CHAPTER 6: CONCLUSION

This study was carried out to identify and estimate the genetic variability within and among six populations of *Channa striata* using microsatellite markers. A total of sixty microsatellite primers pairs which were developed for *Channa striata* were used to screen these populations. Of these, 10 polymorphic microsatellite loci were employed in the genetic variation study of six population of *Channa striata* from different rivers.

In the present research work an investigation was conducted to look for possible cross-species amplifications of the *Cyprinus carpio* microsatellite loci in *Channa striata*. The results suggested that this method saved time and cost for obtaining new microsatellite markers. As it required some experience in primer testing and optimization. However, seven new microsatellite markers were also isolated from *Channa striata* using the Random Amplified Microsatellites (RAMs) based methods. It is faster and easier way to obtain microsatellite in comparison to the other strategies.

From the F_{ST} value, the highest genetic differentiation is between Selangor and Terengganu. The results agree with the geographical origins of these two populations in Malaysia. From the phylip consensus tree (UPGMA), the clustering is according to the geographical area. The west coast of Malaysia i.e Selangor, Kedah, Negeri Sembilan, and Johor were cluster together, while Terengganu (east cost of Malaysia) and Penang (an island) was cluster separately.

In conclusion, the data from the microsatellite loci analysis indicated the high level of heterozygosity in six populations Negeri Sembilan, Johor, Penang, Selangor, Terengganu, and Kedah. Further studies involving greater numbers of samples from different location would be necessary to obtain a more accurate pattern of genetic

structuring in *Channa striata* populations in Malaysia. Furthermore, in order to elucidate genetic structure in detail, we can use more loci and therefore suggest using mitochondrial to infer whether there is unique haplotype (frequencies) for each and between populations.