ Sci Pollut Res Int*, 2020, vol. 27, no. 23, pp. 28899–28911. https://doi.org/10.1007/s11356-020-09171-8.
43. Hedrich S., Schlömann M., Johnson D.B. The iron-oxidizing proteobacteria. *Microbiology (Reading)*, 2011, vol. 157, no. 6, pp. 1551–1564.https://doi.org/10.1099/mic.0.045344-0.
44. Ghosh S., Bagchi A. Protein dynamics and molecular motions study in relation to molecular interaction between proteins from sulfur oxidizing proteobacteria Allochromatium vinosum. *J Biomol Struct Dyn*, 2021, vol. 39, no. 8, pp. 2771–2787. https://doi.org/10.1080/07391102.2020.1754914.
45. Shao M.F., Zhang T., Fang H.H. Sulfur-driven autotrophic denitrification: diversity, biochemistry, and engineering applications. *Appl Microbiol Biotechnol*, 2010, vol. 88, no. 5, pp. 1027–1042. https://doi.org/10.1007/s00253-010-2847-1.
46. Puri A.W. Specialized Metabolites from Methylotrophic Proteobacteria. *Curr Issues Mol Biol*, 2019, vol. 33, pp. 211–224. https://doi.org/10.21775/cimb.033.211.
47. Sánchez-Marañón M., Miralles I., Aguirre-Garrido J.F., Anguita-Maeso M., Millán V., Ortega R., García-Salcedo J.A., Martínez-Abarca F., Soriano M. Changes in the soil

bacterial community along a pedogenic gradient. *Sci Rep*, 2017, vol. 7, pp. 14593. https://doi.org/10.1038/s41598-017-15133-x
48. Lee K.C., Morgan X.C., Dunfield P.F., Tamas I., McDonald I.R., Stott M.B. Genomic analysis of Chthonomonas calidirosea, the first sequenced isolate of the phylum Armatimonadetes. *ISME J*, 2014, vol. 8, no. 7, pp. 1522–1533. https://doi.org/10.1038/ismej.2013.251.
49. Langendries S., Goormachtig S. Paenibacillus polymyxa, a Jack of all trades. *Environ Microbiol*, 2021, vol. 23, no. 10, pp. 5659–5669. https://doi.org/10.1111/1462-2920.15450.
50. Liu L., Wang Z., Ma D., Zhang M., Fu L. Diversity and Distribution Characteristics of Soil Microbes across Forest–Peatland Ecotones in the Permafrost Regions. *Int. J. Environ. Res. Public Health*, 2022, vol. 19, pp. 14782. https://doi.org/10.3390/ijerph192214782.
51. Abinandan S., Subashchandrabose S.R., Venkateswarlu K., Megharaj M. Soil microalgae and cyanobacteria: the biotechnological potential in the maintenance of soil fertility and health. *Crit Rev Biotechnol*, 2019, vol. 39, no. 8, pp. 981–998. https://doi.org/10.1080/07388551.2019.1654972.
52. Nowruzi B., Bouaïcha N., Metcalf J.S., Porzani S.J., Konur O. Plant-cyanobacteria interactions: Beneficial and harmful effects of cyanobacterial bioactive compounds on soil-plant systems and subsequent risk to animal and human health. *Phytochemistry*, 2021, vol. 192, pp. 112959. https://doi.org/10.1016/j.phytochem.2021.112959.
53. Aoyagi T., Inaba T., Aizawa H., Mayumi D., Sakata S., Charfi A., Suh C., Lee J.H., Sato Y., Ogata A., Habe H., Hori T. Unexpected diversity of acetate degraders in anaerobic membrane bioreactor treating organic solid waste revealed by high-sensitivity stable isotope probing. *Water Res*, 2020, vol. 176, pp. 115750. https://doi.org/10.1016/j.watres.2020.115750.
54. Martinez M.A., Woodcroft B.J., Ignacio Espinoza J.C., Zayed A.A., Singleton C.M., Boyd J.A., Li Y.F., Purvine S., Maughan H., Hodgkins S.B., Anderson D., Sederholm M., Temperton B., Bolduc B., Saleska S.R., Tyson G.W., Rich V.I., IsoGenie Project Coordinators, Saleska S.R., Tyson G.W., Rich V.I. Discovery and ecogenomic context of a global Caldiserica-related phylum active in thawing permafrost, Candidatus Cryosericota phylum nov., Ca. Cryosericia class nov., Ca. Cryosericales ord. nov., Ca. Cryosericaceae fam. nov., comprising the four species Cryosericum septentrionale gen. nov. sp. nov., Ca. C. hinesii sp. nov., Ca. C. odellii sp. nov., Ca. C. terrychapinii sp. nov. *Syst Appl Microbiol*, 2019, vol. 42, no. 1, pp. 54–66. https://doi.org/10.1016/j.syapm.2018.12.003.
55. Dyksma S., Gallert C. Candidatus Syntrophosphaera thermopropionivorans: a novel player in syntrophic propionate oxidation during anaerobic digestion. *Environ Microbiol Rep*, 2019, vol. 11, no. 4, pp. 558–570. https://doi.org/10.1111/1758-2229.12759.
56. Zhou S., Wang G., Han. Q., Zhang J., Dang H., Ning H., Gao Y., Sun J. Long-term saline water irrigation affected soil carbon and nitrogen cycling functional profiles in the cotton field. *Front Microbiol*, 2024, vol. 15, pp. 1310387. https://doi.org/10.3389/fmicb.2024.1310387.
57. Rozanov A.S., Bryanskaya A.V., Malup T.K., Meshcheryakova I.A., Lazareva E.V., Taran O.P., Ivanisenko T.V., Ivanisenko V.A., Zhmodik S.M., Kolchanov N.A., Peltek S.E. Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera, Kamchatka, Russia). *BMC Genomics*, 2014, vol. 12, pp. S12. https://doi.org/10.1186/1471-2164-15-S12-S12.
58. Kadnikov V.V., Savvichev A.S., Mardanov A.V., Beletsky A.V., Chupakov A.V., Kokryatskaya N.M., Pimenov N.V., Ravin N.V. Metabolic Diversity and Evolutionary History of the Archaeal Phylum "Candidatus Micrarchaeota" Uncovered from a Freshwater Lake Metagenome. *Appl Environ Microbiol*, 2020, vol. 86, no. 23, pp. e02199-20. https://doi.org/10.1128/AEM.02199-20.
59. Golyshina O.V., Bargiela R., Toshchakov S.V., Chernyh N.A., Ramayah S., Korzhenkov A.A., Kublanov I.V., Golyshin P.N. Diversity of “Ca. Micrarchaeota” in Two Distinct Types of Acidic Environments and Their Associations with Thermoplasmatales. *Genes*, 2019, vol. 10, pp. 461. https://doi.org/10.3390/genes10060461.
60. van Vliet D.M., Palakawong Na Ayudthaya S., Diop S., Villanueva L., Stams A.J.M., Sánchez-Andrea I. Anaerobic Degradation of Sulfated Polysaccharides by Two Novel Kiritimatiellales Strains Isolated From Black Sea Sediment. *Front Microbiol*, 2019, vol. 10, pp. 253. https://doi.org/10.3389/fmicb.2019.00253.
61. Constancias F., Saby N.P., Terrat S., Dequiedt S., Horrigue W., Nowak V., Guillemin J.P., Biju-Duval L., Chemidlin Prévost-Bouré N., Ranjard L. Contrasting spatial patterns and ecological attributes of soil bacterial and archaeal taxa across a landscape. *Microbiologyopen*, 2015, vol. 4, no.3, pp. 518–531. https://doi.org/10.1002/mbo3.256
62. Hu M., Sardans J., Sun D., Yan R., Wu H., Ni R., Peñuelas J. Microbial diversity and keystone species drive soil nutrient cycling and multifunctionality following mangrove restoration. *Environ Res*, 2024, vol. 251, no. 2, pp. 118715. https://doi.org/10.1016/j.envres.2024.118715
63. Sidiki S. Bauxite Mining in the Boké Region (Western Guinea): Method Used and Impacts on Physical Environment. European. *Journal of Sustainable Development Research*, 2019, vol. 3, no. 3, pp. em0087. https://doi.org/10.29333/ejosdr/5735
64. Kolie B., Jun Y., Sunahara G., Camara M. Characterization of the rock blasting process impacts in Lefa gold mine, Republic of Guinea. *Environ Earth Sci*, 2021, vol. 80, pp. 175. https://doi.org/10.1007/s12665-021-09477-x
65. Tabunschik V., Gorbunov R., Bratanov N., Gorbunova T., Mirzoeva N., Voytsekhovskaya V. Fatala River Basin (Republic of Guinea, Africa): Analysis of Current State, Air Pollution, and Anthropogenic Impact Using Geoinformatics Methods and Remote Sensing Data. *Sustainability*, 2023, vol. 15, pp. 15798. https://doi.org/10.3390/su152215798.
66. Sidibé D., Konaté A.A., Kaba O.B., Traoré S. Bauxite Mining Industry in Guinea and the Valorization Prospects of the Resulting Residue for Engineering Purposes. *Novel Perspectives of Engineering Research*, 2021, vol. 4, pp. 94–110. https://doi.org/10.9734/bpi/nper/v4/3680F.
67. Diallo P. Regime Stability, Social Insecurity and Bauxite Mining in Guinea. Developments Since the Mid-Twentieth Century, 1st ed., London, UK, 2019, 142 p. https://doi.org/10.4324/9780429286544.
68. Diallo A.K., Conte M.S.M., Kaba O.B., Soumah A., Camara M. Petrological and Statistical Studies of the Limbiko Bauxite Deposit, Republic of Guinea. *International Journal of Geosciences*, 2023, vol. 14, pp. 351–376. https://doi.org/10.4236/ijg.2023.144020.
69. Wilhelm C., Maconachie R. Exploring local content in Guinea's bauxite sector: Obstacles, opportunities and future trajectories. *Resources Policy*, 2020, vol. 71, pp. 101935. https://doi.org/10.1016/j.resourpol.2020.101935

70. Knierzinger J. The socio-political implications of bauxite mining in Guinea: A commodity chain perspective. *Extractive Industries and Society*, 2014, vol. 1, pp. 20–27. https://doi.org/10.1016/j.exis.2014.01.005.
71. Daniel R. The metagenomics of soil. *Nat Rev Microbiol*, 2005, vol. 3, pp. 470–478. https://doi.org/10.1038/nrmicro1160.
72. Chernov T.I., Kholodov V.A., Kogut B.M., Ivanov A.L. The Method of Microbiological Soil Investigations within the Framework of the Project “Microbiome of Russia”. *Dokuchaev Soil Bulletin*, 2017, vol. 87, pp. 100–113. (In Russian) https://doi.org/10.19047/0136-1694-2017-87-100-113
73. Jones A., Breuning-Madsen H., Brossard M., Dampha A., Dewitte O., Hallett S., Jones R., Kilasara M., Le Roux P., Micheli E., Montanarella L., Spaargaren O., Tahar G., Thiombiano L., Van Ranst E., Yemefack M., Zougmore R. Soil Atlas of Africa. Luxembourg, Luxembourg, 2013, 176 p.
74. Gorbunova, T., Gorbunov, R., Camara, A.I., Bratanov, N., Sow, B.B., Pham, C.N., Safonova, M., Faerman, A., Tabunshchik, V., Nikiforova, A., Lineva, N., Diallo, A.I.P., Keita, I. Heavy Metals in Soils of the Fatala River Basin (Republic of Guinea). *RGSA2024*, vol. 18, pp. e08309. https://doi.org/10.24857/rgsa.v18n9-161

БИБЛИОГРАФИЧЕСКИЙ СПИСОК

1. Mishra A., Singh L., Singh D. Unboxing the black box—one step forward to understand the soil microbiome: A systematic review // Microb Ecol, 2023, vol. 85, pp. 669–683. https://doi.org/10.1007/s00248-022-01962-5
2. Hiraishi A., Matsuzawa Y., Kanbe T., Wakao N. Acidisphaera rubrifaciens gen. nov., sp. nov., an aerobic bacteriochlorophyll-containing bacterium isolated from acidic environments // International Journal of Systematic and Evolutionary Microbiology, 2000, vol. 50, pp. 1539–1546. https://doi.org/10.1099/00207713-50-4-1539
3. Okamura K., Hisada T., Kanbe T., Hiraishi A. Rhodovastum atsumiense gen. nov., sp. nov., a phototrophic alphaproteobacterium isolated from paddy soil // J Gen Appl Microbiol, 2009, vol. 55, no. 1, pp. 43–50. https://doi.org/10.2323/jgam.55.43
4. Ardley J.K., O'Hara G.W., Reeve W.G., Yates R.J., Dilworth M.J., Tiwari R.P., Howieson J.G. Root nodule bacteria isolated from South African Lotononis bainesii, L. listii and L. solitudinis are species of Methylobacterium that are unable to utilize methanol // Arch Microbiol, 2009, vol. 191, no. 4, pp. 311–318. https://doi.org/10.1007/s00203-009-0456-0
5. Kulichevskaya I.S., Ivanova A.O., Baulina O.I., Bodelier P.L., Damsté J.S., Dedysh S.N. Singulisphaera acidiphila gen. nov., sp. nov., a non-filamentous, Isosphaera-like planctomycete from acidic northern wetlands // Int J Syst Evol Microbiol, 2008, vol. 58, no. 5, pp. 1186–1193. https://doi.org/10.1099/ijs.0.65593-0
6. Ivanova A.A., Naumoff D.G., Kulichevskaya I.S., Rakitin A.L., Mardanov A.V., Ravin N.V., Dedysh S.N. Planctomycetes of the Genus Singulisphaera Possess Chitinolytic Capabilities // Microorganisms, 2024, vol. 12, pp. 1266. https://doi.org/10.3390/microorganisms12071266
7. Kruppa O., Czermak P. Screening for Biofilm-Stimulating Factors in the Freshwater Planctomycete Planctopirus limnophila to Improve Sessile Growth in a Chemically Defined Medium // Microorganisms, 2022, vol. 10, pp. 801. https://doi.org/10.3390/microorganisms10040801
8. Jeske O., Surup F., Ketteniß M., Rast P, Förster B., Jogler M., Wink J., Jogler C. Developing Techniques for the Utilization of Planctomycetes As Producers of Bioactive Molecules // Front. Microbiol, 2016, vol. 7, pp. 1242. https://doi.org/10.3389/fmicb.2016.01242
9. Pizzetti I., Gobet A., Fuchs B.M., Amann R., Fazi S. Abundance and diversity of Planctomycetesin a Tyrrhenian coastal system of central Italy // Aquat Microb Ecol, 2011, vol. 65, pp. 129–141. https://doi.org/10.3354/ame01535
10. Vieira S., Luckner M., Wanner G., Overmann J. Luteitalea pratensis gen. nov., sp. nov. a new member of subdivision 6 Acidobacteria isolated from temperate grassland soil // Int J Syst Evol Microbiol, 2017, vol. 67, no. 5, pp. 1408–1414. https://doi.org/10.1099/ijsem.0.001827
11. Mishra A., Singh L., Singh D. Unboxing the black box—one step forward to understand the soil microbiome: A systematic review // Microb Ecol, 2023, vol. 85, pp. 669–683. https://doi.org/10.1007/s00248-022-01962-5
12. Hiraishi A., Matsuzawa Y., Kanbe T., Wakao N. Acidisphaera rubrifaciens gen. nov., sp. nov., an aerobic bacteriochlorophyll-containing bacterium isolated from acidic environments // International Journal of Systematic and Evolutionary Microbiology, 2000, vol. 50, pp. 1539–1546. https://doi.org/10.1099/00207713-50-4-1539
13. Okamura K., Hisada T., Kanbe T., Hiraishi A. Rhodovastum atsumiense gen. nov., sp. nov., a phototrophic alphaproteobacterium isolated from paddy soil // J Gen Appl Microbiol, 2009,vol. 55, no. 1, pp. 43–50. https://doi.org/10.2323/jgam.55.43
14. Ardley J.K., O'Hara G.W., Reeve W.G., Yates R.J., Dilworth M.J., Tiwari R.P., Howieson J.G. Root nodule bacteria isolated from South African Lotononis bainesii, L. listii and L. solitudinis are species of Methylobacterium that are unable to utilize methanol // Arch Microbiol, 2009, vol. 191, no. 4, pp. 311–318. https://doi.org/10.1007/s00203-009-0456-0
15. Kulichevskaya I.S., Ivanova A.O., Baulina O.I., Bodelier P.L., Damsté J.S., Dedysh S.N. Singulisphaera acidiphila gen. nov., sp. nov., a non-filamentous, Isosphaera-like planctomycete from acidic northern wetlands // Int J Syst Evol Microbiol, 2008, vol. 58, no. 5, pp. 1186–1193. https://doi.org/10.1099/ijs.0.65593-0
16. Ivanova A.A., Naumoff D.G., Kulichevskaya I.S., Rakitin A.L., Mardanov A.V., Ravin N.V., Dedysh S.N. Planctomycetes of the Genus Singulisphaera Possess Chitinolytic Capabilities // Microorganisms, 2024, vol. 12, pp. 1266. https://doi.org/10.3390/microorganisms12071266
17. Kruppa O., Czermak P. Screening for Biofilm-Stimulating Factors in the Freshwater Planctomycete Planctopirus limnophila to Improve Sessile Growth in a Chemically Defined Medium // Microorganisms, 2022, vol. 10, pp. 801. https://doi.org/10.3390/microorganisms10040801
18. Jeske O., Surup F., Ketteniß M., Rast P, Förster B., Jogler M., Wink J., Jogler C. Developing Techniques for the Utilization of Planctomycetes As Producers of Bioactive Molecules // Front. Microbiol, 2016, vol. 7, pp. 1242. https://doi.org/10.3389/fmicb.2016.01242
19. Pizzetti I., Gobet A., Fuchs B.M., Amann R., Fazi S. Abundance and diversity of Planctomycetesin a Tyrrhenian coastal system of central Italy // Aquat Microb Ecol, 2011, vol. 65, pp. 129–141. https://doi.org/10.3354/ame01535
20. Vieira S., Luckner M., Wanner G., Overmann J. Luteitalea pratensis gen. nov., sp. nov. a new member of subdivision 6 Acidobacteria isolated from temperate grassland soil // Int J Syst Evol Microbiol, 2017, vol. 67, no. 5, pp. 1408–1414. https://doi.org/10.1099/ijsem.0.001827
21. Challacombe J.F., Eichorst S.A., Hauser L., Land M., Xie G., Kuske C.R. Biological consequences of ancient gene acquisition and duplication in the large genome of Candidatus Solibacter usitatus Ellin6076 // PLoS One. 2011, vol. 6, no. 9, pp. e24882. https://doi.org/10.1371/journal.pone.0024882
22. Rawat S.R., Männistö M.K., Bromberg Y., Häggblom M.M. Comparative genomic and physiological analysis provides insights into the role of Acidobacteria in organic carbon utilization in Arctic tundra soils // FEMS Microbiology Ecology.

2012, vol. 82, no. 2, pp. 341–355. https://doi.org/10.1111/j.1574-6941.2012.01381.x
23. Liu Y., Wang L.H., Hao C.B., Li L., Li S.Y., Feng C.P. Microbial diversity and ammonia-oxidizing microorganism of a soil sample near an acid mine drainage lake // Huan Jing Ke Xue. 2014, vol. 35, no. 6, pp. 2305–2313. (In Chinese). https://doi.org/10.13227/j.hjkx.2014.06.037
24. Игнатьева Д.И., Волков А.А., Шварцев А.А., Алексеев Я.И. Способ выделения тотальной ДНК бактерий из образцов почвы, способ оценки бактериального состава почв посредством метагеномного секвенирования и наборы для осуществления способов. Патент RU 2829656 C1, 2024.
25. Lee J.S., Lee K.C., Kim K.K., Lee B. Complete genome sequence of the Aneurinibacillus soli CB4(T) from soil of mountain // Journal of Biotechnology. 2016, vol. 221, pp. 116–117. https://doi.org/10.1016/j.jbiotec.2016.01.027
26. De Canha M.N., Komarnytsky S., Langhansova L., Lall N. Exploring the Anti-Acne Potential of Impepho [Helichrysum odoratissimum (L.) Sweet] to Combat Cutibacterium acnes Virulence // Frontiers in Pharmacology. 2020, vol. 10, pp. 1559. https://doi.org/10.3389/fphar.2019.01559
27. Rayyan A.A., Kyndt J.A. Genome Sequences of Rhodoplanes serenus and Two Thermotolerant Strains, Rhodoplanes tepidamans and "Rhodoplanes cryptolactis," Further Refine the Genus // Microbiology Resource Announcements. 2023, vol. 12, no. 7, pp. e0009923. https://doi.org/10.1128/mra.00099-23
28. Wu Y., Song Q., Wu J., Zhou J., Zhou L., Wu W. Field study on the soil bacterial associations to combined contamination with heavy metals and organic contaminants // Science of The Total Environment. 2021, vol. 778, pp. 146282. https://doi.org/10.1016/j.scitotenv.2021.146282
29. Too C.C., Keller A., Sickel W., Lee S.M., Yule C.M. Microbial Community Structure in a Malaysian Tropical Peat Swamp Forest: The Influence of Tree Species and Depth // Frontiers in Microbiology. 2018, vol. 9, pp. 2859. https://doi.org/10.3389/fmicb.2018.02859
30. Crnkovic C.M., Braesel J., Krunic A., Eustáquio A.S., Orjala J. Scytodecamide from the Cultured Scytonema sp. UIC 10036 Expands the Chemical and Genetic Diversity of Cyanobactins // ChemBioChem. 2020, vol. 21, no. 6, pp. 845–852. https://doi.org/10.1002/cbic.201900511
31. Adelizzi R., O'Brien E.A., Hoellrich M., Rudgers J.A., Mann M., Fernandes V.M.C., Darrouzet-Nardi A., Stricker E. Disturbance to biocrusts decreased cyanobacteria, N-fixer abundance, and grass leaf N but increased fungal abundance // Ecology. 2022, vol. 103, no. 4, pp. e3656. https://doi.org/10.1002/ecy.3656
32. Nikolaivits E., Taxeidis G., Gkountela C., Vouyiouka S., Maslak V., Nikodinovic-Runic J., Topakas E. A polyesterase from the Antarctic bacterium Moraxella sp. degrades highly crystalline synthetic polymers // Journal of Hazardous Materials. 2022, vol. 434, pp. 128900. https://doi.org/10.1016/j.jhazmat.2022.128900
33. Hervé V., Junier T., Bindschedler S., Verrecchia E., Junier P. Diversity and ecology of oxalotrophic bacteria // World Journal of Microbiology and Biotechnology. 2016, vol. 32, no. 2, pp. 28. https://doi.org/10.1007/s11274-015-1982-3
34. Ling N., Wang T., Kuzyakov Y. Rhizosphere bacteriome structure and functions // Nature Communications. 2022, vol. 13, no. 1, pp. 836. https://doi.org/10.1038/s41467-022-28448-9
35. Gu Z., Feng K., Li Y., Li Q. Microbial characteristics of the leachate contaminated soil of an informal landfill site // Chemosphere. 2022, vol. 287, no. 2, pp. 132155. https://doi.org/10.1016/j.chemosphere.2021.132155
36. Li Y., Zheng B., Yang Y., Chen K., Chen X., Huang X., Wang X. Soil microbial ecological effect of shale gas oil-based drilling cuttings pyrolysis residue used as soil covering material // Journal of Hazardous Materials. 2022, vol. 436, pp. 129231. https://doi.org/10.1016/j.jhazmat.2022.129231
37. Gao H., Wu M., Liu H., Xu Y., Liu Z. Effect of petroleum hydrocarbon pollution levels on the soil microecosystem and ecological function // Environmental Pollution. 2022, vol. 15, no. 293, pp. 118511. https://doi.org/10.1016/j.envpol.2021.118511
38. Brennan F.P., Moynihan E., Griffiths B.S., Hillier S., Owen J., Pendlowski H., Avery L.M. Clay mineral type effect on bacterial enteropathogen survival in soil // Science of The Total Environment. 2014, vol. 468-469, pp. 302–305. https://doi.org/10.1016/j.scitotenv.2013.08.037
39. Callahan M.T., Micallef S.A., Buchanan R.L. Soil Type, Soil Moisture, and Field Slope Influence the Horizontal Movement of Salmonella enterica and Citrobacter freundii from Floodwater through Soil // Journal of Food Protection. 2017, vol. 80, no. 1, pp. 189–197. https://doi.org/10.4315/0362-028X.JFP-16-263
40. Phan-Thien K., Metaferia M.H., Bell T.L., Bradbury M.I., Sassi H.P., van Ogtrop F.F., Suslow T.V., McConchie R. Effect of soil type and temperature on survival of Salmonella enterica in poultry manure-amended soils // Letters in Applied Microbiology. 2020, vol. 71, no. 2, pp. 210–217. https://doi.org/10.1111/lam.13302
41. Kuramae E.E., Yergeau E., Wong L.C., Pijl A.S., van Veen J.A., Kowalchuk G.A. Soil characteristics more strongly influence soil bacterial communities than land-use type // FEMS Microbiology Ecology. 2012, vol. 79, no. 1, pp. 12–24. https://doi.org/10.1111/j.1574-6941.2011.01192.x
42. Han X., Huang C., Khan S., Zhang Y., Chen Y., Guo J. nirS-type denitrifying bacterial communities in relation to soil physicochemical conditions and soil depths of two montane riparian meadows in North China // Environmental Science and Pollution Research International. 2020, vol. 27, no. 23, pp. 28899–28911. https://doi.org/10.1007/s11356-020-09171-8
43. Hedrich S., Schlömann M., Johnson D.B. The iron-oxidizing proteobacteria // Microbiology (Reading). 2011, vol. 157, no. 6, pp. 1551–1564. https://doi.org/10.1099/mic.0.045344-0
44. Ghosh S., Bagchi A. Protein dynamics and molecular motions study in relation to molecular interaction between proteins from sulfur oxidizing proteobacteria Allochromatium vinosum // Journal of Biomolecular Structure and Dynamics. 2021, vol. 39, no. 8, pp. 2771–2787. https://doi.org/10.1080/07391102.2020.1754914
45. Shao M.F., Zhang T., Fang H.H. Sulfur-driven autotrophic denitrification: diversity, biochemistry, and engineering applications // Applied Microbiology and Biotechnology. 2010, vol. 88, no. 5, pp. 1027–1042. https://doi.org/10.1007/s00253-010-2847-1
46. Puri A.W. Specialized Metabolites from Methylotrophic Proteobacteria // Current Issues in Molecular Biology. 2019, vol. 33, pp. 211–224. https://doi.org/10.21775/cimb.033.211
47. Sánchez-Marañón M., Miralles I., Aguirre-Garrido J.F., Anguita-Maeso M., Millán V., Ortega R., García-Salcedo J.A., Martínez-Abarca F., Soriano M. Changes in the soil bacterial community along a pedogenic gradient // Scientific Reports. 2017, vol. 7, pp. 14593. https://doi.org/10.1038/s41598-017-15133-x
48. Lee K.C., Morgan X.C., Dunfield P.F., Tamas I., McDonald I.R., Stott M.B. Genomic analysis of Chthonomonas calidirosea, the first sequenced isolate of the phylum Armatimonadetes // ISME Journal. 2014, vol. 8, no. 7, pp. 1522–1533. https://doi.org/10.1038/ismej.2013.251
49. Langendries S., Goormachtig S. Paenibacillus polymyxa, a Jack of all trades // Environmental Microbiology. 2021, vol. 23, no. 10, pp. 5659–5669. https://doi.org/10.1111/1462-2920.15450
50. Liu L., Wang Z., Ma D., Zhang M., Fu L. Diversity and Distribution Characteristics of Soil Microbes across Forest–Peatland Ecotones in the Permafrost Regions // International

Journal of Environmental Research and Public Health. 2022, vol. 19, pp. 14782. https://doi.org/10.3390/ijerph192214782
51. Abinandan S., Subashchandrabose S.R., Venkateswarlu K., Megharaj M. Soil microalgae and cyanobacteria: the biotechnological potential in the maintenance of soil fertility and health // Critical Reviews in Biotechnology. 2019, vol. 39, no. 8, pp. 981–998. https://doi.org/10.1080/07388551.2019.1654972
52. Nowruzi B., Bouaïcha N., Metcalf J.S., Porzani S.J., Konur O. Plant-cyanobacteria interactions: Beneficial and harmful effects of cyanobacterial bioactive compounds on soil-plant systems and subsequent risk to animal and human health // Phytochemistry. 2021, vol. 192, pp. 112959. https://doi.org/10.1016/j.phytochem.2021.112959
53. Aoyagi T., Inaba T., Aizawa H., Mayumi D., Sakata S., Charfi A., Suh C., Lee J.H., Sato Y., Ogata A., Habe H., Hori T. Unexpected diversity of acetate degraders in anaerobic membrane bioreactor treating organic solid waste revealed by high-sensitivity stable isotope probing // Water Research. 2020, vol. 176, pp. 115750. https://doi.org/10.1016/j.watres.2020.115750
54. Martinez M.A., Woodcroft B.J., Ignacio Espinoza J.C., Zayed A.A., Singleton C.M., Boyd J.A., Li Y.F., Purvine S., Maughan H., Hodgkins S.B., Anderson D., Sederholm M., Temperton B., Bolduc B., Saleska S.R., Tyson G.W., Rich V.I., IsoGenie Project Coordinators, Saleska S.R., Tyson G.W., Rich V.I. Discovery and ecogenomic context of a global Caldiserica-related phylum active in thawing permafrost, Candidatus Cryosericota phylum nov., Ca. Cryosericia class nov., Ca. Cryosericales ord. nov., Ca. Cryosericaceae fam. nov., comprising the four species Cryosericum septentrionale gen. nov. sp. nov., Ca. C. hinesii sp. nov., Ca. C. odellii sp. nov., Ca. C. terrychapinii sp. nov. // Systematic and Applied Microbiology. 2019, vol. 42, no. 1, pp. 54–66. https://doi.org/10.1016/j.syapm.2018.12.003
55. Dyksma S., Gallert C. Candidatus Syntrophosphaera thermopropionivorans: a novel player in syntrophic propionate oxidation during anaerobic digestion // Environmental Microbiology Reports. 2019, vol. 11, no. 4, pp. 558–570. https://doi.org/10.1111/1758-2229.12759
56. Zhou S., Wang G., Han Q., Zhang J., Dang H., Ning H., Gao Y., Sun J. Long-term saline water irrigation affected soil carbon and nitrogen cycling functional profiles in the cotton field // Frontiers in Microbiology. 2024, vol. 15, pp. 1310387. https://doi.org/10.3389/fmicb.2024.1310387
57. Rozanov A.S., Bryanskaya A.V., Malup T.K., Meshcheryakova I.A., Lazareva E.V., Taran O.P., Ivanisenko T.V., Ivanisenko V.A., Zhmodik S.M., Kolchanov N.A., Peltek S.E. Molecular analysis of the benthos microbial community in Zavarzin thermal spring (Uzon Caldera, Kamchatka, Russia) // BMC Genomics. 2014, vol. 12, pp. S12. https://doi.org/10.1186/1471-2164-15-S12-S12
58. Kadnikov V.V., Savvichev A.S., Mardanov A.V., Beletsky A.V., Chupakov A.V., Kokryatskaya N.M., Pimenov N.V., Ravin N.V. Metabolic Diversity and Evolutionary History of the Archaeal Phylum "Candidatus Micrarchaeota" Uncovered from a Freshwater Lake Metagenome // Applied and Environmental Microbiology. 2020, vol. 86, no. 23, pp. e02199-20. https://doi.org/10.1128/AEM.02199-20
59. Golyshina O.V., Bargiela R., Toshchakov S.V., Chernyh N.A., Ramayah S., Korzhenkov A.A., Kublanov I.V., Golyshin P.N. Diversity of “Ca. Micrarchaeota” in Two Distinct Types of Acidic Environments and Their Associations with Thermoplasmatales // Genes. 2019, vol. 10, pp. 461. https://doi.org/10.3390/genes10060461
60. van Vliet D.M., Palakawong Na Ayudthaya S., Diop S., Villanueva L., Stams A.J.M., Sánchez-Andrea I. Anaerobic Degradation of Sulfated Polysaccharides by Two Novel Kiritimatiellales Strains Isolated From Black Sea Sediment // Frontiers in Microbiology. 2019, vol. 10, pp. 253. https://doi.org/10.3389/fmicb.2019.00253
61. Constancias F., Saby N.P., Terrat S., Dequiedt S., Horrigue W., Nowak V., Guillemin J.P., Biju-Duval L., Chemidlin Prévost-Bouré N., Ranjard L. Contrasting spatial patterns and ecological attributes of soil bacterial and archaeal taxa across a landscape // MicrobiologyOpen. 2015, vol. 4, no. 3, pp. 518–531. https://doi.org/10.1002/mbo3.256
62. Hu M., Sardans J., Sun D., Yan R., Wu H., Ni R., Peñuelas J. Microbial diversity and keystone species drive soil nutrient cycling and multifunctionality following mangrove restoration // Environmental Research. 2024, vol. 251, no. 2, pp. 118715. https://doi.org/10.1016/j.envres.2024.118715
63. Sidiki S. Bauxite Mining in the Boké Region (Western Guinea): Method Used and Impacts on Physical Environment // European Journal of Sustainable Development Research. 2019, vol. 3, no. 3, pp. em0087. https://doi.org/10.29333/ejosdr/5735
64. Kolie B., Jun Y., Sunahara G., Camara M. Characterization of the rock blasting process impacts in Lefa gold mine, Republic of Guinea // Environmental Earth Sciences. 2021, vol. 80, pp. 175. https://doi.org/10.1007/s12665-021-09477-x
65. Tabunschik V., Gorbunov R., Bratanov N., Gorbunova T., Mirzoeva N., Voytsekhovskaya V. Fatala River Basin (Republic of Guinea, Africa): Analysis of Current State, Air Pollution, and Anthropogenic Impact Using Geoinformatics Methods and Remote Sensing Data // Sustainability. 2023, vol. 15, pp. 15798. https://doi.org/10.3390/su152215798
66. Sidibé D., Konaté A.A., Kaba O.B., Traoré S. Bauxite Mining Industry in Guinea and the Valorization Prospects of the Resulting Residue for Engineering Purposes // Novel Perspectives of Engineering Research. 2021, vol. 4, pp. 94–110. https://doi.org/10.9734/bpi/nper/v4/3680F
67. Diallo P. Regime Stability, Social Insecurity and Bauxite Mining in Guinea // Developments Since the Mid-Twentieth Century. 1st ed., London, UK, 2019. 142 p. https://doi.org/10.4324/9780429286544
68. Diallo A.K., Conte M.S.M., Kaba O.B., Soumah A., Camara M. Petrological and Statistical Studies of the Limbiko Bauxite Deposit, Republic of Guinea // International Journal of Geosciences. 2023, vol. 14, pp. 351–376. https://doi.org/10.4236/ijg.2023.144020
69. Wilhelm C., Maconachie R. Exploring local content in Guinea's bauxite sector: Obstacles, opportunities and future trajectories // Resources Policy. 2020, vol. 71, pp. 101935. https://doi.org/10.1016/j.resourpol.2020.101935
70. Knierzinger J. The socio-political implications of bauxite mining in Guinea: A commodity chain perspective // Extractive Industries and Society. 2014, vol. 1, pp. 20–27. https://doi.org/10.1016/j.exis.2014.01.005.
71. Daniel R. The metagenomics of soil // Nature Reviews Microbiology. 2005, vol. 3, pp. 470–478. https://doi.org/10.1038/nrmicro1160
72. Чернов Т. И., Холодов В. А., Когут Б. М., Иванов А. Л. Методология микробиологических исследований почвы в рамках проекта “Микробиом России” // Бюл. Почв. ин-та им. В.В. Докучаева. 2017. Т. 87. С. 100–113. https://doi.org/10.19047/0136-1694-2017-87-100-113
73. Jones A., Breuning-Madsen H., Brossard M., Dampha A., Dewitte O., Hallett S., Jones R., Kilasara M., Le Roux P., Micheli E., Montanarella L., Spaargaren O., Tahar G., Thiombiano L., Van Ranst E., Yemefack M., Zougmore R. Soil Atlas of Africa. Luxembourg: Luxembourg, 2013. 176 p.
74. Gorbunova T., Gorbunov R., Camara A.I., Bratanov N., Sow B.B., Pham C.N., Safonova M., Faerman A., Tabunshchik V., Nikiforova A., Lineva N., Diallo A.I.P., Keita I. Heavy Metals in Soils of the Fatala River Basin (Republic of Guinea) // RGSA2024. 2024, vol. 18, pp. e08309. https://doi.org/10.24857/rgsa.v18n9-161

AUTHOR CONTRIBUTIONS

Yakov I. Alekseev, Roman V. Gorbunov, Darya A. Ignateva, Tatiana Yu. Gorbunova, Ibrahima Keita and Vladimir A. Tabunshchik were involved in data analysis, manuscript writing and graphic material creation. Sory Diakité, Abdoulaye M. Baldé, Mamadou D. Sow and Alpha I.P. Diallo participated in data collection and text editing. Aleksey A. Shvartsev, Aleksandr A. Volkov and Yuliya A. Monakhova developed the methodology, analyzed data, and edited the text. All authors are equally responsible for plagiarism, self-plagiarism and other ethical transgressions.

КРИТЕРИИ АВТОРСТВА

Яков И. Алексеев, Роман В. Горбунов, Дарья А. Игнатьева, Татьяна Ю. Горбунова, Ибрагима Кейта, Владимир А. Табунщик принимали участие в анализе данных, написании рукописи и создании графического материала. Сори Диаките, Абдулайе М. Балде, Мамаду Д. Соу, Альфа И. П. Диалло участвовали в сборе данных и редактировании текста. Алексей А. Шварцев, Александр А. Волков, Юлия А. Монахова разработали методологию, проанализировали данные и отредактировали текст. Все авторы в равной степени несут ответственность при обнаружении плагиата, самоплагиата или других неэтических проблем.

NO CONFLICT OF INTEREST DECLARATION

The authors declare no conflict of interest.

КОНФЛИКТ ИНТЕРЕСОВ

Авторы заявляют об отсутствии конфликта интересов.

ORCID

Darya A. Ignateva / Дарья А. Игнатьева https://orcid.org/0000-0003-0432-1760
Tatiana Yu. Gorbunova / Татьяна Ю. Горбунова https://orcid.org/0000-0003-2155-6502
Ibrahima Keita / Ибрагима Кейта https://orcid.org/0009-0001-2560-9117
Yakov I. Alekseev / Яков И. Алексеев https://orcid.org/0000-0002-1696-7684
Roman V. Gorbunov / Роман В. Горбунов https://orcid.org/0000-0002-8222-3819
Aleksey A. Shvartsev / Алексей А. Шварцев https://orcid.org/0000-0002-2786-9860
Aleksandr A. Volkov / Александр А. Волков https://orcid.org/0000-0002-4305-8726
Yuliya A. Monakhova / Юлия А. Монахова https://orcid.org/0000-0002-6772-6098
Vladimir A. Tabunshchik / Владимир А. Табунщик https://orcid.org/0000-0003-3555-6087
Sory Diakité / Сори Диаките https://orcid.org/0009-0009-0284-7495
Abdoulaye M. Baldé / Абдулайе М. Балде https://orcid.org/0009-0003-1231-5608
Mamadou D. Sow / Мамаду Д. Соу https://orcid.org/0009-0005-1297-5424
Alpha I. P. Diallo / Альфа И. П. Диалло https://orcid.org/0000-2603-1959-1992