

Genetic variability of vancomycin-resistant *Enterococcus faecium* and *Enterococcus faecalis* isolates from humans, chickens and pigs in Malaysia

Abstract

Vancomycin-resistant enterococci (VRE) have been reported to be present in humans, chickens, and pigs in Malaysia. In the present study, representative samples of VRE isolated from these populations were examined for similarities and differences by using the multilocus sequence typing (MLST) method. Housekeeping genes of *Enterococcus faecium* (n = 14) and *Enterococcus faecalis* (n = 11) isolates were sequenced and analyzed using the MLST databases eBURST and goeBURST. We found five sequence types (STs) of *E. faecium* and six STs of *E. faecalis* existing in Malaysia. *Enterococcus faecium* isolates belonging to ST203, ST17, ST55, ST79, and ST29 were identified, and *E. faecium* ST203 was the most common among humans. The MLST profiles of *E. faecium* from humans in this study were similar to the globally reported nosocomial-related strain lineage belonging to clonal complex 17 (CC17). Isolates from chickens and pigs have few similarities to those from humans, except for one isolate from a chicken, which was identified as ST203. *E. faecalis* isolates were more diverse and were identified as ST4, ST6, ST87, ST108, ST274, and ST244, which were grouped as specific to the three hosts. *E. faecalis*, belonging to the high-risk CC2 and CC87, were detected among isolates from humans. In conclusion, even though one isolate from a chicken was found clonal to that of humans, the MLST analysis of *E. faecium* and *E. faecalis* supports the findings of others who suggest VRE to be predominantly host specific and that clinically important strains are found mainly among humans. The infrequent detection of a human VRE clone in a chicken may in fact suggest a reverse transmission of VRE from humans to animals.

Keyword: Genetic diversity; Vancomycin-resistant enterococcus; Humans; Chickens; Pigs.