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DETERMINATION OF MICROBIAL DIVERSITY OF INDIGENOUS MICROFLORA OF SOIL SAMPLES CONTAMINATED WITH XENOBIOTICS AND STUDY OF THEIR MICROBIOLOGICAL PROPERTIES

The microbial community that determines the biochemical properties of the soil is a set of living organisms of different species that form a certain ecological and trophic unit. Of all the biotic components of the ecosystem, the microbial community is the most sensitive to changes in environmental conditions that occur during agricultural development of ecosystems, as well as to the presence of other forms of anthropogenic impact, including pollutants. The complexity and diversity of the relationships of various microorganisms with each other and with plants, as well as with other components of the agrobiocenosis, determine the phytosanitary state of the soil and its stability as an integral system.

The aim of the work is to determine the microbial diversity of the native microflora of soil samples contaminated with xenobiotics and to study their biological properties, as well as screening for promising microorganisms. Study of the microbial diversity of the local microflora of soil samples contaminated with xenobiotics in the Turkestan and Kyzylorda regions.

Xenobiotics, getting into the soil, directly or indirectly affect microbial communities. According to modern concepts, microbiological monitoring is a priority area of environmental quality control. Currently, the most developed methods for assessing the impact of pollutants are based on the study of the structural reorganization of communities and the consideration of various groups of microorganisms. In this regard, the work studied the microbial diversity of soils contaminated with xenobiotics in the Turkestan and Kyzylorda regions, and selected promising microorganisms.

Keywords: xenobiotics, microorganisms, screening, destructor, diversity.

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Ксенобиотиктермен ластанған топырақ үлгілерінің жергілікті микрофлорасының микробтық әртүрлілігін анықтау және олардың микробиологиялық қасиеттерін зерттеу

Топырақтың биохимиялық қасиеттерін анықтайтын микробтық қауымдастық – белгілі бір эко-трофикалық бірлікті құрайтын әр түрлі түрдегі бірге тіршілік ететін организмдердің жиынтығы. Экожүйенің барлық биотикалық құрамдас бөліктерінің ішінде микробтық қауымдастық экожүйелердің ауылшаруашылық дамуы кезінде болатын экологиялық жағдайдың өзгеруіне және антропогендік әсердің басқа нысандарының, соның ішінде ластаушы заттардың

барынша сезімтал. Әртүрлі микроорганизмдердің бір-бірімен және өсімдікпен, сондай-ақ агробиоценоздың басқа компоненттерімен қарым-қатынастарының күрделілігі мен әртүрлілігі топырақтың фитосанитарлық жағдайын және тұтас жүйе ретінде оның тұрақтылығын анықтайды.

Жұмыстың мақсаты – ксенобиотиктермен ластанған топырақ үлгілерінің аборигенді микрофлорасының микробтық әртүрлілігін анықтау және олардың биологиялық қасиеттерін зерттеу, перспективалы микроорганизмдерді скринингтен өткізу. Түркістан және Қызылорда облысындағы ксенобиотиктермен ластанған топырақ үлгілерінің жергілікті микрофлорасының микробтық алуан түрлілігін зерттеу.

Топыраққа түсетін ксенобиотиктер микробтық қауымдастықтарға тікелей немесе жанама әсер етеді. Заманауи тұжырымдамаларға сәйкес микробиологиялық мониторинг қоршаған орта сапасын бақылаудың басым бағыты болып табылады. Қазіргі уақытта ластаушы заттардың әсерін бағалаудың ең жақсы дамыған әдістері қауымдастықтардың құрылымдық қайта құрылуын зерттеуге және микроорганизмдердің әртүрлі топтарын есепке алуға негізделген. Осыған байланысты жұмыста Түркістан және Қызылорда облыстарындағы ксенобиотиктермен ластанған топырақтарының микробтық алуан түрлілігі зерттеліп, перспективті микроорганизмдер іріктеліп алынды.

Түйін сөздер: ксенобиотиктер, микроорганизм, скрининг, деструктор.

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Определение микробного разнообразия аборигенной микрофлоры образцов почв, загрязненных ксенобиотиками, и изучение их микробиологических свойств

Микробное сообщество, определяющее биохимические свойства почвы, представляет собой совокупность живых организмов разных видов, образующих определенную эколого-трофическую единицу. Из всех биотических компонентов экосистемы микробное сообщество наиболее чувствительно к изменениям условий окружающей среды, происходящим в процессе сельскохозяйственного освоения экосистем, а также к наличию других форм антропогенного воздействия, в том числе загрязняющих веществ. Сложность и многообразие взаимоотношений различных микроорганизмов между собой и с растениями, а также с другими компонентами агробиоценоза определяют фитосанитарное состояние почвы и ее устойчивость как целостной системы.

Целью работы является определение микробного разнообразия аборигенной микрофлоры образцов почв, загрязненных ксенобиотиками, и изучение их биологических свойств, а также скрининг перспективных микроорганизмов. Изучение микробного разнообразия локальной микрофлоры образцов почв, загрязненных ксенобиотиками в Туркестанской и Кызылординской областях.

Ксенобиотики, попадая в почву, напрямую или косвенно влияют на микробные сообщества. Согласно современным представлениям микробиологический мониторинг является приоритетным направлением контроля качества окружающей среды. В настоящее время наиболее разработаны методы оценки воздействия загрязняющих веществ, основанные на изучении структурной перестройки сообществ и учете различных групп микроорганизмов. В связи с этим в работе изучено микробное разнообразие почв, загрязненных ксенобиотиками в Туркестанской и Кызылординской областях, и отобраны перспективные микроорганизмы.

Ключевые слова: ксенобиотики, микроорганизмы, скрининг, деструктор, разнообразие.

Introduction

Humans and their environment, as well as the nation's health, have always been a priority for the state. Human health depends 12% on the healthcare system, 18% on genetic predisposition, and as much as 70% on lifestyle, including environmental conditions and nutrition. Environmental pollution contributes to an increase in genetic burden and mutation rates within human populations. This is evidenced by the rising incidence of congenital abnormalities, hereditary and multifactorial diseases, particularly in environmentally disadvantaged areas.

In daily life, humans come into contact with numerous chemical substances, extensively used in industry, agriculture, medicine, and households. Experimental studies show that many of these chemical compounds exhibit mutagenic activity. Food products derived from plants and animals may also be contaminated by chemicals used in agriculture for pest and disease control [1].

The industrialization of agriculture has increased the chemical load on natural ecosystems. Intensive chemicalization in agriculture boosts productivity but simultaneously leads to environmental contamination with xenobiotics, pesticides, and other chemical compounds.

Pesticides are widely used in agriculture, as they prevent up to 40% of crop losses. However, poor storage practices and the application of up to 95% of pesticides in ways that fail to target the intended organisms result in significant environmental harm. Misuse of pesticides without considering the natural and climatic features of treated areas or adhering to safety regulations raises serious issues, such as declining biodiversity, wildlife and livestock deaths, poisoning, disruption of natural pest control mechanisms, accumulation of obsolete and unusable chemical substances that pose hazardous environmental risks, contamination of food and feed with pesticide residues, and pollution of surface and groundwater. Contaminated food, feed, and drinking water are the primary sources of pesticide exposure to humans.

Among chemical pollutants in the environment, persistent organic pollutants (POPs) are particularly dangerous [2]. Recently, POPs have become a pressing global environmental issue. POPs are chemical substances containing chlorine, carbon, and hydrogen. These compounds degrade slowly and accumulate in living organisms. POPs are often transported over long distances via air, water, and migratory species, such as insects, birds, and warm-blooded animals. Even in small amounts, POPs pose a threat to humans and nature. They dissolve poorly in water but readily in fats, allowing them to accumulate in the fatty tissues of living organisms. Their concentrations can increase thousands or even tens of thousands of times through food chains [3-4].

In 2001, the Ministry of Natural Resources and Environmental Protection of the Republic of Kazakhstan, together with UNEP Chemicals, conducted a preliminary inventory of obsolete and unnecessary pesticides under a Memorandum of Understanding dated January 8, 2001. A report was prepared, providing information on the inventory of unused pesticide stocks (including POP pesticides) and an analysis of data collected from the official statistics of the Republic of Kazakhstan's Agency for Health Affairs and the Republican Sanitary and Epidemiological Station. With the support of the Central Asia Regional Environmental Center, the project of the "Greenwomen" Environmental News Agency (Kazakhstan) was implemented [5].

Soil salinization, particularly in semi-arid regions, has become a global issue. It is a major factor reducing agricultural productivity worldwide.

Materials and methods

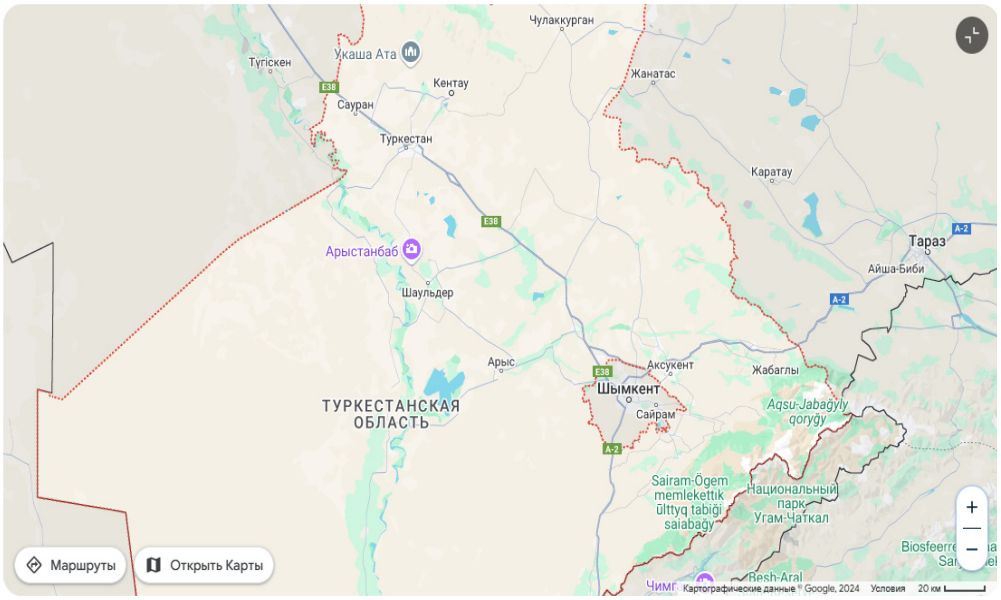
Study of soil samples

We conducted research to study the microbial diversity of soil samples in the Turkestan and Kyzylorda region (Figure 1), contaminated with xenobiotics (pesticides) (test samples) and background territory (control samples).

Collection and preparation of samples for microbiological analysis

To collect samples, use clean, sterile glass vials with tightly closing rubber stoppers and thick paper caps.

Soil samples are collected on each of the areas studied at five points diagonally or along an "envelope" (four points at the corners and one in the center). To prepare an average sample of 0.5 kg, the soil of all samples of one area is poured onto a sterile thick sheet of paper and the soil is thoroughly mixed in a jar. The size of the collected soil samples is dictated by the degree of its contamination and the planned work. Before sowing, the soil is dispersed.



a

b

Figure 1 – Soil sampling points in the Turkestan and Kyzylorda region
(a – Turkestan region, b – Kyzylorda region)

Methods for studying the microbial diversity of environmental objects in areas contaminated with xenobiotics

The determination of the number of different groups of soil microorganisms to identify physiological groups resistant to the pollutant and to compare the microbiological composition of the soil microflora was carried out using the method of successive dilutions of the soil suspension on dense nutrient media.The number of cells was determined using the Koch method. The essence of the method is to sow a certain volume of the studied suspension of microorganisms on a dense medium in Petri dishes and count the colonies that have grown after incubation. The sowing is carried out on agarized media in Petri dishes. To determine the total number of microorganisms, meat-peptone agar (MPA) is used, to determine the content of fungi in the soil – wort

agar (WA), to determine the number of different physiological groups of microorganisms, the corresponding nutrient media are used. Mold fungi were counted on the agarized Czapek-Dox medium, ammonifying bacteria were detected on GRM-agar, nitrogen-fixing bacteria – on Ashby medium, aerobic cellulolytic bacteria were counted on the dense nutrient medium of Hutchinson and Clayton.

The crops were cultivated in a thermostat at 28°C for 2 days when isolating heterotrophic bacteria, 5-7 days when isolating actinomycetes, nitrogen-fixing and mold fungi, and 7-9 days when isolating cellulolytic bacteria. After incubation of the crops, a quantitative count of the grown colonies was carried out and the number of colony-forming units (CFU) in 1 g of soil was determined.

Determination of the titer of colony-forming units of microorganisms

The determination of the number of different groups of soil microorganisms to identify physiological groups resistant to the pollutant and to compare the microbiological composition of the soil microflora was carried out by the method of successive dilutions of the soil suspension on dense nutrient media. Fortiter distribution in samplescolony forming units of microorganismswere carried out using the Koch method. The essence of the method consists of seeding a certain volume of the studied suspension of microorganisms on a dense medium in Petri dishes and counting the colonies that have grown after incubation. The seeding is carried out on agar media in Petri dishes. After incubation of the seedings, a quantitative count of the grown colonies was carried out and the number of colony-forming units (CFU) in 1 g of the sample was determined.

Methods for isolating pure cultures from soil samples. Pure cultures were obtained by mechanical separation on the surface of a dense nutrient medium (the streak method with loop burning) [7]. Individual colonies were checked for purity by microscopy and were seeded onto slanted nutrient agar for cultivation.

Methods for determining the morphological-cultural and physiological-biochemical properties of isolated pure cultures of microorganisms

The study of morphological, physiological and biochemical characteristics of bacteria was carried out using generally accepted methods. The morphological and cultural properties of the isolated pure cultures of microorganisms were studied according to the following characteristics: cell shape and arrangement, cell size, cell motility, presence of endospores, Gram staining, colony description on solid nutrient media, growth pattern in liquid nutrient medium, growth pattern on slant agar. Physiological and biochemical properties of bacteria and yeast were determined according to the following characteristics: bacterial growth at 420C, hydrolysis of gelatin, starch, casein, presence of catalase and use

Pure cultures were obtained by mechanical separation on the surface of a dense nutrient medium (the streak method with loop burning). Individual colonies were checked for purity by microscopy and were seeded onto slanted nutrient agar for cultivation. For isolation, heterotrophic bacteria were cultured for 2-3 days, actinomycetes, nitrogen-fixing bacteria and mold fungi for 7-9 days.

Methods for screening microorganisms of chemical pollutants (xenobiotics)

A wide range of pesticide-resistant microorganisms and their high level of biodegradation capabilities make these organisms promising biotechnological objects for cleaning the environment from pesticides. Soil microorganisms react extremely actively to chemical components of the environment. Screening of sensitive and tolerant microorganisms allows selecting optimal test organisms and bioindicator organisms for pesticide contamination of soil[8].

To search for microorganisms, we used strains from dominant bacterial populations. For this purpose, all isolated strains were seeded on Petri dishes with M9 agar medium (composition, g/l: Na_2HPO_4 – 6.0; KH_2PO_4 – 3.0; NaCl – 0.5;NH_4CL – 1.0; distilled water 1000 ml, 2% starvation agar) with the addition of a pesticide as a carbon source. The strains were cultured for 5 days at 28 °C [9].

Results and discussion

Determination of microbial diversity of local microflora of xenobiotic-contaminated soil samples and study of their biological properties

Isolation of local microorganisms from contaminated soil samples, study of biological properties of isolated microorganisms

Humans and their environment, as well as the nation's health, have always been a priority for the state. Human health depends 12% on the healthcare system, 18% on genetic predisposition, and as much as 70% on lifestyle, including environmental conditions and nutrition. Environmental pollution contributes to an increase in genetic burden and mutation rates within human populations. This is evidenced by the rising incidence of congenital abnormalities,

hereditary and multifactorial diseases, particularly in environmentally disadvantaged areas.

In daily life, humans come into contact with numerous chemical substances, extensively used in industry, agriculture, medicine, and households. Experimental studies show that many of these chemical compounds exhibit mutagenic activity. Food products derived from plants and animals may also be contaminated by chemicals used in agriculture for pest and disease control [209].

The industrialization of agriculture has increased the chemical load on natural ecosystems. Intensive chemicalization in agriculture boosts productivity but simultaneously leads to environmental contamination with xenobiotics, pesticides, and other chemical compounds.

Pesticides are widely used in agriculture, as they prevent up to 40% of crop losses. However, poor storage practices and the application of up to 95% of pesticides in ways that fail to target the intended organisms result in significant environmental harm. Misuse of pesticides without considering the natural and climatic features of treated areas or adhering to safety regulations raises serious issues, such as declining biodiversity, wildlife and livestock deaths, poisoning, disruption of natural pest control mechanisms, accumulation of obsolete and unusable chemical substances that pose hazardous environmental risks, contamination of food and feed with pesticide residues, and pollution of surface and groundwater. Contaminated food, feed, and drinking water are the primary sources of pesticide exposure to humans.

Among chemical pollutants in the environment, persistent organic pollutants (POPs) are particularly dangerous [10]. Recently, POPs have become a pressing global environmental issue. POPs are chemical substances containing chlorine, carbon, and hydrogen. These compounds degrade slowly and accumulate in living organisms. POPs are often transported over long distances via air, water, and migratory species, such as insects, birds, and warm-blooded animals. Even in small amounts, POPs pose a threat to humans and nature. They dissolve poorly in water but readily in fats, allowing them to accumulate in the fatty tissues of living organisms. Their concentrations can increase thousands or even tens of thousands of times through food chains [11-212].

In 2001, the Ministry of Natural Resources and Environmental Protection of the Republic of Kazakhstan, together with UNEP Chemicals, conducted a preliminary inventory of obsolete and unnecessary pesticides under a Memorandum of Understanding dated January 8, 2001. A report was prepared, providing information on the inventory of unused pesticide stocks (including POP pesticides) and an analysis of data collected from the official statistics of the Republic of Kazakhstan's Agency for Health Affairs and the Republican Sanitary and Epidemiological Station. With the support of the Central Asia Regional Environmental Center, the project of the "Greenwomen" Environmental News Agency (Kazakhstan) was implemented [13].

Soil salinization, particularly in semi-arid regions, has become a global issue. It is a major factor reducing agricultural productivity worldwide.

Research results. The aim of the work is to determine the microbial diversity of the local microflora of soil samples contaminated with xenobiotics and to study their biological properties, to screen promising microorganisms.

To study the microbial diversity of the local microflora of soil samples contaminated with xenobiotics in the Turkestan and Kyzylorda regions.

The microbial community, which mainly determines the biochemical properties of the soil, is a set of coexisting organisms of different species that form a certain eco-trophic unit. Of all the biotic components of the ecosystem, the microbial community is the most sensitive to changes in the environmental conditions that occur during the agricultural development of ecosystems and the presence of other forms of anthropogenic impact, including pollutants. The complexity and diversity of the relationships of various microorganisms with each other and with plants, as well as with other components of the agrobiocenosis, determine the phytosanitary state of the soil and its stability as a whole system [14].

Xenobiotics entering the soil directly or indirectly affect microbial communities. According to modern concepts, microbiological monitoring is a priority direction of environmental quality control. Currently, the most developed methods for assessing the impact of pollutants are based on the study of the structural reorganization of communities and the accounting for various groups of microorganisms [15].

From an ecological point of view, soil is a complex heterogeneous system. Soil conditions affect the number and activity of microflora, and also determine the degree of manifestation of the toxic effect of pesticides.

In this regard, the work studied the microbial diversity of soils contaminated with xenobiotics in the Turkestan and Kyzylorda regions. The results of the study of microbial diversity in the studied soils are presented in Figure 2.

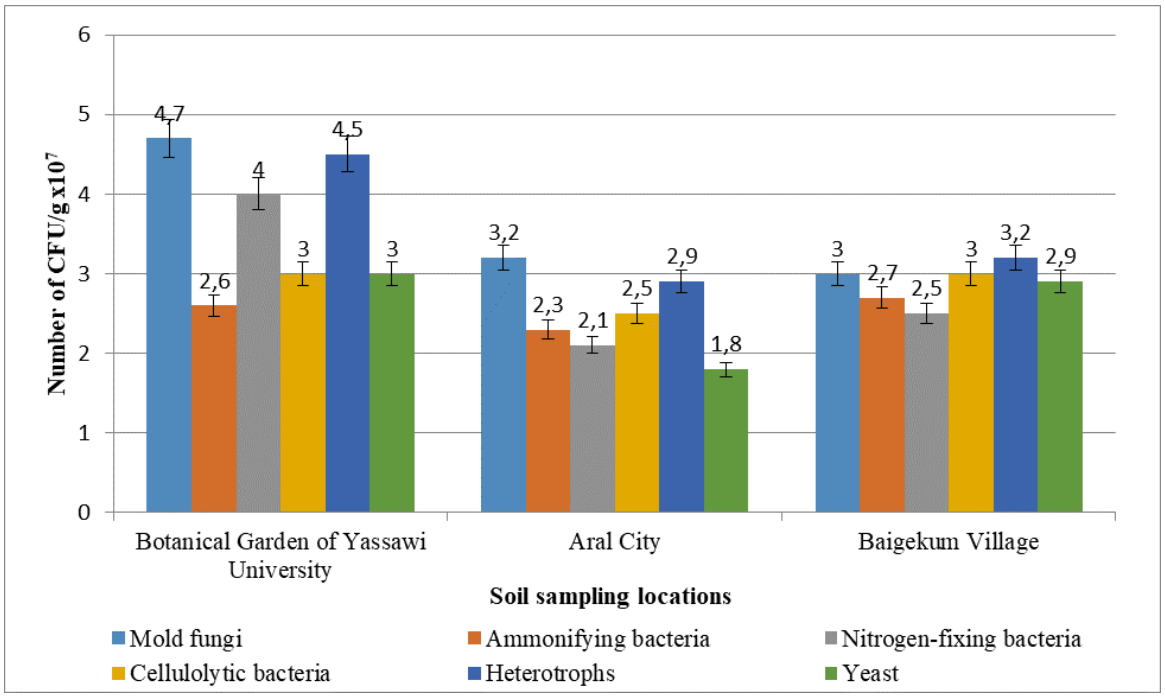


Figure 2 – Microbial diversity of soil samples from South Kazakhstan

Analysis of the microbiological composition of the soil showed that in the contaminated soil of the Turkestan regionthe dominant number of mold fungi is $3.2x10^7$ CFU/g, heterotrophs $2.9x10^7$ CFU/g, aerobic cellulolytic bacteria $2.5x10^7$ CFU/g, ammonifying bacteria $2.3x10^7$ CFU/g, also nitrogen-fixing bacteria $2.1x10^7$ CFU/g, yeast $1.8x10^7$ CFU/g.

The control sample was a soil sample not contaminated with xenobiotics. The total number of mesophilic aerobic and facultative anaerobic microorganisms (MAFAnM) is $1.7x10^2$-$6.9x10^2$ CFU/g. The quantitative indicators of nitrogen-fixing bacteria and microscopic yeasts in the contaminated soil did not differ significantly from the indicators of the control sample.

Thus, ppesticides actively affect the vital activity of both individual cells of microorganisms and soil microbiocenoses. In many ways, the nature of the action of pesticides is determined by their chemical nature and the uniqueness of soil microbiota. There are groups of extremely sensitive and very tolerant microorganisms. However, the toxic effect of pesticides, as a rule, is reversible. The degree of inhibitory effect and the rate of restoration of the original structure of microbiocenoses depend on the chemical composition, dose and stability of the xenobiotic in the environment. Changes in numbers under the influence of pesticides are confirmed by data from other researchers [215]. Also, during the work, the qualitative and quantitative composition of the microflora of the soil sample of the Turkestan region was studied. The results are presented in Figure 3.

As a result of the study of the qualitative and quantitative composition of the microflora of the soil sample of the Turkestan region, it was shown that the microflora is dominated by mold fungi (17-28%), ammonifying bacteria (15%), heterotrophic bacteria (17-18%), yeast (12-18%), and aerobic cellulolytic bacteria (20-27%). The decrease in mold fungi may be due to the presence of pesticides in the contaminated soil that inhibit their growth. Analysis of the number of microorganisms in contaminated soil showed that heterotrophic bacteria were the dominant group, so screening and selection of promising microorganisms was carried out in this group.

An important condition for further microbiological research was the necessary isolation of strains of dominant populations of microorganisms and the production of pure cultures to study their properties.

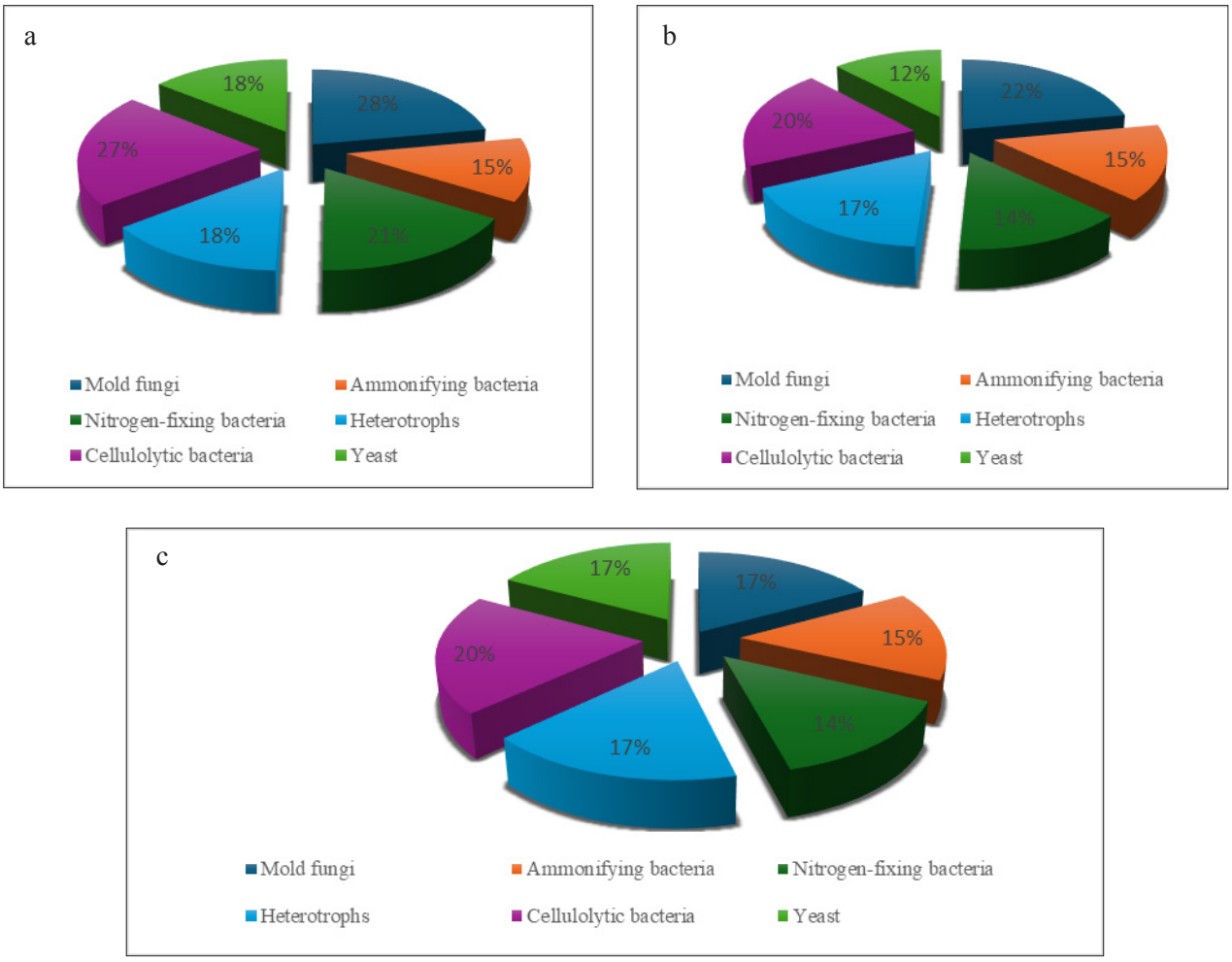


Figure 3 – Qualitative and quantitative composition of the microflora of a soil sample from the Turkestan region (a – Botanical Garden of Yassawi University, b – Aral city, c – Baigekum village)

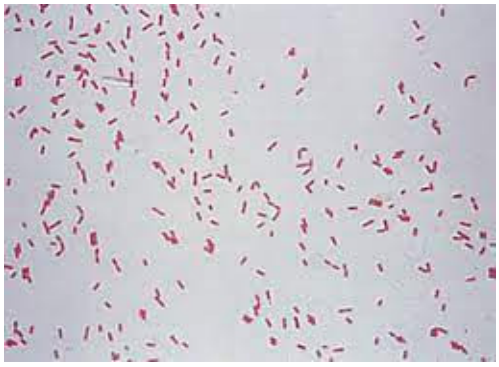
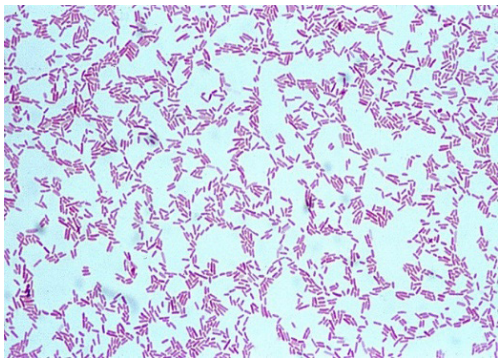
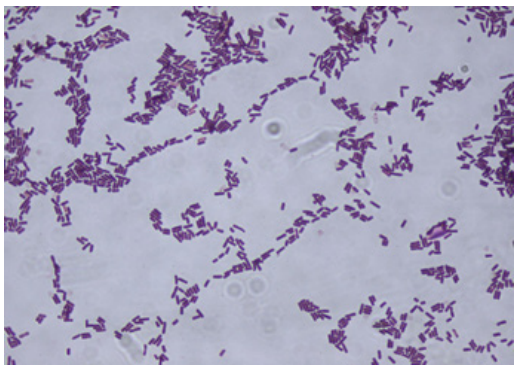
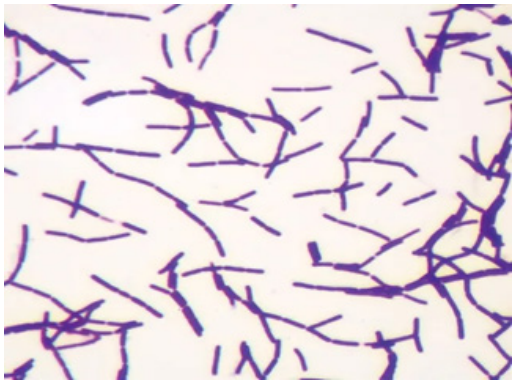
Biotechnological methods for preventing adverse factors for the biosphere are based on the use of microorganisms capable of biotransforming xenobiotic molecules, transforming pollutants into safe forms, and preventing the formation of secondary pollution products. Soil microorganisms play a major role in the decomposition of xenobiotics in the environment. Therefore, the current stage of research into the microbiological destruction of xenobiotics is characterized by interest in studying their physiological and biochemical properties [16].

In this regard, promising strains of microorganisms were isolated in experiments from soil samples contaminated with xenobiotics in the Turkestan and Kyzylorda regions. During the work, 4 strains were isolated for screening promising microorganisms isolated from soil samples containing chemical pollutants.

The description and identification of microorganisms was carried out by studying their cultural, morphological, tinctorial and biochemical properties [17].

The morphological-cultural and physiological-biochemical properties of isolated pure cultures of microorganisms were studied. Table 1 shows the morphological-cultural properties of microorganisms isolated from soil samples.

Table 1 – Morphological and cultural properties of microorganisms

Cell morphology	Morphological and cultural characteristics
1	2
 T1	Gram-negative, rod-shaped, motile bacteria, with straight rods and bipolar filaments, cell size 0.5-1.0 x 1.5 – 5.0 μm. On dense nutrient media, they form thin, shiny, hard, smooth-edged, convex colonies.
 T2	Gram-negative bacteria. Aerobes, small rods with a cell size of 0.9-1.6 μm, a length of 1.5-2.5 μm, do not form spores. On dense nutrient media, they form solid, smooth-edged, convex colonies.
 T3	Gram-positive, spore-forming, aerobic, rod-shaped, cell size 2-5 × 0.4-0.6 μm. Spores are oval, not larger than the cell size, located in the center of the cell. Filaments are peritrichous. Forms dry colonies with wavy edges on dense nutrient media.
 T4	Gram-positive, aerobic rods with centrally or paracentrally located ellipsoid spores, cell size 0.7-0.8 x 2-3 μm. Forms dense, large colonies on dense nutrient media, with uneven edges.

According to morphological and cultural properties, strains T1 and T2 are Gram-negative, short, non-spore-forming rods, while strains T3 and T4 are Gram-positive, spore-forming, motile rods. Table 2 shows the characteristics of the isolated strains according to the main diagnostic characteristics.

Table 2 – Main morphological, tinctorial and biochemical characteristics of isolated strains

No.	Culture	Cell shape	Gram stain	Mobility	Disputes	Hydrolysis of gelatin	Starch hydrolysis	Casein hydrolysis	Presence of catalase	Use of molecular nitrogen	Growth at 420C	Relation to molecular oxygen
1	*T1*	p	-	+	-	+++	++	++	+	+	+++	aerobes
2	*T2*	p	+	+	+	++	++	+	+	-	+++	aerobes
3	*T3*	p	+	+	+	++	+++	+++	+	-	+++	aerobes
4	*T4*	p	-	+	-	+	+	++	+	-	-	aerobes
Note – p – rod-shaped cells; +positive for this feature; -negative for this feature												

Based on the data obtained, gram-positive rods and gram-negative rod-shaped bacteria were identified among the cultures of microorganisms isolated from soil samples. All isolated strains were motile. All cultures grew well at a temperature of 42^0C and actively utilized molecular nitrogen. When studying the growth of cultures in the presence of molecular oxygen, all strains were aerobic. All strains were catalase positive, hydrolyzed starch and casein, and liquefied gelatin.

As a result of the study of morphological, cultural and physiological-biochemical properties, the isolated cultures were conditionally attributed to the genera *Bacillus* and *Pseudomonas.*

Screening and selection of the most promising strains of soil microorganisms of native crops, analysis of their properties

One of the urgent tasks of modern biotechnology is the development of biological products based on strains isolated from local microflora to solve a complex of problems related to the restoration of soils contaminated with xenobiotics [18].

It is known that soil fertility and self-purification are directly related to the activity of microbiological processes, however, as a result of high soil pollution, autochthonous microflora is inhibited [19]. Therefore, the development of complex technologies aimed at restoring the basic functions of soils and increasing their fertility is of significant scientific interest for theoretical and applied microbiology. Currently, biological remediation methods are considered a priority direction for solving the problems of remediation of contaminated soils [20]. Biodestruction is considered the most promising direction in the technologies for the remediation of soil systems contaminated with organic pollutants, including xenobiotics.

The selection of promising strains was carried out among cultures obtained from dominant populations of microorganisms [21]. The activity of the cultures was assessed by their growth rate and preservation of cell viability in the presence of xenobiotics. According to the results of screening studies, 4 strains showed growth activity in a medium with the addition of xenobiotics as the sole source of carbon. Strains T1, T2, T3, T4 had high growth activity in relation to xenobiotics. As a result of the screening, 4 promising strains of microorganisms that actively grow in a nutrient medium containing xenobiotics were identified. The results are shown in Figure 4.

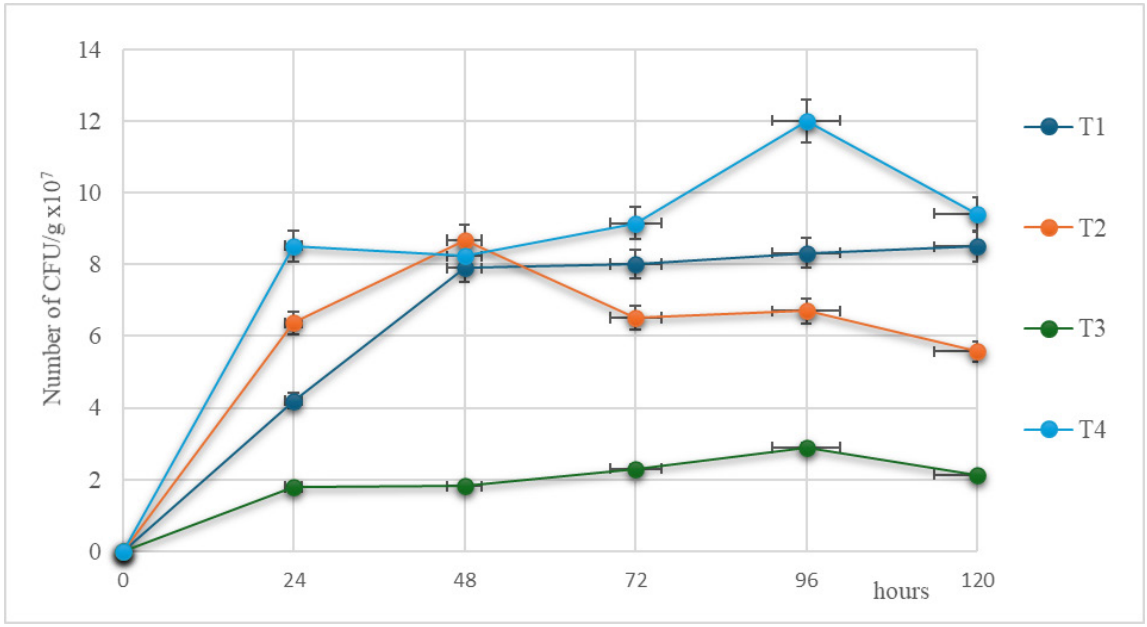
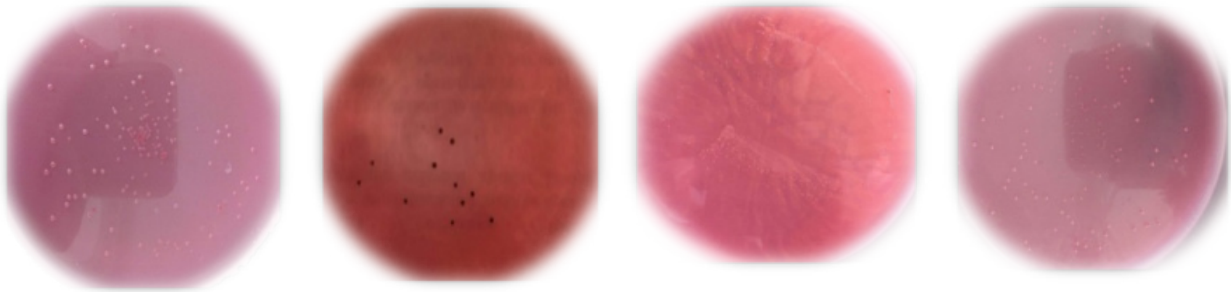


Figure 4 – Growth dynamics of crops in xenobiotic-supplemented media

The growth dynamics of cultures in a nutrient medium supplemented with xenobiotics was studied for 5 days. As can be seen from Figure 4, strains T1, T2, T4 showed active growth compared to strains T3. The cell number of the studied strains after 24 hours was $1.7x10^7$ -$8.6x10^7$ CFU/g, after 120 hours it was $2.1x10^7$ – $1.2x10^7$ CFU/g.

Figure 5 shows the growth of microbial cultures in a medium supplemented with a xenobiotic.



T1 T2 T3 T4

Figure 5 – Growthcultures of microorganisms on a medium with the addition of a xenobiotic

As can be seen from Figure 5, the strains formed uniform colonies of 1-2.5 mm in size in the cultures of microorganisms in the medium with the addition of xenobiotics. When the cultures of microorganisms were grown in M9 medium with the addition of pesticides, the colonies were large, measuring 1.8–3 mm. The colonies were round, with even edges and a smooth surface, dark red in color. The structure of the colonies was homogeneous. During surface cultivation, all strains formed S-type colonies, sometimes mucous (O) colonies appeared. In M9 medium with pesticides, transparent zones were formed around the colonies of all strains.

As a result of the study of promising strains of chemical pollutants, it was found that strains T1, T2, T3, T4 are capable of degrading xenobiotics, which is confirmed by the red color of the colonies and the

medium around them. Thus, the isolated, promising strains can be used in bioremediation of soils contaminated with xenobiotics.

Conclusion

The microbial diversity of local microflora in soil samples contaminated with xenobiotics was studied, and their quantitative and qualitative characteristics were determined. In the contaminated soils of Turkistan and Kyzylorda regions, the dominant microorganism populations were found to include fungal molds (3.2×10^7 CFU/g), heterotrophs (2.9×10^7 CFU/g), aerobic cellulolytic bacteria (2.5×10^7 CFU/g), ammonifying bacteria (2.3×10^7 CFU/g), and nitrogen-fixing bacteria (2.7×10^7 CFU/g).

Indigenous microorganisms were isolated from the contaminated soil samples, and their morphological-cultural, physiological-biochemical, and tintorial properties were studied. Based on the analysis of their morphological, cultural, and physiological-biochemical characteristics, the isolated cultures were tentatively identified as belonging to the genera *Bacillus* and *Pseudomonas*.

Screening and selection of the most promising strains from the native soil microorganisms were performed, followed by an analysis of their properties. The growth dynamics of the studied strains showed cell counts of 1.7×10^7 – 8.6×10^7 CFU/g after 24 hours, and 2.1×10^7 – 1.2×10^7 CFU/g after 120 hours.

The study of promising strains isolated from contaminated soils revealed that strains T1, T2, T3, and T4 are capable of degrading xenobiotics.

Acknowledgments, conflict of interest

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