

Species distribution and resistance phenotypes of vancomycin-resistant enterococcus isolated from pigs in Pulau Pinang, Malaysia

Abstract

Vancomycin-resistant enterococci (VRE) are important nosocomial pathogens. The extensive use of avoparcin as a growth promoter in poultry and pigs is the hypothesized factor for the emergence of vancomycin resistance in enterococci in animals. As pork is one of the major protein sources for 30% of Malaysians, the present study was conducted to elucidate the role of pigs in the epidemiology of VRE. In this study, 220 rectal swabs were collected from pigs at 12 pig farms in Pulau Pinang. The study found 10 of 12 farms (83.3%) and 92 (41.8%) of the sampled pigs were positive for VRE. Of the 92 isolates examined by PCR, *E. faecium* (14%), *E. casseliflavus* (21.7%), *E. gallinarum* (1.1%) and other *Enterococcus* species (63.0%) were identified. VanA was detected in *E. faecium* and *E. gallinarum*. Questionnaire survey indicated that none of the sampled farms had used glycopeptides, either for growth promotion or for therapy. Tylosin, which has also been associated with vancomycin cross-resistance, was used in 41.8% of the sampled farms; however, there was no significant difference ($P>0.05$) between the proportion of VRE detected in the farms which used tylosin to those farms which did not. E-test on selected 49 isolates showed 16.0% of the isolates had $MIC\leq 8$ and 22.0% had $MIC\geq 32$. Single isolates of *E. faecium* and *E. gallinarum*, both possessed the resistance gene vanA, showed very high resistance ($MIC>256$). About 10.0% of the isolates, in which van genes was not detected, had $MIC>32$. In conclusion *E. faecium* and *E. faecalis* were found to be present at a low rate in the pigs sampled in this study. However, detection of vanA with high level of vancomycin resistance ($MIC>256$) highlights the potential public health threat associated with the pigs.

Keyword: Vancomycin-resistant enterococci; VRE; Pigs; Pulau Pinang; Avoparcin