



# Potential of House Mice in Harboring Multiple Bacteria and Threats to Public Health

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**Abstract** | The aim of study was to explore the potential of house mice in carrying bacterial populations. For this purpose, a total of 100 stool samples were collected directly from intestine of individual (n=100) mice. To isolate and characterize bacteria, these samples were cultured on different types of growth media and isolates were identified based on rate of growth, characteristics of colonies, gram staining, acid fast staining, biochemical characteristics and chromogen production. Cumulative outcome of these properties guided the identification of *Mycobacterium kansasii* in 10% samples, *Mycobacterium chelonae* in 8%, *Mycobacterium scrofulaceum* in 7%, *Salmonella typhimurium* in 15%, *Escherichia coli* in 10%, *Shigella dysenteriae* in 30%, *Proteus vulgaris* in 5%, *Pseudomonas aeruginosa* 2% and *Klebsiella pneumoniae* in 3%, *Nocardia asteroides* in 15%, where as *Vibrio cholerae* in 5% of tested samples. Many of these bacteria are important zoonotic pathogens. Therefore, house mice may act as important source of disease to humans. These results highlight the circulation of multiple bacterial populations in Iraqi house mice for the first time.

**Keywords** | Mice, Bacteria, Human

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## INTRODUCTION

The house mouse (*Mus musculus*) is a small mammal and mainly lives in close vicinity with humans and animals. House mice can notoriously contaminate food and water with their feces and may transmit diseases. The infectious agents in house mice may not result in clinical disease but may persistently shed pathogens in feces. In fact, these mammals are associated with subclinical disease and their dropping cause illness in human and other animals in vicinity (Treuting et al., 2012, Nathaniel et al., 2017). Changes in ecological dynamics and food webs enable house mice to establish pathogen populations that expand with human societies (Bonhomme et al., 2011, Frankova et al., 2016). However, any change in behavior and ecology may cause acute impact on the host through increasing in resident bacteria in the small intestine. (Nathaniel et al., 2017). Infection of mice with bacteria such as *Staphylococcus aureus* and *Escherichiacoli* release virulent factors that ef-

fect the infertility of mice (Sharma et al., 2017). It has been proposed that mice can transmit Lymphocytic choriomeningitis virus (LCMV) an infection that may cause lethal impact in pregnant women (Bonthius, 2012). Additionally, mice can transmit endemicty phusrickettsial, chickenpox (Eremeeva et al., 2008), *Leptospirosis* through urine (Brown and Prescott, 2008) and *mycobacteria* through feces. Recent genetic studies in mice indicate that tuberculosis in mice is under multigenic control (Collette et al., 2017). Mice can be infected with *mycobacteria* through ingested food, contaminated with the feces of infected animals or humans. These pathogenic and opportunistic *mycobacteria* resistant to acid and can pass through the stomach of mice without being digested and *mycobacteria* can survive in tissues and organs in mice and can spread over long distances with the migration of mice (Biet et al., 2005). *Salmonella typhi*, causative agent of Typhoid fever, a systemic disease, can also be transmitted by mice as a consequence of systemic bacterial infection (Doutsch et al., 2016). Another study

identified that mice carry *Salmonella* spp and can transmit to humans via the fecal-oral route. *Shigella* produce intestinal damage and bloody mucoid dysentery represents a major threat public health in humans and animal (Benoit and Marteyn, 2016). Nocardiosis is caused by the environmentally actinomycete *Nocardia*. It caused an emerging pyogranulomatous disease causing severe illness in humans and animals worldwide (Munoz et al., 2007). *Escherichia coli* is a major cause of diarrhoea and mortality in low-income countries. *Vibrio* is a facultative anaerobes mainly causing gastroenteritis and septicemia (Thompson et al., 2005) where as *Proteus* is opportunistic pathogen causing septic infection (Jessica et al., 2015). *Klebsiella* cause pneumonia, urinary tract infections, septicemia meningitis and diarrhea (Rashid and Ebringer, 2007).

These studies cumulatively highlight the potential of mice in harboring a plethora of pathogens and thus propose mice as a threat to public health (Guansheng et al., 2017; Claire et al., 2017; Meerburg et al., 2007). It is therefore imperative to investigate the dynamics of pathogens that are circulating in house mice in Iraq where these are widely distributed and are housed in close vicinity to human and animals.

## MATERIALS AND METHODS

Al-huria city of Baghdad was chosen for the study and one hundred house mice were captured to collect feces directly from intestine of mice. These samples were then diluted in PBS and were individually inoculated in enrichment broth media for 24 hr at 37 °C before cultured on different type of media (MacConecky agar, Eosin methylene blue agar, Xylose lysine deoxycholate agar, Salmonella-Shigella agar, Thiosulfate-citrate-bile salts-sucrose agar, Blood agar). These selective and enrichment media were chosen based on the possibility of bacterial population in mice. The suspected pathogens were identified by growth of colony in gram staining, motility and different biochemical reaction. All feces samples were also cultured on Lowenstein-Jenson media after using decontamination (5%), oxalic acid, NaOH (4%) and incubated at 37°C for eight weeks. Diagnosis of mycobacteria was based on the rate of growth, characteristics features of bacterial colonies, acid-fast stain and the ability to production of chromo genes (Quinn et al., 2006).

## RESULTS

Based on chemical characteristics, biochemical tests, growth features, a number of bacterial were identified (Table 1). Several collected samples were positive for more than one bacteria and thus represent a dynamic range of multiple pathogen harbored in these house mice. A dif-

ferential percentage of positivity was mapped within these samples, which ranged from 2-35%. Cumulative results demonstrated that *Mycobacterium kansasii* (10%), *Mycobacterium chelonae* (8%), *Mycobacterium scrofulaceum* (7%), *Salmonella typhimurium* (15%), *Escherichia coli* (10%), *Shigella dysenteriae* (30%), *Proteus vulgaris* (5%), *Pseudomonas aeruginosa* (2%), *Klebsiella pneumoniae* (3%), *Nocardia asteroides* (15%), and *Vibrio cholerae* (5%) were amongst the most common pathogens prevalent in sampled mice.

**Table 1:** Types of bacteria isolated from faecal samples of mice

Type of bacteria	Number of positive isolates	Percentage positivity
<i>Mycobacterium kansasii</i>	10	10%
<i>Mycobacterium chelonae</i>	8	8%
<i>Mycobacterium scrofulaceum</i>	7	7%
<i>Salmonella typhimurium</i>	15	15%
<i>Escherichia coli</i>	10	10%
<i>Shigella dysenteriae</i>	30	30%
<i>Proteus vulgaris</i>	5	5%
<i>Pseudomonas aeruginosa</i>	2	2%
<i>Klebsiella pneumoniae</i>	3	3%
<i>Nocardia asteroides</i>	15	15%
<i>Vibrio cholera</i>	5	5%

## DISCUSSION

House mouse are the most dangerous rodent species and cause multiple damages to human resources by feeding on crops and stored commodities and by their faecal and urine contamination (Frankova et al., 2016). The present study revealed prevalence of different bacterial species in the feces of house mice. Generally, results of this study are in agreement with previous finding that mice tuberculosis excreted through the faeces of infected animals and this maybe a source of infection for vertebrates and lead to spread of tuberculosis (Biet et al., 2005). In another study, it was identified that transmission of *mycobacteria* may occur through inhaling of aerosolized fecal material. Pathogenic *mycobacteria* in house mice were found in organs and excreted in their feces. Therefore, it is plausible that the infection occur through inhalation or ingestion of contaminated material, ectoparasites and animal bites (Fischer et al., 2000). In another study, based on 708 small mammals, different type of *Mycobacterium* species (*M.parascrofulaceum*, *M.chimaera*, *M. arupense*, *intracellulare* where identified in mice (Lies Durnez et al., 2008).

*Salmonella* infection in mice may come from different sources: contact with faeces of infected wild animals or human (Hulst et al., 2004; Guard-Petter et al., 1997). Previous studied have found the presence of *S.enteritidis* in spleens

and livers of house mice and thus can acquire infections from in different parts in livestock houses. On the other hands, *Salmonella* from mice can come from faeces of infected wild animals (Hilton et al., 2002). Three *S. typhimurium* bacteria were isolated from feces of mice (Søndberg et al., 2016). *S. typhimurium* bacteria were isolated from feces, livers and spleens of mice. Another study found that house mice were positive for *salmonella* enteric serotype enteritidis (SE) in house mice with a percentage of 3.7%. The results of other study indicate that *Escherichia coli* can be isolated from intestinal contents (Narayanan et al., 2017). There are evidences that *Shigella* organisms can be isolated from mice and may produce intestinal damage and bloody mucoid dysentery in humans (Ahmed et al., 1990). It has been found that mice can be infected with the eight strains of bacteria, which are localized to different compartments (Martin and Polz, 2004; Meerburg et al., 2009).

Not only human, house mice also threaten other species of animals such as birds. Mice can transmit *Klebsiella spp.*, *Staphylococcus intermedius*, *Escherichiacoli* and *Pseudomonas spp.*, *Enterococcus spp.* (Dagleish et al., 2017) in birds. House mice are recognized carrier of various infective agents and these agents may have zoonotic potential (Roble et al., 2012). In conclusion, this study determined the prevalence of pathogenic bacteria in house mice. These infected mice contaminate their surrounding environment, and may risk public health. Therefore, there is need to not only explore the full spectrum of pathogen in house mice but also to increase awareness in communities to consider isolation and decontamination of possible contaminated premises and food items.

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## CONFLICT OF INTEREST

No conflict of interest in this study.

## AUTHORS CONTRIBUTION

All the works in this research was performed by Maysoun Sabah Abbas.

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