

## Antimicrobial resistance and Plasmid profile of *Vibrio alginolyticus* isolated from Malaysian seawater

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**Abstract :** The present study was aimed to detect the presence of multiple antibiotic resistance, antibiotic resistance genes and plasmid profile of *Vibrio alginolyticus* isolated from seawater and sediment of different beaches in Malaysia. Forty five isolates, including 24 seawater and 21 sediment isolates of *V. alginolyticus* were tested against 14 antibiotics for the antibiogram profile and the presence of the plasmids. Polymerase chain reaction (PCR) was conducted to elucidate the presence of 7 antibiotic resistance genes including Streptomycin resistance (*strB*),  $\beta$ -lactamase resistance (*blaP1*), Chloramphenicol Resistance (*floR*), Tetracycline Resistance (*tetA*), Erythromycin resistance (*ermB*), Quinolone resistance protein (*qnrA*) and Aminoglycosides resistance (*aac(3)-IIa*). Antibiotic resistance studies revealed that in seawater isolates, the highest percentage of antibiotic resistant was obtained against erythromycin E and penicillin P (100%), whereas the lowest antibiotic resistant percentage was obtained from both chloramphenicol C and nalidixic acid NA (16.66 %). The sediment isolates of *V. alginolyticus* showed 100% resistance against both penicillin P and ampicillin AM and the lowest percentage was of gentamycin CN (0 %). There were 17 different antibiotic patterns were observed from the *V. alginolyticus* in this study. The plasmid size was ranged from 2.3 Kb to 21.6 Kb, while there was no detection of plasmid in 19 isolates. The highest resistance gene percentage of seawater isolates was found to be *ermB* (91.66%) which was followed by *blaP1* with 70.83% of resistance gene. The lowest percentage of resistance gene was *floR* with 16.66% of resistance gene. The highest percentage of resistance gene in seawater isolates was found to be *tetA* with 61.9% of resistance gene and the lowest percentage was obtained from *floR* which had 14.28% resistance gene. The finding of this study was shown high percentage of resistance genes in seawater than sediment isolates. These results suggest that the *V. alginolyticus* isolated from seawater and sediments observed in this study were pathogenic, and involved a source of antibiotic resistance genes that could be transmitted to other population of bacteria through mobile genetic elements.

**Key Words :** *V. alginolyticus*; Antibiotic resistance; Resistance gens; Plasmid profiling.