Original article

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MICROBIAL LANDSCAPE AND KERATINOPHILIC PROPERTIES OF SKIN MICROBIOTA OF HEALTHY YOUTH IN ASTANA

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ABSTRACT

The skin microbiome is very diverse. Fungi are a mandatory part of it. The biological role of non-dermatophytic keratinolytic saprophytic fungi is in the decomposition of keratinized skin debris and its appendages in the soil. Non-dermatophytic keratinophils inhabiting human skin may be potential causative agents of opportunistic skin mycoses, making the findings relevant. The aim of the study was to study the microbial landscape of the skin of the hands of adolescents among schoolchildren and students and the keratinophilic properties identified by micromycetes. The object of the study were 43 healthy adolescents aged 12 to 18 years, from whom samples of biomaterial were taken. The health status of young people with physical inactivity, vitamin deficiencies, cases of acute respiratory viral infections and acute respiratory infections was studied by questionnaires. A high rate of carriage of all representatives of pathogens of skin mycosis was established in school-age boys with prevalence of mold (61.5%) and yeast (66.7%) fungi. Among students, carriers of classical dermatophytes were mainly girls (80.0%), mold and yeast fungi - mainly young men (64.0%). A total of 35 isolates were isolated, 13 species of fungi were identified to the genus: *Penicillium* spp. (11%), *T. rubrum* (11%), *Alternaria* spp. (6%), *T. mentagrophytes* (8%), *T. verrucosum* (6%), *A. niger* (9%), *A. flavus* (3%), *M. canis* (3%), *Ch. globosum* (3%), *A. pullulans* (3%), *Cladosporium* spp. (3%) and others. The keratinophilic properties of micromycetes were confirmed by abundant mycelial growth, active spore formation, and accumulation of spores both on the surface of the cuticle (ectothrix) and in the thickness of the hair (endothrix), which were detected by microscopy.

Keywords: human skin microbiome, skin mycoses, spectrum, keratinophilicity, keratinophiles.

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1. INTRODUCTION

The skin is the largest organ of the human body, colonized by a diverse environment of microorganisms, most of which are harmless or even beneficial to their host. Human skin is inhabited by a huge variety of bacteria, viruses, and fungi, and their composition and quantitative ratio are unique for each and determined by the genetic composition of the microbiome [1].

Microbial communities of the skin are very diverse and complex. The qualitative composition of the microbiota present on the skin and mucous surfaces of open cavities includes tens and hundreds of different types of microorganisms. Colonization is determined by the ecology of the skin surface, which varies greatly depending on the topographic location, endogenous host factors, and exogenous environmental factors. Understanding the skin microbiome is necessary to understand the microbial involvement in human skin diseases [2].

Depending on the cleanliness of the skin, 1 cm^2 can contain from several hundred thousand to millions of microorganisms. Most microorganisms inhabiting human skin are harmless, but some of them are associated with dermatological diseases [2, 3, 4]. Skin microbiota can affect human health, and its imbalance and dysbiosis contribute to the development of skin diseases [5, 6].

A properly functioning skin microbiome is a complex set of microorganisms consisting of bacteria, fungi, viruses, microeukaryotes (mites), archaea and phages. Fungi are an essential part of the skin microbiome, mainly belonging to the Ascomycota and Basidiomycota phyla. The dominant genus is *Malassezia*. The highest level of fungal diversity is observed on the feet, where they are colonized by *Aspergillus*, *Cryptococcus*, *Rhodotorula* and *Epicoccum*. Species composition, abundance and distribution on the skin surface can vary depending on internal and external factors [7]. The number of fungi colonizing the skin of the feet reaches 80 on the sole

of the heel. The most frequently isolated genera are *Malassezzia*, *Cryptococcus*, *Aspergillus*, *Rhodotorula*, *Epicoccum*, *Candida*, *Saccharomyces*, *Epidermophyton*, *Trichophyton* and *Microsporum* [8, 9]. An analysis by McCall et al. [10] showed that the fungal profile of human foot skin correlates with urbanization. *Trichosporon*, *Debaryomyces*, and *Saccharomyces* are characterized by a decrease in the number of microorganisms on the feet with urbanization, while an inverse correlation was found for *Candida* and *Aspergillus* [7, 8].

Hands are the most important vector for the transmission of microorganisms between people, pets, various objects, and the environment [11, 12]. The hand microbiota shows high stability over time, despite exposure to adverse environmental factors [13, 14].

Most fungal organisms identified on healthy skin belong to the genus *Malassezia*. *Candida* spp. rarely colonize human skin, but can be determined, causing clinical symptoms of candidiasis in conditions of immunodeficiency, diabetes, or after the use of antibiotics [15, 16]. It is known that the composition of the human skin microbiome is determined by genetics, environmental factors, and the local microenvironment [17, 18]. It is believed that the human skin microbiome remains relatively stable over a long period, despite constant contact with potentially contaminated sources and regular hygiene procedures [6]. However, various publications indicate that the composition of the skin microbiota is constantly changing, with an increase in the number of yeasts and molds in its composition [7, 8, 9, 10, 15].

In turn, the composition of the microbiome can change in the presence of any disease. Thus, the skin microbiome of acne patients is represented by a mixed microbiota. The presence of bacterial biota (*Cutibacterium acnes, Staphylococcus epidermidis, S. aureus*), fungal-bacterial associations, which include the yeast C. albicans, is noted. In the microbiota of the facial skin of patients with seborrheic dermatitis, the presence of *Malassezia furfur* fungi in association with bacteriobiota is dominant, mixed coccal-rod biota is found. A distinctive feature of the microbial landscape of patients with rosacea is the presence of fungal-bacterial associations, mainly due to *C. albicans*, or coccal biota, represented by *S. epidermidis* [19]. In adolescents diagnosed with COVID-19, *Streptococcus pneumoniae* and *Candida albicans* were identified in the skin microbiota [20, 21].

Almost every fifth inhabitant of the Earth faces one or another form of mycosis at least once in their life. According to various estimates, mycoses account for 37-70% of all skin diseases, they are often associated with allergic dermatoses, viral and bacterial infections [22]. The expansion of the spectrum of pathogens of fungal infections is associated with global climate change, with an increased number of professions accompanied by physical inactivity, with a decrease in the immune status due to refusal to vaccinate, the recent COVID-19 pandemic and a number of others [3]. The main pathogens of fungal infections are the genera *Trichophyton*, *Candida*, *Aspergillus* and *Cryptococcus* [5]. In patients with dermatophytosis (trichophytosis, microsporia, scab, rubromycosis, epidermophytosis), the microbiota containing keratinophilic fungi, especially imperfect filamentous fungi *Micropsorum* spp., *Epidermophyton* spp., *Trichophyton* spp., *Nannizzia* spp., *Arthroderma* spp. and a number of other recently added genera, prevails [23, 24, 25, 26, 27, 28]. It has now been established that in addition to classical keratinophiles, or dermatophytes, there are many other keratinophilic ecologically significant species of fungi. Among them are *Chrysosporium* spp., *Psuedogymnoascus* spp., *Geomyces* spp., *Pectinotrichum* spp., *Renispora* spp. and a number of others [29, 30]. Recently, there has been an increase in the number of cases of detection of fungi of the genera *Aspergillus*, *Alternaria*, *Chaetomium*, *Phoma*, *Penicillium*, *Cladosporium*, *Candida* and other representatives of mold fungi and yeast from affected areas of human and animal skin [13, 14].

The biological role of these non-dermatophyte keratinolytic fungi, which are saprophytes, is to decompose keratinized remains of the skin and its appendages in the soil. The ability of saprophytic fungi to destroy and absorb keratin located in the surface tissues transfers them to the category of opportunistic pathogens of skin mycoses and determines the pathogenicity of these fungi [31, 32, 33].

The current state of the problem of skin mycoses, the identification of new pathogens colonizing the skin and causing emergent mycoses in humans, the impact of changes in natural and climatic factors, physical inactivity of adolescent students, COVID-19 and other infectious diseases make the timely detection and identification of human skin microbiota very relevant.

The purpose of the study is to study the microbial landscape of the skin of the hands of adolescents among schoolchildren and students and the keratinophilic properties of the isolated micromycetes.

2. MATERIALS AND METHODS

For the period from 2023 to 2024, 43 healthy adolescents with no skin complaints were observed. The health status of the young people was assessed using questionnaires. The questionnaire included questions regarding immune status, premorbid condition, and the presence or history of chronic non-communicable diseases. Inclusion criteria for the study were age 12–18 years, the absence of complaints and clinical signs of skin diseases at the time of examination, and consent to participate in the study, approval by the ethics committee (Local Bioethics Committee of Astana Medical University, Decision No. 1, Meeting No. 4 dated 01.13.2024), as well as information on the receipt of informed consent from parents/legal representatives and the consent of the adolescents themselves.

Microbiological and mycological studies of skin, nail, and subungual tissue samples were conducted by the national laboratory based at the microbiology laboratoryof the Department of Microbiology and Virology named after Sh.I. Sarbasova of the NJS «Astana Medical University» and the microbiology laboratory of the Scientific and Production Platform of Agricultural Biotechnology of the NJS «Kazakh Agrotechnical Research University named after S. Seifullin».

Sampling was carried out using a standard method [34] on healthy areas of the skin, nails, and subungual space of the hands of young people aged 12 to 18 years, of whom 25 were schoolchildren and 18 were students. All samples from each participant in the experiments were combined and labeled as hand skin samples.

Primary isolation of pathogens was carried out on Sabouraud media: Sabouraud dextrose agar and Sabouraud medium with the addition of chloramphenicol (Titan Biotech Ltd, India) to suppress the growth of extraneous bacterial flora. Cultivation was carried out at 28°C for 12-15 days. Isolation of pure culture was carried out on Sabouraud medium, without the addition of antimycotics [35].

Microscopic analysis of the morphological structures of micromycetes was carried out on a trinocular transmitted light microscope AxioScope A1 (Zeiss, Germany) at a magnification of ×40 [36]. The keratinolytic properties were determined using the classical hair perforation test, which was carried out in accordance with standard mycological procedures [37].

Species identification was performed based on macroscopic and microscopic features visible in the obtained culture (characteristic hyphae and spores) using classical mycological criteria, including colony morphology, pigmentation, and microscopic characteristics [38].

DNA extraction and molecular genetic identification were performed according to the method described by [39].

The collected data were analyzed using descriptive and comparative statistical methods. The prevalence of fungal carriage and the distribution of different fungal groups were calculated as percentages. Categorical variables, including the presence of dermatophytes, mold fungi, and yeast fungi, were summarized using absolute frequencies and proportions. Differences in fungal carriage rates between schoolchildren and university students, as well as between male and female participants, were assessed using the chi-square test or Fisher's exact test, as appropriate. The frequency of keratinophilic activity among the isolated fungal strains was also calculated as a percentage. Statistical significance was set at $p < 0.05$.

3. RESULTS

According to the set objectives, a total of 43 samples of biomaterial were collected from young people aged 12 to 18, schoolchildren and students, permanently or temporarily residing in Astana. Of the total number of young people, 20 samples were collected from girls, 23 samples were collected from boys. Of these, 25 samples were from schoolchildren, including 40.0% from girls, 60.0% from boys; 18 samples were from students, which amounted to 55.6% and 44.4%, respectively. In the group of 25 schoolchildren, girls made up 40.0% (10 people) and boys – 60.0% (15 people). In the group of 18 students, girls made up 55.6% (10 people) and boys – 44.4% (8 people). In total, of all those examined, there were 20 girls (46.5%) and 23 boys (53.5%). The age composition of the examined young people is presented in Figure 1. The health status of the young people who took part in sampling and surveys is presented in Figure 2.

Analysis of 43 samples of biomaterial collected from healthy schoolchildren and students showed that young people are carriers of micromycetes of various species, including dermatophytes. It should be noted that 2 or more isolates were obtained from some samples; the total number of isolates amounted to 35 strains. No micromycete growth was detected in 11 samples (Table 1).

Thus, the isolation of micromycetes from biomaterial of healthy young people in Astana revealed that the prevalence of dermatophytes on the skin of the hands and subungual area was 22.3%, opportunistic mold fungi and yeasts – 58.1%, and in 25.6% of cases, no fungal microflora was detected on the skin of young people.

Analysis of the spectrum of isolated opportunistic mold isolates revealed a high carriage rate of all pathogens causing skin mycoses in boys compared to girls, with molds predominating (61.5%). The distribution by group was as follows: schoolchildren (62.5%) and students (37.5%). Analysis of the spectrum of isolated yeast isolates in the group of boys compared to girls also revealed a high carriage rate of 66.7% (Figure 3).

As can be seen from Figure 3, in schoolgirls these indicators were found in values from 7.6% to 30.7%. Among students, carriers of classical dermatophytes are mainly girls (80.0%), mold and yeast fungi - mainly young men (64.0%). It should be noted that in each group the number of samples with no growth of micromycetes had quite high indicators: schoolchildren (girls and boys) - 27.3%, students - from 9.1% to 45.4%, respectively. There are publications on the appearance in the skin microbiome of new representatives of the microbial world that have adapted to living on the skin. One of the factors in the adaptation of microorganisms to living on the skin is the presence of enzymes that promote the breakdown of human keratin [40]. In nature, there are saprophytic microorganisms-biodestructors, such as *Chrysosporium* spp., *Psuedogymnoascus* spp., *Geomyces* spp., *Pectinotrichum* spp., *Renispora* spp. and a number of others, synthesizing the enzyme keratinase [32, 33]. The most well-known keratinolytic fungi are of the genera *Aspergillus*, *Penicillium*, *Fusarium*, *Microsporum*, *Trichoderma* and *Chrysosporium* [41]. Therefore, their appearance in the microbiome is quite predictable,

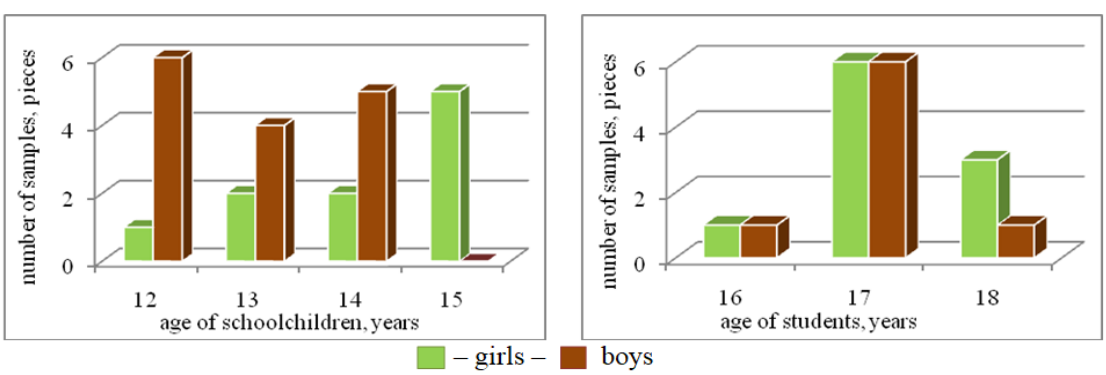


Figure 1 – Age and gender data of the examined groups of healthy youth in Astana.

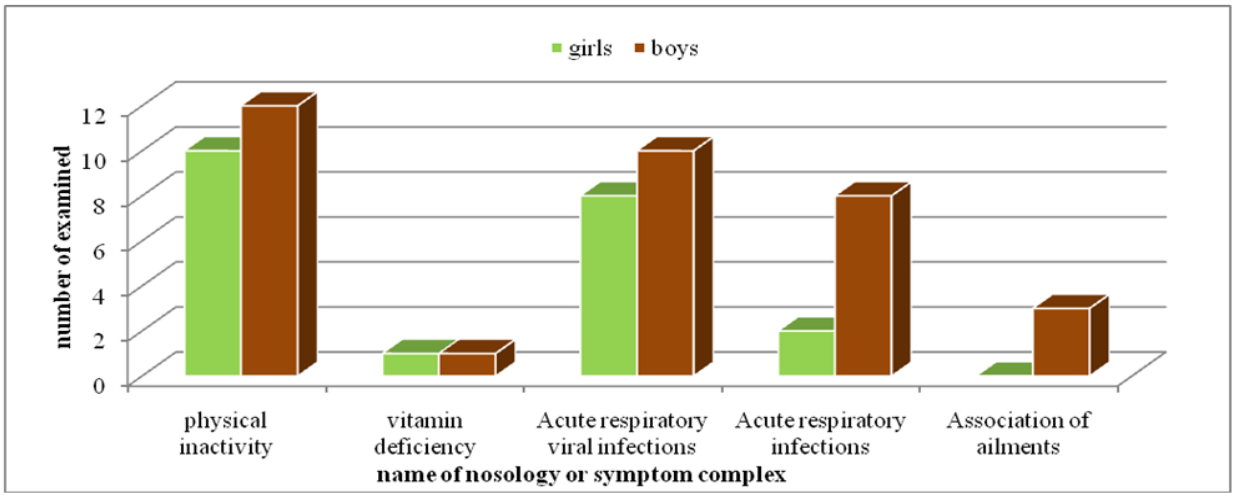


Figure 2 – Health status of the examined groups of healthy young people.

Table 1 – Isolation of pathogens from biomaterial of healthy young people in Astana.

Healthy youth groups		Number of samples	Total number of micromycetes isolated			No growth
			Dermatophytes	Mold fungi	Yeast	
Schoolchildren	female	10	4	4	4	1
	male	15	2	5	5	2
Students	female	10	4	1	-	5
	male	8	-	3	3	3
Total		**43**	**10**	**13**	**12**	**11**

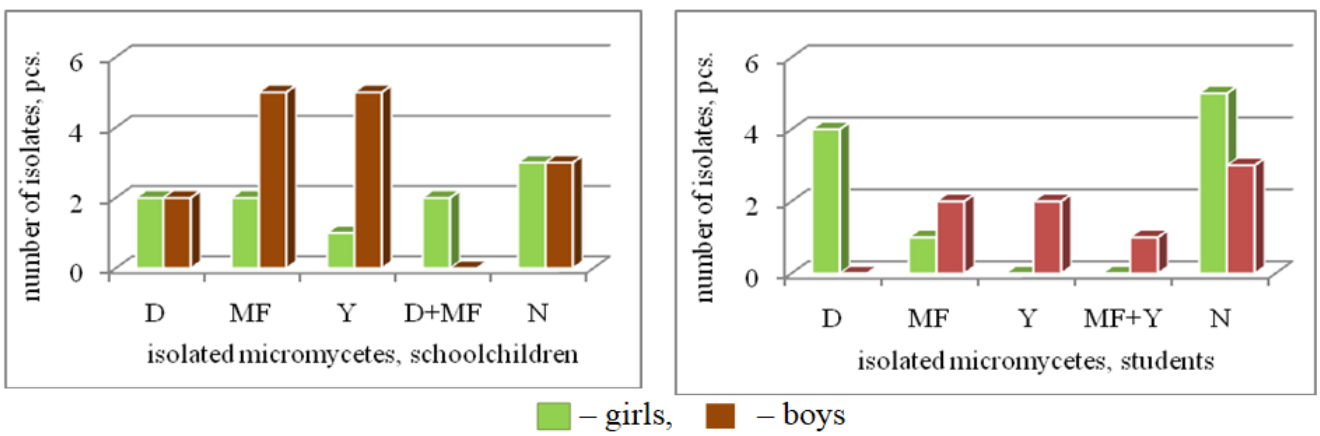


Figure 3 – Age and gender data of the examined groups of healthy youth in Astana: D – dermatophytes, MF – mold fungi, Y – yeast, N – no growth.

especially since keratin is a structural component of skin, hair, and nails in humans [42].

Our results are consistent with the data of foreign authors who reported changes in the composition of the skin microbiota. Thus, from the total number of positive samples, a total of 35 isolates were isolated, 12 fungal taxa were identified to the genus (Figure 4).

As can be seen from Figure 4, the detection rate of dermatophytes of the genus Trichophyton was 28%, including the following species: *T. rubrum* – 11%, *T. mentagrophytes* – 8%, *T. verrucosum* – 6%. The causative agent of microsporia *M. canis* was isolated in 3% of cases.

The detection rate of mold fungi was 37%. Opportunistic filamentous fungi had the following indicators: *Penicillium* spp. – 11%, *A. niger* – 9%, *Alternaria* spp. – 6%, *A. flavus* – 3%, *Ch. globosum* – 3%, *A. pullulans* – 3%, *Cladosporium* spp. – 3%. As can be seen from the obtained data, the highest percentage of isolation was recorded among representatives of *Penicillium* spp., *Aspergillus* spp., *Alternaria* spp. The remaining micromycetes were represented by one strain each (37%).

The detection rate of *Candida* spp. yeasts was 34%, while *Rhodotorula* spp. was 3%. *C. albicans* was the most common yeast species, at 17%. The high detection rate of the opportunistic species *C. parapsilosis* was alarming, at 14%. *Rhodotorula* spp. was detected in only one case (3%).

It should be noted that associations of dermatophytes with molds and yeasts were detected in the skin microbiome of healthy adolescents: *T. rubpum* + *Penicillium* spp. + *Candida* spp. (1 case), *T. verrucosum* + *Penicillium* spp. (1 case), and *T. rubrum* + *Aspergillus* spp. (2 cases).

Samples of micromycetes (10 samples) with cultural and

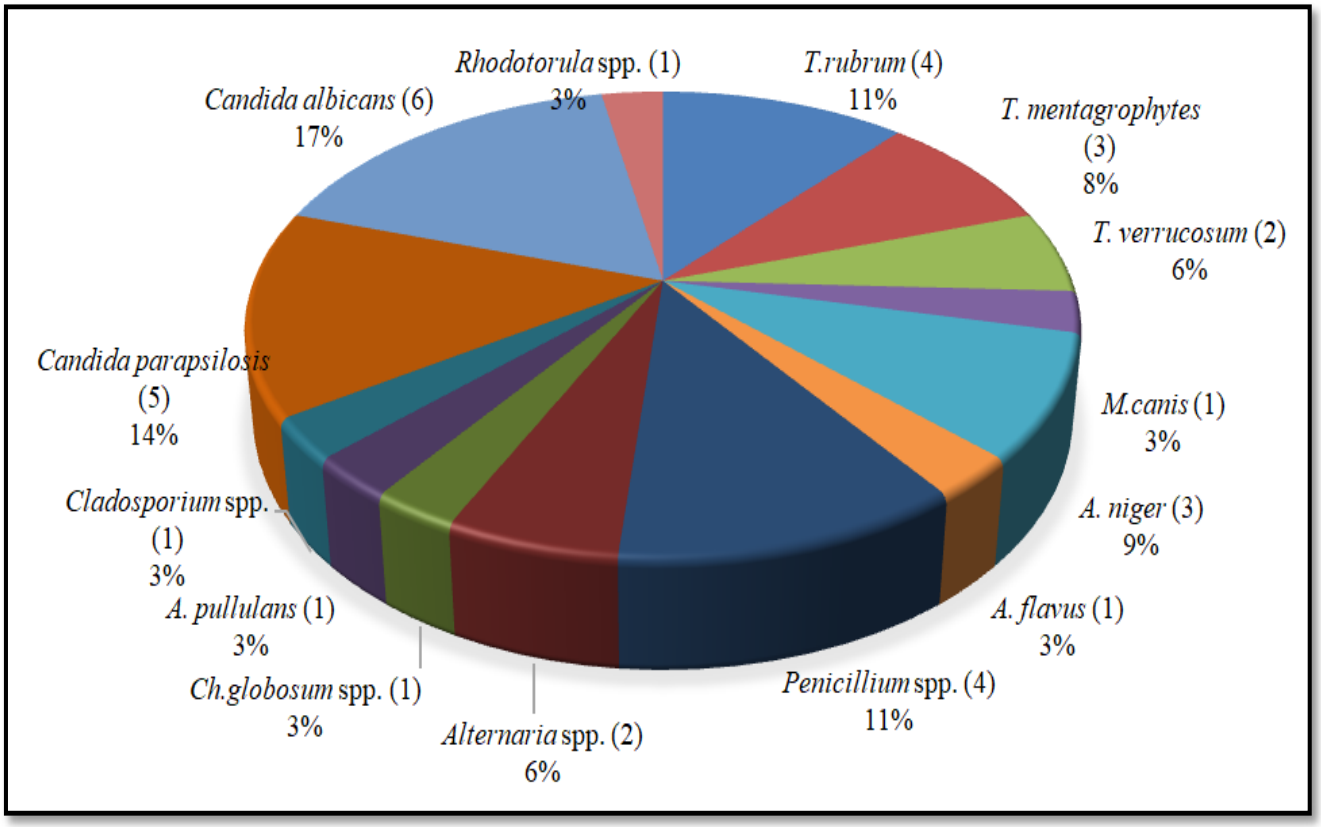


Figure 4 – Taxonomic composition and percentage ratio of fungi isolated from samples of biomaterial of healthy youth.

morphological characteristics that differed markedly from widely known and easily identifiable saprophytes were subjected to molecular genetic identification using universal *ITS/ITS* primers (Table 2).

Based on the results of molecular genetic identification, new species of micromycetes were identified: *P. rubens* – 4 strains, *A. alternata* – 1 strain, *G. galactomycetum* – 1 strain, *C. sphaerospermum* – 1 strain. One strain was identified to the genus level – *Cladosporium*. Two strains were not identified.

Analysis of the keratinophilic properties of isolates raised in pure culture revealed that 71.4% of all strains included in the study possessed keratinophilic properties. The keratinophilic properties of micromycetes were confirmed by abundant mycelial growth, active sporulation, and accumulation of spores both on the surface (ectothrix) and in the thickness of the hair (endothrix) (Figure 5).

As can be seen from Figure 5, 20% of the strains out of the total number were characterized by active mycelial growth, the ability to grow inside the hair and form spores is characteristic of 13% of the strains, 60% of the strains could cause melting and perforation of hair, mycelial growth on hair with longitudinal spore placement on the surface and melting of the hair - 7% of the strains.

The keratinophilic properties of the micromycetes were confirmed by abundant mycelial growth, active spore formation, and spore accumulation both on the surface (ectothrix) and within the hair shaft (endothrix). The pattern of lesions on human hair was clearly visible, revealing both keratinophilic

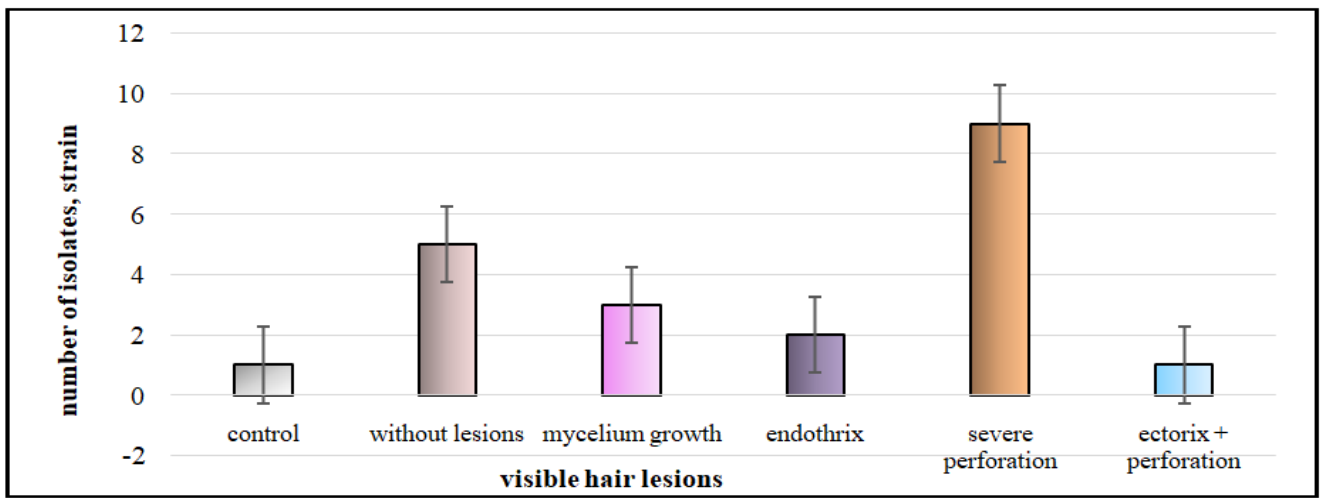


Figure 5 – The number of keratinophilic fungi isolated from the biomaterial of healthy young people and the hair lesions they cause.

Table 2 – Molecular genetic identification of isolates was carried out based on sequencing of the *ITS* region.

Type	Sequence
26 *Penicillium rubens*	ATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTCTGTAGGCCCGGCCGGCGCTTGCCGATCAACCC
18B *Penicillium rubens*	AACTTCACACAAGCTTCCCCGAGGAGGGAATATGAGAACAACCCGAAATCCACGCAAATTCGAACTATCTCCGCGGGTCTCCTAAGGAAGCATCGATGAACAACGCGCGAGTGCTTGCGAATTGTGAATTTCATATTCTCTTTTCATCGAGTCTTTCACCCCGATTGCGCCCCCGGGTATTCCGGGGGGGCATGCTTGTCCGACTCAATTTCTGCCCTCATGCACGGTTGTGTGTTGGGCCCCGTCCTCAGATCCCGGGGGACGGTCCTGACAGCAGCGGTGGTCCGACTCTGGTCTTCAAGCGTATGGGGTTTGCCCCCGCTCTGTAG
18a *Cladosporium sp.*	TTGCGTAACTTTGCAGTCTGAGTAAATTTAATTAATAAATTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAAAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCGACGCGGTCTGCCGCGCTCCTTAAATCGACCGGCTGGGTCTTCTGTCCCCCTCAGCGTTGTGGAAACTATCCCGCT
3 *Penicillium rubens*	CTCCACGGGTCCTCTCTGGTTCAAGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGC
18 cax *Cladosporium sphaerospermum*	TGCGTAACTTTGCAGTCTGAGTAAATTTAATTAATAAATTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCGACGCGGTCCGCCGCGCGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTCAGCGTTGTGGAAACTATTCGCTAAGGTGCCACGGGA
14 *Geotrichum galactomycetum*	ATATTTCTTGTGAATTGCAGAAGTGAATCATCAGTTTTTGAACGCACATTGCACTTTGGGGTATCCCCCAAAGTATACTTGTTTGAGCGTTGTTTCTCTCTTGGAATTGCTTTGCTCTTCTAAAATTTCGAATCAAATTCGTTTGAAAAACAACACTATTCAACCTCAGATCAAGTAGGATTACCCGCTGAACTTAAGCATATCATTAAGCGGAGGAACCCGCAGGTGCGC
010 *Alternaria alternata*	AACTTAAATTTAGCTTCTCGGAGTCAGGGATATGAGAACATCACGAATTACACGTTAATTCAACTGATCTCCGGGGGGCTGGCCTAGAGAAAGAACGCAGCGAAATGCGATAAGTAGTGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTCGAGCGTCATTTGTACCCTCAAGCTTTGCTTGGTGTTGGGCGTCTTGTCTCTAGCTTTGCTGGAGACTCGCCTTAAAGTAATTGGCAGC
13B *Penicillium rubens*	ACACCCTCGTCCTCTGGCTGAAGATTGTAGACTGACCGAAAATATACATTATTTAAAACTTTCTCCACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTAATGTGAATTGCAAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTGCCCTCAAGCACGGCTTGTGTGTTGGGCCCCGTCCTCCGATCCCGGGGGACGGGCCCGAAAGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCCGCTCTGTAGGCCCGGC

and keratinolytic properties in the isolated isolates (Figure 6).

As Figure 6 shows, the activity of keratinolytic enzymes of various dermatomycete fungi allows for the breakdown of hair keratin, which is visually manifested by thinning and melting of the hair, the appearance of darkening at the lateral edges of the hair, foci of perforation in the form of characteristic «pegs,» and uncharacteristic cup-shaped or acute-angled lesions.

4. DISCUSSION

There are publications on the emergence of new microbial representatives in the skin microbiome, adapted to life on the skin. We identified dermatophytes at 28.6%, molds at 37.1%, and yeasts at 34.3%. Our results are consistent with data from international authors reporting changes in the composition of the skin microbiota [7, 8, 9, 10, 15].

One factor in the adaptation of microorganisms to life on the skin is the presence of enzymes that promote the breakdown of human keratin [40]. Saprophytic microorganisms that are biodegraders exist in nature, such as *Chrysosporium* spp., *Psuedogymnoascus* spp., *Geomyces* spp., *Pectinotrichum* spp., *Renispora* spp., and several others, which synthesize the enzyme keratinase [32, 33]. The most well-known keratinolytic

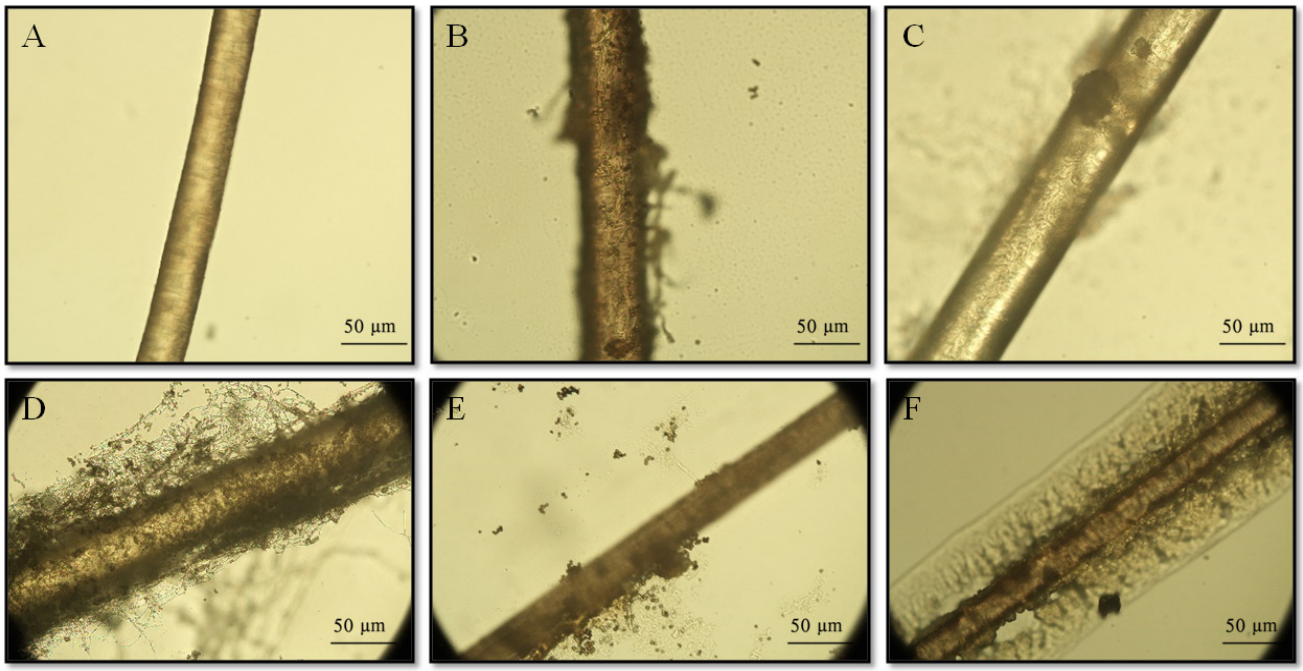


Figure 6 – Hair lesions caused by keratinophilic fungi: A – absence of lesions, B – ectothrix, C – endothrix, D – mycelium growth + perforation, E – cuticle ruptures, F – capsule and hair perforation.

fungi are of the genera *Aspergillus*, *Penicillium*, *Fusarium*, *Microsporum*, *Trichoderma*, and *Chrysosporium* [41]. Therefore, their presence in the microbiome is highly predictable, especially since keratin is a structural component of human skin, hair, and nails [42].

According to our results, dermatophytes were predominantly present on the skin of healthy young people in monoculture (31 samples). Dermatophyte growth in association with molds or yeasts was detected in 4 cases.

Previously, dermatophytes were reported to be associated with micromycetes (17.7%), less frequently with yeast-like fungi (5.9%), and 2.2% of cases were associated with yeast-like fungi and micromycete fungi. The authors also found that fungi of the genus Trichophyton, in monoculture or in association with micromycetes and candida, were isolated from the nails and skin of the hands in 8.1% of cases [34]. These data are consistent with our results, where associations of dermatophytes with mold fungi and yeasts were detected in the skin microbiome of healthy adolescents in four samples: *T. rubpum* + *Penicillium* spp. + *Candida* spp.; *T. verrucosum* + *Penicillium* spp.; *T. rubrum* + *Aspergillus* spp. – a total of 9.3% of the total number of samples (43 samples).

The activity of keratinolytic enzymes in various dermatomycete fungi allows for the breakdown of hair keratin, which is visually manifested by thinning and melting of the hair, the appearance of darkening at the lateral edges of the hair, foci of perforation in the form of characteristic «pegs,» as well as uncharacteristic cup-shaped or acute-angled lesions [26, 27]. It should be noted that the degree of keratin absorption varied. This was mostly manifested by abundant mycelial growth on or near the hair, with the formation of mycelial mass clusters in the form of rounded colonies, the formation of a sheath along the hair, or disordered mycelial growth with chaotic entanglement of the hair fiber. The second criterion was the analysis of sporulation and spore accumulation on, within, or around the hair. The third criterion for assessing keratinophilicity was the ability to alter the hair's appearance and form foci of melting and thinning during mycelial growth, leading to the formation of characteristic pegs or other forms of hair melting. The fourth criterion was the ability to damage the hair cuticle, causing visible damage in the form of cracks or detachment of the superficial cuticle layer.

Keratinolytic properties manifest themselves through hair dissolution [31]. All isolates of micromycetes obtained during the research were analyzed for the presence of keratinolytic properties. In our studies, 42.8% of isolates exhibited classic hair perforation with the formation of pegs or focal hair melting along the entire length or in small areas with a decrease in diameter. 9.5% of isolates developed characteristic «endothrix» lesions – visible spores lying in dense or sparse rows within the hair's thickness. The «ectoctyx» phenomenon was also observed in hair: 14.3% of isolates demonstrated vigorous mycelial growth and active sporulation on the outer hair surface, causing ruptures, cracks, and detachment of the hair cuticle. One isolate (4.8%) exhibited pronounced keratinophilic and keratinolytic properties, causing hair damage in the form of perforation and abundant accumulation of spores and mycelium on the cuticle surface.

Based on the data obtained, it can be concluded that keratinophilia may be the cause of the increased number of ecologically significant saprophytes in the human microbiome. For example, species such as Trichophyton and Microsporum are known for their keratinolytic activity and ability to colonize these tissues. Our opinion is consistent with the authors who believed that «keratinophilicity, or the ability to use keratin, is an important factor in changing the composition and activity of the human microbiome, but the composition and activity of the human microbiome is influenced by a complex interaction of various factors: host genetics, diet, environmental factors, interaction with the immune system, drugs, age and life stage [43]. Therefore, further studies of the fungal biota of human skin are becoming an important aspect in improving

the health and quality of life of the population of Kazakhstan.

The study has several limitations. Firstly, the small sample size: a single study was conducted on healthy schoolchildren and students. Secondly, the lack of a control group; There was no positive control due to the aim of analyzing the skin microbiota of healthy schoolchildren and students.

5. CONCLUSION

35 fungal isolates were isolated from 32 samples in the microbiota of the skin of the hands of healthy adolescents, and up to 13 taxa were identified: *Penicillium* spp. (11%), *T. rubrum* (11%), *Alternaria* spp. (6%), *T. mentagrophytes* (8%), *T. verrucosum* (6%), *A. niger* (9%), *A. flavus* (3%), *M. canis* (3%), *Ch. globosum* (3%), *A. pullulans* (3%), *Cladosporium* spp. (3%), *Candida* spp. (34%), *Rhodotorula* spp. – 3%. No micromycetes were detected in 11 samples (25.6%). Mixed microbiota from one biomaterial accounted for 9%, *Bacillus* spp. and other bacteria – 3%. A high carrier rate of all skin mycosis pathogens was found in boys (schoolchildren and students), with molds (61.5%) and yeasts (66.7%) predominating. Among students, carriers of classic dermatophytes were predominantly female (80.0%), while carriers of molds and yeasts were predominantly male (64.0%).

71.4% of micromycete strains isolated from adolescents possessed keratinophilic properties. The keratinophilic properties of the fungal isolates were confirmed by abundant mycelial growth, active spore formation, and spore accumulation both on the cuticle surface (ectothrix) and within the hair shaft (endothrix), which was detected by microscopy.

AUTHORS' CONTRIBUTIONS

Conceptualization, Y.K; formal analysis, Y.K, A.U; resources, Y.K; preparation of original draft, Y.K; and writing review and editing, Y.K, A.U, G.B, G.K, A.G. All authors have read and agreed with the published version of the manuscript.

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CONFLICT OF INTEREST

There are no conflicts of interest to declare.

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МИКРОБНЫЙ ПЕЙЗАЖ И КЕРАТИНОФИЛЬНЫЕ СВОЙСТВА МИКРОБИОТЫ КОЖИ РУК ЗДОРОВОЙ МОЛОДЕЖИ В Г. АСТАНА

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АБСТРАКТ

Микробиом кожи очень разнообразен. Его обязательной частью являются грибы. Биологическая роль недерматофитныхкератинолитических сапрофитных грибов состоит в разложении ороговевших остатков кожи и ее придатков в почве. Недерматофитныекератинофилы, населяющих кожу человека, могут быть потенциальными возбудителями оппортунистических микозов кожи, что делает актуальными полученные результаты. Целью исследования являлось изучение микробного пейзажа кожи рук подростков среди школьников и студентов и кератинофильных свойств, выделенных микромицетов. Объектом исследования были 43 здоровых подростка в возрасте от 12 до 18 лет, у которых отбирались пробы биоматериала. Анкетированием изучено состояние здоровья молодых людей, у которых выявлена гиподинамия, авитаминозы, случаи ОРВИ и ОРЗ.Установлен высокий показатель носительства всех представителей возбудителей микозов кожи у мальчиков школьного возраста с превалированием плесневых (61.5%) и дрожжевых (66.7%) грибов. Среди студентов носителями классических дерматофитов являлись в основном девушки (80.0 %), плесневых и дрожжевых грибов – в основном юноши (64.0%). Всего выделено 35 изолятов, идентифицировано до рода 13 видов грибов: *Penicillium* spp. (11%), *T. rubrum* (11%), *Alternaria* spp. (6%), *T. mentagrophytes* (8%), *T. verrucosum* (6%), *A. niger* (9%), *M. canis* (3%), *Ch. globosum* (3%), *A. pullulans* (3%), *Cladosporium* spp. (3%) и другие. Изучение кератинофильных свойств микромицетов, выделенных от подростков, показало их наличие у 71,4% штаммов. Кератинофильные свойства микромицетов подтверждались обильным ростом мицелия, активным спорообразованием, накоплением спор как на поверхности кутикулы (эндотрикс), так и в толще волоса (эндотрикс), выявляемых при микроскопии.

Ключевые слова: микробиом кожи человека, микозы кожи, спектр, кератинофильность, кератинофилы

АСТАНА ҚАЛАСЫНДАҒЫ ЖАСӨСПІРІМДЕРДІҢ ҚОЛ ТЕРІСІ МИКРОБИОТАСЫНЫҢ МИКРОБТЫҚ ПЕЙЗАЖЫ ЖӘНЕ КЕРАТИНОФИЛЬДІ ҚАСИЕТТЕРІ

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Түйін

Тері микробиомасы өте алуан түрлі. Оның міндетті бөлігі – саңырауқұлақтар. Дерматофитті емес кератинолитикалық сапрофитті саңырауқұлақтардың биологиялық рөлі топырақтағы терінің және оның қосымшаларының кератинделген қалдықтарының ыдырауынан тұрады. Адам терісін мекендейтін дерматофитті емес кератинофилдер оппортунистік микоздардың ықтимал қоздырғыштары болуы мүмкін, бұл нәтижелерді өзекті етеді. Зерттеудің мақсаты оқушылар мен студенттер арасындағы жасөспірімдердің қол терісінің микробтық пейзажын және оқшауланған микромицеттердің кератинофильді қасиеттерін зерттеу болды. Зерттеу нысаны 12 мен 18 жас аралығындағы 43 сау жасөспірім болды, олардан биоматериал сынамалары алынды. Сауалнама гиподинамия, витамин тапшылығы, ЖРВИ және ЖРА жағдайлары анықталған жастардың денсаулық жағдайын зерттеді. Зең (61,5%) және ашытқы (66,7%) саңырауқұлақтарының басым болуымен мектеп жасындағы ұлдарда тері микозы қоздырғыштарының барлық өкілдерін тасымалдаудың жоғары көрсеткіші белгіленді. Студенттер арасында классикалық дерматофиттердің тасымалдаушылары негізінен қыздар (80,0%), зең және ашытқы саңырауқұлақтары – негізінен ұлдар (64,0%) болды. Барлығы 35 изолят оқшауланған, 13 саңырауқұлақ таксоны тұқымына дейін анықталған: *Penicillium* spp. (11%), *T. rubrum* (11%), *Alternaria* spp. (6%), *T. mentagrophytes* (8%), *T. verrucosum* (6%), *A. niger* (9%), *M. canis* (3%), *Ch. globosum* (3%), *A. pullulans* (3%), *Cladosporium* spp. (3%) және басқалары. Жасөспірімдерден оқшауланған микромицеттердің кератинофильді қасиеттерін зерттеу олардың штаммдардың 71,4%-ында бар екенін көрсетті. Микромицеттердің кератинофильді қасиеттері мицелийдің мол өсуімен, белсенді спораланумен, микроскопия кезінде анықталған кутикула бетінде (эктотрикс) және шаш қалыңдығында (эндотрикс) споралардың жиналуымен расталды.

Кілтті сөздер: адам терісінің микробиомасы, тері микоздары, спектр, кератинофильділік, кератинофилдер.