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Mycological profile of domestic dogs in Port Harcourt Metropolis, Rivers State, Nigeria

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ABSTRACT

Domestic dogs (*Canis lupus familiaris*) are among the closest companion animals to humans, living within the same environment. Their close proximity to humans creates an avenue for the transmission of pathogenic fungi with zoonotic potential from dogs to their handlers. Therefore, this study aimed to assess the mycological profile of domestic dogs in Port Harcourt Metropolis, Rivers State, Nigeria. Using a structured questionnaire and sterile swab sticks, 200 samples were randomly collected from the skin, mouth, ear, and anus of 50 domestic dogs from six locations: Port Harcourt Town, Mgbuoba, Oroazi, Diobu, Rumuomasi, and Woji. The breeds sampled included Lhasa Apso, German Shepherd, German-Caucasian, Pit Bull, Chow Chow, Samoyed, Rottweiler, Aspin, Caucasian, Rottweiler-Canecosor, and Mongrel-Rottweiler, comprising both male and female dogs. The samples were analyzed in the laboratory using standard microbiological techniques. The results identified the presence of *Candida albicans* (80%), *Penicillium* spp. (44%), *Rhizopus* spp. (8%), *Aspergillus flavus* (70%), *Aspergillus niger*, *Fusarium* spp. (22%), and *Rhodotorula* spp. (8%). The highest distribution of fungal isolates was recorded in the mouth (40%), followed by the anus (31%), skin (25%), and ear (19%). Among the study locations, Port Harcourt Town had the highest distribution of fungal isolates (25%), whereas Woji recorded the lowest (8%). The dog breeds with the highest distribution of fungal isolates were Lhasa Apso (86%), Aspin (86%), and Pit Bull (86%). Male dogs (100%) had a higher distribution of fungal isolates than female dogs (86%). The distribution of fungal isolates according to the feeding pattern of the dogs showed that the highest fungal occurrence was observed among dogs fed only dog food/general food (100%), whereas the lowest occurrence was found among dogs fed the same food as their owners only (57%) and those fed dog food/general food supplemented by scavenging (57%). The dogs' healthcare routine also influenced fungal distribution, as dogs bathed daily recorded the lowest prevalence of fungal isolates (14%), compared with those bathed monthly (86%) and quarterly (71%). The presence of potentially pathogenic fungi in all body sites examined suggests that domestic dogs may serve as reservoirs of zoonotic fungal infections, posing a potential health risk to their owners and handlers. Therefore, regular personal hygiene among handlers and routine healthcare practices for dogs are essential to help mitigate the transmission of zoonotic fungal infections and other associated health risks.

Keywords: Mycology, domestic dogs, zoonotic infections, public health risk.

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INTRODUCTION

Domestic dogs (*Canis lupus familiaris*) are highly social animals with a remarkable ability to form strong bonds with humans and other animals (Katagiri and Oliveira-Sequeira, 2008). They possess highly developed senses, particularly an exceptional sense of smell, making them invaluable for tasks such as detection, search and rescue, and tracking (Ogugua et al., 2017). Dogs are highly adaptable to a wide range of environments, from urban settings to rural landscapes, and can thrive under diverse climatic and ecological conditions (Rautenbach et al., 1991). They serve numerous roles in human society, including as companion animals, working dogs, service

animals, and therapy animals (Smith et al., 2019). Working dogs are specifically trained to perform tasks such as herding livestock, guarding property, assisting law enforcement agencies, guiding individuals with disabilities, and detecting narcotics or explosives (Umoh et al., 2017). Throughout history, dogs have played essential roles in hunting, transportation, and protection and have been prominently featured in the art, literature, and mythology of many cultures. In some regions, dog trading is a customary practice in which dog meat is consumed (Seleem et al., 2010; Lucero et al., 2010).

Microorganisms associated with domestic dogs comprise a wide range of pathogens with important implications for both animal and public health (Lucero et al., 2010). Domestic dogs are the most common household animals living in close association with humans (Chelsea, 2023). They are commonly kept as companion animals or for security purposes. However, domestic dogs also serve as reservoirs of numerous pathogens of zoonotic significance that can be transmitted through saliva, aerosols, contaminated urine or feces, and direct physical contact (Azuonwu et al., 2023). Their close association with owners and handlers creates opportunities for the transmission of zoonotic diseases to humans. Therefore, understanding the prevalence, transmission routes, and control measures of these microorganisms is essential for promoting canine health and reducing the risk of zoonotic infections in human populations (Lamichhane et al., 2024).

The fungal microbiome of domestic dogs is a complex community of fungi that inhabit both the external and internal body surfaces of dogs (Cabañes, 2014). This fungal community plays an important role in maintaining the health and well-being of dogs (Handl et al., 2011). The fungal microbiome comprises members of several fungal groups, including Ascomycota, such as *Aspergillus* spp., *Penicillium* spp., and *Candida* spp. (Chermprapai et al., 2019); Basidiomycota, such as *Malassezia* spp., which are commonly found on the skin of dogs (Cabañes, 2014); and Zygomycota, including *Rhizopus* spp. and *Mucor* spp. (Pereira and Clemente, 2021). These fungi colonize different anatomical sites of the dog, including the gastrointestinal tract, which harbors a diverse fungal community comprising species such as *Penicillium* and *Candida* (Handl et al., 2011).

Although many fungal species exist as normal commensals, some are opportunistic or pathogenic and may pose significant health risks to both dogs and humans (Adebiyi and Oluwayelu, 2018). Certain fungal pathogens are zoonotic and can be transmitted from infected animals to humans, resulting in a variety of clinical infections. It has been estimated that approximately 1.5 million fungal species exist worldwide; however, only about 300 are known to cause disease in humans (Ehizibolo et al., 2011). Understanding these fungal pathogens is therefore essential for preventing fungal infections in both dogs and humans.

Among the fungal pathogens commonly associated with domestic dogs are the dermatophytes responsible for ringworm, including *Microsporum canis*, *Microsporum gypseum*, and *Trichophyton mentagrophytes* (Adebiyi and Oluwayelu, 2018). Investigating the mycological profile of domestic dogs provides valuable information on the influence of environmental conditions, management practices, healthcare routines, feeding patterns, and lifestyle on the fungal communities associated with these animals. Such information is essential for developing evidence-based recommendations that will help dog owners and handlers reduce the transmission of zoonotic fungal infections and other pathogens of public health importance.

MATERIALS AND METHODS

Study area

The study was conducted within Port Harcourt Metropolis, Rivers State, Nigeria, among households with domestic dogs whose owners consented to the inclusion of their dogs in the study. Samples were collected from six locations: Port Harcourt Town, Diobu, Mgbuoba, Oroazi, Woji, and Rumuomasi.

Study design

This study employed a cross-sectional design using a convenience sampling technique based on the willingness and availability of dog owners to participate (Nikolopoulou, 2023).

Sampling method

Using the convenience sampling technique, samples were collected from apparently healthy dogs representing 12 different breeds. A total of 50 dogs were sampled. From each dog, one mouth swab, one ear swab, one anal swab, and one skin swab were collected, resulting in a total of 200 swab samples. Structured questionnaires were also administered to obtain information on the dogs' management, healthcare practices, feeding patterns, and daily activities.

Isolation of fungal isolates

Swab samples were cultured following the methods described by previous studies (Azuonwu et al., 2023; Esquivel et al., 2023). Each swab sample was inoculated onto the surface of previously prepared Sabouraud Dextrose Agar (SDA) supplemented with 200 mg of ampicillin (Esquivel et al., 2023). Following inoculation,

the culture plates were incubated at 37°C for 3–5 days. Once fungal colonies appeared, pure cultures were obtained by sub-culturing fungal mycelia or spores from the actively growing edge of each colony onto fresh sterile SDA plates. Fungal growth was monitored daily until pure isolates were obtained (Hizlisoy et al., 2025).

Identification of fungal isolates

Fungal isolates were initially identified macroscopically based on colony characteristics, including colour, texture, growth rate, and pigmentation. Microscopic identification was subsequently performed using a compound microscope. A small portion of fungal mycelium was mounted on a clean glass slide with Lactophenol Cotton Blue stain to examine reproductive structures, hyphae, and conidia. For yeast isolates, characteristic features such as budding cells and pseudohyphae were observed for identification (Becker et al., 2019; Khalil et al., 2021).

RESULTS

Demographic characteristics of the dogs studied

A total of 12 dog breeds were sampled during the study. Lhasa Apso constituted the highest proportion of the sampled dogs (32%), followed by Aspin (16%), while the remaining breeds occurred at varying frequencies, as presented in Figure 1.

The age distribution of the dogs (Figure 2) showed that the majority were between 2 and 4 years of age (52%), followed by those aged 0–2 years (36%). Dogs aged 10–12 years constituted the smallest proportion of the study population (2%).

The gender distribution (Figure 3) indicated that male dogs (76%) outnumbered female dogs (24%). Information obtained from the dog owners further revealed that the majority of the dogs were kept primarily for companionship (46%) and security purposes (32%), as shown in Figure 4.

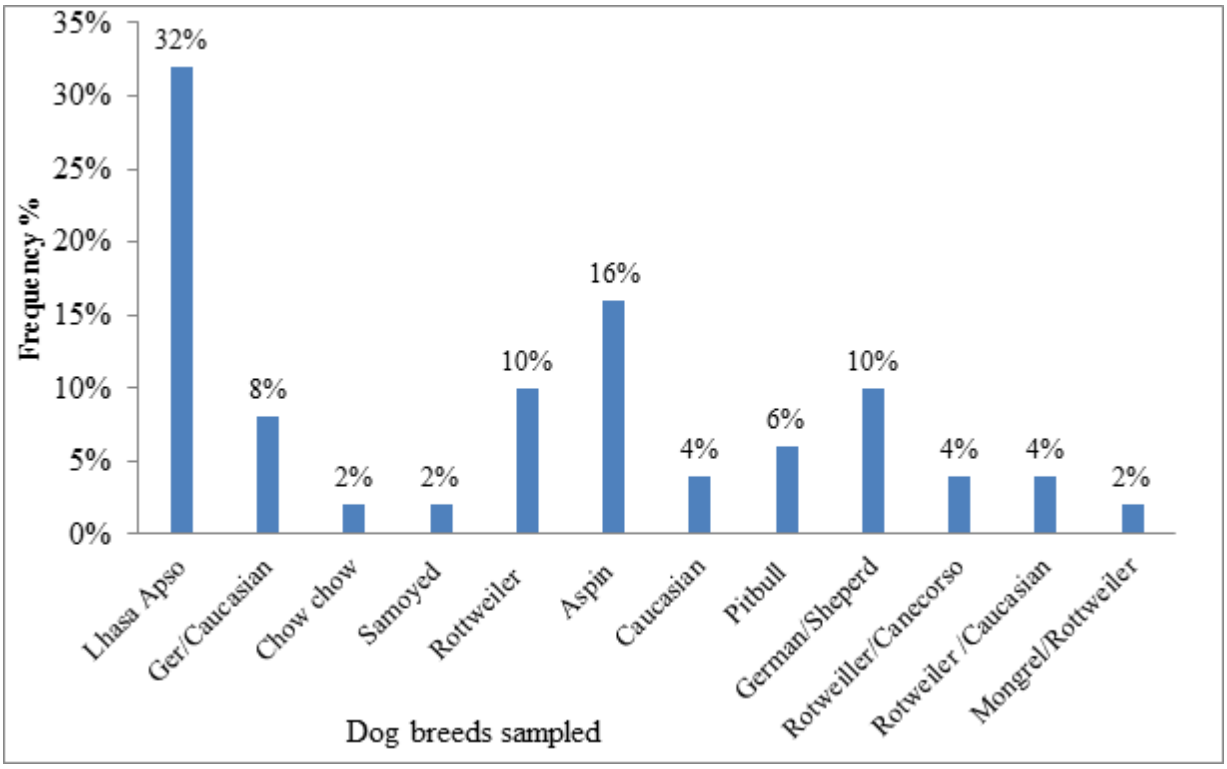

Figure 1. Breeds of the dogs studied.

Fungal isolates identified

The study identified seven fungal taxa. Their colony characteristics and microscopic features, including hyphae and reproductive structures, are presented in Table 1**.** The fungal isolates identified were *Candida albicans* (80%), *Penicillium* spp. (44%), *Rhizopus* spp. (8%), *Aspergillus flavus* (70%), *Aspergillus niger*, *Fusarium* spp. (22%), and *Rhodotorula* spp. (8%). Among these, *Candida albicans* had the highest occurrence, whereas *Rhodotorula* spp. and *Rhizopus* spp. had the lowest occurrence (Figure 5).

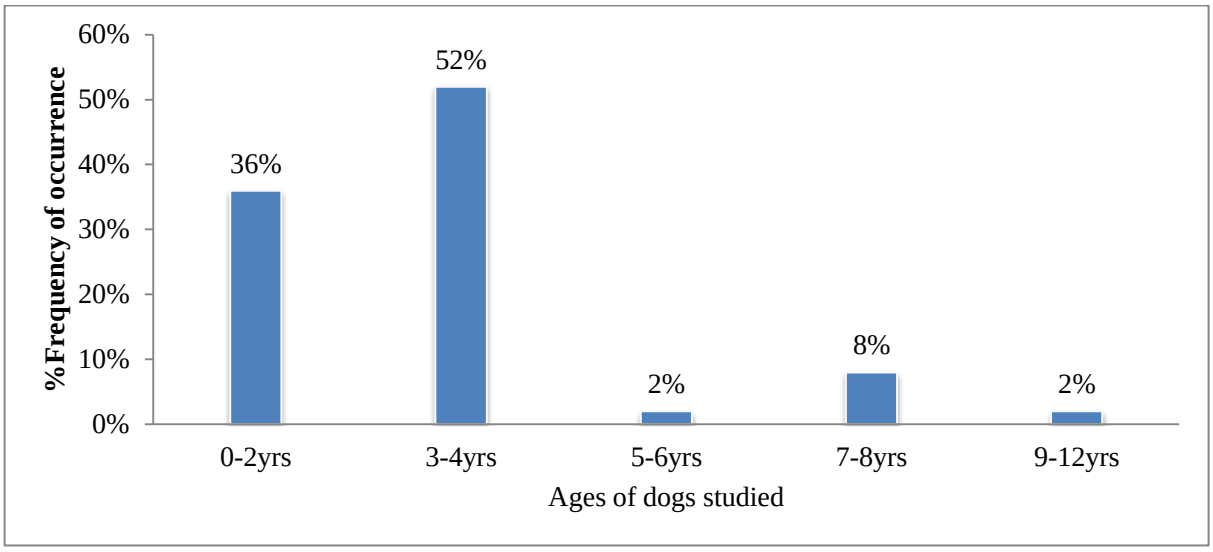

Figure 2. Age distribution of the dogs studied.

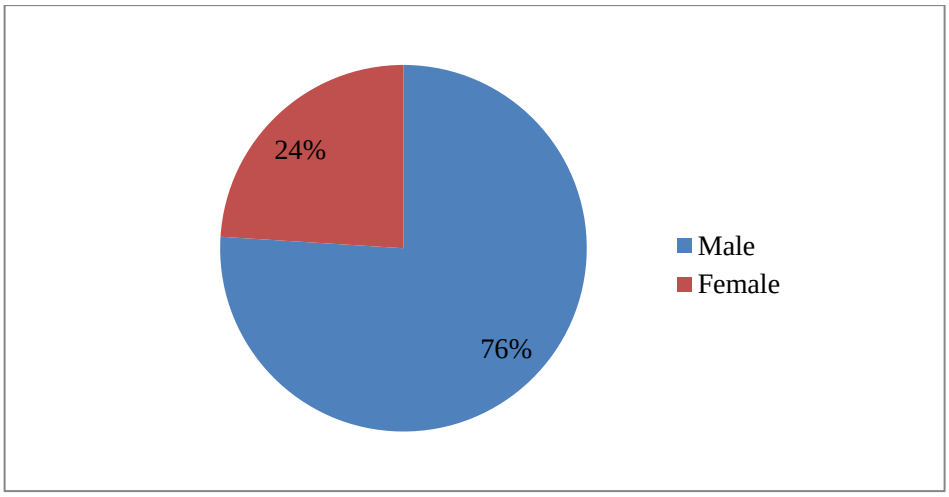

Figure 3. Gender distribution of the dogs studied.

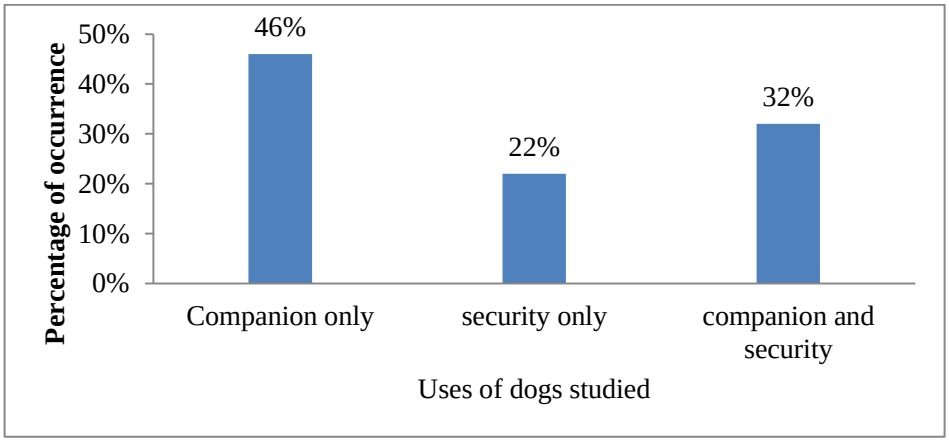

Figure 4. Uses of the Dogs Studied.

Table 1. Morphology of fungi isolates.

Isolate code	Colour surface	Colour reverse	Growth	Hyphae	Conidiophores	Spores	Suspected Microorganisms
MD2	Yellow-green	Brown	Rapid	Septate	Rough and long	Globus conidia	*Aspergillus flavus*
SD7	White-black	Yellow	Rapid	Septate	Long and smooth	Globus conidia	*Aspergillus niger*
AD9	Blue green	Yellow	Rapid	Septate	Short-branched brushlike	Round conidia	*Penicillum* spp.
MD6	White pink	Yellow red	Rapid	Septate	Short branched	Microconidia sickle shaped	*Fusarium* spp.
ED11	White	White	Rapid	Broad aseptate	Long unbranched	Sporangiospores	*Rhizopus* spp.
SD1	White cream	Cream	Moderate	Yeast-like	Absent	Blastoconidia	*Candida* spp.
MD4	Pink- red	Pink	rapid	Yeast-like	Absent	Blastoconidia	*Rhodotorula* spp.

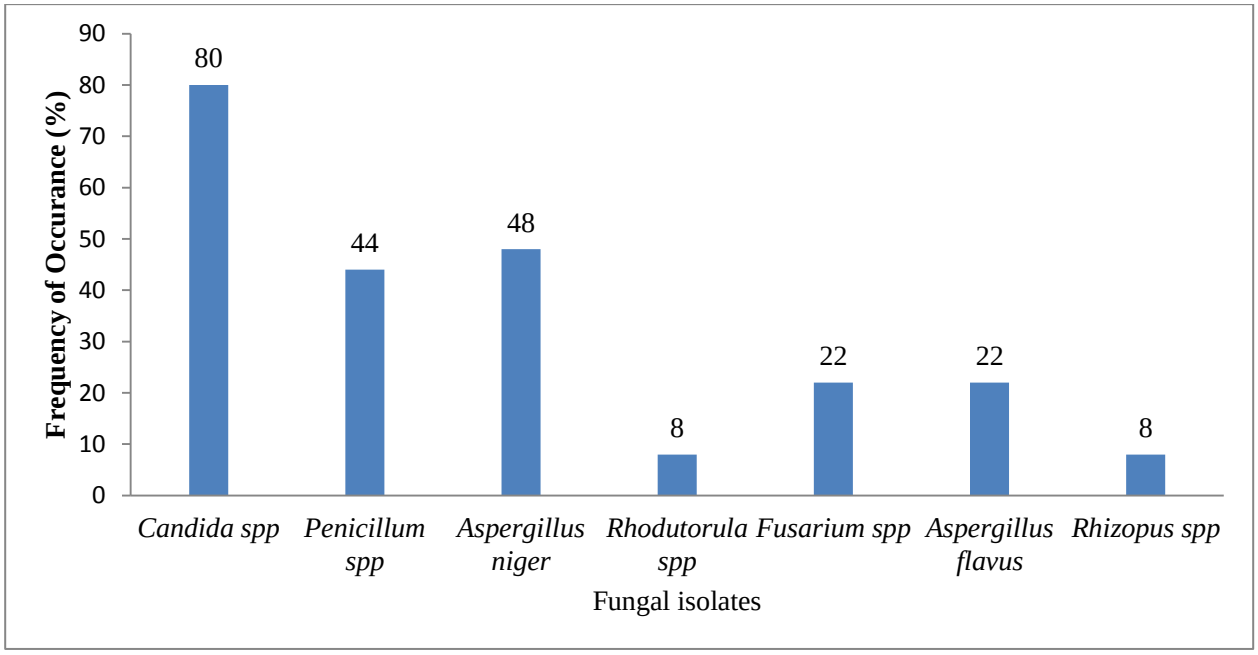

Figure 5. Frequency of occurrence of fungal isolates.

Prevalence and distribution of fungal isolates

The results showed that Lhasa Apso (86%) and Aspin (86%) exhibited the highest prevalence of fungal isolates, whereas the Mongrel-Rottweiler breed had the lowest prevalence (29%), as presented in Table 2**.**

Analysis of fungal distribution according to sex revealed a higher prevalence among male dogs (100%) than female dogs (86%), as shown in Table 3**.**

Among the four anatomical sites sampled, the mouth recorded the highest prevalence of fungal isolates (40%), whereas the ear had the lowest prevalence (19%). *Candida* spp. was the most frequently isolated fungus across all sampled body sites (Table 4).

The distribution of fungal isolates according to sampling location is presented in Table 5**.** Port Harcourt Town recorded the highest prevalence of fungal isolates (25%), whereas Woji had the lowest prevalence (8%).

The distribution of fungal isolates according to feeding pattern (Table 6) showed that dogs fed exclusively on dog feed/general food had the highest prevalence of fungal isolates (100%). In contrast, the lowest prevalence was observed among dogs fed the same food as their owners only (57%) and those fed dog feed/general food in addition to scavenging (57%).

Evaluation of healthcare practices revealed that dogs receiving daily baths and regular tick-removal treatment had the lowest prevalence of fungal isolates, as presented in Table 7.

The living arrangement of the dogs did not appear to

Table 2. Distribution of Fungal Population According to Breeds of Dogs Studied.

Microorganisms	Lhasa n=16(%)	Cau/Ger n=4(%)	Chow n=1(%)	Samoy n=1(%)	Rottwei n=5(%)	Aspin n=8(%)	Caucas n=2(%)	Pitbull n=3(%)	Ger/Shep n=5(%)	Rot/Cane n=2(%)	Rot/Cau n=2(%)	Mon/Rot n=1(%)
Candida spp	14(88)	3(75)	1(100)	1(100)	4(80)	6(75)	2(100)	1(33)	5(100)	1(50)	2(100)	1(100)
Penicillum spp	9(56	2(50)	1(100)	1(100)	1(20)	3(37)	1(50)	1(33)	2(40)	0	1(50)	0
Aspergillus niger	6(38)	2(50)	0	1(100)	3(60)	5(63)	1(50)	2(67)	2(40)	1(50)	1(50)	0
Rhodutorula spp	1(6)	0	1(100)	1(100)	0	1(13)	0	0	0	0	0	0
Fusarium spp	4(25)	0	0	0	1(20)	1(13)	0	1(33)	1(20)	1(50)	1(50)	0
Aspergillus flavus	3(19)	2(50)	0	0	0	2(25)	0	2(67)	1(20)	0	1(50)	0
Rhizopus spp	0	0	0	0	0	0	0	2(67)	0	0	0	1(100)
Total n=7(%)	6(86)	4(57)	3(43)	4(57)	4(57)	6(86)	3(43)	6(68)	5(71)	3(43)	5(71)	2(29)

Key: Lhasa - Lhasa Apso; Cau/Ger - Caucasian German; Chow - Chow Chow; Samoy - Samoyed; Rottwei – Rottweiler; Ger/Shep - German Sherpard; Rot/Cane - Rottweiler-Canecorso; Rot/Cau - Rottweiler-Caucasian; Mon/Rot - Mongrel-Rottweiler.

Table 3. Distribution of fungal populations according to gender of dogs studied.

Microorganisms	Male n=38(%)	Female n=12(%)
Candida spp	31(82)	10(83)
Penicillum spp	16(42)	6(50)
Aspergillus niger	20(53)	4(33)
Rhodutorula spp	2(5)	2(17)
Fusarium spp	11(29)	0
Aspergillus flavus	9(24)	2(17)
Rhizopus spp	1(3)	1(8)
Total n=7(%)	7(100)	6(86)

Table 4. Distribution of fungal population in the different parts of the dogs studied.

Microorganisms	Skin (n=50)	Mouth (n=50)	Ear (n=50)	Anus (n=50)
Candida spp	32(64)	37(74)	22(44)	29(54)
Penicillum spp	5(10)	15(30)	4(8)	12(24)
Aspergillus niger	10(20)	11(22)	5(10)	13(26)
Rhodutorula spp	1(2)	4(8)	0	0
Fusarium spp	1(2)	8(16)	0	3(6)
Aspergillus flavus	0	3(6)	4(8)	4(8)
Rhizopus spp	0	1(2)	2(4)	1(2)
Total=200 (%)	49 (25)	79 (40)	37 (19)	62 (31)

Table 5. Distribution of fungal population according to locations of the dogs studied.

Microorganisms	PH Town (n=10)	Woji (n=6)	Oroazi (n=9)	Diobu (n=11)	Mbuogba (n=8)	Rumuomasi (n=6)	Overall (%) n = 50
Candida spp	8(80)	3(50)	6(67)	10(91)	8(100)	5(83)	40 (80)
Penicillum spp	8(80)	2(33)	1(11)	5(45)	2(25)	4(66)	22 (44)
Aspergillus niger	4(40)	3(50)	4(44)	5(45)	6(75)	2(33)	24 (48)
Rhodutorula spp	1(10)	0	0	2(18)	1(13)	0	04 (8)
Fusarium spp	5(50)	0	2(22)	2(18)	1(13)	1(17)	11 (22)
Aspergillus flavus	2(20)	1(17)	1(11)	3(27)	4(50)	0	11 (22)
Rhizopus spp	1(10)	0	3(33)	0	0	0	04 (8)
Total (%) n=7	7(100)	4(51)	6(86)	6(86)	6(86)	4(51)	7(100)

Table 6. Distribution of fungal population according to feeding pattern of dogs studied.

Microorganisms	DF only n=10(%)	GF only n=5(%)	DF/GF only n=30(%)	DF/GF/Scav n=3(%)	GF/Scavenge n=2(%)
Candida spp	7(70)	4(80)	24(80)	3(100)	2(100)
Penicillum spp	1(10)	3(60)	15(50)	2(67)	1(50)
Aspergillus niger	5(50)	2(40)	14(47)	1(33)	2(100)
Rhodutorula spp	0	1(20)	1(3)	2(67)	0
Fusarium spp	2(20)	0	7(23)	0	1(50)
Aspergillus flavus	3(30)	0	7(23)	0	1(50)
Rhizopus spp	3(30)	0	1(3)	0	0
Total n=7(%)	6(86)	4(57)	7(100)	4(57)	5(71)

Key: DF - Dog food; GF - General food; Scav – Scavenging.

Table 7a. Distribution of microorganisms with respect to health care routines of dogs studied.

	Daily			Weekly			Monthly			Quarterly		
Microorganisms	Bath n=1	TR n=3	Vet n=0	Bath n=23	TR n=12	Vet n=0	Bath n=16	TR n=7	Vet n=22	Bath n=7	TR n=9	Vet n=19
Candida spp	1	3	0	18	10	0	12	5	17	7	7	15
Penicillum spp	0	2	0	8	6	0	10	4	6	3	2	12
Aspergillus niger	0	1	0	10	5	0	7	3	9	6	5	10
Rhodutorula spp	0	2	0	2	0	0	1	0	0	0	1	3
Fusarium spp	0	0	0	3	3	0	5	3	6	2	1	3
Aspergillus flavus	0	0	0	7	2	0	1	0	6	2	4	2
Rhizopus spp	0	0	0	0	2	0	0	0	3	0	0	1
Total n=7(%)	1(14)	4(57)	0	6(86)	6(86)	0	6(86)	5(71)	6(86)	5(71)	6(86)	7(100)

Key: TR - Use of tick remover; Vet - Veterinary care.

Table7b. Distribution of microorganisms with respect to health care routines of dogs studied.

	Biannually			Annually			Never		
Microorganisms	Bath n=3	TR n=3	Vet n=4	Bath n=0	TR n=0	Vet n=2	Bath n=0	TR n=16	Vet n=3
Candida spp	3	3	4	0	0	2	0	13	3
Penicillum spp	1	1	1	0	0	1	0	7	2
Aspergillus niger	1	1	2	0	0	1	0	9	2
Rhodutorula spp	1	1	1	0	0	0	0	0	0
Fusarium spp	0	0	0	0	0	0	0	4	1
Aspergillus flavus	1	1	2	0	0	0	0	4	1
Rhizopus spp	0	0	0	0	0	0	0	0	0
Total n=7(%)	5(71)	5(71)	5(71)	0	0	3(43)	0	5(71)	5(71)

Key: TR - Use of tick remover; Vet - Veterinary care.

Table 8. Distribution of fungal populations according to living arrangement of dogs studied.

Microorganisms	No cage n=37(%)	Cage n=13(%)
Candida spp	29(78)	12(92)
Penicillum spp	16(43)	6(46)
Aspergillus niger	16(43)	8(62)
Rhodutorula spp	2(5)	2(15)
Fusarium spp	6(16)	4(31)
Aspergillus flavus	8(23)	3(23)
Rhizopus spp	2(5)	1(7)
Total n=7(%)	7(100)	7(100)

have a significant influence on fungal occurrence, as fungal isolates were recovered from both caged and free-roaming dogs. However, the proportion of each fungal isolate was generally higher among dogs kept in cages than among those without cages (Table 8).

To determine whether associations existed between the variables studied and the occurrence of fungal isolates, Chi-square analysis was performed. The results of the statistical analysis are presented in Table 9**.**

Table 9. Chi-Square Tests of Independence.

Variable 1	Variable 2	Chi-Square	p-value	Significant (p<0.05)
Location	Breed	67.1415	0.1262	No
Location	Gender	2.7221	0.7427	No
Location	Liv/Arg	4.304	0.5065	No
Location	Nutrition	61.0438	0	Yes
Location	Bath	42.3869	0.0025	Yes
Location	Tick Remover	47.785	0.004	Yes
Location	Vet	44.7025	0.0012	Yes
Location	Skin	62.7591	0.2205	No
Breed	Gender	29.4408	0.0019	Yes
Breed	Liv/Arg	19.443	0.0536	No
Breed	Nutrition	89.4792	0.0001	Yes
Breed	Vet	60.615	0.0488	Yes
Breed	Skin	90.0582	0.984	No
Gender	Liv/Arg	0.2191	0.6397	No
Gender	Nutrition	3.7646	0.4388	No
Gender	Vet	3.5696	0.4674	No
Gender	Skin	23.7736	0.0137	Yes
Liv/Arg	Nutrition	10.6722	0.0305	Yes
Liv/Arg	Tick Remover	3.965	0.5545	No
Liv/Arg	Vet	2.9903	0.5594	No
Nutrition	Bath	60.6487	0	Yes
Nutrition	Tick Remover	86.7014	0	Yes
Nutrition	Vet	40.2246	0.0007	Yes
Nutrition	Skin	44.8514	0.436	No
Bath	Tick Remover	99.7757	0	Yes
Bath	Vet	59.7637	0	Yes
Tick Remover	Vet	52.2453	0.0001	Yes
Vet	Skin	52.5551	0.1765	No
Skin	Mouth	215.158	0.0236	Yes
Skin	Ear	187.92	0	Yes
Skin	Anus	188.1808	0	Yes

DISCUSSION

In assessing the fungal population associated with the domestic dogs studied, seven fungal taxa were identified across the different anatomical sites sampled (mouth, ear, skin, and anus). These included *Candida albicans*, *Penicillium* spp., *Aspergillus flavus*, *Aspergillus niger*, *Fusarium* spp., *Rhodotorula* spp., and *Rhizopus* spp., with *Candida albicans* showing the highest frequency of occurrence. The predominance of *Candida* spp. is consistent with previous studies by Dworecka-Kaszak et al. (2020) and Azuonwu et al. (2023), which similarly identified *Candida* spp. as the most prevalent fungal isolates recovered from domestic dogs. The high occurrence of *Candida* spp. also agrees with the findings of Hizlisoy et al. (2025), who reported that *Candida* spp. are common commensals of the oral cavity of healthy animals but may become opportunistic pathogens in immunocompromised hosts.

The findings of the present study suggest that factors such as inadequate hygiene, dietary practices, and frequent exposure to contaminated environments or objects may contribute to the high prevalence of *Candida* spp. This observation is supported by the finding that all seven dogs with infrequent bathing and poor healthcare routines harboured *Candida* spp. Routine veterinary monitoring of dogs, particularly those with underlying medical conditions, is therefore important for the early detection and management of fungal overgrowth or infection. Furthermore, *Candida* colonization has been reported to be associated with underlying bacterial co-infections and systemic diseases such as diabetes mellitus and canine distemper (Hizlisoy et al., 2025). Future studies should investigate the environmental and

physiological factors influencing the prevalence of *Candida* spp. in domestic dogs across different geographical regions and climatic conditions.

Two species of *Aspergillus*, namely *Aspergillus flavus* and *Aspergillus niger*, were isolated in this study. These fungi are common environmental contaminants capable of causing infections in both animals and humans, particularly respiratory diseases such as aspergillosis (Rafique et al., 2026). Their isolation raises concerns because both species are known producers of mycotoxins and other secondary metabolites that may adversely affect animal and human health (Fakruddin et al., 2015). Although aspergillosis is relatively uncommon in healthy dogs, these fungi may become opportunistic pathogens in immunocompromised animals (Rafique et al., 2026).

Penicillium spp., although generally regarded as non-pathogenic, were also isolated during this study. Species of *Penicillium* are widely distributed in soil and indoor environments, particularly in damp and poorly ventilated areas (Monpierre et al., 2023). While they rarely cause disease in healthy animals, they have been reported as opportunistic pathogens in immunocompromised hosts (Vanittanakom et al., 2006). Their recovery from the skin and oral cavity of dogs suggests environmental contamination and is consistent with previous reports describing widespread exposure to *Penicillium* spp. in domestic environments (Pitt, 1994). The presence of these fungi in the oral and skin microbiota of dogs warrants further investigation, particularly to determine whether chronic exposure reflects environmental conditions such as dampness, poor ventilation, or excessive indoor mould growth (Rafique et al., 2026). Consequently, dog owners should maintain clean, dry, and well-ventilated living environments to minimize fungal exposure.

The detection of *Fusarium* spp., predominantly soil-dwelling saprophytic fungi, is also noteworthy. Members of this genus are well recognized as important pathogens of plants and opportunistic pathogens of both animals and humans, particularly in immunocompromised individuals (Kano et al., 2002). In humans, *Fusarium* spp. have been associated with keratitis and other localized infections following exposure to contaminated soil or plant material (Thornton, 2020). Although infections caused by *Fusarium* spp. are relatively uncommon in dogs, their presence on the skin suggests environmental exposure during outdoor activities or contact with contaminated environments. This observation agrees with the findings of Kano et al. (2002), who reported increased environmental exposure to *Fusarium* spp., thereby increasing the risk of opportunistic infections when predisposing factors such as skin wounds or immunosuppression are present.

Rhodotorula spp. are yeast organisms commonly isolated from moist environments, including soil, water, and indoor air. They have emerged as opportunistic pathogens, particularly among immunocompromised individuals, although their pathogenic significance in dogs remains poorly understood (Aboul-Ella et al., 2025). While these yeasts are generally regarded as having low pathogenic potential, they have been implicated in superficial infections in immunocompromised animals (Aboul-Ella et al., 2025). Further investigations are needed to determine the clinical significance of *Rhodotorula* spp. in domestic dogs, particularly in humid environments where these organisms are more likely to proliferate.

Statistical analysis revealed a significant association between the different anatomical sites sampled, suggesting the possibility of fungal transfer between body sites through grooming behaviour, environmental exposure, or physical contact. Consequently, contamination of one body site with potentially pathogenic fungi may facilitate dissemination to other parts of the animal, thereby increasing the likelihood of transmission to owners and handlers regardless of the site of contact.

CONCLUSION

This study investigated the distribution of fungi across four anatomical sites (skin, mouth, ear, and anus) of domestic dogs in Port Harcourt Metropolis, Rivers State, Nigeria. Seven fungal taxa were identified, namely *Candida albicans*, *Penicillium* spp., *Rhizopus* spp., *Aspergillus flavus*, *Aspergillus niger*, *Fusarium* spp., and *Rhodotorula* spp., from the 50 domestic dogs sampled. These fungi comprised both normal commensal organisms and opportunistic or pathogenic species capable of causing disease in dogs and humans.

The highest prevalence of fungal isolates was observed in the oral cavity of the dogs. This finding is of public health importance because the mouth is frequently involved in close interactions between dogs and humans, including licking, biting, and, in some households, sharing food. Such behaviours may facilitate the transmission of pathogenic fungi, particularly *Candida* spp. and *Aspergillus flavus*, which were recovered from the oral cavity.

Although several of the fungal isolates identified form part of the normal fungal microbiota of dogs, others have recognized zoonotic or opportunistic pathogenic potential, particularly among immunocompromised individuals. The presence of these fungi on apparently healthy domestic dogs suggests that companion animals may serve as reservoirs for fungi capable of causing infections in humans and other animals.

These findings underscore the importance of educating dog owners and the general public about the potential health risks associated with close contact with domestic dogs and the preventive measures required to reduce these risks. Routine veterinary examinations, proper

grooming and healthcare practices, good environmental sanitation, and strict personal hygiene following contact with dogs are strongly recommended. Adherence to these preventive measures will help reduce the risk of zoonotic fungal transmission and contribute to improved public and animal health.

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