

## Fungal Pathogens Isolated From Cyclical Migratory Bats In Jos Metropolis.

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**Abstract:** Bats are distributed worldwide and are among the most diverse species rich mammals on earth. This work was aimed at determining the spectrum of fungal pathogens associated with migratory bats in Jos metropolis. Ninety three bats were randomly captured from their roosting areas in Jos, euthanized and the entire gastrointestinal contents were inoculated into nutrient broth and subsequently subcultured onto sabouraud dextrose Agar (SDA), examined macroscopically and microscopically for fungal growth. A total of 103 isolates were documented as *Penicillium* species 14(13.6%), *Aspergillus* species 42(40.8%) *Torulopsis candida* 22(21.4%), *Rhodotorula rubra* 15(14.6%), *Cryptococcus neoformans* 5(4.9%), *Trichophyton* species 5(4.8%). This study was conducted within the frame work of determining emerging infectious pathogens associated with human and animals. The relevance of public health and emerging infectious disease transmission in migratory bats has been highlighted.

**Key words:** Fungi, migratory, bats, Jos, Nigeria.

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### I. Introduction

Bats can host a range of potentially zoonotic pathogens. In addition to rabies and other lyssaviruses (Kuzmin et al., 2008b; Streicker et al., 2010), bats have been identified as the likely reservoir for severe acute respiratory syndrome (SARS) coronavirus (Li et al., 2005; Cheng et al., 2007; Vijaykrishna et al., 2007), Ebola (Leroy et al., 2005) and Marburg viruses (Monath, 1999; Peterson et al., 2004a,b; Towner et al., 2007). Most recently, a new distinct lineage of influenza A virus has been discovered in little yellow-shouldered bats (*Sturnira lilium*, family Phyllostomidae) in the Americas (Tong et al., 2012) and a range of paramyxoviruses in bats from four continents (Drexler et al., 2012).

Bats have several unique features that may account for their importance in Emerging Infectious Disease (EID) transmission and sustenance. Bats are the second largest order of mammals. Currently, there are in 1,200 recognized bat species worldwide, accounting for approximately 25% of all mammalian species (Turmelle & Olival, 2009). Bats are also unique in their mobility as they are the only mammals capable of flight, allowing them transmit EID during their foraging flights and during seasonal migrations. This extensive mobility, coupled with roosting plasticity and broad food range, means that bats could transport pathogenic material to many different animal species in various locations per unit time.

Bats have a number of trophic specializations. The majority of bats species are frugivorous or insectivorous. In addition, three bat species (all found in Central and South America) are hematophagous (Vampire bats) (Kuzmin et al., 2011). Frugivorous bats often leave behind half eaten fruits that may be contaminated with pathogenic particles from their saliva. Similarly, insectivorous bats will discard contaminated insect parts which can then be consumed by foraging animals (Wong et al., 2007). Omnivorous bats (such as Phyllostomidae, will consume nectar, plants arthropods and small vertebrates as food sources as necessary. (Kuzmin et al., 2011).

Environmental factors can shape pathogen transmission and spillover into a new species as well; periods of resource limitation may bring together diverse species. During the dry season, primates and bats may come into closer contact as they search for limited food supplies enhancing opportunities for cross species transmission (Wong et al., 2007).

It should be noted that infectious diseases emergence also occurs in non humans hosts, including bats themselves, as a result of ecological changes brought by human activity. For examples the recent epizootic of white nose syndrome (WNS) among several bat species in the North eastern United states may be due to the translocation of a fungus from Europe to North America by humans. (Puechmaille et al., 2010). This work was aimed at determining the spectrum of fungal pathogens associated with migratory bats in Jos metropolis.

## II. Materials and methods

### Sample collection

Ninety three bats were randomly captured from their natural habitats from 3 different locations in Jos, Plateau state.

The bats were transported, euthanized and the entire gastrointestinal tract was removed and chopped up in sterile petri dishes using sterile scalpel blades and forceps. The macerated intestines and contents were plated on Sabouraud Dextrose Agar (SDA) (Fuka biochemika, Germany) plates and incubated aerobically at room temperature (25°C) for 2 weeks.

### Isolation and identification of fungi

The cultural characteristics of the fungal growth were examined macroscopically on the Sabouraud Dextrose Agar plates used. Cultures were incubated at (25-27°C for molds and 37°C for yeast) for 2-3 weeks, aerobically and examined every 3 days. Fungal isolates were identified on the basis of colonial morphology and slide cultures (Baker and Breach, 1980., Brook et al., 2004).

### Sugar fermentation:

Five (5) mls of 2% sugar solution each containing glucose, galactose, maltose lactose or sucrose with a 2% Andrade's peptone was prepared and dispensed into test tubes with inverted Durham's tubes. The pH of the solution was adjusted to 7.2 and then closed with cellulose stoppers. The test tubes were heated for 30 minutes in a steam sterilizer on 3 consecutive days.

Suspected yeast cells were inoculated into each sugar solution and incubated for 48hrs at 37°C. The cultures were inspected for colour change and gas production and recorded.

## III. Results

Of the 93 samples screened, a total of 103 fungal isolates which included *Penicillium* species 14(13.6%), *Aspergillus* species 42(40.8%) *Torulopsis candida* 22(21.4%), *Rhodotorula rubra* 15(14.6%), *Cryptococcus neoformans* 5(4.9%), and *Trichophyton* species 5(4.8%) were isolated. Table 1, shows the frequency and percentage positive fungal isolates.

**Table 1: Frequency of isolation and percentage (%) positive of fungal isolates**

Organism	No. positive	% positive
<i>Penicillium</i> species	14	13.6
<i>Aspergillus niger</i>	15	14.6
<i>Aspergillus fumigatus</i>	17	16.5
<i>Aspergillus flavus</i>	10	9.7
<i>Torulopsis candida</i>	22	21.4
<i>Rhodotorula rubra</i>	15	14.6
<i>Cryptococcus neoformans</i>	05	4.9
<i>Trichophyton tonsurans</i>	03	2.9
<i>Trichophyton mentagrophytes</i>	02	1.9
Total	103	100

## IV. Discussions

The hollow bones allow bats to fly, but as a result they do not have bone marrow as similar to non-volant mammals and must produce B-cells in different locations (Dobson, 2005). Whereas certain basic immunological commonalities are shared among all mammals, certain unique anatomical and physiological parameters peculiar to bats may also help to explain the plethora of agents associated with this mammalian order (Kuzmin et al., 2011). Besides their ecological vagility, bats are considered one of the most social groups of mammals that roost together in very large and dense colonies. This dense clustering of individual provides ample opportunities for fungal, viral and bacterial exchange within bat population as reported by Woo et al, (2009).

The diversity of bat species alone, along with their worldwide distribution, contributes to the biodiversity of their pathogens, as documented in our findings.

In this paper, fungal pathogens associated with migratory bats in Jos metropolis has been documented. The significance of bats as reservoirs of such Emerging Infectious Disease (EIDs) has been increasingly appreciated (Calisher et al., 2006). The majority of studies performed to date have focused on infections of significant public health and veterinary concern. This is similar to the findings of Kuzmin et al., 2011 who documented a spectrum of viral pathogens in bats. In this studies, we did not investigate the presence of viral pathogens. Potentially, bats and human could be independently and simultaneously infected from some other sources. (Kuzmin et al., 2011).

Bats have several unique features that may account for their importance in EID transmission and maintenance. Bats are the second largest order of mammals (Kuzmin et al., 2011). Currently there are 1,200 recognized bat species worldwide accounting for approximately 25% of all mammalian species (Turmelle and Olival, 2009). Bats are unique in their mobility as they are the only mammals capable of flight, allowing them to transmit EIDs during their foraging flights and during seasonal migrations. This extensive mobility, coupled with roosting plasticity and broad food range, mean that bats could transport micro-organisms to many different animal species in various locations per unit time; this is a finding which buttresses our studies as documented by Woo et al. (2009).

Increased mobility of people, animal and goods allows for the rapid spread of novel diseases and outbreaks of existing diseases, hence, the cross continental spread of infectious diseases is most likely to occur through flight net-works by bats as reported by (Bobashev et al., 2008). This is further buttressed by our findings of spectrum of fungal pathogens.

The spectrum of fungal pathogens isolated for migratory bat in Jos is similar to the findings of Kosoy et al (2010) who documented the long-standing relationships with certain fungal disease such as histoplasmosis.

Given the potentially devastating effects of these emerging diseases on public health and wildlife conservation (e.g. EBOV and gorillas; Bermejo et al., 2006), it is crucial that we improve our understanding of how bat ecology may influence disease dynamics and their propensity to serve as reservoirs for emerging pathogens (Messenger et al., 2003; Calisher et al., 2006; Wong et al., 2007).

It is anticipated that, with the advent of modern molecular tools and increase scientific activities in this field, additional bat EIDs with public health, veterinary and conservation implications will be uncovered and better understood with practical effective prevention and control modalities necessary for application in the near future.

## V. Conclusion

Bats exists in a large variety of distinct ecologic niches. Many bat species roost near humans, which is of particular interest for research on bat to human transmission of potential zoonotic pathogens. More over migratory bats could act as long distance vectors for several infectious agents. Bats – associated EIDs appear as a “tip of the ice berg” regarding a much more dynamic complex of interacting variables (Kuzmin et al., 2011). Only once well-parameterized models of systems are developed, can perturbations, such as through harvesting or restricting bat movement, be simulated to attempt to predict alterations in infection dynamics. Empirical evidence can be more difficult to produce, in particular because control studies may be difficult to perform, particularly in migratory species, but attempts should be made.

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