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Soil Microbiota and Particulars of Formation thereof under Traditional and Organic Farming on Chernozem Soils of Northern Kazakhstan

The subject matter of the study is soil microbiota of southern carbonate chernozem and particulars of formation thereof under organic and traditional methods of wheat growing under conditions of Northern Kazakhstan. It has been found that soil microbiota varies with arable farming systems. Application of leguminous and cereal above-ground biomass as organic fertilizers contributed to higher numbers of immobilizers that were twice as high as traditional farming variants. When applied as green manure, sweet clover above-ground biomass increased the number of ammonifying soil organisms (up to 6 million CFU/g a.d.s.), while bromegrass biomass increased the number of immobilizers (83.0 million CFU/g a.d.s.) and fungi (8,0 thousand CFU/g a.d.s.). Cellulose-destroying microorganisms were actively propagating in wheat crops (65.0 CFU/g a.d.s.) where wheatgrass biomass was applied as green manure, while sweet clover biomass, on the contrary, contributed to decrease thereof. Under traditional farming conditions, the introduction of ammonium nitrate into rows when planting crops at a dose of N80 stimulated the development of cellulolytic microorganisms and inhibited the development of ammonifying fungi and bacteria. Ammonifiers and immobilizers were actively propagating with reserve application of ammophos in the fallow at the rate of P40.

Keywords: southern carbonate chernozem, soil microbiota, fungi, bacteria, cellulolytic microorganisms, wheat, organic and traditional arable farming.

Introduction

Soil is a heterogeneous environment for the life of most species of microorganisms that is capable to provide for their conservation and survival [1]. Microorganisms act as interlinks in biological cycles and play a significant role in the cycle of matter in Earth ecosystems. Thanks to soil microorganisms, mineralized organic matter turns into available compounds for producers [2, 3]. Besides, microorganisms are essential for soil organic matter mineralization and humification processes, being a key factor of soil formation [4, 5]. They participate in carbon and nitrogen cycles, global trophic web [6, 7]. Each physiological group determines intensity of a certain physiologic and biochemical process performed by taxonomically diversified microorganisms [8], that have various requirements for nutritive conditions and energy sources. Quantitative ratios thereof vary with environmental conditions of formation of a certain microbiota [9]. Microbial pool of microorganisms participating in maintaining homeostatic condition of soil ecosystem also performs significant ecologic functions [10].

Maintenance of diversified revivable and functioning microbial populations in the soil is critical for sustainable farming, since soil fertility depends not only on its chemical composition, but also on quantitative and qualitative character of soil-inhabiting ecologic and trophic microorganism groups [11, 12].

Soil microorganisms perform various systemically important functions. They participate in processes of soil formation, destruction of organic substances and mineralization, stimulation of plant growth and development, and plant protection from phytopathogens [13, 14].

Increased technogenic load on agricultural ecosystems results in a change of soil biota composition. In its turn, it affects microbiological processes influencing soil fertility. Changes in microbiota structure result in increase of the share of some soil microorganisms and decrease of the share of the others. Quite often, such microbiota is dominated by phytopathogens that cause farm crop diseases resulting in partial loss of yield or deteriorated quality thereof. Under modern arable farming conditions, increase of technology intensification contributes to increased farm production, which requires application of large volumes of mineral fertilizers and pesticides [15]. The latter results in changes of soil microbial flora due to modification of quantitative and qualitative composition [16, 17]. When the soil is highly saturated with agricultural chemicals, some bacterial species die, while others, being adapted to nitrogen consumption, develop faster. As the undesirable trends become more obvious, the interest to conservational agricultural practices [18]. In view of

the above, it should be noted that it is necessary to study soil microbiota as a whole, as well as taking into account farming systems in order to reduce unfavorable factors when cultivating crops.

Insufficiency of studies related to soil microbiota in chernozem soils and particulars of formation thereof in traditional and organic farming under conditions of Northern Kazakhstan predetermines comprehensive investigation of the issues in question that are critical for farm production.

The objective of this research is to study environmental trophic groups of soil microbial communities under spring soft wheat grown under conditions of traditional and organic farming.

Materials and Methods

Soil microbiota was studied from 2018 through 2020 at established experimental plots of "A.I. Barayev Research and Production Center for Grain Farming" LLP (N51°36'44,47»; E71°02'40,27») in the grain and fallow three-course rotations (fallow-wheat-wheat). Soil phase is low-humous southern carbonated chernozem of heavy clay-loam texture. In the upper soil level (0–20 cm), humus content is 3.1 %, gross nitrogen and phosphorus content is 0.20 % and 0.11 %, carbonate content, around 5 %. Arable soil layer active acidity is mildly alkaline (pH=7.2). Nitrate nitrogen content is 5.5–30.1 mg per 1 kg of soil, P2O5 (per Machigin): 20.3–35.6 mg per 1 kg of soil, mobile potassium: 550–570 mg per 1 kg of soil.

Soil microbiocenosis was studied in the variants of organic and traditional arable farming on wheat (Shortandinskaya 95 improved), the preceding crop being fallow after sweet clover.

In traditional farming, ammophos (11–46–0) was used, which was added to the fallow at a depth of 12–14 cm at the rate of P40 (control — background); on the same background, ammonium saltpeter (34–0-0) was applied in the rows during planting at various rates (N20, N40, N60, N80).

Organic farming: fertilizers in the form of dry above-ground biomass of various perennial grasses were applied in fallow: sainfoin (*Onobrychis arenaria*) — 4.71 t/ha, alfalfa (*Medicago varia Mart.*) — 4.32 t/ha, sweet clover (*Melilotus officinalis (L.) Pall.)* — 4.71 t/ha, bromegrass (*Bromus inermis Leyss.)* — 5.71 t/ha, wheatgrass (*Agropyron pectiniforme Roem. et Schult)* — 4.85 t/ha.

Organic and mineral fertilizer rates are calculated with due account primarily for soil phosphorus deficit-free balance. The experiments are established in 4 randomized replications on plots of 4.3x30 m (129 m^2).

The timing, norms and depth of sowing spring soft wheat are in accordance with the recommendations for the research area.

Seeding and fertilizer application were performed with the SZS-2.1 duck-foot seed drill. With traditional farming, various herbicides, fungicides and insecticides were applied. At wheat tillering stage, tank mixture of herbicides was used: Esthete (0.6 l/ha) combined with Granstar (15 g/ha) and Trend (120 g/ha); at the booting stage, a combination of Falcon fungicide (0.5 l/ha) + Puma Super 7.5 graminicide (1.0 l/ha) + Angio insecticide (0.1 l/ha) was applied; Falcon fungicide at the rate of 0.6 l/ha was applied at the grain filling stage. No pesticides were applied under organic farming.

Soil samples were taken before wheat seeding and at complete ripeness in various soil profile horizons (0–10, 10–20. 20–3- cm) into sterile envelopes [19]. Microbiological analyses for identification and investigation of environmental trophic groups were performed in fresh soil samples per established practices [20].

Soil weighted portion (10 g) was placed into a sample flask with 100 ml of sterile water and then was stirred for 10 minutes with OS-20 shaker at 120 rpm.

Soil suspension was plated per limited dilution technique on agar media with two replications: ammonifying bacteria on meat-and-peptone agar (MPA); immobilizer bacteria and actinomycetes on starch-and-ammonia agar (SAA); fungi on Czapek medium; cellulose-destroying aerobic bacteria, including micromycetes, on Hutchinson medium (with blotting paper as a source of carbon).

The incubation was performed in a temperature-controlled cabinet at 25–27°C. Soil microorganisms were registered on various dates: on the 3^{rd} day — bacteria; on the 5^{th}–7^{th} day — fungi; on the 30^{th} day — cellulolytic bacteria. The number of microorganisms was expressed as the number of colony-forming units (CFU) per 1 gram of absolutely dry soil (a.d.s.) [21].

To identify microorganisms, classic (based on microorganism microscopy and use of determinants) and biomolecular methods were used.

Classic method. 3–10 days after incubation, soil micromycete colonies that developed on the culture medium were visually inspected with due attention paid to the following: form and margin of the colony, texture of aerial mycelium, color and reversal thereof; with bacteria, form and margin of the colony, as well as pigmentation. To conduct the microscopy, preserved and live microorganism preparations (slide test) were prepared in accordance with the method described in [22].

Soil microorganism microscopy was carried out with *Altami Bio 1* digital binocular microscope with the use of magnifying eyepieces (x15) providing magnification power from 600 to 1500 (for fungi and bacteria, respectively) as depended on the eyepiece magnification power (40x and 100x).

When bacteria were microscoped, morphological characters were taken into account (form and size of cells and relative positions thereof, type of flagellation, existence of capsules, capability of sporulation, particular characteristics of internal constitution), as well as Gram staining related to cell wall configuration, with the use of determinants [23–25].

When identifying soil fungi, major attention was paid to cell morphology and structure. With *Deuteromycetes* (*Fungi imperfecti*), major attention was focused on ways of conidial sporulation. Conidia formed directly on vegetative mycelium or on conidiophore, the so-called specialized offshoots of vegetative mycelium hyphae that differ morphologically from vegetative mycelial paraphyses. Conidia formation is one-step and takes a form of catenulae or heads. Conidiophore development was on hyphae or on a stroma (tight plexus of vegetative hyphae) with formation of various types of conidiophore aggregations: sporodochia, pionnotes or papilliform sporodochia, etc.

The investigation rated conidia form, color and envelope, existence of dissepiments, type of conidia formation, particularly phialospores with *Fusarium, Phyalophora, Cylindrocarpon* fungi. Determinators were used for fungi identifications [26–29].

Biomolecular method. Additionally, to elaborate the specific name of some fungal isolates, a biomolecular method was used that included definition analysis of direct nucleotide sequence of the ITS region (intergenic transcribed spacer region) and subsequent identification of nucleotide identity with sequences deposited in the Gene Bank international database. The PCR reaction was performed with primers ITS 5 5’ — ggaagtaaaagtcgtaacaagg -3’ and ITS 4 5’- tcctccgcttattgatatgc -3’ in the total volume of 30 mcl. The PCR program was implemented with the use of DNA Engine Tetrad 2 Cycler PTC-0240 (Bio-Rad) thermocycler.

Genetic identification of bacterial isolates was conducted on the basis of *16S rRNA* nucleotide sequence analysis. DNA was isolated by the method described by Kate Wilson that allows to effectively isolate DNA from gram-negative and gram-positive bacteria. The PCR reaction was performed with multipurpose primers [30] 8f 5’ — AgAgTTTgATCCTggCTCAg-3 and 806R- 5’ ggACTACCAgggTATCTAAT in the total volume of 30 mcl. The PCR program was implemented with the use of GeneAmp PCR System 9700 (Applied Biosystems) thermocycler.

For statistical data processing, the SNEDECOR software package [31] and Excel (for dispersion and correlation analysis) were used. The results were presented graphically using Microsoft Excel.

Meteorological conditions. During the research period, meteorological conditions were favorable in general, however changeable temperature profile and uneven rainfall distribution across months and weeks were registered during growing seasons.

In May 2018, the temperature profile was 3,7°C lower than the long-term annual average (12.4°C). Rainfall amount in June was 29.0 mm higher than the long-term annual average (Fig. 1).

In July, weather conditions were around the long-term annual averages. In August, the amount of rainfall was substantial, being, in fact, twice higher than the long-term annual averages (40.0 mm), while the temperature profile was 4.8°C lower than normal. Precipitation level in October was within the norm, while the temperature was lower than the long-term annual averages, amounting to 1.2°C.

May 2019 was characterized by actually triple shortfall of rainfall. The monthly precipitation amount was as low as 10.1 mm, while the long-term annual average norm is 32.4 mm. In June, the amount of rainfall was 39.5 mm, i.e. within the long-term annual average norm, which contributed to wheat development. During the first and second ten-day periods of July there was no rainfall, which to a considerable extent inhibited wheat growth. Insufficient rainfall amount was also registered in August (first and second ten-day periods), however, in the third ten-day period the amount of rain shower precipitation was 21.7 mm. Climatic conditions of early spring and summer of 2020 were characterized by higher temperatures. Spring was dryer, there was practically no rainfall in March and in May. However, in April the amount of precipitation was substantial, exceeding the norm 1.9 times. Ambient air temperature over all the months was over 3,0°C higher than normal. Then, severe atmospheric drought was registered for around 50 days (up to 26 June) followed by a heavy rainfall of 39.5 mm (a monthly norm) within two days. Precipitation in July was 46.6 mm, which was actually at the level of the long-term average (57.0 mm). Precipitation that fell at the beginning of the month contributed to sufficient moisture in the root layer. The temperature profile was 2.2°C below the long-term average. The first and third ten days of August were characterized by dry weather.

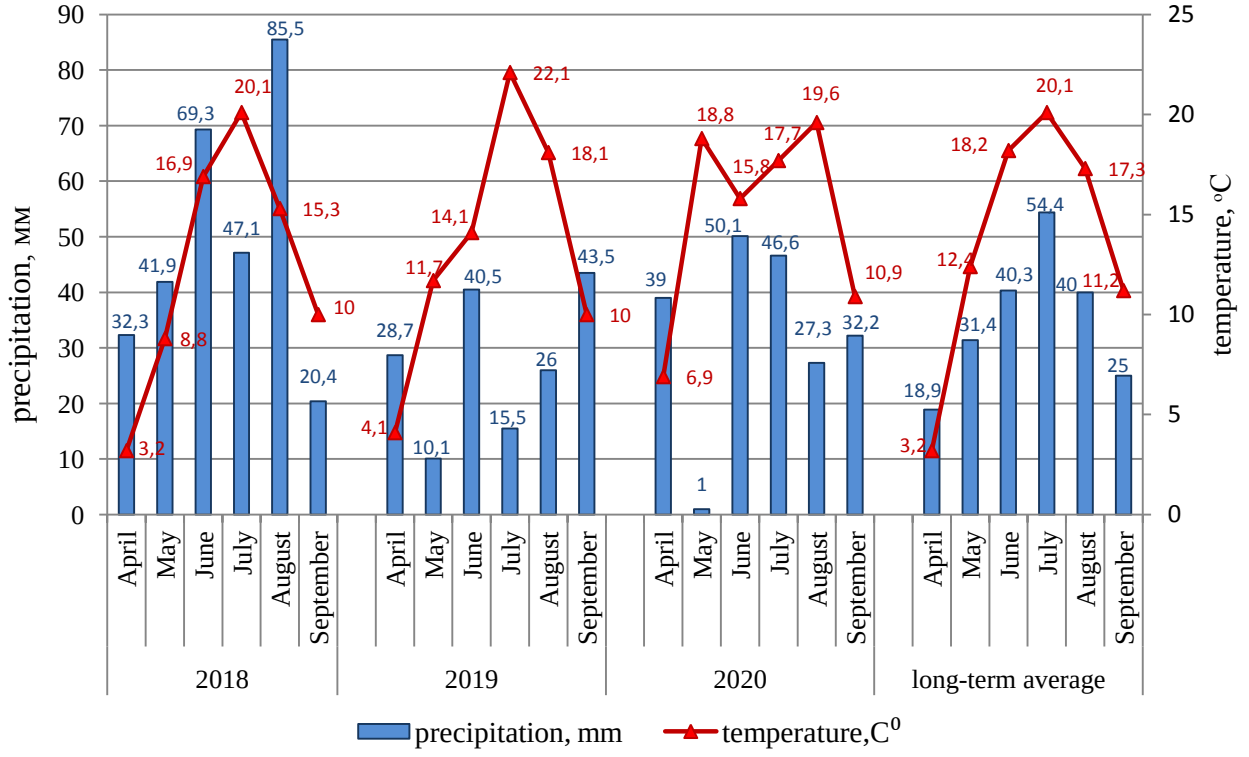

Figure 1. Climatic chart for wheat growing periods

Results and Discussion

Under traditional and organic farming, soil microbiota under spring soft wheat crops was represented by various microorganism groups, population thereof varying with soil horizons and experiment variants.

On average over the three year of the research, under conditions of traditional farming, the population of ammonifiers in the layer of 0–30 cm varied from 1.8 to 6.6 million CFU/g a.d.s. (Fig. 2).

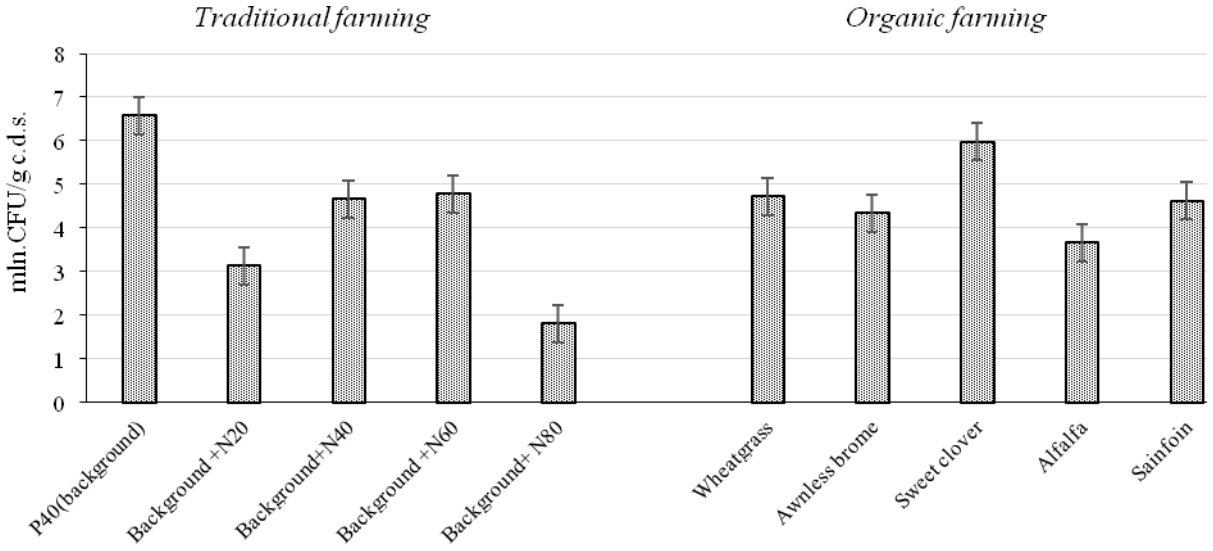

Figure 2. The number of ammonifying bacteria under wheat crops in the soil layer of 0–30 cm (average for 2018–2020)

The active growth of ammonifiers was contributed by application of ammophos into fallows at the rate of P40, when the population thereof grew up to 7.0 million CFU/g a.d.s. The same situation occurred with

the application of sweet clover biomass, which contributed to the growth of ammonifying bacteria up (to 6.0 million CFU/g a.d.s.). Ammonifying microorganisms in the soil, due to emission of enzymes that enrich the soil with nitrogen and other compounds. At the same time, a sanitary role is performed: cleaning the soil of decomposable organic substrate.

All the variants studied were characterized by regular reduction of the number of ammonifiers in the lower layers of the soil plowing horizon. The given group of microorganisms developed actively in soil layers of 0–10 cm and 10–20 cm (Fig. 3). Under traditional farming, the number of ammonifiers was maximal in the layer of 0–10 cm in the variant with sole amorphous and amounted to 6.39 million CFU/g a.d.s., while additional application of ammonium saltpeter ate rate of N40 increased that number to 7.44 million CFU/g a.d.s. In the soil level of 10–20 cm, the maximal number of ammonifying bacteria: 8.71 million CFU/g a.d.s., was registered in variants with ammonium saltpeter application at the rate of N60. In the soil level of 20–30 cm, the maximal number of ammonifying bacteria was registered in the sole phosphorus variant (P40): 7.79 million CFU/g a.d.s.

Under organic farming, the highest number of ammonifying bacteria was detected in the 0–10 cm layer in the variants with the biomass of sweet clover, sainfoin and bromegrass (9.08, 7.45 and 6.29 million CFU/g a.d.s. respectively).

The following ammonifying microorganisms were isolated: sporogenous aerobic bacteria *Bac.mesentericus*, *Bac.subtilis*, *Bac.megatherium*, and non-sporogenous aerobic ammonifiers: *Ps. fluorescens, Proteus vulgaris.*

Therefore, application of perennial grass above-surface biomass as green manure contributes to active development of ammonifiers.

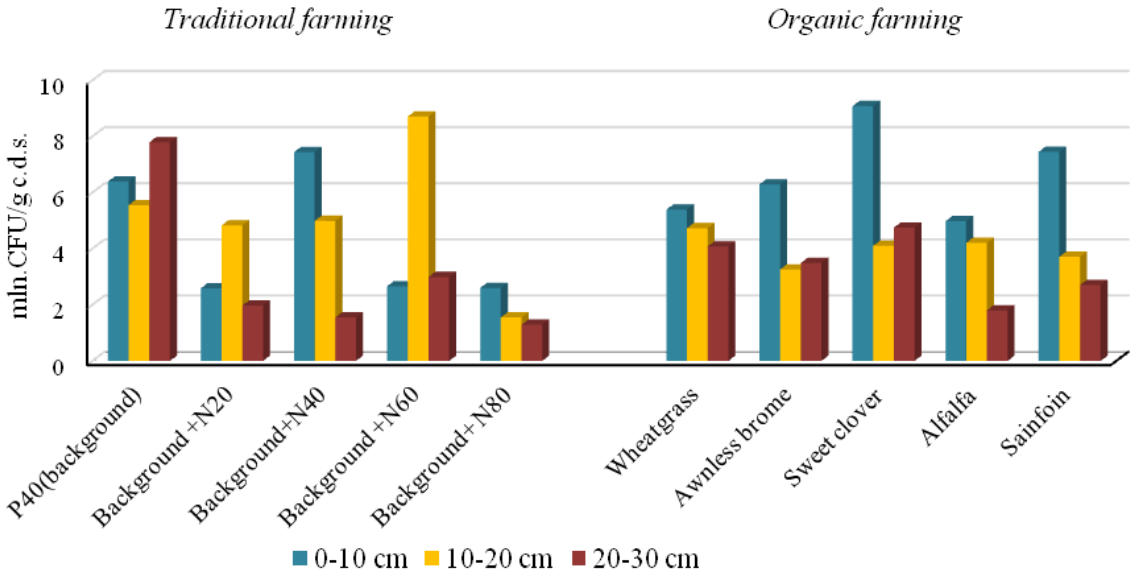

Figure 3. Distribution of ammonifying bacteria in the soil layer of 0–30 cm (on average for 2018–2020)

The bacterial complex was dominated by immobilizers, the population thereof was actually 3 to 19 times higher than that of ammonifying bacteria. On the average, over the years of the research, in the variants with traditional farming their population varied with variants from 7.11 to 36.1 million CFU/g a.d.s., while with organic farming it varied from 16.8 to 82.6 million CFU/g a.d.s. (Fig. 4).

A large population of microorganisms that assimilate inorganic nitrogen was identified in the variant with phosphorus application under traditional farming (32.4 million CFU/g a.d.s.) and in the variant with the application of bromegrass biomass as a fertilizer under organic farming (83.0 million CFU/g a.d.s.).

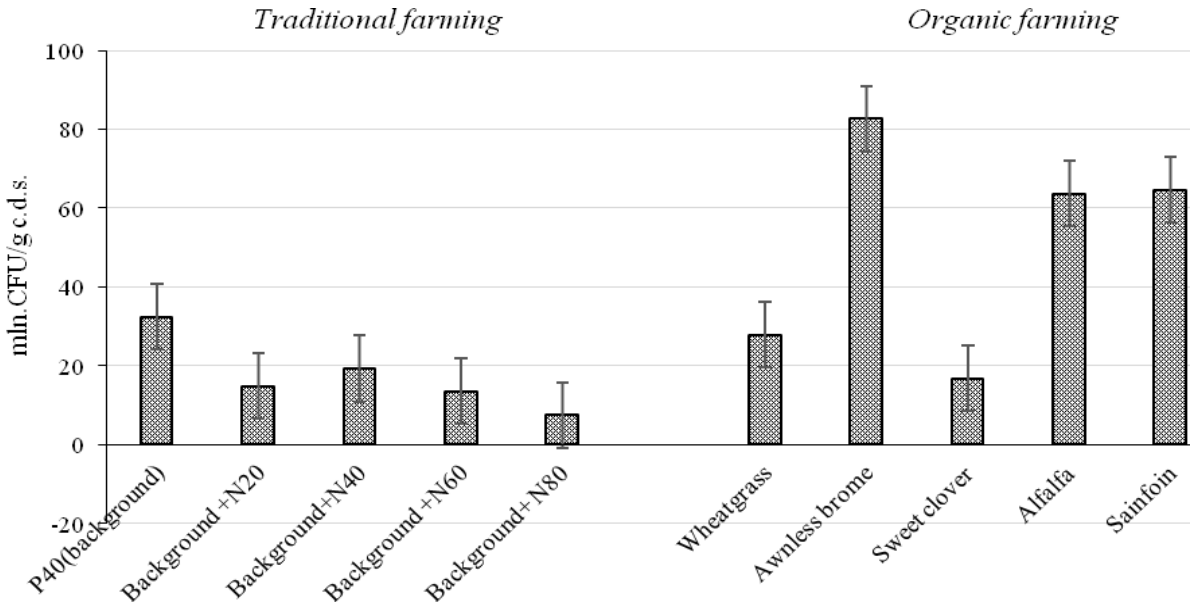

Figure 4. The number of immobilizing bacteria under wheat crops in the soil layer 0–30 cm (average for 2018–2020)

As a whole, it can be noted that both immobilizers and ammonifiers developed most actively in the variants with application of organic fertilizers. Distribution of immobilizers over soil layers was uneven, the development was more active in the layers of 0–10 and 10–20 cm, while in the layer of 20–30 cm the number of immobilizers was low (Fig. 5). That group of microorganisms was represented by various species of bacteria and actinomycetes. Micromycetes were also present, however in singular quantities.

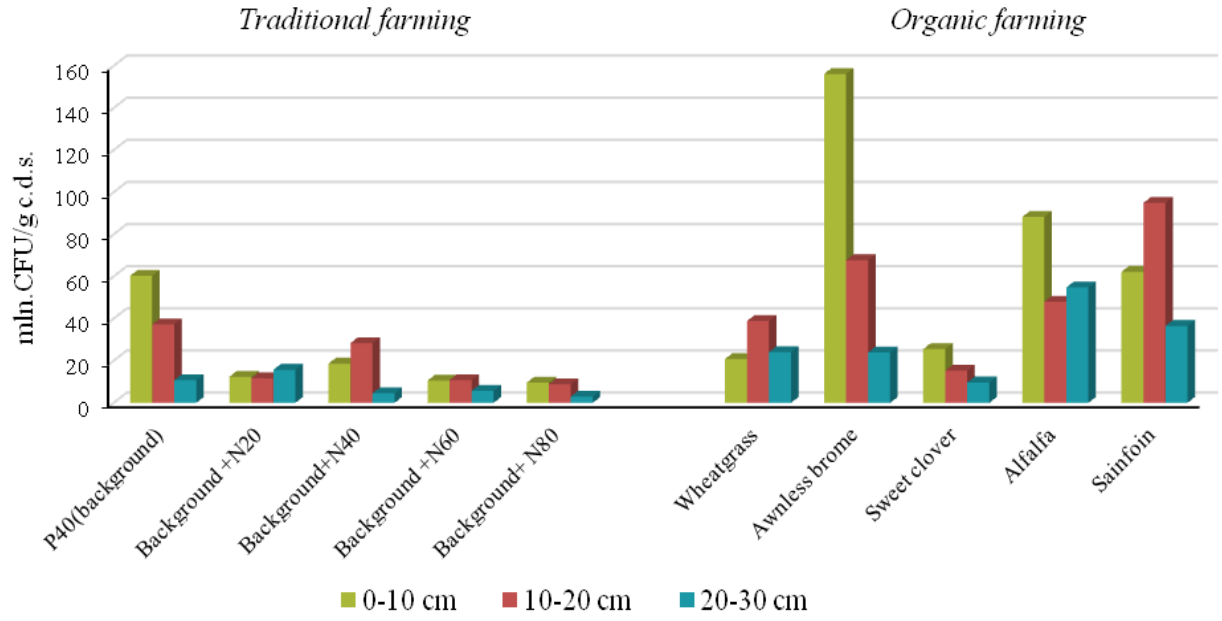

Figure 5. Distribution of immobilizer bacteria over soil layers (average for 2018–2020)

Under traditional farming, the number of immobilizers in the soil layer of 0–30 cm varied from 7.46 million CFU/g a.d.s. (in the variant with nitrogen rate N80) to 32.44 million CFU/g a.d.s. (in the variant with phosphorus). Application of moderate rates of mineral fertilizers contributed to increment of soil bacterial

microflora, which contributed to enhancement of mineralization processes. Similar data were obtained in another research [32].

Under organic farming conditions, the smallest population of immobilizing bacteria in the 0–30 cm soil layer was found in the variant with sweet clover biomass — about 17.0 million CFU/g a.d.s, while with application of bromegrass biomass, the population thereof substantially increased to 82.6 million CFU/g a.d.s., especially in the soil layer of 0–10 cm, where the population of immobilizers was especially large: 156.0 million CFU/g a.d.s. It should also be noted that with application of sainfoin biomass, the population thereof in the soil layer of 10–20 cm increased to 95.0 million CFU/g a.d.s., while with application of alfalfa biomass, the population in the soil layer of 2–30 cm amounted to 54.8 million CFU/g a.d.s.

Application of bromegrass biomass contributed to active development of immobilizer microorganisms.

The fungal complex was represented by various types of soil micromycetes (Penicillium spp., Aspergillus spp., Trichoderma spp., Fusarium spp., Mucor spp., etc.)

On the average for the period of 2018–2020, the number of fungi varied with variants from 4,0 to 6.0 thousand CFU/g a.d.s. The maximal quantity of fungi was registered in the variant with ammonium saltpeter at the rate of N40 (Fig. 6).

It is well known that soil fungi participate in the processes of fermentation of organic compounds and are sensitive to high rates of mineral fertilizers [33], however, with application of ammonium saltpeter at the rate of N80, their population was very low: 3.8 thousand CFU/g a.d.s.

Under organic farming, the total number of fungi varied from 5.6 thousand CFU/g a.d.s. (the variant with alfalfa biomass) to 7.8 thousand CFU/g a.d.s. (variant with bromegrass biomass).

Fungi distribution over soil layers varied significantly, however the fungus pool prominently tended to reduce with depth. That was a consistent pattern on variants with the use of phosphorus (P40) and nitrogen-phosphorus (N60 and N80) fertilizers in traditional farming, as well as with the use of sweet clover, wheatgrass and sainfoin biomass in organic farming (Fig. 7).

In the remaining variants active accumulation occurred in the soil layer of 10–20 cm.

Population dynamics of soil fungi varied with years and variants of the experiment, while the number thereof tended to grow by the third year of the research, especially in the soil layers of 0–10 and 10–20 cm, which is due to soil saturation with fresh plant residues and sufficient soil moisture content during the vegetation period. Under organic farming, bromegrass and sainfoin biomasses used in the capacity of fertilizers contributed to substantial increase of micromycete population.

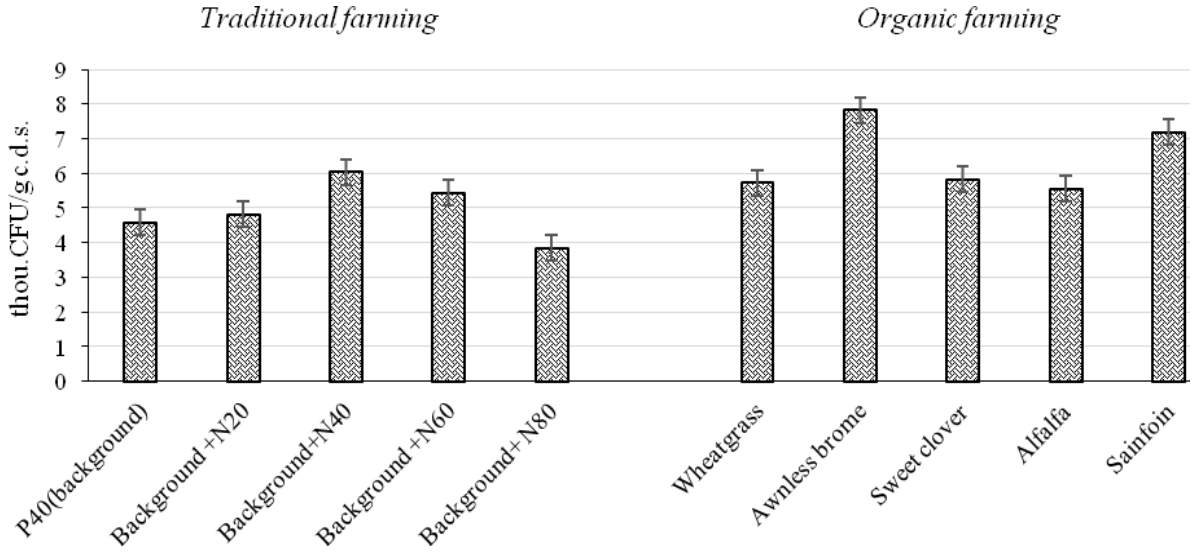

Figure 6. Populations of fungi under wheat crops in the soil layer of 0–30 cm (average for 2018–2020)

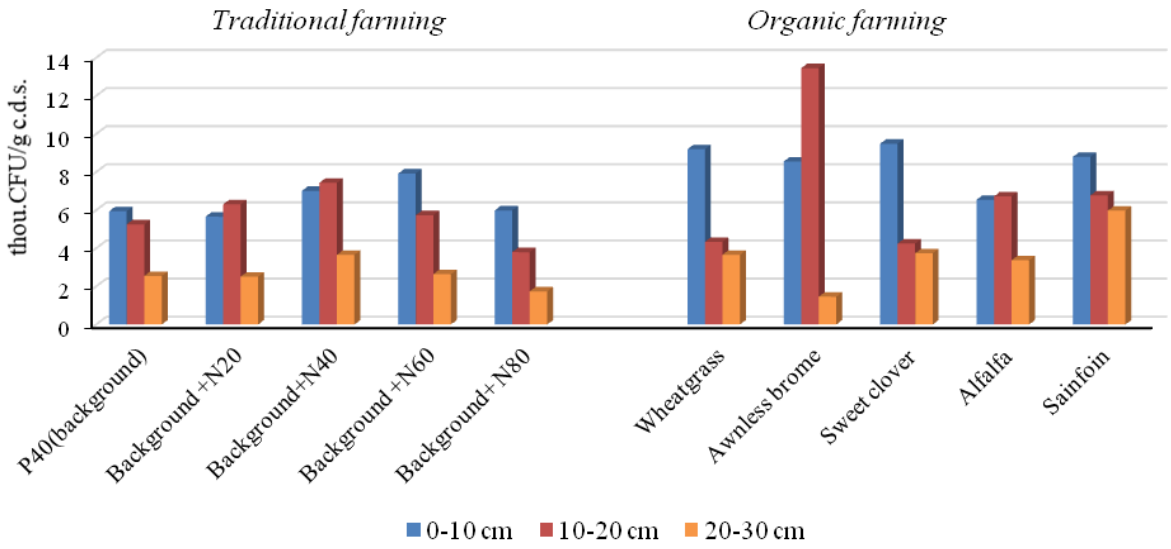

Figure 7. Distribution of fungi over the soil layers (average for 2018–2020)

The number of cellulolytic microorganisms was on the same level irrespective of the farming system. On average, over the three years of research it varied from 39.3 to 63.7 thousand CFU/g a.d.s. under traditional farming and from 32.4 to 64.5 thousand CFU/g a.d.s. under organic farming (Fig. 8).

Under traditional faming, the maximal quantity of cellulolytic organisms was registered in the variant with ammonium saltpeter row application at the rate of N80 (63.7 thousand CFU/g a.d.s.) while the minimal quantity was registered with nitrogen fertilizer application at the rate of N40 (39.3 thousand CFU/g a.d.s.).

Under organic farming, the maximal quantity of cellulolytic bacteria was registered with the application of wheatgrass biomass (64.5 thousand CFU/g a.d.s.), while the application of sweet clover and bromegrass biomass reduced the population thereof by half (32.4 and 32.6 thousand CFU/g a.d.s., respectively).

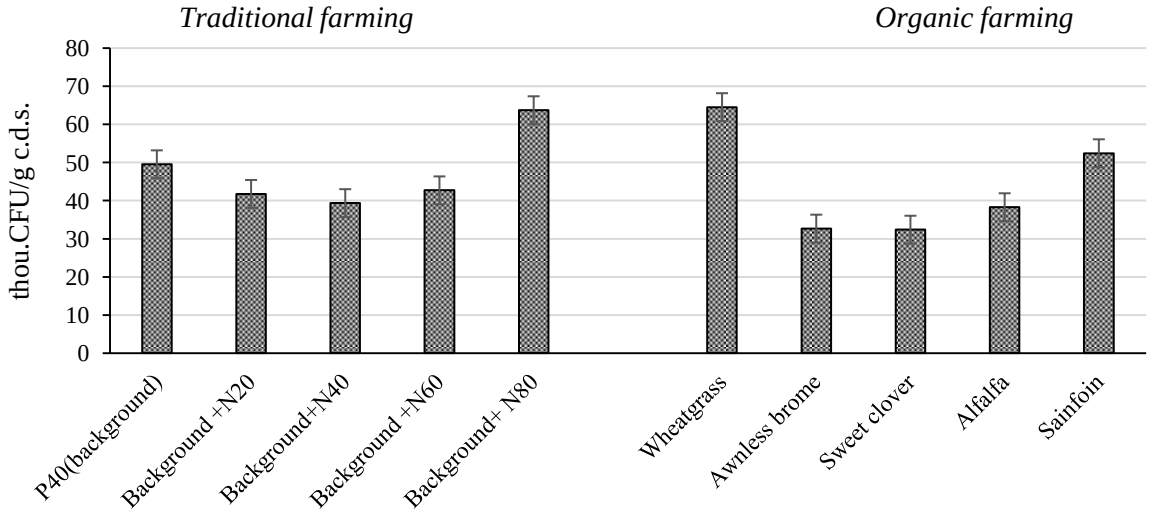

Figure 8. Numerical composition of cellulose-destroying microorganisms under wheat crops in the soil layer of 0–30 cm (2018–2020)

Distribution of cellulose-destroying microorganisms over arable soil layers was uneven. Depending on the experimental options, the largest number of cellulolytic bacteria was identified in the layer of 0–10 cm and 10–20 cm, the smallest — at a depth of 20–30 cm (Fig. 9). This can be explained by the slight accumulation of plant residues on a given soil horizon and their use in cultivating the land. In particular, the use of flat-cutting implements only loosens the soil, but does not cultivate it.

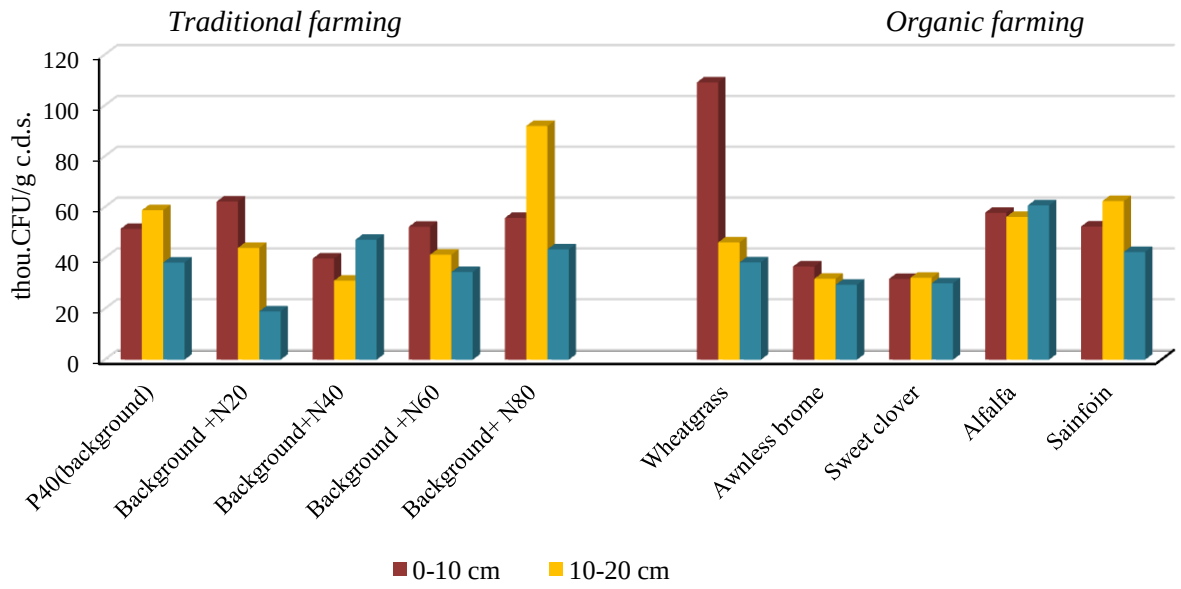

Figure 9. Distribution of cellulolytic microorganisms over soil layers (average for 2018–2020)

Among representatives of cellulolytic microorganisms there were isolated actinomycetes, bacteria and fungi, including *Trichoderma spp., Chaetomium sp., Fusarium spp., Mucor.*

Figure 10 shows major environmental trophic groups of microorganisms isolated from the soil (0–30 cm) under wheat crops grown under traditional and organic farming. Species composition thereof was practically identical with the exception of quantitative ratio.

Figure 10. Soil microorganisms isolated from soil under traditional (A) and organic (B) farming systems

Conclusion

The study of the soil microbiota under wheat crops cultivated under traditional and organic farming allowed made it to identify that make it possible to identify microorganisms belonging to various ecological and trophic groups that participate in various soil biochemical processes.

Regular application of dry biomass of perennial grasses, even more so of bromegrass, in the capacity of organic fertilizers, resulted in increase of population and biodiversity of soil microorganisms, specifically ammonifiers and immobilizers.

Fungi actively propagated with soil application of bromegrass and sainfoin biomass. Application of sainfoin and wheatgrass biomass contributed to the increase of cellulolytic bacteria quantity up to 64.5 thousand CFU/g a.d.s., while application of sweet clover biomass reduced the quantity thereof (down to 32.6 thousand CFU/g a.d.s.).

Distribution of microorganisms over soil layers was uneven. They mostly prevailed in the upper layer (0–10 cm) and the number thereof significantly decreased with depth, especially in the layer of 20–30 cm. No major differences were identified in the species composition.

Under traditional faming, application of ammonium saltpeter at the rate N80 contributed to active development of cellulolytic microorganisms, but retarded development of fungi and ammonifiers. Reserve application of ammophos in the fallow field at the rate P40 contributed to active propagation of bacteria (ammonifiers and immobilizers).

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Топырақ микробценозы және оның қалыптасу ерекшеліктері Солтүстік Қазақстанның қара жер топырақтарында дәстүрлі және органикалық егіншілік

Оңтүстік карбонатты қара топырақтың топырақ микробценозы және Солтүстік Қазақстан жағдайында бидай өсірудің органикалық және дәстүрлі технологиясы кезінде оның қалыптасу ерекшеліктері зерттелді. Топырақ микробценозасы егіншілік жүйесіне байланысты өзгеретіні анықталды. Топыраққа органикалық тыңайтқыш ретінде бұршақ және дәнді шөптердің жерүсті биомассасын енгізу дәстүрлі егіншілік нұсқаларынан екі есе көп иммобилизаторлардың сандық құрамының артуына ықпал етті. Тыңайтқыш ретінде қолданылатын түйежоңышқаның жерүсті биомассасы топырақтағы аммонификациялаушы микроорганизмдердің (6,0 млн. ҚҚБ/г м.қ.т. дейін), ал қылтықсыз арпабас биомассасы — иммобилизаторлар (83,0 млн. ҚҚБ/г м.қ.т.) және саңырауқұлақтардың (8,0 мың ҚҚБ/г м.қ.т.) санын арттырды. Целлюлоза түзетін микроорганизмдер бидай дақылдарының егістігінде белсенді дамыды, онда тыңайтқыш ретінде еркешөп биомассасы енгізілді (65,0 мың ҚҚБ/г м.қ.т.), керісінше, түйежоңышқа мен қылтықсыз арпабастың биомассасы олардың төмендеуіне ықпал етті. Дәстүрлі егіншілікте N 80 дозасында себу кезінде қатарға аммиак селитрасын енгізу целлюлозолитикалық микроорганизмдердің дамуын ынталандырды, бірақ саңырауқұлақтар мен аммонификатор бактерияларының дамуын тежеді. Аммонификаторлар мен иммобилизаторлар Р40 дозасында сүрі танабына енгізу кезінде белсенді дамыды.

Кілт сөздер: оңтүстік карбонатты қара топырақтар, топырақ микробоценозы, саңыраукұлақтар, бактериялар, целлюлозолитикалық микроорганизмдер, бидай, органикалық және дәстүрлі егіншілік.

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Почвенный микробоценоз и особенности его формирования при традиционном и органическом земледелии на черноземных почвах Северного Казахстана

Изучен почвенный микробоценоз чернозема южного карбонатного и особенности его формирования при органической и традиционной технологии возделывания пшеницы в условиях Северного Казахстана. Установлено, что почвенный микробоценоз изменяется в зависимости от системы земледелия. Внесение надземной биомассы бобовых и злаковых трав в качестве органических удобрений в почву способствовало увеличению численного состава иммобилизаторов, которые в два раза превышали варианты традиционного земледелия. Вносимая в качестве удобрения надземная биомасса донника увеличивала количество аммонифицирующих микроорганизмов в почве (до 6,0 млн КОЕ/г а.с.п.), а биомасса костреца — иммобилизаторов (83,0 млн КОЕ/г а.с.п.) и грибов (8,0 тыс. КОЕ/г а.с.п.). Целлюлозоразрущающие микроорганизмы активно развивались под посевами пшеницы, где в качестве удобрения вносили биомассу житняка (65,0 тыс. КОЕ/г а.с.п.), и, наоборот, биомасса донника и костреца способствовала их снижению. В традиционном земледелии внесение аммиачной селитры в рядки при посеве в дозе N80 стимулировало развитие целлюлозолитических микроорганизмов, но сдерживало развитие грибов и бактерий аммонификаторов. Аммонификаторы и иммобилизаторы активно развивались при внесении аммофоса в запас в паровое поле в дозе P40.

Ключевые слова: чернозем южный карбонатный, почвенный микробоценоз, грибы, бактерии, целлюлозолитические микроорганизмы, пшеница, органическое и традиционное земледелие.

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