MJFAS
Malaysian Journal of
Fundamental and Applied
Sciences

RESEARCH ARTICLE

Soil Salinity and Physicochemical Drivers of Microbial Community Composition in the Desiccated Aral Sea Bed

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Abstract For more than six decades following the desiccation of the Aral Sea, soil formation processes on the exposed seabed have undergone continuous development, leading to pronounced changes in physicochemical and biological properties. This study evaluates the influence of soil salinity and physicochemical parameters on microbial communities in newly formed soils of the dried Aral Sea bed. The investigated soils exhibited moderate to high salinity (EC 6.2–8.2 mS cm^{-1}) and slightly alkaline conditions (pH/H_2O 7.7–8.9), with low organic carbon (0.20–0.39%) and humus contents (0.35–0.68%). Carbonate and sulfate–chloride salts predominated, while soil textures ranged from heavy to light. Microbiological analyses indicated the ubiquitous presence of ammonifying and humus-decomposing microorganisms, whereas phosphate-solubilizing and oligonitrophilic bacteria were mainly associated with moderately saline soils. Actinomycetes and micromycetes were detected only sporadically. Statistical analyses revealed a strong positive correlation between electrical conductivity and soil pH ($r = 0.85$, $p < 0.01$), while most microbial indicators showed negative relationships with salinity and alkalinity. These results demonstrate that soil salinity and pH are key environmental drivers constraining microbial diversity and activity during early soil development in arid, saline post-lacustrine ecosystems.

Keywords: Soil salinity, physicochemical properties, microbial community structure, desiccated Aral Sea bed, soil formation, arid saline soils.

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Received: 16 Oct. 2025
Accepted: 28 Feb. 2026

Introduction

The Aral Sea is a large terminal lake located among the deserts of Central Asia, which has dried up and refilled several times over the past 10,000 years. Since the 1960s, the sea has been shrinking rapidly, primarily due to the extensive use of water from the Amu Darya and Syr Darya rivers for irrigation purposes. Consequently, the water level experienced a decline of approximately 23 m, accompanied by a reduction of nearly 74% in the total surface area and an estimated 90% decrease in overall water volume.At the same time, the salinity level increased from 10 g/L to 100 g/L. 19 The drying of the Aral Sea has led to a major environmental crisis in Central Asia, particularly affecting the soils, salinization, and biodiversity of the surrounding regions in Uzbekistan and Kazakhstan. Consequently, 5 million hectares of the dried seabed have been covered with sand and salt. Research is currently being undertaken to address this challenge, stimulate soil formation processes, and mitigate soil salinity. Studies of soils under afforestation projects established in 1991, 2005, 2009, 2010, and 2013 have shown improvements, including a decrease in exchangeable cations (Ca^{2+}, K^+, Mg^{2+}, Na^+), a reduction in soil pH, and an increase in enzyme activity (phosphatase, β-glucosidase, and N-acetylglucosaminidase). 1 Due to soil salinization in the Aral Sea region, 15 fungal genera and 31 species have been identified. 27 The physical and chemical properties of the soil have influenced both microbial communities and plant life in the area. 12 Additionally, denitrification processes in the soil have shown different values depending on soil types. 24 In the saline soils of the Aral Sea region, the genera of microorganisms such as Halomonas and Planococcus have been identified, and they were found to thrive at NaCl concentrations of 8.0%, 10.0%, and 15.0%. 4,17 As a result of the drying of the Aral Sea, Aralkum a new desert rich in salts and toxic substances have emerged, where bacteria such as Alphaproteobacteria and Actinobacteria 34, as well as microorganisms like Gammaproteobacteria, Actinomycetia, and Bacilli, have adapted and been found across vast areas. 34 The drying of the Aral Sea has led to the formation of diverse soil types and significant shifts in microbial communities, and these changes continue to this day. 14-15 Introducing microorganisms into different soils can enhance their proliferation and improve soil properties. 31 The increase or decrease of a single element in the soil influences the composition of microbial communities. 32 Microorganisms have been applied in managing both organic and mineral forms of carbon in the soil, yielding positive results. 35 Soil organic carbon is closely linked to microbial communities, and its abundance has led to the dominance of Proteobacteria, Acidobacteriota, and Actinomycetes, as well as an increase in fungi such as Ascomycetes, Basidiomycetes, and Mortierellomycota. 23 Some immobilized bacteria exhibit high resistance to changes in temperature and pH. 10 The bacteria Acidobacteria, Proteobacteria, and Actinobacteria were found to be most active at soil pH levels of 7.39, 6.09, and 5.41, respectively, whereas fungal species Ascomycota, Basidiomycota, and Mortierellomycota thrived at pH levels of 4.23, 7.39, and 6.48. These findings indicate that soil pH plays a crucial role in determining the diversity and abundance of soil microorganisms. Studying and enhancing the abundance of microorganisms in newly forming soils is of critical importance, as microorganisms play a fundamental role in soil nutrient cycling, including nitrogen, phosphorus, carbon, and sulphur. Phosphate-solubilizing bacteria convert unavailable phosphorus in the soil from an insoluble form into a soluble form, facilitating its uptake by plants as a nutrient unit. 20,36 In the carbon cycle, microorganisms decompose organic matter, leading to the formation of humus in the soil, which enhances soil fertility. 8,18 An analysis of these studies indicates that in different soils, including newly formed soils on the dried seabed of the Aral Sea, the quantity of microorganisms varies depending on soil properties such as organic matter content, pH, salinity levels, and physical characteristics. These microorganisms participate in complex soil processes, contributing to soil formation and positively influencing plant growth.

Materials and Methods

The study area is the dried-up bed of the Aral Sea, one of the four largest lakes in the world, located in Central Asia (Figure 1).

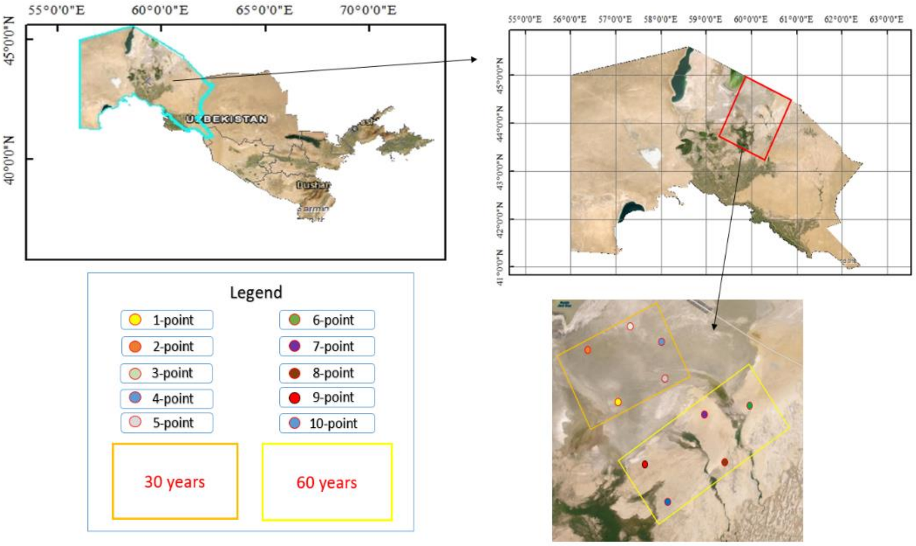


Figure 1. Location of sampling points in the study area.

The desiccation of the Aral Sea commenced in the 1960s, initially affecting the eastern sector, followed sequentially by the southern, western, central, and northern regions. At present, only approximately 10% of the former water surface remains, and the desiccation process is ongoing.

The present study was conducted in the eastern part of the dried Aral Sea bed. Soil samples were collected from the 0–30 cm layer at ten sampling points (Table 1). Sampling locations were selected to represent variations in soil properties and vegetation cover across the study area. The dominant vegetation consisted of Haloxylon ammodendron (C.A. Mey.) Bunge ex Fenzl, Alhagi pseudalhagi (M. Bieb.) Desv. ex Wangerin, Haloxylon persicum Bunge, Halostachys caspica (M. Bieb.) C.A. Mey., Halocnemum strobilaceum (Pall.) M. Bieb., and Caroxylon nitrarium (Pall.) Akhani & Roalson. The regional climate is characterized by extreme aridity, with a mean annual precipitation of approximately 90 mm and an evaporation rate of around 200 mm. Frequent strong winds further intensify aeolian transport of salts and sand.

Table 1. Coordinates of soil sampling points

Coordinates of the sampling points	Points
44°11'51"N 60°02'37"E	1
44°23'42"N 59°53'31"E	2
44°27'12"N 60°19'25"E	3
44°38'34"N 60°04'58"E	4
44°36'29"N 60°16'01"E	5
44°28'05"N 60°37'25"E	6
44°26'38"N 60°30'38"E	7
44°20'13"N 60°37'35"E	8
44°10'29"N 60°21'51"E	9
44°16'50"N 60°16'22"E	10

Field investigations were carried out in September 2024. Ten main soil profiles were excavated to a depth of 0–200 cm, while samples for microbiological analyses were obtained from the 0–30 cm layer. Soil salinity was assessed using electrical conductivity (EC) measurements of soil solutions and classified according to FAO and USDA criteria. Soil classification followed the updated FAO WRB (2022) international classification system.

Soil sampling and storage procedures complied with GOST 17.4.3.01–83 standards. Microbial abundance was determined using Zvyagintsev's method. Soil pH (1:5 H_2O) was measured potentiometrically in accordance with ISO 10390:2005, while soil electrical conductivity was determined following Uz DSt 11265:2013. Humus content was analyzed according to GOST 26213–91. Soil salinity was evaluated using water extraction methods, and granulometric composition was determined using the Kachinsky method.

For microbiological analyses, selective nutrient media were employed: GPA for ammonifiers, Pikovskaya medium for phosphorus-solubilizing bacteria, Zakh medium for potassium-solubilizing bacteria, Ashby medium for oligonitrophils, starch ammonium agar (KAA) for actinomycetes and nitrogen-assimilating microorganisms, soil agar for humus-decomposing microorganisms, Ashby and soil agar media for Azotobacter, Czapek and PDA media for micromycetes, Vinogradsky liquid medium for nitrifiers (phases I and II), and Giltay solid medium for denitrifiers. Microbial identification was performed using MALDI-TOF mass spectrometry. Incubation was carried out for 20–25 days at a temperature of 28–30 °C.

Laboratory data were analyzed using descriptive statistics, analysis of variance (ANOVA), regression analysis, and correlation analysis. These methods were applied to evaluate relationships between soil pH, electrical conductivity, and variations in microbial abundance across the different sampling sites.

Results and Discussion

For 65 years have passed since the drying of the Aral Sea, soil formation is still in progress, and its properties are gradually developing. To confirm the soil formation process, it is essential to identify the presence of microorganisms and study their quantity in relation to soil characteristics. According to the results, the organic carbon content in the soil ranged between 0.20–0.39%, while the humus content was found to be within 0.35–0.68%. The salinity level of the soils was classified as moderate to high, with EC values ranging from 6.2 to 8.2. Correspondingly, due to the salinity level, the pH of the soil environment was between 7.8 and 8.9 (Table 2).

Table 2. Soil Indicators of the Study Area

Point	SOC (%)	Humus (%)	EC1:1 (mS cm^{-1})	$\text{pH}_{1:5\ H_2O}$	Salinity Level	Salinity Chemistry	Texture Composition
1	0.23±0.01	0.41±0.05	8.2±0.01	8.9±0.02	High	Sulfate-Chloride	Heavy
2	0.23±0.01	0.40±0.04	8.2±0.02	8.8±0.01	High	Sulfate-Chloride	Heavy
3	0.22±0.02	0.38±0.05	8.1±0.02	8.3±0.02	High	Sulfate-Chloride	Heavy
4	0.22±0.01	0.39±0.04	8.1±0.02	8.4±0.03	High	Sulfate-Chloride	Heavy
5	0.20±0.02	0.35±0.04	8.0±0.01	8.0±0.01	High	Sulfate-Chloride	Heavy
6	0.32±0.01	0.56±0.02	6.2±0.03	7.8±0.01	Moderate	Carbonate	Medium
7	0.31±0.02	0.54±0.05	6.4±0.02	7.8±0.03	Moderate	Carbonate	Medium
8	0.39±0.01	0.68±0.02	6.6±0.01	7.9±0.03	Moderate	Carbonate	Light
9	0.34±0.02	0.59±0.05	6.6±0.02	7.9±0.01	Moderate	Carbonate	Light
10	0.33±0.01	0.57±0.03	6.2±0.01	7.7±0.01	Moderate	Carbonate	Light

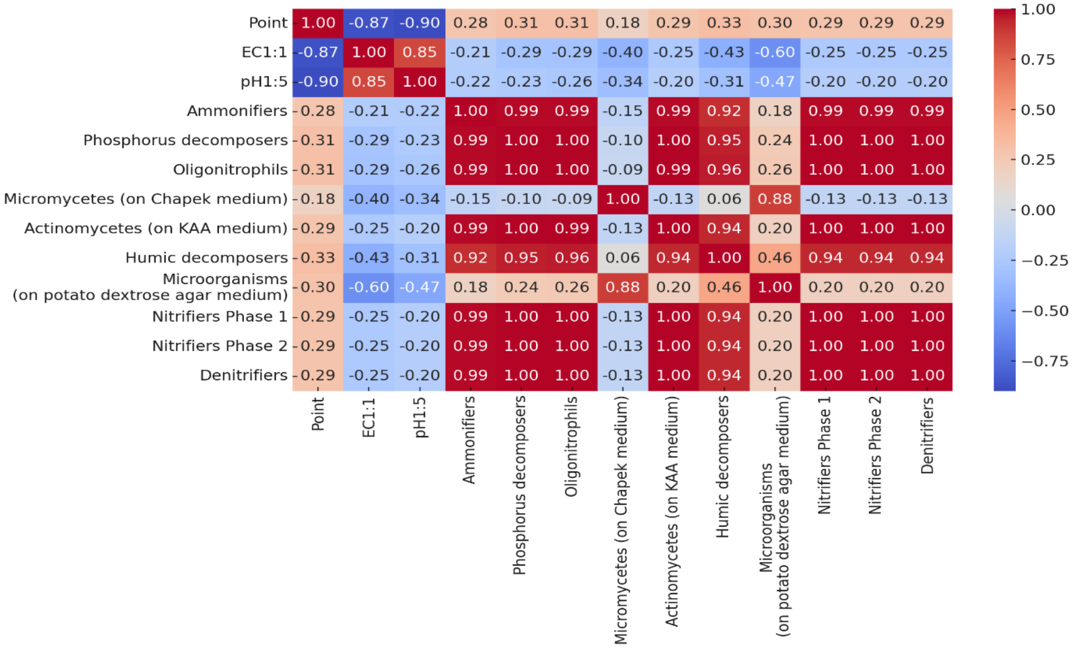
SOC-Soil Organic Carbon.

The identified salt assemblages were dominated by carbonate and sulfate–chloride types. Based on granulometric characteristics, the soils were classified into heavy-, medium-, and light-textured categories. Owing to pronounced spatial variability in salinity levels, pH conditions, granulometric composition, and humus content within the dried Aral Sea bed, the composition and diversity of soil microbial communities exhibited substantial variation. According to the results, ammonifying bacteria were detected in all ten soil sampling points, with their quantity ranging between 4×1014 \times 10^14×101 and 3×1053 \times 10^53×105 CFU/g of soil. The number of phosphorus-decomposing bacteria was significantly low, found only in soil samples from points 6, 7, 8, and 9, with a concentration between 1×1011 \times 10^11×101 and 3×1023 \times 10^23×102 CFU/g. Oligonitrophilic bacteria were identified in soil samples from points 5, 6, 7, 8, 9, and 10, with a quantity ranging from 3×1013 \times 10^13×101 to 7×1037 \times 10^37×103 CFU/g. Microfungi were found to be very rare in the study area, detected only in soil samples from points 6 and 7. Similarly, actinomycetes were identified in only a few locations, specifically in soil samples from points 2 and 8 (Table 3).

Table 3. The Quantity of Microorganisms Identified in the Study Areas

Microorganisms	Soil samples									
	1	2	3	4	5	6	7	8	9	10
Ammonifiers	1.x10^2	3x10^3	3x10^2	7x10^3	4x10^4	3x10^3	2x10^3	3x10^5	7x10^2	4x10^1
Phosphate Solubilizers	-	-	-	-	-	1x10^1	1x10^1	3x10^2	1x10^1	-
Oligonitrophiles	-	-	-	-	4x10^2	6x10^2	3x10^2	7x10^3	6x10^1	3x10^1
Micromycetes (Czapek Nutrient Medium)	-	-	-	-	-	1x10^1	6x10^1	-	-	-
Actinomycetes (KAA Nutrient Medium)	-	1x10^1	-	-	-	-	-	9x10^2	-	-
Humus Decomposers	3x10^2	1x10^3	4x10^2	4x10^2	1x10^2	3x10^3	2x10^3	9x10^3	1x10^3	1x10^2
Microorganisms (Potato Dextrose Agar Nutrient Medium)	3x10^1	6x10^1	4x10^1	3x10^1	3x10^1	4x10^2	7x10^2	3x10^2	9x10^1	1x10^1
Nitrifiers (Phase 1)	-	-	-	-	2x10^2	1x10^1	6x10^1	70x10^3	-	-
Nitrifiers (Phase 2)	-	-	-	-	-	-	-	2x10^2	-	-
Denitrifiers	-	-	-	-	-	-	-	2x10^1	-	-

Humus decomposers were identified in soil samples from all points of the study area, with quantities ranging between 1×10² and 9×10³. This study examined the distribution of physiological groups, species composition, and abundance of soil microorganisms in relation to the desiccation history and physicochemical properties of soils in the dried seabed of the Aral Sea. The results demonstrate that microbial community structure and abundance are strongly controlled by soil salinity, pH, organic carbon and humus contents, granulometric composition, and the duration of soil exposure following desiccation. Soils from the earliest desiccated zones (approximately 60 years since drying) were characterized by high salinity (EC 8.0–8.2 mS cm^{-1}), sulfate–chloride salinization, heavy-textured granulometric composition, and relatively low humus contents (0.35–0.41%). In contrast, soils from more recently dried areas exhibited moderate salinity (EC 6.2–6.6 mS cm^{-1}), carbonate-type salinization, medium- to light-textured composition, and higher humus contents ranging from 0.54 to 0.68%. Across all sampling sites, humus-decomposing microorganisms, ammonifiers, and microorganisms cultivated on potato dextrose agar were consistently detected. However, phosphorus-solubilizing bacteria, oligonitrophiles, micromycetes, actinomycetes, nitrifiers (phases I and II), and denitrifiers were either absent or present in very low abundances in highly saline sulfate–chloride soils characterized by heavy texture, alkaline conditions (pH 8.0–8.9), low organic carbon (0.20–0.23%), and reduced humus content. Microbial species composition varied spatially among sampling points and reflected differences in soil formation stage and environmental conditions. Identified taxa included *Micrococcus luteus* (Point 1), Proteobacteria spp. (Point 2), *Propionibacterium freudenreichii* (Point 3), *Exiguobacterium aurantiacum* (Point 4), *Kocuria palustris* (Points 5 and 6), *Halomonas pacifica* (Points 7 and 10), *Streptomyces rochei, Micrococcus luteus*, and *Bacillus subtilis* (Point 8), and Halobacterota (Point 9). The highest microbial diversity was observed at Point 8, where Haloxylon plantations had been established and agro-technical measures were applied. This finding indicates that vegetation establishment and soil management practices substantially enhance microbial diversity and functional complexity in the soils of the desiccated Aral Sea bed (Figure 2).



	Point	EC1:1	pH1:5	Ammonifiers	Phosphorus decomposers	Oligonitrophils	Micromycetes (on Chapek medium)	Actinomycetes (on KAA medium)	Humic decomposers	Microorganisms (on potato dextrose agar medium)	Nitrifiers Phase 1	Nitrifiers Phase 2	Denitrifiers
Point	1.00	-0.87	-0.90	0.28	0.31	0.31	0.18	0.29	0.33	0.30	0.29	0.29	0.29
EC1:1	-0.87	1.00	0.85	-0.21	-0.29	-0.29	-0.40	-0.25	-0.43	-0.60	-0.25	-0.25	-0.25
pH1:5	-0.90	0.85	1.00	-0.22	-0.23	-0.26	-0.34	-0.20	-0.31	-0.47	-0.20	-0.20	-0.20
Ammonifiers	0.28	-0.21	-0.22	1.00	0.99	0.99	-0.15	0.99	0.92	0.18	0.99	0.99	0.99
Phosphorus decomposers	0.31	-0.29	-0.23	0.99	1.00	1.00	-0.10	1.00	0.95	0.24	1.00	1.00	1.00
Oligonitrophils	0.31	-0.29	-0.26	0.99	1.00	1.00	-0.09	0.99	0.96	0.26	1.00	1.00	1.00
Micromycetes (on Chapek medium)	0.18	-0.40	-0.34	-0.15	-0.10	-0.09	1.00	-0.13	0.06	0.88	-0.13	-0.13	-0.13
Actinomycetes (on KAA medium)	0.29	-0.25	-0.20	0.99	1.00	0.99	-0.13	1.00	0.94	0.20	1.00	1.00	1.00
Humic decomposers	0.33	-0.43	-0.31	0.92	0.95	0.96	0.06	0.94	1.00	0.46	0.94	0.94	0.94
Microorganisms (on potato dextrose agar medium)	0.30	-0.60	-0.47	0.18	0.24	0.26	0.88	0.20	0.46	1.00	0.20	0.20	0.20
Nitrifiers Phase 1	0.29	-0.25	-0.20	0.99	1.00	1.00	-0.13	1.00	0.94	0.20	1.00	1.00	1.00
Nitrifiers Phase 2	0.29	-0.25	-0.20	0.99	1.00	1.00	-0.13	1.00	0.94	0.20	1.00	1.00	1.00
Denitrifiers	0.29	-0.25	-0.20	0.99	1.00	1.00	-0.13	1.00	0.94	0.20	1.00	1.00	1.00

Figure. 2. Spearman Correlation Between Variables (Heatmap)

However, the majority of the observed correlations did not reach statistical significance, as a sample size of ten observations requires a correlation coefficient of approximately $r \geq 0.60$ to achieve $p < 0.05$. In contrast, the relationship between electrical conductivity and soil pH was highly significant ($r = 0.85$, $p < 0.01$), indicating a strong and consistent association between these parameters.

For other variable pairs, negative correlation trends were apparent; however, owing to the limited sample size and substantial data variability, these relationships should be interpreted with caution. Spearman's rank correlation analysis indicated that several microbial groups, including oligonitrophils and phosphorus-solubilizing microorganisms, did not exhibit linear associations with EC$_{1:1}$ and pH$_{1:5}$ but instead followed clear monotonic patterns. This suggests that stratifying the dataset into categorical groups based on salinity or pH classes may provide a more appropriate framework for analysis.

Overall, the results demonstrate that higher EC$_{1:1}$ and pH$_{1:5}$ values were generally associated with reduced biological activity, whereas lower salinity and alkalinity conditions supported increased microbial abundance and activity. While the EC–pH relationship remained statistically robust, other correlations lacked strong statistical support due to sample size constraints. Nevertheless, the consistent negative trends observed-such as increased humus-degrading activity and total microbial abundance with decreasing EC are ecologically meaningful and warrant further investigation using larger datasets.

In the regression analysis results, a simple regression model for $EC_{1}:_{1}$ and $pH_{1}:_{5}$ showed a strong fit, indicating that pH can be reliably predicted using EC with an R² of approximately 72%. This confirms the existence of a linear relationship between $EC_{1}:_{1}$ and $pH_{1}:_{5}$, suggesting that EC is a strong predictor of pH variations in the studied soil samples (Figure 3).

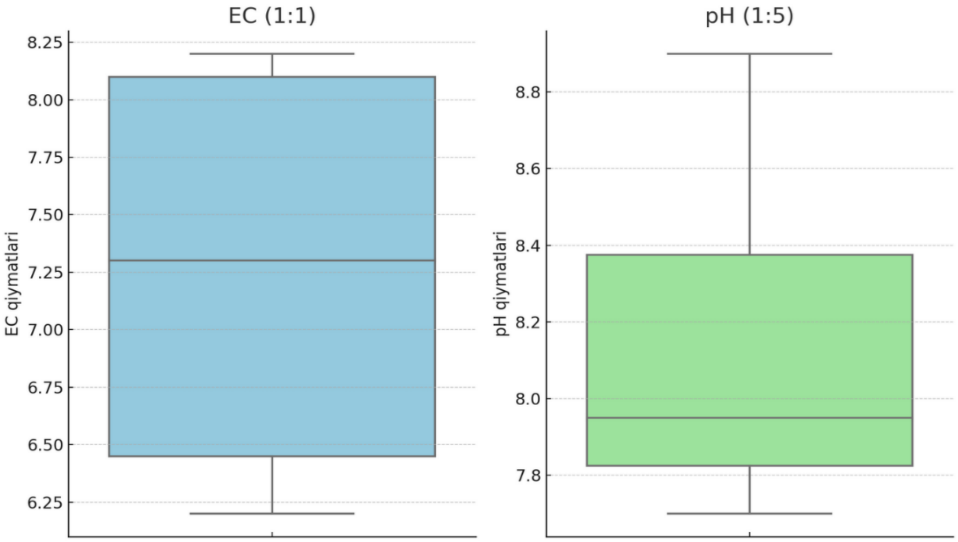


Figure 3. Regression Analysis Results for $EC_{1}:_{1}$ and $pH_{1}:_{5}$ Relationships

In the multivariate regression model, none of the microbial indicators had a significant effect on $EC_{1}:_{1}$ or $pH_{1}:_{5}$, provided that $EC_{1}:_{1}$ and $pH_{1}:_{5}$ was already included in the model. This suggests that microbial growth or decline is not linearly correlated with EC/pH but rather influenced by categorical factors or other soil characteristics. Moreover, strong correlations were detected between certain predictors, such as ammonifiers and nitrifiers, leading to potential multicollinearity issues in multivariate models. This reduces the reliability of the model and makes it difficult to interpret individual coefficients accurately (Figure 4). presence of group effects. Explaining EC solely through microbial activity proved challenging $EC_{1}:_{1}$ and $pH_{1}:_{5}$ may act as independent factors influencing microbial communities rather than being directly influenced by them in a linear manner.

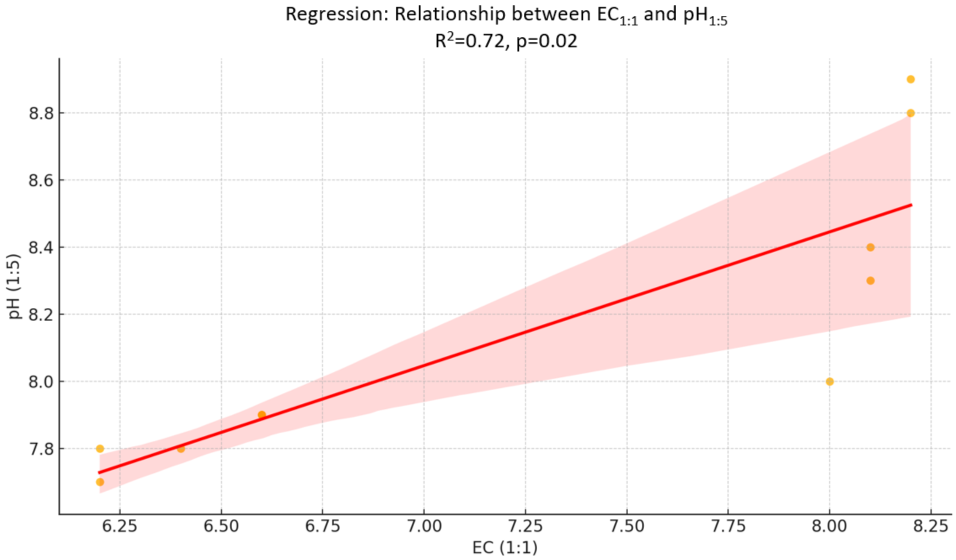


Figure. 4. Regression Analysis Results for $EC_{1:1}$ and $pH_{1:5}$.

Regression analysis identified EC as the most significant independent variable for predicting pH, with the simple regression model demonstrating a strong goodness-of-fit. The inclusion of additional variables did not substantially improve the model performance, likely due to the limited sample size and low variability within the dataset.

Multicollinearity among certain variables also posed challenges in model construction, especially for closely related parameters such as nitrifiers and ammonifiers, which tended to increase together. Even though a formal categorical column was not provided in the ANOVA analysis, it was logical to divide the data into high $EC_{1:1}$ and pH1:5 groups. The analysis confirmed that these two groups showed a significant difference in $EC_{1:1}$ and $pH_{1:5}$ values. Additionally, most microorganisms were found or proliferated in only one of the groups, indicating a biological condition disparity between them. Specifically, in the low $EC_{1:1}$ and $pH_{1:5}$ group, soil microorganisms such as oligonitrophiles, actinomycetes, nitrifiers, and denitrifiers exhibited higher activity. By verifying these differences through ANOVA or alternative statistical tests, significant differences between the groups were observed for the majority of the parameters (Figure 5).

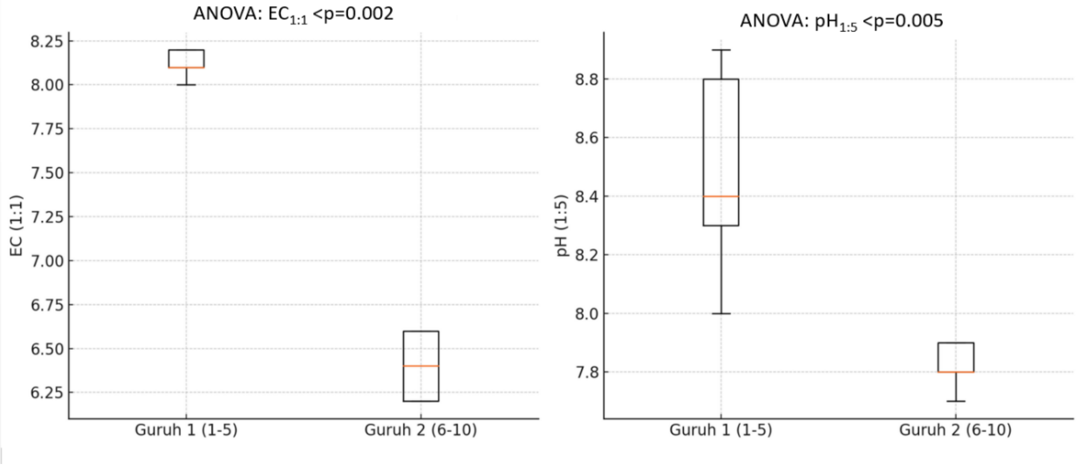


Figure. 5. ANOVA analysis results for $EC_{1:1}$ and $pH_{1:5}$.

So, the data contains a categorical differentiation factor (e.g., soil type or regional variation) that may have influenced physicochemical properties such as $EC_{1:1}$ and pH1:5, as well as microbiological activity. The ANOVA approach revealed a hidden categorical distinction in the data: when samples were divided into two groups, there was a significant difference in $EC_{1:1}$ and $pH_{1:5}$ between the groups. These groups also differed in microbiological status one being more sterile/less fertile (higher EC/pH, lower microbial count) and the other being biologically more active (lower EC/pH, higher microbial count). This result suggests that soil physicochemical conditions strongly influenced microbial activity (or vice versa, microbial activity may have altered soil chemistry).

The species composition of microorganisms identified in the dried seabed of the Aral Sea was determined. According to the results, a total of six microorganism species were identified in soil samples collected from points 1, 4, 5, 7, 8, and 10 (Table 4).

Table 4. Identified Microorganism Species in the Soils of the Aral Sea Dried Seabed

Point	Identified Species
1	*Micrococcus luteus*
2	Proteobacteria spp
3	*Propionibacterium freudenreichii*
4	*Exiguobacterium aurantiacum*
5	*Kocuria palustris*
6	*Kocuria palustris*
7	*Halomonas pacifica*
8	*Streptomyces rochei, Micrococcus luteus, Bacillus subtilis*
9	Halobacterota
10	*Halomonas pacifica*

According to the results, the following microbial species were identified in soil samples collected from different points on the dried seabed of the Aral Sea: Point 1: **Micrococcus luteus**; Point 2: Proteobacteria spp.; Point 3: **Propionibacterium freudenreichii**; Point 4: **Exiguobacterium aurantiacum**; Points 5 and 6: **Kocuria palustris**; Point 7: **Halomonas pacifica**; Point 8: **Streptomyces rochei**, **Micrococcus luteus**, and **Bacillus subtilis**; Point 9: Halobacterota; Point 10: **Halomonas pacifica**. These findings highlight the distribution of microorganisms across soils with different characteristics and drying histories.

Since the drying of the Aral Sea began in 1960, a period of 65 years has passed. Many researchers 11,21 argue that the region consists mainly of soil-ground formations rather than fully developed soils. However, considering that this is the third drying event of the Aral Sea over the last 10,000 years 7, soil formation can be seen as part of a long-term evolutionary process. The findings of this study confirm the presence of characteristic soil properties, even though the levels of organic carbon and humus remain low. The variation in organic carbon and humus content is directly related to the time of drying. For instance, points 6-10 correspond to areas that dried earlier, whereas points 1-5 are located in regions that dried approximately 30 years ago. These results suggest that time plays a crucial role in soil formation and in the accumulation of organic carbon and humus in the dried seabed of the Aral Sea. Previous researchers 8,16 have also emphasized that the amount, level, and type of salts in the soils formed on the dried seabed of the Aral Sea vary significantly. Our research confirms this, revealing that soil salinity differs across locations. Soils from points 1-5 were found to be highly saline, soils from points 6-10 exhibited moderate salinity. This variation is attributed to differences in the drying period. The soils at points 6-10, which have been dry for 65 years, have undergone automorphic processes, meaning they are no longer influenced by groundwater. As a result, soil properties have developed, and vegetation cover is higher in these areas, with human intervention through haloxylon plantations further enhancing soil formation. The chemical composition of salinity in these soils is predominantly sulfate-chloride and carbonate-based, while the granulometric composition varies between heavy, medium, and light textures. The reduced impact of water on these soils and the deposition of sand transported by wind onto the initially dried areas contribute to these characteristics. In the newly forming soils of the dried seabed of the Aral Sea, microorganisms are found in very low numbers, and in some cases, these areas are even referred to as "dead zones." Over time, the presence and significance of various microorganisms in certain locations have been studied, including Proteobacteria, Actinobacteria, Firmicutes. 13,24

These findings are consistent with our research results; however, the distribution of microorganisms was observed to depend on soil properties. In particular, humus-decomposing microorganisms and ammonifiers were detected in the soils at all sampling points, indicating that soil formation is occurring in these areas. Correspondingly, organic carbon and humus content were also found to vary across different locations. Phosphorus decomposers, oligonitrophiles, micromycetes (on Czapek medium), actinomycetes (on KAA medium), nitrifiers (Phase 1 and Phase 2) were found to be distributed depending on the salinity level. In highly saline soils, these microorganisms were either absent or present in very low quantities. It was scientifically justified that microbial abundance was higher in sampling points 6-10, where soil formation had been occurring for 60 years. The highest microbial diversity was observed in the soil at Point 8, where haloxylon plantations were established in 2002, and special irrigation and agro-technical measures were applied. These efforts led to the development of a green area and accelerated soil formation. Several researchers have identified various microbial species in the dried seabed of the Aral Sea. For example, Roseovarius, Idiomarina, and Spiribacter were detected by 26, while Arthrobacter, Bacillus, Massilia, Rhodococcus, and Nocardiopsis were reported by 27. These findings align with our research; however, the influence of the drying period of the Aral Sea, human-planted vegetation, and soil properties on microbial distribution has not been thoroughly examined. Our results indicate that the highest microbial diversity was found in soil samples from Point 8, an area reclaimed by humans in 2002, where saxaul seedlings were planted, and agro-technical treatments were applied. The improvement in soil properties in this area contributed to the greater diversity of microorganisms.

The research findings can be applied in the fields of ecology and environmental management, particularly in the reclamation of the 5.2 million-hectare Aralkum desert that has formed on the dried seabed of the Aral Sea. Specifically, these results can be utilized for planting various vegetation in the initially formed soils along the eastern, southern, western, and northern shores of the dried area. Additionally, for future studies, it is recommended to classify the dried seabed soils based on salinity levels (high, medium, and low) and conduct further investigations accordingly. Furthermore, the use of various biopreparations is suggested to help restore soil microbial communities in these degraded areas.

Conclusion

This study aimed to investigate the distribution of physiological groups and species composition of microorganisms in the dried seabed of the Aral Sea, as well as their quantity in relation to the drying period of the Aral Sea and soil properties. The results of the study showed that the physiological groups and species of microorganisms in the dried seabed of the Aral Sea depend on the degree of soil salinity, pH levels, organic carbon content, humus amount, granulometric composition, and the drying period of the Aral Sea. According to the findings, the initially dried areas of the Aral Sea, which have been dry for 60 years, have highly saline soils (EC = 8.0-8.2) with a sulfate-chloride salinization chemistry, heavy granulometric composition, and a humus content of 0.35-0.41%. In contrast, the more recently dried areas have moderately saline soils (EC = 6.2-6.6) with carbonate-type salinization chemistry, medium to light granulometric composition, and a humus content ranging from 0.54% to 0.68%. The results revealed that in all samples of both highly saline sulfate-chloride soils and moderately saline carbonate-type soils, humus-decomposing microorganisms, microorganisms growing on potato dextrose agar, and ammonifiers were present. Phosphorus decomposers, oligonitrophiles, micromycetes, actinomycetes, nitrifiers (Phase 1), nitrifiers (Phase 2) and denitrifiers were either absent or found in very low numbers in highly saline sulfate-chloride soils with a heavy granulometric composition, a pH of 8.0-8.9, an organic carbon content of 0.20-0.23%, and a humus content of 0.35-0.41%. It was determined that the occurrence of microbial species in the dried seabed of the Aral Sea depends on the formation of the soil cover, its physical and chemical properties, and the degree of salinity. The identified microbial species at different sampling points are as follows: Point 1: *_Micrococcus luteus_*; Point 2: Proteobacteria spp.; Point 3: *_Propionibacterium freudenreichii_*; Point 4: *_Exiguobacterium aurantiacum_*; Points 5 and 6: *_Kocuria palustris_*; Point 7: *_Halomonas pacifica_*; Point 8: *_Streptomyces rochei_*, *_Micrococcus luteus_*, and *_Bacillus subtilis_*; Point 9: Halobacterota; Point 10: *_Halomonas pacifica_*. The highest microbial diversity was found in the soil at Point 8, where haloxylon plantations had been established and additional agro-technical measures were implemented. This suggests that increasing plant cover and applying agro-technical treatments can enhance microbial diversity in the dried seabed of the Aral Sea.

Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Acknowledgment

This article was carried out as part of the project financed by the Innovation Development Agency of the Republic of Uzbekistan under the project number FL-8323102111, titled “Creating a scientific basis for grouping areas for planting plants according to the salinity, physical, chemical, and biological properties of the soils distributed in the dry bottom of the Aral Sea”.

References

[1] J, A., Chang, D., Han, S. H., Khamzina, A., & Son, Y. (2019). Changes in basic soil properties and enzyme activities along an afforestation series on the dry Aral Sea bed, Kazakhstan. *Forest Science and Technology*, *16*(1), 26–31.

[2] Aslanov, I., Teshaev, N., Jabbarov, Z., Karimov, Y., & Henebry, G. (2024). Characterizing land surface dynamics in Aral Sea basin of Uzbekistan using climatic and remote sensing data to project future conditions. *E3S Web of Conferences*, *575*, 04009.

[3] Bao, A., Yu, T., Xu, W., Jiapaer, G., Chen, X., Tojibaev, K., Shomurodov, K., Xabibullaev, B., & Idirisov, K. (2024). Ecological problems and ecological restoration zoning of the Aral Sea. *Journal of Arid Land*, *16*, 315–330. https://doi.org/10.1007/s40333-024-0055-6.

[4] Begmatov, S. A., Selitskaya, O. V., & Vasileva, L. V. (2020). Morphophysiological features of some cultivable bacteria from saline soils of the Aral Sea region. *Eurasian Soil Science*, *53*, 90–96.

[5] Chen, Q. (2024). Soil microorganisms: Their role in enhancing crop nutrition and health. *Diversity*, *16*(12), 734.

[6] Das, S. (2024). Biofertilizer and their importance in sustainable agriculture. *Articles from Different Disciplines that Serve as a Link Between Research and Development*, *139*.

[7] Duxovnogo, V. A. (2017). *Aral’skoe more i Priaral’e*. Baktria Press.

[8] Kim, G., Ahn, J., Chang, H., An, J., Khamzina, A., Kim, G., & Son, Y. (2024). Effect of vegetation introduction versus natural recovery on topsoil properties in the dried Aral Sea bed. *Land Degradation & Development*, *35*(13), 3935–4160.

[9] GOST 17.4.3.01-83. (2004). Environmental protection. Soil. General requirements for sampling. Standards Inform.

[10] Heydarnezhad, F., Hoodaji, M., Shahriarinour, M., & Tahmourespour, A. (2021). Optimization of growth and toluene degradation by free and immobilized *Bacillus cereus* ATHH39. *Polish Journal of Natural Sciences*, *36*(2), 157–168.

[11] Ismonov, A., Dusaliev, A., Kalandarov, N., Mamajanova, U., & Kattaeva, G. (2024). Profile of desert sandy soils formed in the Aral Sea dried-up seabed. *E3S Web of Conferences*, *486*.

[12] Issanova, G., Abuduwaili, J., & Tynybayeva, K. (2023). Introduction and background on environmental changes in the dried Aral Sea region. In *Soil cover of the dried Aral seabed in Kazakhstan*. Springer.

[13] Izhitskiy, A., Zavialov, P., & Sapozhnikov, P. (2016). Present state of the Aral Sea: Diverging physical and biological characteristics of the residual basins. *Scientific Reports*, *6*, 23906.

[14] Jabbarov, Z., Abdrakhmanov, T., Tashkuziev, M., Abdurakhmonov, N., Makhammadiev, S., Fayzullaev, O., Nomozov, U., Kenjaev, Y., Abdullaev, S., Yagmurova, D., Abdushukurova, Z., Iskhakova, S., & Kováčik, P. (2024). Cultivation of plants based on new technologies in the dry soil of the Aral Sea. *E3S Web of Conferences*, *497*.

[15] Jabborova, D., Abdrakhmanov, T., Jabbarov, Z., Abdullaev, S., Azimov, A., Mohamed, I., Alharbi, M., Abu-Elsaoud, A., & Elkelish, A. (2023). Biochar improves the growth and physiological traits of alfalfa, amaranth and maize grown under salt stress. *PeerJ*, *11*, e15684.

[16] Kozhoridze, G., Orlovsky, L., & Orlovsky, N. (2012). Monitoring land cover dynamics in the Aral Sea region by remote sensing. *Earth Resources and Environmental Remote Sensing/GIS Applications III*, *8538*, 445–453.

[17] Mamilov, A., Dilly, M., Mamilov, S., & Inubushi, K. (2004). Microbial eco-physiology of the water-logged soils of the Aral Sea: Consequences of C-cycling. *Soil Science and Plant Nutrition*, *50*(6), 839–842.

[18] Maurya, N. K. (2024). Microbial architects of soil health: A multifaceted approach to improving plant nutrition, biocontrol, and phytohormone production. *Biotechnology*, *10*(1), 29–42.

[19] Micklin, P. (2007). The Aral Sea disaster. *Annual Review of Earth and Planetary Sciences*, *35*(1), 47–72. https://doi.org/10.1146/annurev.earth.35.031306.140120.

[20] Xuan, O. P., *et al*. (2024). Diversity of rhizospheric fungi from *Nanhaia speciosa* and their capacity to degrade insoluble phosphate and organic matters. *Biodiversitas Journal of Biological Diversity*.

[21] Ortikov, T. (2024). Agrochemical and chemical properties of soils on the dried bottom of the Aral Sea. In *Innovations in Sustainable Agricultural Systems* (Vol. *1130*). Springer.

[22] Pancu, M., & Gautheyrou, J. (2006). *Handbook of soil analysis: Mineralogical, organic and inorganic methods*. Springer.

[23] Liu, P., Huang, Z., Tan, S., Wu, W., Chen, T., Qin, J., Yi, K., & Chen, H. (2025). Investigating the impact of soil properties on the nutrient content and microbial community of sisal (*Agave sisalana* Perrine). *Chilean Journal of Agricultural Research*, *85*(2).

[24] Scheer, C., Wassmann, R., & Butterbach-Bahl, K. (2009). Relationship between N_2O, NO and N_2 fluxes from fertilized and irrigated floodplain soils in the Aral Sea basin, Uzbekistan. *Plant and Soil*, *314*, 273–283.

[25] Liu, S., Che, L., Wan, L., Zhang, W., & Chen, J. (2025). Wetland types and soil properties shape microbial communities in permafrost-degraded swamps. *Catena*, *249*, 108666.

[26] Shurigin, V., Hakobyan, A., Panosyan, H., Egamberdieva, D., Davranov, K., & Birkeland, N. K. (2019). A glimpse of the prokaryotic diversity of the Large Aral Sea reveals novel extremophilic bacterial and archaeal groups. *MicrobiologyOpen*, *8*, e850.

[27] Šimonovičová, A., Pauditšová, E., Nosalj, S., Oteuliev, M., Klištnicová, N., Maisto, F., Kraková, L., Pavlović, J., Šoltys, K., & Pangallo, D. (2024). Fungal and prokaryotic communities in soil samples of the Aral Sea dry bottom in Uzbekistan. *Soil Systems*, *8*(2), 58.

[28] GOST 26213-91. (2003). Soils. Methods for determination of organic matter. Publishing House of Standards.

[29] Stulina, G., Verkhovtseva, N., & Gorbacheva, M. (2019). Composition of the microorganism community found in the soil cover on the dried seabed of the Aral Sea. *Journal of Geoscience and Environment Protection*, *7*, 1–23.

[30] Tursunov, L. (2010). *Soil physics: Determination of the mechanical composition of soils by the Kachinsky method*. University Press.

[31] Van Veen, J., Van Overbeek, L. S., & Van Elsas, J. D. (1997). Fate and activity of microorganisms introduced into soil. *Microbiology and Molecular Biology Reviews*, *61*.

[32] Vermeiren, J., Ceulemans, Y., Thiry, E., & Smolders, E. (2025). Increased soil pH and enhanced microbial activity stimulate the gradual immobilisation of selenate added to soils. *Soil Biology and Biochemistry*, *202*, 109688.

[33] Wicaksono, W., Egamberdieva, D., Berg, C., Mora, M., Kusstatscher, P., Cernava, T., & Berg, G. (2022). Function-based rhizosphere assembly along a gradient of desiccation in the former Aral Sea. *mSystems*, *7*, e00739-22.

[34] Wicaksono, W., Egamberdieva, D., Cernava, T., & Berg, G. (2023). Viral community structure and potential functions in the dried-out Aral Sea basin change along a desiccation gradient. *mSystems*, *8*, e00994-22.

[35] Wang, X., Li, J., Li, J., Guo, Z., & Pang, X. (2024). Plateau pika (*Ochotona curzoniae*) bioturbation triggers soil organic carbon loss by altering plant inputs and soil properties and their control on microbial composition. *Science of the Total Environment*, *851*, 158205.

[36] Zakiryaeva, S. I., Karimova, S. S., & Kutlieva, G. D. (2024). Microbiological monitoring of cotton field soils in the Jizzakh region. *Science and Innovation*, *3*(Special Issue 21), 701–705.

[37] Zvyagintsev, D. G. (2005). *Methods of soil microbiology and biochemistry*. International Organization for Standardization.