

CHAPTER V

CONCLUSIONS

1. The (GT)_n microsatellites are abundant in *P. monodon* genome.
2. The average distance between neighbouring (GT)_n microsatellites in *P. monodon* genome was 92.8 kb.
3. One hundred and thirty one microsatellites isolated from *P. monodon* genome were classified as perfect, imperfect and compound microsatellites. The predominant category was imperfect. The most common size-class in all categories contained sequences with lengths of 30-35 repeats.
4. Seven sets of PCR amplified were designed based on the flanking DNA sequences of microsatellites and PCR methods were developed for amplifications of these microsatellite loci.
5. Two microsatellite loci, namely, Pmo 18 and Pmo 386, yielded scorable PCR products. Polymorphism tests showed that these two loci were highly polymorphic which have a potential for further population studies and parentage analysis.