2. REVIEW OF LITERATURE
Accurate identification of species and its subunits or stocks is a pre-requisite to the modern scientific management of fisheries resources. There is a large volume of literature published on the concept of STOCK in the field of fisheries research and management and various methods/techniques used for its identification.

In the early history of fisheries research, morphologically and meristically differentiated races were considered as practical units of fisheries management (Heinke, 1899; Schmidt, 1917). Later, the concept of stock and its different forms were introduced. The term fish stock has been defined and used in many contexts by different investigators, ranging from a production or management unit (Marr, 1957; Larkin, 1972) to that emphasises genetic discreetness (Moller, 1971; Ihssen, 1977). Murray (1961) has explained variety of usage and different meanings of the word "stock". Ricker (1972) has explained that fish stocks probably have genetic individuality. The term sympatric stocks has been used by Ihssen et al. (1981a) to denote stocks that are not isolated by physical barriers. Booke (1981) has also reviewed the stock concept along with different definitions as applied in fishery science and also has presented a working definition of the "stock". His general definition of stock is "a species-group or population of fish that maintains and sustains itself over a time in a definable area". In this respect, the most popular unit stock concept applied in fisheries research and management is based on the Mendelian populations. It is defined as a "reproductive community of sexual and cross fertilized individuals among whom matings regularly occur

The identification of distinct genetic stocks, if any, is basic to the conservation and rational exploitation of fisheries resources (Leberg, 1990). Smith et al. (1990) argues that the biological stock concept developed with the studies on cod (Gadus morhua), herring (Clupea harengus) and plaice (Pleuronectes platessa). Critical importance of stock concept to the formulation of any comprehensive long term fisheries management has been emphasised by many investigators (Uttter and Hodgins, 1972; Allendorf and Utter, 1979; Altukhov, 1981; Ihssen et al., 1981a; Larkin, 1981; Mac Lean and Evans, 1981; Philipp et al., 1981; Allendorf et al., 1987; Kapuscinski and Philipp, 1988; Gulland, 1989; Lavery and Shaklee, 1989; Utter et al., 1989; Smith, 1990; Waples et al., 1990; Utter and Ryman, 1993).

Ihssen et al. (1981a) have reviewed some of the materials and methods that have been traditionally used to identify and delineate different stocks. They have discussed a wide variety of population parameters such as abundance, age composition, recruitment, mark recapture-procedures (tagging) etc. and various characters ranging from morphometric, meristic and calcareous to biochemical and cytogenetic characters which have been used to identify
fish stocks. Traditionally, studies on anatomical characters such as morphometrics and meristics have been conducted to identify different fish stocks. But phenotypic variations of these characters have not been directly correlated to particular differences in the genome and hence their application in stock identification is complicated (Clayton, 1981). Moreover, the effects of physiological and epigenetic constraints on morphology in response to certain environmental parameters such as temperature and oxygen are poorly understood (Bock, 1980; Todd et al., 1981). However, anatomical characters also have indicated stock differences which were agreeing to the data from alternative methods (Sharp et al., 1978; Casselman et al., 1981; Ihssen et al., 1981a).

Stock identification based on fish chromosome morphology has been done since 1945 (Booke, 1968) as reported by Ihssen et al. (1981a). Recently many modern practices have been evolved for isolation and resolution of fish chromosomes which are invariably of small size and great number. This enabled many researchers to adopt chromosome characters for stock delineation. However, Ihssen et al. (1981a) and Bye and Ponniah (1983) have indicated about the limitations in accepting intraspecific chromosomal variation as an indication of stock difference. Moreover, Boothroyd (1959) and Rees (1967) have reported that most of the intraspecific chromosomal differences are due to errors in methodologies or techniques rather than true genetic differences. Above all, live specimens are to be used for the extraction of chromosomes which may be difficult especially in the case of truly marine species like S. longiceps.
Realising the role of environmental parameters on the phenotypic expression in fishes, modern investigators started applying biochemical genetic techniques for identification of gene controlled phenotypes such as proteins and enzymes in different tissues of fishes. Biochemical techniques designed to compare species on the basis of protein differences dates back to 1904 when Nuttal used immunological methods to compare the serum of humans with that of other primates. Later on the classical paper electrophoresis work of Pauling *et al.* (1949) showed phenotypically different haemoglobins in human blood. Then the introduction of starch gel electrophoresis by Smithies (1955) demonstrated human serum protein variations. The innovation of starch gel zymogram methods by Hunter and Markert (1957) revealed a world of enzyme polymorphism in organisms ranging from Drosophila to humans. Meanwhile, Raymond and Weintraub (1959) introduced polyacrylamide as an effective electrophoretic medium. Its high resolving power due to adjustable pore size made it a better gel medium than starch gel. Then, Davis (1964) provided simple polyacrylamide disc gel electrophoretic unit as a popular method for protein/enzyme separation. Using both starch and polyacrylamide gel media, researchers in biology widely published the natural phenomenon of genetic variations in different proteins and enzymes. Shaw (1965) reviewed electrophoretic variation of enzymes in vertebrates and invertebrates. Harris (1966) detected polymorphic forms of many enzymes in man. Lewontin and Hubby (1966) and Hubby and Lewontin (1966) discovered high genetic variability within the species, *Drosophila pseudoobscura*. Meanwhile, attempts were made to apply blood groups and serum protein characteristics in fish
population genetic studies (Sick, 1961; Marr and Sprague, 1963; Cushing, 1964; de Ligny, 1969; Tsuyuki et al., 1969). Studies on serological and biochemical aspects involving eyefens protein, muscle protein and enzymatic proteins have been reviewed by de Ligny (1969).

The biochemical and serological methods have been discussed with special reference to identification of fish stocks during the ICES special meeting held at Dublin (de Ligny, 1971). It is evident from different reports that general proteins and some enzymatic proteins were useful for stock identification programmes. Among general proteins, muscle proteins and eyefens proteins were widely used for stock identification studies by most of the investigators (Tsuyuki et al., 1965a,b, 1968; Tsuyuki and Roberts, 1966; Eckroat and Wright, 1969; Uthe and Ryder, 1970; Peterson and Shehadeh, 1971; Menezes, 1976a,b; Rao and Dhole, 1976; Jamieson and Turner, 1980; Smith et al., 1980; Winans, 1980; Andersson et al., 1983; Fujio et al., 1983; Basiao and Taniguchi, 1984; Sbordoni et al., 1986; Smith, 1986; Mahobia, 1987; Philip Samuel, 1987; Present, 1987; Feveldon and Haug, 1988; Salini and Shaklee, 1988; Menezes, 1990; Vijayakumar, 1992).

The electrophoretic techniques and staining procedures for detection of different enzyme systems published by Shaw and Koehn (1968), Brewer (1970), Shaw and Prasad (1970) enabled different researchers to discover and publish large volume of information on electrophoretic characteristics of different enzyme systems. Publication of books on electrophoresis with different methods and techniques to detect at least 40 enzyme systems (Smith,
1968, Brewer, 1970), laboratory manual or practical guide specifically designed to detect electrophoretic variations of these enzymes in prawns (Siciliano and Shaw, 1976; Redfield and Salini, 1980), fishes and shell fishes (Benson and Smith, 1989) and method of interpretation of electrophoretic phenotypes as genetic variants and for purpose of stock identification of fish (Utter et al., 1987) greatly helped in applying biochemical genetic techniques in the fisheries research and management. The very basis of identification of distinct genetic stocks is the expected evolutionary processes occurring within the species. The degree of evolutionary diversification between identified discrete stocks may also be expressed in terms of genetic identity and genetic distance measured according to the method of Nei (1972). Its application in biochemical genetics of populations was explained using models (Utter, 1987; Ayala and Kiger, 1980).

The major reason for world wide application of biochemical genetic techniques involving gel electrophoresis is the implication of genetic stock concept in fisheries management (Moller, 1968, 1970; de Ligny, 1969, 1972; Utter et al., 1974; Allendorf and Utter, 1979). Since most of the biochemical processes involve catalytic participation of large number of enzyme systems, they have been investigated as potential source of genetic variation studies. Thus major portion of literature available on modern fish stock identification studies are based on enzyme allelic frequencies. Among different group of enzyme systems, dehydrogenases are studied in detail for stock identification programmes, especially in different species of salmon and trout by many of the investigators (Hodgins et al., 1969; Northcote et al., 1970; Wilkscroft

Using dehydrogenases, many other fishes have also been thoroughly investigated for stock identification such as New Zealand snapper (Smith et al., 1978), walleye pollock (Grant and Utter, 1980), Coregonus clupeaformis (Casselman et al., 1981), jackmackerel (Richardson, 1982a), jackass (Richardson, 1982b), Atlantic herring (Grant, 1984), damsel fish (Shaklee, 1984), Pacific herring (Grant and Utter, 1984), Atlantic cod (Mork et al., 1985).

In addition to dehydrogenase enzymes, esterase enzyme system has also been investigated in large number of fishes like cat fish (Koehn and Rasmussen, 1967; Koehn, 1970), Pacific hake (Utter et al., 1970), American eel (Williams et al., 1973), European hake (Mangaly, 1974; Mangaly and Jamieson, 1978), sun fish (Avise and Smith, 1974), Zoarces (Christiansen and Frydenberg, 1974), Cichlids (Kornfield and Koehn, 1975; Mahobia, 1987),
Menidia (Johnson, 1975), guppy (Shami and Beardmore, 1978), New Zealand snapper (Smith et al., 1978; Smith, 1979), Atlantic mackerel (Smith and Jamieson, 1980; Smith et al., 1981a), milk fish (Winans, 1980), walleye pollock (Grant and Utter, 1980), sprat (Smith and Robertson, 1981; Ryman and Stahl, 1981), New Zealand hoki (Smith et al., 1981b), Catostomus (Buth and Crabtree, 1982), paddle fish (Carlson et al., 1982), tilapia (Cruz et al., 1982; Mc Andrew and Majumder, 1983; Basiao and Taniguchi, 1984); Australian barramundi (Shaklee and Salini, 1983; Salini and Shaklee, 1988), Orizias (Sakaizumi et al., 1983), Salvelinus (Andersson et al., 1983), Atlantic herring (Grant, 1984), Pacific herring (Grant and Utter 1984), perch (Gyllesten et al., 1985), Northern pike (Seeb et al., 1987), Pacific cod (Grant et al., 1987), shark (Lavery and Shaklee, 1989), tuna (Richardson and Habib, 1987), grey mullet (Vijayakumar, 1992) and crustaceans (Johnson et al., 1974; Lester, 1975; Kannupandi, 1980; Mulley and Latter, 1980; De Matthiseis et al., 1983; Philip Samuel, 1987).

Studies on biochemical genetics of Indian fishes are only a few and are of preliminary nature. These were mainly attempts to find out interspecies or species specific protein differences. Some of the examples are: flat fish (Kasinathan et al., 1972), marine fishes (Manohar and Velankar, 1973), goboids (Natarajan et al., 1975), Bombay duck (Kurian, 1977), oil sardine (Rao and Dhulkhed, 1976), mackerel (Dhulked and Rao, 1976; Menezes, 1986; Menezes et al., 1990), M. cephalus (Bhosle, 1977), mullets (Rao, 1981), Channa stewartii and Danio dangila (Bhattacharya and Alfred, 1982), Etroplus suratensis Liza macrolepis and Mystus gulio (Kamalakara Rao et al., 1985), grass carp
(Padhi and Khuda-bukhsh, 1989), carangids (Menezes, 1990). Similar investigations have also been carried out in shrimps and oysters (Sriraman and Reddy, 1977; Kulkarni et al., 1980; Thomas, 1981; Puthran Prathibha, 1984; Ponniah, 1988).

However, there are also a few Indian reports on the biochemical genetics of fishes and shrimps with due importance to stock identification studies, namely, mullets (Reddy, 1977; Rao, 1981), cichlids (Mahobia, 1987), penaeid prawns (Philip Samuel, 1987) and *Mugil cephalus* (Vijayakumar, 1992). The application of genetics in aquaculture was also emphasised in the C.M.F.R.I. Special publication (Bye and Ponniah, 1983). An awareness on the importance of fish genetic resources, its conservation and management in India has been published by Jhingran (1984), Das and Jhingran (1989) and Das et al. (1989).

The above review of the literature gives sufficient justification for the choice of the present thesis problem, its objectives, its methods of investigation/interpretation of data and the conclusions drawn from the results of the investigation.