

Hydrobiological Diversity and Adaptive Microbial Communities in the Dried Aral Sea Basin (Muynak and Shegekul Areas)

Tukhtaboeva Y. A.^{1,*}, Ikramov N. B.², Tursunova Sh. A.³, Mirzaolimova M. M.¹, Rakhmatov A.²

¹KIUT Namangan Branch, Namangan, Uzbekistan

²Namangan State University, Uzbekistan

³Kokand State University, Uzbekistan

Abstract The desiccation of the Aral Sea has resulted in the formation of extreme and highly transformed ecosystems characterized by high salinity, aridity, and unstable hydrological conditions. These environmental changes have significantly influenced the structure and diversity of hydrobiological communities in the region. The present study investigates the hydrobiological diversity and adaptive microbial communities of the dried Aral Sea basin, focusing on the Muynak and Shegekul areas. Field sampling was conducted in residual water bodies and dried seabed zones of the southern Aral Sea region. Hydrobiological analyses included the identification of phytoplankton, microalgae, cyanobacteria, and associated microbial taxa using standard microscopic and algological methods. Taxonomic identification was performed according to modern hydrobiological classification systems. A total of 56 taxa belonging to six major taxonomic groups were identified. Cyanobacteria represented the dominant group (41.1%), followed by Bacillariophyta (25.0%) and Chlorophyta (21.4%). The microbial communities were primarily composed of stress-tolerant and ecologically flexible taxa, including representatives of the genera *Microcystis*, *Oscillatoria*, *Lyngbya*, *Navicula*, and *Cymbella*. Comparative analysis demonstrated notable spatial differences between the Muynak and Shegekul sites, mainly associated with hydrological stability, salinity gradients, and habitat variability. The results indicate that microorganisms play a critical role in ecosystem adaptation and stabilization under post-desiccation environmental stress. The dominance of adaptive cyanobacteria and diatoms reflects ongoing ecological restructuring processes in the dried Aral Sea basin. The findings contribute to the understanding of biodiversity patterns and microbial adaptation mechanisms in extreme environments and provide a scientific basis for future ecological monitoring and restoration studies in the Aral Sea region. Samples were analyzed using standard microscopic and algological methods at the Algology Laboratory of Namangan State University. Taxonomic identification was performed based on modern classification systems, and particular attention was given to the ecological role and adaptability of microorganisms in high-salinity environments.

Keywords Aral Sea, Hydrobiology, Microbial diversity, Cyanobacteria, Microalgae, Biodiversity, Salinity, Ecological adaptation, Muynak, Shegekul

1. Introduction

The Aral Sea, formerly one of the largest inland water bodies in the world, has experienced one of the most severe environmental transformations caused by human activities. Intensive diversion of the Amu Darya and Syr Darya rivers for agricultural irrigation during the twentieth century led to a dramatic reduction in water inflow, resulting in progressive desiccation, increased salinity, habitat fragmentation, and the formation of extensive exposed seabed areas [1,3]. As a

consequence, large territories of the former seabed have been converted into highly dynamic and environmentally stressed ecosystems characterized by extreme salinity, aridity, temperature fluctuations, and unstable hydrological conditions [3,5].

The desiccation of the Aral Sea has not only altered regional hydrology but has also profoundly affected biological diversity and ecosystem functioning. Previous investigations have documented significant changes in species composition, trophic relationships, nutrient cycling, and ecological processes throughout the Aral Sea basin [1,4]. The emergence of newly exposed sediments and residual water bodies has created novel ecological niches where only highly adapted organisms are capable of surviving and maintaining ecological functions.

* Corresponding author:

toxtaboyevayulduzxon934@gmail.com (Tukhtaboeva Y. A.)

Received: Jun. 2, 2026; Accepted: Jun. 26, 2026; Published: Jun. 30, 2026

Published online at <http://journal.sapub.org/ijvmb>

Microorganisms constitute one of the most important biological components of these transformed ecosystems. Cyanobacteria, microalgae, diatoms, and other hydrobiological organisms contribute substantially to primary productivity, nutrient turnover, organic matter accumulation, and ecosystem stabilization. Due to their rapid response to environmental changes and high physiological plasticity, microbial communities serve as valuable indicators of ecological transformation and environmental stress [9,7].

Among these organisms, cyanobacteria are particularly important in saline and arid habitats because of their exceptional adaptive capabilities. Many cyanobacterial taxa possess physiological mechanisms that enable them to tolerate osmotic stress, prolonged desiccation, nutrient limitation, and elevated salinity levels. Furthermore, their ability to produce extracellular polysaccharides contributes to sediment stabilization and biological soil crust formation, which are essential processes in newly developing ecosystems [8]. Diatoms and green algae also play significant ecological roles by participating in nutrient cycling and serving as indicators of environmental conditions and habitat quality [10,11].

Recent studies conducted in arid and degraded ecosystems have emphasized the importance of microbial diversity for ecosystem resilience and recovery. Investigations of saline soils and extreme terrestrial habitats in Central Asia have demonstrated that cyanobacteria and microalgae form highly specialized communities capable of adapting to severe environmental stress while supporting ecosystem stability and biological productivity [12,13]. Such findings highlight the necessity of understanding microbial adaptation mechanisms in regions undergoing rapid environmental change.

The Muynak and Shegkul areas represent ecologically significant sectors of the southern Aral Sea region. These territories include dried seabed surfaces, residual lakes, temporary wetlands, and periodically flooded depressions formed as a consequence of long-term desiccation processes. Variations in hydrological stability, salinity gradients, and moisture availability create heterogeneous environmental conditions that influence the composition and distribution of hydrobiological communities.

Although considerable attention has been devoted to hydrological changes and environmental consequences of the Aral Sea crisis, detailed hydrobiological investigations of microbial communities inhabiting post-desiccation ecosystems remain relatively limited. In particular, information concerning species diversity, community structure, and ecological adaptation of microorganisms in the Muynak and Shegkul areas is still insufficient despite their importance for understanding ecosystem transformation processes and biodiversity conservation in the Aral Sea basin [6].

Understanding the taxonomic composition and ecological characteristics of microbial communities in these environments is essential for evaluating ecosystem functioning, biological

adaptation, and long-term environmental sustainability. Hydrobiological studies provide valuable information regarding ecological succession, habitat quality, and resilience of biological communities under extreme environmental stress.

Therefore, the aim of the present study was to investigate the hydrobiological diversity and adaptive microbial communities of the dried Aral Sea basin, with particular emphasis on the Muynak and Shegkul areas. The objectives were to identify dominant taxonomic groups, evaluate patterns of species distribution, characterize adaptive microbial assemblages, and assess their ecological significance under conditions of elevated salinity and post-desiccation environmental stress.

2. Materials and Methods

Study Area

The study was conducted during 2024–2025 in the southern part of the former Aral Sea basin, including the residual lakes of Muynak and Shegkul and the surrounding desiccated seabed areas. These sites represent post-desiccation ecosystems that developed following the retreat of the Aral Sea and are characterized by high salinity, arid climatic conditions, limited water availability, and unstable hydrological regimes.

Sampling was performed in both aquatic and terrestrial habitats. Aquatic samples were collected from residual water bodies (remnant lakes) located within the dried Aral Sea basin, whereas soil samples were obtained from adjacent desiccated sediments and exposed seabed surfaces surrounding the lakes. These habitats represent different stages of ecological succession and provide suitable conditions for the development of diverse hydrobiological and microbial communities.

The geographic coordinates of selected sampling points included: 43.558510° N, 59.136313° E; 43.571312° N, 59.092565° E; and 43.558008° N, 59.202872° E (Fig. 1).

Sampling Procedure

Field sampling was conducted seasonally during 2024–2025 in the residual lakes of Muynak and Shegkul and in the surrounding dried seabed areas of the former Aral Sea. Water samples were collected from remnant lakes, shallow littoral zones, and temporary water bodies, while soil samples were obtained from adjacent desiccated sediments and exposed seabed surfaces. Sampling in both aquatic and terrestrial habitats allowed assessment of microbial diversity under different environmental conditions associated with post-desiccation ecosystem development.

To ensure spatial representativeness, soil samples were taken from the upper 0–10 cm layer at regular intervals across selected sampling plots. All samples were collected using standard hydrobiological and microbiological techniques, labeled in the field, and transported to the laboratory under controlled conditions for further analysis.

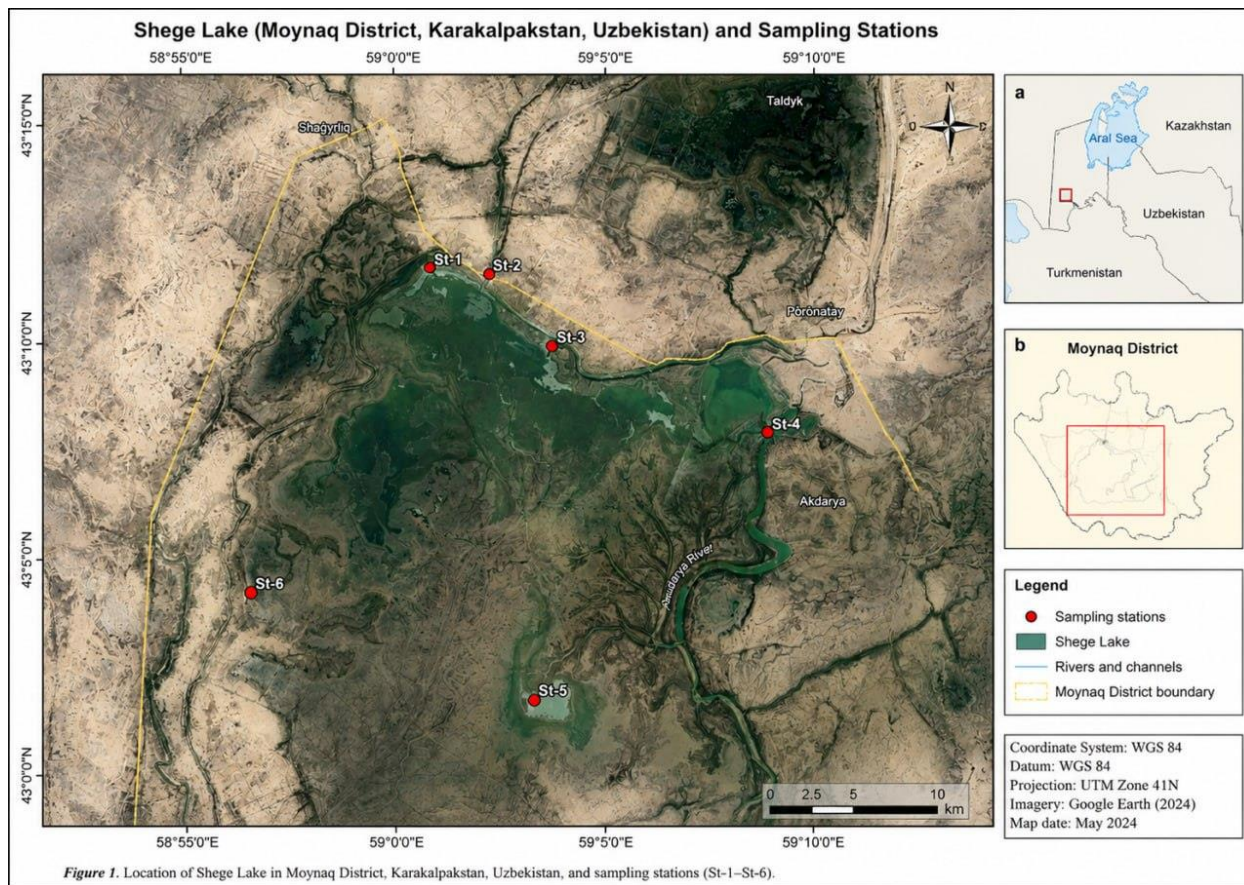


Figure 1. Location of sampling sites in the Muynak and Shegekul areas within the dried Aral Sea basin

Laboratory Analysis

All hydrobiological and algological analyses were conducted at the **Algology Laboratory of Namangan State University**, equipped for detailed microscopic and microbiological investigations. Microscopic examination was performed using light microscopy to identify phytoplankton, zooplankton, microalgae, and cyanobacteria based on their morphological characteristics.

Cultivation and Isolation of Microorganisms

To isolate microbial strains, water samples were inoculated onto BG-11 agar medium, which is widely used for the cultivation of cyanobacteria and microalgae [8]. Pure algological cultures were obtained through repeated streak plating and isolation of individual colonies using a sterile Pasteur pipette.

The isolated strains were cultivated on solid BG-11 medium supplemented with nitrogen under controlled laboratory conditions: pH 7.0, agar concentration 1.4%, temperature 23–25 °C, light intensity 60–75 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$, and a 12-hour light/dark photoperiod. These conditions were maintained in a climate-controlled chamber to ensure stable growth and reproducibility of results.

Taxonomic Identification

Taxonomic identification was performed using standard identification keys and modern classification systems widely accepted in hydrobiology and phycology [7,8,11].

Species composition was determined, and dominant and subdominant taxa were identified for each sampling site. The systematic analysis allowed the assessment of biodiversity and community structure.

Data Analysis and Documentation

The obtained data were systematized and comparatively analyzed to evaluate differences in species composition and community structure between the Muynak and Shegekul areas. Photographic documentation of selected taxa was performed using microscope imaging techniques, providing visual confirmation of species identification and supporting morphological analysis.

3. Results and Discussion

Species Composition and Biodiversity

The hydrobiological analysis of the studied areas revealed a high diversity of microorganisms in the dried Aral Sea basin, particularly in the Muynak and Shegekul regions. The taxonomic composition included representatives of several major groups, such as **Cyanobacteria**, **Bacillariophyta (diatoms)**, **Chlorophyta (green algae)**, **Euglenophyta**, **Dinophyta**, and **Xanthophyta (Table 1)**.

The taxonomic composition of hydrobiological communities identified in the study area is summarized in **Table 1**. The analysis revealed that the studied ecosystems are dominated

by representatives of Cyanobacteria, Bacillariophyta, and Chlorophyta, which together constitute the core of the microbial community structure.

As shown in Table 1, cyanobacteria exhibited a high level of diversity and ecological significance, with dominant genera such as *Microcystis* and *Oscillatoria*. Similarly, diatoms (Bacillariophyta) were represented by a wide range of taxa, particularly *Navicula* and *Cymbella*, indicating their adaptability to benthic and periphytic habitats.

The presence of green algae (Chlorophyta), including *Scenedesmus* and *Spirogyra*, reflects the variability of environmental conditions and the availability of microhabitats within the dried seabed ecosystem. Minor groups such as Euglenophyta, Dinophyta, and Xanthophyta were also recorded, contributing to overall biodiversity but with lower representation.

A total of 56 taxa (including species, varieties, and forms) were identified, indicating relatively high biodiversity despite the extreme environmental conditions of the region. Among the identified taxa, cyanobacteria and microalgae constituted the most diverse and ecologically significant groups.

Cyanobacteria were widely represented by genera such as *Microcystis*, *Oscillatoria*, *Lyngbya*, *Spirulina*, and *Phormidium*, which are known for their tolerance to high salinity and environmental stress. For instance, species such as *Microcystis aeruginosa*, *Oscillatoria limosa*, and *Lyngbya confervoides* were frequently observed and can be considered characteristic components of the studied ecosystems.

Diatoms (Bacillariophyta) were also highly diverse, with numerous species belonging to genera such as *Navicula*, *Cymbella*, *Gomphonema*, and *Pinnularia*. These taxa are known indicators of environmental conditions and were widely distributed across sampling sites, suggesting the persistence of benthic and periphytic communities in the dried seabed habitats.

Green algae (Chlorophyta) were represented by species of *Scenedesmus*, *Ankistrodesmus*, *Cladophora*, *Ulothrix*, and *Spirogyra*, indicating the presence of both planktonic and filamentous forms adapted to fluctuating environmental conditions.

The hydrobiological communities of the studied areas demonstrated considerable ecological heterogeneity associated with variations in salinity, moisture availability, and hydrological

stability. Cyanobacteria represented the dominant functional group, accounting for 41.1% of the identified taxa, which confirms their high ecological plasticity under hypersaline and arid conditions.

Among cyanobacterial taxa, representatives of the genera *Oscillatoria*, *Microcystis* and *Lyngbya* were particularly abundant in the Muynak sites, indicating their tolerance to fluctuating salinity and temperature regimes. In contrast, the Shegekul area exhibited relatively higher diversity of Chlorophyta and Bacillariophyta, reflecting more stable aquatic microhabitats and temporary wetland conditions.

Diatoms constituted 25.0% of the total taxa and were represented predominantly by benthic and periphytic forms, including *Navicula* and *Cymbella* species. Their occurrence suggests the persistence of ecologically functional sediment-water interfaces despite severe post-desiccation transformation processes.

Comparative ecological analysis revealed that biodiversity indices were comparatively higher in the Shegekul area than in the Muynak region. This pattern is likely associated with differences in hydrological persistence, nutrient distribution, and microclimatic variability between the studied ecosystems.

The predominance of stress-tolerant microorganisms indicates that biological communities in the dried Aral Sea basin are undergoing adaptive ecological restructuring. Such microbial assemblages may play a significant role in primary productivity, nutrient cycling, and the gradual stabilization of newly formed post-desiccation ecosystems.

Comparison with Previous Studies

The hydrobiological patterns observed in the present study are generally consistent with previous investigations conducted in the Aral Sea basin and other saline ecosystems of Central Asia. Earlier studies have demonstrated that the desiccation of the Aral Sea resulted in profound ecological restructuring, leading to the replacement of many freshwater organisms by stress-tolerant and halophilic taxa capable of surviving under conditions of elevated salinity and hydrological instability [1,2]. The predominance of cyanobacteria observed in the Muynak and Shegekul areas reflects this long-term ecological transition and confirms the adaptive capacity of microbial communities inhabiting post-desiccation environments.

Table 1. The taxonomic composition of hydrobiological communities identified in the study area

Taxonomic group	Number of taxa	Percentage (%)	Dominant genera (examples)
Cyanobacteria	23	41.1%	<i>Microcystis</i> , <i>Oscillatoria</i> , <i>Lyngbya</i>
Bacillariophyta	14	25.0%	<i>Navicula</i> , <i>Cymbella</i> , <i>Gomphonema</i>
Chlorophyta	12	21.4%	<i>Scenedesmus</i> , <i>Spirogyra</i> , <i>Cladophora</i>
Euglenophyta	4	7.1%	<i>Euglena</i> , <i>Phacus</i>
Dinophyta	2	3.6%	<i>Peridinium</i>
Xanthophyta	1	1.8%	<i>Tribonema</i>
Total	56	100	

Our results revealed that Cyanobacteria constituted 41.1% of the total identified taxa, making them the dominant taxonomic group within the studied ecosystems. Similar trends have been reported in saline and arid habitats where cyanobacteria frequently become the principal primary producers due to their high ecological plasticity, resistance to osmotic stress, and ability to survive prolonged desiccation [8]. The abundance of genera such as *Microcystis*, *Oscillatoria*, and *Lyngbya* in the present study supports previous observations that these taxa are among the most successful colonizers of environmentally stressed aquatic and semi-aquatic habitats.

The substantial representation of Bacillariophyta (25.0%) is also in agreement with previous hydrobiological studies that identified diatoms as important components of benthic and periphytic communities in transitional aquatic ecosystems. According to Round *et al.* (1990), genera such as *Navicula* and *Cymbella* exhibit considerable tolerance to fluctuations in salinity and nutrient availability, allowing them to persist in unstable habitats undergoing ecological succession. Their widespread occurrence in the studied sites indicates the continued existence of functional sediment-associated microbial communities despite extensive environmental degradation.

The relatively high diversity of Chlorophyta recorded in the Shegekul area may be associated with the presence of more stable aquatic microhabitats and temporary wetlands. Similar relationships between hydrological stability and increased algal diversity have been reported in residual water bodies of the Aral Sea region and other arid landscapes [7,9]. The occurrence of genera such as *Scenedesmus*, *Spirogyra*, and *Cladophora* suggests the persistence of ecological niches capable of supporting both planktonic and filamentous algal communities.

The observed differences between the Muynak and Shegekul sites further emphasize the importance of local environmental conditions in shaping microbial community structure. Muynak was characterized by a greater abundance of stress-tolerant cyanobacteria, whereas Shegekul supported comparatively higher taxonomic diversity due to more favorable hydrological conditions. Similar spatial heterogeneity has been documented in previous ecological assessments of the southern Aral Sea region, where variations in salinity, moisture availability, and water permanence were identified as major determinants of biological diversity [6].

The findings of the present investigation are also consistent with recent studies of cyanobacteria and microalgae in arid ecosystems of Uzbekistan. Tukhtaboeva *et al.* (2025a; 2025b) reported that microbial communities inhabiting degraded and saline environments are dominated by highly adaptive taxa capable of tolerating multiple environmental stressors. The dominance of ecologically flexible microorganisms observed in the Muynak and Shegekul areas supports the hypothesis that microbial adaptation represents one of the primary mechanisms driving ecosystem stabilization and biological succession within post-desiccation landscapes.

Overall, the results demonstrate that the dried Aral Sea basin continues to support diverse and functionally important

hydrobiological communities. Although environmental conditions remain extreme, microbial assemblages have developed adaptive strategies that enable them to maintain ecosystem processes and contribute to the gradual ecological stabilization of newly formed habitats. These observations reinforce the importance of microorganisms as indicators of ecosystem transformation and as key components of future restoration and monitoring programs in the Aral Sea region.

Ecological Significance

The results highlight the importance of hydrobiological communities in the formation and functioning of ecosystems in the dried Aral Sea region. Despite extreme environmental stress, the studied areas maintain considerable biodiversity, largely due to the adaptability of microorganisms.

These findings emphasize that the dried seabed is not a biologically inactive environment but rather a dynamic system where new ecological structures are being formed. Understanding these processes is essential for predicting future ecosystem development and for designing effective environmental management strategies in the Aral Sea region.

4. Conclusions

The present study provides a comprehensive analysis of the hydrobiological structure and species diversity of microorganisms in the dried Aral Sea bed, focusing on the Muynak and Shegekul areas. Despite the extreme environmental conditions associated with desiccation, including high salinity, aridity, and unstable hydrological regimes, the studied ecosystems support a relatively diverse assemblage of microorganisms.

A total of 56 taxa belonging to six major taxonomic groups were identified, with Cyanobacteria (41.1%), Bacillariophyta (25.0%), and Chlorophyta (21.4%) forming the core of the hydrobiological community. The dominance of cyanobacteria reflects their high ecological plasticity and adaptability to stress conditions, while the significant presence of diatoms indicates the persistence of microhabitats capable of supporting benthic and periphytic communities.

Comparative analysis revealed spatial differences between the Muynak and Shegekul areas, which are primarily associated with variations in hydrological stability and environmental conditions. The Shegekul region demonstrated relatively higher biodiversity due to more stable water bodies, whereas the Muynak area was characterized by the prevalence of stress-tolerant taxa.

The results are consistent with previous studies on the Aral Sea region, which have documented substantial ecological restructuring and increasing dominance of stress-tolerant microorganisms following desiccation processes [1,2]. Microorganisms, particularly cyanobacteria and microalgae, play a crucial role in these processes by contributing to primary production, nutrient cycling, and ecosystem stabilization.

Overall, the findings demonstrate that the dried Aral Sea bed represents a dynamic and biologically active system

rather than a degraded and lifeless environment. This study contributes to a deeper understanding of biodiversity patterns and adaptive mechanisms in extreme environments and provides a scientific basis for future ecological monitoring and restoration strategies in the Aral Sea basin.

Funding: This research was supported by the Ministry of Higher Education, Science and Innovation of the Republic of Uzbekistan under Project No. AL-9424115044.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data are available upon reasonable request from the corresponding author.

Conflicts of Interest: The authors declare no conflict of interest.

Author ORCIDs

Yulduzkhon Tukhtaboeva

<https://orcid.org/0009-0008-2209-3582>

Nuriddin Ikramov <https://orcid.org/0009-0002-9853-1151>

REFERENCES

- [1] Micklin, P. (2007). The Aral Sea disaster. *Annual Review of Earth and Planetary Sciences*, 35, 47–72.
- [2] Micklin, P., & Aladin, N. V. (2008). Reclaiming the Aral Sea. *Scientific American*, 298(4), 64–71.
- [3] Aladin, N. V., Plotnikov, I. S., & Potts, W. T. W. (1995). The Aral Sea desiccation and possible ways of rehabilitating and conserving its northern part. *Environmental Conservation*, 22(1), 17–29.
- [4] Zholdasova, I. M. (1997). The ecosystem of the Aral Sea and its changes. *Journal of Marine Systems*, 13, 1–8.
- [5] Dukhovny, V. A., & de Schutter, J. (2011). Water in Central Asia: Past, present, future. CRC Press.
- [6] Kalabaev, M. (2022). Hydrological and morphometric changes of water bodies in the Southern Aral Sea region. *Hydrobiology and ecology*.
- [7] Wehr, J. D., & Sheath, R. G. (2003). Freshwater algae of North America. Academic Press.
- [8] Komárek, J., & Anagnostidis, K. (2005). Cyanoprokaryota. Elsevier.
- [9] Reynolds, C. S. (2006). The ecology of phytoplankton. Cambridge University Press.
- [10] Prescott, G. W. (1978). How to know the freshwater algae. Wm. C. Brown Company.
- [11] Round, F. E., Crawford, R. M., & Mann, D. G. (1990). The diatoms: Biology and morphology. Cambridge University Press.
- [12] Tukhtaboeva, Y., Krivina, E., Redkina, V., Portnov, A., Sinetova, M., & Temraleeva, A. (2025a). Species delimitation in the genus *Klebsormidium* (Klebsormidiophyceae, Charophyta), including description of *Klebsormidium mirabile* sp. nov. with high content of polyunsaturated fatty acids. *PhytoKeys*, 266, 53–74. <https://doi.org/10.3897/phytokeys.266.158514>.
- [13] Tukhtaboeva, Y.A., Redkina, V.V., Bukin, Y.S. *et al.* Diversity of Cyanobacteria and Algae in Eroded Soils of the Fergana Valley (Uzbekistan) According to Light Microscopy Data and High-Throughput Sequencing. *Arid Ecosyst* 15, 232–245 (2025b). <https://doi.org/10.1134/S2079096125700143>.