

Virulence Genes Detection among the Antibiotic Resistant *Enterococcus faecalis* Isolated from Bird Industry in Borneo

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ABSTRACT

The abuse of antibiotics usage in bird industry has resulted in the emerging antibiotic resistant *Enterococci* worldwide which has posed a threat clinically to human health. The present study was to screen and identify the potential virulence agents in antibiotic resistance *E. faecalis* in bird industry in Borneo. *Enterococcus* bacteria collected from the birds' faeces and indoor air inside ten birdhouses were identified to species level and their antibiotic resistance was checked using antibiotic susceptibility discs. Specific primers using PCR assay were intended for the detection of four potential virulence genes (*ace*, *AS*, *efaA*, *geIE*). Out of the thirty-seven *Enterococci* faecal bacteria, the prevailing bacteria found were *Enterococcus gallinacum* (51%), *Enterococcus faecalis* (35%) and *Enterococcus harae* (8%). The airborne bacteria were reported as *Enterococcus faecalis* (5%) and *Enterococcus gallinacum* (1%). Twenty-seven percent of isolates were reported to have Multiple Antibiotic Resistance (MAR) index ≥ 0.2 with 9 distinct resistance patterns formed. *E. faecalis* showed higher resistance to vancomycin. Virulence genes were successfully reported in the 15 *E. faecalis* isolates. Sixty-seven percent of isolates were detected positive for four virulence genes, 27% possessed three (*AS*, *efaA*, *geIE*) genes and 6% possessed two (*ace*, *AS*) genes. Antibiotic resistance and virulence genes detection were significantly correlated. These virulence genes or antibiotic resistance genes were important in the pathogenesis of *E. faecalis* infections.

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