WORLD SCIENCE PUBLISHING
LONDON LTD
LONDON
London International Monthly Conference on Multidisciplinary Research and Innovation

CHARACTERIZATION AND IDENTIFICATION OF ISOLATES OBTAINED FROM THE SOILS AND SEDIMENTS OF THE DRIED ARAL SEA BED

T.Abdrakhmanov, Z. Jabbarov,
Q. Normurodova, M. Karimboyeva
Candidate of Agricultural Sciences, Professor. Department of Soil Science, Faculty of Biology and Ecology, National University of Uzbekistan, Tashkent, 100174, Uzbekistan;
Doctor of Biological Sciences, Professor. Department of Soil Science, Faculty of Biology and Ecology, National University of Uzbekistan, Tashkent, 100174, Uzbekistan;
Doctor of Biological Sciences, Professor. Department of microbiology and biotechnology, Faculty of Biology and Ecology, National University of Uzbekistan, Tashkent, 100174, Uzbekistan;
Independent researcher. Department of Soil Science, Faculty of Biology and Ecology, National University of Uzbekistan, Tashkent, 100174, Uzbekistan;

Abstract. A study was conducted on microorganisms found in the soil and substrate of the dried Aral Sea bed. Using the MALDI-TOF method, Halomonas pacifica, Bacillus licheniformis, Actinomyces oris, Streptomyces rochei, Bacillus subtilis, and Micrococcus luteus were identified. Among these, Bacillus subtilis stood out due to its enzymatic activity; consequently, the isolate identified as Bacillus subtilis via MALDI-TOF was further verified using molecular-genetic methods to confirm its identity. To definitively establish the taxonomic species of the Bacillus subtilis strain, an analysis of the 16S rRNA gene sequence was performed.

Keywords: MALDI-TOF, 16S rRNA gene sequence, Bacillus subtilis strain 70/85, NCBI GenBank

Introduction. The Aral Sea region has experienced profound environmental transformation following the progressive desiccation of the Aral Sea and the development of extensive desertification processes. The drying of the Amu Darya Delta, which historically supplied a substantial proportion of the inflow to the Aral Sea, began in the 1960s. Over subsequent decades, increasing water diversion for irrigation, climatic aridification, and changes in river discharge contributed to the progressive shrinkage of the sea and the exposure of extensive areas of the former seabed. The exposed sediments, consisting mainly of sands, sandy loams, loams, and clayey deposits, have subsequently become subject to active pedogenic and desertification processes [2,3,7].

In particular, sandy soils with relatively low salinity supported greater vegetation activity, whereas heavy and highly saline soils were associated with lower biodiversity and the dominance of halophytic species. However, the establishment of vegetation plantations in the newly formed Aralkum Desert requires a comprehensive and site-specific assessment of the physical, chemical, and biological properties of the soil. Arid regions cover approximately 30% of the Earth's land surface, yet their microbial biodiversity remains insufficiently characterized. Persistent aridification and water stress can negatively affect the abundance, structure, and activity of soil microbial communities [9].

In the current era, one of the most significant consequences of global climate change is aridity. Drought is a hazardous abiotic stressor that alters soil conditions. It reduces the populations of microorganisms responsible for ecosystem processes, disrupts their functional composition, and diminishes microbial activity—including enzyme production. Drought directly affects plant morphology, anatomy, physiology, and biochemistry. However, it is possible to mitigate these adverse effects by promoting plant growth through the action of rhizosphere microbial communities.

© 2026 London International Monthly Conference on Multidisciplinary Research and Innovation. All Rights Reserved.

The prolonged process of aridification negatively affects the abundance, structure, and activity of the soil microbiome [9] As a result of reduced microbiological activity, potential metabolic processes in the soil—such as the mineralization of nutrients (N, P, K, C) and respiration—also decrease [8] Recent literature has examined various drought-adapted microorganisms, such as Rhodococcus jostii [4], Microbacterium sp., Arthrobacter siccitoleran, Rhodococcus sp. [5], Pseudomonas putida [10], Azospirillum sp. [1], Lactobacillus paracasei [6], and others. Such drought-adapted microorganisms survive by producing xeroprotectants within their cells, enabling them to adapt to the environment. Our research has focused specifically on isolating these types of microorganisms.

It is possible to mitigate the adverse effects of drought. To achieve this, soil amendments are required. For instance, the application of various organic materials—such as biochar, compost, and sewage sludge—as well as biopreparations of diverse compositions, can enhance soil enzymatic activity, create favorable alternative conditions for the soil microbiome, and enable plants to rapidly adapt to and thrive in adverse conditions.

In our studies, the microorganisms present in the dried-up seabed soils and sediments of the Aral Sea were investigated. The isolated isolates were analyzed by MALDI-TOF. MALDI-TOF MS enabled species-level identification of several bacterial and actinomycete isolates recovered from the investigated soils. The identified microorganisms included Halomonas pacifica, Bacillus licheniformis, Bacillus subtilis, Actinomyces oris, Micrococcus luteus and Streptomyces rochei. Their occurrence demonstrates that, despite the harsh physicochemical conditions, the exposed seabed supports a taxonomically diverse culturable microbial assemblage.

Among these isolates, Bacillus subtilis exhibited the highest activity in α- amylase synthesis. A unique isolate, previously identified as Bacillus subtilis using the MALDI-TOF method, was subjected to molecular-genetic identification to confirm its identity as Bacillus subtilis. To verify the precise taxonomic species of the Bacillus subtilis strain, the sequence of the 16S rRNA gene was analyzed. Its classification as the bacterial species Bacillus subtilis was confirmed through molecular-genetic analysis, and it was designated as strain Bacillus subtilis 70/85. Additionally, strain Bacillus subtilis 70/85 was registered in the NCBI GenBank database under accession number PQ738242.1. [11].

Isolating salinity-adapted bacterial strains from the dried bed of the Aral Sea and studying their unique properties enables the creation of a new generation of biological preparations; when applied, these products improve plant nutrition, protect crops against various phytopathogens, enhance soil fertility and agricultural yields, and accelerate seed germination and growth, thereby offering opportunities for their widespread use in agriculture.

In addition, a field experiment was conducted to observe the effect of the culture fluid of Bacillus subtilis strain 70/85 on the growth and development of elm and black saxaul (Haloxylon aphyllum) seedlings planted in the soil of the dried Aral Sea bed. For this purpose, at the National University of Uzbekistan’s educational and research site established near the "Ship Graveyard" in the Muynak district, 30 elm seedlings and 50 black saxaul seedlings were planted; the experiment included control groups and groups treated with the Bacillus subtilis strain 70/85 culture fluid (at a 1:5 ratio).

The results of the field research (shown in Figure 4.2.3) indicated that the survival rate of the 30 elm seedlings in the control group was 29.3%, whereas the survival rate of seedlings treated with the Bacillus subtilis strain 70/85 culture fluid was 41%. Similarly, for the black saxaul plants, a survival rate of up to 66% was observed in the group treated with the Bacillus subtilis strain 70/85 culture fluid, compared to 53% in the control group.

© 2026 London International Monthly Conference on Multidisciplinary Research and Innovation. All Rights Reserved.

References

1. Arzanesh, M.H., Alikhani, H.A., Khavazi, K., Rahimian, H.A., Miransari M. Wheat (Triticum aestivum L.) growth enhancement by Azospirillum sp. under drought stress. World J. Microbiol. Biotechnol. 2011, 27, 197–205. 42
2. Jabbarov, Z., Abdrakhmanov, T., Abdullaev, Sh., Makhammadiev, S., Nomozov, U., Imomov, O., & Makhkamova, D. (2025a). Accumulation, distribution, and transformation of heavy metals in the dried bottom soils of the Aral Sea. Egyptian Journal of Soil Science, 65(2), 1231–1200. https://doi.org/10.21608/ejss.2025.369277.2070
3. Jabbarov, Z., Abdrakhmanov, T., Abdullaev, Sh., Nomozov, U., Karimov, H., Makhkamova, D., Zafarjonov, N., & Aslanov, I. (2026). Soil salinity and physicochemical drivers of microbial community composition in the desiccated Aral Sea bed. Malaysian Journal of Fundamental and Applied Sciences, 22(2), 411–421.
4. Leblanc J.C., Gonçalves, E.R. Mohn W.W. Global response to desiccation stress in the soil actinomycete Rhodococcus jostii RHA1. Appl. Environ. Microbiol. 2008, 74, 2627–2636. 29.
5. Narváez-Reinaldo J.J., Barba I., González-López J., Tunnacliffe A., Manzanera M. Rapid method for isolation of desiccationtolerant strains and xeroprotectants. Appl. Environ. Microbiol. 2010, 76, 5254–5262. 30
6. Palud A., Salem K., Cavin J.F., Beney L., Licandro H. Identification and transcriptional profile of Lactobacillus paracasei genes involved in the response to desiccation and rehydration. Food Microbiol. 2020, 85, 103301. 32
7. Qo‘ziev, R. Q., Abduraxmonov, N. Yu., & Ramazonov, B. R. (2020). Orolbo‘yi hududlarining tuproq resurslari va ulardan samarali foydalanishning ilmiy asoslari. Zilol-Buloq
8. Schimel J., Balser T.C., Wallenstein M. Microbial stress-response physiology and its implications for ecosystem function. Ecology 2007, 88, 1386–1394
9. Siebielec, S., Siebielec, G., Klimkowicz-Pawlas A., Gałazka A., Grzadziel, J., Stuczynski, T. (2020). Impact of water stress on microbial community and activity in sandy and loamy soils. Agronomy, 10, 1429.
10. Vílchez J.I., García-Fontana C., Román-Naranjo D., González-López J., Manzanera M. Plant drought tolerance enhancement by trehalose production of desiccation-tolerant microorganisms. Front. Microbiol. 2016, 7, 1577
11. https://www.ncbi.nlm.nih.gov/nuccore/PQ738242.1?report=gbwithparts&log$=seqview

© 2026 London International Monthly Conference on Multidisciplinary Research and Innovation. All Rights Reserved.