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Occurrence of *Escherichia coli* in Wildlife from Different Habitats of Sarawak, Malaysia

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ABSTRACT

This study was carried out to assess the occurrence of *Escherichia coli* (*E. coli*) in the bats, birds and rodents as representative of wildlife from different habitats in Sibu and Kapit, Sarawak, Malaysia. A total of 682 swab samples were collected from wildlife hosts and screened for the bacteria *E. coli* and *E. coli* O157:H7 using standard microbiological methods and molecular techniques. The overall occurrence rates of *E. coli* among these hosts were 14%, 17% and 54% for bats, birds and rodents, respectively. The occurrence of *E. coli* was the highest in rodents regardless of the habitats. Isolated *E. coli* were then screened for *E. coli* O157:H7 by using a multiplex PCR with four primer pairs targeting for Shiga toxin producing genes (*slt*-I and *slt*-II), and the genes involved in biosynthesis of O157 antigen (*rfb*E) and H7 antigen (fliC$_{H7}$). *slt*-I, *slt*-II and *rfb*E genes were not detected in any of the *E. coli* isolates. However, the gene encoding for H7 antigen was detected in 23 *E. coli* isolates. This indicated that *E. coli* O157:H7 strain was not detected in the wildlife studied. Absence of *E. coli* O157:H7 in the wildlife studied indicated these wild animals do not serve as an important reservoir of *E. coli* O157:H7. However, precautions have to be taken as other group of pathogenic *E. coli* may pose a zoonotic risk for humans and other animals.

Keywords: *Escherichia coli*, occurrence, Sarawak, wildlife

INTRODUCTION

Escherichia coli belong to the family *Enterobacteriaceae* and is part of the normal microflora of the gastrointestinal tract of mammals and birds. However, some strains are identified as pathogenic *E. coli* by their ability to possess specific virulence factors and specific toxin-encoding genes (Nataro & Kaper, 1998). Virulence factors for *E. coli* O157:H7 include the production of one or more shiga-toxin (Mead & Griffin, 1998). Enterohemorrhagic *E. coli* O157:H7 are zoonotic pathogens associated with severe human illness such as hemorrhagic colitis, hemolytic uremic syndrome and thrombocytopenic thrombotic purpura (Caprioli *et al.*, 2005).

E. coli O157:H7 was first recognized as a pathogen in 1982 during an outbreak of hemorrhagic colitis caused by the consumption of undercooked meat in Oregon and Michigan (Riley *et al.*, 1983). Ground beef, cattle and other bovine sources have been identified as the main natural reservoir for *E. coli* O157:H7. Birds and rodents have also been reported to harbour *E. coli* O157:H7. For example, Wallace *et al.* (1997) reported the isolation of *E. coli* O157 from wild birds in Morecambe Bay and Lancaster, UK which implicated that wild bird can serve as potential vectors for the dissemination of *E. coli* O157:H7. Other animals such as swine in the United State also harboured potentially pathogenic *E. coli* O157 (Feder *et al.*, 2003).

Polymerase Chain Reaction (PCR) assay represents good alternative to traditional typing methods for the diagnosis of Shiga toxin producing *E. coli* due to their simplicity,

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