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MICROBIAL SUCCESSION OF SALINE IRRIGATED SOILS OF THE DJIZAKH STEPPE OF UZBEKISTAN

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ABSTRACT:

Microbial succession of Djizakh steppe soils under salinization was studied. It was revealed that microorganism's development in the soils of various salinization levels occurs unequally and depends on the salinization level and season. The dominance of ammonification agents and ray fungi was revealed. The cellulose-fermenting bacteria content in the soils varies dramatically depending on the salinization level. The middle- and highly-saline soils were notable for low content of the nitrifying microorganisms. The microorganism's generic composition in the irrigated soils with various salinization levels was studied.

Keywords: salinization, soil, microbial succession, seasons, ammonifires, nitrifires, denitrifiers

[1] INTRODUCTION

The soils salinization is an essential environmental factor influencing soil microorganism's development. The over-content of water-soluble salts is the limiting factor of soil fertility, which reduces the crops harvest and activity of the microorganisms.

The microorganisms are rather sensitive to the slightest change of medium conditions. The matters of soils succession microflora and their biological activity remain debatable [9].

For understanding of the microorganisms functioning, all researches are to be carried out interactively. It concerns both the determination of microorganisms quantity and qualitative composition, recovery of the physiologically active agents microbes-producers and the soils fermentation activity. Many parameters of the soils biological activity are so dynamical that their disposable determination misleads only [7].

The comprehension that microorganism's population is not a simple amount of cells, but the unique over-organism system similar to multicellular organism, however, not identical to the latter in the certain relation has grown recently. Such systems feature is the separate cells interaction (cooperation), where their coordinated activity is directed on achievement of the same result [14].

For most trustworthy information, we set the goal to reveal the regular and systematic change of the microorganisms quantity and quality under saline stress in the soil – microorganisms system.

[II] MATERIAL AND METHODS

The researches had been carried out in the irrigated soils of the Djizakh steppe in 2008-2011 yy.

The soils samples were taken seasonally on horizons. For analyses, the samples selected from three replications were used. For estimation of content of the microorganisms ecological-trophic groups the standard methods were applied [2, 3, 4, 5, 6, 7]. The soils

microbiological analyses were conducted in the dynamics of spring-summer-autumn. Microbial communities quantitative count on the basic rank groups was made under the standard soil microbiology methods of limiting dilutions by inoculating the soil suspension into the elective nutrient mediums [1, 9, 10, 11, 15, 16, 18].

The ammonification agents were counted on MPA, the oligonitrophils and aerobic nitrogen-fixing microorganisms – on the anazotic medium of Rushman, the 1st phase nitrifying microorganisms - on the medium of Soriano and Walker, the 2 nd phase nitrifying microorganisms - on the medium of Watson and Wotbery, the denitrifiers - on the medium of Guiltay, and the aerobic cellulose-fermenting microorganisms - on the medium of Getchinson and Clayton. The quantity of soil microorganisms physiological groups considered on liquid nutrient mediums was determined according to the table of Mac-Credy. The recalculation of microorganisms amount was made on 1 g. of abs. dry soil. Statistical data processing was carried out by means of software package Microsoft Exel-2003.

[III] RESULTS AND DISCUSSION

The microbial successions research demands determination of several revealing parameters of population changes. On the assumption of above-stated, we chose the poic-sierozem **[Figure-1]**, sierozem-poic **[Figure-2]**, paludal-poic **[Figure-3]**, and poic soils **[Figure-4]** with mild, middle, and high salinization level.

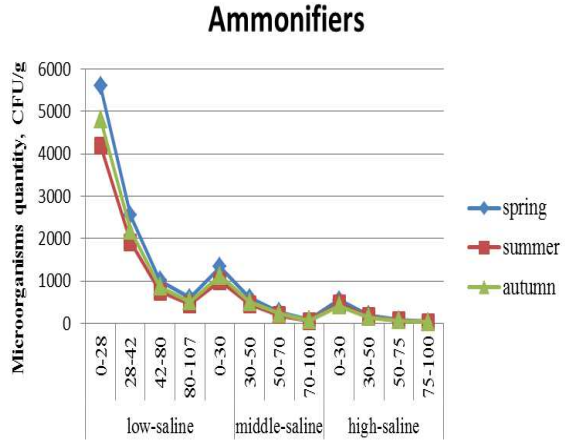
On the basis of quantitative analyses was revealed that microorganisms development in the soils of various salinization level occurs unequally and depends on salinization level and season.

In non saline soils, the microorganism's quantity growing on MPA reached the maximum quantities in comparison with other soils.

In all tested samples of soils, the quantity of ammonification agents predominated over the amount of microorganisms consuming mineral nitrogen forms, which indicated to weak mineralization process. Concerning the number of aforesaid, there followed the ray fungi, nitrifying microorganisms, nitrogen-fixing microorganisms, denitrifiers, and aerobic nitrogen-fixing and butyric-acid bacteria and fungi. The content of cellulose-fermenting bacteria in the tested soils samples varied dramatically depending on the salinization level.

It is known that saprophytic microorganisms ability to live is closely related to organic matter.

Under the similar count, where the humus content in the upper horizon of irrigated meadow soils is from 0, 96 to 1, 10%, in the meadow - gray soils - from 0.73 to 2.60%, in the gray- meadow soils - from 0.88 to 1.13%, and in paludal-poic soils to 0.80%, the quantity and composition of microorganisms accordingly changed.



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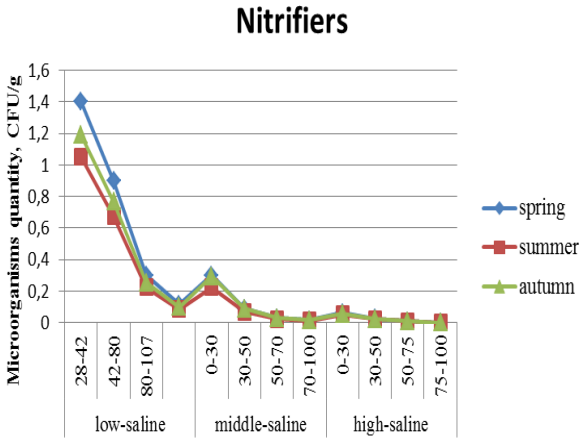

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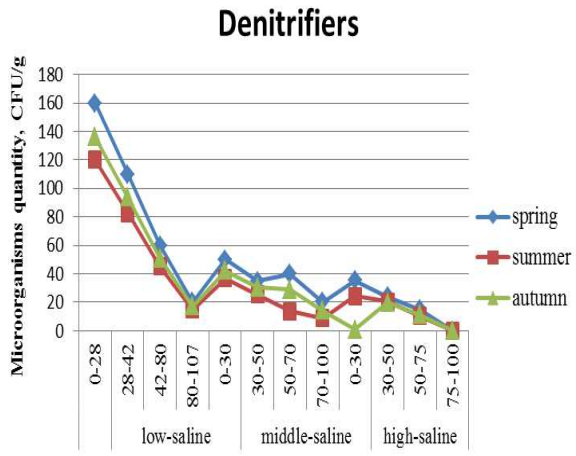

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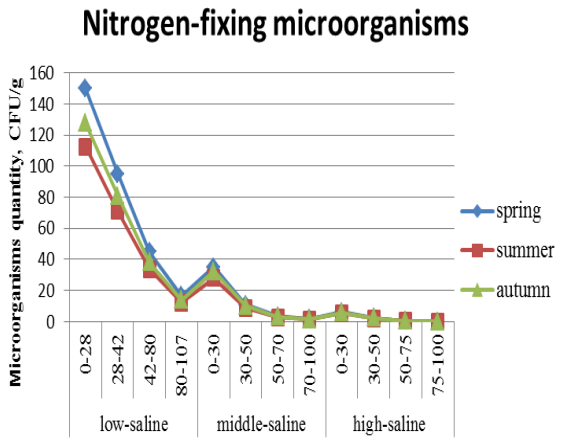

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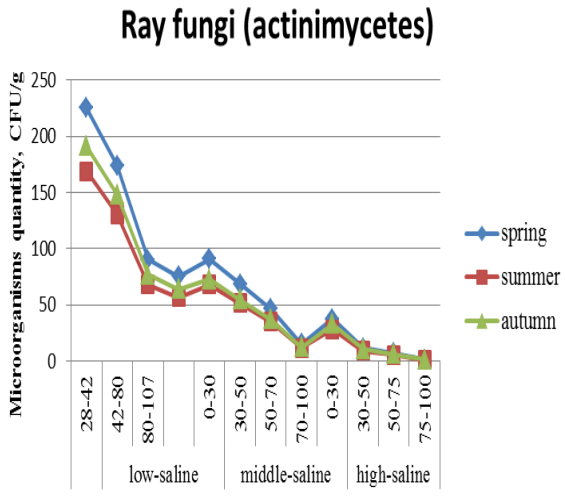

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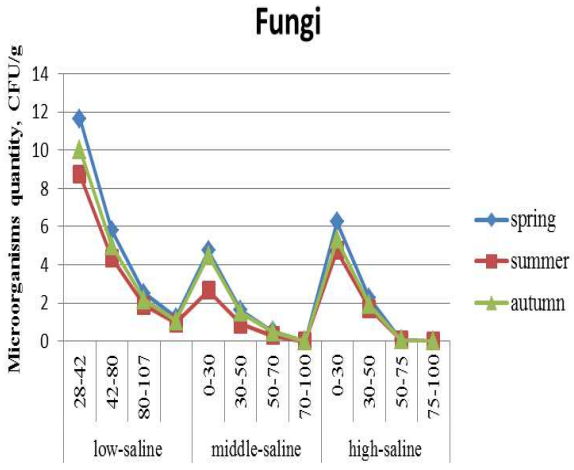

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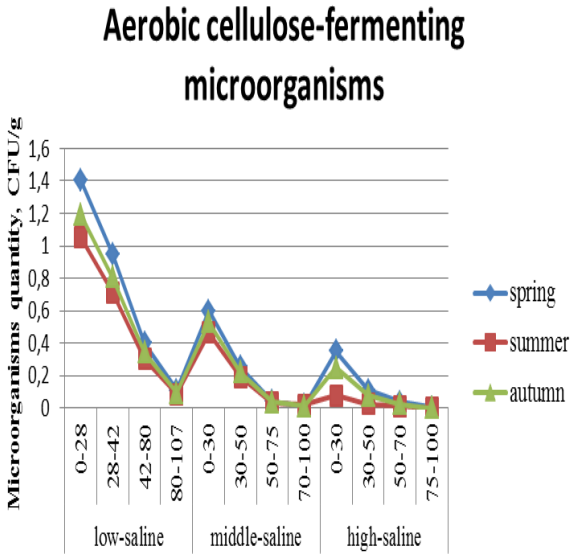

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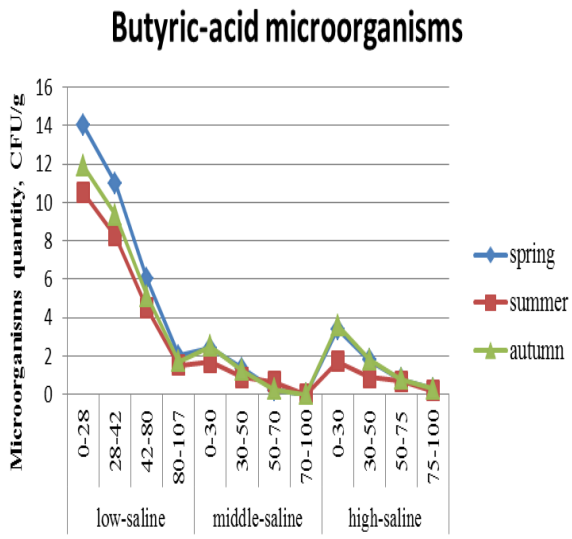

(h)

Fig: 1. Microbial succession of the irrigated poic-sierozem soils of the Djizakh steppe depending on salinization level.

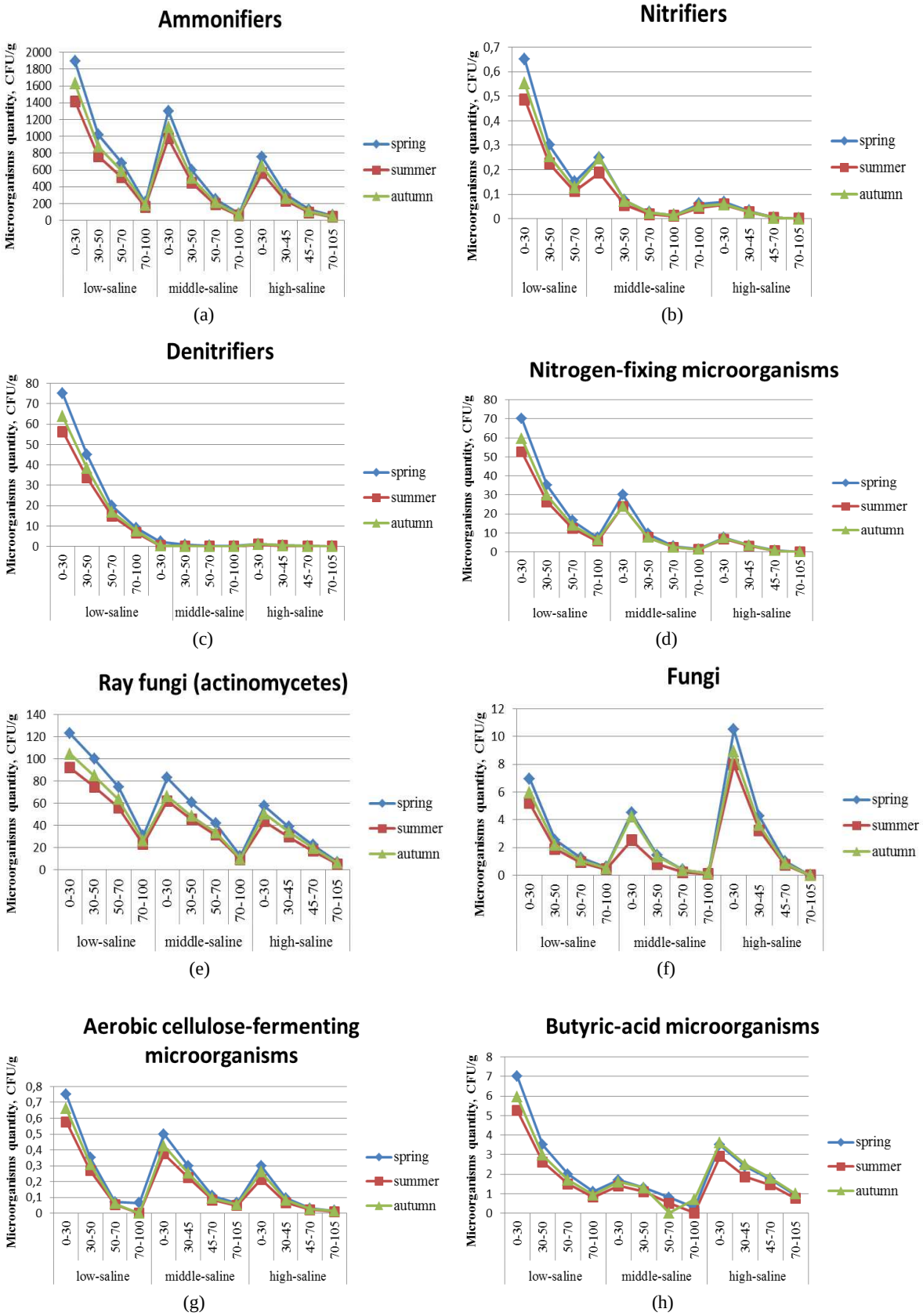

Fig: 2. Microbial succession of microorganisms of the irrigated sierozem-poic soils of the Djizakh steppe depending on salinization level.

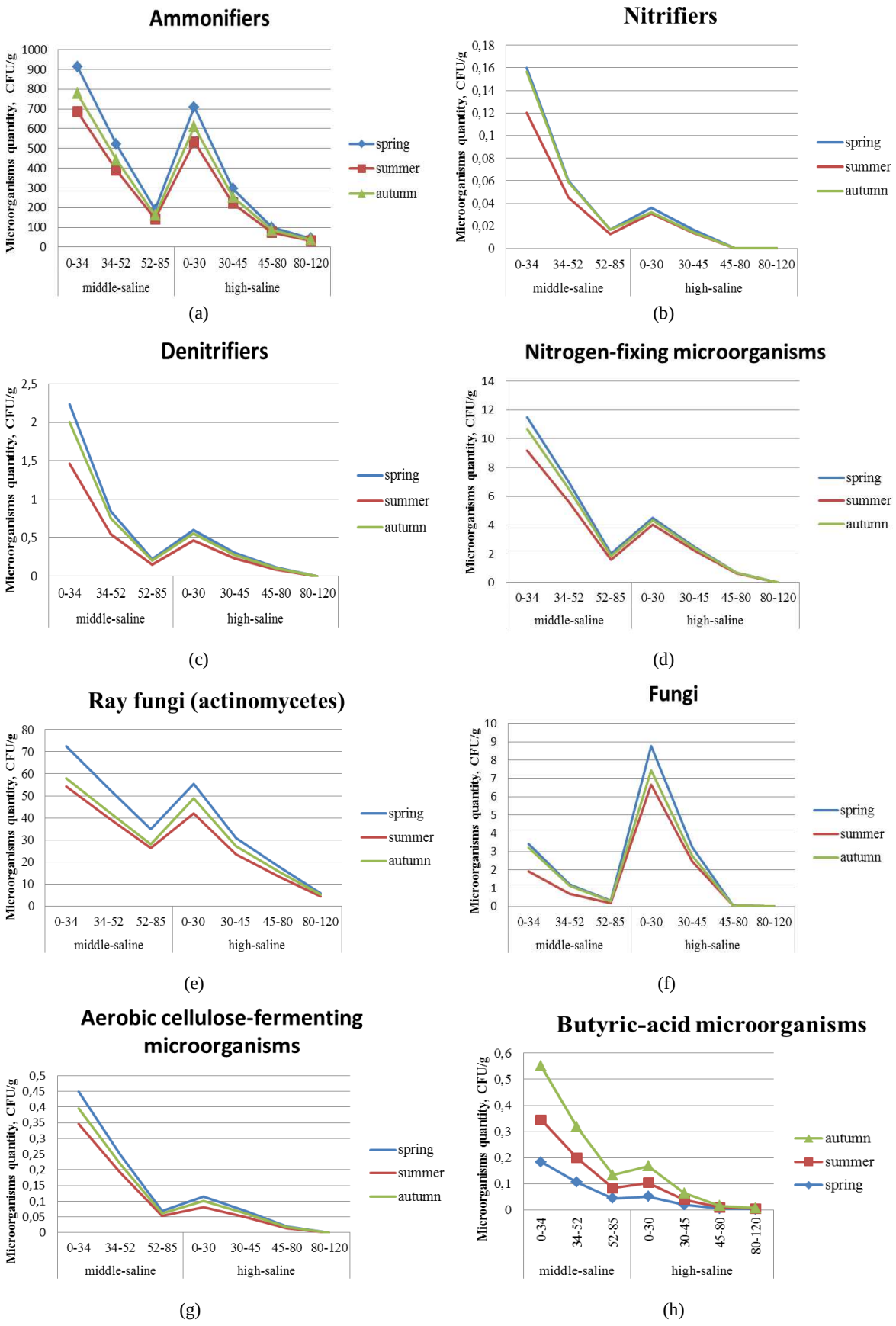

Fig: 3. Microbial succession of the irrigated paludal-poic soils of the Djizakh steppe depending on salinization level.

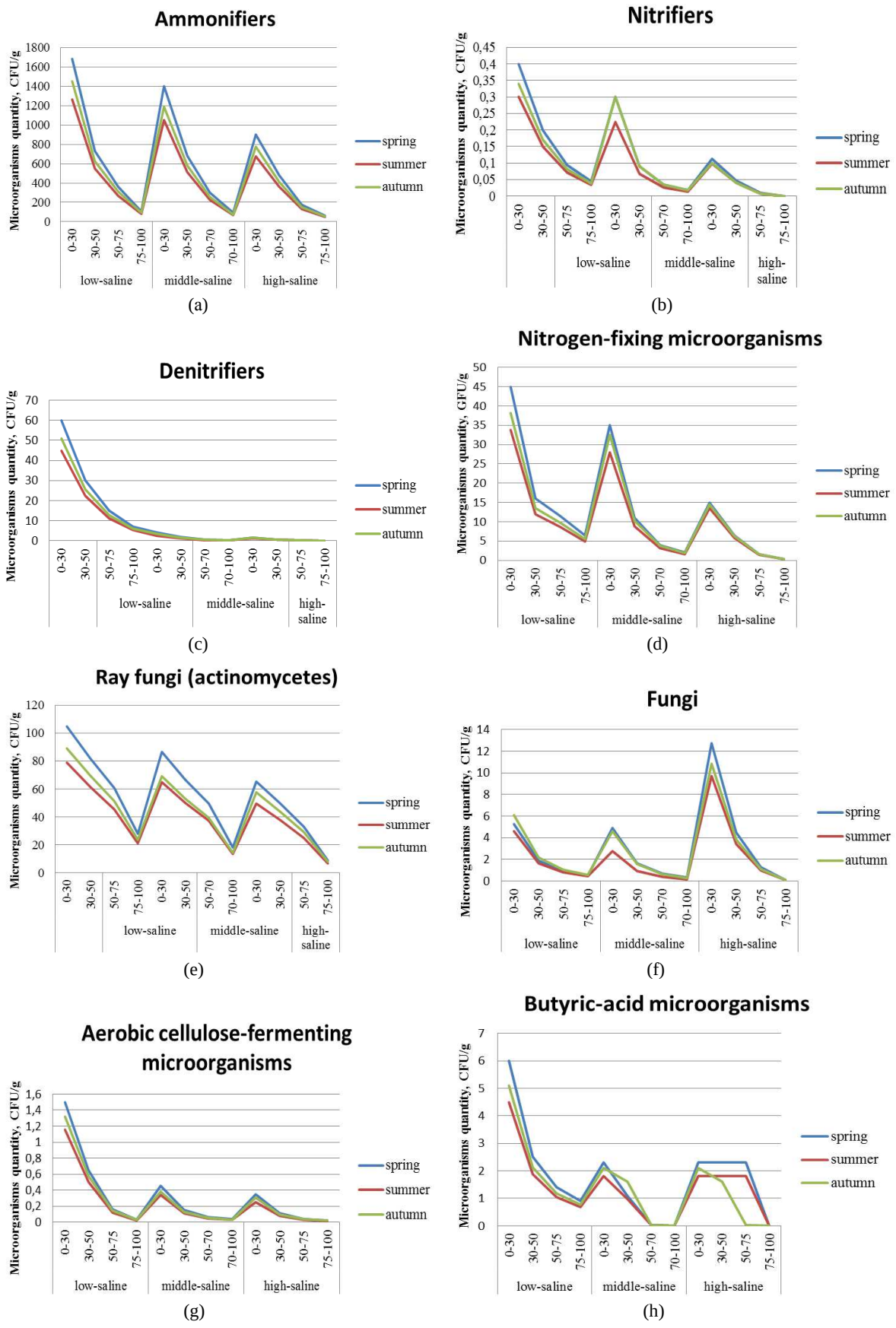

Fig: 4. Microbial succession of the irrigated poic soils of the Djizakh steppe depending on salinization level.

As the irrigated paludal-poic soils developed in the lowered relief parts of soil, they formed heavy texture soils more often. As a result of researches, it was revealed that they are poor of humus; therefore, the ammonification microorganism's content was low in the upper horizon, whereas, the nitrifying, denitrifying, and aerobic cellulose-fermenting microorganisms were not revealed in the bottom soil horizons.

For all researched soils, the total amount of microorganisms reduced on the soil profile, which, probably, was connected with the aerations deterioration and insufficiency of nutrients, as well as the water-soluble salts toxic effect near to the ground waters. Any toxic agent's accumulation in the soil leads to lowering of the microorganism's growth energy, as well as the lack of any nutrients makes the soil not suitable for their development [12].

As there are always much more easily accessible organic substances in the soil (undecomposed stubble remains of previous year, etc.) in the spring, microorganisms strengthen the mineralizing activity just in the spring. Their gradual consumption by the summer and parallel accumulation of the antibiotic substances in the soil leads to lowering of the activity in the summer as well. New arrival of the organic substances in the autumn and inactivation of antimicrobial substances within the summer leads to activation of the microbiological processes in the autumn again. This way, probably, there is a change of more active periods of microorganisms growth to less active ones, finally, the basis for seasonal prevalence of the microbiological processes in the soil, which is necessary to be considered at practical conditions of agricultural production.

As a result of analyses, the plentiful growing of bacteria on Eshbi agar, from the earliest development phases and in the radical plant's zones, was noticed.

Such quantity of oligonitrophiles in the plants rhizosphere and their selectivity by the roots can serve as an indicator of their certain role in the nitric plants balance [13]. In addition, the phenomenon can be explained by the microorganism's ability to adapt to the medium. The high enough concentration of salts in the soil can stand those microorganisms, in which protoplasm occurs the reserve substances hydrolysis and emission of the osmotic active agents depressing the creation of more raised salts content in cells.

In the summer, some decrease of the microorganisms quantity in the poor-saline soils is observed in comparison with the spring period and in the autumn again lifting, which is especially well traced at counting of bacteria growing on MPA.

In the poor-saline soils, the ammonification microorganisms and ray fungi were dominating physiological groups **[Table-1].**

In the middle-saline soils, the amount of ammonification and cellulose-fermenting microorganism's reduction was noted. In comparison with the poor-saline soil, the quantity of nitrogen-fixing microorganisms did not change sharply.

Basically met types of microorganisms	Degree of soil salinity		
	Poor-saline soils	Middle-saline soils	Highly-saline soils
Arthrobacter	++	+	+
Azotobacter	++	++	+
Bacillus	++	++	++
Chromobacterium	-	-	+
Micrococcus	+	+	-
Pseudomonas	++	++	+
Rhodococcus	++	++	++
Myxococcus	+	-	-
Sarcina	+	++	++
Spirosarcina	+	++	++
Sterptomyces	++	++	++
Penicillium	+	+	-
Xantomonas	++	+	-
Flavobacterium	++	+	+
Aspergillus	++	+	+
Clostridium	+	+	++
Botritiscinereae	++	+	++
Verticillium	++	+	++
Fusarium	++	+	++

Note: ++ - dominating types, + often met types. – not revealed.

Table: 1. Microbial communities in saline soils of the Djizakh steppe

The middle- and highly-saline soils differed by the low nitrifying microorganisms content.

Proceeding from the literary data, it is known that nitrifying bacteria are sensitive to the environment, their cells are easily penetrated by toxic substances, and they use only up to 9% of the energy emitted at the ammonification oxidative processes. They quickly react to change of the soil medium reaction. This feature can be consider as salted soils indicator [17].

The researchers showed that, in the highly-saline soils of the arable soil layer, was revealed reduce of bacteria growing on MPA up to 1.4 times, fungi – up to 2 times, nitrifying microorganisms – up to 3.18 times, denitrifiers – up to 2.8 times, nitrogen-fixing microorganisms – up to 2.6 times, aerobic cellulose-fermenting microorganisms – up to 3.5, and butyric-acid bacteria – up to 2 times less than in the poor-saline soils.

Under the high content of chlorine and sulphate ions, first of all, the cellulose-fermenting, nitrifying, and denitrifying microorganisms were depressed. The fungi and butyric-acid bacteria were stable therein.

Within the seasons, among the cellulose-fermenting groups in the spring and the nitrifying microorganisms considerable growth in the autumn, by the vegetation period's end, was observed.

On the basis of carried out experiments, it can be noted that salinization influenced various physiological groups and complexes of microorganisms unequally. Within the seasons, some groups gave way to another.

[IV] CONCLUSION

Under the irrigated zones conditions of Djizakh steppe, the non-uniform distribution of microorganisms on the soil horizons and salinization level was noticed. Among the physiological groups, the ammonification microorganisms and ray fungi were of the greatest amount. Within the seasonal dynamics, the microorganism's maximum was revealed in the spring that can be related to the optimal soil conditions for microorganisms growth. The salinization influenced negatively the nitrifying microorganisms growth and activity. With increasing of salts concentration, the microorganisms type composition differed as well; in the soils which combined temperature and humidity, the microorganisms consuming nitrate nitrogen gave way to the microorganisms using the ammoniates nitrogen.

Proceeding, from the above-stated data, it follows that microorganisms adapted to the soils ecological conditions are peculiar to the certain soil conditions.

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