Original Article

Aerobic Bacterial Flora In The False Vampire Bat Megaderma Lyra

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Abstract

Bats play an important ecological role all over the world, and their presence is thought to be an indicator of a healthy ecosystem. Microorganisms play an important role in maintaining the delicate ecological balance of the earth. But frequently, they have a negative public image as a vector of disease-causing microbes. Megaderma lyra, a common carnivorous bat, was chosen to study the impact of their microbial flora. The oral cavity and intestinal bacterial florawas collected. Nutrient agar, Blood agar, MacConkeyagar, and Salmonella shigella agar culture medium were prepared to identify the aerobic organisms. Bacterial species isolated from M.lyra harboured twelve species belonging to three different families; ten from Enterobacteriaceae, one from Streptococcaceae and one from Pseudomonadaceae. Studies on the oral aerobic flora of this bat species revealed, that they have the same microbial flora as any mammal, including humans. Dietary items of carnivorous bats are also a major influencing factor on bacterial oral cavity bacterial floral composition. This work made an attempt of focus the bacterial flora of M.lyra.

Key Words: Microorganisms, Megaderma lyra, Culture medium, Aerobic flora, Oral Cavity.

INTRODUCTION: Insectivorous bats represent 70% of all bat species and are widely distributed [1]. They play an importantecological role in the transfer of nutrients in ecosystems[2]. Microorganisms are ubiquitous in nature. Every day we have intimate contact with an enormous number and variety of microorganisms. Microorganisms play an important role in preserving the earth's delicate ecological balance. In a gram of soil, approximately 10^8bacteria are present and these are estimated to represent over10,000species. There are more 10^{30}bactera on earth, compared with fewer than 10^{10} humans[3].Among the bio control agent, the carnivorous bat is one of the pest controllers of an agro ecosystem[4]. This bats roost in caves, temples, forts, old ruined buildings, underground tunnels and shallow soapstone mines[5,6].Megaderma lyra is primarily carnivorous, feeding on large insects, spiders, and small vertebrates such as bats, birds, rodents, and fish. Prey are detected either by passive listening or with the help of echolocation, then gleaned from the substrate and removed to a night roost where they are consumed[7,8,]. The human body contains large number of bacteria; 500-1000 different species, most of them performing tasks that are useful for human survival[9]. Paster et al., [10] is reported that up to 500 species can be found as normal oral flora. The initial part of the colon, cecum, has 10^8 bacterial cells per milliliter and many of these species are different from those found in the mouth [11]. Vander Waaij [12] is reported that they even stimulate the immune system and inhibit the entry of harmful bacteria.Bats as mammals exhibit a marvelous symbiosis with microorganisms. Earlier studies on bats also revealed that bacteria have a symbiotic association with bats and help them in odour production, digestion and disease resistance [13,14,15]. People fear that temple roosting bats give a large exposure to the public with bat zoonotic microbes. This initiated a strong belief that bats transmit diseases and because of this reason in India people never like bats. Lack of bat- bacterial association studies with Indian tropical species and the awareness regarding bat biology and their

ecological role is the main drawback in Indian culture. Since the bat species vary in their dietary relation all bat species including the temple bats are important members in any biodiversity assemblage of the agro and forest-ecosystem. Bats play important ecological roles worldwide and their presence is considered an indicator of a healthy ecosystem. The outcome of the present study about the bat associated microbes especially of temple bat species will help to understand bats better and to remove some of the misconceptions and misunderstandings about bats the existence of bats in the ecosystem.

METHODOLOGY:

1. Study Area:

In the present study area isVenkatachalapathy Thirukoil has located at Krishnapuram (8° 41' N lat 77°37'E long) were selected for this study. During the study visit the single bat was captured at from their roosting site by mist netting (Avinet NY 18m wide, 38mm mesh 3m high and 6 shelves). According to biodiversity conservation status of IUCN, this bat is under least concern and it is not in the scheduled animal category. The captured adult bat was assessed as healthy on the basis of physical examination and the single bat was sacrificed for bacterial analysis.

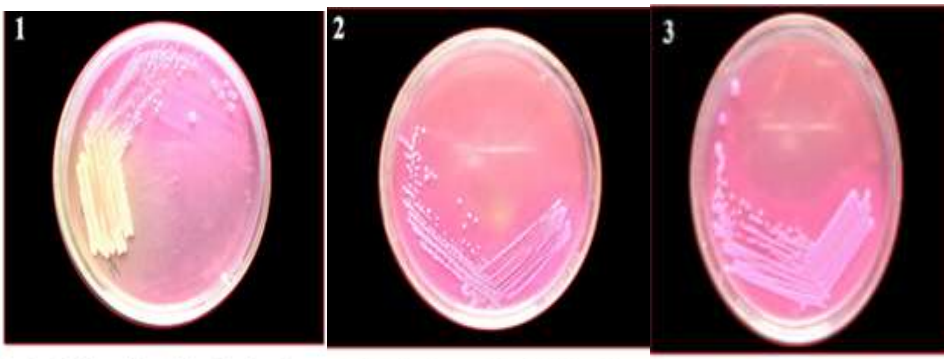
2. Sample Collection:

Sterile swabs were used to collect the bacterial flora of oral cavity. The intestine was dissected aseptically. Swabs and intestines were inoculated in peptone water, alkaline peptone water and selenite F broth for enrichment. After enrichment, cultures were made for aerobic organisms on Nutrient agar (Basal media), MacConkey agar (Moderately selective and differential media), and Salmonellashigella agar (Highly selective Media). The culture plates were incubated at 37 ºC for 24 hours. The colonies were picked up and were completely characterized by standard bacteriological procedures[16].

RESULT:

The aerobic bacterial species were isolated from the samples collected during the study period. The Plate and Table depicted the bacterial species isolation and percentage of bacterial flora. M.lyra harboured twelve species belonging to three different families; ten of them were from Enterobacteriaceae,onefrom Streptococcaceae (Group-D)and one from Pseudomonadaceae. In all the studied bat species, bacterial members of the family Enterobacteriaceae dominated the other bacterial isolates.The results of the present study clearly indicate that, there is a slight disparity in their normal flora. E. coli, the enterobacteria and Enterococcus faecalis of the enterococci group were isolated throughout the study period. Isolation of E. coli, Klebsiella oxytoca, K. pneumoniae, Citrobacter freundii, C. diversus, Proteus vulgaris, Enterobacter cloacae and Pseudomonas aeruginosa both from the oral cavity and intestine indicates that this bacterial assemblage is involved in a mutualistic relationship.From the results obtained, it is clear that most of the members of Family Enterobacteriaceae were isolated from the bat species selected for the present study and they show a slight difference in their normal bacterial flora by harboring Salmonella sp in carnivorous bat, M.lyra.

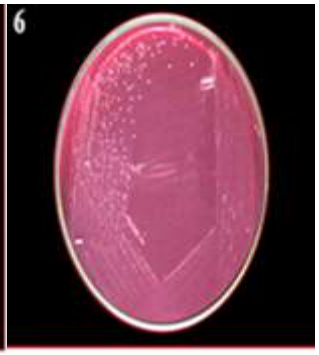
Plate:Bacterial species isolation



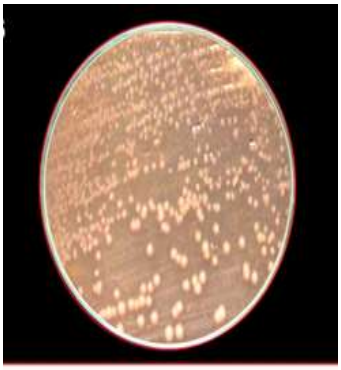
Escherichia coli on MacConkey Agar *Citrobacter on MacConkey Agar* *Klebsiella on MacConkey Agar*

Proteus on Nutrient Agar

Pseudomonas on Nutrient Agar

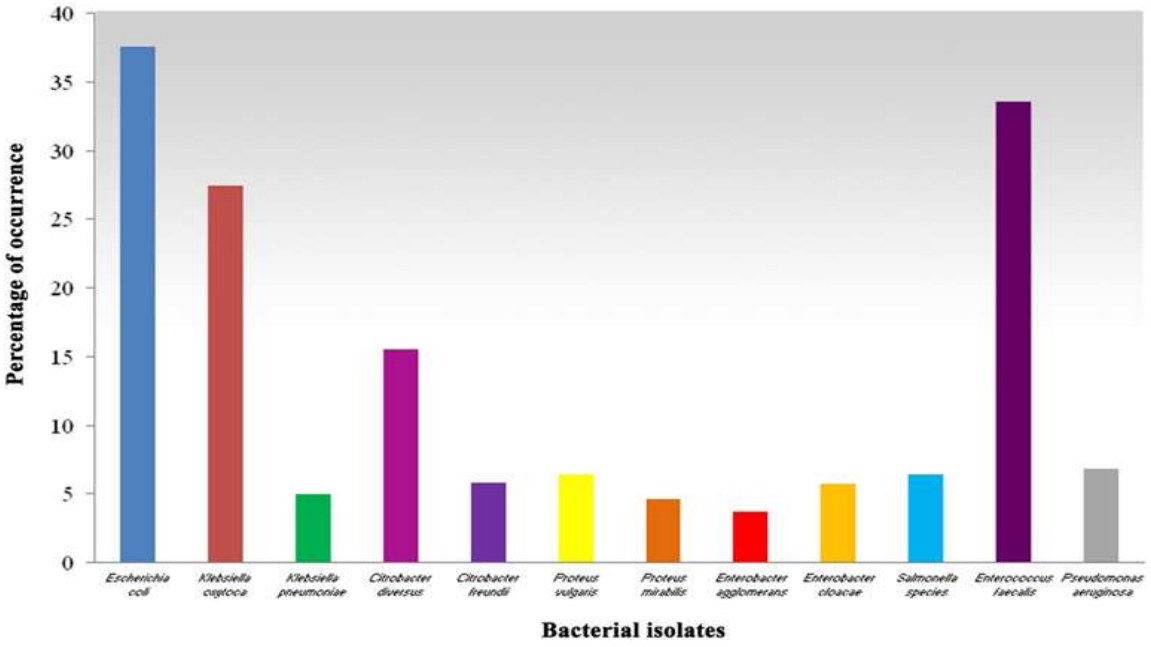


Enterococcus faecalis on MacConkey Agar



Salmonella

Table : Percentage of occurance of aerobic bacterial species incidence in Megaderma lyra.



DISCUSSION:

Bats are gregarious and their roosting sites are contaminated by the faecal pellets, urinary and glandular scent markings. The bacterial flora indigenous to bat species is the normal symbiotic bacterial flora very similar to that of any mammalian species including man[17]. Documented that up to 500 bacterial species are found as normal flora in human body and are beneficial to man. Bacterial symbionts found in insects can significantly impact the biology of their host[18]. Inthe studied carnivorous bat, members of the bacterial family Enterobacteriaceae were the dominant group among the bacterial isolates. In general, members of this bacterial family are called enteric organisms because they so often reside in the gastrointestinal tract of animals[19]. Enterobacteriaceae is one of the largest families including a large number of species. These bacteria are rod-shaped, gram-negative, facultative anaerobes, fermenting sugars to produce lactic acid and various other end products.This bacterial characterization aids in the conversion of the high protein content in the food of the bats. The studied bat species are carnivorous; they consume a lot of Lepidoptera order insects[20].The Enterobacteriaceae members within the bats convert these dietary items into the nitrite rich guano. This transformation enriches the bat guano as a very good natural fertilizer, the "black gold". A few species of Enterobacteriaceae are also found in water and soil [21].In the present study, among the isolated aerobic bacterial species, under the family Enterobacteriaceae the predominant genera were Escherichia coli in the bat. E. coli is believed to be one of the most common bacterial floras in the intestinal tract of vertebrates. Furthermore, E. coli plays an important role in the synthesis of some vitamins (B, K and C) and utilization of food[22]. Without the presence of E. coli even the human gastrointestinal tract could be overgrown by harmful bacteria and fungi. Bat as a mammal is not an exception to this. M. lyra bat species posses a high percentage of E. coli as their major aerobic bacterial.Insectivorous bats' dietary items are also one of the major influencing factors on bacterial floral composition. A few studies regarding insect associated bacterial flora are as follows: houseflies[23], larvae of Culex quinquefasciatus, Psorophoracolumbiae[24] and cockroaches [25]. They have documented the following different Enterobacteriaceae members: E. coli, Klebsiella pneumoniae, K.ozonae, Citrobacter freundii, Enterobacter cloacae,E. agglomerans, Proteus sp, and Serratia marcescens and other family members like Pseudomonas aeruginosa species.Earlier studies about the bacterial assemblage in a few lepidopteran insect pests revealed the presence Pseudomonas fluorescens, and Streptococcus faecalis[26,27].Next to E. coli, Klebsiella oxytoca (Enterobacteriaceae) is the second major species in the bacterial assemblage of bat species.After studying 642 mammalian hosts from Australia, have confirmed that K. oxytoca is one of the frequent inhabitants of the oral cavity to intestinal carriage[28].

Normally, this microbe is an associate of insects and some of these insect possessors are included in the dietary items of the bats [29].The bat species of the present study possess Enterobacter agglomerans, E. cloacae, and except M. lyra species also possess Enterobacter asburiae, E. aerogenes sp. as their normal flora and symbiotic associate.

The enterobacteriaceae, Psudomonadaceae, Salmonella was isolated only from M. lyra. Even though M. lyra as a carnivorous bat comes under the group of insectivorous bats, it prefers to select small vertebrates like rodents, amphibians, lizards, small mammals, birds and fishes as its food item[30][8].Earlier studies have proved that reptiles and amphibians harbour Salmonella as a natural part of flora. It is noteworthy that Salmonella has an association with the household lizard gecko [31,32] and wild tortoises[33]. Results of the present study clearly show that the bat species have Enterococcus faecalis and Pseudomonas aeruginosa as their normal oral cavity to intestinal flora. Enterococci are widely distributed in nature. The oral cavity to intestinal tract of animals and humans is the natural habitat of these organisms. Enterococci naturally occur in large numbers in the intestines of mammals, birds, reptiles and insects. But,Salmonellafrom M. lyra, the study on their dietary habits will prove that the food habits of an animal has an immense impact on their bacterial associates. The dietary habit analysis of the bats confirmed that their dietary items include insects of the orders Lepidoptera, Diptera, Hemiptera, Coleoptera, Tricoptera etc..,[20].It is also evident that frogs, toads, lizards and other reptiles have Salmonella as their normal flora.This facilitates the entry of Salmonella as its normal oral cavity to intestinal flora of carnivorous bat.

CONCLUSION:

The present work has contributed information about the normal aerobic bacterial flora in carnivorous bat and it suggests that they are similar to those of human beings.The majority of bacteria isolated from bats are harmless and some are beneficial. Certain bacteria can be beneficial to some animals and pathogenic to others.Bacteria that are normally harmless can become lethal under certain conditions. Bacteria help the host in digestion, production of vitamins and protection from competing pathogens. This work concludes that the normal bacterial flora of the selected bat species, M. lyra are similar to that of any other mammal.

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