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Isolation and Characterization of Antibiotic Resistant Bacteria from Swiftlet Feces in Swiftlet Farm Houses in Sarawak, Malaysia

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There is a growing concern on the occurrence of antimicrobial resistance. Development of multiple antibiotic resistant bacteria has overtaken new drug development and threatened the patients with untreatable infections. This study was conducted to isolate and characterize the antibiotic resistant bacteria from swiftlet farm houses located in various places including Kota Samarahan, Semarang, Saratok, Betong, Sarikei, Sibul, Sepinang, Maludam, Miri, and Kuching in Sarawak, Malaysia. Five feces samples were collected randomly from each site. One gram of the feces sample was diluted in 9 mL of 0.85% normal saline solution. The diluted sample was plated on Trypticase Soy agar plates and incubated at 37±1 °C for 24 h. A total of 500 bacteria isolates were then identified using 16S rRNA analysis method. Disc diffusion method was then used to confirm the resistant phenotypes of these isolates. The results showed that the means of the bacterial colony count were significantly different ($p < 0.05$) from one another, with the highest \log_{10} CFU g^{-1} (9.22 ± 0.72) found in Kota Samarahan and the lowest \log_{10} CFU g^{-1} (6.03 ± 0.62) in Betong. Besides, the isolated bacteria were identified as 96% Gram positive bacteria and 4% Gram negative bacteria. The isolated bacteria were highly resistant to penicillin G ($36.80 \pm 23.87\%$), ampicillin ($28.60 \pm 17.13\%$), and rifampicin ($16.90 \pm 13.70\%$). Thus, swiftlet feces are good reservoir for a range of antibiotic resistant bacteria which may pose a potential health hazard to human.

Key words: antibiotic resistance, bacteria, isolation, swiftlet feces

Dewasa ini, tingkat kekhawatiran pada munculnya resistensi terhadap antimikroba semakin meningkat. Laju kemunculan bakteri dengan resistensi ganda terhadap antibiotik lebih tinggi dibandingkan dengan penemuan obat baru, sehingga membahayakan pasien-pasien dengan infeksi yang tidak tertangani. Penelitian ini ditujukan untuk mengisolasi bakteri yang resisten terhadap antibiotik dari peternakan walet (swiftlet) yang tersebar di Kota Samarahan, Semarang, Saratok, Betong, Sarikei, Sibul, Sepinang, Maludam, Miri, dan Kuching di Sarawak, Malaysia dan mengkaraktisasinya. Lima sampel feses diambil secara acak dari masing-masing situs. Satu gram sampel feses didilusi dalam 9 mL 0.85% larutan salin normal. Sampel terdilusi kemudian di sebar pada media agar *Trypticase Soy* dan diinkubasi pada 37±1 °C selama 24 jam. Lima ratus isolat bakteri kemudian diidentifikasi berdasarkan urutan 16S rRNA. Resistensi dibuktikan menggunakan metode cakram difusi (*disk diffusion method*). Hasil penelitian ini menunjukkan bahwa nilai rata-rata penghitungan koloni bakteri berbeda secara signifikan ($p < 0.05$) antara isolat satu dengan lainnya. Nilai \log_{10} CFU g^{-1} tertinggi ditemukan di Kota Samarahan (9.22 ± 0.72) sementara nilai terendah ditemukan di Betong (6.03 ± 0.62). Identifikasi juga menunjukkan bahwa 96% isolat adalah bakteri gram positif sementara hanya 4% bakteri gram negatif. Bakteri terisolasi menunjukkan resistensi tinggi terhadap Penisilin G ($36.80 \pm 23.87\%$), Ampisilin ($28.60 \pm 17.13\%$), dan Rifampisin ($16.90 \pm 13.70\%$). Maka dapat disimpulkan bahwa feses walet merupakan sumber bakteri yang resisten antibiotik, sehingga boleh jadi berpotensi berbahaya terhadap manusia.

Kata kunci: bakteri, feses walet, isolasi, resistensi antibiotik

Abuse of antibiotic use is becoming a major concern of today's society. It is also the major cause of antibiotic resistance in clinical practice. Since the discovery of penicillin in the 1940s, the emergence of antibiotic resistance has been highlighted. According to Dorsch (2007), the excessive use of antibacterials in agriculture and clinical therapy has led to the phenomenon of antibiotic resistance. Antibiotic resistan-

ce decreases our ability in treating infections and diseases, affecting the proper infection control, and prevention strategies (Dorsch, 2007). Antibiotic resistant bacteria have also widely spread in the environment. Transmission of resistant gene in these pathogenic bacteria may cause health problem to human. According to Varaldo (2002), *Streptococcus pyogenes* has become resistant to erythromycin and able to enter human respiratory cells. *Staphylococcus aureus* has also been found to be resistant to a variety of antibiotics (Akano *et al.* 2009). Thus, the studies of

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