

Antibiotic resistance and molecular typing among cockle (*Anadara granosa*) strains of *Vibrio parahaemolyticus* by polymerase chain reaction (PCR)-based analysis

ABSTRACT

Genomic DNA of *Vibrio parahaemolyticus* were characterized by antibiotic resistance, enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR) and random amplified polymorphic DNA-polymerase chain reaction (RAPD-PCR) analysis. These isolates originated from 3 distant locations of Selangor, Negeri Sembilan and Melaka (East coastal areas), Malaysia. A total of 44 (n = 44) of tentatively *V. parahaemolyticus* were also examined for the presence of *toxR*, *tdh* and *trh* gene. Of 44 isolates, 37 were positive towards *toxR* gene; while, none were positive to *tdh* and *trh* gene. Antibiotic resistance analysis showed the *V. parahaemolyticus* isolates were highly resistant to bacitracin (92 %, 34/37) and penicillin (89 %, 33/37) followed by resistance towards ampicillin (68 %, 25/37), cefuroxime (38 %, 14/37), amikacin (6 %, 2/37) and ceftazidime (14 %, 5/37). None of the *V. parahaemolyticus* isolates were resistant towards chloramphenicol, ciprofloxacin, ceftriaxone, enrofloxacin, norfloxacin, streptomycin and vancomycin. Antibiogram patterns exhibited, 9 patterns and phenotypically less heterogenous when compared to PCR-based techniques using ERIC- and RAPD-PCR. The results of the ERIC- and RAPD-PCR were analyzed using GelCompare software. ERIC-PCR with primers ERIC1R and ERIC2 discriminated the *V. parahaemolyticus* isolates into 6 clusters and 21 single isolates at a similarity level of 80 %. While, RAPD-PCR with primer Gen8 discriminated the *V. parahaemolyticus* isolates into 11 clusters and 10 single isolates and Gen9 into 8 clusters and 16 single isolates at the same similarity level examined. Results in the presence study demonstrated combination of phenotypically and genotypically methods show a wide heterogeneity among cockle isolates of *V. parahaemolyticus*.

Keyword: Antibiotic resistance; Molecular typing; *Vibrio parahaemolyticus*; ERIC-PCR; RAPD-PCR