CHAPTER VII

CONCLUSION

Seventy *Vibrio parahaemolyticus* isolates obtained from several aquatic sources and clinical isolates were identified by 23 selected biochemical test and the MIC were determined by Etest to find isolates with MIC value $\geq$ 1 μg/ml. Twenty-one environmental *Vibrio parahaemolyticus* isolates with MIC value $\geq$ 1 μg/ml were confirmed as *Vibrio parahaemolyticus* by PCR method using *gyrB* primer to support the biochemical results then A 200 bp of *gyrA* QRDR and 214 bp of *parC* QRDR were amplified using *gyrA* and *parC* primer by PCR and nucleotide sequences of QRDR were analyzed.

The results have showed the mutations of 19 isolates in *gyrA* QRDR at codon 83 resulting in amino acid substitution from Serine (AGT) to Leucine (ATT) with *gyrA* QRDR of 2 isolates, SMV37 and SMV43, cannot be amplified. The mutation in *parC* QRDR were found in 20 isolates at codon 85 resulting in amino acid substitution from Serine (TCT) to Phenylalanine (TTT) with 1 isolate, SMV48,was found to have a mutation only in *gyrA*.

The further study is suggested to be done at the lower level then susceptible break point used in this study (MIC $<$ 1 μg/ml) to examine MIC ranges which have caused the mutation in parC as the mutation in parC found in this study were not corresponded to previous study by Okuda et al., 1999.