European Journal of Interdisciplinary Research and Development
Volume- 51 May- 2026
Website: www.ejird.journalspark.org ISSN (E): 2720-5746

COMPOSITION AND QUANTITATIVE INDICATORS OF MICROFLORA IN IRRIGATED MEADOW-ALLUVIAL SOILS OF BUKHARA DISTRICT

M.I.Akhmedov1, O.B.Sharipov2

[1] Akhmedov Mukhammad Ismatovich
Director of the Bukhara Scientific Experimental Station,
Research Institute of Cereals and Leguminous Crops,
Candidate of Agricultural Sciences, Professor
Email: 202807499@mail.ru
ORCID iD: 0009-0002-0090-7254

[2] Sharipov Odiljon Bafoyevich
PhD in Biological Sciences, Associate Professor
Bukhara State University, Deputy Director for Science and Innovation,
Bukhara Scientific Experimental Station
Email: sharipov4004@gmail.com: +998 91 442 88 22
ORCID iD: 0000-0002-4332-668X

Abstract

This article analyzes the composition, distribution patterns, and quantitative indicators of microflora in irrigated meadow-alluvial soils of Bukhara district. Soil samples were collected from the 0–5, 5–15, 15–30, 30–50, and 50–70 cm layers and studied using classical microbiological methods on meat-peptone agar, Ashby, Hutchinson, Czapek, and starch-ammonia agar nutrient media. The results showed that total microflora, including rod-shaped bacteria and actinomycetes, was more abundant on meat-peptone agar, whereas nitrogen-fixing microorganisms similar to Azotobacter were detected on Ashby medium. In general, the upper soil horizons were characterized by higher microbial abundance and greater morphological diversity of colonies. However, a local maximum recorded in the 30–50 cm layer of profile R-3 indicates the heterogeneity of microbial activity within the soil profile. During the summer period, the activity of cellulose-decomposing microorganisms and filamentous fungi increased, confirming the existence of seasonal microbiological dynamics. The obtained data can be used to assess the biological activity, fertility level, and reclamation status of irrigated soils.

Keywords: Irrigated soils, meadow-alluvial soils, microflora, nitrogen-fixing bacteria, actinomycetes, Azotobacter, soil horizon, biological activity, salinity.

Introduction

Microbiological processes in irrigated soils play an essential role in maintaining soil fertility, mineralization of organic residues, nutrient cycling, nitrogen transformation, and biochemical processes occurring in the plant rhizosphere. Soil microorganisms participate in the decomposition of organic matter, the formation of humus, the mobilization of nutrients, and the stabilization of agroecosystem productivity. Therefore, the assessment of microflora composition and its quantitative dynamics across soil horizons is of great agroecological and practical importance.

Under the conditions of Bukhara region, irrigated meadow-alluvial soils are characterized by a specific water regime, high evaporation, different degrees of salinity, and changing reclamation conditions. These factors directly influence the structure, abundance, and physiological activity of microbial communities. The number and diversity of microorganisms in such soils may vary depending on soil depth, season, moisture conditions, aeration, organic matter content, root exudates, and nutrient availability.

The purpose of this study was to analyze the composition of microflora, the main physiological groups of microorganisms, and their quantitative indicators in irrigated meadow-alluvial soils of Bukhara district. The study was carried out using classical microbiological methods widely applied for the cultivation, isolation, and morphological characterization of soil microorganisms [1, 2].

Literature Review

Soil microflora is one of the most important biological indicators of soil fertility and ecological stability. In irrigated agricultural soils, microbial communities are strongly influenced by salinity, sodicity, soil moisture, aeration, organic matter, root exudates, and seasonal hydrothermal conditions. Previous studies have shown that irrigation-induced salinity and sodicity reduce microbial biomass, weaken enzymatic activity, and form a smaller and more stressed microbial community [3]. These findings are especially relevant for irrigated soils of the Bukhara region, where salinity and irrigation regime are among the main factors affecting soil biological activity.

Modern studies also confirm that soil salinization changes not only the quantity of microorganisms but also the structure and ecological functions of bacterial and fungal communities. Salinity stress affects microbial diversity and weakens the role of microorganisms in carbon and nitrogen cycling processes [4]. Therefore, the decrease in microbial abundance with depth and the differences between soil profiles observed in the present study may be explained by changes in organic matter content, oxygen availability, salinity level, and rhizosphere influence.

Nitrogen-fixing microorganisms are particularly important in irrigated agricultural soils because they participate in biological nitrogen accumulation and improve soil fertility. Among them, representatives of the genus *Azotobacter* are considered free-living nitrogen-fixing bacteria with high agronomic value. They may contribute to plant nutrition, improve nitrogen availability, and support yield stability [5]. In the present study, the detection of colonies similar to *Azotobacter* on Ashby medium indicates the presence of a certain nitrogen-fixing potential in irrigated meadow-alluvial soils. However, since identification was based mainly on morphological features, further biochemical and molecular studies are necessary for accurate taxonomic confirmation.

Studies conducted in the Bukhara oasis also show that the degree of soil salinity has a direct effect on the number of taxonomic and physiological groups of microorganisms in meadow-alluvial soils. With increasing salinity and soil depth, the number of bacteria, fungi, actinomycetes, nitrogen-fixing microorganisms, nitrifiers, ammonifiers, nitrate reducers, and cellulose-decomposing microorganisms tends to decrease. These conclusions correspond to the results of the present research, where microbial abundance was generally higher in the upper horizons, while deeper layers showed lower microbial activity.

Thus, the reviewed literature confirms that the microbiological activity of irrigated meadow-alluvial soils depends on salinity level, soil horizon, seasonal conditions, root activity, nutrient availability, and local microecological features. Microbiological indicators can therefore be used as important criteria for assessing the biological activity, fertility level, and reclamation status of irrigated soils.

Materials and Methods

The research object was the irrigated meadow-alluvial soils of the "Bafo Mardoni Sharif" farm located in Bukhara district. Soil samples were collected from five depth layers: 0–5, 5–15, 15–30, 30–50, and 50–70 cm. Microbiological analyses were conducted using three representative soil profiles designated as R-1, R-2, and R-3.

For each soil horizon, 10 g of soil sample was placed into 100 mL of sterile water and thoroughly mixed to obtain a soil suspension. Serial tenfold dilutions were then prepared from 10^{-1} to 10^{-9}. The obtained dilutions were inoculated onto different nutrient media in order to determine the number of colony-forming microorganisms, colony morphology, and cellular structure.

The following nutrient media were used in the experiment:

- meat-peptone agar — for determining the total number of microorganisms;
- Ashby medium — for nitrogen-fixing bacteria;
- Hutchinson medium — for cellulose-decomposing microorganisms;
- Czapek medium — for filamentous fungi;
- starch-ammonia agar — for actinomycetes and yeasts.

Morphological analysis was carried out by observing stained and living cells under microscopy according to generally accepted microbiological methods [1, 2]. The obtained results were interpreted using descriptive analysis. Particular attention was paid to the vertical distribution of microorganisms, the diversity of colony morphology, and seasonal changes in the activity of specific physiological groups.

Results and Discussion

The results of the study showed that microbial groups were not evenly distributed across the studied soil profiles and horizons. On meat-peptone agar, spore-forming and non-spore-forming rods, actinomycetes, and coccoid forms were detected relatively frequently. On Ashby medium, nitrogen-fixing microorganisms, including mucous and spreading colonies morphologically similar to *Azotobacter*, were observed.

On meat-peptone agar, the highest microbial titer in profile R-1 was recorded in the 0–5 cm layer and amounted to 2×10^7 cells/mL. With increasing depth, this value gradually decreased to 2×10^5 cells/mL. A similar tendency was observed in profile R-2, where microbial abundance decreased in deeper horizons and ranged from 2×10^4 to 2.5×10^4 cells/mL in the 15–70 cm layers. In profile R-3, however, a local maximum of 2.5×10^7 cells/mL was recorded in the 30–50 cm layer, indicating the presence of a specific microbiologically active zone within the soil profile.

According to colony morphology, the upper horizons were characterized by greater diversity in shape, color, surface structure, and consistency. In the 0–5 and 5–15 cm layers, white, grey, semi-transparent, convex, and spreading colonies were observed. In addition, dry and pigment-forming colonies typical of actinomycetes were also detected. In deeper layers, colony diversity decreased, and small white-grey colonies became dominant.

Nitrogen-fixing bacteria on Ashby medium were mainly recorded within the range of 10^2–10^3 cells/mL. In profile R-3, nitrogen-fixing microflora was detected in almost all studied horizons. Colonies similar to *Azotobacter* were colorless or greyish, mucous, and spreading. Over time, some colonies produced yellow-green or dark-grey pigmentation.

During spring sampling, microbial growth on Hutchinson and, in some cases, Czapek media was weak or almost absent. However, during the summer season, the number of cellulose-decomposing microorganisms and filamentous fungi increased significantly. This indicates that seasonal changes in temperature and moisture conditions stimulate the decomposition of organic residues and the development of specialized physiological groups of microorganisms.

The obtained data show that the main microbiological activity is generally concentrated in the upper soil layers. This can be explained by the relatively high amount of organic residues, better aeration, and higher concentration of root exudates in these horizons. Nevertheless, the local maximum observed in the 30–50 cm layer of profile R-3 suggests that the soil profile is not microbiologically homogeneous. This phenomenon may be associated with buried organic matter, localized moisture conditions, or increased root activity in certain microzones.

Table 1 Number of microorganisms detected on meat-peptone agar, cells/mL

Soil profile	0–5 cm	5–15 cm	15–30 cm	30–50 cm	50–70 cm
R-1	2×10^7	5×10^6	2×10^6	2×10^5	2×10^5
R-2	5.0×10^6	2.5×10^5	2×10^4	2.5×10^4	2.5×10^4
R-3	1×10^6	6×10^5	2.5×10^5	2.5×10^7	1.7×10^5

Note: The high value observed in the 30–50 cm layer of profile R-3 indicates a local increase in microbiological activity and should be interpreted as an exception to the general vertical decreasing trend.

Table 2 Number of nitrogen-fixing microorganisms detected on Ashby medium, cells/mL

Soil profile	0–5 cm	5–15 cm	15–30 cm	30–50 cm	50–70 cm
R-1	2.5×10^2	2×10^2	2×10^2	1×10^2	1×10^2
R-2	2.5×10^3	2×10^2	1×10^2	1×10^2	–
R-3	2×10^3	1×10^3	1×10^2	2×10^2	2×10^2

Note: The dash symbol indicates that microbial growth was not detected. The value originally presented as “2,103” was normalized to 2×10^3 according to the logical range of the data.

Scientific Interpretation of the Results

The data presented in the tables confirm the presence of vertical stratification in the soil microflora. In most cases, microbial abundance was higher in the upper horizons and decreased with depth. This pattern is mainly associated with the higher content of organic matter, better oxygen availability, and stronger influence of plant roots in the surface soil layers.

The detection of nitrogen-fixing bacteria in the range of 10^2–10^3 cells/mL on Ashby medium indicates that irrigated meadow-alluvial soils possess a certain functional potential for biological nitrogen cycling. However, it should be noted that colonies similar to *Azotobacter* were identified only on the basis of morphological characteristics. Therefore, further biochemical tests or molecular methods are required for accurate taxonomic identification at the species level.

Seasonal changes were also evident in the activity of cellulose-decomposing microorganisms and filamentous fungi. Their increased development in the summer period suggests the intensification of organic matter decomposition and humus formation processes under favorable hydrothermal conditions. Thus, microbiological processes in these soils depend not only on soil depth but also on seasonal environmental factors.

At the same time, the present study has a primarily descriptive character. For a deeper interpretation of the results, microbiological indicators should be combined with physical and chemical soil properties such as humus content, salinity level, pH, soil moisture, and mechanical composition. Such an integrated approach would allow a more accurate assessment of the biological and reclamation status of irrigated soils.

Conclusion

1. The composition and quantitative indicators of microorganisms in irrigated meadow-alluvial soils of Bukhara district differed considerably depending on soil profile, depth layer, and nutrient medium.
2. On meat-peptone agar, the total microflora was represented mainly by rod-shaped bacteria, actinomycetes, and coccoid forms. In most cases, the highest microbial abundance was recorded in the upper soil horizons.
3. On Ashby medium, nitrogen-fixing bacteria, including colonies morphologically similar to Azotobacter, were detected. Their most stable occurrence was observed in profile R-3.
4. The increased activity of cellulose-decomposing microorganisms and filamentous fungi during the summer period confirmed the presence of seasonal microbiological dynamics in the studied soils.
5. The local maximum recorded in the 30–50 cm layer of profile R-3 indicates the presence of microbiologically active microzones within the soil profile. Therefore, the heterogeneity of the soil profile should be taken into account when interpreting microbiological data.
6. Salinity, soil depth, organic matter content, aeration, and seasonal hydrothermal conditions are among the main factors influencing the abundance and activity of soil microflora in irrigated meadow-alluvial soils.

7. Further studies combining microbiological indicators with physical and chemical soil parameters are necessary to accurately assess the influence of salinity and other reclamation factors on soil microflora.

Practical Significance.

The results of this study can be used to assess the biological condition of irrigated soils, conduct microbiological monitoring, and scientifically justify fertilization and reclamation measures. The data presented in the article may also serve as a basis for further studies of rhizosphere microbiocenoses in cotton-growing and other irrigated farming systems.

From a practical point of view, the determination of microbial abundance in different soil horizons makes it possible to evaluate the biological activity of irrigated soils and identify layers with relatively high or low microbiological potential. Such information is important for improving soil fertility management, optimizing irrigation and fertilization practices, and developing measures aimed at maintaining the ecological stability of agricultural soils.

Limitations of the Study

Species-level identification of some taxa and the confirmation of causal relationships between environmental factors and microbial dynamics require additional molecular-biological and statistical approaches.

In addition, the interpretation of microbiological data would be strengthened by the inclusion of soil physical and chemical parameters such as salinity, pH, humus content, soil moisture, and mechanical composition. Future research should combine microbiological, biochemical, and molecular methods in order to obtain a more complete understanding of microbial processes in irrigated meadow-alluvial soils.

References

1. Netrusov, A.I. (Ed.). Practical Course in Microbiology: Textbook for Higher Educational Institutions. Moscow: Akademiya, 2005. 603 p.
2. Netrusov, A.I., & Kotova, I.B. Microbiology: Textbook for Higher Educational Institutions. Moscow: Akademiya, 2006. 350 p.
3. Rietz, D.N., & Haynes, R.J. Effects of irrigation-induced salinity and sodicity on soil microbial activity. Soil Biology and Biochemistry, 2003, Vol. 35, Issue 6, pp. 845–854. DOI: 10.1016/S0038-0717(03)00125-1.
4. Zhang, G., Bai, J., Zhai, Y., Jia, J., Zhao, Q., Wang, W., & Hu, X. Microbial diversity and functions in saline soils: A review from a biogeochemical perspective. Journal of Advanced Research, 2024, Vol. 59, pp. 129–140. DOI: 10.1016/j.jare.2023.06.015.
5. Aasfar, A., Bargaz, A., Yaakoubi, K., Hilali, A., Bennis, I., Zeroual, Y., & Meftah Kadmiri, I. Nitrogen Fixing Azotobacter Species as Potential Soil Biological Enhancers for Crop Nutrition and Yield Stability. Frontiers in Microbiology, 2021, Vol. 12, Article 628379. DOI: 10.3389/fmicb.2021.628379.