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ECOLOGICAL CHARACTERISTICS OF MICROMYCETE COMPLEXES OF PLANTS OF LEGUME FAMILY (FABACEAE LINDL.)

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Summary

Plants of the family Fabaceae Lindl. hold strategic importance both in maintaining the equilibrium of natural ecosystems and in modern agriculture due to their role in restoring soil fertility and biological nitrogen fixation. In this research, the structural-functional and ecological characteristics of micromycete complexes associated with *Trifolium pratense*, *Medicago sativa*, *Lupinus luteus*, and other leguminous plants were comprehensively investigated across various ecological conditions and different levels of technogenic load in the Lankaran natural region of Azerbaijan. A total of 120 fungal species were identified from the rhizosphere and phylloplane environments. Microbiological analyses revealed that the genera *Fusarium*, *Alternaria*, *Aspergillus*, and *Penicillium* dominate the formation of the microbiota. The results of the study indicate that increasing anthropogenic and technogenic pressure directly influences the reduction of species diversity and the simplification of community structures in micromycete complexes. Particularly in agrocenoses with high technogenic loads, a sharp decrease in the number of beneficial antagonists (e.g., *Trichoderma* spp.) was observed, while the frequency of pathogenic and toxigenic fungi increased by 20-25%. Calculated biodiversity indices (Shannon index $H' = 3.2 \pm 0.12$; Simpson index $D = 0.92 \pm 0.02$) confirmed that *Trifolium pratense* possesses the richest microbial complex. As a scientific novelty, the "microbial signatures" of leguminous plants in the specific soil-climatic conditions of the Lankaran region were determined for the first time, integrating traditional morphological methods with modern molecular ITS rDNA sequencing. The practical significance of the research lies in providing a scientific basis for predicting plant diseases, organizing phytosanitary monitoring, and developing ecologically clean biopesticides based on local *Trichoderma* strains. These findings are of vital importance for the management of sustainable agroecosystems and the biological restoration of degraded soils.

Keywords: micromycetes, mycoflora, phytopathogen, agrocenosis, rhizosphere, phylloplane, mycotoxins, diversity indices

Introduction

Plants of the *Fabaceae* family play a vital role in ecosystems and agriculture by improving soil fertility through biological nitrogen fixation and providing high-protein crops [1, 2]. These plants interact with numerous microorganisms, including micromycetes inhabiting the rhizosphere, phyllosphere, and seeds. Such fungi can be pathogenic, saprotrophic, or symbiotic, affecting plant health and productivity [2, 11, 12].

Recent anthropogenic impacts and the intensification of agroecosystems significantly influence micromycete diversity and distribution. Therefore, studying the ecological characteristics of micromycete complexes associated with *Fabaceae* plants is crucial for sustainable agriculture and ecosystem management [10].

Objective of the work

The aim of this work is to determine the ecological characteristics of the micromycete complexes of the rhizosphere and phylloplane of the legume family (*Fabaceae* Lindl.) in different ecosystems. To achieve this goal, the following tasks were set:

1. To determine the distribution patterns of micromycete complexes in natural conditions and agrocenoses.
2. To characterize the formation of micromycete complexes in biotopes with various technogenic loads.
3. To assess the structural characteristics of the phyllosphere micromycetes in agrocenoses.
4. To evaluate the impact of soil parameters on fungal diversity.

Materials and methods

Study area and Sampling: The study was conducted in the Lankaran region, representing three ecosystems: natural meadows (low impact), agrocenoses with moderate technogenic load, and high-load crop rotation fields. A total of 360 samples were collected. For each species (*Trifolium pratense, T. repens, Medicago sativa, Lupinus luteus, and Vicia faba*), exactly 12 plant samples were collected per site. All experiments and isolations were performed with three biological replicates (n = 3) during the period from April to September 2025.

Soil analysis: Soil parameters were measured using standard procedures: pH was determined potentiometrically in a 1:5 soil-water suspension, and organic matter by the Walkley-Black method [9].

Isolation and İdentification: Micromycetes were isolated using Potato Dextrose Agar (PDA) and Czapek Dox Agar (CDA) via serial dilution [7]. For molecular identification of selected pathogenic isolates, the Internal Transcribed Spacer (ITS) region was amplified using universal primers ITS1 and ITS4 according to the protocol by White et al. [14].

Resultsand discussion

A total of 120 fungal species were identified across the studied sites (Table 1). The dynamics of the rhizosphere microbial community are significantly influenced by root exudates, which act as primary substrates for fungal assembly [15].

Table 1. Checklist of Micromycete Species Identified (n=120)

№	Genus	Species (Latin Name)	Trophic Group
1-25	*Fusarium*	*F. oxysporum, F. solani, F. culmorum, F. moniliforme, F. verticillioides, F. avenaceum, F. graminearum, F. equiseti, F. poae, F. sporotrichioides, F. semitectum, F. sambucinum, F. acuminatum, F. proliferatum, F. subglutinans, F. tricinctum, F. heterosporum, F. chlamydosporum, F. dimerum, F. merismoides, F. nivale, F. anthophilum, F. lateritium, F. tabacinum, F. udum*	*Phytopathogen*
26-45	*Aspergillus*	*A. niger, A. flavus, A. fumigatus, A. terreus, A. clavatus, A. ochraceus, A. candidus, A. versicolor, A. nidulans, A. wentii, A. glaucus, A. restrictus, A. sydowii, A. tamarii, A. ustus, A. amstelodami, A. chevalieri, A. repens, A. oryzae, A. parasiticus*	*Saprotroph / Toxigenic*
46-70	*Penicillium*	*P. chrysogenum, P. expansum, P. digitatum, P. italicum, P. cyclopium, P. frequentans, P. funiculosum, P. purpurogenum, P. citrinum, P. brevicompactum, P. decumbens, P. fellutanum, P. glabrum, P. janczewskii, P. janthinellum, P. miczynskii, P. oxalicum, P. paxilli, P. raistrickii, P. roqueforti, P. rugulosum, P. simplicissimum, P. verrucosum, P. viridicatum, P.*	*Saprotroph*

		waksmanii	
71-85	*Alternaria*	*A. alternata, A. tenuissima, A. brassicicola, A. infectoria, A. solani, A. citri, A. radicina, A. japonica, A. cheiranthi, A. cucumerina, A. dauci, A. maritima, A. nucis, A. triticina, A. tomato*	*Phytopathogen*
86-95	*Trichoderma*	*T. harzianum, T. viride, T. koningii, T. hamatum, T. aureoviride, T. reesei, T. pseudokoningii, T. virens, T. longibrachiatum, T. atroviride*	*Antagonist / Saprotroph*
96-105	*Mucor / Rhizopus*	*M. mucedo, M. hiemalis, M. racemosus, M. piriformis, M. plumbeus, R. stolonifer, R. nigricans, R. oryzae, R. microsporus, R. arrhizus*	*Saprotroph*
106-120	*Other Genera*	*Rhizoctonia solani, Ulocladium botrytis, Cladosporium herbarum, C. cladosporioides, Botrytis cinerea, Verticillium dahliae, V. albo-atrum, Acremonium strictum, Gliocladium roseum, Humicola grisea, Nigrospora oryzae, Stemphylium botryosum, Chaetomium globosum, Aureobasidium pullulans, Epicoccum nigrum*	*Various*

The quantitative analysis of biodiversity in the rhizosphere of different legume species showed that environmental stability is directly linked to the host plant species (Table 2). The calculated indices are presented below.

Table 2. Rhizosphere micromycete diversity indices (Mean ± SD)

Species	***H’*(Shannon)**	***D* (Simpson)**	**Evenness (*E*)**
Trifolium pratense	3.2 ± 0.12	0.92 ± 0.02	0.85
Medicago sativa	3.0 ± 0.15	0.91 ± 0.03	0.83
Lupinus luteus	2.8 ± 0.10	0.88 ± 0.04	0.80

The data in Table 2 suggests that *Trifolium pratense* supports a more complex and stable fungal community compared to other studied legumes.

Furthermore, the colonization of the phylloplane (leaf surface) was evaluated. The relative abundance of the main fungal genera on the leaves varied according to the host plant and the level of technogenic stress in the region (Table 3).

Table 3. Relative abundance of micromycete genera on leaves of Fabaceae species (%)

Species	**Fusarium**	**Alternaria**	**Aspergillus**	**Penicillium**	**Trichoderma**	**Ulocladium**
Trifolium pratense	20%	15%	10%	10%	25%	5%
Medicago sativa	15%	10%	25%	10%	20%	5%
Lupinus luteus	10%	25%	15%	20%	10%	5%
Trifolium repens	15%	20%	15%	10%	20%	5%
Vicia faba	15%	10%	30%	10%	15%	5%

On the phylloplane, colonization was mainly by phytopathogens such as *Alternaria alternata*, *Ulocladium botrytis*, and saprotrophic fungi [3, 10]. The relative abundance of genera varied among species and according to anthropogenic pressure, as shown in Table 3. For example, *Trifolium pratense* leaves were dominated by *Fusarium* (20%) and *Trichoderma* (25%), while *Medicago sativa* showed higher abundance of *Aspergillus* (25%) under moderate technogenic load [6, 11]. Lupinus luteus leaves were dominated by *Alternaria* (25%) and *Penicillium* (20%), and *Vicia faba* leaves exhibited increased toxigenic *Aspergillus* in highly impacted agroecosystems.

Sites with higher technogenic load showed a significant reduction in species evenness and a 20-25% increase in the abundance of phytopathogenic fungi. This shift suggests that anthropogenic stress disruptions reduce the population of beneficial antagonists like *Trichoderma*, creating an ecological niche for opportunistic pathogens.

Correlation analysis revealed a positive relationship between soil nitrogen content and *Trichoderma* abundance ($r = 0.68$, $P < 0.05$), while a negative correlation was found between soil pH and *Fusarium* frequency ($r = -0.54$, $P < 0.05$). On the phylloplane, colonization was dominated by *Alternaria alternata* and *Aspergillus* species, particularly in highly impacted agroecosystems.

Scientific novelty

This study provides one of the first comprehensive ecological descriptions of the micromycete communities associated with both wild and cultivated *Fabaceae* species in the specific soil-climatic conditions of the Lankaran natural region of Azerbaijan. Unlike previous general mycological surveys, this research establishes a high-resolution taxonomic baseline by integrating traditional morphological methods with molecular ITS rDNA sequencing, ensuring the precise identification of species-specific assemblages [5, 14].

A key novelty of this work is the quantitative evaluation of how varying levels of technogenic load (anthropogenic pressure) act as a selective driver for fungal community assembly. We demonstrate that technogenic stress disrupts the ecological equilibrium of the rhizosphere, specifically favoring the proliferation of opportunistic phytopathogens at the expense of beneficial soil microflora. Furthermore, this study identifies the species-specific "microbial signatures" for *Trifolium pratense* and *Medicago sativa*, highlighting their role as host plants for diverse and ecologically stable fungal complexes even under moderate environmental stress.

Practical significance

The findings of this research have direct applications for sustainable agriculture and environmental management. The established database of 120 micromycete species serves as a critical resource for long-term phytosanitary monitoring and disease forecasting in the Lankaran region. By identifying the prevalence of *Fusarium* and *Alternaria* species in agrocenoses, agricultural stakeholders can implement more effective crop rotation strategies; for instance, determining the optimal fallow period or selecting non-host subsequent crops to prevent the accumulation of residual soil-borne pathogens [8, 13].

Moreover, the identification of indigenous *Trichoderma* strains with high frequency in natural meadows suggests a significant potential for the development of local biological control agents. These native strains are better adapted to the regional climate and soil properties compared to imported commercial products. Utilizing these indigenous antagonists as "biopesticides" can significantly reduce the agricultural sector's reliance on chemical fungicides, thereby mitigating soil pollution and promoting the production of ecologically clean legume crops. These results also provide a scientific basis for the ecological restoration of technogenically degraded soils through the reintroduction of beneficial microbial complexes.

Conclusion

1. The rhizosphere and phylloplane micromycete complexes of *Fabaceae* plants exhibit distinct structural differences depending on the ecosystem type. Natural ecosystems maintain a higher level of microbial diversity, whereas agroecosystems subjected to anthropogenic pressures show a specialized but less diverse fungal composition [1, 5].

2. High technogenic load acts as an environmental stressor that shifts the microbial balance toward a higher prevalence of phytopathogenic and opportunistic fungi (e.g., *Fusarium* and *Aspergillus* spp.), which may pose risks to both plant productivity and human health [6, 11].

3. Saprotrophic and endophytic fungi identified in the rhizosphere play a fundamental role in maintaining agroecosystem stability by facilitating nutrient cycling and enhancing plant tolerance to abiotic stresses [3, 10]. The interaction between these beneficial micromycetes and *Fabaceae* plants significantly improves soil fertility through enhanced nitrogen enrichment [2, 8].

4. The research findings establish a robust scientific basis for integrated phytosanitary monitoring and disease forecasting in the Lankaran region. Maintaining balanced microbial communities is essential for developing sustainable management practices and resilient agricultural systems [4, 9].

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PAXLALILAR AİLƏSİNƏ (FABACEAE LİNDL.) AİD OLAN BİTKİLƏRİN MİKROMİSET KOMPLEKSLƏRİNİN EKOLOJİ XÜSUSİYYƏTLƏRİ

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Xülasə

Fabaceae Lindl. (Paxlalılar) ailəsinə aid bitkilər həm təbii ekosistemlərin müvazinətində, həm də müasir kənd təsərrüfatında torpaq münbitliyinin bərpası və bioloji azot fiksasiyası baxımından strateji əhəmiyyət kəsb edir. Təqdim olunan tədqiqat işində Azərbaycanın Lənkəran təbii vilayətinin müxtəlif ekoloji şəraitlərində və fərqli texnogen yüklənməyə məruz qalmış ərazilərində *Trifolium pratense*, *Medicago sativa*, *Lupinus luteus* və digər paxlalı bitkilərlə assosiasiya olunan mikromiset komplekslərinin struktur-funksional və ekoloji xüsusiyyətləri kompleks şəkildə araşdırılmışdır. Tədqiqat zamanı rizosfer və filoplan mühitlərindən ümumilikdə 120 göbələk növü identifikasiya edilmişdir. Aparılan mikrobioloji analizlər nəticəsində müəyyən edilmişdir ki, mikrobiotanın formalaşmasında *Fusarium, Alternaria, Aspergillus* və *Penicillium* cinsləri dominantlıq təşkil edir. Tədqiqatın nəticələri göstərir ki, antropogen və texnogen təzyiqin artması mikromiset komplekslərinin növ müxtəlifliyinin azalmasına və icmaların strukturunun sadələşməsinə birbaşa təsir göstərir. Xüsusilə yüksək texnogen yükə malik aqrosenozlarda faydalı antaqonistlərin (məsələn, *Trichoderma* spp.) sayının kəskin azalması, patogen və toksigen göbələklərin yayılma tezliyinin isə 20-25% artması müşahidə olunmuşdur. Hesablanmış biomüxtəliflik göstəriciləri (Şennon indeksi $H' = 3.2 \pm 0.12$; Simpson indeksi $D = 0.92 \pm 0.02$) *Trifolium pratense* bitkisinin ən zəngin mikrob kompleksinə malik olduğunu təsdiq edir. Elmi yenilik kimi, ilk dəfə olaraq Lənkəran bölgəsinin spesifik torpaq-iqlim şəraitində paxlalı bitkilərin "mikrob imzaları" müəyyən edilmiş və ənənəvi morfoloji metodlar müasir molekulyar ITS rDNA sekvenləşdirmə üsulları ilə inteqrasiya olunmuşdur. Tədqiqatın praktiki əhəmiyyəti bölgədə bitki xəstəliklərinin proqnozlaşdırılması, fitosanitar monitorinqin təşkili və yerli *Trichoderma* ştammları əsasında ekoloji təmiz biopestisidlərin hazırlanması üçün elmi baza yaratmasındadır. Bu tapıntılar dayanıqlı aqroekosistemlərin idarə olunması və deqradasiyaya uğramış torpaqların bioloji bərpası üçün mühüm əhəmiyyət daşıyır.

Açar sözlər: mikromisetlər, mikromofauna, fitopatogen, agrocenosis, rizosfer, filoplan, mikotoksinlər, müxtəliflik indeksləri

ЭКОЛОГИЧЕСКИЕ ОСОБЕННОСТИ КОМПЛЕКСОВ МИКРОМИЦЕТОВ РАСТЕНИЙ СЕМЕЙСТВА FABACEAE LINDL

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Аннотация

Растения семейства Fabaceae Lindl. (Бобовые) имеют стратегическое значение как для поддержания равновесия природных экосистем, так и для современного сельского хозяйства благодаря их роли в восстановлении плодородия почвы и биологической фиксации азота. В данной исследовательской работе комплексно изучены структурно-функциональные и экологические характеристики комплексов микромицетов, ассоциированных с *Trifolium pratense, Medicago sativa, Lupinus luteus* и другими бобовыми растениями, в различных экологических условиях и при разной степени техногенной нагрузки в Лянкяран природном регионе Азербайджана. В ходе исследования из ризосферы и филлоплана было идентифицировано в общей сложности 120 видов грибов. Микробиологический анализ показал, что в формировании микробиоты доминируют роды *Fusarium*, *Alternaria*, *Aspergillus* и *Penicillium*. Результаты исследования указывают на то, что усиление антропогенного и техногенного воздействия напрямую влияет на снижение видового разнообразия и упрощение структуры сообществ микромицетов. В частности, в агроценозах с высокой техногенной нагрузкой наблюдалось резкое сокращение численности полезных антагонистов (например, *Trichoderma* spp.), в то время как частота встречаемости патогенных и токсигенных грибов увеличилась на 20-25%. Рассчитанные показатели биоразнообразия (индекс Шеннона H' = 3.2 ± 0.12; индекс Симпсона D = 0.92 ± 0.02) подтвердили, что *Trifolium pratense* обладает наиболее богатым микробным комплексом. Научная новизна работы заключается в том, что впервые в специфических почвенно-климатических условиях Лянкяранского региона были определены «микробные сигнатуры» бобовых растений, а традиционные морфологические методы были интегрированы с современным молекулярным секвенированием ITS рДНК. Практическая значимость исследования состоит в создании научной базы для прогнозирования болезней растений, организации фитосанитарного мониторинга и разработки экологически чистых биопестицидов на основе местных штаммов *Trichoderma*. Эти выводы имеют важное значение для управления устойчивыми агроэкосистемами и биологического восстановления деградированных почв.

Ключевые слова: микромицеты, микрофлора, фитопатоген, агроценоз, ризосфера, филлоплан, микотоксины, индексы разнообразия

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