

## Microorganisms in the Soil of Arid Pastures – Indicators of Health and Assistants in the Evaluation of Biostimulants

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### ABSTRACT

Microorganisms living in the soil of arid rangelands play a key role in maintaining their health. These tiny creatures are agents of organic matter decomposition on which soil fertility depends. Species and quantitative composition of microorganisms is an indicator reflecting the direction of biological processes in the soil. In natural conditions, the ratio of different groups of microorganisms shows whether decomposition or synthesis of organic compounds, including humus, prevails. In agroecosystems where humans use organic and inorganic fertilizers, the study of microorganisms helps to assess the availability of nutrient elements to plants. Analysis of the soil microbial community also allows direct assessment of the effectiveness of biostimulant application, i.e. how well plants assimilate the applied macronutrients. The purpose of our study was to determine the health of the soil by the number and ratio of different groups of microorganisms, to identify whether the processes of decomposition (mineralization) or synthesis (immobilization) of nutrients prevail in the soil and to obtain reliable information on the availability of nutrients for plants. The study of microorganisms in the soil of arid pastures is a valuable tool for assessing their ecological state, as well as for developing more efficient and environmentally friendly farming methods.

**Keywords:** arid pastures, biostimulator, catalase, soil microorganisms, urease.

### INTRODUCTION

Arid grasslands are vast areas covered with herbaceous vegetation where annual rainfall does not exceed 400 mm. Covering about 30% of the land surface, these harsh lands are enchanting in their wild beauty and hold many secrets. The arid grasslands are under a regime of severe water conservation. Plants that have adapted to the arid climate have deep roots that allow them to extract moisture from deep layers of soil (Baymagambetova et al. 2024). The leaves of many plant species are covered with a waxy coating that prevents evaporation of moisture. Animals inhabiting these areas have also developed unique types of adaptations. The plant world of arid grasslands is represented by grasses, sedges, wormwoods, astragals and other *xerophytic species*. These plants, able

to survive in drought conditions, provide food for herbivorous animals. The fauna of arid pastures is quite diverse: there are rodents, ungulates, predators, as well as many birds. Arid pastures are traditionally used for grazing. However, overgrazing can lead to pasture degradation, soil erosion, and desertification. It is necessary to manage these fragile areas sustainably to preserve them for future generations (Xue et al. 2023; Czigány et al. 2023). To this end, the authors investigated microorganisms in arid pastures, which in these agroecosystems they play the role of real giants, performing many functions that directly affect soil fertility and productivity.

Thanks to their great diversity, bacteria and fungi living in the soil play a key role in the nutrient cycle. These microscopic creatures synthesize many enzymes and possess specific genes

that allow them to participate in almost all stages of this vital process (Jiapeng Zhang et al. 2024; Wydro et al. 2014). The abundance of bacteria and fungi in the soil contributes to the formation of humus, a valuable component that ensures fertility. Microorganisms produce specific metabolites, biomass and enzymes that participate in the synthesis and formation of precursors of humic compounds. Thus, microorganisms are not just invisible soil inhabitants but real motors that ensure nutrient cycling and formation of fertile layer (Patel et al. 2023).

Soil is a complex and multi-component world inhabited by a colossal variety of microorganisms. These microscopic creatures, with their unique metabolic abilities, play a key role in organic matter decomposition and nutrient cycling. The composition and abundance of the soil microbial community are directly influenced by various factors, both natural and anthropogenic. Studying these relationships is an important task that will allow us to better understand the functioning of soil ecosystems and predict the effects of various exposures on their health (Wu et al. 2024).

Understanding of interrelationships between physical-chemical and biological characteristics of soil, as well as the influence of various factors on them, is the key to optimizing its fertility. Studying these interrelationships will allow us to manage trophic and biological processes, purposefully regulate the course of transformation of nutrient elements, and develop methods for managing the reproduction of soil fertility. Understanding the complex interrelationships in soil will allow us to increase its fertility and, consequently, ensure food security.

Research on soil microorganisms has received considerable attention in recent years (Herman et al. 2012; Cotrufo, et al. 2013; Krause et al. 2014; Fierer 2017; Jansson and Hofmockel 2020; Janie Zhang et al. 2021). The structure of soil microbial communities is particularly important for soil ecosystems to function at maximum efficiency (Gonzalez et al. 2011; Ochoa-Hueso 2017; Tripathi et al. 2017). Soils characterized by high abundance and diversity of microorganisms have been shown to provide essential ecosystem services (Torsvik and Øvreås 2002; Scherer-Lorenzen et al. 2022). Studies by many scientists have identified increases in soil functional diversity and microbiome complexity as one mechanism by which organic additives promote soil health (Schlatter et al. 2019; Bailey and Lazarovits 2003).

The role of different microbial species in biogeochemical cycles that significantly influence the responses of soil ecosystem depending on environmental situations is poorly understood and evaluated (Bhattacharjee et al. 2020). In addition, the metagenomic studies conducted in this research will provide a more detailed assessment of the role of microorganisms in soil ecosystem functioning under different management intensities, which is very important under climate change. Also, soil microbiome studies will allow the assessment of soil fertility and sustainable agriculture to realistically predict how soil ecosystems will respond to anthropogenic environmental changes.

The aim of our study is to determine the health of the soil by the number and ratio of different groups of microorganisms, to identify whether the processes of decomposition (mineralization) or synthesis (immobilization) of nutrients prevail in the soil and, as a result, to obtain reliable information on the availability of nutrients for plants.

## MATERIALS

Previously treated soil with biostimulant - MERS based on plant extract with soil microorganisms, and biofertilizer - based on biohumus with addition of biostimulant MERS (Baymagambetova et al. 2024). Soil samples for analysis were taken from 2022 to 2023 during the vegetation period of plants. For granulometric parameters in spring, when plant vegetation is underway. Samples for physical analysis were taken twice: in spring when plant growth starts and in fall (before fall rains). Coordinates of soil sampling locations are presented in Table 1 and marked in Figure 1.

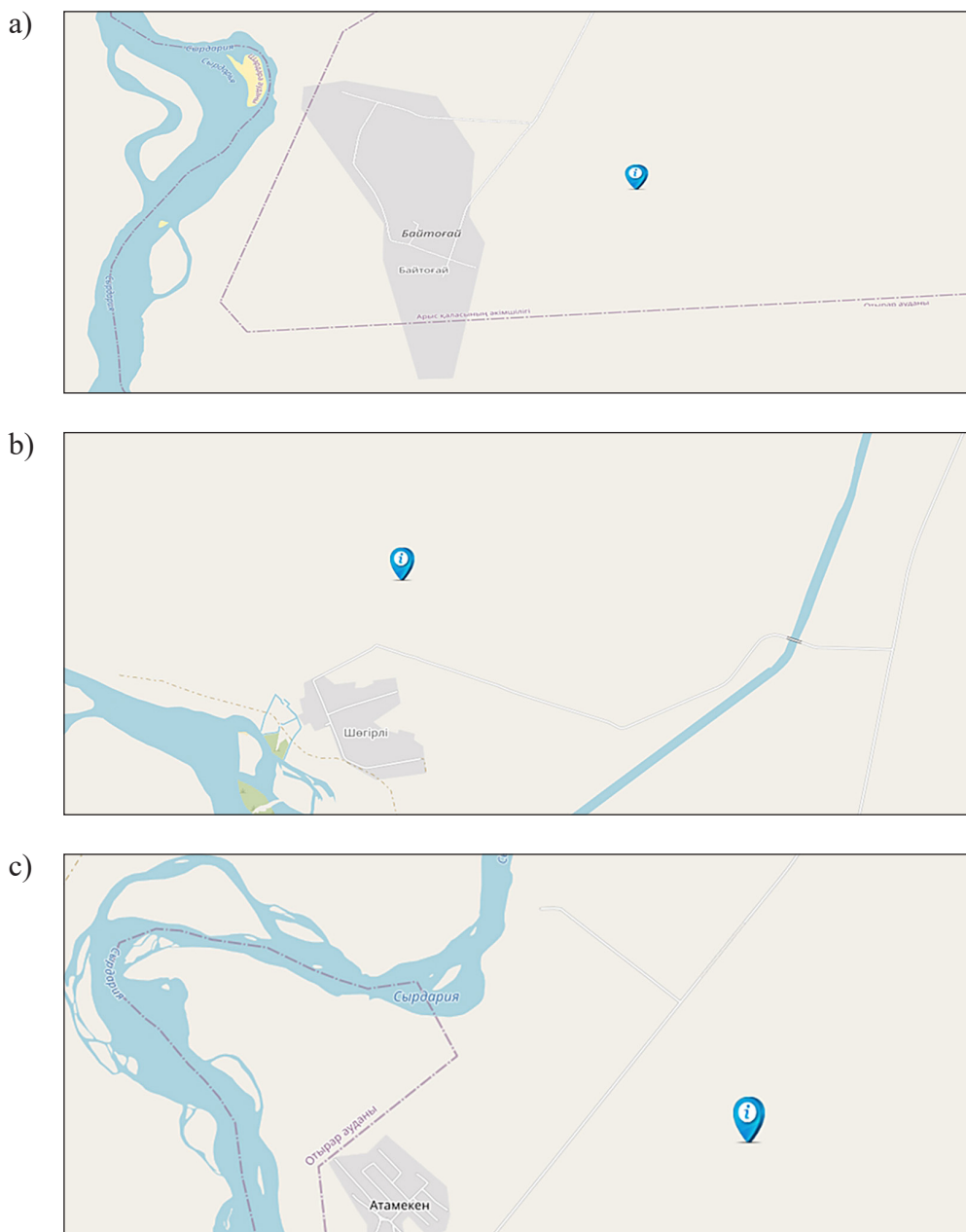
## METHODS

### Bacteriological analysis

Determination of the number of microorganisms of different ecological and trophic groups was carried out according to (Nidhin and Chattopadhyay 2022), by the method of limiting dilutions of soil suspension and surface seeding on selective nutrient media - meat-peptone agar (MPA) for ammonifiers, starch-ammonia agar - SAA (for amylolytic bacteria and actinomycetes), oligotrophic microorganisms on Lockheed soil agar, oligonitrophilic microorganisms on

**Table 1.** Soil characterization

No.	Soil coordinates	Soil type	Vegetation
1	41.91429 N. - north latitude 68.16055 E. - east longitude	Light loamy gray soils (Darbaza)	<i>Artemisia diffusa</i>
2	41.91429 N. - north latitude 68.16055 E. - east longitude	Strengthened soilsand <i>Calcisol</i> (Kozhatogai)	<i>Herbaceous-shrub</i> <i>Goebellia pachycarpa</i> <i>Alhgi pseudalhagi</i> <i>Heliotropium arguzioides</i> <i>Astragalus-unifoliolatus</i> <i>Cousinia epectispina</i> <i>Ammodendron conollyi</i>
3	41.91429 N. - north latitude 68.16055 E. - east longitude	Light loamy soil (Atameken)	<i>Artemisia diffusa</i> <i>Goebellia pachycarpa</i> <i>Heliotropium arguzioides</i> <i>Astragalus-unifoliolatus</i> <i>Artemisia scoporia</i>



**Figure 1.** Coordinates of received soil samples on arid pastures: (a) Baitogai village, soil light loamy gray soil; (b) Shogirli village, soil accreted gray soil sands; (c) Atameken village, soil light loamy gray soil

Ashby medium (Wolny-Kołodka et al. 2022). The mineralization and immobilization coefficient (KMC) were calculated by the ratio of amyolytic and ammonifying microorganisms, and the pedotrophic index was calculated by the ratio of oligotrophic and ammonifying microorganisms. The number of microorganisms was determined by surface sowing of soil suspension in dilution 10<sup>2</sup>–10<sup>5</sup>. Repetition of sowing for each dilution was three times. For desorption of cells from the surface of soil aggregates, the soil suspension was mixed on the MX-S Vortex Mixer (manufacturer IKA-Werke GmbH, Germany) for 5 minutes (according to a stopwatch) at a speed of 250 rpm. Petri dishes with cultures were incubated in thermostats for 5–10 days, at 26 °C. Microbial numbers were expressed in colony forming units (CFU in 1 g of soil) (Hafeez and Aslanzadeh 2018; Salwan, Rana, and Sharma 2023; Green 2015).

### Statistical analysis

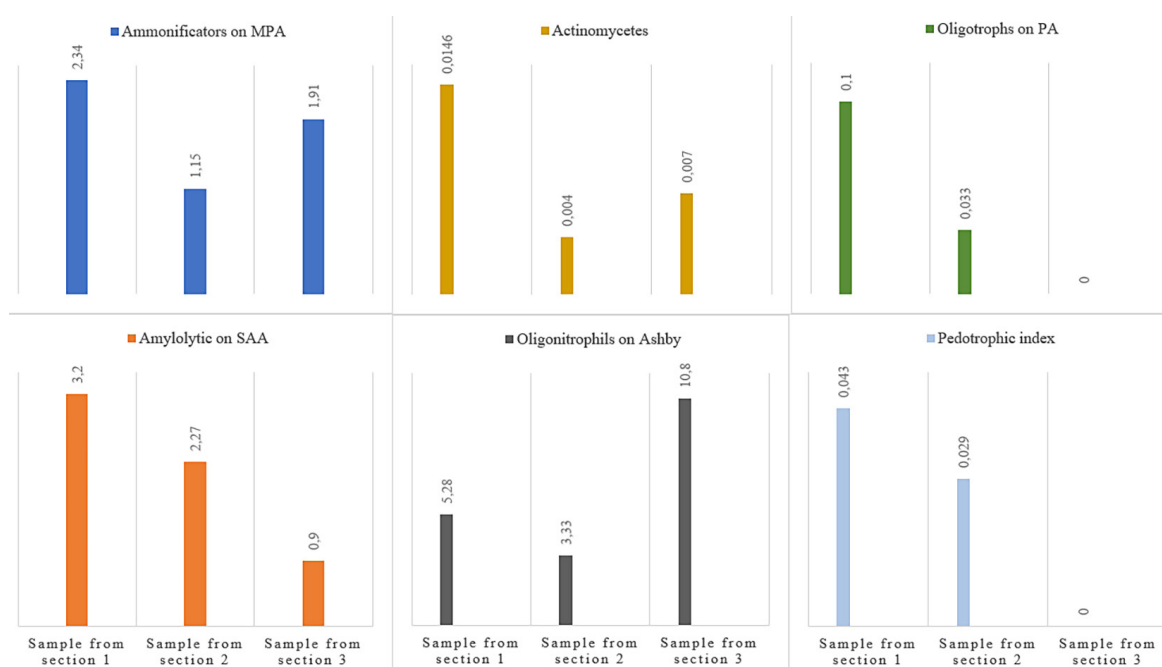
Differences between each treatment and control and between individual treatments were evaluated using one-factor analysis of variance (ANOVA, Duncan's criterion,  $p \leq 0.05$ ). Within-treatment variation was determined by calculating standard deviation ( $\pm$ SD) values. Correlation coefficient values were calculated using the nonparametric Spearman's criterion for chemical and biological properties. All

statistical analyses were performed using Statistica PL 13 and MiniTab 21.1.1 software.

## RESULTS AND DISCUSSION

In soil, microorganisms are grouped into groups according to the type of functions they perform. The ammonifying group decomposes nitrogen-containing substances, the amyolytic group converts mineral nitrogen into organic nitrogen (Xu et al. 2024), and the oligonitrophilic group transforms nitrogen-free and other high molecular weight components. The oligotrophic group prefers environments with low nutrient element content and dominates in low-humus soils. Actinomycetes, due to their powerful enzyme apparatus, are responsible for the destruction of complex organic compounds at deep stages of decomposition, and also produce humic-like pigments (Peng et al. 2023).

This paper presents the results of research on the number of microorganisms in soil. The authors studied the relationship between the number of microbes and various processes occurring in the soil, as well as with indices characterizing its quality. The numbers of microorganisms of the main ecological and trophic groups of three different soils are presented in Table 2, and Figure 2.



**Figure 2.** Numbers of microorganisms of some ecological-trophic groups in soils in Kozhatogai district (south of Kazakhstan). \*Number of microorganisms (million CFU in 1 g of soil), reliable interval  $p < 0.05$

The initial stages of transformation of organic compounds in soil take place in several stages. Ammonification carried out by ammonifying microorganisms is the first stage of this process. Ammonifiers decompose readily available nitrogen-containing organic matter, converting it into ammonium. These include various bacteria (*Bacillus*, *Bacterium*, *Pseudomonas*), fungi (*Penicillium*, *Trichoderma*, *Aspergillus*) and streptomycetes. The essence of this stage is the decomposition of complex organic molecules to simpler ones available to other microorganisms. Ammonification is a nonspecific process, so it can be performed by different groups of microorganisms, but with the same “food” preferences.

It was found that the abundance of ammonifying microorganisms is greatly influenced by both climatic and agrotechnical conditions - aeration, moistening-drying regimes, temperature, cultivation culture, in agrocenoses - by the application of mineral and organic fertilizers, and especially manure (Bian et al. 2024; Wang et al. 2024; Sychina et al. 2023).

Judging from the abundance of ammonifying microorganisms (ranging from 1.15–2.34 million CFU in 1 g of soil), there is a small amount of readily available organic nitrogen in all soil samples. The low number of ammonifiers in sample 2 (1.15 million CFU) reflects the low intensity of organic nitrogen-containing compounds cycling inherent directly in the soil. In samples 1 and 3, the number of representatives of this group is 2.03 and 1.66 times higher than in sample 2, which is probably due to the presence of more plants or another source of nitrogenous compounds. The low nitrogen content in these soils confirms the presence of a large number of oligonitrophils (3.33–10.80 million CFU) preferring trace amounts of nitrogen.

Oligotrophs, due to their metabolism and abundance, play an important role in the formation of soil fertility (Tsolova et al. 2021). This group of microorganisms is able to be satisfied with substrates poor in nutrients and, as a rule, under normal nutrient regime they do not dominate in the soil. High abundance of pedotrophs indirectly indicates active processes of organic matter destruction. Their abundance is usually lower on non-cultivated plots. In particular, the number of pedotrophic microorganisms decreases in the row: arable land – virgin land. In gray forest soils, the number of pedotrophic microorganisms decreases in the row: conventional field

- organic fields - background virgin area. In poor soils with nutrient deficiency this group survives due to deep mineralization of organic matter inaccessible to other representatives of the microbial community. The results of the study of the number of this group of microorganisms are shown in Figure 2. The studied soil is characterized by very low content of oligotrophs: at site 1 - only 0.1 million (i.e. 100 thousand) CFU in 1 g of soil; at site 2 - 3 times less - 0.033 million CFU, while at site 3 oligotrophs were not found. Such a low number of oligotrophs is rare in both virgin and cultivated soils, and indicates rather the processes of immobilization of organic matter than its destruction.

One of the most important indicators characterizing the direction of microbiological transformation of soil organic matter is the pedotrophic index (PI) - the ratio of oligotrophic and ammonifying microorganisms. A number of authors believe that the higher the PI is, the more the soil is close to the state of natural biogeocenosis, while the lower it is, the more negative effect of anthropogenic load is noticeable. However, there are also contradictory results. For example, Zavyalova et al., 2019, report the level of IP equal to 0.99 in forest soil, while in meadow soil - 2.2. On arable land, the IP decreases immediately by 62%, with increasing doses of mineral fertilizers (in increments of 30 kg/ha) the IP uniformly decreases by 9–20%.

Despite the fact that the studied soils were not subjected to anthropogenic load, the IP has a very low level of 0.043 and 0.029, whereas in variant 3 the IP cannot be calculated due to the absence of oligotrophs in the bacteriological crops. The reason for such suppression of the number of oligotrophs and their small share in the structure of soil microbial community should probably be explained by climatic or weather factors.

Another important indicator of the activity of biological processes in soil and the composition of the soil microbial community is the ratio of the number of microorganisms developing on starch-ammonia agar (SAA) and characterizing the process of ammonia nitrogen transformation to the number of microorganisms on meat-peptone agar (MPA) and controlling the transformation of soil protein substances. The mineralization and immobilization coefficient (KMI) calculated by this formula shows the intensity of decomposition of readily available matter and activation of the

initial stage of humus formation process (Zlenko 2012). According to the conducted studies, CMI in the studied soil indicates the processes of immobilization (fixation) of readily available nitrogen in the soils of site 1 and 2 (1.37 and 1.97) and, on the contrary, decomposition of organic nitrogen in the soil of site 3 (0.47).

Enzymes play a huge role in the vital activity of animals, plants and microorganisms. Soil enzymes are involved in the breakdown of plant, animal and microbial residues, as well as in the synthesis of organic matter, including humus. Hard-to-access nutrients are broken down to forms that are easily digestible for plants and microorganisms. Enzymes are characterized as highly specific and highly active proteins, providing all chemical reactions of decomposition-synthesis, redox and other processes. Enzyme activity of soils can serve as a reliable criterion to clarify the level of soil fertility, as well as the impact of climatic or anthropogenic factors. As a result of researches, the dependence between activity of microbiological and enzymatic processes and realization of measures increasing soil fertility has been established. Soil treatment, fertilizer application significantly changes the ecological situation of microorganisms development. Currently, several thousand individual enzymes have been found in biological objects, and several hundred of them have been isolated and studied (Labarthe et al. 2024).

N- and P-cycle enzymes play a special role in the transformation of nitrogen and phosphorus compounds. Soils contain a large amount of phosphorus in the form of organic compounds, which comes with dying remains of plants, animals and microorganisms. The release of phosphoric acid from these compounds is carried out by a relatively narrow group of microorganisms with specific phosphatase enzymes. Among the enzymes of phosphorus metabolism, the activity of orthophosphorus monophosphoesterases has been most fully investigated. Producers of phosphatases are predominantly cells of soil microorganisms. Soil phosphatase activity is determined by its genetic features, physical, agrochemical, biological properties, and the level of agrotechnics. Soil physical and chemical characteristics such as acidity are most important for phosphatase activity. Acidic soils predominantly contain acid phosphatases, slightly alkaline soils contain alkaline phosphatases. The level of phosphatases in soils dependent on acidity was found to be

determined by the composition of microflora. In general, soil phosphatase activity is directly related to the level of organic carbon and phosphorus as substrate for this enzyme. The highest phosphatase activity is characterized by chernozems. Phosphatase activity is dynamic during the vegetation period. In active phases of plant growth at high soil temperature and sufficient moisture in summer months phosphatase activity of soils is maximum. In some soils correlation of phosphatase activity with the total number of microorganisms and the number of microorganisms mineralizing organic phosphorus compounds was observed, in other soils correlation of phosphatase activity with the number of microorganisms was not established. The influence of humus is manifested in the nature of changes in the enzyme activity along the profile, in particular, during agrotechnical measures and application of organic fertilizers. Studies of many authors indicate a direct dependence of soil phosphatase activity on the content of organic phosphorus in the soil. On the contrary, there is evidence that phosphatase activity increases as readily available phosphorus in the soil decreases. The role of higher plants in the formation of the phosphatase pool of soils used in agriculture is lower than that of microorganisms and is mainly related to the input of crop residues and root excreta into the soil. From the agrochemical point of view, the end result is important - the growth of the enzyme pool of soils with an increase in the capacity of plant root systems. Impoverishment of agrocenoses with plants leads to a decrease in rhizosphere effect and, as a consequence, to a decrease in soil phosphatase activity. A significant decrease in soil phosphatase activity was observed under monoculture cultivation. On the contrary, crop change creates conditions for improved hydrolytic processes, which leads to increased metabolism of phosphorus compounds (Elhawat et al. 2024; Sun et al. 2024).

Based on the above, it can be concluded that the maximum contribution to the phosphatase pool under natural vegetation is made by microorganisms and crop residues as substrate. Judging from the very low phosphatase activity, the studied soils have a small amount of organic matter (and possibly poor vegetation) and, consequently, a low content of microorganisms. Thus, the lowest phosphatase activity is observed in variant 2 (1.386 mg P<sub>2</sub>O<sub>5</sub>, which is only 70 and 50% of variants 1 and 3). On the contrary, the highest activity

was noted in variant 3, slightly lower in variant 1. Judging by the confidence interval (0.809), the difference between the variants is highly significant and reliable.

The enzyme urease (amidase) also belongs to the class of hydrolytic enzymes, and its activity is the most important indicator of biological “well-being”, “health” of soils (Hu and Schmidhalter 2024). Urease is the most important enzyme involved in the nitrogen transformation cycle in soil, it catalyzes the hydrolysis of urea to ammonia and carbon dioxide, causing hydrolytic cleavage of the nitrogen-carbon bond in organic matter molecules. Of the enzymes of nitrogen metabolism, urease is the best studied. It is found in all soils. Its activity correlates with the activity of all major enzymes of nitrogen metabolism. In soil, urease exists in intracellular and extracellular forms.

In the soil profile, the humus horizon has the highest urease activity; the distribution in the profile depends on the natural characteristics of the soil. High urease activity of anthropogenically used soils reduces the efficiency of urea due to nitrogen losses in the form of ammonia. In order to improve plant nitrogen nutrition and prevent unsustainable losses, various compounds, urease inhibitors, are being developed to slow down urea hydrolysis (Hu and Schmidhalter 2024). The rate of urea hydrolysis in soil is influenced by temperature, soil acidity, level of agronomic practices, crop grown and other factors (Sunling et al. 2024).

It should be noted that the soils we studied were also characterized by very high urease activity, ranging from 60.76 to 92.95 mg N-NH<sub>4</sub> in 100 g of soil, sample 1, 2 and 3, respectively, 60.76; 82.73 and 92.95 mg N-NH<sub>4</sub> in 100 g of soil.

Considering the low levels of microorganisms involved in the nitrogen cycle (ammonifiers, amylolytic and oligonitrophils) in these soils and

in this season (month of February), it can be assumed that the urease activity is rather indicative of the self-cleaning potential of the soil, and probably the accumulation of a large amount of bound nitrogen over the summer period.

Importantly, no significant correlation was found between the two enzymes, phosphatase and urease ( $r = 0.39$ ), but sample 3 was characterized by the highest activity of urease, just as in the case of phosphatase (Table 2). Catalase belongs to the class of redox enzymes. The role of catalase in soil is that it breaks down hydrogen peroxide, which is poisonous to plants, into water and molecular oxygen. Hydrogen peroxide is formed during plant respiration and during biochemical reactions of organic matter oxidation (Golnari et al. 2024). Indices of catalase activity (along with invertase, urease) are widely used in the diagnosis and classification of soils, in assessing the degree of cultivation, erodibility and pollution of soils, and the degree of fertilizer exposure. As a rule, soils under plants with powerful deep penetrating root system are characterized by higher catalase activity. Down the profile, catalase activity changes little, and its level has an inverse dependence on soil moisture and a direct dependence on temperature. Catalase activity depends on localization in different structural aggregates. While hydrolytic enzymes are mainly concentrated in microaggregates (less than 0.25 mm), the redox enzyme catalase is concentrated in larger aggregates. Water-stable aggregates are characterized by greater activity (Xing et al. 2024).

The catalase activity is higher inside the aggregates. In addition, it is proved that the increase in anthropogenic load leads to a decrease in catalase activity of soil (Table 3). The enzymatic analysis showed very low catalase activity, with soil samples 2 and 3 being lower in activity by 28.2 and 17.5% relative to sample 1 in the dynamics

**Table 2.** Level of phosphatase and urease activity in soils of Kozhatogai district (south of Kazakhstan)

Variant no.	Phosphatase in 100 g of soil in 1 hour		Urease mg N-NH <sub>4</sub> in 100 g of soil	
	M	±M	M	±M
Sample 1	1.982	0.069	60.76	2.126
Sample 2	1.386	0.042	82.73	2.482
Sample 3	2.810	0.076	92.95	2.510
Standard, deviation	0.715		16.449	
Reliable interval p<0.05	0.809		18.614	

**Table 3.** Catalase activity in soils of Kozhatogai district (south of Kazakhstan)

Variant no.	1 minute		2 minute		3 minute		4 minute		5 minute		Avarage	
	M	m	M	m	M	m	M	m	M	m	M	m
Sample 1	2.4	0.30	3.57	0.45	4.7	0.59	5.67	0.71	6.6	0.83	4.59	0.57
Sample 2	1.57	0.21	2.5	0.34	3.33	0.45	4.13	0.56	4.93	0.67	3.29	0.44
Sample 3	1.63	0.57	2.8	0.98	3.93	1.38	4.83	1.69	5.73	2.01	3.79	1.33
Standard, deviation	0.46	0.19	0.55	0.34	0.69	0.50	0.77	0.62	0.84	0.73	0.66	0.48
Reliable interval p<0.05	0.52	0.21	0.62	0.39	0.78	0.57	0.87	0.70	0.95	0.83	0.74	0.54

**Table 4.** Pearson’s matrix evaluating the interdependence of biological and biochemical characteristics of soil of Kozhatogai district (south of Kazakhstan)

Specification	AM*	AC	OT	AML	ON	PI	MC	Cat	Phosph	Ure
AM	1.0									
AC	0.92	1.0								
OT	0.53	0.82	1.0							
AML	0.25	0.61	0.95	1.0						
ON	0.40	0.01	-0.56	-0.79	1.0					
PI	0.17	0.54	0.92	1.00	-0.84	1.0				
MC	-0.54	-0.16	0.43	0.68	-0.99	0.74	1.0			
Cat	0.96	0.99	0.75	0.52	0.12	0.44	-0.27	1.0		
Phosph	0.56	0.18	-0.41	-0.66	0.98	-0.73	-1.00	0.29	1.0	
Ure	-0.54	-0.83	-1.00	-0.95	0.55	-0.92	-0.42	-0.76	0.39	1.0

**Note:** AM – ammonificators, AC – actinomycetes, OT – oligotrophs, AML – amylolytic, ON – oligonitrophils, PI – pedotrophic index, MC – mineralization coefficient, Cat – catalase, Phosph – phosphatase, Ure – urease.

over 5 minutes of measurements. The correlation matrix is an important tool in data analysis, allowing the study of relationships between different variables. It provides an opportunity to assess the degree of linear relationship between pairs of variables and to identify strong and weak relationships. A correlation matrix can also be used to make predictions and identify relationships in the data. Using the package “Data Analysis” in MiniTab 21.1.1, Pearson’s correlation matrix was calculated, describing the relationship and interdependence of the studied soil characteristics (Table 4). In particular, a direct (positive) correlation of great strength between:

- Ammonificators and actinomycetes ( $r = 0.92$ );
- Amylolytic and oligotrophic microorganisms ( $r = 0.95$ );
- Oligotrophs and actinomycetes ( $r = 0.82$ ).

A close inverse relationship was established between:

- Oligonitrophils and amylolytic microorganisms ( $r = -0.79$ );
- Oligonitrophils and oligotrophs ( $r = -0.56$ ).

Interestingly, the level of catalase activity had a significantly high correlation with all isolated groups of microorganisms ( $r = 0.52-0.99$ ) except oligonitrophils. In contrast, urease was negatively correlated with the same groups of microorganisms ( $r=-0.54$  to  $-0.95$ ), except for oligonitrophils, where a direct correlation was recorded ( $0.55$ ).

## CONCLUSIONS

The authors investigated previously treated experimental soils on the productivity impact of plant growth stimulants. The obtained samples from arid pastures showed a low content of microorganisms involved in the nitrogen cycle, this is due to the low content of organic matter in the studied soils. It was found reliable high activity of urease may indicate the potential of self-purifying ability of soil and accumulation of bound nitrogen during the summer period. The level of catalase activity indicates low biological activity of soil. The obtained data can be used to develop



measures to improve soil fertility. It is recommended to use organic plant or manure composts with the addition of growth biostimulants based on microbial consortia. Such interventions improve soil fertility in a natural way.

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## REFERENCES

- Bailey K.L., Lazarovits G. 2003. Suppressing soil-borne diseases with residue management and organic amendments. *Soil and Tillage Research*, Soil Agroecosystems: Impacts of Management on Soil Health and Crop Diseases, 72(2), 169–80. [https://doi.org/10.1016/S0167-1987\(03\)00086-2](https://doi.org/10.1016/S0167-1987(03)00086-2).
- Baymagambetova Z., Kedelbayev B.S., Seitkarimov A., Kalymbetov G., Sapargaliyeva B. 2024. Biostimulator for Arid Pastures in the South of Kazakhstan. *Journal of Ecological Engineering*, 25(1), 131–45. <https://doi.org/10.12911/22998993/174332>.
- Bhattacharjee, A., Dusan Velickovic D., Wietsma T.W., Bell S.L., Jansson J.K., Hofmockel K.S., Anderson C.R. 2020. Visualizing Microbial Community Dynamics via a Controllable Soil Environment. *Systems*, 5(1). 10.1128/msystems.00645-19. <https://doi.org/10.1128/msystems.00645-19>.
- Bian Q., Zhao L., Cheng K., Jiang Y., Li D., Xie Z., Sun B., Wang X. 2024. Divergent Accumulation of Microbe- and Plant-Derived Carbon in Different Soil Organic Matter Fractions in Paddy Soils under Long-Term Organic Amendments. *Agriculture, Ecosystems and Environment*, 366. <https://doi.org/10.1016/j.agee.2024.108934>.
- Cotrufo M.F., Wallenstein M.D., Boot C.M., Denef K., Paul E. 2013. The Microbial Efficiency-Matrix Stabilization (MEMS) framework integrates plant litter decomposition with soil organic matter stabilization: do labile plant inputs form stable soil organic matter? *Global Change Biology*, 19, 988–95. <https://doi.org/10.1111/gcb.12113>.
- Czigány S., Sarkadi N., Lóczy D., Cséplő A., Balogh R., Fábrián S.A., Ciglič R., et al. 2023. Impact of Agricultural Land Use Types on Soil Moisture Retention of Loamy Soils. *Sustainability*, 15(6), 4925. <https://doi.org/10.3390/su15064925>.
- Elhawat N., Kovács A.B., Antal G., Kurucz E., Domokos-Szabolcsy É., Fári M.G., Alshaal T. 2024. Living Mulch Enhances Soil Enzyme Activities, Nitrogen Pools and Water Retention in Giant Reed (*Arundo Donax* L.) Plantations. *Scientific Reports*, 14(1). <https://doi.org/10.1038/s41598-024-51491-z>.
- Fierer N. 2017. Embracing the unknown: disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology*, 15(10), 579–90. <https://doi.org/10.1038/nrmicro.2017.87>.
- Golnari M., Bahrami N., Milanian Z., Rabbani Khorasgani M., Asadollahi M.A., Shafiei R., Fatemi S.S.-A. 2024. Isolation and Characterization of Novel *Bacillus* Strains with Superior Probiotic Potential: Comparative Analysis and Safety Evaluation. *Scientific Reports*, 14(1). <https://doi.org/10.1038/s41598-024-51823-z>.
- Gonzalez A., Clemente J.C., Shade A., Metcalf J.L., Song S., Prithiviraj B., Palmer B.E., Knight R. 2011. Our microbial selves: what ecology can teach us. *EMBO reports*, 12(8), 775–84. <https://doi.org/10.1038/embor.2011.137>.
- Green L.H. 2015. Diagnostic Medical Microbiology. *Practical Handbook of Microbiology*, Third Edition, 135–52. <https://doi.org/10.1201/b17871>.
- Haféez S., Aslanzadeh J. 2018. Biochemical Profile-Based Microbial Identification Systems. *Advanced techniques in diagnostic microbiology: Volume 1: Techniques*, Third Edition, 33–67. [https://doi.org/10.1007/978-3-319-33900-9\\_3](https://doi.org/10.1007/978-3-319-33900-9_3).
- Herman D.J., Firestone M.K., Nuccio E., Hodge A. 2012. Interactions between an arbuscular mycorrhizal fungus and a soil microbial community mediating litter decomposition. *FEMS Microbiology Ecology*, 80(1), 236–47. <https://doi.org/10.1111/j.1574-6941.2011.01292.x>.
- Hu Y., Schmidhalter U. 2024. Annual consumption and types of synthetic nitrogen fertilizers: ammonia emission indicators for mitigation strategies in the European Union. *Environmental and Sustainability Indicators*, 22. <https://doi.org/10.1016/j.indic.2024.100365>.
- Jansson J.K., Hofmockel K.S. 2020. Soil microbiomes and climate change. *Nature Reviews Microbiology*, 18(1), 35–46. <https://doi.org/10.1038/s41579-019-0265-7>.

16. Krause, S., Le Roux X., Niklaus P.A., Van Bodegom P.M., Lennon J.T., Bertilsson S., Grossart H.P., Philippot L., Bodelier P.L.E. 2014. Trait-based approaches for understanding microbial biodiversity and ecosystem functioning. *Frontiers in microbiology*, 5(May). <https://doi.org/10.3389/fmicb.2014.00251>.
17. Labarthe M.M., Maroniche G.A., Lamattina L., Creus C.M. 2024. Nitric oxide synthase expression in *Pseudomonas Koreensis* MME3 improves plant growth promotion traits. *Applied Microbiology and Biotechnology*, 108(1). <https://doi.org/10.1007/s00253-024-13029-1>.
18. Ye G., Banerjee S., He J.Z., Fan J., Wang Z., Wei X., Hu H.W., Zheng Y., Duan C., Wan S., Chen J., Lin Y. Manure application increases microbiome complexity in soil aggregate fractions: results of an 18-year field experiment. 2021. *Agriculture, Ecosystems & Environment*, 307, 107249. <https://doi.org/10.1016/j.agee.2020.107249>.
19. Nidhin, I.K., Chattopadhyay I. 2022. Emerging technologies in environmental microbiology: microbes in the environment. *Environmental Microbiology: Emerging Technologies*, 33–58. <https://doi.org/10.1515/9783110727227-002>.
20. Ochoa-Hueso R. 2017. Global change and the soil microbiome: a human-health perspective. *Frontiers in Ecology and Evolution*, 5(July). <https://doi.org/10.3389/fevo.2017.00071>.
21. Patel C., Singh J., Karunakaran A., Ramakrishna W. 2023. Evolution of Nano-Biofertilizer as a Green Technology for Agriculture. *Agriculture*, 13(10), 1865. <https://doi.org/10.3390/agriculture13101865>.
22. Peng Q., Zheng H., Yu H., Meng K., Cheng Y., Yang X., Xie G., Zheng X. 2023. Environmental Factors drive the succession of microbial community structure during wheat qu fermentation. *Food bioscience*, 56. <https://doi.org/10.1016/j.fbio.2023.103169>.
23. Salwan R., Rana A., Sharma V. 2023. Characterization of microbes using molecular methods. <https://doi.org/10.1016/B978-0-323-95078-7.00013-9>.
24. Scherer-Lorenzen M., Gessner M.O., Beisner B.E., Messier C., Paquette A., Petermann J.S., Soininen J., Nock C.A. 2022. Pathways for cross-boundary effects of biodiversity on ecosystem functioning. *Trends in Ecology & Evolution*, 37(5), 454–67. <https://doi.org/10.1016/j.tree.2021.12.009>.
25. Schlatter, D.C., Paul N.C., Shah D.H., Schillinger W.F., Bary A.I., Sharratt B., Paulitz T.C. 2019. Biosolids and Tillage Practices Influence Soil Bacterial Communities in Dryland Wheat. *Microbial Ecology*, 78(3), 737–52. <https://doi.org/10.1007/s00248-019-01339-1>.
26. Sun X., Gao W., Li H., Zhang J., Cai A., Xu M., Hao X. 2024. Animal Manures Increased Maize Yield by Promoting Microbial Activities and Inorganic Phosphorus Transformation in Reclaimed Soil Aggregates. *Applied Soil Ecology*, 198. <https://doi.org/10.1016/j.apsoil.2024.105352>.
27. Sunling Y., Shahzad A., Wang M., Xi Y., Shaik M.R., Khan M. 2024. Urease and nitrification inhibitors with drip fertigation strategies to mitigate global warming potential and improve water-nitrogen efficiency of maize under semi-arid regions. *Agricultural Water Management*, 295. <https://doi.org/10.1016/j.agwat.2024.108750>.
28. Syrchina N.V., Pilip L.V., Kolevatykh E.P., Ashikhmina T.Y., Kuznetsov D.A. 2023. Effect of sodium hypochlorite on the microbiota and odor of manure effluents. *Biology Bulletin*, 50(10), 2736–40. <https://doi.org/10.1134/S1062359023100278>.
29. Torsvik V., Øvreås L. 2002. Microbial diversity and function in soil: from genes to ecosystems. *Current Opinion in Microbiology*, 5(3), 240–45. [https://doi.org/10.1016/S1369-5274\(02\)00324-7](https://doi.org/10.1016/S1369-5274(02)00324-7).
30. Tripathi B.M., Itumeleng Moroenyane, Chen Sherman, Yoo Kyung Lee, Jonathan M. Adams, and Yosef Steinberger. 2017. Trends in taxonomic and functional composition of soil microbiome along a precipitation gradient in Israel. *Microbial Ecology*, 74(1), 168–76. <https://doi.org/10.1007/s00248-017-0931-0>.
31. Tsoлова V., Nedyalkova K., Tomov P., Kolchakov V. 2021. Microbiome status and determinants in soils from the region of maritsa-iztok coal mine (Bulgaria). ii. spolic technosols. *Bulgarian Journal of Agricultural Science*, 27(4), 727–35.
32. Wang C., Guo L., Cai Z.J., Chen J., Shen R.F. 2024. Different Contributions of Rare Microbes to Driving Soil Nitrogen Cycles in Acidic Soils under Manure Fertilization. *Applied Soil Ecology*, 196. <https://doi.org/10.1016/j.apsoil.2024.105281>.
33. Wolny-Kołodka K., Jarosz R., Marcińska-Mazur L., Lośák T., Mierzwa-Hersztek M. 2022. Effect of mineral and organic additions on soil microbial composition. *International Agrophysics*, 36(May), 131–38. <https://doi.org/10.31545/intagr/148101>.
34. Wu Y., Yang W., Li Q., Qiao Q., Zhao S., Zhang Y., Yu Y., Zhang S., Li X., Kou J. 2024. Microbial community response to alpine meadow degradation and its impact on soil nutrient cycling. *Agronomy*, 14(1), 195. <https://doi.org/10.3390/agronomy14010195>.
35. Wydro U., Wolejko E., Łoboda T., Matejczyk M., Butarewicz A. 2014. Influence of sewage sludge on the chosen soil properties and microbiological parameters of urban grass mixtures rhizosphere. *Journal of Ecological Engineering*, 16(1), 171–77. <https://doi.org/10.12911/22998993/604>.
36. Xing Y., Qiu J., Chen J., Cheng D., Yin Q., Chen X., Xu L., Zheng P. 2024. Unveiling hidden interactions: microorganisms, enzymes, and mangroves

- at different stages of succession in the shankou mangrove nature reserve, China. *Science of the Total Environment*, 923. <https://doi.org/10.1016/j.scitotenv.2024.171340>.
37. Xu Z., Li R., Zhang X., Wang S., Xu X., Ho Daniel Tang K., Emmanuel Scriber II K., Zhang Z., Quan F. 2024. Molecular mechanisms of humus formation mediated by new ammonifying microorganisms in compost. *Chemical Engineering Journal*, 483. <https://doi.org/10.1016/j.cej.2024.149341>.
38. Xue Z., Yan H., Zhen L. 2023. For a better quality of beef: the challenge from growing livestock on limited grasslands with a production–consumption balance perspective. *Foods*, 12(17), 3231. <https://doi.org/10.3390/foods12173231>.
39. Zhang J., Cook J., Nearing J.T., Zhang J., Raudonis R., Glick B.R., Langille M.G.I., Cheng Z. 2021. Harnessing the plant microbiome to promote the growth of agricultural crops. *Microbiological Research*, 245(April), 126690. <https://doi.org/10.1016/j.micres.2020.126690>.
40. Zhang J., Zhao S., Miao Q., Feng L., Chi Z., Li Z., Li W. 2024. Effect of Subsurface Drainage in Regulating Water on Desalinization and Microbial Communities in Salinized Irrigation Soils. *Agronomy*, 14(2), 282. <https://doi.org/10.3390/agronomy14020282>.
41. Zlenko B.I. 2012. Formation of microbocenoses at the initial stages of biological reclamation of reclaimed lands of the Nikopol manganese ore basin. B In *Biological reclamation and monitoring of disturbed lands: materials of the IX All-Russian scientific conference with international participation*, Ekaterinburg, 113–18.