Chapter IV

Conclusions

1. A Randomly Amplified Polymorphic DNA analysis (RAPD) can be used to assess the genetic variation among populations of *P.monodon*.
2. Optimized PCR temperature profile for amplification of *P.monodon* DNA is 35 cycles; 94°C, 5 sec; 36°C, 45 sec and 72°C, 90 sec.
3. The percentages of polymorphic bands and the values of similarity index within population showed that samples from Angsila were more similar among themselves than samples from Satun-Trang, Trad and Medan, respectively.
4. The values of similarity index between population and genetic distances indicated a high genetic similarity between samples of Thai *P.monodon*, but indicated a lower genetic similarity between Thai and Indonesian *P.monodon*.
5. The UPGMA dendrograms could divide samples of *P.monodon* into two clearly distinct gene pools which were composed of Satun-Trang, Trad and Angsila as Group 1, and Medan as Group 2.
6. A monte Carlo simulation could divide samples of *P.monodon* into three distinct groups which were composed of Satun-Trang as group 1, Trad and Angsila as Group 2, and Medan as group 3.

7. Amplification by primer 428 gave region-specific marker for samples from the Andaman Sea.