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Identification of the Most Common Dust Fungi at Universiti Pendidikan Sultan Idris, Malaysia

Mai Shihah Abdullah*, Ghassan Hadi Kttafah

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Abstract: Fungi are eukaryotic organisms that live as saprophytes, parasites or symbionts in their plant or animal hosts. Despite extensive research on the involvement of fungal allergens in the pathophysiology of allergic diseases, studies on fungi as a prominent source of allergens are still lacking in basic research and clinical practice. Hence, this study was conducted to identify ten common airborne fungal species as a preliminary work prior to conducting a sensitisation study on common fungal allergens. Fifty-four dust samples were collected from offices, laboratories lecturers' rooms that are situated within three blocks of the Sultan Azlan Shah Campus, UPSI, Tanjong Malim, Perak, Malaysia by using a vacuum cleaner. The sieved dust was cultured with potato dextrose agar media, incubated at room temperature to propagate pure cultures and sent to the Malaysian Agricultural Research and Development Institute for identification viapolymerase chain reaction. The most common species found in the premises were Penicilliumsimplicissimum (94%), Aspergillus aculeatus (85%), Rhodosporidiobolusruineniae (74%), Ceriporialacerata (92%), A.caliodustus (57%), Syncephalastrumsp. (62%), Aspergillus sp. (72%), A. fumigatus (77%), Fusarium sp. (77%) and P.canescens (83%). A number of species identified in this study do not trigger fungal allergies. Therefore, further studies must be conducted to confirm their potential as fungi allergens. Due to high frequency of Penicillium and Aspergillus, The three-block research area in this study could be categorised as sick building and mycoremediation was recommended to minimise mould growth.

Keywords: Fungi Allergy, Fungi Identification, Sick Building, Universiti Pendidikan Sultan Idris.

Introduction

Indoor air is made up of many airborne particles, including mould, bacteria allergens and dust. In a typical indoor environment, such as home, school and workplace, the particle level is generally influenced by the occupants' activities, internal maintenance practices, quality of interior maintenance and external air brought into the facility through the ventilation system [1], spend 90% of our lives indoors, and the quality of indoor air we breathe is critical to human health and well-being [2]. Similar to other chemical and particulate pollutants, microorganisms can also impact indoor air quality. Airborne microorganisms, which are allergens or pathogens, are of primary concern. Bacteria, fungi and viruses are ubiquitous in indoor air with concentrations that typically exceed 100,000 cells or viral particles per cubic meter of air [3]. The majority of fungi cannot be identified by only using standard techniques [4], and researchers have begun using molecular methods recently to perform comprehensive assessments of the amounts and types of bacteria and fungi found in indoor air [5]. To avoid the problems of culture dependency and being too time-consuming, molecular tools are increasingly being used to detect indoor airborne mould.

Building-related factors, such as ventilation, relative humidity, temperature and occupants can

Mai Shihah Abdullah*, Department of Biology, Faculty of Science and Mathematics, Universiti Pendidikan Sultan Idris, Tanjong Malim, Perak, Malaysia.
Ghassan HadiKttafah, Department of Biology, Faculty of Science and Mathematics, Universiti Pendidikan Sultan Idris, Tanjong Malim, Perak, Malaysia.

influence the diversity and composition of microbes found indoors [6]. Although fungi found indoors are primarily influenced by the type of fungi found outdoors [7], the occupants of a given building can have significant effect on the types of fungi found indoors. The presence of airborne fungi allergen at work sites was significantly associated with poor ventilation systems and this was, in turn, associated with low efficiency of filters. AtUniversiti Pendidikan Sultan Idris (UPSI), the ducts of the central cooling system are loaded with fungal growth (Figure 1a), which is likely causes allergies. Such ducts are rarely cleaned, and the accumulated fungal and other growth can be substantial in buildings, such as Blocks 1, 2 and 3 at UPSI, which are more than nine years of age. The occupants with allergies may be suffering due to exposure to fungal spores or dust mites in their office, lecture hall, tutorial room or laboratories, where they stay for at least 40 hours weekly. A high concentration of fungal material was observed outside the old buildings and may aggravate allergies in people working in such buildings (Figure 1b).

Fungi grow within the premises of UPSi (Figures 1a and 1b). Therefore, this study aims identify the common fungi within the research area or further allergy study.

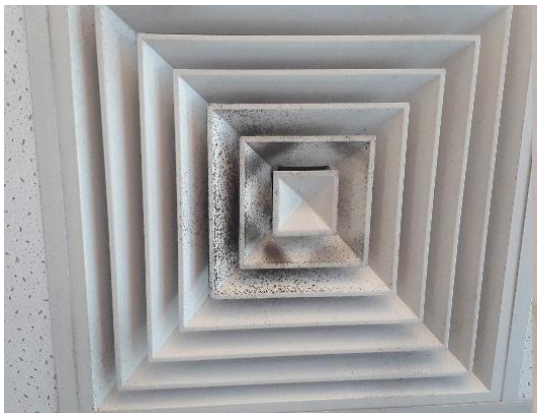

Figure 1a: Fungi growth in the duct indoor

Figure1b: Fungi growth in the outdoor

Several studies have reported that exposure to airborne fungi is linked with different health problems[8]. Approximately 1 million to 1.5 million fungal species exist worldwide. However, only 80,000 have been described thus far. Amongst these, 112 genera are allergen sources. The four genera most commonly associated with the development of allergies are *Alternaria*, *Cladosporium*, *Penicillium* and *Aspergillus*. Such genera belong to the phylum Ascomycota, but allergens have also been described from Basidiomycota and Zygomycota, which cause allergies in approximately (2–6 %)of the general population in developed countries [9], [10]. Overall, 107 allergens from 28 fungal genera have been confirmed by the International Allergen Nomenclature Subcommittee [11]. Many fungal roteinsareimmunoglobulin E-reactive.

Amongst the indoor fungi, certain types may be pathogenic and can secrete toxic metabolites, which cause allergies and serious diseases.

After entering from the outdoor environment, fungi increase in the indoor environmentunder optimal conditions and can cause health problems not only to those having insusceptible deficiency but also to healthy people.

The main factors that contribute to the growth and development of both pathogenic and nonpathogenic fungi are heat, stickiness and disinfection conditions in the different areas of the habitat. The optimal conditions that fungi need are dampness, i.e., from water that escapes from the roof and pipes, and increased moisture or wetness.

Fungi grow within the premises of UPSi (Figures 1a and 1b). Therefore, this study aims identify the common fungi within the research area or further allergy study.

Material and Methods

Study Location

The study was conducted in the buildings in Blocks 1, 2 and 3 of the Faculty of Science and Mathematics, Sultan Azlan Shah Campus, UPSI (English: Sultan Idris Education University). UPSI is a public university in the town of Tanjong Malim in Perak, Malaysia. Its coordinates are 3°43'19.5"N 101°31'24.1"E. This campus was built in an 800-acre (3.2 km^2) site in the new township of Proton City.

Figure 2: An aerial view of Universiti Pendidikan Sultan Idris

Sample Processing and Analysis

A total of 54 rooms located in the three blocks were used. People that stay in these rooms approximately 6–7 hours daily and 5 days weekly were randomly selected from offices, laboratories and lecturers rooms. Such rooms had a mechanical ventilation system, openable windows and vertical blinds. The buildings were first occupied in 2011. To date, the buildings are aged more than 9 years. From general observation, eight lecturers' rooms had visible indoor mould growth on the wooden furniture. In addition, the external wall along the corridor to offices and laboratories also contained mould. The occupants of the rooms in Blocks 1, 2 and 3 were informed about the dust vacuuming by circulating a letter to everyone on the notice board a few days before sampling.

The dust samples were collected between August and September 2017 by using a handheld vacuum cleaner (vo. Temm two-way power, 650 W China), which was operated for 5–10 min The dust was collected from the floors, carpets, chairs, corners, computers and furniture inside the room. The vacuum filter cab was decontaminated with a 95% ethanol wipe between each room sampling and allowed to dry. All dust samples were placed in a plastic bag with a zipper; the dust was passed through a 400 μmmes in the laboratory and kept at 20 ^{o}C[12]. The dust samples were then cultured on PDA 0edia. The 10 most common species were identified via molecular methods with polymerase chain reaction (PCR), which was carried out by the Malaysian Agricultural Research and Development Institute.

The indoor relative humidity and temperature were measured by using a hygrometer (Extech EA20, Taiwan), and the daily data of air temperature, humidity and rainfall of this area from July until September 2017 were obtained from the regional meteorological station situated at FELDA Sungai Behrang.

Characterisation and examination of typical fungal distributions can be helpful in identifying the associations between domestic fungal characteristics and clinical diagnoses and preventing seasonal allergic diseases in a particular region [13]. The high prevalence of both *Penicillium* (94%–83%) and *Aspergillus* (87%–57%)in the UPSI samples colonised in the indoor materials; such fungiwere isolated from a wide variety of environments (faculty offices and teaching, learning and research laboratories). Savill and Fadok [14] stated that if *Penicillium* and/or *Aspergillus* are dominant in indoor dust or aerosol, then the environment supports the indoor growth of fungi. In this study, four species of genera *Aspergillus* were identified. Amongst them, *A. fumigatus* and *A. niger* were isolated and reported as the primary agents of invasive Aspergillos [15]. *Syncephalastrum* sp. was also isolated and reported as a disease-causing agent [16], [17]. Although genera *Penicillium* was isolated and highly prevalent in this study, *P. simplicissimum* and *P. canescens* were not proven to be allergenic fungi by the IUIS Allergen Nomenclature Subcommittee.

The indoor relative humidity and temperature were measured by using a hygrometer (Extech EA20, Taiwan) and the daily data of air temperature, humidity and rainfall of this area from July until September 2017 were obtained from the regional meteorological station situated at FELDA Sungai Behrang.

RESULTS

The Fungi Identification

Ten most common species were identified by molecular methods using polymerase chain reaction (PCR) carried out by the Malaysian Agricultural Research and Development Institute (Figure 3-12).

Sequence =
CCAACCTCCCACCCGTGTTTATCGTACCTTGTTGCTTCGGCGGGCCCGCCTCACG
GCCGCCGGGGGGCATCCGCTCCCGGGCCCGCGCCCGCCGAAGACACCAATGAAC
TCTGTCTGAAGATTGCAGTCTGAGCAGATTAGCTAAATCAGTTAAAACTTTCAAC
AACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATACGTA
ATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCC
CTGGTATTCCGGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTCAAGCACGGC
TTGTGTGTTGGGCTCCGCCCCCCGGCTCCCGGGGGGCGGGCCCGAAAGGCAGCG
GCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTCGTCACCCGCTCTGTAGGC
CCGGCCGGCGCCCGCCGGCGACCCCAATCAATCTATCCAGGTTGACCTCGGATCA
GGTAGGGATACCCGCTGAACTTAAGCA

Figure 3: DNA sequence of Penicilliumsimplicissimum

Sequence =
CCGTGCTTACCGTACCCTGTTGCTTCGGCGGGCCCGCCTTCGGGCGGCCCGGGGC
CTGCCCCCGGGACCGCGCCCGCCGGAGACCCCAATGGAACACTGTCTGAAAGCG
TGCAGTCTGAGTCGATTGATACCAATCAGTCAAAACTTTCAACAATGGATCTCTT
GGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAACTAATGTGAATTGCA
GAATTCAGTGAATCATCGAGTCTTTGAACGCACATTGCGCCCCCTGGTATTCCGG
GGGGCATGCCTGTCCGAGCGTCATTTCTCCCCTCCAGCCCCGCTGGTTGTTGGGC
CGCGCCCCCCCGGGGGCGGGCCTCGAGAGAAACGGCGGCACCGTCCGGTCCTCG
AGCGTATGGGGCTCTGTCACCCGCTCTATGGGCCCGACCGGGGCTCGCCTCGACC
CCCAATCTTCTCAGATTGACCTCGGATCAGGTAGGGATA

Figure 4: DNA sequence of Aspergillus aculeatus

Sequence =
GTCCGAACTCTCACTTTCTAACCCTGTGCATTTGTTTTGGCTAGTAGGATGCTTGC
GTCCGAACACCTCTTCATTTACAAACACAAAGTCTATGAATGTTTAATTTTATAA
CAAAACAAAACTTTCAACAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGC
AGCGAAATGTGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT
GAACGCATCTTGCACTCCTTGGTATTCCGAGGAGTATGCCTGTTTGAGTGTCATG
AATTCTTCAACCCTCTCTTTTCTTAGTGATTAGAGAAGAGCTTGGATTCTGAGTGT
TGCTCCTTACCCGAGCTCATTCGTAATACATTAGCATCCATATTCGAACTTTCGGA
TTGACTTGGCGTAATAGACTATTCGCTGAGGAATCTAACTTCGGTTAGAGCCGGG
TTTGAACTAGGAAGCTCCTAATCTAGCTTAGTCTACTTTTAGATTAGATCTCAAAT

Figure 5: DNA sequence of Rhodosporidiobolusruineniae

Sequence =
AGCTGGCCTTTAACGAGGTATGTGCACGCCTGGCTCATCCACTCTCAACCTCTGT
GCACTTTATGTAAGAAACGGTGTAAGCCAGCTATTTAATAGTCGGTAATAAGCCT
TTCTTATGTTTACTACAAACGCTTCAGTTATAGAATGTTTACTGTGTATAACACAA
TTATATACAACTTTCAGCAACGGATCTCTTGGCTCTCGCATCGATGAAGAACGCA
GCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTTG
AACGCACCTTGCACTCCTTGGTATTCCGAGGAGTATGCCTGTTTGAGTCTCATGG
AATTCTCAACCCCTAAATTTTGTAATGAAGTTTAGTGGGCTTGGACTTGGAGGTT
GTGTCGGCTTCTAGTCGACTCCTCTGAAATGTATTAGCGTGAATCTTACGGATCG
CCTTCAGTGTGATAATTATCTGCGCTGTGGTGTTGAAGTATTTATTAGTTCATGCT
TATAGTCGTCTCTTACCGAGACAATTTATGACAATCTGAGCTCAAATCAGGTAGG
ACTACCCGCTGAACTTAAGCATATCAATAAGCGGGAGG

Figure 6: DNA sequence of Ceriporialacerata

Sequence =
AGGCCTAACCTCCCACCCGTGAATACCTGACCAACGTTGCTTCGGCGGTGCGCCC
CCCCCCCCCGGGGGTACCCCCCGGAAACCCCCCCAAACCCCCGGTTTTTAGGGTT
TTCTGACTTTGATACCAAACCTTTTAAAATTTTCAAAAAGGGTTCTTTGGTTTCCG
GCTTCAATAAAAAACCCACCAAACTGCAAAAATTAATGGAAATTGCAAAATTCA
TGGAATCTTCAATTTTTTAAACCCCCTTTGCCCCCCCCGGGCTTTCCGGGGGGAAT
GCCTGCCCAAGCGTCTTTGCTCCCCTTAAACCCCGGTTTGGGGGTGGGGCCCCCC
CCCCCCCCGGGGGACGGGCCCAAAAGGAAGGGGCGGCCCCCCGCCCGGCCCCCA
AGGGAAGGGGGTTTTTCCCCCCCCCCAATTAGGGCCGGCCGGGCCCCACCCGGC
TTTCCCAACCTTTTTTTTTACCGGGTTAACCTCGAATCAGGGGGGGAACCCCCCT
AAACTT

Figure 7: DNA sequence of Aspergillus caliodustus

Sequence =
GAGGAAGAATTTGGTATTCACCCAGTCTATTGCAACGATTCCTGGGTTAACAAAG
AATGGATTTTCAATTAAAAACATTTTTTTTAATACCAATTGATTCTTAATTGAATT
GAAGTATAAAAAAAAAAAAGAAGGCTCCCAATTGAGACTTTGGACTTTTTTAAA
CAACTTTAAGCAATGGATCTCTTGGCTCTCCCACCGATGAAAAGCGTACCAAATT
GCGATAATTAGTGCGATCTGCATTCTGCGAATCATCAAGTTCTTGAACGCACCTT
GCACCCTTTGGGTGGTCCTTGGGGGATGCTTGTTTCAGTCCAACTATAAACCCCC
AAATGACATTTTTTTATTGAAATGTCCATTGGGATTGGGAGGGCAAAGGGAAAC
CTTTCTTCCTGAAAATGAGTCCCTAGGATTAAAAAACAATTGAGGGTTTTTTTTTT
TTTTCCCAGCCAATTTTTTTTATTTAAAAAAAAATGCTGTGGAAAAAAAAA

Figure 8: DNA sequence of Syncephalastrum sp

Sequence =
AGCGAGCCCACCTCCCACCCGTGTTTACTGTACCTTAGTTGCTTCGGCGGGCCCG
CCATTCATGGCCGCCGGGGGCTCTCAGCCCCGGGCCCGCGCCCGCCGGAGACAC
CACGAACTCTGTCTGATCTAGTGAAGTCTGAGTTGATTGTATCGCAATCAGTTAA
AACTTTCAACAATGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAAT
GCGATAACTAGTGTGAATTGCAGAATTCCGTGAATCATCGAGTCTTTGAACGCAC
ATTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCA
TCAAGCACGGCTTGTGTGTTGGGTCGTCGTCCCCTCTCCGGGGGGGACGGGCCCC
AAAGGCAGCGGCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCTTTGTCACCC
GCTCTGTAGGCCCGGCCGGCGCTTGCCGAACGCAAATCAATCTTTTTCCAGGTTG
ACCTCGGATCAGGTAGGGA

Figure 9: DNA sequence of Aspergillus sp

Sequence =
TCCACCTCCCACCCGTGTCTATCGTACCTTGTTGCTTCGGCGGGCCCGCCGTTTCG
ACGGCCGCCGGGGAGGCCTTGCGCCCCCGGGCCCGCGCCCGCCGAAGACCCCAA
CATGAACGCTGTTCTGAAAGTATGCAGTCTGAGTTGATTATCGTAATCAGTTAAA
ACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATG
CGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGAACGCACA
TTGCGCCCCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCTC
AAGCACGGCTTGTGTGTTGGGCCCCCGTCCCCCTCTCCCGGGGGACGGGCCCGAA
AGGCAGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTTGTCACCTGCT
CTGTAGGCCCGGCCGGCGCCAGCCGACACCCAACTTTATTTTTCTAAGGTTGACC
TCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA

Figure 10: DNA sequence of Aspergillus fumigatus

Sequence =
GACATACCTATACGTTGCCTCGGCGGATCAGCCCGCGCCCCGTAAAACGGGACG
GCCCGCCCGAGGACCCCTAAACTCTGTTTTTAGTGGAACTTCTGAGTAAAACAAA
CAAATAAATCAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAGAA
CGCAGCAAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAAT
CTTTGAACGCACATTGCGCCCGCCAGTATTCTGGCGGGCATGCCTGTTCGAGCGT
CATTTCAACCCTCAAGCTCAGCTTGGTGTTGGGACTCGCGGTAACCCGCGTTCCC
CAAATCGATTGGCGGTCACGTCGAGCTTCCATAGCGTAGTAATCATACACCTCGT
TACTGGTAATCGTCGCGGCCACGCCGTAAAACCCCAACTTCTGAATGTTGACCTC
GGATCAGGTAGGAA

Figure 11: DNA sequence of Fusarium sp

Sequence =
CCTCCCACCCGTGTCTCTCTCTACCTGTTGCTTTGGCGGGCCCACCGGGGCCACCC
GGTCGCCGGGGGACGTCGTCCCCGGGCCCGCGCCCGCCGAAGCGCTCTGTGAAC
CCTGATGAAGATGGGCTGTCTGAGTCGAATGAAAATTGTCAAAACTTTCAACAAT
GGATCTCTTGGTTCCGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATG
TGAATTGCAGAATTCCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTG
GCATTCCGGGGGGCATGCCTGTCCGAGCGTCATTTCTGCCCTCAAGCCCGGCTTG
TGTGTTGGGCGTGGTCCCCCCGGGGACCTGCCCGAAAGGCAGCGGCGACGTCCG
TCTGGTCCTCGAGCGTATGGGGCTCTGTCACTCGCTCGGGACGGATCGGCGGAGG
TTGGTCACCACCACAGTTTTACCACGGTTGACCTCGGATCAGGTAGGAGTTACCC
GCTGAACTTAAGCATATCAATA

Figure 12: DNA sequence of Penicilliumcanescens

The species were identified as *Penicilliumsimplicissimum*, *Aspergillus aculeatus*, *Rhodosporidiobolusruineniae*, *Ceriporialacerata*, *Aspergillus caliodustus*, *Syncephalastrum*sp., *Aspergillus* sp., *Aspergillus fumigatus*, *Fusarium* sp. and *Penicilliumcanescens*. Six genera were identified that made up the ten species. Aspergillus gave rise to four species, namely Asp. *aculeatus*, Asp. *caliodustus*, Asp. *fumigatus,* and one unidentified *Aspergillus* sp., followed by Penicillium genus with P. *simplicissimum* and P. *canescens*. Remaining genera were Rhodosporidiobolus *(R. ruineniae*), Ceriporia *(C. lacerata*, Syncephalastrum, and Fusarium (both were not identified to specific taxa).

The Fungi Prevalence

Ten different species of fungi were detected and their frequency is between 51 (94%) to 31 (57%). *Penicilliumsimplicissimum* was found to be the most prevalent (94%) while *Aspergillus caliodustus* was the least (57%) as shown in Table 1.

Table 1: The occurrence of the most prevalent fungi sampled at UPSI

Genera	Species	Frequency	Percentage (%)	Rank
Penicillium	*P. simplicissimum*	51	94	1
Penicillium	*P. canescens*	45	83	4
Ceriporia	*C. lacerata*	50	92	2
Aspergillus	*Asp. aculeatus*	46	85	3
Aspergillus	*Asp. fumigatus*	42	77	5
Aspergillus	*Asp.* sp.	39	72	8
Aspergillus	*Asp. caliodustus*	31	57	10
Fusarium	*Fusarium* sp.	42	77	6
Rhodosporidiobolus	*R. ruineniae*	40	74	7
Syncephalastrum	*Syncephalastrum*sp.	34	62	9

Figure 13 displays the six genera with Penicillium was the most prevailed ranged between (94-83%), followed by Ceriporia (92%), Aspergillus (85-57%), Fusarium (77%), Rhodosporidiobolus (74%), and Syncephalastrum (62%).

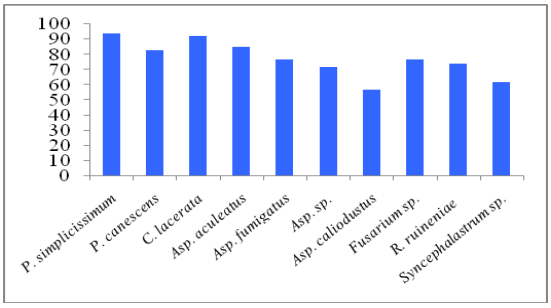

Figure 13: The prevalence of most common fungi genera at UPSI, Tanjong Malim, Perak

Temperature, Relative Humidity and Rainfall

The mean values of indoor temperature and relative humidity at Universiti Pendidikan Sultan Idris, Sultan Azlan Shah campus were at 24.8°C, 68% respectively, whereasthe mean values of outdoor temperature (27.15°C), relative humidity (85.49%), and rainfall (6.80mm) recorded at the FELDA Sungai Behrang, Perak regional meteorological station.

DISCUSSION

The Fungi Identification

The ten identified species were mapped and included in the taxonomical tree as shown in Figure 14. R *hodosporidiobolusruineniae*, *Ceriporialacerata* and *Syncephalastrum.sp* have not been reported as source of type 1 allergy with reference to the taxonomical tree provided by [13]WHO/IUIS Allergen Nomenclature Sub-Committee database 2019 (http://www.allergen.org). *Asp.aculeatus* and *Asp.caliodustus* were also not reported within Aspergillus genera causing allergy with exemption to *Asp. fumigatus.* Identification of the other Aspergillus species was unsuccessful.

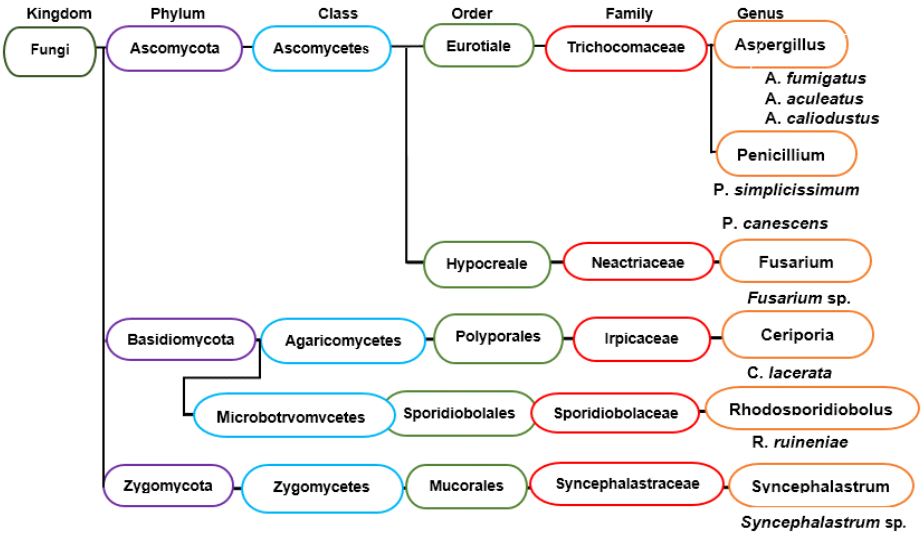

Figure 14: The taxonomical tree for fungal species identified at Universiti Pendidikan Sultan Idris

Study of characterization and examination of typical fungal distributions can be helpful in identifying associations between domestic fungal characteristics and clinical diagnosis and in the prevention of seasonal allergic diseases in a particular region [13] (Wu et al. 2000). The highly prevalent of both Penicillium (94-83%) and Aspergillus (87-57%)sampled at UPSI which colonized indoor materials has been isolated from a wide variety of environments (faculty offices, teaching and learning laboratories, research laboratories).According to Savill and Fadok [14]ifPenicillium and/or Aspergillus are dominant in the indoor dust or aerosol, the environment is usually considered to be supporting indoor growth. In this study four species from genera Aspergillus were identified. Among them, Asp. *fumigatus* was isolatedand reported as the primary effective agents of invasive Aspergillosis along with Asp. *niger*,[15]. *Syncephalastrum*sp. was also isolated and reported causing disease agent [16], [17].Although genera Penicillium was isolated and highlyprevalent in this study, both *P. simplicissimum*and *P. canescens* are not approved as allergenic fungi by IUIS Allergen Nomenclature Sub-committee.

Relationship of Relative Humidity and Temperature to Fungi Prevalence

The EPA recommends that the relative humidity levels in homes remain below 60%, ideally between 30% and 50%, to prevent mould growth [6]. The recommended values were relatively lowerthan our data from the regional meteorological station located at FELDA Sungai Behrang with mean indoor and outdoor values of 68% and 85.49%, respectively. The high average monthly rainfall of 680 mm in this area was higher than the Malaysian average of 400 mm. Thus, average monthly rainfallwas an added factor to theabundance of fungi at UPSI.

The UPSI indoor temperature (24.8 °C) was lower than that of the outdoortemperature (27.15°C). Both were relatively low compared with the average temperature in Malaysia (32 C to 33°C). A similar scenario was observed in Hulu Langat, which is one of the largest districts in Selangor, Malaysia.

A study conducted in this area revealed that the frequently isolated genera in selected primary school buildings during the study period were *Aspergillus*, *Penicillium*, *Fusarium* and *Rhizopus* [18]. *Aspergillus* spp., *Penicillium*spp. and *Fusarium*spp. were also isolated from thepremises ofUniversitiSains Malaysia, which was declared as a 'sick building' in 2012 [19]. Therefore, the three blocks in this study could be categorised as 'sick buildings'.

In another study, *P.simplicissimum*, whichalso had high frequency in this study,and *Aspergillus* spp. were isolated and identified as having the highest growth and were the most effective for mycoremediation of spent engine oil in Peninsular, Malaysia [20]. In summary, the high occurrence of *Aspergillus* spp. at UPSI university campus buildings indicated fungal contamination in these buildings. *A. niger*, *A. flavu*and *A. fumigatus* spores have a direct correlation with the incidence of Aspergillosis amongst immunosuppressed patients;and such spores have been associated with human allergies [19].

The diversity and abundance of fungi are influenced strongly by the microclimate [21].Outdoor air is an important source of indoor fungi. Their results showed that outdoor and indoor culturable fungi were highly correlated with location, building construction and maintenance, ventilation, moisture control, surface materials, the occupants themselves and their activities and lifestyles. Other factors include current and historical use of the building and fungal particles that may be transported by humans on their clothes, skin, hair and shoes when they come inside from outside [22].These factors then contribute to the growthperformance of individual species. Exposure to these fungi may eventually increase the risk of developing fungal allergies.

Subsequently, further allergy tests will be performed to assess the prevalence of fungus allergies amongst the occupants. To date, the results of the study recommend remediation to prevent indoor and outdoor mould growth at UPIS.

Conclusion

In this study, ten species from six genera were identified.Five of these species have not been reported as sources of allergens, as confirmed by the IUIS Allergen Nomenclature Subcommittee. Fungi are abundant in the premises with an average temperature of 24.8 °C andrelative humidity of 68%. The buildings at Blocks 1, 2 and 3 at UPSI could be categorised as 'sick buildings'. This study showed that further allergy testsmust be performed to assess the fungal diversity and the prevalence of fungus allergies amongst the occupants.

References

[1] Abdulmumin, U.A., Manga, S.B., Shinkafi, S.A., Rabah, A.B., Gambo, A., & Odeh, P. A. (2014). Annals of Biological Sciences Fungi associated with carpets and floor dust samples as an indicator for indoor air quality. *Department of Microbiology, Usmanu Danfodio University, P.M. B 2346, Sokoto State-Nigeria Department of Microbiology, Bayero U, 2*(4), 16–19.

[2] Luongo, J. C., Barberán, A., Hacker-Cary, R., Morgan, E. E., Miller, S. L., & Fierer, N. (2017). Microbial analyses of airborne dust collected from dormitory rooms predict the sex of occupants. *Indoor air, 27*(2), 338-344.

[3] Prussin, A. J., Garcia, E. B., & Marr, L. C. (2015). Total concentrations of virus and bacteria in indoor and outdoor air. *Environmental Science and Technology Letters*, *2*(4), 84–88.

[4] Amann, R. I., Ludwig, W., & Schleifer, K. H. (1995). Phylogenetic identification and in situ detection of individual microbial cells without cultivation. *Microbiological Reviews*, *59*(1), 143–169.

[5] Whitley, B. E., & Kite, M. E. (2018). *Principles of research in behavioral science*. Routledge.

[6] Dannemiller, K. C., Weschler, C. J., & Peccia, J. (2017). Fungal and bacterial growth in floor dust at elevated relative humidity levels. *Indoor Air*, *27*(2), 354-363.

[7] Barberán, A., Ladau, J., Leff, J. W., Pollard, K. S., Menninger, H. L., Dunn, R. R., & Fierer, N. (2015). Continental-scale distributions of dust-associated bacteria and fungi. *Proceedings of the National Academy of Sciences*, *112*(18), 5756-5761.

[8] Ghiasian, S. A., Maghsood, A. H., & Aghamirian, M. R. (2016). Aeromycological analysis of allergenic airborne fungi in Qazvin, Iran. *Current medical mycology*, *2*(3), 5–9.

[9] Żukiewicz-Sobczak, W. A. (2013). The role of fungi in allergic diseases. *Advances in Dermatology and Allergology/Postępy Dermatologii I Alergologii*, *30*(1), 42-45.

[10] Fukutomi, Y., & Taniguchi, M. (2015). Sensitization to fungal allergens: resolved and unresolved issues. *Allergology International*, *64*(4), 321-331.

[11] Twaroch, T. E., Curin, M., Valenta, R., & Swoboda, I. (2015). Mold allergens in respiratory allergy: from structure to therapy. *Allergy, asthma & immunology research*, *7*(3), 205-220.

[12] Macher, J.M. (2001). Review of methods to collect settled dust and isolate culturable microorganisms. *Indoor Air*, *11*(2), 99–110.

[13] WHO/IUIS Allergen Nomenclature Sub-Committee database 2019.

[14] Savill, J., & Fadok, V. (2002). Dustborne fungi in large office buildings. *Mycopathologia*, *154*(2), 93–106.

[15] Abarca, M.L. (2000). Taxonomy and identification of the species involved in nosocomial aspergillosis. *Revista iberoamericana de micologia*, *17*(3), S79—84.

[16] Neofytos, D., Horn, D., Anaissie, E., Steinbach, W., Olyaei, A., Fishman, J., & Marr, K. (2009). Epidemiology and outcome of invasive fungal infection in adult hematopoietic stem cell transplant recipients: analysis of Multicenter Prospective Antifungal Therapy (PATH) Alliance registry. *Clinical Infectious Diseases*, *48*(3), 265-273.

[17] Kubak, B. M., & Huprikar, S. S. (2009). Emerging & rare fungal infections in solid organ transplant recipients. *American Journal of Transplantation*, *9*(s4).

[18] Hussin, N. H. M., Sann, L. M., Shamsudin, M. N., & Hashim, Z. (2011). Characterization of bacteria and fungi bioaerosol in the indoor air of selected primary schools in Malaysia. *Indoor and Built Environment*, *20*(6), 607-617.

[19] Rahman, W. A., Rosli, H., Baharuddin, S. N., & Salleh, B. (2012). Incidence and remediation of fungi in a sick building in Malaysia: a case study. *Aerobiologia*, *28*(2), 275-283.

[20] Hock, O. G., Cheng, H. C., Fang, V. L. B., Yong, W. Y., & Shing, W. L. (2018). Isolation and identification of potential fungal species for spent engine lubrication oil remediation in Peninsular Malaysia. *Remediation Journal*, *28*(3), 91-95.

[21] Talley, S. M., Coley, P. D., & Kursar, T. A. (2002). The effects of weather on fungal abundance and richness among 25 communities in the Intermountain West. *BMC ecology*, *2*(1), 7–10.

[22] Nevalainen, A., Täubel, M., & Hyvärinen, A. (2015). Indoor fungi: companions and contaminants. *Indoor air*, *25*(2), 125-156.