DOI: https://doi.org/10.17816/ecogen50901



Thermophilic aerobic organoheterotrophic soil bacteria from anthropogenically changed territories of Saint Petersburg and Leningrad region

© A.S. Zhuravleva^{*1}, E.N. Volkova², A.S. Galushko¹

¹ Agrophysical Research Institute, Saint Petersburg, Russia;

² Saint Petersburg State University of Industrial Technologies and Design, Higher School of Technology and Energy, Saint Petersburg, Russia

Anthropogenically altered soils of Saint Petersburg and Luga (Leningrad Region) were investigated for the presence of thermophilic aerobic chemoorganoheterotrophic bacteria, potentially capable of decomposing hydrocarbons at elevated temperatures (60°C). 6 strains of pure spore-forming cultures of bacteria were isolated. Analysis of the nucleotide sequences of the 16S rRNA genes showed that they belong to the genera *Geobacillus* and *Aeribacillus*. For the first time, we obtained information on the presence of representatives of the genus *Aeribacillus*, which are typical inhabitants of hot springs and zones with geothermal activity, in the soils of the regions of Saint Petersburg and the Leningrad Region.

Keywords: aerobes; thermophilic bacteria; acetate-decomposing bacteria; oil pollution; anthropogenic soil pollution.

To cite this article:

Zhuravleva AS, Volkova EN, Galushko AS. Thermophilic aerobic organoheterotrophic soil bacteria from anthropogenically changed territories of Saint Petersburg and Leningrad region. *Ecological genetics*. 2021;19(1):47–58. DOI: https://doi.org/10.17816/ecogen50901

Received: 23.11.2020



Accepted: 15.02.2020

Published: 23.03.2021

DOI: https://doi.org/10.17816/ecogen50901

Термофильные аэробные органогетеротрофные бактерии антропогенно измененных территорий Санкт-Петербурга и Ленинградской области

© А.С. Журавлева*¹, Е.Н. Волкова², А.С. Галушко¹

 Федеральное государственное бюджетное научное учреждение «Агрофизический научно-исследовательский институт», Санкт-Петербург;
Государственное бюджетное образовательное учреждение высшего образования «Санкт-Петербургский государственный университет промышленных технологий и дизайна», Высшая школа технологии и энергетики, Санкт-Петербург

Исследованы антропогенно измененные грунты Санкт-Петербурга и Луги (Ленинградская область) на предмет присутствия термофильных аэробных хемоорганогетеротрофных бактерий, потенциально способных к разложению углеводородов при повышенной температуре (60 °C). Выделено 6 штаммов чистых культур спорообразующих бактерий. Анализ нуклеотидных последовательностей генов 16S pPHK показал их принадлежность к родам *Geobacillus* и *Aeribacillus*. Сведения о присутствии представителей рода *Aeribacillus*, типичных обитателей горячих источников и зон с геотермальной активностью, в почвах регионов Санкт-Петербурга и Ленинградской области получены нами впервые.

Ключевые слова: аэробы; термофильные бактерии; ацетатразлагающие бактерии; нефтезагрязнение; антропогенное загрязнение почв.

Как цитировать:

Журавлева А.С., Волкова Е.Н., Галушко А.С. Термофильные аэробные органогетеротрофные бактерии антропогенно измененных территорий Санкт-Петербурга и Ленинградской области // Экологическая генетика. 2021. Т. 19. № 1. С. 47–58. DOI: https://doi.org/10.17816/ecogen50901



Рукопись одобрена: 15.02.2021

Опубликована: 23.03.2021

INTRODUCTION

Numerous studies of anthropogenically modified soils and grounds in different climatic zones have shown that the composition of the microbial community, in particular, the consortium of crude oil degraders, is different [1-4]. Most of the microorganisms inhabiting places remote from geothermal areas are mesophiles growing at temperatures from 0°C-10°C to 40°C-45°C, with the natural optimal temperature of 37°C [5, 6]. Thermophilic microorganisms are considered as an ecologically separate group of microorganisms; the optimum temperature for the growth of moderately thermophilic bacteria is 50°C-75°C, and for extreme thermophilic and hyperthermophilic bacteria and archaea, it is within the range of 75°C–105°C, with the maximum temperature reaching 100°C and above [5, 6]. The main distinguishing traits of these groups are the specific chemical composition and strength of cell membranes, thermostable proteins and enzymes, increased lipid content in the cell wall, saturated fatty acid content, and accelerated metabolism, which, among other things, enables restoration of quickly damaged cell structures [6].

The natural habitats of thermophilic microorganisms in the contemporary biosphere are thermal springs, deep-sea hydrothermal springs, high-temperature underground biosphere, as well as ecosystems associated with human activities, namely, composts, waste water, storage sites for manure, peat, and hay [5]. Numerous studies have shown the presence of thermophilic microorganisms in various geographic areas such as in Indonesia, New Zealand, Mexico, China, Nepal, Thailand, India, People's Republic of China, Japan, Turkey, Algeria, Saudi Arabia, Iran, Tunisia, Germany, Italy, Bulgaria, Russia, Armenia, Kazakhstan, and Antarctica [6-37]. Microorganisms discovered are mainly representatives of the microbiota of thermal springs, reservoir waters of high-temperature oil fields, and ecosystems associated with them; however, they also include inhabitants of soils and even subglacial lake waters [21], which indicate the adaptability of these microorganisms to various habitat conditions. Thus, according to the literature, the presence of thermotolerant bacteria was also confirmed in the soils of the northern regions [38], which is presumably associated with anthropogenic effect and climate change. The study of microorganisms adapted to the climatic conditions of a particular region must be taken into account for the selection of a system for bioremediation of oil-contaminated soils and the use of agents in it based on the application of microbial cultures [19]. In addition, thermophilic microorganisms, one of the main characteristics of which is rapid metabolism, can accelerate significantly the decomposition of oil products in the soil. We have revealed previously the presence of thermophilic hydrocarbon-oxidizing microorganisms in

the soils of St. Petersburg [39]; nevertheless, in general, their representatives living in the soils of the northern regions free of geothermal activity are still under-investigated.

Under natural conditions in the southern regions, where thermophilic microorganisms are typical inhabitants, the soil surface can be heated by solar radiation up to 60°C-75°C [40, 41], and in the northern regions, it can be heated up to 46°C-57°C [42, 43]. While heating is also naturally influenced by the state of the vegetation cover, the dry-weight percentage of the soil, and its moisture capacity [44], sandy soils warm up to a greater extent than cold ones and cool faster; the contrast ratio of the temperature regime is also typical for anthropogenically modified territories with deterioration or absence of soil and vegetation cover [45], as well as for areas where the soil cover is completely replaced by bulk ground. Landfills and areas of railways represent such anthropogenically altered landscapes with a locally increased ambient temperature and the regular introduction of alien flora and microflora into the ecosystem [46, 47]. This prompts the hypothesis that thermophilic microorganisms that are resistant to pollution and able to adapt to the conditions of a lack of organic compounds can inhabit the surface layer of soils of such altered landscapes.

Thus, *this work aimed* to reveal the presence of thermophilic bacterial crude oil degraders in anthropogenically altered soils of St. Petersburg and Leningrad region as well as to isolate pure cultures and characterize and identify strains.

MATERIALS AND METHODS

The study objects were samples of anthropogenically contaminated soil from the landfill in St. Petersburg (samples K2 and K6) and soil samples from the Luga railway tracks (samples L1 and L2) taken in 2019. Sample K2 was soil from the landfill in the Kudrovo area, sample K6 was the background soil near the landfill, sample L1 was the background soil on the slope of the railway in Luga, and sample L2 was the sandy soil from the railway track in Luga with visible oil contamination. Samples of the surface layer of soil or ground (0–5 cm) were taken into sterile vessels at 5 points on an area of 1 m², and then they were mixed under sterile conditions and solid inclusions and plant residues were manually removed.

For identification of the presence of thermophilic bacteria and obtaining enrichment cultures in averaged samples, the samples were inoculated into a modified Voroshilova–Dianova (VD) liquid mineral nutrient medium [48] with the addition of Na acetate as the only source of energy and carbon for the growth of microorganisms. The VD medium (per 1 L) was composed of 1.0 g of NH_4Cl ,

1.0 g of NaCl, 1.0 g of K_2 HPO₄, 1.0 g of KH₂PO₄, 0.2 g of MgSO₄, 0.02 g of CaCl₂, and 1.36 g of CH₃COONa \cdot 3H₂O. The medium pH was adjusted to 7.0–7.4. The medium was sterilized by autoclaving for 30 min at 1 atm and 121°C. Trace element solutions prepared as described in the source [49] were added at 1 ml/L of each to a sterile medium before inoculation. The bacteria were cultivated aerobically in a thermostat at a constant temperature of 60°C. Initially, 0.5 ml of an aqueous extract of soil was added to a test tube with VD medium of 5 ml [1 g of soil was introduced into a test tube with 10 ml of distilled water, shaken on a Vortex V-1 plus (Biosan). Inoculation with a pipette from the upper part of the extract was performed after 15-min settling of sedimentation of soil particles]. Subsequently, the method was adjusted, and 0.05 g of a soil sample was introduced directly into a test tube with the medium.

To isolate pure cultures, enrichment cultures were subcultured in test tubes with a liquid VD medium with sodium acetate (method of serial dilutions) and cultured in a thermostat. After shaking on a Vortex using a pipette, 0.1 ml of the culture liquid was inoculated from the upper part of the test tube onto plates with solid fish meal hydrolyzate (FMH) medium with agar (composition per 1 L included 12.0 g of pancreatic FMH, 12.0 g of enzymatic peptone, 6.0 g of NaCl, 12.0 g of microbiological agar) and triturated evenly with a spatula, and cultivation took place within 1 day, after which pure cultures were isolated from the grown colonies by the bacto-streep method.

Microscopic examination to check the purity of the cultures was performed on a Zeiss Axiostar plus microscope equipped with a phase-contrast device at a total magnification of ×400. A day-old culture grown on solid FMH medium was used.

To test the ability of the cultures to use oil as the only carbon source, isolated cultures were inoculated in a liquid VD medium with the addition of oil as a substrate (10 ml/L). After the surface introduction of oil into the medium, the bacterial suspension was inoculated and cultivated in a thermostat at a constant temperature of 60°C. To confirm the growth of bacteria using oil hydrocarbons as the only carbon source, the bacterial suspension obtained from oil was subcultured three times on a similar medium with oil, followed by cultivation with measurement of optical density.

The dynamics of culture growth in a liquid medium was determined by the change in the optical density of the medium using a PE 3000-UV spectrophotometer (Promecolab) at a wavelength of 570 nm in absorption units (abs). Based on the results of measurements for 2.5 days (until the growth curve reached a plateau), the culture growth curve was plotted. The experiment was performed in triplicate, and the culture optical density for each point was measured twice in a 2.5-ml cuvette; statistical processing and plotting with the display of the relative error were performed in MS Excel 2007. The range of values lies within the error limits ($\Delta = 0.05$).

Strains were identified by molecular genetic methods at Evrogen (Moscow) based on the analysis of the nucleotide sequence of the 16S rRNA gene obtained using standard primers 27F (5'-AGAGTTTGATCCTGGCTCAG3') and 1492R (5'-ACGGYTACCTTGTTACGACTT3').

For analysis of nucleotide sequences and construction of a phylogenetic tree, we used the NCBI BLAST libraries and neighbor-joining and maximum likelihood methods [49–53] (MUSCLE, Gblocks, PhyML, TreeDyn programs). The length of the sequences analyzed was 1439–1444 nucleotides.

Nucleotide sequences of 16S rRNA gene fragments were deposited in the GenBank NCBI database under numbers MW676172–MW676177.

RESULTS AND DISCUSSION

Isolation of pure cultures

Inoculation of water extracts of soil in variants K2 and K6 on a liquid VD medium and subsequent incubation did not lead to the expected result, the growth of thermophilic microorganisms was not detected, probably due to a small number of their cells in the soil. Therefore, the technique was subsequently modified, and 0.05 g of a soil ground sample was used as an inoculum, which was introduced directly into a test tube with the medium. In this case, the growth of microorganisms started 1 day after inoculation. Microorganisms capable of growing at a temperature of 60°C were detected in all studied samples K2-2, K6, L1, and L2.

As a result of several serial dilutions and successive transfers of microorganisms grown from the studied soil samples (K2 and K6, and L1 and L2), stable growing enrichment cultures of thermophilic bacteria were obtained. Subsequently, pure cultures K2-2, K6, as well as L1, L2-1, L2-2, and L2-3 were isolated from enrichment cultures. The L2-1 culture stopped growing after several reinoculations and was not used in further experiments. Isolation of enrichment cultures K2 and K6 was described by Volkova et al. [39]. The isolation of pure cultures of bacteria from the Kudrovo and Luga samples is described in this publication.

Inoculation of the L2 enrichment culture on the surface of the agar medium of FMH resulted in the growth of bacterial colonies visually different in color and growth pattern. Three pure cultures of bacteria, namely, L2-1, L2-2, and L2-3, were isolated by the depletion bactostreep method on this medium, while the L1 culture was initially a homogeneous monoculture. A greater diversity of cultivated thermophilic microorganisms was detected in a sample of contaminated soil compared with

the background, which indicates a greater adaptability of the microbial community under conditions of technogenic pollution.

Characteristics of cultures

Microscopic examination of the cultures showed that cultures K2-2, K6, L1, L2-2, and L2-3 are immobile, sporulating small thin rods, and L2-1 are immobile sporulating long rods.

The general view of microbial cells and spores is presented in Fig. 1.

All isolated cultures were able to grow by using acetate as a source of energy and carbon. The growth dynamics of cultures K2-2 and K6 are demonstrated in Figs. 2 and 3. The maximum optical density (0.25 ± 0.012) was registered after 2-3 days for the K2-2 culture and 1.7 days for the K6 culture.

The isolated bacterial strains were tested for their ability to grow by the use of oil. Strains K2-2 and K6 were able to grow by using petroleum hydrocarbons. The ability to use petroleum hydrocarbons by strains isolated from Luga's samples requires further study.



DOI: https://doi.org/10.17816/ecogen50901

Fig. 1. General view of cells and spores: a - L1, b - L2 - 1, c - L2 - 2, d - L2 - 3, e - K2 - 2, f - K6





Fig. 2. Growth curve of a bacterial culture K2-2 in a liquid VD medium with sodium acetate and without an organic substrate for 2.5 days. OD, optical density of the culture

Fig. 3. Curve of the change in the optical density of the bacterial culture K6 in VD medium with sodium acetate and without an organic substrate for 2.5 days. OD, optical density of the culture

The maximum optical density of the K2-2 and K6 cultures at the end of the experiment during their cultivation for 2.5 days on a liquid VD medium added with oil was 0.143 ± 0.011 for the K2-2 culture and 0.064 ± 0.005 for the K6 culture, which indicated the ability of these cultures to use various petroleum hydrocarbons as a growth substrate. The K2-2 strain isolated from the contaminated soil at the landfill territory is possibly capable of decomposing more oil components and, accordingly, appears more promising for further research in this field.

Identification of strains

The study of the phylogenetic position of the isolated cultures based on the analysis of the nucleotide sequence of the 16S rRNA genes obtained with universal primers 27F and 1492R revealed that they represent different genera of gram-positive spore-forming bacteria belonging to *Firmicutes* of the *Bacilli* class of the order *Bacillales* of the *Bacillaceae* family. Thus, strain L2-1 belongs to the genus *Geobacillus*, and strains K2-2, K6, L1, L2-2, and L2-3 belong to the closely related genus *Aeribacillus* (Fig. 4), which was relatively recently separated from *Geobacillus* [10]. This genus currently comprises two species [10, 55].

According to the literature, strains Aeribacillus pallidus and Geobacillus thermodenitrificans, which are bacterial species most similar to those we found based on the results of 16S rRNA sequencing, are inhabitants of hot geographic regions, and they were found in Mexico [11], Iran [35], and Turkey [9]; there is little information about their ability to decompose hydrocarbons. Moreover, some strains of these species are capable of decomposing petroleum hydrocarbons (alkanes <C17, aromatic hydrocarbons, naphthalene, phenanthrene), namely, Aeribacillus pallidus 8m3, SL1, VP3, XS2, and XS3 [20, 24, 56-59] and Geobacillus thermodenitrificans NG80-2 [60]. As a rule, thermophilic bacilli of the genus Aeribacillus were found in thermal springs and geothermal activity zones [12, 13, 20, 61]; we obtained information on their presence in the soils of the regions of St. Petersburg and Leningrad for the first time. According to literature data, some other thermophilic representatives of the genus Geobacillus were revealed on the territory of Russia [18, 62, 63], and these species were also found mainly in thermal springs. While there is very little information



0.01

Fig. 4. Phylogenetic tree of closely related strains obtained by applying the neighbor-join and BioNJ algorithms to the matrix of pairwise distances [50–54]. Branch length is presented to scale and is measured by the number of nucleotide substitutions per site

nowadays on their presence in soil on the territory of Russia, there are only a few data on the presence of thermophilic microorganisms in anthropogenically modified soils, such as timber stockpiling areas [64], as well as of agricultural soils after the application of wastewater treatment products [65].

Thus, the hypothesis of the presence of thermophilic bacteria in anthropogenically altered soils of St. Petersburg and Leningrad region was confirmed, and the results of this study demonstrated that, in general, representatives of thermophilic bacteria with rapid metabolism, atypical for the northern regions, are capable of adapting and surviving under conditions of anthropogenic contamination, using a short period of elevated temperatures for reproduction and waiting out of unfavorable periods in a state of spores.

CONCLUSION

The microflora of anthropogenically altered soils of the Kudrovo region (St. Petersburg) and the city of

REFERENCES

1. Panicker G, Aislabie J, Saul D, Bej AK. Cold tolerance of *Pseudomonas* sp. 30–3 isolated from oil-contaminated soil, Antarctica. *Polar Biol.* 2002;25:5–11.

2. Andreolli M, Albertarelli N, Lampis S, et al. Bioremediation of diesel contamination at an underground storage tank site: a spatial analysis of the microbial community. *World J Microbiol Biotechnol.* 2016;32:6.

3. Yan L, Sinkko H, Penttinen P, Lindström K. Characterization of successional changes in bacterial community composition during bioremediation of used motor oil-contaminated soil in a boreal climate. *Science of the Total Environment*. 2016;542:817–825. DOI: 10.1016/j.scitotenv.2015.10.144

4. Kim DD, O'Farrell C, Toth CRA., et al. Microbial community analyses of produced waters from high-temperature oil reservoirs reveal unexpected similarity between geographically distant oil reservoirs. *Microb Biotechnol.* 2018;11(4):788–796. DOI: 10.1111/1751-7915.13281

5. Bonch-Osmolovskaja E.A. Termofil'nye mikroorganizmy: obshhij vzgljad. *Trudy In-ta mikrobiologii im. S.N. Vinogradskogo*. M.: MAKS Press, 2011. P. 5–14. (In Russ.)

6. Wiegel J. Anaerobic alkalithermophiles, a novel group of extremophiles. *Extremophiles*. 1998;2:257–267.

7. Chamkha M, Mnif S, Sayadi S. 2008. Isolation of a thermophilic and halophilic tyrosol-degrading *Geobacillus* from a Tunisian hightemperature oil field. *FEMS Microbiol Lett.* 2008;283:23–29. DOI: 10.1111/j.1574-6968.2008.01136.x

8. Saw JH, Mountain BW, Feng L, et al. Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium *Anoxybacillus flavithermus* WK1. *Genome Biol.* 2008;9: R161. D0I: 10.1186/gb-2008-9-11-r161

9. Adiguzel A, Ozkan H, Baris O, et al. Identification and characterization of thermophilic bacteria isolated from hot springs in Turkey. *J Microbiol Methods*. 2009;79(3):321–328. DOI: 10.1016/j. mimet.2009.09.026

Luga (Leningrad region) was investigated. This study revealed the presence of thermophilic aerobic bacteria with growing capability due to the destruction of acetate at an elevated temperature (60°C). Pure bacterial cultures (6 strains) were isolated and described, and the obtained strains were identified based on molecular genetic methods, which showed that they belong to the genera *Geobacillus* and *Aeribacillus*. For the first time, we obtained information about representatives of the genus *Aeribacillus* in the regions of St. Petersburg and Leningrad.

Future studies should identify the adaptability of bacterial cultures obtained under different temperature conditions, as well as the ability to decompose individual hydrocarbons.

ADDITIONAL INFORMATION

Funding. The research was partially supported by the Russian Foundation for Basic Research (Grant No. 19-34-90156).

10. Miñana-Galbis D, Pinzón DL, Loren JG, Manresa A, Oliart-Ros RM. Reclassification of *Geobacillus pallidus* (Scholz et al. 1988) Banat et al. 2004 as *Aeribacillus pallidus* gen. nov., comb. nov. *Int J Syst Evol Microbiol*. 2010;60:1600–1604.

11. Pinzón-Martínez DL, Rodríguez-Gómez C, Miñana-Galbis D, et al. Thermophilic bacteria from Mexican thermal environments: isolation and potential applications. *Environ Technol*. 2010;31(8–9):957–966. DOI: 10.1080/09593331003758797

12. Yasawong M, Areekit S, Pakpitchareon A, et al. 2011. Characterization of thermophilic halotolerant *Aeribacillus pallidus* TD1 from Tao Dam Hot Spring, Thailand. *Int J MolSci.* 2011;12(8):5294–5303. DOI: 10.3390/ijms12085294

13. Zheng C, He J, Wang Y, et al. Hydrocarbon degradation and bioemulsifier production by thermophilic *Geobacillus pallidus* strains. *Bioresour Technol.* 2011;102;(9155–9161).

14. Inan K, Belduz AO, Canakci S. *Anoxybacillus kaynarcensis* sp. nov., a moderately thermophilic, xylanase producing bacterium. *J Basic Microbiol.* 2013;53:410–419.

15. Radchenkova N, Vassilev S, Panchev I, et al. Production and properties of two novel exopolysaccharides synthesized by a thermophilic bacterium *Aeribacillus pallidus* 418. *Appl Biochem Biotechnol*. 2013;171:31–43. DOI: 10.1007/s12010-013-0348-2

16. Cihan AC, Cokmus C, Koc M, Ozcan B. *Anoxybacillus calidus* sp. nov., a thermophilic bacterium isolated from soil near a thermal power plant. *Int J Syst Evol Microbiol.* 2014;64:211–219.

17. Palanisamy N, Ramya J, Kumar S, et al. Diesel biodegradation capacities of indigenous bacterial species isolated from diesel contaminated soil. *J Environ Heal Sci Eng.* 2014;12:1–8. DOI: 10.1186/s40201-014-0142-2

18. Bryanskaya AV, Rozanov AS, Slynko NM, et al. *Geobacillus icigianus* sp. nov., a thermophilic bacterium isolated from a hot spring. *Int J Syst Evol Microbiol.* 2015;65:864–869. DOI: 10.1099/ijs.0.000029 **19.** Delegan JA, Vetrova AA, Chernjavskaja MI, et al. Termotolerantnye aktinomicety kak agenty remediacii neftezagrjaznennyh gruntov i vod v uslovijah zharkogo aridnogo klimata. *Izvestiya Tula State University.* 2015(4):248–258. (In Russ.)

20. Filippidou S., Jaussi M., Junier T., et al. Genome sequence of *Aeribacillus pallidus* strain GS3372, an endospore-forming bacterium isolated in a deep geothermal reservoir. *Genome Announc*. 2015;3(4); e00981–15. DOI: 10.1128/genomeA.00981-15

21. Delegan JA. *Termotolerantnye bakterii-destruktory uglevodorodov nefti* [dissertation]. Pushchino: Pushchino State Institute of Natural Science, 2016. (In Russ.) Available from: https://dlib.rsl. ru/01008734496.

22. Mesbaiah FZ, Eddouaouda K, Badis A, et al. Preliminary characterization of biosurfactant produced by a PAH-degrading *Paenibacillus* sp. under thermophilic conditions. *Environ Sci Pollut Res.* 2016;23:14221–14230. DOI: 10.1007/s11356-016-6526-3

23. Poltaraus AB, Sokolova DS, Grouzdev DS, et al. Draft genome sequence of *Aeribacillus pallidus* strain 8m3, a thermophilic hydrocarbon-oxidizing bacterium isolated from the Dagang oil field (China). *Genome Announc*. 2016;4(3): e00500–16. DOI: 10.1128/genomeA.00500-16

24. Poltaraus AB, Sokolova DS, Grouzdev DS, et al. Draft genome sequence of *Geobacillus subterraneus* strain K, a hydrocarbon-oxidizing thermophilic bacterium isolated from a petroleum reservoir in Kazakhstan. *Genome Announc*. 2016;4(4): e00782–16. DOI: 10.1128/genomeA.00782-16

25. Pugazhendi A, Wazin HA, Qari H, et al. Biodegradation of low and high molecular weight hydrocarbons in petroleum refinery wastewater by a thermophilic bacterial consortium. *Environ Tech.* 2016:2381–2391. DOI: 10.1080/09593330.2016.1262460

26. Nazina TN, Shestakova NM, Semenova EM, et al. Diversity of metabolically active bacteria in water-flooded high-temperature heavy oil reservoir. *Front Microbiol.* 2017;8:707. DOI: 10.3389/fmicb.2017.00707

27. Khan IU, Habib N, Xiao M, et al. *Anoxybacillus sediminis* sp. nov., a novel moderately thermophilic bacterium isolated from a hot spring. *Antonie Van Leeuwenhoek*. 2018;111(12):2275–2282. DOI: 10.1007/s10482-018-1118-5

28. Panosyan H, Di Donato P, Poli A, Nicolaus B. Production and characterization of exopolysaccharides by *Geobacillus thermode-nitrificans* ArzA-6 and *Geobacillus toebii* ArzA-8 strains isolated from an Armenian geothermal spring. *Extremophiles*. 2018;22(5): 725–737. DOI: 10.1007/s00792-018-1032-9

29. Radchenkova N, Vassilev S, Panchev I, et al. Production and properties of two novel exopolysaccharides synthesized by a thermophilic bacterium *Aeribacillus pallidus* 418. *Appl Biochem Biotechnol.* 2013;171:31–43. DOI: 10.1007/s12010-013-0348-2

30. Yadav P, Korpole S, Prasad GS, et al. Morphological, enzymatic screening, and phylogenetic analysis of thermophilic bacilli isolated from five hot springs of Myagdi, Nepal. *J Appl Biol Biotechnol.* 2018;6(3):1–8. DOI: 10.7324/JABB.2018.60301

31. Mantiri FR, Rumende RRH, Sudewi S. Identification of a-amylase gene by PCR and activity of thermostable a-amylase from thermophilic *Anoxybacillus thermarum* isolated from Remboken hot spring in Minahasa, Indonesia. *IOP Conf. Ser.: Earth Environ.* 2019;217:012045. DOI: 10.1088/1755-1315/217/1/012045

32. Mechri S, Bouacem K, ZaraîJaouadi N, et al. Identification of a novel protease from the thermophilic *Anoxybacillus kamchatkensis*

M1V and its application as laundry detergent additive. *Extremophiles*. 2019;23:687–706. DOI: 10.1007/s00792-019-01123-6

33. Elumalai P, Parthipan P, Narenkumar J et al. Role of thermophilic bacteria (*Bacillus* and *Geobacillus*) on crude oil degradation and biocorrosion in oil reservoir environment. *3 Biotech*. 2019;9:79. DOI: 10.1007/s13205-019-1604-0

34. Yamprayoonswat W, Sittihan S, Jumpathong W, Yasawonga M. Draft genome sequence of thermophilic halotolerant *Aeribacillus pallidus* TD1, isolated from Tao Dam hot spring, Thailand. *Microbiol.* 2019;8(17): e00204–19. DOI: 10.1128/MRA.00204-19

35. Harirchi S, Etemadifar Z, Mahboubi A, et al. The efect of calcium/magnesium ratio on the biomass production of a novel thermoalkaliphilic *Aeribacillus pallidus* strain with highly heat-resistant spores. *Curr Microbiol*. 2020;77:2565–2574. DOI: 10.1007/s00284-020-02010-6

36. Miyazaki K, Hase E, Tokito N. Complete genome sequence of *Geobacillus* sp. strain E55-1, isolated from mine geyser in Japan. *Microbiol Resour Announc*. 2020;9: e00339–20. DOI: 10.1128/ MRA.00339-20

37. Puopolo R, Gallo G, Mormone A, et al. Identification of a new heavy-metal-resistant strain of *Geobacillus stearothermophilus* isolated from a hydrothermally active volcanic area in southern Italy. *Int J Environ Res Public Health*. 2020;17(8):2678. DOI: 10.3390/ ijerph17082678

38. Delegan JA, Vetrova AA, Akimov VN, et al. Thermotolerant oil-degrading bacteria isolated from soil and water of geographically distant regions. *Applied biochemistry and microbiology*. 2016;52(4):383–391. (In Russ.) DOI: 10.7868/S0555109916040024

39. Volkova EN, Zdorovceva AG, Galushko AS. Poisk termofil'nyh nefterazrushajushhih pochvennyh bakterij na meste nesankcionirovannoj svalki na okraine g. Sankt-Peterburga. Proceedings of the National Scientific and Practical Conference dedicated to the memory of Doctor of Medical Sciences, Professor L.F. Zykin "Zykinskie chtenija". Larionova OS, Sazonova IA, eds. Saratov: Saratovskij GAU, 2020. P. 41–46. (In Russ.)

40. Portillo MC, Santana M, Gonzalez JM. Presence and potential role of thermophilic bacteria in temperate terrestrial environments. *Naturwissenschaften*. 2012;99:43–53. DOI: 10.1007/s00114-011-0867-z

41. Dorzhiev SS, Bazarova EG, Rosenblum MI. Jekologicheskij karkas dlja optimizacii teplovogo rezhima pochvy na aridnyh territorijah. Proceedings of the Russian science conference "Jekologija: vchera, segodnja, zavtra". 2019:155–160. (In Russ.)

42. Makhatkov I.D., Ermolov Y.V. The thermal regime of active layer of pit-covered terrain in northern taiga. *Mezhdunarodnyj zhurnal prikladnyh i fundamental'nyh issledovanij.* 2015(11–3):400–407. (In Russ.)

43. Wong ML, An D, Caffrey SM, et al. Roles of thermophiles and fungi in bitumen degradation in mostly cold oil sands outcrops. *Appl Environ Microbiol.* 2015;81:6825–6838.

44. Shkadova AK. *Temperaturnyj rezhim pochv na territorii SSSR*. Leningrad; 1979: P. 75–81. (In Russ.)

45. Marchik TP, Efremov AL. *Pochvovedenie s osnovami rastenievodstva*. Grodno: GrGU, 2006. 249 p. (In Russ.)

46. Skvortsova IV, Berezutski MA. Railway embankment flora in the southern Volga height. *Povolzhskij jekologicheskij zhurnal.* 2008(1):55–64. (In Russ.)

47. Sudakova SS. Features of railway flora of Ulynovsk Region. *I. Yakovlev Chuvash State Pedagogical University Bulletin.* 2013;2(78):150–154. (In Russ.)

48. Voroshilova AA, Dianova EV. Okisljajushhie neft' bakterii — pokazateli intensivnosti biologicheskogo okislenija nefti v prirodnyh uslovijah. *Mikrobiologiya*. 1952; XXI(4):408–415. (In Russ.)

49. Palatinszky M, Herbold C, Jehmlich N, et al. Cyanate as an energy source for nitrifiers. *Nature*. 2015;524:105–108. DOI: 10.1038/ nature14856

50. Tamura K, Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. *Mol Biol Evol*. 1993;10:512–526.

51. Chevenet F, Brun C, Banuls AL, et al. TreeDyn: towards dynamic graphics and annotations for analyses of trees. *BMC Bioinformatics*. 2006;7:439. DOI: 10.1186/1471-2105-7-439

52. Dereeper A, Guignon V, Blanc G, et al. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Res.* 2008;36(2):465–469. DOI: 10.1093/nar/gkn180

53. Dereeper A, Audic S, Claverie JM, Blanc G. BLAST-EXPLORER helps you building datasets for phylogenetic analysis. *BMC Evol Biol.* 2010;10:8. DOI: 10.1186/1471-2148-10-8

54. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res.* 2004;(5):1792–1797. DOI: 10.1093/nar/gkh340

55. Finore I, Gioiello A, Leone L, et al. *Aeribacillus composti* sp. nov., a thermophilic *bacillus* isolated from olive mill pomace compost. *Int J Syst Evol Microbiol*. 2017;67:4830–4835. DOI: 10.1099/ijsem.0.002391

56. Zheng C, Li Z, Su J, et al. Characterization and emulsifying property of a novel bioemulsifier by *Aeribacillus pallidus* YM-1. *J Appl Microbiol*. 2012;13(44–51). DOI: 10.1111/j.1365-2672.2012.05313.x

57. Mnif S, Sayadi S, Chamkha M. Biodegradative potential and characterization of a novel aromatic-degrading bacterium isolated from a geothermal oil field under saline and thermophilic conditions. *Int Biodeterior Biodegradation*. 2014;86(C):258–264. DOI: 10.1016/j. ibiod.2013.09.015

СПИСОК ЛИТЕРАТУРЫ

1. Panicker G., Aislabie J., Saul D., Bej A.K. Cold tolerance of *Pseudomonas* sp. 30–3 isolated from oil-contaminated soil, Antarctica // Polar Biol. 2002. Vol. 25. P. 5–11.

2. Andreolli M., Albertarelli N., Lampis S., et al. Bioremediation of diesel contamination at an underground storage tank site: a spatial analysis of the microbial community // World J Microbiol Biotechnol. 2016. Vol. 32. P. 6.

3. Yan L., Sinkko H., Penttinen P., Lindström K. Characterization of successional changes in bacterial community composition during bioremediation of used motor oil-contaminated soil in a boreal climate // Science of the Total Environment. 2016. Vol. 542. P. 817–825. DOI: 10.1016/j.scitotenv.2015.10.144

4. Kim D.D., O'Farrell C., Toth C.R.A., et al. Microbial community analyses of produced waters from high-temperature oil reservoirs reveal unexpected similarity between geographically distant oil reservoirs // Microb Biotechnol. 2018. Vol. 11, No. 4. P. 788–796. DOI: 10.1111/1751-7915.13281

5. Бонч-Осмоловская Е.А. Термофильные микроорганизмы: общий взгляд // Труды Ин-та микробиологии им. С.Н. Виноградского. М.: МАКС Пресс, 2011. С. 5–14.

58. Mehetre GT, Dastager SG, Dharne MS. Biodegradation of mixed polycyclic aromatic hydrocarbons by pure and mixed cultures of biosurfactant producing thermophilic and thermo-tolerant bacteria. *Sci Total Environ*. 2019;679:52–60. DOI: 10.1016/j.scitotenv.2019.04.376 **59.** Tao W, Lin J, Wang W, et al. Biodegradation of aliphatic and polycyclic aromatic hydrocarbons by the thermophilic bioemulsifierproducing *Aeribacillus pallidus* strain SL-1. *Ecotoxicol Environ Saf*. 2020;189:1–9. DOI: 10.1016/j.ecoenv.2019.109994

60. Wang L, Tang Y, Wang S, et al. Isolation and characterization of a novel thermophilic *Bacillus* strain degrading long-chain n-alkanes. *Extremophiles*. 2006;10(4):347–356. DOI: 10.1007/s00792-006-0505-4

61. Mechri S, Berrouina MBE, Benmrad M O, et al. Characterization of a novel protease from *Aeribacillus pallidus* VP3 with potential biotechnological interest. *Int J Biol Macromol.* 2017;94(A):221–232. DOI: 10.1016/j.ijbiomac.2016.09.112

62. Nazina TN, Lebedeva EV, Poltaraus AB, et al. *Geobacillus gargensis* sp. nov., a novel thermophile from a hot spring, and the reclassification of *Bacillus vulcani* as *Geobacillus vulcani* comb. nov. *Int J Syst Evol Microbiol.* 2004;(6):2019–2024. DOI: 10.1099/ijs.0.02932-0

63. Rozanov AS, Logacheva MD, Peltek SE. Draft genome sequences of *Geobacillus stearothermophilus* strains 22 and 53, isolated from the Garga hot spring in the Barguzin river valley of the Russian Federation. *Genome Announc*. 2014;2(6): e01205–14. DOI: 10.1128/genomeA.01205-14 **64.** Junicyna OA, Kisil' OJ, Rudakova VA. Termofil'nye bakterii, vydelennye iz othodov lesopilenija, — producenty ksilanoliticheskih i amiloliticheskih fermentov. Proceedings of the Russian science conference "Tehnologii i oborudovanie himicheskoj, biotehnologicheskoj i pishhevoj promyshlennosti"; May 22–242019. Bijsk. P. 433–437. (In Russ.)

65. Ahtemova GA. *Izmenenie struktury mikrobnogo kompleksa pochvy pri ispol'zovanii produktov pererabotki stokov svinootkor-mochnyh predprijatij v kachestve udobrenija* [dissertation]. Saint Petersburg: VNI ISM, 1998. 22 p. (In Russ.) Available from: https://dlib.rsl.ru/01000796688.

6. Wiegel J. Anaerobic alkalithermophiles, a novel group of extremophiles // Extremophiles. 1998. Vol. 2. P. 257–267.

7. Chamkha M., Mnif S., Sayadi S. Isolation of a thermophilic and halophilic tyrosol-degrading *Geobacillus* from a Tunisian high temperature oil field // FEMS Microbiol Lett. 2008. Vol. 283. P. 23–29. DOI: 10.1111/j.1574-6968.2008.01136.x

8. Saw J.H., Mountain B.W., Feng L., et al. Encapsulated in silica: genome, proteome and physiology of the thermophilic bacterium *Anoxybacillus flavithermus* WK1 // Genome Biol. 2008. Vol. 9. R161. D0I: 10.1186/gb-2008-9-11-r161

9. Adiguzel A., Ozkan H., Baris O., et al. Identification and characterization of thermophilic bacteria isolated from hot springs in Turkey // J Microbiol Methods. 2009. Vol. 79, Is. 3. P. 321–328. DOI: 10.1016/j.mimet.2009.09.026

10. Miñana-Galbis D., Pinzón D.L., Loren J.G., et al. Reclassification of *Geobacillus pallidus* (Scholz et al. 1988) Banat et al. 2004 as *Aeribacillus pallidus* gen. nov., comb. nov // Int J Syst Evol Microbiol, 2010. Vol. 60. P. 1600–1604.

11. Pinzón-Martínez D.L., Rodríguez-Gómez C., Miñana-Galbis D., et al. Thermophilic bacteria from Mexican thermal environments:

Экологическая генетика

Ecological genetics

isolation and potential applications // Environ Technol. 2010. Vol. 31, no. 8–9. P. 957–966. DOI: 10.1080/09593331003758797

12. Yasawong M., Areekit S., Pakpitchareon A., et al. 2011. Characterization of thermophilic halotolerant *Aeribacillus pallidus* TD1 from Tao Dam Hot Spring, Thailand // Int J MolSci. 2011. Vol. 12, No. 8. P. 5294–5303. DOI: 10.3390/ijms12085294

13. Zheng C., He J., Wang Y., et al. Hydrocarbon degradation and bioemulsifier production by thermophilic *Geobacillus pallidus* strains // Bioresour Technol. 2011. Vol. 102. P. 9155–9161.

14. Inan K., Belduz A.O., Canakci S. *Anoxybacillus kaynarcensis* sp. nov., a moderately thermophilic, xylanase producing bacterium // J Basic Microbiol. 2013. Vol. 53. P. 410–419.

15. Radchenkova N., Vassilev S., Panchev I., et al. Production and properties of two novel exopolysaccharides synthesized by a thermophilic bacterium *Aeribacillus pallidus* 418 // Appl Biochem Biotechnol. 2013. Vol. 171. P. 31–43. DOI: 10.1007/s12010-013-0348-2

16. Cihan A.C., Cokmus C., Koc M., Ozcan B. *Anoxybacillus calidus* sp. nov., a thermophilic bacterium isolated from soil near a thermal power plant // Int J Syst Evol Microbiol. 2014. Vol. 64. P. 211–219.

17. Palanisamy N., Ramya J., Kumar S., et al. Diesel biodegradation capacities of indigenous bacterial species isolated from diesel contaminated soil // J Environ Heal Sci Eng. 2014. Vol. 12. P. 1–8. DOI: 10.1186/s40201-014-0142-2

18. Bryanskaya A.V., Rozanov A.S., Slynko N.M., et al. *Geobacillus icigianus* sp. nov., a thermophilic bacterium isolated from a hot spring // Int J Syst Evol Microbiol. 2015. Vol. 65. P. 864–869. DOI: 10.1099/ijs.0.000029.

19. Делеган Я.А., Ветрова А.А., Чернявская М.И., и др. Термотолерантные актиномицеты как агенты ремедиации нефтезагрязненных грунтов и вод в условиях жаркого аридного климата // Известия Тульского государственного университета. Естественные науки. 2015. Вып. 4. С. 248–258.

20. Filippidou S, Jaussi M, Junier T, et al. Genome sequence of *Aeribacillus pallidus* strain GS3372, an endospore-forming bacterium isolated in a deep geothermal reservoir // Genome Announc. 2015. Vol. 3, No. 4. P. e00981–15. DOI: 10.1128/genomeA.00981-15

21. Делеган Я.А. Термотолерантные бактерии-деструкторы углеводородов нефти: дис. ... канд. биол. наук. Пущино: Пущинский государственный естественно-научный институт, 2016. Режим доступа: https://dlib.rsl.ru/01008734496. Дата обращения: 01.11.2016.

22. Mesbaiah F.Z., Eddouaouda K., Badis A., et al. Preliminary characterization of biosurfactant produced by a PAH-degrading *Paenibacillus* sp. under thermophilic conditions // Environ Sci Pollut Res. 2016. Vol. 23. P. 14221–14230. DOI: 10.1007/s11356-016-6526-3

23. Poltaraus A.B., Sokolova D.S., Grouzdev D.S., et al. Draft genome sequence of *Aeribacillus pallidus* strain 8m3, a thermophilic hydrocarbon-oxidizing bacterium isolated from the Dagang oil field (China) // Genome Announc. 2016. Vol. 4, No. 3. P. e00500–16. DOI: 10.1128/genomeA.00500-16

24. Poltaraus A.B., Sokolova D.S., Grouzdev D.S., et al. Draft genome sequence of *Geobacillus subterraneus* strain K, a hydrocarbon-oxidizing thermophilic bacterium isolated from a petroleum reservoir in Kazakhstan // Genome Announc. 2016. Vol. 4, No. 4. P. e00782–16. DOI: 10.1128/genomeA.00782-16

25. Pugazhendi A., Wazin H.A., Qari H., et al. Biodegradation of low and high molecular weight hydrocarbons in petroleum refinery wastewater by a thermophilic bacterial consortium // Environ Tech. 2016. P. 2381–2391. DOI: 10.1080/09593330.2016.1262460

26. Nazina T.N., Shestakova N.M., Semenova E.M., et al. Diversity of metabolically active bacteria in water-flooded high-temperature heavy oil reservoir // Front Microbiol. 2017. Vol. 8. P. 707. DOI: 10.3389/fmicb.2017.00707

27. Khan I.U., Habib N., Xiao M., et al. *Anoxybacillus sediminis* sp. nov., a novel moderately thermophilic bacterium isolated from a hot spring // Antonie Van Leeuwenhoek. 2018. Vol. 111, No. 12. P. 2275–2282. DOI: 10.1007/s10482-018-1118-5

28. Panosyan H., Di Donato P., Poli A., Nicolaus B. Production and characterization of exopolysaccharides by *Geobacillus thermodeni-trificans* ArzA-6 and *Geobacillus toebii* ArzA-8 strains isolated from an Armenian geothermal spring // Extremophiles. 2018. Vol. 22, No. 5. P. 725–737. DOI: 10.1007/s00792-018-1032-9

29. Radchenkova N., Vassilev S., Panchev I., et al. Production and properties of two novel exopolysaccharides synthesized by a thermophilic bacterium *Aeribacillus pallidus* 418 // Appl Biochem Biotechnol. 2013. Vol. 171. P. 31–43. DOI: 10.1007/s12010-013-0348-2

30. Yadav P., Korpole S., Prasad G.S., et al. Morphological, enzymatic screening, and phylogenetic analysis of thermophilic bacilli isolated from five hot springs of Myagdi, Nepal // J Appl Biol Biotechnol. 2018. Vol. 6, No. 3. P. 1–8 DOI: 10.7324/JABB.2018.60301

31. Mantiri F.R., Rumende R.R.H., Sudewi S. Identification of a-amylase gene by PCR and activity of thermostable a-amylase from thermophilic *Anoxybacillus thermarum* isolated from Remboken hot spring in Minahasa, Indonesia // IOP Conf. Ser.: Earth Environ. 2019. Sci. 217. 012045. DOI: 10.1088/1755-1315/217/1/012045

32. Mechri S., Bouacem K., ZaraîJaouadi N. et al. Identification of a novel protease from the thermophilic *Anoxybacillus kamchat-kensis* M1V and its application as laundry detergent additive // Extremophiles. 2019. Vol. 23. P. 687–706. DOI: 10.1007/s00792-019-01123-6

33. Elumalai P., Parthipan P., Narenkumar J., et al. Role of thermophilic bacteria (*Bacillus* and *Geobacillus*) on crude oil degradation and biocorrosion in oil reservoir environment // 3 Biotech. 2019. Vol. 9. P. 79. DOI: 10.1007/s13205-019-1604-0

34. Yamprayoonswat W., Sittihan S., Jumpathong W., Yasawonga M. Draft genome sequence of thermophilic halotolerant *Aeribacillus pallidus* TD1, isolated from Tao Dam hot spring, Thailand // Microbiol. 2019. Vol. 8, No. 17. P. e00204–19. DOI: 10.1128/ MRA.00204-19.

35. Harirchi S., Etemadifar Z., Mahboubi A., et al. The efect of calcium/magnesium ratio on the biomass production of a novel thermoalkaliphilic *Aeribacillus pallidus* strain with highly heat-resistant spores // Curr Microbiol. 2020. Vol. 77. P. 2565–2574. DOI: 10.1007/ s00284-020-02010-6

36. Miyazaki K., Hase E., Tokito N. Complete genome sequence of *Geobacillus* sp. strain E55–1, isolated from mine geyser in Japan // Microbiol Resour Announc. 2020. Vol. 9. P. e00339–20. DOI: 10.1128/ MRA.00339–20

37. Puopolo R., Gallo G., Mormone A., et al. Identification of a new heavy-metal-resistant strain of *Geobacillus stearothermophilus*

isolated from a hydrothermally active volcanic area in southern Italy // Int J Environ Res Public Health. 2020. Vol. 17, No. 8. P. 2678. DOI: 10.3390/ijerph17082678

38. Делеган Я.А., Ветрова А.А., Акимов В.Н., и др. Термотолерантные бактерии-нефтедеструкторы, выделенные из проб грунта и воды географически удаленных регионов // Прикладная биохимия и микробиология. 2016. Т. 52, № 4. С. 383–391. DOI: 10.7868/S0555109916040024

39. Волкова Е.Н., Здоровцева А.Г., Галушко А.С., и др. Поиск термофильных нефтеразрушающих почвенных бактерий на месте несанкционированной свалки на окраине г. Санкт-Петербурга // Материалы национальной научно-практической конференции, посвященной памяти д. м. н., профессора Л.Ф. Зыкина: «Зыкинские чтения» / под ред. О.С. Ларионовой, И.А. Сазоновой. Саратов: Саратовский ГАУ, 2020. С. 41–46.

40. Portillo M.C., Santana M., Gonzalez J.M. Presence and potential role of thermophilic bacteria in temperate terrestrial environments // Naturwissenschaften. 2012. Vol. 99. P. 43–53. DOI: 10.1007/s00114-011-0867-z

41. Доржиев С.С., Базарова Е.Г., Розенблюм М.И. Экологический каркас для оптимизации теплового режима почвы на аридных территориях // Материалы Всероссийской научно-практической конференции: Экология: вчера, сегодня, завтра. 2019. С. 155–160.

42. Махатков И.Д. Ермолов Ю.В. Температурный режим деятельного слоя верхового болота северной тайги // Международный журнал прикладных и фундаментальных исследований. 2015. № 11, ч. 3. С. 400–407.

43. Wong M.L., An D., Caffrey S.M., et al. Roles of thermophiles and fungi in bitumen degradation in mostly cold oil sands outcrops // Appl Environ Microbiol. 2015. Vol. 81. P. 6825–6838.

44. Шкадова А.К. Температурный режим почв на территории СССР. Ленинград, 1979. С. 75–81.

45. Марчик Т.П., Ефремов А.Л. Почвоведение с основами растениеводства. Гродно: ГрГУ, 2006. 249 с.

46. Скворцов И.В., Березуцкий М.А. Флора железнодорожных насыпей Приволжской возвышенности // Поволжский эколо-гический журнал. 2008. № 1. С. 55–64.

47. Судакова С.С. Особенности флоры железнодорожных путей Ульяновской области // Вестник Чувашского государственного педагогического университета им. И.Я. Яковлева. 2013. Т. 2, № 78. С. 150–154.

48. Ворошилова А.А., Дианова Е.В. Окисляющие нефть бактерии — показатели интенсивности биологического окисления нефти в природных условиях // Микробиология, 1952. Т. 21, № 4. С. 408–415.

49. Palatinszky M., Herbold C., Jehmlich N., et al. Cyanate as an energy source for nitrifiers // Nature. 2015. Vol. 524. P. 105–108. DOI: 10.1038/nature14856

50. Tamura K., Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees // Mol Biol Evol. 1993. Vol. 10. P. 512–526.

51. Chevenet F., Brun C., Banuls A.L., et al. TreeDyn: towards dynamic graphics and annotations for analyses of trees // BMC Bioinformatics. 2006. Vol. 7. P. 439. DOI: 10.1186/1471-2105-7-439

52. Dereeper A., Guignon V., Blanc G., et al. Phylogeny.fr: robust phylogenetic analysis for the non-specialist // Nucleic Acids Res. 2008. Vol. 36, No. 2. P. 465–469. DOI: 10.1093/nar/gkn180

53. Dereeper A., Audic S., Claverie J.M., Blanc G. BLAST-EXPLORER helps you building datasets for phylogenetic analysis // BMC Evol Biol. 2010. Vol. 10. P. 8. DOI: 10.1186/1471-2148-10-8

54. Edgar R.C. MUSCLE: multiple sequence alignment with high accuracy and high throughput // Nucleic Acids Res. 2004. Vol. 32, No. 5. P. 1792–1797. DOI: 10.1093/nar/gkh340

55. Finore I., Gioiello A., Leone L., et al. *Aeribacillus composti* sp. nov., a thermophilic *bacillus* isolated from olive mill pomace compost // Int J Syst Evol Microbiol. 2017. Vol. 67. P. 4830–4835. DOI: 10.1099/ijsem.0.002391

56. Zheng C., Li Z., Su J., et al. Characterization and emulsifying property of a novel bioemulsifier by *Aeribacillus pallidus* YM-1 // J Appl Microbiol. 2012. Vol. 13. P. 44–51. DOI: 10.1111/j.1365-2672.2012.05313.x

57. Mnif S., Sayadi S., Chamkha M. Biodegradative potential and characterization of a novel aromatic-degrading bacterium isolated from a geothermal oil field under saline and thermophilic conditions // Int Biodeterior Biodegradation. 2014. Vol. 86, part C. P. 258–264. DOI: 10.1016/j.ibiod.2013.09.015

58. Mehetre G.T., Dastager S.G., Dharne M.S. Biodegradation of mixed polycyclic aromatic hydrocarbons by pure and mixed cultures of biosurfactant producing thermophilic and thermo-tolerant bacteria // Sci Total Environ. 2019. Vol. 679. P. 52–60. DOI: 10.1016/j. scitotenv.2019.04.376

59. Tao W., Lin J., Wang W., et al. Biodegradation of aliphatic and polycyclic aromatic hydrocarbons by the thermophilic bioemulsifier-producing *Aeribacillus pallidus* strain SL-1 // Ecotoxicol Environ Saf. 2020. Vol. 189. P. 1–9. DOI: 10.1016/j.ecoenv.2019.109994

60. Wang L., Tang Y., Wang S., et al. Isolation and characterization of a novel thermophilic *Bacillus* strain degrading long-chain n-alkanes // Extremophiles. 2006. Vol. 10, No. 4. P. 347–356. DOI: 10.1007/s00792-006-0505-4

61. Mechri S., Berrouina M.B.E., Benmrad M.O., et al. Characterization of a novel protease from *Aeribacillus pallidus* VP3 with potential biotechnological interest // Int J Biol Macromol. 2017. Vol. 94, part A. P. 221–232. DOI: 10.1016/j.ijbiomac.2016.09.112

62. Nazina T.N., Lebedeva E.V., Poltaraus A.B., et al. *Geobacillus gargensis* sp. nov., a novel thermophile from a hot spring, and the reclassification of *Bacillus vulcani* as *Geobacillus vulcani* comb. nov // Int J Syst Evol Microbiol. 2004. Vol. 54, No. 6. P. 2019–2024. DOI: 10.1099/ijs.0.02932-0

63. Rozanov A.S., Logacheva M.D., Peltek S.E. Draft genome sequences of *Geobacillus stearothermophilus* strains 22 and 53, isolated from the Garga hot spring in the Barguzin river valley of the Russian Federation // Genome Announc. 2014. Vol. 2, No. 6. P. e01205–14. DOI: 10.1128/genomeA.01205-14

64. Юницына О.А., Кисиль О.Я., Рудакова В.А. Термофильные бактерии, выделенные из отходов лесопиления, — продуценты ксиланолитических и амилолитических ферментов // Материалы конференции «Технологии и оборудование химической, биотехнологической и пищевой промышленности»; 22–24 мая 2019 г. Бийск. С. 433–437.

65. Ахтемова Г.А. Изменение структуры микробного комплекса почвы при использовании продуктов переработки стоков свинооткормочных предприятий в качестве удобрения: автореф. дис. ... канд. биол. наук. Санкт-Петербург: ВНИ ИСМ, 1998. 22 с. Режим доступа: https://dlib.rsl.ru/01000796688. Дата обращения: 05.05.2008.

AUTHORS INFO

*Anna S. Zhuravleva, junior researcher, PhD student; address: 14 Grazhdanskiy pr., Saint Petersburg, 195220, Russia; ORCID: https://orcid.org/0000-0001-7204-9653; e-Library SPIN: 3084-1394; e-mail: zhuravlan@gmail.com

Elena N. Volkova, Dr. Sci. (Agriculture), Professor; ORCID: https://orcid.org/0000-0001-7429-4046; e-Library SPIN: 6437-9252; e-mail: ele-ven@yandex.ru

Alexander S. Galushko, PhD, Cand. Sci. (Biol.), Leading Researcher; ORCID: https://orcid.org/0000-0002-0387-7997; eLibrary SPIN 9759-9942; e-mail: galushkoas@inbox.ru

ОБ АВТОРАХ

*Анна Сергеевна Журавлева, младший научный сотрудник, аспирант; адрес: 195220, Санкт-Петербург, Гражданский просп., д. 14; ORCID: https://orcid.org/0000-0001-7204-9653; e-Library SPIN: 3084-1394; e-mail: zhuravlan@gmail.com

Елена Николаевна Волкова, д-р с.-х. наук, профессор; ORCID: https://orcid.org/0000-0001-7429-4046; e-Library SPIN: 6437-9252; e-mail: ele-ven@yandex.ru

Александр Сергеевич Галушко, канд. биол. наук, ведущий научный сотрудник; ORCID: https://orcid.org/0000-0002-0387-7997; eLibrary SPIN 9759-9942; e-mail: galushkoas@inbox.ru