

Chapter V

Conclusions

1. Three microsatellite loci, CUPmo18, Di25 and Di27, were shown to be highly polymorphic with number of alleles at each locus of 37, 34 and 32 alleles respectively. Population analyses based on 3 loci revealed heterozygosities between 0.66-0.80 and average alleles per locus were ranged from 22.23-26.33.
2. The effective number of alleles and mean heterozygosity for overall loci indicated that the level of genetic polymorphisms of *P. monodon* originating from the Gulf of Thailand was slightly greater than that of the Andaman samples.
3. For determination of intraspecific population structure, CUPmo18 and Di25 were equally effective. Although Di27 did not provide an ability to detect geographic heterogeneity among Thai *P. monodon* samples, all microsatellite loci used in this study are useful for breeding programs of this economically important species.
4. Analysis of geographic heterogeneity and phylogenetic reconstruction using the Neighbor - joining approach divided 5 geographic *P. monodon* samples to three different gene pools (stocks) constituting of Satun, Trang and Phang-nga(A), Chumphon(B) and Trad(C).

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