



General characteristics of pathogenic mycobiota of fodder plants of Azerbaijan

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Abstract

In the conducted researches fodder plants growing in the conditions of Azerbaijan were analyzed according to the fungal biota. It was found that 110 species of fungi are involved in the formation of the mycobiota of fodder plants, and 74.5% of the total mycobiota belong to Ascomycota, 18.2% to Basidiomycota and 7.3% to Zygomycetes (Mucormycota). According to the specific weight of phytopathogens, *Artemisia vulgaris* and *Medicago sativa* differ from other plants, and in this case, the difference is manifested by the fact that the specific weight of phytopathogens in *A. vulgaris* is the lowest in the total mycobiota, and *M. sativa* is the highest. It became clear that 70 species of these fungi belong to phytopathogens, of which 37.1% has specific characteristics of necrotrophic, 35.7% of biotrophs, and 27.1% of hemibiotrophs.

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Introduction

The increasing number of the world's population and the fact that this is happening on the Earth, which is stable against the background of the reduction of the areas used by people for food purposes, has put humanity in the face of a number of problems. This includes issues such as lack of food, energy, raw materials for industry and others. If we add to these the global problems of the globalized world, first of all, such as global warming and biodiversity loss, then we can see that the situation on Earth is not so encouraging. Among the mentioned problems, the problems related to the demand for food and fodder of the Earth's population, as well as other living beings, are of particular importance. Today, serious problems are felt in providing people with quality food products. It would be appropriate to touch on some facts in this regard.

According to the estimates of the UN FAO, 783 million people are currently suffering from hunger and this number is increasing (<https://www.who.int/news/item/12-07-2023-122-million-more-people-pushed-into-hunger-since-2019-due-to-multiple-crises--reveals-un-report>, Oluwole *et al.*, 2023). So, according to various forecasts, the number of the Earth's population in 2050 is likely to be 9.3 billion, that is, the population is expected to increase by 1.33 times. In return for this increase, it will be necessary to increase the production of agricultural products by about 1.5 times in order to meet the demand for food products of the people living on the Earth. This forecast is based on crops grown on the Earth's land used by humans for food production today. If we take into account the lands that lose their suitability for cultivation due to salinization, desertification and other conditions every year as a result of global warming, urbanization and other processes, then it will be necessary to increase the productivity per hectare more.

The basis of human food is traditionally the products of plants and animals. Nevertheless, among the food products used by people, there are also products obtained with the participation of

microorganisms, primarily bacteria and fungi, and the proportion of products obtained from the mentioned sources is gradually changing in favor of microorganisms. Nevertheless, plants and animals still remain the main source of food for humans and for this reason, first of all, the protection of plants, their effective use, is one of important tasks that needs to be solved due to the realities of today's globalized world.

It should be noted that the data on the number of species of living things on the Earth at the moment differ sharply from each other, and this number is recorded from 2 (Costello *et al.*, 2012) million to 3 (Lennon and Locey, 2016) trillion. Different systems are built (Wiens, 2023) by approaching these numbers from the point of view of what is known to science and what is actual in nature and according to those systems, the number of species currently known to science on Earth is 8.7 (± 1.3) million species, of which 2.2 (± 0.18) million live in seas, and the rest live on land. Currently, a total of 1.2 million species of these creatures have been catalogued. 86% of the living things on earth and 91% of those in the sea are waiting for their description (Mora, 2011). Nevertheless, according to 2023 date, the number of species of flowering plants known to science is shown to be 369 thousand species. Nevertheless, according to 2023 date, the number of species of flowering plants known to science is shown to be 369 thousand species. If we add primitive plants here, the total number of species included in the plant world is around 550 thousand (<https://www.statista.com/statistics/264674/biodiversity-worldwide>) which makes up 9% of the world's flora. Nevertheless, the fact that most types of plants are found in a not so large area makes it possible to note the richness of the flora of Azerbaijan (<https://science.gov.az/az/news/open/18429>). In order to use them effectively, these plants are systematized in another way, as in the world, that is, they also use artificial systematization for plants. Medicinal plants, technical plants, oil plants, decorative plants, fodder plants come from such systems.

Both cultivated and wild forage plants are an indispensable group of plants necessary for the development of animal husbandry that these plants are also widespread in Azerbaijan, and the number of their species is expressed in hundreds (Humbatov *et al.*, 2013).

The majority of fodder plants grow wild or are cultivated in almost all regions of Azerbaijan, but their cultivated areas, productivity, and fodder value are different. Both cultivated and wild forage plants are not only important as fodder, but also actively participate in a number of processes typical of plants in general.

It should be noted that fodder plants contain enough nutrients for various organisms, including disease-causing organisms, which makes the spread of these organisms inevitable.

Microorganisms differ in the form of distribution in plants as well as in feed materials, that is they are characterized as epiphytes and pathogens, the latter of which cause various pathologies in plants, causing changes in their biological productivity, as well as changes in the quality indicators of those used for practical purposes. Unfortunately, in all cases, these changes are evaluated in a negative direction from a practical point of view. For this reason, the study of plants in this direction, more precisely according to phytopathogens, is one of the current research directions in most countries of the world, including in Azerbaijan. Thus, 20-40% (Ayaz *et al.*, 2023) of plant-based agricultural products are lost every year due to phytopathogenic microorganisms (bacteria, fungi, fungi-like organisms, viruses, etc.), of which at least 14.1% (<https://www.cphdforum.org/index.php/2022/05/26/plant-disease-crop-loss/>) is caused by pathogens. This is 220 billion USA dollars per year. This is a serious loss in modern times, mainly because the Earth's population is constantly increasing and this is happening within a fixed area, so today hundreds of millions of people are

already experiencing food shortages. Therefore, it is important, more precisely necessary, to conduct research aimed at preventing that loss.

Although pathogenic organisms include bacteria, fungus-like organisms, fungi, and viruses, the 70-80% of plant diseases are caused by fungi (Li *et al.*, 2021). Fungal diseases differ from others not only because of their high specific weight in common diseases, but also because of their danger and the yield loss can be 50% or more during the epiphytosity of fungal diseases (<http://agroAtlas.ru/ru/content/diseases/index.html>) and even cause the destruction of entire plants. In addition, there was no plant species in nature that fungi could not use or cause disease in. Therefore, this issue should be studied in order to keep it under control, to make their activities manageable or completely restricted. The first stage of the work carried out in this direction is the determination of the species composition of the causative agents of those diseases and the correct diagnosis of the diseases caused by them.

Although fodder plants containing enough nutrients for the spread of fungi are widespread in Azerbaijan (Humbatov *et al.*, 2013), their research in comparison with other plants, especially from the mycological (Bakhshaliyeva *et al.*, 2020) point of view, is poor and some studies are mainly related to the background of common plants (Bakhshaliyeva *et al.*, 2022). More precisely, during the mycological research of plants of various purposes, the name of the fungi (Bakhshaliyeva *et al.*, 2019) found on fodder plants, and sometimes their occurrence frequency on those plants is also found (Muradov *et al.*, 2022). All this is not enough for the general characterization of mycobiota of fodder plants, especially its pathogenic species.

Therefore, the purpose of the presented work was to study the species composition, frequency of occurrence, and the nature of the diseases caused by phytopathogens involved in the formation of the mycobiota of a number of fodder plants growing wild and cultivated in the territory of Azerbaijan.

Materials and methods

Researches were carried out in the geomorphological units of the Republic of Azerbaijan like as Kur-Araz plain, In the Greater and Male Caucasus, Talysh mountains and Lankaran plain which differ from each other in terms of climatic conditions, flora and fauna, and leading soil types (<https://eco.gov.az/az>).

Sampling for the study was carried out according to the planned route method (Tomashevich, 2015) according to accepted methods and approaches (Methods of experimental..., 1982) in mycology. In the research, samples were taken from 25 plant species which include both wild and cultivated plants.

In the course of research for the removal of fungi into pure culture were used nutrient media such as Saburo agar, agarized malt juice, agarized Çapek, potato and rice agar (Methods of experimental..., 1982).

The identification of fungi was carried out according to the known identifiers (<https://www.mycobank.org>, Kirk *et al.*, 2008, Seifert, 2011, Sutton *et al.*, 2001), which were compiled based on their cultural-morphological and physiological characteristics.

The frequency of occurrence of fungi recorded in studies and the degree of spread of diseases caused by them were determined based on the formula $P=(n/N) \times 100$, so that here P -is the incidence (or prevalence) of the disease expressed in %, N - the total number of sampled plants (number), a - the number (number) in which the fungus was identified (or diseased plants) in the samples taken.

The numerical composition of fungi was determined based on the formula $A = a \times b \times c / d$ (Mirchnik, 1988), so that where a -is the mean number of colonies in the Petri dish, b- is the amount of dilution, c- is the initial weight of the sample, d- is the dry weight of the sample.

Results and Discussion

As a result of the mycological analysis of about 1000 samples collected in different years in the research

areas determined distribution of 110 species, and the information about them was summarized in Table 1.

Table 1. Quantitative and qualitative characterization of the taxonomic structure of fungi, which are generally distributed in fodder plants, by departments

Ascomycota	Bazidiomycota	Mucormycota
82	20	8

As it can be seen, the vast majority of recorded fungi that is 74.5% of the total mycobiota, belong to *Ascomycota*, 18.2% to *Basidiomycota* and 7.3% to *Zygomycetes (Mucormycota)*. Fungi species differed in their distribution by individual taxa and the number of species belonging to each genus and the number of species of recorded fungi varied between 1-8 (Table 2).

It should be noted that fodder plants differ from each other according to a number of indicators. This difference covers areas such as their taxonomic affiliation, chemical composition, intended purpose, and so on.

One of them is related to the chemical composition of fodder plants, as they differ from each other in terms of both quantitative and qualitative indicators of their constituent components. As this difference affects their mycobiota from both a scientific and a practical point of view, the spread of fungi on individual plant species has also become the subject of research. From the results obtained from the research conducted in this regard, it became clear that the mycobiota of plants differs from each other in terms of the number of species, and this situation manifests itself in relation to both cultivated and wild plants (Table 3). Thus, from the carried out of research became clear that the richest mycobiota of forage plants is characterized *Medicago sativa* (23 species), and by the poorest mycobiota *Artemisia vulgaris* (9 species). The number of fungal species involved in the formation of the mycobiota of the rest ranges from 10 to 20.

Table 2. Distribution of fungi recorded in studies by genera

Ascomycota		Bazidiomycota		Mucormycota	
Genus	Number of species	Genus	Number of species	Genus	Number of species
<i>Aspergillus, Fusarium, Penicillium</i>	8	<i>Puccinia</i>	7	<i>Mucor</i>	5
<i>Eryshiphe</i>	6			<i>Absidia</i>	1
<i>Septoria, Trichoderma</i>	5	<i>Ustilago</i>	4	<i>Rhiso-bus</i>	
<i>Alternaria, Ascochyta, Phoma, Verticillium</i>	4	<i>Urocystis</i>	3		
		<i>Uromyces</i>			
<i>Cercospora, Sclerotina</i>	3	<i>Rhizoctonia</i>	1		
<i>Cladosporium, Colletotrichum, Ramularia</i>	2	<i>Tilletia</i>			
<i>Blumeria, Botrytis, Cephalosporium</i>	1				
<i>Claviceps, Cochliobolus</i>					
<i>Gibberella, Monilia, Paecilomyces</i>					
<i>Phomopsis, Pyrenophora, Trichothecim</i>					

As mentioned, various relationships between fungi and plants have been formed over the years, one of which is manifested in the fact that fungi cause various pathologies in plants. Among the fungi recorded in fodder plants in the course of research, there are species with sufficient information about causing various pathologies. *Alternaria, Ascochyta, Botrytis, Fusarium, Phoma, Puccinia, Septoria, Urocystis, Uromyces, Verticellium* and other genera species can be examples of this. During the determination of the distribution of the registered fungi, as well as the phytopathogenicity confirmed by us or according to literature data, on individual plants, it became clear that according to the number of species of phytopathogens, the *Medicago sativa* plant is characterized by the highest indicators, while *Artemisia vulgaris* is characterized by the lowest indicators (Table 3). Thus, more than half of the 23 fungal species involved in the formation of the mycobiota of the *Medicago sativa* plant, or more precisely 65.2%, belong to phytopathogens. In the formation of the mycobiota of *A.vulgaris* plant involved only 4 species of fungi (*Fusarium sporotrichioides, Phoma artemisiae, Puccinia artemisiicola, V. nigrescen*), whose phytopathogenicity has been confirmed according to our observations and literature data. The number of species of phytopathogenic fungi involved in the formation of the general mycobiota of the rest plant varies between 5-11. For example, 18 species of fungi are involved in the formation of the mycobiota of *Onobrychis viciaefolia* plants, 11 of which belong to phytopathogens, and these phytopathogens are

Alternaria alternata, Ascochyta sojicola, Botrytis cinerea, Fusarium oxysporium, F.solani, Phoma destructiva, Rhizoctonia solani, Stemphium botryosum, Thielaviopsis basicola, Trichothecim roseum, Verticillium albo-atrum. In the formation of the mycobiota of nother plant belonging to the leguminous family-*Trifolium repens* are involved a total 18 species, 50% of which belong to phytopaogens and those phytopathogens are fungi such as *Alternaria alternata, A.tenuissima, Botrytis cinerea, Cercospora medicaginis, Colletotrichum trifolii, Erysiphe trifolii, Fusarium moniliforme, Ramularia medicaginis* and *Trichothecim roseum.* Although the corn plant does not belong to legumes, 10 of the 18 fungal species involved in the formation of its mycobiota belong to phytopathogens and these are composed of species such as *Alternaria alternata, Botrytis cinerea, Botrytis cinerea, Cochliobolus heterostrophus, Fusarium moniliforme, F. oxysporium, F. sporotrichioides, Phoma destructiva, Septoria nodorum, Ustilago zae.* From these data is clear that, regardless of the taxonomic affiliation of this or that plant, the same species of fungi can sometimes cause disease in many and sometimes in a specific plant and depending on the plants, the combination of participation of universals and specifics is different. The specific weight of specifics is relatively high in sugar beet. Thus, a total of 17 species participate in the formation of mycobiota of the mentioned plant, and 10 (*Alternaria solani, Ascochyta betae, Cercospora beticola, Erysiphe betae, Fusarium moniliforme, F. oxysporium, Phoma betae, Ramularia betae, Trichothecim roseum,*

P.coronata) of them belong to phytopathogens. More than half of these phytopathogens, more precisely 60% (*Asc. betae*, *Cercospora beticola*, *Erysiphe betae*, *Phoma betae*, *Ramularia betae* and *Puccinia coronata*), were determined to spread only in this plant and cause the relevant disease during the course of research. In these studies, specific plants are the most represented plants. In our opinion, this is due to the fact that sugar beet root is a fruit-bearing plant,

more precisely, a succulent fodder plant, and for this reason its chemical composition has different components.

It should be noted that the main reason why fungi have become an object of research is not only the large number of diseases they cause, but also the different forms of disease they cause (Nazarov *et al.*, 2020).

Table 3. Evaluation of the investigated fodder plants according to their total and phytopathogenic mycobiota

SL	Plants	Total number of species, number	Phytopathogens	
			Number of species	Specific gravity,%
1	<i>Agrostis alba</i>	11	5	45,5
2	<i>Artemisia vulgaris</i>	9	4	44,4
3	<i>Beta vulgaris</i>	17	10	58,8
4	<i>Bromopsis inermis</i>	12	6	50,0
5	<i>Cynodon dactylon</i>	12	6	50,0
6	<i>Helianthus annuus</i>	16	9	56,3
7	<i>Hordeum vulgare</i>	18	10	55,6
8	<i>Lathyrus sativus</i>	14	7	50,0
9	<i>Malva neglecta</i>	15	8	53,3
10	<i>M. sylvestris</i>	14	7	50,0
11	<i>Medicago sativa</i>	23	15	65,2
12	<i>Melilotus officinalis</i>	10	5	50,0
13	<i>Onobrychis viciaefolia</i>	18	11	61,1
14	<i>Panicum miliaceum</i>	15	8	53,3
15	<i>Phleum pratense</i>	15	7	46,7
16	<i>Pisum arvense</i>	18	10	55,6
17	<i>Poa pratensis</i>	14	7	50,0
18	<i>Sorghum sudanense</i>	13	7	53,8
19	<i>Trifolium pratense</i>	20	11	55,0
20	<i>T. repens</i>	18	9	50,0
21	<i>Triticum aestivum</i>	16	9	56,3
22	<i>T. durum</i>	15	8	53,3
23	<i>Vicia sativa</i>	13	5	38,5
24	<i>V. villosa</i>	12	6	50,0
25	<i>Zea mays</i>	18	10	55,6
Total		110	70	53,3

As mentioned, about 80% of recorded plant diseases are caused by fungi, and about 19,000 species of fungi are known to cause plant diseases (Jain *et al.*, 2019). In addition, diseases caused by phytopathogenic fungi are generally divided into 3 groups (necrotrophs, fungal-biotrophs and hemibiotrophs) (Dyakov and Elansky, 2016). Based on this, it was considered appropriate to characterize the phytopathogenic fungi recorded in research from this aspect. From the research conducted in this regard, it became clear that 25 (*Blumeria graminis*, *Erysiphe betae*, *E. cichoracearum*, *E. communis*, *E. cruciferarum*, *E. pisi*, *E. trifolii*, *Puccinia artemisiicola*, *P. coronata*, *P.*

cynodontis, *P. graminis*, *P. helianthi*, *P. hordei*, *P. recondita*, *Tilletia caries*, *Urocystis cepulae*, *U. tritici*, *Uromyces fabae*, *U. striatus*, *U. trifolii-repentis*, *Ustilago cynodontis*, *U. nigra*, *U. hordei*, *U. tritici* and *U. zae*) species of fungi that cause rust, powdery mildew belong to biotrophs, 26 (*Alternaria alternata*, *A. solani*, *A. tenuissima*, *A. tenuis*, *Asc. betae*, *Asc. hordei*, *Asc. pisi*, *Asc. sojikota*, *Cercospora beticola*, *C. fabae*, *C. medicaginis*, *Colletotrichum gloesporioides*, *C. trifolii*, *Phoma artemisiae*, *Ph. betae*, *Ph. destructiva*, *Ph. medicaginis*, *Ramularia medicaginis*, *Rhizoctonia solani*, *Septoria helianthi*,

S. nodorum, *S. pisi*, *S. sojae*, *S. tritici*, *Thielaviopsis basicola*, *Trichothecium roseum*) species are necrotrophic fungi, and 19 (*Botrytis cinerea*, *Claviceps purpurea*, *Cochliobolus heterostrophus*, *Fusarium avenaceum*, *F. culmorum*, *F. gibbosum*, *F. moniliforme*, *F. oxysporium*, *F. solani*, *F. semitectum*, *F. sporotrichioides*, *Gibberella fujikuroi*, *Monilia sitophila*, *Pyrenophora graminea*, *Sclerotinia sclerotiorum*, *S. trifoliorum*, *Stemphiliium botryosum*, *Verticillium albo-atrum* and *V. dahliae*) species are hemibiotrophs.

More precisely, 37.1% of registered phytopathogens belong to fungal-necrotrophs, 35.7% to fungal-biotrophs, and 27.1% to hemibiotrophs. Based on this fact, it can be said that the specific weight of hemibiotrophs is low and the specific weight of biotrophs is relatively high, which can be evaluated as a positive situation. So, in terms of adaptation and substrate specificity, hemibiotrophs are considered more active, that is, their adaptability is higher, and substrate specificity is weak, that is, they are universal. Among the biotrophs, since there are more of those with substrate specificity, neither they are widespread in phytocenoses, nor do they occur in epiphytotoy.

It would be appropriate to touch on one point regarding the division of fungi according to the effect of the diseases they cause, which is related to the fact that some of the fungi belong to both hemibiotrophs and endophytes at the same time. Thus, some fungi, for example, fungi belonging to the genus *Fusarium*, can behave as both necrotrophic fungi and hemibiotrophs, as well as endophytes, by causing various diseases in plants (Vrabka *et al.*, 2029). This fact itself allows us to note that fungi are a very interesting object from a scientific and practical point of view, but a number of their properties, more precisely, their potentials, have not been revealed until the end. Among the disease-causing organisms in the world, fungi are now seriously different from other disease-causing organisms both in terms of the number of diseases they cause and the negative effect of the disease on plant productivity and have

advantages. For this reason, those phytopathogenic fungi are studied in various aspects and their degree of danger is determined individually. According to one such study, the 10 most dangerous phytopathogenic fungi are species such as *Manaportha oryzae*, *Botrytis cinerea*, *Puccinia* sp., *Fusarium graminearum*, *F.oxysporum*, *Blumeria graminis*, *Mycosphaerella graminicola*, *Colletotrichum* spp, *Ustilago mayds* and *Melampsora lini* (Dean *et al.*, 2012). By clarifying the information about some of these fungi (*Colletotrichum* spp., *Mycosphaerella graminicola*, *Puccinia* sp.), it would be reasonable to try to estimate the specific weight and the current situation of the phytopathogenic species of the mycobiota of fodder plants that are spread or cultivated in Azerbaijan.

First of all, about the studies related to *Colletotrichum* spp. can be noted that fungi belonging to this genus cause anthracnose disease in the host plant, and analysis of literature data shows that one or more of the cultivated plants in the world are susceptible to fungi belonging to this genus. These fungi become more active after harvest and can even cause 100% spoilage of stored produce. They are hemibiotrophs, their sexual reproduction is unknown, and plants such as (Manova *et al.*, 2022) *C. capsici*, *C. gloeosporioides*, *C. graminicola*, *C. trifoli* and others are among the species that cause disease.

The fungus *Mycosphaerella graminicola* belongs to teleomor, whose anamorphic form is the fungus *Septoria tritici*. The name of the disease caused by these two fungi is called septoria spotting, and studies have found its distribution in a number of areas where grain crops are grown. Fungi known as *Puccinia* spp. cause rust disease in grain plants, of which 3 forms are and considered particularly dangerous: stem rust (caused by *P. graminis*), striped (yellow) rust (*P. striiformis*) and brown (leaf) rust (*P. triticina*) (Figuroa *et al.*, 2018). The participation of the *P. graminis* fungi in the formation of the phytopathogenic mycobiota of the fodder plants of Azerbaijan has been confirmed in the course of

research. Taking into account the last mentioned data, when comparing with the phytopathogenic fungi recorded in the fodder plants of Azerbaijan, it is clear that 4 (*Botrytis cinerea*, *F.oxysporum*, *Blumeria graminis* and *Ustilago mayds*) of the 10 most dangerous fungi are species that recorded in the course of research and cause diseases. In the course of research, it was confirmed that *C. gloeosporioides*, *C. trifoli*, *P. graminis* and *Septoria tritici* species belonging to fungi like *Colletotrichum* spp., *Mycosphaerella graminicola* and *Puccinia* spp. are involved in the formation of the pathogenic mycobiota of fodder plants of Azerbaijan. In short, 7 of the 10 most dangerous fungi in the world are involved in the formation of the pathogenic mycobiota of Azerbaijan's fodder plants to one or another degree.

On the other side, the presence of fungi such as *Alternaria alternata*, *A. solani*, *Erysiphe pisi*, *Rhizoctonia solani*, *Tilletia caries*, *Trichothecium roseum*, *Verticillium dahliae* and others, which participate in the formation of the mycobiota of Azerbaijan's fodder plants, and the fact that they are the causative agents of dangerous diseases has also been experimentally confirmed in other studies (Jain *et al.*, 2019) too. Interestingly, recent studies (El-Baky and Amara, 2021) show that both the number of such fungi and their degree of danger continue to increase.

It would be appropriate to touch on a fact about the fungi belonging to the genus *Fusarium* recorded in the studies. As mentioned, the distribution of 8 *Fusarium* cinsinə aid 8 (*Fusarium avenaceum*, *F. culmorum*, *F. gibbosum*(=*F. equiseti*), *F. Moniliforme* (= *Fusarium verticillioides*), *F. oxysporium*, *F. solani*, *F. Semitectum* (= *F. incarnatum*) and *F. sporotrichioides*,) species belonging to the genus *Fusarium* was determined in the research. All these fungi, as well as their teleomorphic form - *Gibberella fujikuroi* - are involved in the development of fusariosis - the most dangerous disease of the century in fodder crops, especially grains and legumes and they are involved in the

occurrence of this disease either individually or in various combinations.

In other studies conducted on fungi of this genus, was determined that 12 (*F. acuminatum*, *F. avenaceum*, *F. equiseti*, *F. falciforme*, *F. incarnatum*, *F. oxysporium*, *F. proliferatum*, *F. redolens*, *F. solani*, *F. tricinatum*, *F. verticillioides* and *F. virguliforme*) of its species have pathogenic (Wang, 2023) activity, and they separately or combined cause fusarium root rot in the lucerne. 7 of the mentioned fungi are found in cultivated or wild fodder plants in Azerbaijan, which gives a serious reason for keeping these fungi in the center of attention and preparation of preventive measures against them.

It would not be right to mention that the situation regarding the phytopathogenic mycobiota of fodder plants is so sad today, at least for the reason that none of these fungi that cause dangerous diseases is currently not part of the dominant core of the mycobiota of fodder plants, and most of them have indicators that are characteristic of random and rare species in terms of frequency of occurrence. Nevertheless, the situation can be considered potentially dangerous. However, it is advisable to always keep this in mind and implement preventative and environmentally justified preventative measures to prevent the spread of fungal diseases. Special attention should be paid to the ecological justification of the prepared measures, which is based on the following considerations.

First, the changes in nature as a result of an increasing anthropogenic impact on the environment in modern times do not bypass living things, including plants and fungi. As a result of this, mutually formed changes occur in plant-fungus relations. In order to clarify this, it is necessary to pay special attention to the changes in the habitat of plants and fungi, especially to its ecobiological aspects.

Second, according to changes in the environment there is an inverse dependency between the flexibility

of living things to adapt to changing conditions and the level of development of living things. In this regard, fungi are at a lower level of development than plants, so they adapt to changed conditions faster, that is, the adaptability of the pathogen is higher than that of the host. This ultimately determines the occurrence of resistance events.

Thirdly, a number of fungi are universal in terms of the characteristics they carry, that is, they are characterized by a wide variety of diseases (hemibiotrophs and necrotrophs) caused by them, can function as endophytes in their interactions with plants, and can lead the same lifestyle as typical soil saprotrophs. This makes it necessary to develop newer approaches in their study, more specifically, those that allow determining which of these features to use.

Finally, the last one is taking measures to combat diseases observed in plants is prepared based on the use of either separate physical-mechanical, chemical and biological control methods, or the joint use of them in various combinations. Although each of the mentioned has positive and negative aspects, the control measures based on biological methods and approaches are considered more favorable. Thus, physical and mechanical control measures do not allow obtaining results that would compete with either chemical or biological control methods. Control measures based on chemical and biological control are currently widely used, but the means used during chemical control cause new ecological problems and are more likely to promote the emergence of more resistant forms of microorganisms, including fungi. It is quite difficult to create resistant forms against the means used in biological control and their use does not create additional environmental problems.

In connection with the above mentioned, one of the points observed in the studies and paid attention to in the future is related to the control methods applied during the cultivation of fodder plants. Thus, biological and complex control measures based on it are not systematically used in the fight against fungal diseases in the country. In addition, despite the fact

that the sources used in biological control, primarily fungi that are antagonistic to phytopathogens, are widespread in Azerbaijan, there is not found organization of some product in their base. Solving all these should be the main task of future research to solve the problems that arise in accordance with the principles of sustainable development of the country. It can be specially noted that solving the above-mentioned issues at a high level and preparing preventive measures against fungal diseases, as well as organizing the production of biological agents at the expense of local sources, are among the issues of great importance in terms of the development of the non-oil sector for Azerbaijan, a traditional oil country.

Finally, it would be appropriate to touch on one of the issues that should be paid attention to in the future, which is related to the assessment of the risk of natural and agrocenoses due to fungal diseases. So, currently, there was no evaluation system that was used or proposed based on the research conducted in the conditions of Azerbaijan. True, in some studies, such attempts are found for local areas, and according to those evaluation systems, the degree of spread of the disease caused by this or that fungus is taken as a basis (Majnunova, 2015). This approach is correct, because the degree of spread of the disease is one of the main indicators in terms of assessing the phytosanitary status of the senoses, but the research materials used in those works cover specific areas, not all of Azerbaijan, and are useful in terms of general impression. For this reason, it is appropriate to continue researches aimed at developing a more perfect evaluation system in the future.

Conclusion

From the research results, it became clear that fodder plants are also one of the habitats of fungi, and phytopathogens are also actively involved in their formation. Thus, phytopathogenic fungi are characterized by diversity both in terms of their distribution on individual plants and the effect of the diseases they cause, however, it is advisable to develop a more perfect evaluation system in the future to determine their dangerousness.

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