

Diversity of Culturable Enteric Bacteria Among International Tourists Visiting Phuket, Thailand

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Introduction

Pathogen detection among international tourists visiting Thailand is necessary, as food is one of the primary factors contributing to diarrhea. The objective of this study was to determine the diversity of gut bacteria among travelers (except our neighboring countries) visiting Phuket, the most popular tourist attraction area in Southern Thailand

Materials and Methods

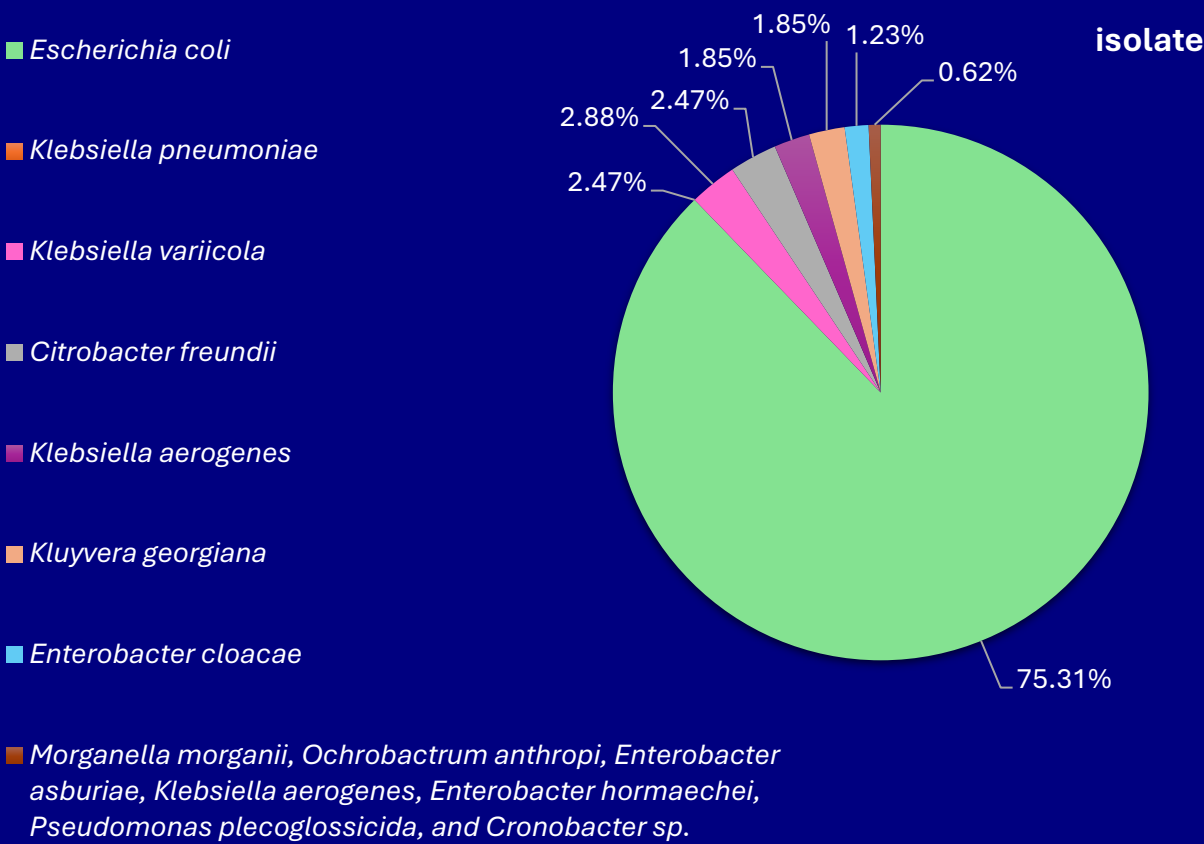
Stool samples were collected from the participants. Enteric pathogens were isolated from the samples by streaking on MacConkey agar, *Salmonella-Shigella* agar, and thiosulfate citrate bile salt sucrose agar. All culture plates were incubated at 37°C for 24 hours. After incubation, the colonies were sub-cultured onto tryptic soy agar (TSA) to obtain a pure colony for stock storage at -80°C. Bacterial identification was performed using Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrophotometry (MALDI-TOF MS).

Results

A total of 162 isolates from 125 stool samples were isolated and identified. *Escherichia coli* (n = 122, 75.31%) was the most frequent species, followed by *Klebsiella pneumoniae* (n = 18, 11.11%). A few isolates were classified as *Klebsiella variicola* (n = 4, 2.47%), *Citrobacter freundii* (n = 4, 2.47%), *Klebsiella aerogenes* (n = 3, 1.85%), *Kluyvera georgiana* (n = 3, 1.85%), and *Enterobacter cloacae* (n = 2, 1.23%). Furthermore, *Morganella morganii*, *Ochrobactrum anthropi*, *Enterobacter asburiae*, *Klebsiella aerogenes*, *Enterobacter hormaechei*, *Pseudomonas plecoglossicida*, and *Cronobacter* sp. were only found in one isolate (0.62%).

Discussion

This study revealed the diversity of enteric bacteria among international tourists visiting Phuket. *Escherichia coli* was the predominant species, which is expected as it represents both commensal and diarrheagenic strains. The detection of *Klebsiella pneumoniae* and *Enterobacter cloacae* is of concern, since these organisms are often associated with antimicrobial resistance. The recovery of less common species, such as *Morganella morganii* and *Ochrobactrum anthropi*, may indicate exposure from food or environmental sources during travel. However, unculturable pathogens and other bacteria may play a crucial role in altering the gut microbiota of tourists. Therefore, a metagenomic study is warranted to investigate this further.



Conclusion

Our findings provide a preliminary overview of the gut microbial landscape associated with international travel in Phuket, Thailand, which may be beneficial for public health surveillance, disease prevention, and the development of targeted interventions.

references

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