VI. SUMMARY

The freshwater prawn, *Macrobrachium rosenbergii* is one of the widely cultured freshwater prawn species all over the world. Culture of this species has expanded rapidly not only within Asia but also in regions far remote from the natural distribution of the species and is now cultured in at least 43 countries across five continents. The application of genetic markers has allowed rapid progress in aquaculture investigations of parentage assignments, genetic variability and inbreeding. Microsatellite markers have been shown to be very useful for verifying pedigrees in prawn lines and pedigree tracing of hatchery populations. Genetic studies on *M. rosenbergii* using DNA markers are very rare. At the global level, India follows China and Thailand in freshwater prawn production and occupies the third position. The species are believed to be declining as a result of over-exploitation. So understanding the genetic diversity in wild stocks is important for developing sound conservation strategies. Populations with a high level of genetic variation have greater prospects in terms of higher growth rate, developmental stability, viability, fecundity and resistance to environmental stress and disease. Therefore knowledge of the genetic background of a species and its population structure is essential for success in any breeding management for the selection of genetically diverse brood stock.

The present research is aimed at identifying microsatellite loci in the genome of giant freshwater prawn, *M. rosenbergii* from India and understanding their usefulness to study genetic
diversity of wild populations. For most efficient marker development, microsatellite enriched genomic DNA libraries are made. In this study, we have successfully amplified the microsatellite region containing (GA) and (CT) repeats using PCR primers. The PCR fragments were purified and sequenced. From the sequence information generated microsatellite loci were identified. For the initial microsatellite detection and enrichment, total genomic DNA was extracted from the muscle tissue of *M. rosenbergii*. In the case of studies involving characterization of microsatellite loci and population structure, DNA was extracted from the pleopods of live animals without sacrificing the sampled freshwater prawns.

Thirteen well identifiable, highly polymorphic microsatellite marker loci in the ‘western’ form of *M. rosenbergii* genome have been developed. Among the thirteen microsatellite loci developed and used in this study, all were found to be highly polymorphic and showed considerable variation in the tested population samples of *M. rosenbergii*. A total of 59 different alleles were found over all the microsatellite loci tested and the number of alleles per locus ranged from 3 to 9. The average observed and expected heterozygosities ranged between 0.6785 ± 0.1883 and 0.6881 ± 0.1117 respectively. The number of genotypes estimated across all the microsatellite loci in both the tested populations of giant freshwater prawn found in the range of 21 to 35 genotypes. The locus MRMB1 exhibited the highest range of the number of genotypes (2–19) and the locus MRMB13 showed the least (3–10). None of the loci showed significant linkage disequilibrium for all pairs of loci. Both the major populations of giant freshwater prawn from south India tested have a very high genetic variability and thereby present significance in commercial breeding operations.

Cross species amplification was performed using different types of crustacean species including freshwater prawns, shrimps and crabs. The freshwater prawn *M. idella* showed considerable
amplification of all the microsatellite regions with the microsatellite primers developed for *M. rosenbergii*. We observed a correlation between the prevalence of these viruses with certain microsatellite repeat regions identified and characterized in *M. rosenbergii* viz (GA)$_{44}$, (GA)$_{36}$, (GA)$_{26}$, (GA)$_{10}$ and (CT)$_{17}$. These markers could serve as a unique tool for marker–assisted selection since these are associated with disease phenotypes in scampi.

The data generated in this study provide useful information on the genetic variation and differentiation in two major wild populations of *M. rosenbergii* from southern peninsular India. This information can be applied for future genetic improvement by selective breeding, and to design suitable management guidelines for these genetic materials. Availability of such data could be very useful for stock management, selective breeding programme and sustainable use of wild resources.