Advanced Studies in Biology, Vol. 16, 2024, no. 1, 35 - 43
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https://doi.org/10.12988/asb.2024.91841

General Characteristics of Some Fruit Plants Included in the Flora of Azerbaijan and Their Mycobiota

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Abstract

In the conducted studies, a number of fruits and berries distributed in the Greater Caucasus part of Azerbaijan were analyzed according to fungal microbiota. It was found that in the formation of the microbiota of the 20 plant genera sampled are involved 86 species of which 81 belong to true fungi and 5 belong to bacteria. Recorded fungi are characterized by a wide diversity both in terms of their distribution on individual plants, and their mofo-biological characteristics, as well as the manifestation form and degree of spread of the diseases they cause. Thus, of the registered species fungi 9 are involved in the occurrence of powdery mildew, 11 of rust, 35 of spotting and wilting, and the remaining 44 species are participates in the occurrence of rotting disease. The total prevalence of diseases recorded on plants on average is 16.1%.

Keywords: fruits and berries, microbiota, phytopathogenic fungi, bacteria, prevalence rate, disease

Introduction

Regardless of their form, plants have been used by living beings for various purposes since the dawn of life and are still being used today[5]. It should be noted that plants are a resource that has no alternative yet, both in terms of volume and biological value, in directly and indirectly satisfying the human need for food.

The increasing number of the world's population and the fact that this process takes place within a fixed area leads to an increase in the demand for plants. At the same time, the reduction of plant resources due to anthropogenic effects is an inevitable process. For this reason, the degradation of biodiversity has been one of the global problems of the world for a long time. Thus, the range of many species is gradually shrinking, the number of individuals of a number of species is rapidly decreasing and they are registered as objects of the "Red Book". For this reason, the protection of biodiversity is not the work of one country or regional states, it is a global issue[1]. In order to prevent this, first of all, it is very important to correctly assess the conditions that lead to the deterioration of biodiversity.

One of the reasons for the narrowing of the areas of plants and the decrease in the number of individuals is the diseases caused by living things, especially microorganisms[18]. Although the regulation of biodiversity from an ecological point of view is a characteristic feature of a certain group of living things, as a result of the performance of this function, the areas of plants can shrink, and the number of individuals can decrease. It is worth noting one fact that, the number of individuals that die every year as a result of diseases caused by microorganisms is expressed in hundreds of millions [22]. Therefore, for the protection of plants, mainly those used for food, fodder and medical, as well as technical purposes is important to study the species composition of disease agents observed in these plants, their ecotophyic relationships, development cycles and other characteristics.

Although the organisms that cause disease in plants are mainly viruses, bacteria and fungi, the latter differ from other organisms in terms of the number of pathologies they cause and the damage they cause to plant productivity[7, 13, 15] and we can say that this feature of them is one of the main goals of research conducted all over the world today.

The territory of the Republic of Azerbaijan consists of ecosystems of different nature, and each ecosystem carries specific characteristics along with the general signs of the nature of Azerbaijan. It should be noted that, 8 of the 11 climate types are found in the not so large (86.6 thousand km^2) territory of the Republic of Azerbaijan[10]. Such diversity has also influenced the flora of Azerbaijan and in the studies carried out so far, the distribution of about 5000 plant species has been determined in the territory of the Republic of Azerbaijan. The recorded plants are characterized by a wide diversity according to their taxonomic structure, life forms, purposes, resources, areas of use and other features[14]. The above-mentioned cases, which primarily lead to the narrowing of the range of plants and the decrease in the number of individuals, are not alien to the Republic of Azerbaijan, and researches have been conducted in this direction for a long time, the species composition, ecotrophic relationships and other characteristics of disease-causing microorganisms in various groups of plants are also being studied [2, 6, 17]. Despite this, there are not enough materials about the comprehensive study of plants, primarily fruits and berries, characteristic of the nature of Azerbaijan in this aspect.

Therefore, the purpose of the presented work is dedicated to the study of phytopathogens involved in the formation of the mycobiota of a number of fruits and berries included in the flora of Azerbaijan according to their species composition and the degree of spread of the diseases they cause.

Material and methods

Researches were conducted in the areas of Azerbaijan located in the Greater Caucasus, which is related to the fact that this region is the area where both wild and cultivated fruits and berries are more widespread. In this regard, it should be noted that 49% of the country's forests are located here [10].

The samples were taken from the above-ground part of fruits(*Castanea Mill., Cerasus Juss., Cornus Link., Corulus L., Crataegus Pall., Cydonia Mill., Gerasus L., Malus Mill., Persica Mill., Pistacia L., Prunus Nill., Pyurus L*. and etc.), and berries(*Rubus L., Morus L*., etc. total 20 genera), where fungi (micromycetes) are likely to be present, and from the fruiting bodies of fungi (macromycetes) living in trees. Special care was taken to ensure that all the selected trees were alive at the time of sampling that is, samples were taken mainly from plant species that are alive and currently capable of bearing fruit.

Sampling was carried out according to the planned route method[21], passporting, preparation for laboratory analysis, transfer of samples to nutrient mediums, and obtaining pure culture carried out according to traditional methods and approaches accepted in microbiology, mycology, and phytopathology[18, 20], as well as those used in our own work[2].The identification of fungi and bacteria recorded in the studies was carried out using known determinants according to classical approaches[3-4, 8, 11-12, 16, 19].

Obtained results and their discussion

In research, samples were taken from about -20 species of plant genera, as well as the varieties created on their basis. As a result of the analysis, it became clear that a total of 86 species of microorganisms participate in the formation of the microbiota of the mentioned plants, and the information about them is summarized in Table 1. As seen, a total of 86 species of microorganisms are involved in the formation of the microbiota of the trees selected as the research object, of which 93.8% belong to fungi and 6.2% to bacteria. Since it is necessary to carry out

Table 1. Information about the taxonomic structure of the microbiota of fruits and berries plants

Kingdom	Division	Class	Order	Family	Genus/species	Share in total microbiota (%)
Bacteria	1	1	2	3	4/5	4,6
Mycota or Fungi	*Mucormycota*	1	1	1	2/3	2,8
	Ascomycota	4	8	12	22/48	44,4
	Bazidiomycota	2	10	14	33/52	48,2
Total						108(100)

Table 2. Characteristic of recorded fungi genera by the number of species

№	Department	Species number those between 1-3	Number of which 4 and more
1	*Mucor-mycota*	*Mucor(2) və Rhisopus(*1)	-
2	*Asco-mycota*	*Alternaria*(3), *Ascochyta*(3), *Cercospora*(3), *Cylindrocarpon*(1), *Cytospora(3), Erysiphe*(5), *Gloeosporium* (3), *Microsphaera*(1), *Monilia(2), Mycosphaerella*(1), *Naemospora*(1), *Nectria*(2), *Phyllosticta*(2), *Podosphaera*(3), *Septoria*(4), *Sphaerotheca*(1), *Sporotrichum*(1), *Cylindrosporium*(1), *Taphrina*(1), *Venturia*(1) *və Verticillium* (2)	*Penicillium*(4)
3	*Bazidio-mycota*	*Abortiporus(1), Armillaria(2), Bjerkandera(2), Cerrena (1), Climacodon (1) , Cronartium*(1) , *Daedalea (1), Daedaleopsis (1), Fomes(1), Fuscoporia (1), Ganoderma (2), Gymnosporangium(3) Laetiporus (1), Lenzites(1), Melampsora (2), Phaeolus(1), Pholiota (1), Phragmidium*(2), *Pleurotus (2), Polyporus (2), Porodaedalea (1), Puccina(2), Pycnoporus (1) , Schizophyllum (1) Spongipellis*(1), *Stereum*(2), *Trametes(2), Trametopsis*(1), *Trichaptum*(1) və *Vuilleminia*(1)	*Fomitopsis(4)* *İnonotus(4)* *Phellinus(6)*

additional experiments in order to clarify some aspects of the findings related to bacteria, it was considered appropriate to touch upon the findings related to fungi in the presented work.

First of all, it should be noted that fungi are characterized by higher indicators due to their participation in the formation of the microbiota of the studied plants, the number of pathologies they cause and the extent of their spread.

The number of species of fungi belonging to different groups that participate in the formation of the general mycobiota of the studied trees is also different(tab. 2). As seen, in this regard, genera such as *Fomitopsis*, *Inonotus*, *Phellinus* and *Trametes* are represented among basidiomycetes, and *Penicillium* genus is represented by more species in the Ascomycota division. So that, in the first it varies between 4-6 species, and in the second between 4 species. For the rest of the genus, this indicator ranges from 1-3.

In general, the distribution of recorded fungi on individual plant species has a unequal character, and in a certain sense, they participate in different combinations(tab. 3). As can be seen, plants belonging to the *Pistacia L.* genus (individual species and varieties) are characterized by the richest microbiota, and *Corylus L.* by the poorest microbiota. On the other side, some of the recorded fungi are universal and some are characterized by substrate specificity.

Table 3. Quantitative characterization of the distribution of recorded fungi on individual tree species

№	Plant species where the samples were taken	The number of recorded fungi species	Number of species with substrate specificity
1	*Castanea* Mill.	26	2
2	*Cerasus* Juss .	21	2
3	*Cornus* Link.	17	2
4	*Corulus* L.	16	1
5	*Crataegus* Pall.	26	2
6	*Cydonia* Mill	17	2
7	*Gerasus* L.	19	3
8	*Malus* Mill.	21	1
9	*Persica* Mill.	26	2
10	*Pistacia* L.	29	2
11	*Prunus* Nill.	21	1
12	*Pyurus* L.	21	2
13	*Rubus* L.	21	2
14	*Morus* L.	18	2
15	*Digərləri*	30	3
Total		103	29

It should be noted that when characterizing the distribution of fungi on trees chosen as an object of study: by the color of the decay they cause in natural conditions and their ecotrophic relationships, that fungi are also characterized by diversity in this aspect. Thus, 20.4% of the total recorded fungi (*Armillaria* - 1 species, *Erysiphe* - 5 species, *Fomes* - 1 species, *Gymnosporangium* - 3 species, *Inonotus* - 1 species, *Melampsora* - 2 species, *Phragmidium* - 2 species, *Podosphaera* - 3 species, *Puccinia* – 2 species and *Taphrina* – 1 species) in terms of ecotrophic relationships belonged to biotrophs, and the remaining 79.6% belonged to facultatives, i.e. those that do not have true saprotrophy and biotrophy.

According to their relation to substrates, 28.5% of the recorded fungi belong to true stenotrophs (those has substrate specificity), 22.3% to conditional stenotrophs (those has relative substrate specificity) and 49.2% to eurytrophs, that is, to those without substrate specificity.

It should be noted that various relationships are formed between fungi and plants, including trees, one of which is parasitism, and the manifestation of this relationship manifests itself in plants with various pathologies. The existence of these relationships between the fungi recorded in the studies and the studied trees has been confirmed in various studies. For this reason, it was considered appropriate to characterize the registered fungi from this aspect and to determine the diseases they cause in the studied plants. It was clear from the obtained results that the recorded fungi cause various diseases in the studied plants, which its spread rate is characterized by different quantitative indicators. In addition, the form of observation of diseases caused by fungi also differs. Taking into account the above, it was considered appropriate to divide the diseases caused by polytrophs and true biotrophs into 4 conditional groups, which were recorded in the studied plants in the course of the research, based on the same name and similar symptoms.

1. Fungi that cause powdery mildew are included in this group.9 recorded species belonging to the genera *Erysiphe*, *Podosphaera* and *Taphrina* belonged to this group. The fungi included in this group belong to true biotrophs, and the diseases they cause are found in almost all studied fruit plants, and the general prevalence rate of this disease varies between 0.5-1.7% on the mentioned trees. In this case, the highest index was observed in the Pear genus, and the lowest index was observed in the Quince genus.
2. This group includes rust-causing fungi, and 10 species belonging to the genera *Cronartium*, *Gymnosporangium*, *Melampsora*, *Phragmidium*, and *Puccinia*, which were recorded in the course of the research, corresponded to this characteristic. In terms of eco-trophic relations, the prevalence of rust caused by these fungi, which belong to true biotrophs, varies from 1.1 to 3.2%, which is the most observed.

3. Pathogenic micromycetes that cause leaf spotting, wilting and other diseases belong to the third group, they mainly consisted of 35 species belonging to genera such as *Alternaria, Ascochyta, Cercospora, Cylindrocarpon, Cytospora, Gloeosporium, Microsphaera, Monilia, Mycosphaerella, Naemospora, Nectria, Phyllosticta, Septoria, Sphaerotheca, Sporotrichum, Cylindrosporium, Venturia* and *Verticillium* belonging to the Ascomycota division. Diseases of this type, especially various (white, gray, brown, black, etc.) colored spotting diseases, are found in all studied fruit and berry plants, and their prevalence varies from 1.7 to 21.4%.
4. 44 species belonging to the genera *Abortiporus, Armillaria, Bjerkandera, Cerrena, Climacodon, Daedalea, Daedaleopsis, Fomes, Fomitopsis, Fuscoporia, Ganoderma, İnonotus, Laetiporus, Lenzites, Phaeolus, Phellinus, Pholiota, Pleurotus, Polyporus, Porodaedalea, Pycnoporus, Schizophyllum, Spongipellis, Stereum, Trametes, Trametopsis, Trichaptum* and *Vuilleminia*, which cause white, brown, and mixed-colored decay, belong to this group. The prevalence of diseases caused by these fungi varies from 0.8 to 12.4%.

The overall prevalence of recorded diseases on fruit plants is an average 16.1% , which this indicator is 16.0% for fruit plants and 16.7% for berries. Based on these indicators, it can be noted that the fruits and berries that grow wild in the Great Caucasus region of the Republic of Azerbaijan and are culturally cultivated are at a potentially dangerous level from a phytopathological point of view. Thus, according to the normative documents adopted in a number of countries[9, 23], the prevalence of one or another disease up to 20% is considered as not potentially dangerous.

Conclusion

Thus, the conducted research allows us to note that the situation is not at a dangerous level in terms of fungal biota of fruits and berries grown in Azerbaijan. So, in general, the prevalence of fungal diseases on neither fruits nor berries is higher than 16.1%. Nevertheless, in a situation where the existence of global problems on Earth is real, this indicator should be considered as a dangerous situation, and the implementation of preventive measures against their perpetrators should be one of the main tasks. This situation is not only for the Republic of Azerbaijan, it is also valid for every country in the world, least because the spread of disease-causing microorganisms, including fungi, knows no boundaries.

Acknowledgements. This work was supported by the Azerbaijan Science Foundation – Grant AEF-MCG-2023- 1(43)-13/10/3-M-10.

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Received: May 5, 2024; Published: May 22, 2024