

CHAPTER V

CONCLUSIONS AND RECOMMENDATIONS

1. High genetic diversity of five oysters in Thailand; *C. belcheri*, *C. iredalei*, *S. cucullata*, *S. forskali* and *S. mytiloides* was revealed by RAPD analysis using primers OPA09, OPB01, OPB08, UBC210 and UBC220.
2. Two hundred and fifty-four reproducible and polymorphic fragments (200 - 2500 bp in length) were generated across investigated oyster species. Intraspecific genetic distances between pairs of geographic samples were lower than genetic distance between different species.
3. A neighbor-joining tree indicated distant relationships between *Crassostrea* and *Saccostrea* oysters but closer relationships were observed within each genus.
4. Ten, five and two species-specific markers were found in *C. belcheri*, *C. iredalei*, and *S. cucullata*, respectively. No species-specific markers were observed in *S. forskali* and *S. mytiloides*.
5. Three *C. belcheri*-specific RAPD fragments were cloned and sequenced. The sensitivity of detection of each designed primer set reached approximately 30 pg of *C. belcheri* total DNA template.
6. A 536 bp fragment amplified by pPACB1-F/R primers was only found in *C. belcheri* but disappeared in other species indicating the species-specific nature of the developed SCAR marker in this economically important species.