

Chapter 1

GENERAL INTRODUCTION

Like all successful groups of animals, the molluscs have explored with enterprise and ingenuity, the possibilities latent in their basic structure during the course of a long evolutionary history. Even when the extent of the plasticity of their basic form is seen, the variety of the 'Mollusca' remains 'exceptional and spectacular' among the various phyla of the animal kingdom (Morton and Yonge, 1964). Molluscs are the most numerous group of animals comprising a total of 100,000 species inhabiting all possible habitats except aerial (Abbot, 1954).

The class Bivalvia (Phylum : Mollusca) can be divided into two sub-classes - Protobranchia and Lamellibranchia, of which the latter comprises the clams, mussels and oysters (Newell, 1965; 1969; Boss, 1982). The unique pattern of distribution, polymorphism and other genetic variations among bivalves have been subject to extensive research in recent times. Over the past few years, several excellent discussions have appeared in scientific journals concerning the treatment of the lower taxonomic characters. The enormous diversity of Mollusca, which ranks about a third in the number of living species of animals makes it difficult to formulate a definition which will apply to all members of this group but none outside it, and at the same time be reasonably brief. Perhaps, this could be the reason why the phylogeny of this group have received so much attention in elucidating what the molluscs are.

The categorisation of phylum Mollusca as suggested by Burch (1956) seems inadequate on the basis of the statement that "sub-species should

be based on characters resulting from the environment". This implies that (1) the variations result entirely through natural selection of genotypes most compatible to the environments, (2) infraspecific variation results as a direct effect of the environment on the genetic system or (3) variations result by expression of the gene complex in different ways in different environments. Among molluscs, the third possibility appears to be more frequent and the fact that it leads to "ecotypes" and "ecophenotypes" and is well known to malacologists.

Molluscs in general and bivalves in particular are known to form isolated local populations because of their sedentary habits and wide distribution. Often these populations show a marked homogeneity among members of each population and in most cases, every local population may be morphologically distinguished from others. These "micro-geographical races" may either be genetically determined or ecophenotypically conditioned. The separation of an ecophenotype as a taxonomic unit with a sub-specific name is erroneous (Hubendick, 1951). This is because, if the morphological characters of populations are genetically determined, recognizing each population as a sub-species or species is absurd since there exists a clear-cut discontinuity of characters. Thus, there is more to systematics than merely the identification of the animals involved and it is essential to understand the underlying mechanisms and principles of variation, speciation and evolution, to realize the inadequacy of our system of nomenclature of animals.

India enjoys a luxuriant molluscan resource and has been widely used as food for man and as a source of lime besides other purposes. Among them, bivalves are of remarkable interest with regard to their

abundance and the growing importance in fisheries. Bivalves are by far the most important group compared to gastropods for commercial exploitation and utilisation as food. In recent years, there has been a spectacular advance in the utilisation of these forms in India and abroad. Hulse (1982) stated that the yield of high quality protein by bivalves per hectare of surface seawater far exceeds the protein that could be produced on a hectare of land by any known terrestrial plant or animal. Besides, they are of particular interest as indicator or sentinel organisms reflecting the level of environmental contamination in a manner amenable to both short term and long term monitoring.

Recent trends in aquaculture practice involve domestication of an animal by their shielding from unfavourable environmental conditions and long term genetic adaptation to an artificial environment (Doyle and Hunte, 1981). This may lead to increasing divergence between domesticated organisms and their wild population due to reduction of variability. Therefore, any information gathered on the genetics of change in fitness of each cultivable species would be useful as more and more bivalve species are being brought under cultivation. Although some success has been achieved in developing breeding technology of shellfishes especially bivalves, literature available on the genetic make up or genetic variability of these shellfishes is rather scarce. An understanding of the little known effects of aquaculture practices and related fields in fisheries on these species will help to promote their breeding and hybridization. The growing trend in the application of genetic principles envisages the necessity for scientific data pertaining to information on grounds of taxonomy and population genetics of bivalves.

Despite the fact that advanced researches have been initiated towards problems related to production, quality and maintenance of better stocks, scant attempts have been made towards the study of the systematic position and affinities of bivalve species. The present study was therefore taken up with a view to delineate the systematic position, interrelationships and variations among populations of three commercially important bivalve species representing the three major families of the class Bivalvia from Cochin and nearby waters. The species selected for the study are Villorita cyprinoides, Crassostrea madrasensis and Perna viridis belonging to the three major families Corbiculidae, Ostreidae and Mytilidae respectively.