

Characterization of vancomycin-resistant *Enterococcus* isolates from broilers in Selangor, Malaysia.

Abstract

Vancomycin-resistant *Enterococcus* (VRE) is an emerging nosocomial pathogen in humans. The use of antibiotics in human therapy and in the production of food animals has been incriminated in the emergence of this organism. The present study describes the distribution of VRE species, the vancomycin-resistant genes detected, the vancomycin resistance pattern observed, and the genetic diversity of the isolates found in live broiler chickens in Malaysia. Overall 140 VRE were isolated with species comprising *Enterococcus faecalis* (48%), *Enterococcus faecium* (25.7%), *Enterococcus gallinarum* (12.1%), *Enterococcus casseliflavus* (1.4%) and other *Enterococcus* species (12.8%). Vancomycin resistance gene *vanA* and intrinsic genes *vanC1* and *vanC2/3* were detected in the study population. *VanA* was detected in 15 (63.9%) of *E. faecium*, 23 (22.4%) of *E. faecalis* and in 3 (17.6%) *E. gallinarum* isolates. E-test was conducted on randomly selected 41 of the isolates and the minimum inhibition concentration (MIC) of vancomycin for five (11.9%) of tested isolates is more than 256µg/ml. Genotypic analysis using random amplified polymorphic DNA (RAPD) showed genetic diversity within the *Enterococcus* species.

Keyword: *Enterococcus*; Vancomycin-resistant *Enterococcus*; Broiler; Selangor.