SCIENCE AND INNOVATION
INTERNATIONAL SCIENTIFIC JOURNAL VOLUME 3 ISSUE 6 JUNE 2024
ISSN: 2181-3337 | SCIENTISTS.UZ

MICROBIAL COMMUNITY IN SALINE SOILS OF COTTON FIELDS IN KASHKADARYA REGION

[1]Zakiryaeva S.I., [2]KarimovX.X., [3]Khamidova Kh.M., [4]Shakirov Z.S.
[1,2,3,4]The Institute of Microbiology, Academy of Sciences of the Republic of Uzbekistan
https://doi.org/10.5281/zenodo.12609130

Abstract*. The microbial communities within soil layers (0-10 cm, 10-20 cm, and 20-30 cm) of cotton fields at the "Yuksalish" MFY farm, Nishon district, Kashkadarya region, were analyzed. Microbiological analysis revealed low populations of microorganisms from the main physiological groups, with some groups entirely absent. Ammonifying bacteria were significantly more abundant in the 20-30 cm layer (1.5 × 10^5 CFU/g) compared to upper layers, whereas oligonitrophilic microorganisms were less prevalent (4.5×10^3 CFU/g) in this layer. Fungi belonging to Aspergillus and Fusarium genera were observed in soil layers of 10-20 cm and 20-30 cm.*

Keywords*: saline soil, microbial community, ammonifying bacteria, oligonitrophilic microorganisms, actinomycetes, micromycetes, cellulose-decomposing microorganisms.*

Introduction

Salinity poses a significant threat to soil fertility on a global scale. Understanding its impact on soil microbial communities is challenging due to the intertwined effects with other variables influenced by salinity [1]. Soil degradation induced by salinity is increasingly recognized as a pressing global issue, leading to soil compaction, diminished nutrient availability, and inhibited plant growth. These factors collectively undermine agricultural productivity, resulting in economic losses, unsustainable agricultural practices, and jeopardizing global food security [2-4].

Soil microorganisms play a crucial role as biological factors influencing plant growth in saline environments. Numerous studies have demonstrated the substantial impact of salinity on microbial communities [5]. Salinity can disrupt microbial metabolic functions by modifying enzyme activities and substrate availability, thereby affecting nutrient cycling and overall soil health [6].

Soil microorganisms play a pivotal role in soil formation and enhancing productivity. The rate of microbiological processes in soil, as well as the quantity and composition of microflora, depend significantly on factors such as soil temperature, texture, moisture content, organic matter content, relief erosion, and agricultural practices including fertilizer use, tillage depth, and other related practices.

Organic matter decomposition is facilitated by microbial activity, whereby microorganisms break down organic materials in the soil. Soil hosts a vast array of microorganisms including bacteria, actinomycetes, fungi, algae, yeasts, lichens, and small benthic animals. Their populations vary widely, with millions to billions present in just one gram of soil.

Microbiological activity in soil shapes its properties, regimes, and fertility. Understanding soil microbiological activity is crucial for comprehending soil processes, properties, regimes, and current fertility conditions. This understanding allows for effective management practices aimed at optimizing soil productivity and ensuring sustainable agricultural outcomes.

Based on several scientific studies, it has been established that cotton yields decrease significantly under varying levels of soil salinity: by 20% in mildly saline soils, 50% in moderately

saline soils, and 85% in highly saline soils. Soil microorganisms with high biological activity play a crucial role in decomposing organic residues, mineralizing nutrients, and forming humus. However, biological processes are typically less active in saline soils due to the inhibitory effects of salinity on microbial metabolism under low moisture conditions, disrupting nutrient and osmotic balances and impeding plant growth and development.

Given these challenges, studying and restoring the microbiological health of saline soils in our region is crucial for enhancing agricultural productivity.

Our research aims to investigate the microbial community in saline soils of the Kashkadarya region.

Standard methods of soil microbiology were employed for the microbiological analysis of soil samples collected from the cotton fields of the "Yuksalish" MFY grain and vegetable farm in the Nishon district, Kashkadarya region, at depths of 0-10 cm, 10-20 cm, and 20-30 cm.

The microbial community of moderately saline soil was studied according to the generally accepted method of D.G. Zvyagintsev [7].

Micro-organisms in soil samples, including: ammonifying bacteria - MPA, phosphorus-decomposing bacteria - Pikovsky, oligonitrophils and azotobacteria - Eshbi, actinomycetes - starch ammonium agar (SAA), micromycetes - Chapeka and Sabura, yeast bacteria - potato dextrose agar, and cellulose-degrading microorganisms - Getchenson was studied. Cellulose-degrading aerobic microorganisms were identified in Getchinson-Clayton liquid nutrient medium. Composition of Getchinson-Clayton liquid nutrient medium, g/l (tap water): K_2HPO_4 – 1.0; $MgSO_4 \times 7H_2O$ – 0.3; $SaCl_2$ – 0.1; NaCl - 0.1; $FeCl_3$ – 0.01; $NaNO_3$ – 2.5; pH 7.2–7.3. The number of anaerobic cellulose-degrading microorganisms was determined in Omelyansky's liquid nutrient medium. Filter paper was placed at the bottom of test tubes in the form of strips. Composition of Omelyansky liquid nutrient medium, g/l: K_2HPO_4 – 1.0; $MgSO_4 \times 7H_2O$ – 1.0; NaCl - 1.0; $(NH_4)_2SO_4$ – 2.0; $SaCO_3$ – 2.0. As a rule, sowing is carried out from 3, 4 and 5 diluted test tubes. Fatty acid-producing microorganisms were identified in Vinogradsky's liquid nutrient medium. The incubation period is 20-25 days, at a temperature of + 28-30 °C.

A suspension was prepared from the soil samples taken for microbiological analysis. For this, 10 grams of the soil sample was taken, mixed with 90 ml of sterile water and shaken in a shaker for 30 minutes. This process was continued serially, diluted to 1:1000000 and repeated. 1 ml of the liquid in the test tube was inoculated into specific solid selective nutrient media in a Petri dish, on a "dilution" basis in triplicate, and tested.

The amount of bacteria, yeasts, actinomycetes and fungi per 1 gram of dry soil was calculated using the following formula;

$$a = \frac{b \times c \times g}{d}$$

in this; a - the number of cells in 1 g of dry soil, b - the average number of colonies in a Petri dish, c - the separation used for sowing, g - the number of drops in 1 ml of suspension, d - the weight of dry soil taken for analysis.

The McCready table was used to determine the amount of microorganisms cultured in the liquid nutrient medium.

The agrochemical parameters of the soil are as follows: pH – 7.95; salinity – 1.72%; electrical conductivity - 3.79 ES / m; density - 1.91%, humus - 0.61%; total nitrogen content -

0.15%; total phosphorus content - 0.12%; total amount of potassium - 0.51%; Carbon C - 0.35%, mobile phosphorus - 10.5 mg/kg and mobile potassium - 250.5 mg/kg.

Results

Ammonifying microorganisms are putrefactive bacteria. Among them, the most famous are *Bacillus* (*Bacillus subtilis*, *Bacillus mycoides*) and *Clostridium* (*Clostridium tetani*, *Clostridium perfringens*, *Bacillus histolyticum*, *Clostridium putrificum*), as well as bacteria of the family, *Enterobacteriaceae* (*Proteus*, *Escherichia coli*).

As a result of the conducted microbiological analysis, it was found that the total amount of ammonifying bacteria in the studied soil samples is on average 10^4 to 10^5 CFU cells per 1 gram of soil. Ammonifying bacteria were less common in the 0-10 and 10-20 cm soil layers than in the 20-30 cm soil layer and averaged 1.5-6.7x10^4 CFU/g.

It was observed that representatives of phosphorus-decomposing bacteria and azotobacter were not found in all analyzed soil samples.

Microorganisms that use mineral forms of nitrogen are oligonitrophils. The amount of oligonitrophilic microorganisms in the 0-10 and 10-20 cm soil layers was one order higher than in the 20-30 cm soil layer, and it was 2.2-2.4x10^4 CFU/g in 1 gram of soil.

The amount of micromycetes in the 0-10, 10-20 and 20-30 cm layers of the studied soil was in the same order, and the average number of 1 gram of soil was 1.5-3x10^2 CFU spores, respectively. In the soil layers of 10-20 and 20-30 cm, fungi belonging to the genera *Aspergillus* and *Fusarium* were observed.

The amount of actinomycetes in the 0-10 cm layer of the soil surface was an order of magnitude higher than in the lower, i.e., 10-20 and 20-30 cm soil layers, on average 4.5x10^3 CFU/g in 1 gram of soil. Among the actinomycetes, species belonging to the genus *Streptomyces* were found. According to color, actinomycetes of black, yellow, gray, pink color were distinguished.

The amount of bacteria grown in the potato dextrose agar nutrient medium was one order higher in the 10-20 cm soil layer than in the 0-10 cm and 20-30 cm soil layers, and averaged 9.7x10^4 CFU/g in 1 gram of soil. In the Saburo nutrient medium, their amount was on average 1.9x10^5 CFU/g in 1 gram of soil at 0-10 cm of the soil layer, 3.7x10^3 CFU/g at the 10-20 cm layer, and 3.7x10^3 CFU/g at the 20-30 cm soil layer. it was observed that no bacteria were found. In starch ammonium agar medium, bacteria were found in all soil layers in the same order (7.5-4.6-4.3x10^3 CFU/g). Cellulose-decomposing bacteria and fungi were detected in Getchenson's agar nutrient medium. It was found that the amount of these microorganisms in the 0-10 and 10-20 cm layers of the soil is one order higher than in the 20-30 cm soil layer, that is, on average, 3.7-1 per gram of soil, respectively. It was 5x10^3 CFU/g. In the 10-20 cm layer of the soil, the fungus *Aspergillus niger* belonging to the genus *Aspergillus* was found (Foto. 1).

Eubacteria belonging to different taxonomic groups have the ability to break down cellulose in anaerobic and aerobic conditions: individual representatives of the genus Clostridium, a number of actinomycetes, myxobacteria, some representatives of the genus Pseudomonas, representatives of the genera *Cellulomonas*, *Ruminicoccus*, *Bacteroides*, *Butyrivibri*o, etc. The only thing these organisms have in common is the ability to synthesize enzymes that break down cellulose.

It has the property of breaking down cellulose under aerobic conditions: representatives of the genera *Penicillum*, *Aspergillus*, *Fusarium*, *Botrytis* of eukaryotic micromycetes; Bacteria belonging to the genera *Cytophaga* and *Cellfalcicula*, etc.

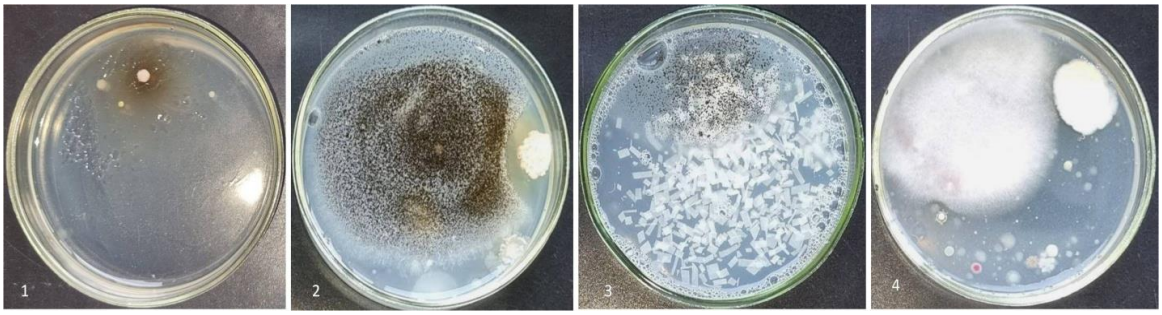

Foto 1. Kashkadarya region Nishon district "Yuksalish" MFY grain growing vegetable farm cotton crop area 10-20 cm soil layer the total number and appearance of the main physiological group of microorganisms in different nutrient environments
1-Meat peptone agar nutrient medium; 2- Chapeka nutrient medium;
3-Getchenson nutrient medium; 4- Starch ammonium agar nutrient medium.

It was observed that fatty acid-producing bacteria were on average $2.0x10^3$ CFU/g in the 0-10 cm layer of the soil, while their amount in the lower 10-20 cm layer was one order less ($7x10^2$ CFU/g), and in the 20-30 cm layer isolated colonies were found. Fatty acid-producing bacteria are anaerobes, representatives of the genus *Clostridium*. Fatty acid-producing bacteria are widespread in the soil, and they decompose large amounts of organic matter under anaerobic conditions. Some species fix nitrogen. Cellulose-degrading anaerobic microorganisms formed $2x10^2$ CFU in 1 gram of soil in the 20-30 cm soil layer, and isolated colonies were found in the 0-10 and 10-20 cm soil layers. The amount of cellulose-degrading aerobic microorganisms was the same in all soil layers, and isolated colonies were observed (Fig. 1).

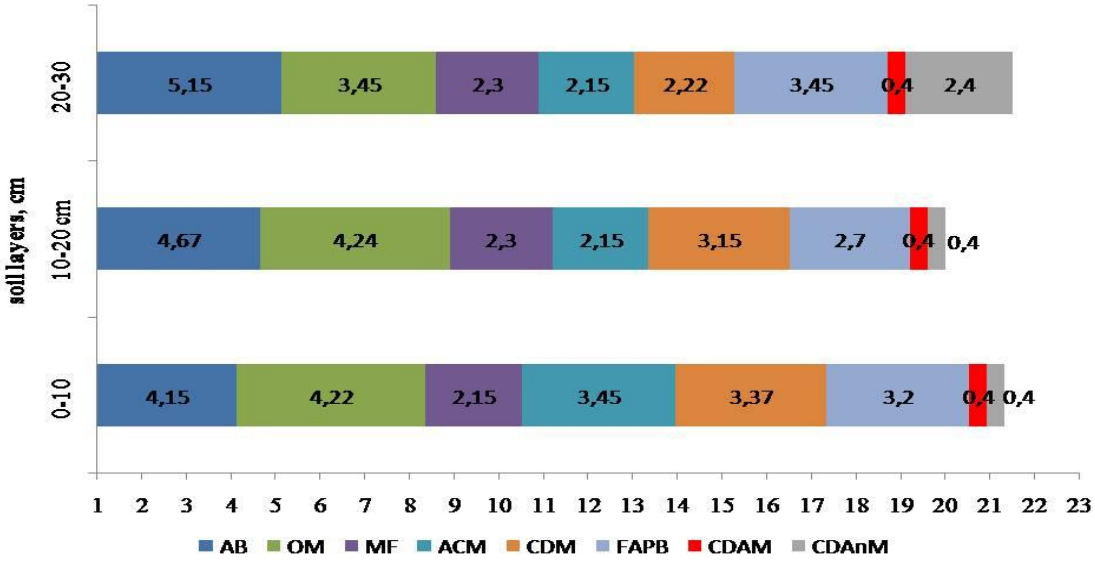

Figure 1. Kashkadarya region, Nishon district, "Yuksalish" MFY, the average amount of the main physiological group of microorganisms in the soil of the grain growing vegetable farm, cotton cultivation area, lg CFU/g of soil

AB - ammonifying bacteria; OM - oligonitrophilic microorganisms; MF – microscopic fungi; ACM - actinomycetes; CDM-cellulose-decomposing microorganisms (in a solid nutrient medium); FAPB-fatty acid producing bacteria; CDAM - cellulose-decomposing aerobic microorganisms; CDAnM - cellulose-decomposing anaerobic microorganisms:

Thus, microbiologically analyzed Kashkadarya region, Nishon district "Yuksalish" MFY, grain and vegetable farm, cotton crop area, it was observed that the main physiological group of

microorganisms are much less than the norm, and phosphorus-decomposing microorganisms were not found at all. This indicates low absorption of phosphorus element.

Summary. Soil serves as the primary habitat for microorganisms, crucial for their survival and reproductive processes. Salinity poses significant challenges to agriculture by reducing nutrient absorption in crops, inducing physiological drought, and potentially leading to crop failure. Soil microorganisms actively participate in the natural metabolism of substances and energy, playing a pivotal role in mitigating salinity issues in saline fields [8]. Research indicates that soil microorganisms contribute to plant growth promotion and facilitate beneficial interactions between plants and their microbial environment [3, 9]. Given their critical role, soil microorganisms are essential for enhancing saline soils. The microbial community within saline soils represents a vital component of ecosystems capable of adapting to extreme conditions and performing essential ecological functions. Therefore, studying the microbial community in salinized cotton fields is imperative. This research aims to develop effective strategies that harness native microbial communities to enhance soil fertility, rehabilitate degraded lands, and increase cotton yields under saline conditions. Such efforts are crucial for sustainable agricultural practices and ecosystem resilience.

REFERENCES

1. Kristin M. Rath , Noah Fierer, Daniel V. Murphy, Johannes Rousk. Linking bacterial community composition to soil salinity along environmental gradients //ISME J. 2019 Mar;13(3): 836-846. doi: 10.1038/s41396-018-0313-8.
2. Qadir M., Quillerou E., NangiaV., Murtaza G., Singh M., Thomas R.J., etal. (2014). Economics of salt-induced land degradation and restoration. Nat. Resour. Forum 38, 282–295. doi:10.1111/1477-8947.12054.
3. Liu B., Hu Y., Wang Y., Xue H., Li Z. and Li M. (2022). Effects of saline-alkalistress on bacterial and fungal community diversity in *Leymus chinensis* rhizosphere soil. Environ. Sci. Pollut. Res. Int. 29, 70000–70013. doi: 10.1007/s11356-022-20270-6.
4. Shan S., Wei Z., Cheng W., Du D., Zheng D. and Ma G. (2023) Biofertilizer based on halotolerant microorganisms promotes the growth of riceplants and alleviates the effects of saline stress. Front. Microbiol. 14:1165631. doi: 10.3389/fmicb.2023.1165631.
5. Rath K.M., Fierer N., Murphy D.V., Rousk J. Linking bacterial community composition to soil salinity along environmental gradients. ISME J.2019; 13: 836–846.
6. Dang C., Morrissey E.M., Neubauer S.C., Franklin R.B. Novel microbial community composition and carbon biogeochemistry emerge over time following saltwater intrusion in wetlands. GlobalChangeBiol. 2019; 25: 549–561.
7. Zvyagintsev D.G. (1991). Methods of soil microbiology and biochemistry. Moscow, 365 p.
8. Wang M., Chen S., Chen L., and Wang D. (2019a). Responses of soil microbial communities and their network in teractions to saline-alkaline stress in Cd-contaminated soils. Environ. Pollut. 252, 1609–1621. doi:10.1016/j.envpol.2019.06.082.
9. Zhou Y., Hao L., Ji C., Zhou Q., Song X., Liu Y., et al. (2021). The effect of salt-tolerantant agonistic bacteria CZ-6 on the rhizosphere microbial community of winter jujube (*Ziziphus jujubamill*.“Dongzao”) in saline-alkaliland. Biomed Res. Int. 2021, 5171086. doi:10.1155/2021/5171086.