



Fungal Contamination in Thermal Springs: A Comparative Study Between Pool Water and Air Samples

Derya BERİKTEN¹ * Meliha KOLDEMİR GÜNDÜZ²

¹ Kütahya Health Sciences University, Faculty of Engineering and Natural Sciences, Department of Molecular Biology and Genetics, Kütahya, Türkiye.

² Kütahya Health Sciences University, Faculty of Engineering and Natural Sciences, Department of Basic Sciences of Engineering, Kütahya, Türkiye.

Received: 8 September 2025; Revised: 24 October 2025; Accepted: 8 November 2025

*Corresponding author : derya.berikten@ksbu.edu.tr

Citation: Berikten, D., & Koldemir Gündüz M. (2025). Fungal contamination in thermal springs: a comparative study between pool water and air samples. *International Journal of Chemistry and Technology*, 2025, 9(2), 333-343. <http://dx.doi.org/10.32571/ijct.1780205>

ABSTRACT

Thermal springs have been used for therapeutic purposes in Türkiye for centuries and remain popular for both health-related treatments and recreational activities. However, the increasing use of thermal pools without strict hygiene measures has been associated with rising incidences of infections such as folliculitis, dermatitis, otitis, conjunctivitis, and respiratory, genitourinary, and gastrointestinal infections. In this study, 24 water and air samples from eight indoor spa pools were examined, yielding 205 fungal isolates. Microfungal counts ranged from 5 to 1,228 cfu/m³ in air and 2,000 to 228,000 cfu/m³ in water. The isolates belonged to genera including *Aspergillus*, *Penicillium*, *Alternaria*, *Paecilomyces*, *Mucor*, *Rhizopus*, *Fusarium*, *Pythium*, and others. The fungal community was dominated by *Penicillium* (35%) and *Aspergillus* (29%). Among the 69 *Aspergillus* isolates, medically important species such as *A. fumigatus*, *A. terreus*, *A. niger*, and *A. flavus* were detected. These findings demonstrate that thermal pools may serve as reservoirs for opportunistic fungi, underscoring the need for molecular surveys and stricter monitoring to minimize public health risks.

Keywords: *Aspergillus*, thermal waters, indoor air, airborne microfungi.

1. INTRODUCTION

Natural spring waters, an important part of life in almost all cultures since prehistoric times, have been used by humans for therapeutic purposes such as healing wounds and relieving pain, and sometimes for mystical purposes (Mias et. Al., 2025; Velikova, 2025). Thermal spring pools used for therapeutic purposes pose significant microbiological risks. However, indoor pools, especially due to the warm and humid environments found in thermal springs, are particularly suitable for the growth and spread of fungi. Fungi can

grow in many environments with sufficient carbon sources and moisture, including ceiling tiles, wood products, paint, pictures, carpets, some furniture, books, plaster, wallpaper (drywall), laundry, and other fabrics (Robins and Morell, 2007). Fungal spores, introduced to pools by air, water, and human sources, can thrive in these areas due to the high humidity levels (Gots and Layton, 2003).

Indoor air quality is very important for human health (Yeşiltaş, 2024). A number of studies have examined the health risks associated with the presence of fungi in

indoor environments and have found a positive correlation between fungal levels and health problems (Xiao et al., 2025; Groot et al., 2023; European Environment and Health Information System, 2007). Spores of some airborne microfungi can cause disease processes such as aspergillosis and histoplasmosis when inhaled by immunocompromised individuals. Respiratory diseases are the most common health problems in fungal colonized environments (Maaranen et al., 2025; Holden et al., 2023).

Since the indoor pools in spas are open to public use, the risk of microorganisms being transmitted from outside the pool, such as through entrances, changing rooms, and shower cabins, is higher than the risk of contamination from pool water. Therefore, the areas where community treatments are most frequently encountered in spas are the pools where public treatments are conducted. Furthermore, the immune systems of people using spas may be weaker than those of the general population. This situation is quite favorable for the development of opportunistic pathogenic fungi. Most people who breathe air contaminated with fungal spores can be identified by symptoms such as headache, vomiting, nausea, stuffy noses, asthmatic rhinitis, wheezing, conjunctival irritation, skin rashes, chest tightness, difficulty breathing, runny nose, fever, muscle aches, and diarrhea. Volatile products of molds present in the environment can cause toxic diseases or mycotoxicoses (Abbot, 2002; Straus and Wilson, 2006).

A large number of fungi have been identified in different indoor air environments in many parts of the world. Airborne fungi commonly found in indoor environments are: *Alternaria* sp., *Aspergillus glaucus* group, *A. versicolor*, *A. fumigatus*, *A. sydowii*, *Penicillium aurantiogriseum*, *P. chrysogenum*, *Stachybotrys chartarum*, *Chaetomium globosum*, *Cladosporium cladosporoides*, *Ulocladium*, *Aspergillus nidulans* and *Alternaria alternata* (Ayanbimpe et al., 2012). In studies conducted to determine fungal contamination in public swimming pools of various countries, samples were taken from various surfaces, air and pool water and as a result *Aspergillus* sp., *Cladosporium* sp., *Fusarium* sp., *Acremonium* sp., *Penicillium* sp., *Alternaria* sp., *Candida* sp., *Rhizopus* sp. species were found to be frequently encountered fungi. Studies have shown that *Aspergillus* sp. species are among the most common fungi (Adamowicz et al., 2019; Agababova and Hon, 2018; Brandi et al., 2007; Hanbakhsh et al., 2004).

Thermal tourism has become quite popular in our country in recent years. However, due to the use of thermal pools without following hygiene rules, the incidence of various infections, such as follicular dermatitis and dermatitis, ear and eye infections, skin irritation, and respiratory, genitourinary, and

gastrointestinal tract infections, has increased significantly in recent years (Alim et al., 2002; Yılmaz Sarıözlü et al., 2012). Furthermore, many sources generally focus on bacterial and viral infections when discussing these infections, while fungal infections are overlooked (Savcı and Şahin, 2019). Conducting quantitative studies to simultaneously determine the water and air quality of indoor pools in thermal facilities located in different districts of Kütahya, which are important for thermal tourism, is crucial for gaining insight into the epidemiology of opportunistic pathogens that cause infections in these regions (Sarmadian et al., 2020). In this study, the isolation of potentially pathogenic microfungi from hot spring pool water and indoor air, the qualitative determination of microfungi density, the identification of isolates at genus level and the identification of *Aspergillus* sp. containing potentially pathogenic species at species level using morphological identification criteria by macroscopic and microscopic examination were carried out.

2. EXPERIMENTAL

2.1. Materials

2.2.1. Site description and characterization of hot springs

The research material was obtained by sampling hot water and indoor air samples taken from indoor thermal pools in Kütahya province, Çiftlikköy thermal springs in Yoncalı district, Ilıca thermal springs in Gediz district, Eynal, Çitgöl and Naşa thermal springs in Simav district, Osmanlı, Dereli and Kaynarca thermal springs in Emet district, Göbel thermal springs in Tavşanlı district and Esire thermal springs in Hisarcık district (Table 1) twice on 18.10.2020 and 23.10.2021. The temperatures of the sampled pool waters and the humidity rate of the pool environments were measured during sampling.

Table 1. Coordinates of the sampled hot springs.

Region No. Name	Coordinates
1. Yoncalı Çiftlikköy Hot Springs	39.47561, 29.83089
2. Gediz Ilıca Hot Springs	38.94666, 29.26532
3. Simav Çitgöl Hot Springs	39.13098, 28.95576
4. Simav Eynal Hot Springs	39.09582, 28.98632
5. Simav Naşa Hot Springs	39.14909, 28.96950
6. Emet Hot Springs	39.46350, 29.27251
7. Tavşanlı Göbel Hot Springs	39.52555, 29.50690
8. Hisarcık Esire Hot Springs	39.21055, 29.30675

2.2. Methods

2.2.1. Water and air sampling

A total of 12 different water and air samples were collected from the selected hot springs during each of the two sampling sessions, resulting in 24 water samples

and 24 air samples being used for fungal isolation studies. Water samples were collected in 1 L sterile polypropylene bottles and transported to the laboratory in an insulated bag, where microbiological analyses were conducted on the same day. A total of 200 L of indoor air was sampled from the enclosed thermal pool environment using a microbial air sampler (AirIDEAL), with two replicate samplings of 100 L each.

2.2.2. Isolation and counting of microorganisms from hot water/air samples

The membrane filtration method was used for the enumeration and isolation of fungi from hot spring water. 500 ml of each water sample taken from the indoor thermal pools of the hot springs into sterile bottles was filtered using sterile membrane filters with 0.22 µm pore diameter, and these filters were placed in petri dishes containing Potato dextrose agar (PDA) (Merck, Germany) supplemented with 500 mg streptomycin (Yarita et al., 2007), which was used as an isolation medium, and incubated at 30 °C for 7-14 days. Experiments were performed in 2 replicates. On the other hand, a total of 200 L of air was aspirated from the indoor air of the indoor thermal pools of the selected hot springs using a Microbial Air Sampling Device (AirIDEAL), 100 L per sampling (in 2 replicates). Dichloran Glycerol Agar (DG 18) (Merck, Germany) media was used in the sampling process (Samson et al., 2010) and then brought to the laboratory and incubated at 30 °C for 7-14 days. The Petri dishes were examined at intervals of 24 to 48 hours. After incubation period, the count of fungi in the water/air samples was determined and expressed as colony-forming unit per m³ of the water/air (cfu/m³). The isolates obtained in pure form were stored at both +4 °C and -20 °C.

2.2.3. Identification of microfungi

All isolates were grown on Malt Extract Agar (MEA) at 25°C 7 days for identification. Microfungi were identified to the genus level on the basis of their microscopic and colonial characteristics (Barnett and Hunter, 1999; Hasenekoğlu, 1991). Lacto-Cotton Blue (Lacto-Cotton Blue – LCB- Mounting Medium) (Sime et al., 2002) was used as an examination medium to enable examination under light microscopy after incubation of microfungi in the media.

For species-level identification of *Aspergillus* isolates, fresh cultures were inoculated onto Petri dishes containing Czapek Dox Agar (CDA), Czapek Yeast Extract Agar supplemented with 20% sucrose (CY20S), Czapek Yeast Extract Agar (CYA), and Malt Extract Agar (MEA). Plates were incubated at 25 °C for 7 days, with additional CYA plates incubated at 37 °C for the same period (Klich, 2002; Samson et al., 2010). Following incubation, macroscopic characteristics—including colony diameter, texture, surface and reverse

coloration, pigmentation, exudate production, and sclerotia formation—were systematically recorded. Micromorphological features such as spore dimensions and pigmentation, vesicle morphology, stipe size, and the presence of Hülle cells, ascospores, and cleistothecia were examined using light microscopy. Species-level identification was achieved by comparing the observed characteristics with established taxonomic keys (Klich, 2002). The current names of fungi identified at the genus and/or species level, along with the corresponding author citations, were standardized in accordance with the Index Fungorum Partnership database (Hawksworth et al., 2011).

2.2.4. Statistical analysis

Statistical analyses were performed using SPSS 23.0 (Statistical Package for Social Sciences). Descriptive statistics were presented as mean ± standard deviation (SD) for continuous variables. The independent samples t-test was used for comparisons of means between two or more groups. The Mann-Whitney-U test was used for variables that did not show a normal distribution in comparisons between paired groups. The Kruskal-Wallis test was used to assess differences between three or more independent groups when parametric assumptions were not met. A p value of <0.05 was considered statistically significant

3.RESULTS

3.1.Features of hot springs

The temperatures of the sampled pool waters vary between 24-30 °C. The humidity rates in the pool environments where air samples were taken were determined as 65% in Çiftlikköy hot springs in Yoncalı district, 55% in Ilıca hot springs in Gediz district, 59%, 55%, 54% in Eynal, Çitgöl and Naşa hot springs in Simav district, respectively, 75%, 70%, 68% in Osmanlı, Dereli and Kaynarca hot springs in Emet district, respectively, 48% in Göbel hot springs in Tavşanlı district and 69% in Esire hot springs in Hisarcık district.

3.2. Microfungal enumeration

A total of 12 different pool water and air samples were taken in two sampling runs to isolate filamentous microfungi. The number of colonies that developed on the petri dishes after the isolation inoculations are shown in Table 2. Morphologically distinct colonies were purified from the isolates mixed in the isolation petri dishes. As a result of the purification processes, the first isolation run yielded a total of 103 isolates: 74 from air samples and 29 from water samples. The second isolation run yielded a total of 102 isolates: 69 from air samples and 33 from water samples. The total number of isolates was 205, of which 143 were isolated from air

samples and 62 from water samples. The pure isolates were stored at both +4°C and -20°C. The distribution of air and water samples of the first isolation by region was found to be statistically significant ($p=0.0003$, $p=0.0018$, respectively) (Table 2). The distribution of

air and water samples of the second isolation by region was found to be statistically highly significant ($p=0.0003$, $p=0.0005$, respectively) (Table 2).

Table 2. Number of microfungi obtained in the first and second isolation study.

Isolation		Sample Codes*												p
		1.1 (n=5)	1.2 (n=5)	2.1 (n=5)	3.1 (n=5)	4.1 (n=5)	4.2 (n=5)	5.1 (n=5)	6.1 (n=5)	6.2 (n=5)	6.3 (n=5)	7.1 (n=5)	8.1 (n=5)	
1	Air (CFU/m ³)	samples	5 ± 0.63	75 ± 0.75	220 ± 1.02	40 ± 0.63	M ± SD 65 ± 0.75 95 ± 0.63		45 ± 1.02	185 ± 0.75	15 ± 0.75	75 ± 0.63	140 ± 1.41	0.0003***
	Water (CFU/m ³)	samples	2000 ± 7.1	68000 ± 32.2	2000 ± 7.1	3800 ± 7.2	4000 ± 32.2	-	8000 ± 32.6	20000 ± 38.5	2000 ± 7.7	4000 ± 20.6	-	0.0018**
2	Air (CFU/m ³)	samples	115 ± 3.22	1228 ± 15.97	205 ± 3.41	165 ± 3.22	165 ± 1.72	590 ± 54.13	10 ± 0.63	64 ± 1.79	180 ± 17.03	85 ± 0.63	110 ± 0.89	0.0003***
	Water (CFU/m ³)	samples	20000 ± 70.7	168000 ± 63.2	-	6000 ± 77.2	18000 ± 114	14000 ± 63.6	12000 ± 68.1	2000 ± 66	8000 ± 63.3	228000 ± 69.4	4000 ± 63.4	0.0005***

* In code numbers, the 1st digit indicates the region and the 2nd indicates the sample number

** $p<0.01$, *** $p<0.001$, M: Average, SD: Standard deviation

When the amounts of microorganisms in the first and second isolations of air samples were compared, the samples from the second isolation in regions 1.1, 1.2, 3.1, 4.1, 4.2, 6.2, 6.3 and 8.1 were found to be

statistically higher ($p<0.001$) (Figure 1). The samples from the second isolation in regions 2.1, 5.1, 6.1 and 7.1 were found to be statistically lower ($p<0.001$) (Figure 1).

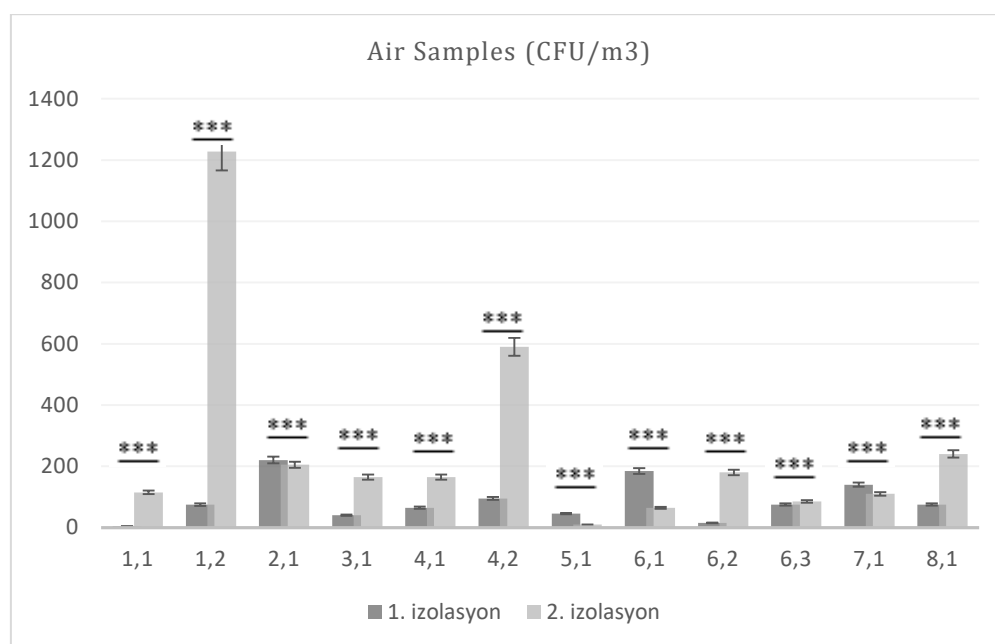


Figure 1. Comparison of the amount of microorganisms in the air samples of the first and second isolation *** $p<0.001$

When the amounts of microorganisms in the first and second isolations of water samples were compared, the samples from the second isolation in regions 1.1, 1.2, 4.2, 6.1, 6.3 and 7.1 were found to be statistically higher ($p<0.001$) (Figure 2). The samples from the second isolation in regions 4.1 and 6.2 were found to be statistically lower ($p<0.001$) (Figure 2). In the first isolation, microorganisms from air samples were significantly different from those from 12 different

locations (Mean = 86.3, SD = 63.08) compared to those from water samples at 9 different locations (Mean = 16443.8, SD = 21695.9), $t(103) = -5.84$ $p<0.00001$. In the second isolation, microorganisms from air samples were significantly different from those from 12 different locations (Mean = 263.08, SD = 325.8) compared to those from water samples at 11 different locations (Mean = 43818.18, SD = 74706.6), $t(133) = -4.52$ $p<0.00001$.

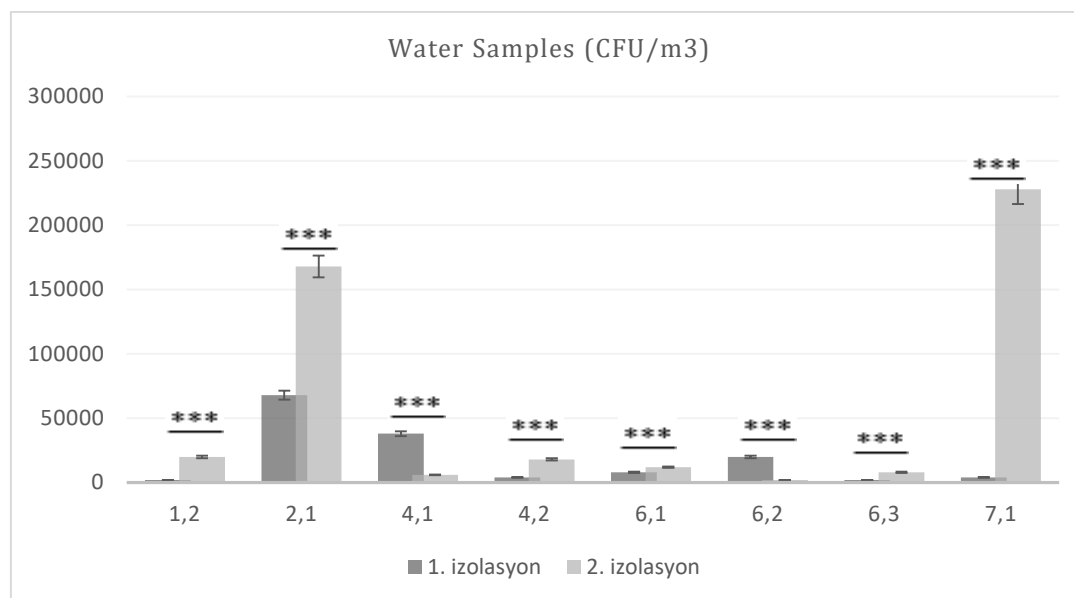


Figure 2. Comparison of the amount of microorganisms in the water samples of the first and second isolation
*** $p < 0.001$

3.3. Fungal isolates

The isolated fungi were identified based on their morphological characteristics. During identification based on morphological criteria, macroscopic and microscopic examinations were used to determine which of the main fungal genera all isolates belonged to. These genera and the hot spring air and water samples from which they were obtained are listed in [Tables 3-6](#). Among the fungal isolates obtained in this study, members of the genus *Penicillium* sp. were the most dominant, representing 35% of the total community. When all identified *Aspergillus* taxa were considered collectively as *Aspergillus* sp., ([Figure 3](#)) they

accounted for 29% of the isolates, highlighting the ecological prominence of this genus within the sampled habitats. *Alternaria* sp. comprised 10% of the isolates, whereas non-spore-forming fungi represented 6%. The remaining fraction, constituting 20% of the total, consisted of less frequently encountered genera, including *Paecilomyces* sp., *Mucor* sp., *Rhizopus* sp., *Pythium* sp., *Fusarium* sp., and unidentified *Ascomycota* spp. As a result of the analysis, 69 isolates were identified as *Aspergillus*, 56 of which were isolated from air samples and 13 from water samples. The species distribution of isolates within the *Aspergillus* genus is given in [Figure 4](#).

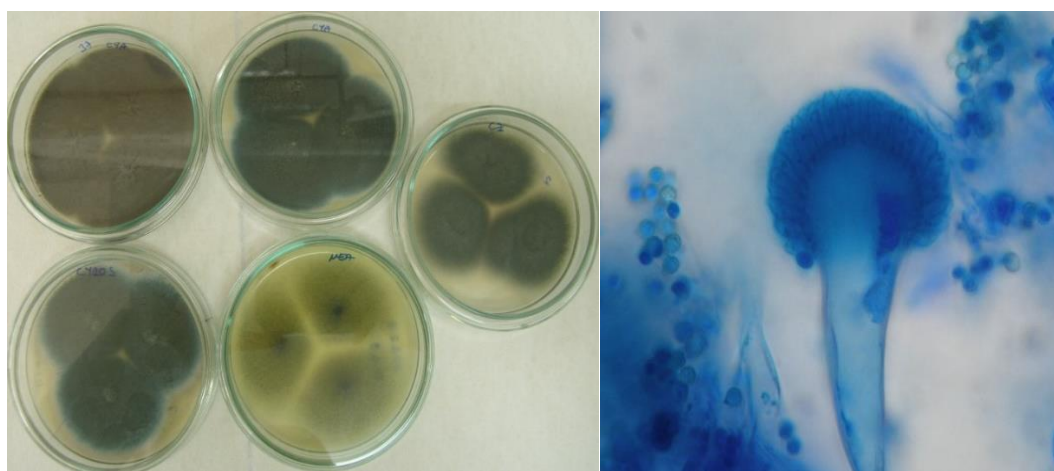


Figure 3. a-Macroscopic (on CYA 37 °C, CYA, CDA, CY20S, MEA) and b-microscopic (light microscope 100x; ascosporic head structure, conidia) images of *Aspergillus fumigatus*

Table 3. Microfungi identified in the first isolation from air samples.

Region No	Isolate Code *	Genus/Species
1	1.1.1.1	<i>Aspergillus fumigatus</i>
	1.1.2.1	<i>Alternaria</i> sp.
	1.1.2.2	<i>Aspergillus europaeus</i>
	1.1.2.3	<i>Aspergillus amstelodami</i>
	1.1.2.4	<i>Ascomycota</i> sp.
	1.1.2.5	<i>Ascomycota</i> sp.
	1.1.2.6	<i>Penicillium</i> sp.
2	1.1.2.7	<i>Alternaria</i> sp.
	1.2.1.1	<i>Penicillium</i> sp.
	1.2.1.2	<i>Penicillium</i> sp.
	1.2.1.3	<i>Penicillium</i> sp.
	1.2.1.4	<i>Alternaria</i> sp.
	1.2.1.5	<i>Alternaria</i> sp.
	1.2.1.6	<i>Alternaria</i> sp.
	1.2.1.7	Non-spore forming fungi
	1.2.1.8	<i>Alternaria</i> sp.
	1.2.1.9	<i>Aspergillus terreus</i>
	1.2.1.10	<i>Alternaria</i> sp.
3	1.2.1.11	<i>Aspergillus niger</i>
	1.3.1.1	<i>Ascomycota</i> sp.
	1.3.1.3	<i>Penicillium</i> sp.
	1.3.1.4	<i>Alternaria</i> sp.
	1.3.1.5	<i>Alternaria</i> sp.
	1.3.1.6	<i>Penicillium</i> sp.
4	1.4.1.1	<i>Aspergillus sclerotiorum</i>
	1.4.1.2	<i>Aspergillus montevidensis</i>
	1.4.1.3	<i>Aspergillus montevidensis</i>
	1.4.1.4	<i>Penicillium</i> sp.
	1.4.1.5	<i>Paecilomyces</i> sp.
	1.4.1.6	<i>Aspergillus tubingensis</i>
	1.4.1.7	<i>Aspergillus montevidensis</i>
	1.4.1.8	<i>Aspergillus flavus</i>
	1.4.2.1	<i>Aspergillus flavus</i>
	1.4.2.2	<i>Aspergillus neoniveus</i>
	1.4.2.3	Non-spore forming fungi
	1.4.2.4	<i>Ascomycota</i> sp.
	1.4.2.5	<i>Aspergillus flavus</i>
	1.4.2.6	<i>Aspergillus tabacinus</i>
	1.4.2.7	<i>Aspergillus chevalieri</i>
	1.4.2.8	<i>Bipolaris</i> sp.
	1.4.2.9	<i>Aspergillus tabacinus</i>
	1.4.2.10	<i>Aspergillus chevalieri</i>
	1.4.2.11	<i>Ascomycota</i> sp.
	1.4.2.12	<i>Aspergillus tabacinus</i>
	1.4.2.13	Non-spore forming fungi

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

Table 3. Microfungi identified in the first isolation from air samples (continue)

Region No	Isolate Code *	Genus/Species
5	1.5.1.1	<i>Penicillium</i> sp.
	1.5.1.2	<i>Alternaria</i> sp.
	1.5.1.3	<i>Penicillium</i> sp.
	1.5.1.4	<i>Aspergillus flavus</i>
	1.5.1.5	<i>Alternaria</i> sp.
	1.5.1.6	<i>Alternaria</i> sp.
	1.5.1.7	Non-spore forming fungi
	1.5.1.8	<i>Alternaria</i> sp.
6	1.6.1.1	<i>Aspergillus terreus</i>
	1.6.1.2	<i>Penicillium</i> sp.
	1.6.1.3	<i>Aspergillus ochraceus</i>
	1.6.2.1	<i>Curvularia</i> sp.
	1.6.2.2	<i>Aspergillus tubingensis</i>
	1.6.3.1	<i>Paecilomyces</i> sp.
7	1.7.1.1	<i>Aspergillus magaliesburgensis</i>
	1.7.1.2	<i>Aspergillus magaliesburgensis</i>
	1.7.1.3	Non-spore forming fungi
	1.7.1.4	<i>Mucor</i> sp.

8	1.7.1.5	<i>Aspergillus chevalieri</i>
	1.7.1.6	<i>Penicillium</i> sp.
	1.7.1.8	<i>Aspergillus magaliesburgensis</i>
	1.7.1.9	<i>Alternaria</i> sp.
	1.7.1.10	<i>Aspergillus ostianus</i>
	1.7.1.11	<i>Penicillium</i> sp.
	1.7.1.12	<i>Penicillium</i> sp.
	1.7.1.13	<i>Penicillium</i> sp.
	1.7.1.14	<i>Penicillium</i> sp.
	1.8.1.1	<i>Alternaria</i> sp.
	1.8.1.2	<i>Aspergillus niger</i>

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

Table 4. Microfungi identified in the first isolation from water samples.

Region No	Isolate Code *	Genus/Species
1	S.1.1.1.1	Non-spore forming fungi
	S.1.1.2.1	<i>Aspergillus unguis</i>
	S.1.1.2.2	<i>Aspergillus niger</i>
	S.1.1.2.3	<i>Paecilomyces</i> sp.
2	S.1.1.2.4	<i>Paecilomyces</i> sp.
	S.1.2.1.1	<i>Alternaria</i> sp.
3	S.1.3.1.1	<i>Fusarium</i> sp.
	S.1.3.1.2	<i>Penicillium</i> sp.
	S.1.3.1.3	Non-spore forming fungi
	S.1.3.1.4	<i>Paecilomyces</i> sp.
	S.1.3.1.5	<i>Fusarium</i> sp.
	S.1.3.1.6	Non-spore forming fungi
4	S.1.4.1.1	<i>Rhizomucor</i> sp.
	S.1.4.1.2	<i>Aspergillus austwickii</i>
	S.1.4.2.1	Non-spore forming fungi
	S.1.4.2.2	<i>Paecilomyces</i> sp.
5	S.1.5.1.1	<i>Aspergillus niger</i>
	S.1.5.1.2	<i>Pythium</i> sp.
	S.1.5.1.3	<i>Pythium</i> sp.
6	S.1.6.1.1	<i>Pythium</i> sp.
	S.1.6.1.2	<i>Pythium</i> sp.
	S.1.6.1.3	<i>Pythium</i> sp.
	S.1.6.1.4	<i>Pythium</i> sp.
	S.1.6.1.5	<i>Aspergillus niger</i>
	S.1.6.2.1	<i>Aspergillus flavus</i>
	S.1.6.2.2	<i>Penicillium</i> sp.
	S.1.6.2.3	<i>Aspergillus niger</i>
	S.1.6.3.1	<i>Pythium</i> sp.
	S.1.6.3.2	<i>Mucor</i> sp.

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

Table 5. Microfungi identified in the second isolation from air samples.

Region No	Isolate Code *	Genus/Species
1	2.1.1.1	<i>Penicillium</i> sp.
	2.1.1.2	<i>Penicillium</i> sp.
	2.1.1.3	<i>Paecilomyces</i> sp.
	2.1.1.4	<i>Penicillium</i> sp.
	2.1.1.5	<i>Penicillium</i> sp.
	2.1.1.6	<i>Rhizopus</i> sp.
	2.1.2.1	<i>Aspergillus flavipes</i>
	2.1.2.2	<i>Penicillium</i> sp.
	2.1.2.3	<i>Penicillium</i> sp.
	2.1.2.4	<i>Aspergillus flavus</i>
	2.1.2.5	<i>Penicillium</i> sp.
2	2.2.1.1	<i>Aspergillus flavus</i>
	2.2.1.2	<i>Aspergillus terreus</i>
	2.2.1.3	<i>Penicillium</i> sp.
	2.2.1.4	<i>Penicillium</i> sp.
	2.2.1.5	<i>Penicillium</i> sp.
	2.2.1.6	<i>Penicillium</i> sp.
3	2.3.1.1	<i>Penicillium</i> sp.

	2.3.1.2	<i>Penicillium</i> sp.
	2.3.1.3	<i>Alternaria</i> sp.
	2.3.1.4	<i>Penicillium</i> sp.
	2.3.1.5	<i>Aspergillus niger</i>
	2.3.1.6	<i>Penicillium</i> sp.
	2.3.1.7	<i>Alternaria</i> sp.
	2.3.1.8	<i>Rhizopus</i> sp.
	2.4.1.1	<i>Aspergillus chevalieri</i>
	2.4.1.2	<i>Penicillium</i> sp.
	2.4.1.3	<i>Alternaria</i> sp.
	2.4.1.4	<i>Penicillium</i> sp.
	2.4.1.5	<i>Penicillium</i> sp.
	2.4.1.6	<i>Alternaria</i> sp.
	2.4.1.7	<i>Aspergillus sydowii</i>
4	2.4.1.8	<i>Helminthosporium</i> sp.
	2.4.1.9	<i>Aspergillus terreus</i>
	2.4.1.10	<i>Penicillium</i> sp.
	2.4.2.1	<i>Aspergillus tubingensis</i>
	2.4.2.2	<i>Ascomycota</i> sp.
	2.4.2.3	<i>Aspergillus niger</i>
	2.4.2.4	<i>Aspergillus flavus</i>
	2.4.2.5	<i>Mucor</i> sp.
5	2.5.1.1	<i>Penicillium</i> sp.
	2.5.1.2	<i>Penicillium</i> sp.

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

Table 5. Microfungi identified in the second isolation from air samples (continue).

Region No	Isolate Code *	Genus/Species
	2.6.1.1	Non-spore forming fungi
	2.6.1.2	<i>Talaromyces</i> sp.
	2.6.1.3	<i>Paecilomyces</i> sp.
	2.6.1.4	<i>Penicillium</i> sp.
	2.6.1.5	<i>Penicillium</i> sp.
	2.6.1.6	<i>Penicillium</i> sp.
	2.6.2.1	<i>Aspergillus sydowii</i>
	2.6.2.2	<i>Penicillium</i> sp.
	2.6.2.3	<i>Aspergillus tubingensis</i>
6	2.6.2.4	<i>Aspergillus flavus</i>
	2.6.2.5	<i>Penicillium</i> sp.
	2.6.2.6	<i>Penicillium</i> sp.
	2.6.3.1	<i>Penicillium</i> sp.
	2.6.3.2	<i>Aspergillus tennesseensis</i>
	2.6.3.3	<i>Aspergillus jensenii</i>
	2.6.3.4	Non-spore forming fungi
	2.6.3.5	<i>Penicillium</i> sp.
	2.6.3.6	<i>Penicillium</i> sp.
	2.6.3.7	<i>Aspergillus fumigatus</i>
	2.7.1.1	<i>Aspergillus sydowii</i>
7	2.7.1.2	<i>Aspergillus terreus</i>
	2.7.1.3	<i>Paecilomyces</i> sp.
	2.7.1.4	<i>Penicillium</i> sp.
	2.8.1.1	<i>Aspergillus montevidensis</i>
8	2.8.1.2	Non-spore forming fungi
	2.8.1.3	<i>Aspergillus niger</i>

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

Table 6. Microfungi identified in the second isolation from water samples.

Region No	Isolate Code *	Genus/Species
	S.2.1.1.1	<i>Penicillium</i> sp.
	S.2.1.1.2	<i>Penicillium</i> sp.
	S.2.1.1.3	<i>Penicillium</i> sp.
	S.2.1.1.4	<i>Penicillium</i> sp.
1	S.2.1.2.1	<i>Penicillium</i> sp.
	S.2.1.2.2	<i>Penicillium</i> sp.
	S.2.1.2.3	<i>Penicillium</i> sp.
	S.2.1.2.4	<i>Alternaria</i> sp.
	S.2.1.2.5	<i>Penicillium</i> sp.

	S.2.1.2.6	<i>Penicillium</i> sp.
	S.2.3.1.1	Non-spore forming fungi
	S.2.3.1.2	<i>Penicillium</i> sp.
	S.2.4.1.1	<i>Mucor</i> sp.
	S.2.4.1.2	<i>Penicillium</i> sp.
4	S.2.4.1.3	<i>Penicillium</i> sp.
	S.2.4.2.1	<i>Aspergillus niger</i>
	S.2.4.2.2	<i>Penicillium</i> sp.
	S.2.5.1.1	<i>Penicillium</i> sp.
5	S.2.5.1.2	<i>Penicillium</i> sp.
	S.2.5.1.3	<i>Aspergillus fumigatus</i>
	S.2.5.1.4	<i>Penicillium</i> sp.
	S.2.6.1.1	<i>Penicillium</i> sp.
	S.2.6.2.1	<i>Aspergillus sydowii</i>
	S.2.6.2.2	<i>Myriococcum</i> sp.
	S.2.6.2.3	<i>Penicillium</i> sp.
6	S.2.6.3.1	<i>Aspergillus chevalieri</i>
	S.2.6.3.2	<i>Aspergillus cheber</i>
	S.2.6.3.3	<i>Penicillium</i> sp.
	S.2.6.3.4	<i>Penicillium</i> sp.
	S.2.6.3.5	<i>Penicillium</i> sp.
7	S.2.7.1.1	<i>Penicillium</i> sp.
	S.2.7.1.2	<i>Penicillium</i> sp.
8	S.2.8.1.1	<i>Aspergillus fumigatus</i>

[* In code numbers, the 1st digit indicates the second isolate, the 2nd digit indicates the region, the 3rd digit indicates the sample number, and the 4th digit indicates the isolate number.]

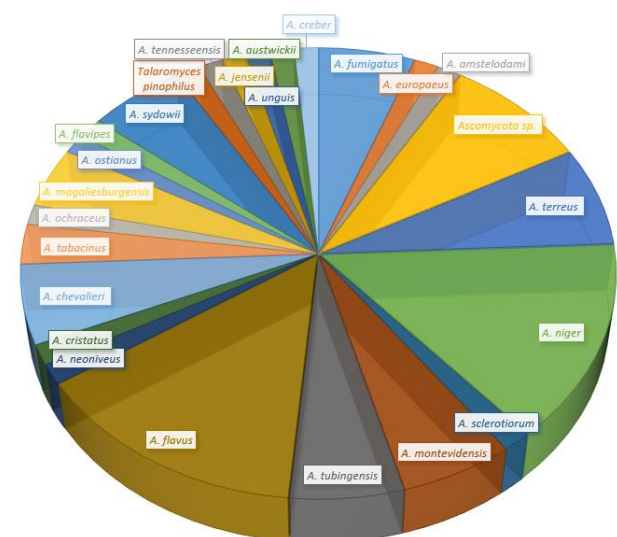


Figure 4. Species distribution (%) of isolates within the *Aspergillus* genus.

4. DISCUSSION

Examining the water and air of thermal spring pools in Kütahya province allowed us to identify mold growth in the water and air and to determine whether the observed mold counts and fungal profiles are a concern for the health of pool personnel and visitors. Our fungal screening study, conducted with air and water samples from indoor thermal spring pools located in six districts and eight different facilities in Kütahya province, was conducted on two different dates. Fungal loads in air samples from pool environments were found to be 5-220 CFU/m³ in the first isolation run and 10-1255 CFU/m³ in the second isolation run. Fungal loads in water samples were found to be 0-68,000 CFU/m³ in the first isolation run and 0-228,000 CFU/m³ in the second

isolation run. Given that there was no seasonal change during the first and second isolation runs, we believe that the increases in both air and water samples are related to the intensity of thermal spring pool use. This is because our first isolation study was conducted during a period when the number of people in indoor spaces was limited as part of the precautions taken during the Covid-19 pandemic, while the second isolation study was conducted when this was not the case. This demonstrated how fungal loads can vary depending on usage intensity and that an increase in fungal load is inevitable in a crowded pool environment. In the first isolation study, the spa with the highest airborne fungal load was found at Gediz Ilica Hot Springs, the spa with the lowest was found at Yoncalı Çiftlikköy Hot Springs. The spa with the highest waterborne fungal load was found at Yoncalı Çiftlikköy Hot Springs, and the spas with the lowest loads were found at Simav Eynal, Tavşanlı Göbel, and Hisarcık Esire Hot Springs. In the second isolation study, the hot spring with the highest airborne fungal load was found at Yoncalı Çiftlikköy Hot Springs, and the lowest at Simav Naşa Hot Springs. The hot spring with the highest waterborne fungal load was found at Emet Hot Springs, and the lowest at Gediz Ilica Hot Springs. It is believed that there is no consistent relationship between the mold density values obtained from the different hot springs in the first and second isolation studies, and that this finding is not related to humidity and temperature values.

In a study in Italian indoor swimming pools, monitoring the air quality of 10 facilities, the total fungal load in the air of one of the pools was found to be 25.5 CFU/m³ (Brandi et al., 2007). In another study, fungi were detected in the air of 6 indoor swimming pools in the Toronto area during the winter season of 2017, and the loads in zones 1 to 6 ranged from 18 CFU/m³ to 81 CFU/m³ (Agababova and Hon, 2018). Viegas et al. (2010) found a total fungal load of 135 CFU/m³ in air samples taken from gyms with indoor swimming pools (Viegas et al., 2010). The colony counts obtained from the air samples in our study are similar to these studies conducted by various researchers. However, most studies in this area have been conducted for regular swimming pools, not spa pools.

In our study, *Aspergillus* sp., *Penicillium* sp., *Alternaria* sp., *Paecilomyces* sp., *Bipolaris* sp., *Curvularia* sp., *Mucor* sp., *Rhizopus* sp., and *Helminthosporium* sp. were identified in samples taken from the ambient air of the hot spring pool, and the most frequently encountered species were *Aspergillus* sp. and *Penicillium* sp. There was no significant difference in species diversity in the first and second isolations. The mold genera we isolated from the air samples in our study overlap with those found in the study by Brandi et al. (2007) (*Aspergillus*, *Penicillium*, *Cladosporium* and *Alternaria*). In a study on bioaerosol microbial diversity in sports facilities, including swimming pools, *Cladosporium* sp., *Fusarium*

sp., *Acremonium* sp., *Penicillium* sp., *Alternaria* sp., and *Aspergillus* sp. were found, and it was demonstrated that these species affect human health and performance (Adamowicz et al., 2019). The species found in this study are parallel to our study, and the same risks apply to the spas where we worked.

In another study identifying fungi in the air of six indoor swimming pools in the Toronto area, the most common fungal groups were *Cladosporium* (59.8%), *Penicillium* (19.2%), and *Alternaria* (5.5%). Among the fungi isolated from all pools, *Alternaria*, *Nigrospora*, *Rhizomucor*, *Aspergillus niger*, *Aspergillus fumigatus*, and *Aspergillus versicolor*, all known to be harmful to human health, were found (Agababova and Hon, 2018). Despite the significant geographical differences between this Toronto study and ours, the diversity of fungal genera obtained was quite similar. Furthermore, the fact that *Aspergillus* constituted the majority of the species harmful to human health isolated from the pool air by the researchers further validates the use of this group for species-level identification in our study.

In our study, *Penicillium* sp., *Aspergillus* sp., *Alternaria* sp., *Paecilomyces* sp., *Fusarium* sp., *Pythium* sp., *Myriococcum* sp., *Mucor* sp., and *Rhizomucor* sp. were determined in samples taken from hot spring pool water. *Penicillium* sp. was the most frequently encountered species, followed by *Aspergillus* sp. and *Pythium* sp. In a study conducted to determine fungi in swimming pools in Urmia, Iran, *Aspergillus* sp. was found to be 56.25%, *Candida* sp. 22.9%, *Rhizopus* sp. 4.16%, other filamentous fungi 16.6%, and other yeast species 2.8% in samples taken from various surfaces and pool water (Hanbakhsh et al., 2004). Ten indoor public swimming pools in Ahwaz, Iran, were investigated for six months and the dominant groups among the molds isolated from the pool waters were *Aspergillus* and *Penicillium*, while *Alternaria*, *Cladosporium*, *Mucor*, *Rhizopus*, *Ulocladium*, *Paecilomyces* and various yeasts were also identified (Rafiei and Amirrajab, 2010).

Aspergillus fumigatus, *A. terreus*, *A. niger*, *A. montevidensis*, *A. tubingensis*, and *A. flavus* were the most frequently encountered *Aspergillus* species in our study (Figure 4). A total of 69 isolates identified as *Aspergillus* sp. were obtained from the air and water samples of the hot springs examined in the study, 56 of which were isolated from the air samples and 13 from the water samples. This revealed that the *Aspergillus* spore density in the air was higher than in the water. Furthermore, there was no significant difference in the number of *Aspergillus* spores between the first and second isolations, nor in the density of air and water samples. Similar to our study, in terms of members of the *Aspergillus* genus, air and surface samples were collected at four different times of the year in a study examining 10 indoor swimming pool facilities in Italy. The identification and identification of isolated species were carried out using cultural and morphological

methods. *A. flavipes*, *A. flavus*, *A. fumigatus*, *A. glaucus*, *A. nidulans*, *A. niger*, *A. ustus* and *A. versicolor* species belonging to the genus *Aspergillus* were obtained in air and surface samples (Brandi et al., 2007).

The biodiverse filamentous fungal profile found at various sites in our study included mold groups associated with adverse health effects in humans, such as *Alternaria*, *Rhizomucor*, and *Aspergillus* species (Table 7). These species are known allergens and are associated with respiratory diseases (Goldstein et al., 1992; Knutsen et al., 2012). *Rhizomucor* exposure has been associated with healthy individuals developing infections in the lungs, gastrointestinal tract, and paranasal sinuses (Goldstein et al., 1992). *Alternaria* has been associated with the development of asthma in individuals without previous health problems. *A. fumigatus* has been associated with the development of asthma, allergic bronchopulmonary aspergillosis, and hypersensitivity to increased exposure to *A. fumigatus* in individuals with asthma and/or cystic fibrosis (Knutsen et al., 2012).

Although there are no known published safe exposure thresholds for airborne mold spores, they have been associated with adverse health effects on surrounding areas and can pose a risk to many individuals. Indoor air quality monitoring is commonly performed by comparing mold species and concentrations found indoors with those of the outdoor environment; this is used as a reference point for assessing the presence of mold contamination in the indoor environment (Viegas et al., 2010). While there is no standard information for airborne mold spore exposure limits, studies suggest that exposure limits are only necessary if a single fungal group has >50 CFU/m³ or if multiple fungal groups have >150 CFU/m³ (Miller et al., 1988). Therefore, the mold spore concentrations found in this study may be considered low for some hot springs but quite high for others. The geographic location of the hot spring, the presence of agricultural activities in the area, the intensity of pool use, and hygiene conditions are thought to account for these differences.

Numerous studies have been conducted worldwide to investigate the physical, chemical, and microbiological elements of swimming pool water. The results indicate the presence of various chemical and infectious agents in these pools, posing a serious health threat to those who come into contact with them. Because indoor spa pools attract people year-round, water safety and hygiene are of particular importance. Human skin infections have increased significantly in recent years, and one of the most significant reasons for this is frequent human contact with contaminated indoor water environments. Fungal skin infections are a worldwide problem, regardless of age or gender (Mavridou et al., 2018). Although this was a pilot study, the results from the water samples in our study indicate that species that

could pose a risk to human health were also isolated from the water.

5. CONCLUSION

In conclusion, modern spa facilities offer an increasing variety of uses, including sports, fitness, wellness, and rehabilitation. The proliferation of swimming pools, water parks, spas, saunas, and wellness centers is therefore crucial for addressing a wide range of users, special needs, and health-related issues. Constant vigilance and appropriate sanitary measures are essential to protect the safety of staff, patients, and clients. In addition to bacteria and protozoa, biological risk sources include pathogenic fungi, whose ubiquitous aquatic presence makes them particularly viable in humid, hot, and crowded spa environments. Monitoring air, surfaces, and water, along with the application of integrated microbiological and molecular techniques, appears crucial for effective monitoring and strategic control procedures. The epidemiological study presented in this study on fungal contaminants was conducted at an indoor spa pool in the Kütahya province, which can be considered a pilot study for Turkey, from 24 different water and air samples collected from eight different regions in the districts of the province. Interestingly, considering the results, despite adherence to existing local recommendations regarding swimming pool safety, a high level of fungal biodiversity was observed in a complex ecosystem. Although there is a regulation for spa environments, this regulation does not include any provisions regarding the presence limits of filamentous fungi in air and water. This pilot study highlights the seriousness of this situation and the need for further, more comprehensive research on this topic.

Acknowledgements

We would like to thank Prof. Dr. Merih KIVANÇ for her consultancy support for our study. We would also like to thank the Governorship of Kütahya for providing permission to collect samples at the thermal spring facilities.

Funding

This work has been supported by Kutahya Health Sciences University Scientific Research Projects Coordination Unit under grant number TSA-2020-28.

Ethics Committee Approval

Since the article does not contain any studies with human or animal subject, its approval to the ethics committee was not required.

Data Sharing Statement

All data are available within the study.

Conflict of Interest

The authors have no conflicts of interest to declare.

REFERENCES

- Abbot, S.P., 2002. Mycotoxins and indoor moulds. *Indoor Environment Connections*, 3(4), 14-24.
- Adamowicz, M.M., Kubera, L., Jankowiak, E., & Dembowska, E., 2019. Microbial diversity of bioaerosol inside sports facilities and antibiotic resistance of isolated *Staphylococcus* spp. *Aerobiologia*, 35, 731-42. <https://doi.org/10.1007/s10453-019-09613-y>
- Agababova, M., Hon, C.Y., 2018. Pilot study: Assessment of the presence of mold in indoor swimming pools. *Environmental Health Review*, 61(2), 35-38. <https://doi.org/10.5864/d2018-009>
- Alim, A., Hakgüdener, Y., Poyraz, O., 2002. Investigation of *Legionella pneumophila* in thermal pool waters of hot springs in the Central Anatolia Region. *Microbiology Bulletin*, 36(3-4), 237-246.
- Ayanbimpe, G.M., Danjuma, W. S., Okolo, M. O., 2012. Relationship between fungal contamination of indoor air and health problems of some residents in Jos. in: Sunil Kumar & Rakesh Kumar (Eds.), *Air quality - monitoring and modeling*. InTech. pp. 1-18. <https://doi.org/10.5772/32160>
- Barnett, H.L., Hunter, B.B., 1999. *Illustrated genera of imperfect fungi* (4th ed.). APS Press, USA.
- Brandi, G., Sisti, M., Paparini, A., Gianfranceschi, G., Schiavano, G.F., Santi, M., Santoni, D., Magini, V., Romano-Spica, V., 2007. Swimming pools and fungi: An environmental epidemiology survey in Italian indoor swimming facilities. *International Journal of Environmental Health Research*, 17(3), 197-206. <https://doi.org/10.1080/09603120701254862>
- European Environment and Health Information System. 2007. Children living in homes with problems of damp (Fact Sheet No. 3.5, Code RPG3_Hous_Ex2).
- Goldstein, M.F., Dvorin, D.J., Dunskey, E.H., Lesser, R.W., Heuman, P.J., Loose, J.H., 1992. Allergic Rhizomucor sinusitis. *Journal of Allergy and Clinical Immunology*, 90(3), 394-404. [https://doi.org/10.1016/S0091-6749\(05\)80020-X](https://doi.org/10.1016/S0091-6749(05)80020-X)
- Gots, R.E., Layton, N.J., 2003. Indoor health: Background levels of fungi. *Journal of Occupational Health and Hygiene*, 64(4), 427-438. <https://doi.org/10.1080/15428110308984836>
- Groot, J., Nielsen, E.T., Nielsen, T.F., Andersen, P.K., Pedersen, M., Sigsgaard, T., Loft, S., Nybo Andersen, A. M., Keller, A., 2023. Exposure to residential mold and dampness and the associations with respiratory tract infections and symptoms thereof in children in high-income countries: A systematic review and meta-analyses of epidemiological studies. *Paediatric Respiratory Reviews*, 48, 47-64. <https://doi.org/10.1016/j.prrv.2023.06.003>
- Hanbakhsh, H., Diba, K., & Hazarti, K., 2004. Study of fungal contamination of indoor public swimming pools. *Iranian Journal of Public Health*, 33(1), 60-65.
- Hasenekoğlu, İ., 1991. *Soil moulds* (Vol. 7). Atatürk University Publications, Faculty of Education Publications, Erzurum.
- Hawksworth, D.L., Crous, P.W., Redhead, S.A., 2011. The Amsterdam declaration on fungal nomenclature. *IMA Fungus*, 2, 105-112. <https://doi.org/10.5598/imafungus.2011.02.01.14>
- Holden, K.A., Lee, A.R., Hawcutt, D.B., Sinha, I.P., 2023. The impact of poor housing and indoor air quality on respiratory health in children. *Breathe*, 19(2), 230058. <https://doi.org/10.1183/20734735.0058-2023>
- J.D., Laflamme, A.M., Sobol, Y., Lafontaine, P., Greenhalgh, R., 1988. Fungi and fungal products in some Canadian houses. *International Biodeterioration*, 24(2), 103-120. [https://doi.org/10.1016/0265-3036\(88\)90053-X](https://doi.org/10.1016/0265-3036(88)90053-X)
- Klich, M.A., 2002. Identification of common *Aspergillus* species. *Centraalbureau voor Schimmelcultures*.
- Knutsen, A.P., Bush, R.K., Demain, J.G., Denning, D.W., Dixit, A., Fairs, A., Greenberger, P.A., Kariuki, B., Kita, H., Kurup, V.P., et al., 2012. Fungi and allergic lower respiratory tract diseases. *Journal of Allergy and Clinical Immunology*, 129(2), 280-291. <https://doi.org/10.1016/j.jaci.2011.12.970>
- Maaranen, J., Hugg, T.T., Paciência, I., Jaakkola, M.S., Jaakkola, J.K.J., Rantala, A.K., 2025. Home dampness and molds and occurrence of respiratory tract infections in the first 27 years of life: the Espoo Cohort Study. *American Journal of Epidemiology*, kwaf200. <https://doi.org/10.1093/aje/kwaf200>
- Mavridou, A., Pappa, O., Papatzitze, O., Dioli, C., Kefala, A.M., Drossos, P., Beloukas, A., 2018. Exotic tourist destinations and transmission of infections by swimming pools and hot springs: A literature review. *International Journal of Environmental Research and Public Health*, 15(12), 2730. <https://doi.org/10.3390/ijerph15122730>
- Mias, C., Theunis, J., Noharet J., Baradat S., C. Satgé, C., Bes Vuillermoz D., Houcine, A., Chlasta, J., Stennevin, A., Doat, G., Bessou-Touya, S.,

- Duplan, H., 2025. 0474 Sensitive skin and low mineralized thermal spring water: Biomechanical and microbiota benefits. *Journal of Investigative Dermatology*, 145(8), S81.
- Rafiei, A., Amirrajab, N., 2010. Fungal contamination of indoor public swimming pools, Ahwaz, southwest of Iran. *Iranian Journal of Public Health*, 39(3), 124-128.
- Robins, C., Morell, J. 2007. Mold housing and wood. Western Wood Products Association. Oregon.
- Samson, R. A., Houbbraken, J., Thrane, U., Frisvad, J. C., Andersen, B., 2010. Food and indoor fungi. CBS-KNAW Fungal Diversity Centre, Utrecht.
- Sarmadian, H., Hazbavi, Y., Didehdar, M., 2020. Fungal and parasitic contamination of indoor public swimming pools in Arak, Iran. *Journal of the Egyptian Public Health Association*, 95, 8. <https://doi.org/10.1186/s42506-020-0036-3>
- Savcı, Ü., Şahin, M., 2019. Investigation of fungal flora in hammams, Turkish baths: A field study. *Journal of Surgery and Medicine*, 3(9), 640–643. <https://doi.org/10.28982/josam.611224>
- Sime, A.D., Abbott, L.L., Abbott, S.P., 2002. A mounting medium for use in indoor air quality spore-trap analyses. *Mycologia*, 94(6), 1087-1088. <https://doi.org/10.1080/15572536.2003.11833165>
- Straus, D.C., Wilson, S.C., 2006. Respiratory trichothecene mycotoxins can be demonstrated in the air of *Stachybotrys chartarum*-contaminated buildings. *Journal of Allergy and Clinical Immunology*, 118, 760. <https://doi.org/10.1016/j.jaci.2006.06.025>
- Velikova, E., 2025. Sustainable Use of Mineral Springs as Sustainable Development of Water and Environment: Proceedings of ICSDWE 2024.
- Viegas, C., Alves, C., Carolino, E., Rosado, L., Silva Santos, C., 2010. Prevalence of fungi in indoor air with reference to gymnasiums with swimming pools. *Indoor and Built Environment*, 19(5), 555-561. <https://doi.org/10.1177/1420326X10380120>
- Xiao, H., Yang, J., Lou, H., Luo, M., 2025. Potential respiratory hazards of fungal exposure in the residential indoor environment: A systematic review. *Atmospheric Pollution Research*, 16(10), 102634. <https://doi.org/10.1016/j.apr.2025.102634>
- Yarita, K., Sano, A., Murata, Y., Takayama, A., Takahashi, Y., Ohori, Y., Kamei, K., Miyaji, M., Nishimura, K., 2007. Pathogenicity of *Ochroconis gallopava* isolated from hot springs in Japan and a review of published reports. *Mycopathologia*, 167, 135-147. <https://doi.org/10.1007/s11046-007-9034-7>
- Yeşiltaş, H.K., 2024. Thermal bridge in the building, energy loss and environmental effects. *International Journal of Chemistry and Technology*, 8(1), 1-9. <https://doi.org/10.32571/ijct.1208607>
- Yılmaz Sarıözlü, N., Demirel, R., Kıvanç, M., 2012. Microbial population of hot spring waters in Eskişehir/Turkey. *Anadolu University Journal of Science and Technology C - Life Sciences and Biotechnology*, 2(1), 31-39.