

Fungal flora isolated from the skin of healthy dromedary camels (*Camelus dromedarius*)

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Abstract

Hair samples from 58 healthy camels were examined for the presence of saprophytic fungi. One hundred and seventy-four samples were obtained from three different locations of dromedary camel's body. Several fungal specific media were used for isolating and identifying the saprophytes. Fungal isolates belonged to 15 genera. The most common in order of frequency were members of the genera *Aspergillus* (48% of the total examined camels), *Penicillium* (16.1%), *Mucor* (14.2%), *Alternaria alternata* (5.6%), *Rhizopus* (3.1%), *Chrysosporium* (2.7%), *Acremonium* (1.1%), *Scoupolariopsis* (1%), *Cladosporium* (0.8%), *Fusarium*, *Psuedallescheria boydii* and *Stachybotrys atra* (0.2%). The highest frequently yeasts isolated were related to *Candida* species (6%), followed by *Geotrichum candidum* (0.6%) and *Malassezia* species (0.2%). Skin infections caused by any of the contaminants were not encountered. The study demonstrates that *Aspergillus*, *Penicillium* and *Mucor* species were the common components of healthy camel skin mycoflora, and that camel hair analyzed in this study was free from true dermatophyte.

Introduction

The skin is the largest organ of the body, and depending on the species and age can represent 12-24% of an animal's body weight. It has many functions, including acting as a barrier for the body and providing environmental protection, regulating temperature, producing pigment and vitamin D and sensory perception, amongst others (Aiello, 1998). Changes in the skin may occur as a consequence of different biological agents, bacteria, fungi, parasites and viruses, but may also be a consequence of allergy, immunology disorders, endocrine disturbances, inborn diseases, environmental factors and nutritive deficits (Popovi and Lazarevi, 1999). These changes can influence the normal functioning of the skin and the effectiveness of its role as an enclosing barrier.

Among etiological agents, fungi are taxonomically related groups of organisms that can infect the cornified epidermis, hair, horns, nails and feathers in man and animals. Most fungal contaminants are not known to produce infections in healthy individuals, but some are known to become invasive in conditions of decreased resistance, thus being opportunistic in their pathogenicity (Khosravi, 1996). Cases of suspected fungal infections caused by saprophytic fungi have been described in domestic and wild animals throughout the world during research over the last two

decades. Previous investigations have shown that the most common isolated fungi from the skin or hair of different animals were *Penicillium*, *Aspergillus*, *Alternaria*, *Mucor*, *Scoupolariopsis* and *Chrysosporium* (Aho, 1983; Efuntoye and Fashanu, 2001; Bourdeau *et al.*, 2004; Stojanov *et al.*, 2007; Rostami *et al.*, 2010). Until now, no complete investigation had been performed on the frequency and population size of fungal flora on the skin and hair of camels, and little was known on their role in the occurrence of skin lesions in this animal (Kuttin *et al.*, 1986; Fadlelmula *et al.*, 1994; Khosravi *et al.*, 2007). The present study evaluates the fungi present on predisposed skin locations in healthy camels.

Materials and methods

Camels

Fifty-eight dromedary camels (males and females) were studied with ages that ranged from 6 months to 9 years old, with a mean age of 6.5 years. Camels were selected from various farms in Iran (Najafabad and Tehran regions) and all were considered clinically healthy in dermatological examinations during this study in 2010.

Sampling and fungal identification

A total of 174 samples comprising skin and hair

material were taken from neck, hump and flank surfaces, and submitted to the mycology laboratory for fungal analysis. Samples were cultured onto Sabouraud dextrose agar (Merck Co., Darmstadt, Germany) containing chloramphenicol (0.005%), Mycosel agar (Merck Co., Darmstadt, Germany), Dixon agar and blood agar. Plates were then incubated aerobically at 30°C and examined daily from day two post inoculation, for a 10-day period. *Aspergillus* species were identified following Raper and Fennel's keys (Raper and Fennel, 1965), while identification of other filamentous fungi was achieved to the genus level. Yeast colonies were identified for macro- and micromorphological characteristics, and on the basis of physiological characteristics, such as presence of capsule by India ink testing, urease production at 25°C, and the germ tube test. Carbohydrate assimilation test was performed on all isolates. Colonies were counted and the frequency of each fungal isolate in the three sample areas of each camel was calculated.

Statistics

The chi-square (χ^2) test was used to assess statistical differences between groups. Probabilities of 5% were taken to be statistically significant. Results were analyzed and described using frequency and percentage distribution.

Results

From 58 dromedary camels, the presence of fungal genera and/or species was identified in 57 animals (98.3%). One animal (1.7%) was identified to have no positive cultures from the three different body's sites sampled. A total of 620 fungal isolates were obtained from the 57 animals samples. Fungal isolates belonged to 15 genera. The following fungal genera and species were recovered: *Aspergillus* (48% of the total examined camels), *Penicillium* (16.1%), *Mucor* (14.2%), *Alternaria alternata* (5.6%), *Rhizopus* (3.1%), *Chrysosporium* (2.7%), *Acremonium* (1.1%), *Scoupolariopsis* (1%), *Cladosporium* (0.8%), *Fusarium*, *Psuedallescheria boydii* and *Stachybotrys atra* (0.2%) (Table 1).

Among the five *Aspergillus* species isolated, *A. flavus* occurred most frequently (15.7%), followed by *A. fumigatus* (14%), *A. niger* (11%), *A. penicillioides* (1.1%), *A. versicolor* (0.6%). Thirty-five *Aspergillus* isolates were not identified at the species level, so they were reported as *Aspergillus* spp (5.6%). No significant differences were found in the frequency among *Aspergillus* species, and between *Aspergillus* species and other filamentous fungi species in samples.

The highest frequency yeasts isolated were related to *Candida* species (6%), followed by *Geotrichum candidum* (0.6%) and *Malassezia* species (0.2%). The yeasts were not accompanied by filamentous fungi in

the skin surface of most subjects. Filamentous fungi (93.2%) were found to occur at a significantly greater frequency in samples than yeasts (6.8%) isolated from healthy camels skin ($P < 0.05$) (Figure 1).

Fungal isolates were recovered from all three parts of the body surfaces including neck (30.8%), hump (38.9%) and flank (30.3%). The mean number of fungal colonies in the hump was found to be higher than those in other sample areas, but this was not found to be statistically significant.

The prevalence of fungal isolation was 79.3% in males and 20.7% in females, indicating a significant difference between two sexes ($P < 0.05$). Based on the maturity age of camels, 13.8% of the isolated fungi were found in animals less than 5 years old, and 86.2% were found on adult camels. This result was found to be statistically significant ($P < 0.05$).

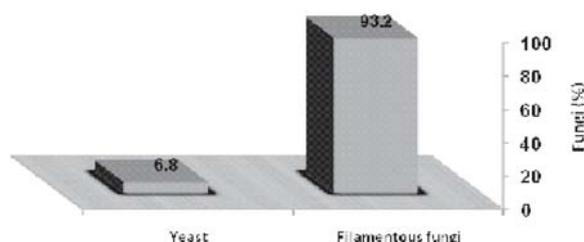
Discussion

Camels can live in areas that are inhospitable to other domestic animals, and are therefore of great assistance to humans surviving in and making use of drier regions of the planet. These animals seem to be

Table 1: The frequency of filamentous fungi and yeasts from 58 healthy skins of dromedary camels according to body sites

	Body sites			Total
	Neck (No., %)	Hump (No., %)	Flank (No., %)	
Filamentous fungi				
<i>Aspergillus niger</i>	10(1.6)	38(6.1)	20(3.2)	68(11)
<i>Aspergillus fumigatus</i>	36(5.8)	25(4)	26(4.2)	87(14)
<i>Aspergillus flavus</i>	31(5)	40(6.5)	26(4.2)	97(15.7)
<i>Aspergillus versicolor</i>	0(0)	1(0.2)	3(0.5)	4(0.6)
<i>Aspergillus penicillioides</i>	0(0)	0(0)	7(1.1)	7(1.1)
<i>Aspergillus</i> spp.	12(1.9)	14(2.3)	9(1.5)	35(5.6)
<i>Mucor</i> spp.	28(4.5)	29(4.7)	31(5)	88(14.2)
<i>Rhizopus</i> spp.	5(0.8)	10(1.6)	4(0.6)	19(3.1)
<i>Penicillium</i> spp.	30(4.8)	46(7.4)	24(3.9)	100(16.1)
<i>Chrysosporium</i> spp.	4(0.6)	6(1)	7(1.1)	17(2.7)
<i>Alternaria alternata</i>	15(2.4)	9(1.5)	11(1.8)	35(5.6)
<i>Fusarium</i> spp.	1(0.2)	0(0)	0(0)	1(0.2)
<i>Cladosporium</i> spp.	3(0.5)	1(0.2)	1(0.2)	5(0.8)
<i>Acremonium</i> spp.	2(0.3)	1(0.2)	4(0.6)	7(1.1)
<i>Scoupolariopsis</i> spp.	0(0)	5(0.8)	1(0.2)	6(1)
<i>Stachybotrys atra</i>	0(0)	1(0.2)	0(0)	1(0.2)
<i>Psuedallescheria boydii</i>	0(0)	0(0)	1(0.2)	1(0.2)
Yeasts				
<i>Geotrichum candidum</i>	0(0)	0(0)	4(0.6)	4(0.6)
<i>Candida</i> spp.	14(2.3)	15(2.4)	8(1.3)	37(6)
<i>Malassezia</i> spp.	0(0)	0(0)	1(0.2)	1(0.2)
Total	191(30.8)	241(38.9)	188(30.3)	620(100)

Figure 1: Comparison of the frequency of filamentous and yeast fungi isolated from dromedary camels during 2010.



spared from the devastating epidemic infections that threaten other livestock species in the same regions, e.g. rinderpest, contagious pleuropneumonia and foot and mouth disease. Camel diseases that are shared with other species of livestock are well-known, but camel-specific diseases, although well-known to pastoralists for generations, still remain a mystery to the scientific community and some have still yet to be identified (Wernery and Kaaden, 1995). This paper provides observations on laboratory descriptions of fungal flora of healthy camel skin, which were either poorly described, or not described in the literature. In the present study, the most common fungi isolated from skin of healthy camels were saprobes, particularly *Aspergillus*, *Penicillium* and *Mucor* species. This may be due to the commonality of these fungi, which are frequently found in soil, air, plants and on other materials; these are therefore in constant contact with the animals (Mancianti and Papini, 1996). Nevertheless, in certain circumstances such as chronic disease, anticancer therapy, prolonged antibiotic treatment, and steroids therapy, some fungi commonly considered saprobe can assume pathogenic properties and invade tissues. Investigations on the fungal flora from skin of various mammal species throughout the world have identified the most common isolated fungi from the skin or hair as *Microsporum canis*, *Penicillium* and *Aspergillus* species in cat (Khosravi, 1996), *Aspergillus*, *Penicillium* and *Alternaria* species in dog (Stojanov *et al.*, 2007), *Scoupolariopsis*, *Penicillium* and *Acremonium* in horse (Bourdeau *et al.*, 2004), *Mucor*, *Penicillium* and *Aspergillus* species in squirrel (Rostami *et al.*, 2010) and *Mucor*, *Penicillium* and *Cladosporium* species in cow (Aho, 1983). The results of this study are greatly similar to those obtained by other investigators and agree with the findings of Bagy and Abdel Hafez (1985), where *Chrysosporium*, *Aspergillus* and *Cladosporium* were reported as the most common genera isolated from the hair and skin of camels in Egypt. The amount of discrepancy between the results of this study and Bagy and Abdel Hafez (1985) may be due to the different climates. Our results have also demonstrated that camel's hair was free from true dermatophyte. However, Kuttin (1986) isolated *Trichophyton verrucosum* from 25% of young camels, and found that less than 0.5% of the animals suffered from *T. mentagrophytes* infection. In another study conducted by Manefield and Tinson (1997), *T. mentagrophytes* was listed as the only dermatophyte isolated from Australian camels, especially in the young that are less than 3 years of age. *Candida* species are known to occur as commensal yeasts in the mouth, gastrointestinal tract, vagina and on the skin of healthy animals, and are more commonly found in temperate zones (Khosravi *et al.*, 2005). Although our observations could be supported by the above statement, Jaiswal (1990) from India and Shaikh *et al.*

(1993) from Iran reported that *Candida* species were the predominant etiological agents of dermatomycoses. Isolation of these yeasts in camels had not been reported previously. The frequency of occurrence of *Candida* species in this study (6%) was in agreement with frequencies reported for the skin of different healthy animals (6.8%) (Paixão *et al.*, 2001). In normal conditions, only a small amount of yeast species can be sporadically isolated from the skin; however, in immunosuppressed situations, some *Candida* species can be isolated. *C. albicans* are predominantly found and its excessive population can lead to dermatomycosis (Kennis *et al.*, 1996). The results of the present study are closely similar to aforementioned studies in humans and other animals, but identify a difference from other animals in the fungal agents isolated from camels' skin without clinical signs. However, this discrepancy may be due to sampling technique used, the lesser areas of skin sampled and arid and semiarid climates in Iran. As camels live in temperate climates, it is expected that the prevalence and intensity of fungal flora in healthy skin to be significantly lower than that of fungi found in warm-humid climates. Warm-humid climates are good conditions for sporulation of the fungi and their consequent spread in the environment (Anaissie *et al.*, 2003). The study identified camels over 5 years of age carried the greater percentage of the filamentous fungi and yeasts identified, agreeing with the findings of other investigations carried out in animals with slight differences (Logas, 1994; Bernardo, Martins and Martins, 1998). Age variation among the different studies may be due to varying methods of handling, hygiene and the geographical regions where the research was made.

In conclusion, the results show saprobe fungi, such as *Aspergillus*, *Penicillium* and *Mucor* species are possible etiological agents of dermatomycoses in camels. This suggests greater veterinarian concern is needed to be placed on identification of these fungi. The involvement of saprobe fungi as pathogenic agents of mycoses in camels must be carefully analyzed by an experienced mycologist and veterinarian.

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