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RESEARCH PAPER

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General characteristics of the mycobiota of vegetable and melon plants cultivated in Azerbaijan

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ABSTRACT

The present study was undertaken to address the limited and fragmented knowledge of fungal diversity associated with vegetable and melon crops in Azerbaijan, particularly in terms of their ecological roles and phytosanitary significance. Understanding the composition and functional structure of the mycobiota is essential for improving crop protection strategies, minimizing yield losses, and ensuring sustainable agricultural production in regions with diverse environmental conditions. The work is therefore important both from a scientific perspective, as it contributes to regional mycological knowledge, and from an applied perspective, as it informs disease management practices. Field sampling was conducted in the Kur-Araz lowland and the Greater Caucasus under both open-field and protected cultivation systems. Approximately 400 samples were collected from different plant organs of major vegetable and melon crops. Fungi were isolated using standard culture-based techniques on Čapek–Doks medium, followed by morphological identification using established taxonomic keys and atlases. The identified taxa were classified at multiple taxonomic levels and further analyzed based on their ecotrophic and functional characteristics using descriptive statistical methods. A total of 178 fungal species were identified, with Ascomycota dominating the mycobiota (84.3%), followed by Basidiomycota (6.7%), Oomycota (5.1%), and Mucoromycota (3.9%). At the ecological level, facultative forms constituted the majority (80.9%), while true saprotrophs and biotrophs accounted for 10.1% and 9.0%, respectively. Functionally, 124 species (69.7%) were phytopathogenic, 20 species (11.2%) were associated with spoilage, and 34 species (19.1%) had unknown roles. Additionally, 8 species were recorded for the first time in Azerbaijan. Overall, the study demonstrates a high diversity and predominance of phytopathogenic fungi, highlighting the need for continuous monitoring and integrated disease management strategies to support sustainable crop production.

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INTRODUCTION

The growing demand for food driven by rapid population increase has intensified the pressure on agricultural systems worldwide. Ensuring a stable supply of high-quality plant-based products, particularly vegetables and melons, has therefore become a central concern in modern agricultural research (Valiyev *et al.*, 2025; Macieira *et al.*, 2021). These crops are of considerable nutritional and economic importance and are widely cultivated across diverse agro-climatic regions. However, their productivity and quality are significantly constrained by plant diseases, among which fungal pathogens play a dominant role (Gai and Wang, 2024).

Fungi are responsible for a substantial proportion of plant diseases, often accounting for up to 70–80% of all recorded phytopathologies (Simões *et al.*, 2023). Many phytopathogenic fungi, including species of *Fusarium, Colletotrichum,* and *Septoria*, exhibit broad host ranges and can cause severe yield losses, sometimes reaching complete crop failure under favorable conditions (Zhou *et al.*, 2024). In addition to field-level infections, fungi also contribute to post-harvest deterioration, further exacerbating economic losses and food insecurity (Macieira *et al.*, 2021). These impacts highlight the importance of understanding fungal diversity, ecology, and functional roles in agricultural systems.

The Republic of Azerbaijan, characterized by diverse climatic conditions and rich vegetation, provides favorable habitats for a wide range of fungal species. Previous studies conducted in the region have largely focused on phytopathogenic fungi associated with fruit crops and forest ecosystems (Bakshaliyeva *et al.*, 2024), while investigations into the mycobiota of vegetable and melon plants remain relatively limited. Although some research has addressed the species composition of fungi in agricultural systems (Muradov *et al.*, 2019), existing studies are often fragmentary and do not provide a comprehensive assessment of fungal diversity across different ecological zones and cultivation systems. Moreover, earlier works have primarily emphasized taxonomic identification without adequately integrating ecological (ecotrophic) and functional (pathological) perspectives. As a result, there remains a significant gap in understanding how fungal communities associated with vegetable and melon crops are structured in terms of their ecological strategies (saprotrophic, biotrophic, facultative) and their roles in plant health, including disease causation, spoilage, and unknown interactions. Such integrated knowledge is essential for developing effective phytosanitary and crop protection strategies. In this context, the present study aims to provide a comprehensive evaluation of the mycobiota associated with vegetable and melon plants cultivated in different regions of Azerbaijan. Specifically, the objectives of the study were:

(i) to determine the taxonomic composition of fungal communities at different hierarchical levels;
(ii) to assess the distribution of fungal species across genera and divisions;
(iii) to analyze the ecotrophic structure of the recorded fungi;
(iv) to evaluate their functional roles, particularly in relation to phytopathogenicity and spoilage; and
(v) to identify new fungal records for the mycobiota of Azerbaijan.

By addressing these objectives, the study seeks to fill existing knowledge gaps and contribute to a more integrated understanding of fungal diversity and its implications for sustainable vegetable and melon production in the region.

MATERIALS AND METHODS

Study areas

The study was conducted in two major agro-ecological regions of the Republic of Azerbaijan, namely the Kur-Araz lowland and the Greater Caucasus. These regions differ in soil-climatic conditions, relief, and vegetation characteristics, providing a representative basis for assessing fungal diversity associated with vegetable and melon crops. The Kur-Araz lowland is dominated by irrigated plains with gray and graybrown soils, whereas the Greater Caucasus includes mountainous, foothill, and plain ecosystems (Fig. 1).

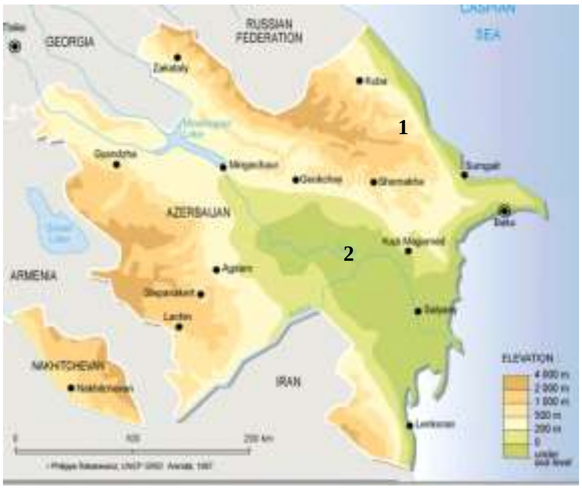

Fig. 1. General view of the study areas
1- Greater Caucasus, 2 - Kur-Araz lowland

Sampling strategy and plant material

Field surveys were carried out under both open-field and protected (greenhouse) cultivation conditions. Samples were collected from major vegetable and melon crops, including cucumber (*Cucumis sativus* L.), tomato (*Solanum lycopersicum* L.), eggplant (*Solanum melongena* L.), cabbage (*Brassica oleracea* L.), pepper (*Capsicum annuum* L.), carrot (*Daucus carota* L.), watermelon (*Citrullus lanatus*), melon (*Cucumis melo* L.), and pumpkin (*Cucurbita pepo* L.).

Sampling targeted both vegetative and generative plant organs (leaves, stems, flowers, and fruits) showing visible symptoms or potential fungal colonization. Standard route-based (transect) and stationary observation methods commonly used in mycological studies were applied. Sampling was conducted across different seasons to capture temporal variability. In total, approximately 400 samples were collected.

Isolation and identification of fungi

Fungal isolation was performed using conventional mycological techniques. Plant tissues were surface-processed and inoculated onto agarized Čapek–Doks medium supplemented with chloramphenicol (100 mg/L) to inhibit bacterial growth. Pure cultures were obtained through repeated sub-culturing.

Microscopic examination was carried out using a compound microscope (up to 2500× magnification) to observe morphological characteristics. Identification of fungal taxa was based on classical taxonomic approaches using standard identification manuals and atlases. Both true fungi (Ascomycota, Basidiomycota, Mucoromycota) and fungus-like organisms (Oomycota, Chromista) were included in the analysis to provide a comprehensive assessment of the mycobiota.

Taxonomic and ecological classification

Identified taxa were classified according to hierarchical taxonomic levels (division, class, order, family, genus, and species). Quantitative summaries were generated to determine the contribution of each taxonomic group to the overall mycobiota.

In addition, all recorded taxa were categorized based on their ecotrophic relationships into three main groups:
(i) true saprotrophs,
(ii) true biotrophs, and
(iii) facultative forms.

Furthermore, fungi were classified according to their functional (pathological) roles into:
(i) phytopathogenic species causing plant diseases,
(ii) storage-associated spoilage organisms, and
(iii) species with unknown or insufficiently studied pathogenicity.

Data processing and statistical analysis

The study employed descriptive statistical methods to analyze fungal diversity and composition. The number of taxa at each taxonomic level was calculated, and their relative proportions (%) were determined based on the total number of recorded species ($n = 178$). No diversity indices (e.g., Shannon, Simpson) were calculated.

Similarly, the distribution of fungi among ecotrophic groups and functional categories was quantified and expressed as percentages. No inferential statistical tests were applied, as the study focused on the descriptive characterization of species composition, ecological structure, and functional roles of the mycobiota.

RESULTS

The analysis of samples collected from vegetable and melon plants cultivated in different agro-ecological zones of Azerbaijan revealed a considerable diversity of fungi associated with these crops. In total, 178 species were identified, encompassing both true fungi and fungus-like organisms.

Taxonomic structure of the mycobiota

The taxonomic composition of the identified fungi is presented in Table 1. The results indicate a clear predominance of Ascomycota, which accounted for 150 species (84.3%) of the total mycobiota. In comparison, other divisions were represented to a much lesser extent, with Basidiomycota comprising 12 species (6.7%), Oomycota 9 species (5.1%), and Mucoromycota 7 species (3.9%).

At lower taxonomic levels, the identified fungi were distributed across 7 classes, 9 orders, 13 families, and 39 genera (Table 1). The overwhelming representation of Ascomycota across these hierarchical levels highlights its dominant ecological role in both open-field and protected cultivation systems.

Table 1. Taxonomic structure of fungi isolated during the research

Division (Phylum)	Class	Order	Family	Genus	Species	%
Oomycota	1	1	2	3	9	5.1
Mucoromycota	1	1	1	2	7	3.9
Ascomycota	3	6	10	32	150	84.3
Basidiomycota	2	3	5	7	12	6.7
Total	7	9	13	39	178	100

Note: Oomycota belongs to the kingdom Chromista, while Mucoromycota, Ascomycota, and Basidiomycota belong to the kingdom Fungi.

Table 2. Distribution of fungal species found in vegetables and melons by genera

Genus name	Number of species	%
Colletotrichum	15	8.4
Phoma	14	7.9
Ascochyta	13	7.3
Fusarium	12	6.7
Septoria	12	6.7
Penicillium	10	5.6
Alternaria, Phyllosticta	7-8	4.2*
Aspergillus, Cladosporium, Diplodina, Mucor, Verticillium	4-6	2.8*
Botrytis, Cephalosporium, Cercospora Cylindrosporium, Dicoccum, Erysiphe, Hormiscium, Macrophoma, Macrosporium, Monilia, Peronospora, Pestolotia, Phomopsis, Plasmopara, Plectosphaerella, Puccinia, Rhizopus, Sclerotina, Spongospora, Sporotrichum, Stagonospora, Stemphylium, Trichothecium, Trichoderma, Urocystis, Uromyces, Ustilago	1-3	1.1*

Note: Total species = 178; *=% per species; Species numbers for grouped genera are presented as ranges; midpoint values were used to estimate percentage contribution.

Table 3. Ecotrophic structure of the recorded fungi (n = 178)

Ecotrophic group	Number of species	%
True saprotrophs	18	10.1
True biotrophs	16	9.0
Facultative forms	144	80.9
Total	178	100

Distribution at the genus level

The distribution of fungal species among genera is summarized in Table 2. The genus Colletotrichum showed the highest species richness, represented by 15 species (8.4%). This was followed by Phoma (14 species; 7.9%) and Ascochyta (13 species; 7.3%). Other prominent genera included Fusarium and Septoria, each with 12 species (6.7%), and Penicillium, which accounted for 10 species (5.6%). In addition to these dominant genera, a wide range of other taxa were recorded with moderate (4–8 species) or low (1–3 species) representation (Table 2). Although individually less abundant, these genera collectively contributed to the overall diversity and structural complexity of the mycobiota.

Ecotrophic structure of the fungi

The ecological-trophic classification of the recorded fungi is shown in Table 3. The results demonstrate that the majority of the fungi belonged to facultative forms, accounting for 144 species (80.9%). In contrast, true saprotrophs and true biotrophs were represented by 18 species (10.1%) and 16 species (9.0%), respectively (Table 3).

This distribution indicates that most fungi associated with the studied plants exhibit ecological flexibility, allowing them to adapt to varying environmental conditions and host interactions.

Functional (pathological) roles

The functional categorization of the recorded fungi is presented in Table 4. A substantial proportion of the identified species were phytopathogenic, with 124 species (69.7%) directly involved in causing plant diseases.

In addition, 20 species (11.2%) were associated with post-harvest spoilage, contributing to the deterioration of plant materials during storage. The remaining 34 species (19.1%) could not be conclusively linked to any specific pathological role and were therefore categorized as having unknown or insufficiently studied status (Table 4).

Table 4. Functional (pathological) role of recorded fungi

Functional category	Number of species	%
Phytopathogenic (disease-causing)	124	69.7
Storage spoilage organisms	20	11.2
Unknown/undetermined role	34	19.1
Total	178	100

Table 5. Taxonomic affiliation of mushroom species first recorded in the nature of Azerbaijan

Division	Species
Ascomycota	*Fusarium equiseti* (Corda) Sacc., *Rasamsonia argillacea* (Stolk, H.C. Evans & T. Nilsson) Houbraken & Frisvad, *Neonectria punicea* (J.C. Schmidt) Castl. & Rossman, *Alternaria cucumerina* (Ellis & Everh.) J.A. Elliott, *Plenodomus lingam* (Tode) Höhn., *Boeremia diversispora* (Bubák) Aveskamp, *Pseudocercospora fijiensis* (M. Morelet) Deighton, *Stagonosporopsis cucurbitacearum* (Fr.) Aveskam

Newly recorded species

The study also revealed 8 fungal species recorded for the first time in Azerbaijan, as detailed in Table 5. Most of these species were identified in open-field conditions, while one species was detected under protected cultivation. All newly recorded taxa belong to the division Ascomycota and are associated with plant pathologies.

Overall, the results highlight a high level of taxonomic and functional diversity within the mycobiota of vegetable and melon plants in Azerbaijan, with a marked dominance of Ascomycota and a significant proportion of facultative and phytopathogenic species across the studied regions.

DISCUSSION

The present study provides a comprehensive overview of the taxonomic and functional structure of the mycobiota associated with vegetable and melon plants cultivated in Azerbaijan. The identification of 178 species reflects a relatively high level of fungal diversity, which is consistent with the ecological richness and heterogeneity of the studied regions. The Kur-Araz lowland and the Greater Caucasus differ substantially in climatic and edaphic conditions, and such environmental variability is well known to promote microbial diversity, particularly among fungi.

A key finding of this study is the pronounced dominance of Ascomycota, which accounted for the majority of the identified taxa. This observation aligns with numerous previous studies indicating that Ascomycota represents the most diverse and ecologically versatile group of fungi in terrestrial ecosystems, particularly in agroecosystems (Simões *et al.*, 2023). Members of this division are known for their ability to colonize a wide range of substrates and hosts, which explains their extensive representation in both open-field and protected cultivation systems. The comparatively lower representation of Basidiomycota and Mucoromycota is also consistent with earlier findings, where these groups typically play more specialized or limited ecological roles in plant-associated environments.

At the genus level, the predominance of Colletotrichum, Phoma, Ascochyta, Fusarium, and Septoria further emphasizes the phytopathological significance of the recorded mycobiota. These genera are widely recognized as major plant pathogens responsible for a variety of economically important diseases in agricultural crops (Gai and Wang, 2024; Zhou *et al.*, 2024). In particular, species of *Fusarium* are known for their broad host range and ability to cause severe diseases such as wilting and root rot, often leading to significant yield losses. The high representation of such genera in the present study suggests that vegetable and melon crops in Azerbaijan are exposed to considerable phytosanitary pressure.

The ecological-trophic structure of the fungal community revealed a clear predominance of facultative forms, which constituted more than four-fifths of the total species. This finding is ecologically meaningful, as facultative fungi possess adaptive flexibility, enabling them to function both as saprotrophs and opportunistic pathogens depending on environmental conditions and host susceptibility. Such versatility enhances their survival and dissemination in agroecosystems, where environmental conditions and cultivation practices are often dynamic. The relatively lower proportion of strict saprotrophs and biotrophs further supports the idea that fungal communities associated with cultivated plants are largely shaped by opportunistic and adaptable species.

From a functional perspective, the high proportion of phytopathogenic fungi (69.7%) underscores the potential risk posed by fungal diseases to vegetable and melon production. This result is in agreement with previous reports indicating that fungi are responsible for a substantial proportion of plant diseases globally, often accounting for up to 70–80% of known plant pathologies (Simões *et al.*, 2023; Gai and Wang, 2024). In addition, the presence of species associated with post-harvest spoilage highlights the importance of considering not only field-level infections but also storage-related losses, which can significantly affect food quality and safety (Macieira *et al.*, 2021).

Another noteworthy outcome of this study is the identification of species with unknown or insufficiently studied functional roles. Although these fungi were not directly associated with plant diseases based on current knowledge, their ecological roles cannot be fully excluded. It is possible that some of these taxa may act as latent pathogens or opportunistic colonizers under specific environmental conditions. Therefore, further investigations, including pathogenicity tests and molecular characterization, are required to clarify their biological significance.

The detection of ten fungal species recorded for the first time in Azerbaijan further highlights the incompleteness of current knowledge regarding the country's mycobiota. This finding is consistent with earlier observations that fungal diversity in many regions remains underexplored, particularly in agricultural systems (Bakshaliyeva *et al.*, 2024; Muradov *et al.*, 2019). The fact that all newly recorded species belong to Ascomycota and are associated with plant pathologies reinforces the dominant role of this group in shaping phytopathogenic communities.

Overall, the results of the present study demonstrate that the mycobiota of vegetable and melon crops in Azerbaijan is characterized by high taxonomic diversity, ecological adaptability, and significant phytopathological potential. These findings have important implications for crop protection strategies, as effective disease management requires a detailed understanding of the composition and functional roles of fungal communities. In this context, integrated approaches combining monitoring, early detection, and targeted control measures are essential to minimize yield losses and ensure sustainable agricultural production.

CONCLUSION

The present study provides a comprehensive assessment of the taxonomic composition, ecological structure, and functional roles of the mycobiota associated with vegetable and melon plants cultivated in Azerbaijan. A total of 178 fungal species were identified, reflecting a high level of diversity shaped by the heterogeneous environmental conditions of the Kur-Araz lowland and the Greater Caucasus.

The results clearly demonstrate the dominance of Ascomycota, as well as the significant representation of key phytopathogenic genera such as *Colletotrichum, Phoma, Ascochyta, Fusarium,* and *Septoria*. The predominance of facultative ecological forms (80.9%) indicates that most fungi associated with these crops possess considerable adaptive flexibility, enabling them to persist under varying environmental and host conditions.

From a functional perspective, the high proportion of phytopathogenic species (69.7%) highlights the substantial phytosanitary risk posed by fungal communities to vegetable and melon production. In addition, the presence of spoilage-associated and functionally uncharacterized species suggests that fungal impacts extend beyond field-level infections to post-harvest losses and potentially unexplored ecological interactions.

The identification of ten species newly recorded for Azerbaijan further emphasizes the need for continued mycological investigations in the region. Overall, the findings underline the importance of systematic monitoring and integrated disease management strategies to mitigate the impact of fungal pathogens and ensure sustainable crop production.

Future research should focus on the molecular characterization, pathogenicity assessment, and ecological interactions of the identified fungi, particularly those with unknown functional roles, in order to develop more effective and targeted phytosanitary measures.

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