

ANTIBIOTIC POLLUTION IN THE CONTEXT OF BIOPHYSICAL DEGRADATION OF ARABLE CHERNOZEMS (CONCEPTUAL- SYNTHETIC APPROACH)

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Abstract. The antibiotic pollution is evaluated as a component of the biophysical degradation of genetically arable chernozems determined both by the input of antibiotics into the soil with organic fertilizers based on waste from livestock, composts and biohumus obtained from them, with plant residues of crops that accumulate antibiotics in tissues, with phytosanitary products (fungicides) and by antibiotic substances produced by the soil biome in polluting quantities under the action of stress factors induced by climatic instability and agrogenetics. Its achievement is supported by unidirectional bioenergetic (humic) and structural-functional (aggregate) degradation responsible for reducing the impact and effects caused by the accumulation of antibiotics. Many processes modulated by antibiotics may be inherently critical for the producing bacteria, such as substrate acquisition or the initiation of developmental changes that will ensure survival under stress conditions. Antibiotics may also have many and important roles in more complex interactions, including virulence on host plants or shaping the outcomes of multitrophic interactions. The innate functions of antibiotics for producing bacteria in their native ecosystem are only beginning to emerge, but current and recent research highlights also a wide range of activities that go far beyond the historical perspective of antibiotics as participation in microbial competitions.

Keywords: antibiotic pollution, chernozem soils, organic fertilizers, soil microbiome

INTRODUCTION

The problem of soil pollution with antibiotics has come to the attention of research relatively recently due to its increasingly noticeable effects as well as its multilateral impacts on the soil ecosystem, especially the microbial community (Fig 1). In this context, its magnitude is comparable to pollution with phytosanitary products, especially pesticides.

In the context of what is presented in Fig. 1. We consider that the production of antibiotics is a basic function of the soil ecosystem and a product of its evolution on the pedological scale of time, conforming/adapting to changes in environmental factors, especially climatic and biological. Through this prism of ideas it was found that even in very low concentrations of antibiotics in the soil (below the minimum inhibitory concentration) they create conditions for genetic changes in bacterial genomes and the transfer of antibiotic resistance genes (ARG) (Cycon et al., 2019).

In this context, soil microorganisms (actinomycetes, bacteria, fungi) produce antibiotics to suppress the growth of competitors and capture resources (space, nutrients).

At the same time, plants, through root exudates, secrete organic antibiotics (phytoncides) into the soil that protect plants and rhizospheric microflora by suppressing pathogenic organisms. At the same time, symbiotic bacteria that develop on plant roots produce antibiotics that protect the plant from various pathologies.

Thus, the environments associated with soil and plants harbor numerous species of bacteria that produce antibiotic metabolites with specific or broad-spectrum activities against coexisting microorganisms.

The function and ecological importance of antibiotics have long been considered to provide a survival advantage to producer bacteria in highly competitive, but resource-limited soil environments, through direct suppression.

Although specific antibiotics can increase the persistence of producers when challenged by competitors or predators in soil habitats, at subinhibitory concentrations, they have a wide variety of other roles and functions in the life cycle of producer bacteria.

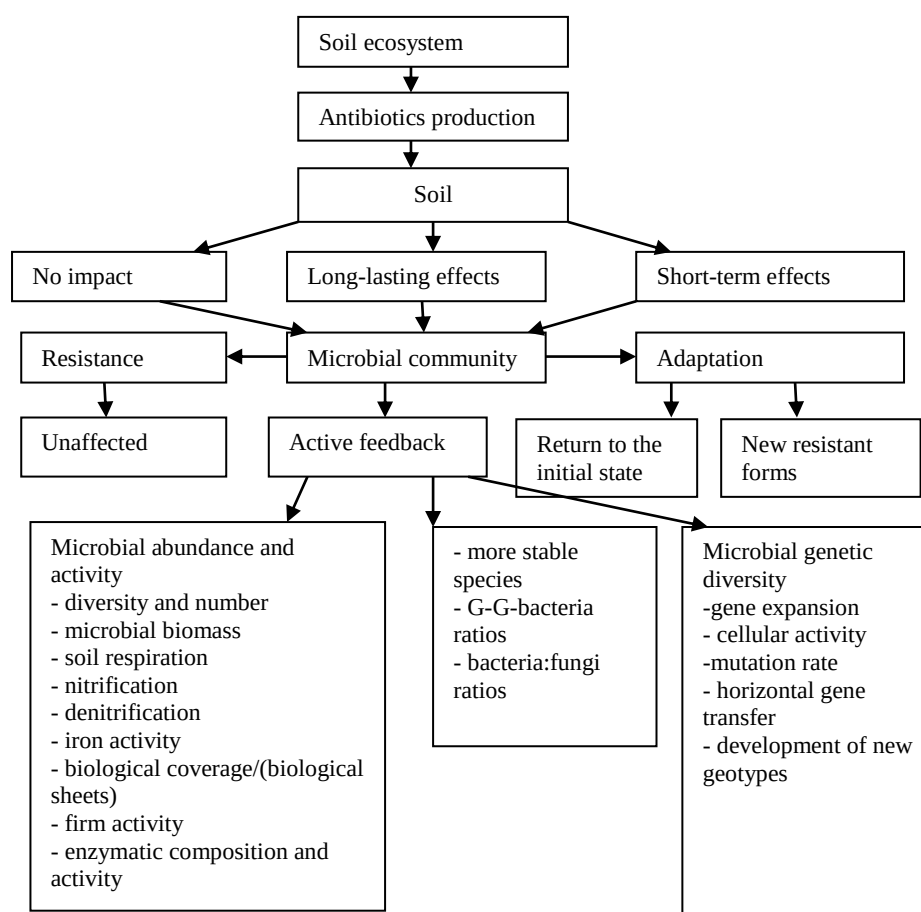


Figure 1. Diversity and natural functions of antibiotics produced by beneficial and phytopathogenic bacteria

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Although specific antibiotics can increase the persistence of producers when challenged by competitors or predators in soil habitats, at subinhibitory concentrations, they have a wide variety of other roles and functions in the life cycle of producer bacteria.

Many processes modulated by antibiotics may be inherently critical for the producing bacteria, such as substrate acquisition or the initiation of developmental changes that will ensure survival under stress conditions. Antibiotics may also have roles in more complex interactions, including virulence on host plants or shaping the outcomes of multitrophic interactions. The innate functions of antibiotics for producing bacteria in their native ecosystem are only beginning to emerge, but current research highlights a wide range of activities that go far beyond the historical perspective of antibiotics as participation in microbial competitions (Raaijmakers & Mazzola, 2012).

In addition to soil contamination with antibiotics, the accumulation of their breakdown products in agricultural products and the identified negative impact on the bacterial genome through the formation of resistance genes, the influence of antibiotics on the activity and structure of soil microbial communities should be mentioned.

Soil microorganisms perform numerous vital processes and contribute to maintaining soil health and fertility. In addition, many microorganisms act as biological control agents, inhibiting the growth of plant pathogens.

When released into the soil, antibiotics exhibit high antimicrobial activity, inhibiting the growth of not only pathogenic microorganisms, but also beneficial ones in the soil, while disrupting the composition and abundance of the microbial community and altering the ecological function of the soil.

In high concentrations, antibiotics inhibit nitrification, phosphate mobilization and the activity of ferrous bacteria, which has a direct impact on the availability of nitrogen and phosphorus for agricultural crops. At the same time, the reverse action of antibiotics on denitrifying bacteria has been observed - they can intensify this process, inevitably leading to nitrogen loss from the soil.

From the perspective of the systemic approach to the soil ecosystem, the degree of vulnerability to antibiotic pollution and the negative effects induced by them depend on the condition of the soils.

From the perspective of the concept of eco/agroecosystemic and eco/agroecological functions and services of soils, the negative impact of antibiotics on the soil ecosystem is determined by the properties of the soil, especially the granulometric composition and the degree of its homogeneity, the structural composition and the degree of hydrostability of the aggregates, the apparent density, the volume and composition of the pore space, the humus content and the composition of the humic system, the aerohydric and hydrothermal regimes materialized in the abundance and composition of the soil microflora, the antibiotic capacity/antibiotic activity and antibiotic resistance of the soil.

MATERIAL AND METHODS

The conceptual-theoretical framework for assessing and managing the antibiotic status of soils, especially chernozems, is provided by the concept of soil ecosystem health, which is based on its self-regulating capacity as a parabiotic bioroutine system in which microorganisms (bacteria, fungi, actinomycetes) produce antibiotics for competition (space) and competition (resources). This system contributes to maintaining soil health, fertility and resistance to pathogens, materialized in the antibiotic resistome, antibiotic capacity.

The synthetic analysis of the approach to soil antibiotic degradation implies the conclusion that it, in most cases, is examined without taking into account the functionality of the soil ecosystem, with emphasis placed on external sources of contamination: fertilization with manure of various origins, organic fertilizers, especially composts and biohumus obtained based on them, the return to soils of plant residues, including crops that extract antibiotics from the soil and accumulate them in tissues, the use of fungicides and insecticides based on antibiotic substances (Chec-Sanford et al., 2009; Pepper et al., 2018; Verlicchi & Alaukidy, 2012). At the same time, however, antibiotic resistance genes have also been identified in microorganisms that have never previously had contact with the products of human activity (Finley et al., 2013), indicating the connection between the problem of antibiotic resistance and the complex ecological and evolutionary relationships between microorganisms established long before the emergence of man as a species (Supotnitskiy, 2011).

Antibiotic resistance of microorganisms is an indispensable attribute of any microbial community, and its mechanisms reflect the ability to restore the community in the event of various disturbances and is materialized in the buffering capacity of the soil to antibiotic contamination (Baquero et al., 2009).

This represents a complex of ecosystem processes determined by the intersection of the physical, chemical and biological subsystems of the soil system, materialized in the properties of absorbing antibiotics and decomposing them over time.

From the perspective of the biophysical concept of the functioning of chernozems, the antibiotic capacity/antibiotic activity is their ability to regulate, through the dynamics of aerohydric and hydrothermal regimes, the mass, number, diversity and activity of the soil microbiome in accordance with the bioenergetic potential (organic matter resources), as well as the ratio between beneficial and pathogenic microorganisms due to the formation of antibiotic substances secreted by the soil microbiota.

This mechanism constitutes the core of the soil resistome (Kozevin et al., 2013; Vinogradova et al., 2013).

In this context, in our research, the soil is examined for the first time as a functional component of the ecosystem, a saprotrophic biological community (pedocenosis) a living global reservoir of antibiotic resistance genes constituted within the process of evolution of the soil microbiome at the pedological time scale, the driving force of the constitution process being the interaction of the soil ecosystem with the environmental factors of the agroecosystem (Jigău et al., 2025).

In this sense, recently in the framework of functional ecology a new concept has been formulated about the ecosystem as a symbiotic unit of biocenoses, specialized by types of nutrition (phytocenosis, zoocenosis and pedocenosis) united by a common metabolic circuit, and the soil as a component of it, performs a very specific function within it and has its own unique mechanism for this function which is part of the ecosystem functioning mechanism (Kerzentsev, 2006).

Through this prism of ideas, the issue of intelligent management of soil functions to increase its health, fertility and resistance to various stresses and pathologies (soil degradation) is one of the most pressing (Jigău et al., 2025).

The specified features materialize in the antibiotic state of the soil - a complex ecofunctional property that characterizes the capacity of the soil ecosystem microbiome to produce antibiotic substances to perform its protective functions, minimize the impact of external antibiotics and support the unidirectional realization of eco/agroecosystemic and eco/agroecological functions and services responsible for soil health and fertility.

In the context of the above, this is a genetically determined feature, a product of the interdetermined and interdetermined interactive development of typogenetic processes, and as a result varies depending on the type and subtype of pedogenesis.

Through this prism of ideas, chernozems are characterized by a high degree of antibiotic resistance, a product of the interdependent and interdetermined quantitative and qualitative interconnection of humification and aggregation-structuring processes materialized in the humus and structural-aggregate state.

In this sense, the antibiotic state of the soil is a function of the content and composition of humus manifested in the aggregation-structuring of the soil mass (the basic function of humus) and of the structural-aggregate composition manifested in the aërohydric and hydrothermal regimes (the basic function of the aggregate structure of soils).

In this context, humus plays a decisive role in soil detoxification, having an active action on the decomposition and neutralization of antibiotics, both those incorporated with organic fertilizers and those of microbial origin. Some antibiotics can be present in organic/vegetable residues being adsorbed in plants during vegetation.

Humic substances are characterized by high adsorption capacity determined by the large specific area and functional groups (carboxylic, hydroxylic, phenolic, amine).

In this sense, we mention that antibiotics, similar to other substances of biological origin, have amphiphilicity, manifesting hydrophobic-hydrophilic properties.

Through this prism of ideas, we consider that these, similar to humic substances, can be adsorbed on the surface of fine particles (<0.005 mm) of clay minerals. The first are absorbed hydrophilic substances, coating the clay particles and subsequently attracting hydrophobic substances to the surface of the newly created organomineral complex.

Thus, antibiotics are stabilized in organomineral compounds. At the same time, antibiotics are adsorbed by humus, the mechanism being similar to the one described above and involves the retention of hydrophilic fulvic acids on the surface of mineral particles, and the newly formed fulvic organomineral compound can easily absorb hydrophobic antibiotic

substances. In this sense, we consider that this mechanism is determined by the content and composition of humus in the soil. In this case, humic substances reduce the mobility of antibiotics and the degree of their accessibility to plants and microorganisms.

The role of humus in reducing antibiotic contamination is also determined by its quality, since humus is a nutritional bioenergetic source for soil microorganisms. In our research, from the perspective of the biophysical concept of the chernozem pedogenesis process, humus is a bioroutine system in which the vast majority of soil microorganisms are concentrated. Thus, the high humus content supports the biological activity of the microflora, which is capable of decomposing complex organic compounds, including antibiotics. At the same time, humus provides conditions in which microorganisms adapt and are able to use some antibiotics as a source of nutrition by decomposing them.

In the context of the described mechanisms, the aggregate structure of the soil plays a key role in ensuring optimal bioaerohydric and biohydrothermal conditions for their decomposition.

Structural aggregates, especially aggregates >1 mm, represent refuges for soil microbiota.

The decisive role in the decomposition of antibiotics belongs to the species Actinomycetes, Pseudomonas, Bacillus, Azotobacter, Azospirillum and Trichoderma fungi.

Actinomycetes develop more intensively in agronomically valuable chernozem aggregates 0.25-5 mm, the content of which in chernozems makes up more than 50%. They are characterized by a predominantly aerobic aerohydric regime that favors the intensive decomposition of organic compounds with a high degree of stability (cellulose, lignin, chitin) including antibiotic substances.

The Pseudomonas species develops in the pores of all agronomically valuable aggregates (0.25-10 mm), more intensively, but their activity is in aggregates with a diameter of 1-2 mm and in interaggregate pores. The Bacillus species develops in aggregates 0.25-10 mm, but optimal conditions for the decomposition of antibiotics are provided in aggregates 0.25-5 mm.

Trichoderma is characterized by higher functional intensity in the pores of aggregates >0.25 mm in the rhizosphere of crop plants.

Azospirillum and Azotobacter species are found in all 0.25-10 mm aggregates, but optimal conditions for them are created in 2-10 mm aggregates.

Through this prism of ideas, the aggregate structure of the soil is the key factor that determines not only the antibiotic activity of soils but also its dynamics during the vegetation period.

In this context, we mention that in arable chernozems, unlike native ones, the structural-aggregate composition is very dynamic, being influenced by the cultivation systems practiced and their degree of compatibility with the self-reproduction potential of the aggregate structure, the particularities of the cultivated crops and the moisture regime of the soils.

The content of fine clay and humus in the structural aggregates determines the degree of retention ensuring physical protection for antibiotics. Strong sorption/physical protection reduces the degree of their exposure to microbial action, reducing their decomposition. At the same time, however, in such a state (absorbed) they are not active nor toxic for the environment.

The interdependent and interdetermined interacting functions of humus and the aggregate structure of soils are achieved through their state of settlement materialized in the apparent density, total volume and composition of the porous space.

Through this prism of ideas, the volume, composition and functions of the porous space are indispensably dependent on the interdependent and interdetermined interacting development of the humification process and the aggregation-structuring process. This involves the quantitatively and qualitatively balanced intercalation of the basic function of humus and the basic function of the soil structure materialized in the dynamics of porous spaces with various functions in the soil (Tab. 1) and in the functioning of the soil ecosystem determined by the totality of processes that occur in the soil under the action of both the modification of the internal pedogenetic environment (pedogenetic and pedofunctional regimes) and the external one, the latter being determined, first of all, by climatic conditions (Tab. 2).

The total volume of pores, the composition of the porous space and the hydrophysical parameters of soils in terms of soil water content (CC), the degree of mobility (CO) and their accessibility depend on the dynamics of the apparent density of soils (Tab. 3).

Table 1

Functions of pores with various dimensions (Jigău, 2022)

Pore Sizes, μ	Meanings/Implications
>500	Microcracks that form preferential water movement paths; cause excessive increase in infiltration rate and water loss from the active biopedogenetic layer.
250-500	Transmission pores that ensure gas exchange in the soil-environment system.
250-100	Regime-determining pores that ensure the balance between oxidation and reduction processes in soils.
100-50	Draining pores that ensure the dynamics of elementary processes in soils.
50-0,5	Moisture-conducting pores that ensure water reserves in the soil.
0,5-0,005	Residual moisture-protective pores that determine unproductive water reserves with implications on the thermal characteristics and physical-mechanical properties of soils.
<0,005	Textural pores that ensure the stability of micro- and macroaggregates

Table 2

The role of pore space in the functioning of the soil ecosystem (Jigău, 2022)

Pore group	Pore diameter		Water relations	Root Access	Redox regime	Features of biochemical processes
	mm	mkm				
Macropores	10	10000	Easy to drain	Accessible	Oxidant	Intensive mineralization, low content of freshly produced humus
	1	1000				
	0,1	100				
Mesopores	0,01	10	Moisture conductors and protectors	Accessible	Redox	Processes of humification and mineralization of unstable humic substances. Processes of condensation, maturation, sequestration and stabilization of humic substances
	0,001	1				
Micropores	0,00001	0,1	Permanently	Inaccessible	Reducer	Processes of

	0,00001	0,01	occupied by physically bound water			formation of organo- mineral compounds
	0,000001	0,001				

Table 3

Differential porosity and hydrophysical parameters of arable chernozems depending on the degree of compactness (loamy, clayey and clay soils)

Apparent density, g/cm ³	Total porosity, %	Differential porosity, %					Hydrophysical indices, % g/g		
		<0,2 mKm	0,2-1,0 nKm	1,0-60 mKm	60-300 mKm	>300 mKm	CO	CC	DAU
1,00-1,25	54,7	7,3	8,8	24,0	7,9	6,7	10,3	28,8	18,5
1,26-1,40	48,8	10,8	9,2	19,6	5,9	2,8	11,4	27,6	15,2
1,41-1,45	46,7	11,3	9,4	20,0	4,3	1,7	12,0	26,9	14,9
1,46-1,50	43,7	13,2	10,4	18,2	1,9	0	12,6	26,3	13,7
1,51-1,55	42,0	16,9	10,5	12,9	1,7	0	13,3	26,4	12,8
1,56-1,60	39,7	16,9	10,3	11,2	1,3	0	14,8	25,5	10,7

CO – wilting coefficient

CC – field water capacity

DAU – usable water range

RESULTS AND DISCUSSIONS

Management of the antibiotic status of arable chernozems through the concept of biophysical degradation

Biophysical degradation of soils involves the development of an interdependent and interdetermined interaction in soils of a complex of physical and biological processes of degradation of the structural-functional organization of the soil ecosystem manifested in the disruption of eco/agroecosystem functions and services responsible for its self-organization, self-regulation, self-purification and self-reproduction. Its quantitative and qualitative expression is soil health and fertility.

Through this prism of ideas, soil health and fertility are interdependent and interdetermined interacting features produced by chernozem typogenetic processes a) formation-accumulation of humus b) aggregation-structuring of the soil mass with stabilization of humus in the soil (Jigau, 2009; Jigau, 2017; Jigau et al., 2022; Vislozilova et al., 2016).

In this sense, according to our research, the genesis of chernozems involves the quantitatively and qualitatively interdependent and interdetermined interactive development of the humification process and the aggregation-structuring process manifested in the intercalation of the humiferous profile and the structural-aggregate one materialized in the chernozem progressive accumulative pedogenetic profile.

Through this prism of ideas, eco/agroecosystemic functions and services are genetically determined and are receptive to the degradative impacts induced by changing environmental factors but also those induced by agrogenic pedogenetic processes.

In this sense, in our research, through the perspective of the biophysical concept of chernozem genesis within the current phase of evolution of arable chernozems, the chernozem process of solification is determined by the syntransformational processes determined by the changes in the internal pedogenetic environment, especially in the pedogenetic (hydric, thermal, aeration) and pedofunctional (aerohydric, hydrothermal, deoxido-reduction) regimes materialized in the modification of the soil climate, which, together with the specific particularities of agrophytocenoses, led to the radical modification of the soil biota, especially

the composition, diversity, number and mass, the space of vital activity and its duration (Sincovscaia, 2012).

In this context, the specified research showed that the microbial carbon content in the arable layer (0-30 cm) is 1.3-1.6 times lower than in standard soils. Biomass reserves in the 0-100 cm layer have decreased from 5.9-12.7 t/ha dry mass in cultivated and fallowed soils to 3.6-7.2 t/ha in arable soils.

As a result of the change in the way of storing plant residues and their quantity in the composition of fungi and bacteria, the groups characteristic of the steppe litter have decreased. At the same time, in the composition of microorganisms that decompose humic substances, the ratio between bacteria and fungi increases 3-4 times. In the composition of fungi, species of the genus *Penicillium* (49.5-82.2%) predominate. At the same time, representatives of the genera *Aspergillus* (13.1%), *Mucor* (6.0-12.7%), *Trichoderma* (6.5-7.5%) and *Fusarium* (1.0-7.9%) are also present. In this regard, we mention that the genera *Penicillium*, *Trichoderma* and *Aspergillus* are active producers of antibiotics that suppress the growth of bacteria and other fungal species.

We draw attention to the fact that they account for 69.1 to 100% of the entire fungal community in arable chernozems (Sincovscaia, 2012).

After the inclusion of chernozems in the agricultural circuit (the sixties of the last century), the amount of saprophages in chernozems and the mass of the Lumbricidae family decreased by 25-35%, the number of their species decreasing from 9 to 5 of them, the major share returning to two species *Apporectodea roscus* and *Lumbricus terrestris*. Among microorganisms, species that can survive in conditions of lower humus contents, lower organic matter contents and less qualitative parameters of physical and biophysical conditions develop.

Enzymatic activity compared to the initial state during the period of intensive use (50-60 decans) was reduced by 40-70% in soils, establishing a stable trend of reducing the activity of polyphenol oxidase responsible for the transformation of organic matter into humus and increasing the activity of peroxidase that favors the mineralization of organic matter.

Our more recent research has shown that the arable layer of arable chernozems is characterized by an extremely short period (3-4 weeks at the beginning of the biologically active period) of biological activity of invertebrate mesofauna (Fala et al., 2018). As a result, in arable chernozems, the microbiological processes of decomposition and transformation of plant residues are intensified, and the mineralization energy increases approximately 2 times, manifested in the disruption of the natural balance between the mineralization and humification processes characteristic of natural chernozem ecosystems in favor of mineralization (Lebedeva et al., 2013).

The truncated cycle of organic matter, the anthropogenic systematization through works, and in the last 20-25 years and through the application of various biological and biohumic preparations, of the natural processes of decomposition of plant residues, characteristic of agricultural monocultures, have modified the cycle and regime of accumulation of organic carbon and its related biophilic elements in the soil, reducing its volume and general structure.

Disturbance of natural patterns of interaction between soil organic matter and mineral substrate (mineral matrix) in common with strong mechanical impacts of agricultural machinery limits the process of self-restoration of the structural and aggregate state of arable chernozems and, respectively, of the reproduction processes of the chernozem process of pedogenesis, and is manifested in the unidirectional physical degradation of arable chernozems.

Through this prism of ideas, the direct cause of the biophysical degradation of chernozems are the negative transformations in the structural and aggregate composition, accompanied by a decrease in the total amount of organic matter accumulated in the soil and the change in its location in the structural aggregates that re-aggregate under conditions of organic matter deficit and systematic agricultural pressures.

The degradation of the structural and aggregate composition, the essence of which consists in the total reduction of the hydrostability of aggregates >5 mm, significantly of those 5-3 mm, and partial of aggregates 2-3 mm, is accompanied by a significant weakening of the mechanisms of stabilization of organic matter in the soil, which in the form of feedback stimulates the subsequent negative transformation of the physical state of arable chernozems.

The combined negative modification of the organic matter in the soil in its quality as a biotic component and of the structural and aggregate composition in its quality as a modeled abiotic component of chernozems determines the disruption of the functioning of the genetic-evolutionary system [humic system]↔[aggregate system] responsible for the reproduction of typogenetic processes and, respectively, of chernozem typogenetic processes.

Through this prism of ideas, biophysical degradation is genetically determined.

In this context, the fact that the morphogenetic profile of chernozems bears features largely characteristic of native chernozems, including static properties, implies the conclusion that their profile is inherited from the pre-agrogenic period of solifaction (Jigau et al., 2026). At the same time, however, appreciated, through the prism of the hierarchy of levels of structural-functional organization of the soil ecosystem, implies the conclusion that it manifests itself only at the higher level "Profile". Already at the "horizon" level within the ecological system of arable chernozems the arable horizon is distinguished by features and functions and pedofunctional services that are not characteristic of the humus-accumulative chernozem horizon of native chernozems.

From the perspective of the hierarchy and functional interaction of the chernozem profile the specified changes in the arable layer inevitably lead to changes in the cycle of substances in the soil profile and, respectively, on the composition and functioning of the soil biota manifested in the reduction of biological activity and, respectively, increased vulnerability to antibiotic pollution.

In our research these aspects are evaluated from the perspective of the evolution of the aggregate structure of soils and, respectively, their biological activity, including antibiotic activity.

In this sense, from the perspective of the examined concept, the structural-aggregate composition of chernozems is one of the main factors that determine the activity of the respective soil biota, and the activity of antibiotic decomposition, this being a function of the degree of structuring of the soil mass and its stability and is materialized in the interdependent laws between the structural-aggregate state and the settlement indices of the soil.

According to them, the settlement state indices (apparent density, total pore volume and composition of the porous space) are, indispensably dependent on the degree of soil structuring and the degree of stability.

In general, it is considered that the higher the degree of aggregation-structuring of the soil mass, the greater the volume of the porous space, and, respectively, the lower the apparent density values.

The achievement of this law requires the presence of equal contents (50:50) of 5-10 mm and 0.25-5 mm aggregates in soils.

According to our research, despite the agrogenesis-induced transformation in the aggregation-structuring process in arable chernozems in the area between the Prut and the Dniester, this law is achieved (Jigău et al., 2022). In this sense, the content of agronomically valuable aggregates (0.25-10 mm) makes up, in most cases, 75-85%. In their composition, about 35-40% belongs to coarse aggregates (5-10 mm) and another about 60-65% belongs to 0.25-5 mm aggregates. At the same time, however, the content of hydrostable aggregates >0.25 mm in rare cases exceeds 65%. In most cases, it makes up 40-55%.

As a result, arable chernozems are characterized by a high degree of vulnerability to compaction caused by the loosening of aggregates upon wetting and only partial self-restoration of the profile. Based on this, we propose to use the parameters of the hydrostability state of structural aggregates (Tab. 4) to evaluate the degree of stability of the arable chernozem profile and, respectively, the state of settlement indices manifested in the stability of the aeration regime, the aerohydric regime and biological activity, and the parameters presented in Tab. 5 and 6 to evaluate the aeration porosity.

Table 4

Stability of the aerohydric regime of arable chernozems in the degree of hydrostability of structural aggregates

Hydrostable aggregate content >0.25 mm, %	Degree of stability of the aggregate profile	Dynamics of settlement indices (apparent density, pore space)	Aeration regime	Aerohydric regime	Biological activity
>65	Very high	Stable	Stable optimal	Optimal	High
55-65	High	Attenuated	Optimal	Optimal	High
50-55	Moderate	Weak-moderate-disturbed	Relatively optimal	Relatively optimal	Good
40-50	Satisfactory	Disturbed	Satisfactory	Satisfactory	Low
<40	Poor	Pronounced	Critical	Critical	Low

Table 5

Ranges of values of aeration space (aeration porosity) depending on apparent (loamy and clayey grain size composition) (n=884 profiles)

Apparent density	Total porosity, %	Aeration porosity	Specifications	Aerohydric regime
<1,10	>55,0	>25,0	Excessive	Strongly aerobic with periods of anaerobic respiration
1,10-1,25	55,0-50,0	20,0-25,0	Optimal	Aerobic
1,25-1,30	50-48,0	20,0-15,0	Moderate	Aerobic Anaerobic
1,30-1,40	48,0-45,0	15,0-12,0	Satisfactory	Anaerobic-aerobic
1,40-1,50	45,0-42,0	12,0-8,0	Critical	Anaerobic
>1,50	<42	<8,0	Unsatisfactory	Pronounced Anaerobic

Table 6

Norms of the parameters of the chernozem settlement indices for the purpose of controlled management of the content of antibiotics/organic contaminants in the chernozems of the area between the Prut and the Dniester (layer 0-30 cm)

Parameters	Normative values		
	optimal	admissible	critical
Carbonate and typical weakly humiferous clayey and clayey loamy chernozems			
Equilibrium bulk density,	1,15-1,25	1,25-1,35	>1,35

g/cm ³			
Total porosity, %	55,0-51,0	50,0-47,0	<47,0
Aeration porosity (W=CC), %	15,0-25,0	15,0-10,0	<10,0
Porosity of aggregates 5-7 mm, %	40,0-42,0	40,0-35,0	<35,0
Porosity of aggregates 3-1 mm, %	38,0-40,0	33,0-35,0	<33,0
Typical moderately humus-rich, clayey and clay-loamy chernozems			
Equilibrium bulk density, g/cm ³	1,10-1,30	1,30-1,35	>1,35
Total porosity, %	56,0-51,0	50,0-46,0	<46,0
Aeration porosity (W=CC), %	15,0-25,0	15,0-10,0	<10,0
Porosity of aggregates 5-7 mm, %	42,0-44,0	41,0-38,0	>37,0
Porosity of aggregates 3-1 mm, %	40,0-42,0	39,0-35,0	<34,0
Clayey and clayey-loamy livigated chernozems			
Equilibrium bulk density, g/cm ³	1,10-1,25	1,30-1,40	<1,41
Total porosity, %	55,0-60,0	53,0-46,0	<46
Aeration porosity (W=CC), %	15,0-25,0	14,0-10,0	<10
Porosity of aggregates 5-7 mm, %	40,0-42,0	39,0-31,0	<33,0
Porosity of aggregates 3-1 mm, %	35,0-40,0	34,0-32,0	<32
Clay-iluvial chernozems, clayey and clayey loams			
Equilibrium bulk density, g/cm ³	1,15-1,30	1,31-1,40	>1,42
Total porosity, %	55,0-49,0	47,0-44,0	<44,0
Aeration porosity (W=CC), %	15,0-25,0	14,0-12,0	<12,0
Porosity of aggregates 5-7 mm, %	40,0-42,0	39,0-34,0	<34,0
Porosity of aggregates 3-1 mm, %	33,0-35,0	32,0-30,0	<30,0

In light of the parameters specified in Table 6, we draw attention to the relatively identical values regardless of taxonomic affiliation at the subtype level. This implies the conclusion that the degradative processes established in soils have led to the development of an identical degradative trend in soils. In this sense, we consider that the evolution of antibiotic resistance and its state is determined exclusively by the antibiotic factor. Therefore, the unidirectional development of biophysical degradation, especially bioenergetic (humic) and structural-functional (aggregate) degradation, will inevitably lead to an increase in the vulnerability of arable chernozems to antibiotic degradation, and this in turn to an intensification of typogenetic degradation.

At the same time, according to our research, the current phase of anthropo-natural chernozem pedogenesis arable chernozems are receptive to external energy inputs within the framework of pedoregenerative practices based on controlled humification.

CONCLUSIONS

Antibiotic pollution represents a new form of genetic degradation determined by the increase, over time, of anthropogenic pressures on soils (fertilization with manure, of various origins, composts and biocomposts obtained based on them, use of phytosanitary products, especially fungicides) of stress factors caused by the intercalated action of climatic instability and pedodegradative processes. In this sense, antibiotic pollution is an indispensable process dependent on the biophysical state of soils, a component part of biophysical degradation. The unidirectional development of biophysical degradation involves the risk of an accelerated increase in the vulnerability of arable chernozems to antibiotic pollution. Its reduction involves the substantiation and promotion of pedoregenerative agrobiotechnologies based on controlled humification.

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