

## CHAPTER 5

### CONCLUSIONS

1. A randomly amplified polymorphic DNA (RAPD) technique can be used to assess the genetic patterns between normal and viral tolerance *P. monodon*.
2. Twenty-six of 47 screening arbitrary primers were selected to examine differences in RAPD patterns between normal viral tolerance *P. monodon*.
3. From the RAPD patterns using 26 selected primers, two primers, OPA-04 and OPB-20 yielded a band of 800 bp and 1,250 bp, respectively, which were present only in normal *P. monodon* but absent in viral tolerance shrimps.
4. By increasing the number of samples to the final twenty individuals in each group, the 800 bp fragment still existed in all normal shrimp but the 1,250 bp was found in 12 of 19 individuals (63.2 %).
5. Cloning of the 800 bp DNA fragment yielded the recombinant clone (no. 28) which contained the DNA insert of expected size.
6. Sequence analysis of the 800 bp DNA fragment revealed no similarity of this DNA fragment to any gene in the GenBank suggested that it could represent the intron or a part of a new gene. However, conversion of nucleotide sequences to amino acid sequences showed no sequence similar to any known proteins.
7. PCR amplification using specific primers designed from the sequence of the 800 bp fragment yield a PCR product with size 173 bp which was found only in

normal shrimps. The result suggested that this method could offer a specific detection of normal and viral tolerance shrimps.

8. The presence of a 173 bp PCR product was examined in other geographically separated *P. monodon*. Unfortunately, no PCR product was detected. The results suggested that further investigation of this marker required a larger sample size and careful sample collections.



สถาบันวิทยบริการ  
จุฬาลงกรณ์มหาวิทยาลัย