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Detection of *Escherichia coli* O157:H7 in Wildlife from Disturbed Habitats in Sarawak, Malaysia

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ABSTRACT

This study was carried out to assess the occurrence of *Escherichia coli* and to detect the pathogenic strain *Escherichia coli* O157:H7 in birds, bats and rodents from disturbed habitats comprising of two urban forests and an oil palm plantation habitats located along the Rejang Basin, Sibu in the state of Sarawak, using both standard microbiological and molecular techniques. A total of 105 bird hosts, 44 of rodent hosts and 84 bat hosts represented 48 species of birds, one species of rodent and ten species of bats were screened for the presence of *Escherichia coli*. The representative isolates were cultured on a highly selective agar, Cefaxime-tellurite sorbitol MacConkey agar for the detection of *Escherichia coli* O157:H7. From the microbiological analysis, the overall occurrences of *Escherichia coli* in the hosts were 43% in rodents, 18% in birds and 11% in bats. The isolates were tested for the presence of pathogenic *Escherichia coli* O157:H7 strain by multiplex PCR method targeting the *slt-I*, *slt-II*, *rfbE* and fliC_{H7} genes. The *slt-I*, *slt-II*, *rfbE* genes were not detected in any of the *E. coli* isolates. This study indicated that bats, birds, or rodents from these habitats in Sarawak did not serve as an important reservoir of *Escherichia coli* O157:H7 and thus were of no risk in the epidemiologic cycle of emerging enteric bacterial zoonoses in the state of Sarawak, Malaysia.

Key words: E. coli, occurrence, multiplex PCR, disturbed habitats, Sarawak

INTRODUCTION

Wildlife is well-known to be involved in most of the zoonotic diseases (Kruse et al., 2004). The zoonotic agents, typically various bacteria, carried by wildlife, serves as the major reservoirs for microbial transmission to both human and domestic animals. Outbreaks of zoonoses have recently received increased attention worldwide due to their major impact on human health, agriculture production, wildlife-based economies and wildlife conservation (Chomel et al., 2007). Wild animals are thought to be the source of more than 70% of all emerging infections (Kuiken et al., 2005). According to World Health Organization (2008), millions of people are infected by zoonotic diseases every year.

Enterobacteriaceae are among the best-characterized group of microflora in the gastro-intestinal tract of wildlife. The Enterobacteriaceae and Escherichia coli (E. coli) are among the most common

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