CHAPTER V

CONCLUSIONS

- 1. The (GT)_n microsatellites are abundant in *Penaeus monodon* genome.
- 2. The average distance between neighboring (CT)_n and (GT)_n microsatellites in *P. monodon* genome was 164 and 42 kb, respectively.
- 3. The predominant category of microsatellites isolated from *P. monodon* genome was imperfect.
- 4. The most common size-class in all dinucleotide repeat categories of *P.monodon* was 12-17 copies for (CT)_n and 36-55 copies for (GT)_n.
- Six pairs of PCR primers were designed from the flanking regions of microsatellite clones. Two microsatellite loci, namely Pmo 195 and Pmo 519, were successfully amplified.

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