# The aerobic bacterial population of the respiratory passageways of healthy dromedaries in Najaf-abbad abattoir, central Iran

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#### Abstract

The aerobic bacteria of the respiratory passageways were investigated using 30 healthy camels randomly selected from animals brought to the Najaf-abbad abattoir in central Iran. Samples were collected asceptically from the nasal cavity, tonsils, trachea, and the lungs for bacteriological examination. Standard microbiological techniques were used for isolation and identification of bacterial genera.

From a total of 120 samples collected for bacteriological examinations, 313 isolates representive different genera were identified. Identified bacteria were staphylococci (52.7%), *Neisseria* spp (20.4%), *Bacillus* spp (16.6%), streptococci (4.5%) and *Escherichia coli* (2.2%). Gram-positive bacteria were dominant in this environment, followed by *Neisseria* spp, *Escherichia coli* and *Klebsiella* spp.

Keywords: Aerobic bacteria, Camel respiratory tract, Iran.

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#### **1. Introduction**

Bacterial flora in a mammalian host can be considered as either resident or transitory, of which the resident population is constant for a given anatomical area at a specific age of the the resident host animal. When microbiom becomes disturbed, the initial balance tends to be restored quickly. However transitory microorganisms from the environment remain for only short periods within the host. The animals body is not a uniform bacterial habitat as each organ system differs, creating a selective medium where certain microorganisms are more favoured than others (Mcfarland 2000, Sorum and Sunde 2001).

Some studies conducted on the bacterial population of the respiratory

tract of domestic animals (Ajuwape et al, 2006; Megra et al., 2006, Yimeri and Asseged, 2007) but for the camel they mainly focus on lungs (Al-Doughaym et al., 1999, Zubair et al., 2004), and studies the on bacteria of respiratory passageways of healthy camels are scarce (Shigidi, 1973). In Iran there are some camel rearing areas (east center, south and south east), mainly for meat producing purposes but camel slaughtering is performed only in a few cities within Iran such as Najaf-abbad (a city in centre of Iran). Camels from all over the country are brought to the Najafabbad slaughterhouse. So, this study was designed to isolate and characterize bacteria from different anatomical sites the respiratory passageways of of apparently healthy camels in Iran.

# 2. Material and Methods

The study was carried out weekly through June to October 2008 on 30 camels randomly selected from animals brought to the Najaf-abbad abattoir for slaughter. The camels originated from east center, south and south east of Iran where camel rearing are common.

Although records were not available concerning the age and previous health status, all camels were adults and were found to be apparently healthy at the ante-mortem examination.

Nasal samples were collected, during ante-mortem inspection, by inserting sterile cotton-tipped applicator sticks into the nasal passageways after proper cleaning and disinfection of the external nares. After slaughter the trachea of each camel was opened using a sterile scalpel blade to take a sample by inserting sterile cotton tipped swab into the tracheal tube. The mucosa were thoroughly rubbed by rolling the swabs to attain effective contact. The swabs were put in separate sterile test tubes containing Stuart transport media (Quelab cat. QB-65-5015), labeled and kept in a cool box and transported to the veterinary microbiology laboratory of Shahrekord University on the day of sampling for further processing.

Before collecting tonsils and lung samples, the external surfaces were disinfected with 70% alcohol to minimize surface contamination. Using sterile scissors and tissue forceps, pieces of the lung and the corresponding tonsils were collected separately into sterile screwcapped universal bottles and transported in a cool box for further processing.

For bacteriological examination, the swabs were removed from the bottles and streaked over the duplicate plates of blood agar-base (Scharlau 01-352)

supplemented with 7% sheep blood and Maconkey agar (Merck 1.05465.0500). Whereas, the surfaces of lung and tonsil samples were seared with a hot spatula, incised and printed on mentioned media and streaked with a wire loop. The streaking was further spread with inoculating loop to aid colony isolation. The plates were labeled and incubated aerobically at 37°C for 24-48 h (Carter, Mycoplasma and 1984). anaerobic culture were not included in the examinations.

One colony was selected from those colonies that have similar morphologies and sub-cultured on blood agar plates for further analysis. After gram staining, catalase and oxidase tests, identification of the isolated microorganisms was done using a standard biochemical scheme according to Quinn et al., (1994).

## 3. Results and Discussion

Out of 120 specimens collected from the nasal cavity, trachea, tonsils and lung (30 from each site), 313 bacterial isolates (representative of 313 different colony morphologies) were identified, table 1.

The predominant species among the isolates were staphylococci (52.7%), followed by Neisseria spp (20.4%), Bacillus spp (16.61%) and streptococci (4.5%). Whereas, *Klebsiella* (1.3%). Nocardia (0.003%)and Serratia (0.006%) were the least encountered bacterial genera. The majority of the isolates colonized all the anatomical sites investigated with the exception of E. coli and, streptococci, which were absent from the lung, and Klebsiella which was absent from the nasal tract. Grampositive bacteria were dominant in this environment, followed by Neisseria spp, *E. coli* and *Klebsiella* spp.

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Bacteria	Nasal tract	Tonsils	Trachea	Lung	Total
Staphylococus spp	49 (29%)	40 (24%)	52 (31%)	24 (14%)	165 (52.725)
Neisseria spp	16 (25%)	24 (42%)	21 (32%)	3 (4.6%)	64 (20.44%)
Bacillus spp	7 (13%)	22 (42%)	14 (26%)	9 (18%)	52 (16.61%)
Streptococcus spp	5 (35%)	5 (35%)	4 (28%)	0 (0%)	14 (4.47%)
Klebsiella spp	0 (0%)	1 (25%)	2 (50%)	1 (25%)	4 (1.27%)
Escherichia coli	4 (57%)	1 (14%)	2 (28%)	0 (0%)	7 (2.23%)
Serratia	1 (50%)	0 (0%)	1 (50%)	0 (0%)	2 (0.006%)
Nocardia	0 (0%)	0 (0%)	1 (50%)	0 (0%)	1 (0.003%)
Yeast	2 (50%)	1(25%)	1 (25%)	0 (0%)	4 (0.01%)
Total	84 (26.83%)	94 (30.03%)	98 (31.30%)	37 (11.82%)	313 (100%)

**Table 1**. Relative frequency of the different groups of microorganisms isolated from the respiratory tract of healthy camels.

This study has shown that a variety of bacterial species colonizes the respiratory of apparently passageways healthy camels. The normal bacteria of a healthy individual can however be altered by several factors such as the nutritional and immunological status of the animal or the environment. The suppression of the normal bacteria frequently allows the development of potential pathogens, leading to the presentation of a variety of pathologies (Herthelius et al., 1989). Our results show that 20.4 % of the isolations belong to Neisseria spp. Several other workers have studied the aerobic bacteria from different healthy animals such as the caprine respiratory tract (Mergra et al., 2006), canine upper respiratory tract (Ajuwape et al., 2006), Sea lion nasal tract (Hernandez-Castro et al., 2005), but only the latter reported Neisseria spp from the respiratory tract. Although it seems that this bacteria is a part of oral bacterial population of some animals (Bailie et al., 1978), but reports concerning its isolation from animal respiratory tract are rare. Likewise, there are no reports on the isolation of Neisseria spp in camels. Our study high isolation showed rate of staphylococci from camels (52.7%) compared to 26.2% coagulase negative staphylococci, 2.6% staphylococcus *aureus* (Shigidi, 1973), and 24.8% in lungs (Al-Doughaym et al, 1999).

We had no success for isolation of Pasteurella spp. or Manheimia hemolytica from studied anatomical sites, whereas Mergra et al. (2006) reported the isolation of these bacteria from respiratory tract of healthy goats. In most other mammals also they may be a part of respiratory tract microbiome (Mohamed and Abdelsalam, 2008). In present study Bacillus spp were isolated from all examined sites while Shemsedin, (2002) isolated it only from camel's lung.

Streptococcus was one of encountered genera (4.5%), Buxton and Fraser, (1977) indicated that streptococcus species are widely distributed in nature and live as a commensals in the respiratory tract of many species of domestic animals. Isolation of Lancefield group B streptococci from nasopharynx of healthy camels was reported by Younan and Bornstein, (2007).

The present study has indicated that several bacterial genera inhabit the respiratory passageways of apparently healthy camels. Considering factors which may subject the animals to stresses, the pathogenic role of these apparently commensal organisms could be important. We recommend a detailed study to look into anaerobic bacteria and mycoplasmas inhabit camels.

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