5. DISCUSSION

The Knowledge of the pattern and range of distribution of organisms throw light on their ecology, adaptation intra and site-specific relationships. Every species has its own niche in nature. Especially, when two closely related forms coexist in a habitat, they exhibit niche preference. Biological studies are never complete and make no sense until the natural habitats are taken to consideration. Notable contribution are made on the ecology and distribution of the freshwater prawns (Williams 1977, Carpenter 1977a, 1977b, 1978, 1983, Anatharaman et al., 1986, Benzie and de Silva 1988) Yet, the scanning of literature reveals the fact that information on the distribution and abundance of the freshwater prawns of Tamil Nadu is extremely scant.

The advent of molecular technique made possible not only the genetic analysis and also the study of evolutionary relationship among the species or phylogeny. Although there are many ways to study phylogenetic relationships example amino acid sequence of protein, nucleotide sequence of nucleic acid and presence or absence of enzyme, it is now recognized that ribosomal RNA is important indices or phylogeny. Ribosomal RNA has the characteristics that are important in studying the evolutionary divergences. These universal characteristics have identical functions in all living organisms. This functional constancy makes rRNA ideal molecular chronometers to measure evolutionary changes. Because rRNA is a small molecule that cannot tolerate much structural changes and still retains its function, its
sequences moderately well conserved or constant across phylogenetic lines. Consequently small differences in rRNA sequence can be used to determine evolutionary distance. Among the rRNAs, 16S is used most commonly as phylogenetic tool. Small size rRNA limits the amount size rRNA makes this molecule more difficult to experimentally analyze.

There are many different ways to measure genetic diversity. The modern causes for the loss of animal genetic diversity have also been studied and identified. A 2007 study conducted by the National Science Foundation found that genetic diversity and biodiversity are dependent upon each other, that diversity within a species is necessary to maintain diversity among species, and vice versa. According to the lead researcher in the study, Dr. Richard Lankau, If any one type is removed from the system, the cycle can break down, and the community becomes dominated by a single species.

Genetic diversity is a level of biodiversity that refers to the total number of genetic characteristics in the genetic makeup of a species. It is distinguished from genetic variability, which describes the tendency of genetic characteristics to vary. The academic field of population genetics includes several hypotheses and theories regarding genetic diversity. The neutral theory of evolution proposes that diversity is the result of the accumulation of neutral substitutions. Diversifying selection is the hypothesis that two subpopulations of a species live in different environments that select for different alleles at a particular locus. This may occur, for instance, if a species has a large range relative to the mobility of individuals within it. Frequency-dependent selection is the hypothesis that as alleles become more common, they become less fit. This is often invoked in host-pathogen interactions,
where a high frequency of a defensive allele among the host means that it is more likely that a pathogen will spread if it is able to overcome that allele.

Genetic diversity plays a very important role in survival and adaptability of a species because when a species’s environment changes, slight gene variations are necessary to produce changes in the organisms anatomy that enables it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variations from which to choose the most fit alleles. Increase in genetic diversity is also essential for an organism to evolve. Species that have very little genetic variation are at a great risk. With very little gene variation within the species, healthy reproduction becomes increasingly difficult, and offspring often deal with similar problems to those of inbreeding. The vulnerability of a population to certain types of diseases can also increase with reduction in genetic diversity.

A total of five prawn samples of each species were typed using the six RAPD primers and had generated RAPD markers. Scoring was done on bands generated by each primer within the molecular weight of 15 to 1500 bp as shown in Fig - 60. The percentage of polymorphic markers detected in all the primers was quite large in all the six species. All the three species of Caridina, M. lamerrai lamerrai and M. scabriculum, M. scabriculum and M. canare shows higher percentage of polymorphism, where as M. lamerrai lamerrai and M. canare shows lower percentage of polymorphism when compared with other species. Optimization of the protocol is necessary in order to obtain reproducible and interpretable RAPD banding pattern. Scoring of the banding pattern was done within the range of 250 to 1500 bp due to this range showing
good reproducibility and any amplified products falls out of this range showed low reproducibility (Ambak et al., 2006).

*C. gracilirostris* has been reported from Indo-Malayan archipelago by several workers (de Man, 1892, Kemp, 1918, Natarajan, 1942, Johnson, 1961 & 1963, Arudprakasam & Costa, 1962, Pillai, 1964, Holthius, 1965; Tiwari & Pillai, 1971; Costa, 1972; Ravindranath, 1977; Richard and Chandran, 1994)

In 1892 de Man established a new variety to *Caridina nilotica* (Roux) from Celebes. Later he (1908a, 1908b) described a variety to *C. nilotica* (Roux), viz. var. *bengalensis*. He obtained the specimens from Port Canning Lower Bengal. He synonymised Henderson’s (1893) *C. wyckii* from Madras and Nobile’s (1903) *C. wyckii* from Pondichery to this new variety. While described his new variety de Man (1908b) was prompt to insist that “it present a great resemblance to the var. *gracilipes* de Man from Celebes”. He listed few differences between the two varieties.

*Macrobrachium lamarrei* is confined to India (Holthuis 1950). De Man (1908) collected this species from port Canning near Calcutta and described it extensively solving most of the problems that existed in this confusing species.

*Macrobrachium canarae* was first described by Tiwari (1958) from South Kanara district of Karnataka providing the diagnostic characters.
Later Jalihal et al., (1988) while studying the freshwater prawns of Karnataka, collected this material from the type locality and made an extensive study of this species along with the type material from Z.S.I. he compared *M. canarae* with the other closely related forms, *M. lamarrei* and *M. lamarrei lamarroides* and distinguished *M. canarae* from these forms by five characters.

### 5.1 CONCLUSIONS

RAPD fingerprinting is to yield reliable and useful results. Therefore, the risk of misinterpretation in a genetic analysis different RAPD patterns have similar size can be minimized by the use of several RAPD primers so that the genetic analysis are based on a large number of pooled RAPD markers (Bidochka et al., 1994). RAPD marker had been applied in studies at the individual level as well as in genetic identification and in the studies involving closely related species. Due to their very high genomic abundance, they have also been applied in gene mapping studies. Several advantages in genetic mapping providing by RAPD markers are a universal set of primers, which can be used for genomic analysis in a wide variety of species, no preliminary work such as isolation of cloned DNA probes, preparation of filters for hybridizations or nucleotide sequencing is needed and each marker is the equivalent of a Sequence Tagged Site, which can greatly simplify information transfer in collaborative research programs (Williams et al., 1990). In addition, this method is easy and quick to assay, requires low quantities of template DNA and no sequence data for primer construction.