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Abstract

Polymorphism is a unique aspect of genetic variability. Polymorphism means the presence of two or more alternative forms of a phenotype in a population and can show its presence in any genetic character, in any segment of DNA. Biochemical diversity is popularly known as biochemical polymorphism and it is the occurrence of the varieties which is attributed to biochemical dissimilarities, which is under the charge of genetics. When two or more distinct inherited varieties coexist in the same individuals, a population is said to exhibit genetic polymorphism.

Fishes exhibit the highest genetic diversity in terms of size, shape, biology and in the habitats they occupy. Conservation of this fragile genetic diversity is extremely important to maintain ecological balance. Genetic variability is an important attribute of the species, since those with higher levels of variation are most likely to present high additive genetic variance for productive traits.

Keywords: Polymorphism, fish, genetic variability

Introduction

The term 'protein' is derived from the Greek word 'Proteios' which means primary. The first recognizable and the distinctive expression of genetic information is the protein. Proteins act as catalysts which help in controlling the rates of all biological reactions, they also serve as regulators, the carriers of essential substances in an organism and also as building blocks for cellular and organic structures ^[3]

Protein molecules are basically gene products and it is sensible to assume that the data provided by two homologous proteins of different organisms makes sense. If two or more discontinuous forms of proteins occur in a species in such a proportion that the rarest protein cannot be maintained by recurrent mutation it is known as protein polymorphism. It has been proved experimentally by scientists that all traits such as production, reproduction and genetic diseases are controlled in the body of the fish species by the biochemical activities and these are fulfilled by many different types of proteins such as serum proteins, enzymes, hormones etc. ^[3]. The effect shown by each of these different proteins is through different ways *viz.* anabolic, catabolic, substrate activation etc. which controls the growth, production and reproduction of the individuals. Proteins are useful in studying the genetic variations within and among organisms.

A new dimension in the understanding of variations in the proteins has its basis in the two events of the 1950's. The DNA molecule structure as proposed by Watson and Crick (1953) led to an understanding of the direct relationship between genes and proteins.

Protein polymorphism is also known as simultaneous occurrence of two or more alleles at a single locus of a group. Relatively high degree of interspecific polymorphism is apparent at classification level and thus, where the tissue from a creature is in a suitable condition, useful distinguishing characters are readily available from proteins ^[27]. The concept related to proteins is that different species possess unique proteins or species can be differentiated on the basis of structural polymorphisms of a protein. In order to assay polymorphism in fish species, three types of protein based techniques have been used namely serological methods, total protein analyses, and locus specific allozyme indicator ^[9]. An attribute of genetic variations in species is that it enhances the capability of an individual to adjust to the changing environment and these variations are necessary for survival of the species.

Biochemical diversity is popularly known as biochemical polymorphism and it is the occurrence of the varieties which is attributed to biochemical dissimilarities, which is under

the charge of genetics. When two or more distinct inherited varieties coexist in the same individuals, a population is said to exhibit genetic polymorphism.

Due to normal cellular operations or relations with the surroundings, all organisms are subjected to variations, leading to genetic variation or polymorphism. Biochemical variations have a wide occurrence in nature.

It is assumed that all types of biochemical variations are controlled by only one or more than one allelic pair of genes. It has also been proved that many types of protein polymorphism are due to the difference in the number of amino acids in the protein molecules that show their consequence in different manners ^[3]. In the participation of formation of a protein, a triplet code of nucleotide of DNA and RNA is responsible. In a specific DNA or RNA the different triplet codes present, sends separate codes to separate amino acids to come in a particular arrangement to form a specific protein which is permanently or temporarily required for a specific function of the body. Allelic pair of genes which have the same nucleotide sequences in one as well as the other gene can send the same type of codes to the amino acids to come in contact to form the similar type of protein that is a monomorphic protein but if the allelic pair of genes having distinct codes for distinct amino acids reach a particular sequence of nucleotide in the DNA or RNA they form the distinct protein molecules. A unique kind of polymorphic protein is formulated within the body by this and it puts forth its effects in numerous ways ^[3].

In most natural populations, genetic variation in the form of multiple alleles of numerous genes exists. No two organisms (barring identical twins or alternative multiple identical births) is expected to possess the identical genotype for all genes in most sexually reproducing populations ^[19]. For the identification of genetic variation and stock structure of a population, Ihssen *et al.* (1981) studied the population parameters, physiological, behavioral, morphometric, meristic, calcareous, cytogenetical and biochemical characteristics.

Protein variations used for comparison of species dates back to 1906, when Nuttal used immunological methods to compare serum of human therewith of other primates.

A scientist must be able to identify the extent of genetic variation within and among populations in order to manage any biological resources effectively. Genetic variability is directly assessed through molecular, allozyme, RAPD, RFLP, mtDNA, minisatellite and microsatellite markers. Initial studies in genetic science were restricted to proteins such as hemoglobin and transferring during the 1960's, however attention quickly turned to enzymatic proteins, allozymes ^[12] and allozymes was the dominant technique, widely used throughout the 1960s and also during the starting of 1980s^[49]. To analyze stock structure in exploited species, numerous ways and characteristics have been used (parasite distribution, tagging, ecological, physiological and behavioral traits, morphometrics and meristics, blood pigments, calcified structures, immunogenetics, molecular genetic tools ^[22, 23], it was only by the utilization of separate, heritable macromolecules such as proteins [40] and nucleic acid [14] heterogeneity that provided an often and universally ample array of markers.

Protein Polymorphism in Fishes

All organisms are subjected to micro and macro evolutionary processes endlessly at organism as well as at molecular levels.

Genes are the main elements that decide the phenotypic characters of any organism. It is only because of the variations that happen at the gene level that the production of organisms, those are different either at the molecular level or at the organism level take place. It is robustly believed that species may be subjected to micro-evolutionary processes and differentiate into genetically distinct sub-populations or stocks in a span of time, if geographically and reproductively isolated. In recent times, there has been a widespread degradation of natural aquatic habitat due to numerous anthropogenic activities and this has resulted in radical decline and extinction of many fish species. The assessment of the genetic diversity of fish resources in such species assumes importance. Correct information of the genetic makeup and variability of fish stocks can facilitate proper management, conservation of endangered species and improvement of stocks of species that can be cultivated. The distribution of subpopulation in mixed fisheries may also be calculated simply if the population genetic structure of a species is well-known. Lack of information regarding the genetic structure of such populations might result in the differential harvest of the populations which will ultimately have a severe and long term consequence. In order to deal with this problem, there is a necessity for investigations encompassing the genetic variations at the intra and interspecific population levels as well as at the intra and inter specific levels of the fish and shellfish resources of any nation [1]

Apart from their economic value and from the biodiversity point of view, fishes are known to have the very best species diversity among all vertebrate taxa. They exhibit highest diversity in terms of size, shape, biology and in the habitats they occupy. There are many latest reviews on the applications of molecular genetic techniques in fisheries and associated areas ^[8, 10, 12, 13, 15, 17, 24, 25, 33, 36, 42, 43, 47].

Within the species itself, organisms may form separate groups and such groups form the fundamental genetic units of evolution. In wild fish populations or cultivable stocks the measurement of genetic diversity is important for understanding, interpretation and effective management of populations or stocks. Genetic diversity has been measured inferentially and indirectly through performance studies and controlled breeding or by classical systematic analysis of phenotypic traits. The different characteristics and ways needed to analyze stock structure in fish populations are ecological, tagging, parasite distribution, physiological and behavioral traits, morphometrics and meristics, calcified structures, cytogenetic, immunogenetic and blood pigments [22].

In order to assess genetic variability at intra specie level, most of the previous studies were based solely on morphological characters but it is very difficult and tedious to assess genetic variation based only on morphological characters ^[2, 41]. Between fishes of different origin, the morphological variations are caused by factors such as environmental factors and a huge fraction of evidence for genetic differences is inferential ^[30]. Realizing the significant role of environmental factors on phenotypic expression in fishes ^[31], present investigators applied biochemical techniques for the identification of gene-controlled phenotypes like proteins and enzymes of diverse tissues of fishes. The important economic traits of a fish like hatchability, age at sexual maturity, bodyweight, fertility, egg production and egg shell quality are less or more genetically linked with completely diverse

protein polymorphs^[3].

Different methodologies have been developed by scientists almost everywhere in the world so as to evaluate genetic variation and to differentiate and characterize fish stocks. One of the conventional methods for characterizing fish stocks has been the comparative examination of morphological characters of the fishes ^[20]. However the traditional morphometric measurements are usually inefficient and biased, as they can produce an uneven coverage of the body form. Histochemical staining and protein electrophoresis ^[39] methods ^[21] gained advantage over morphological studies during the mid 50's, by providing rapidly collected genetic figures. This technique is capable of unveiling the invisible variations that occur at the molecular level as visible biochemical phenotypes through allozyme electrophoresis.

For defining genetic markers for stock identification in fishes, protein electrophoresis can prove to be helpful specially in anadromous species, as proved by various studies that document differences in protein allele frequencies between stocks ^[1, 4, 6, 16, 34, 46, 47].

In the varied array of biological disciplines, studies on genetic variation at protein levels guided to some major contributions ^[45]. Proteins are considered as gene products and electrophoretic mobility's of various proteins in closely linked species or in diverse populations can be explained genetically ^[5]. Different electrophoretic techniques are used to recognize the variations among fish species and muscle protein is most usually used to assess the polymorphism among fish species ^[18, 28, 38].

Among the individuals of the like species, the incidence of polymorphic locus that occurs at molecular level can be a valuable tool to establish heterozygosity that determines the potential of a population. Intra-specific muscle protein variation in marine fish species was reported for the first time in *Anoplomoma fimbria*^[44]. The in-depth study on intra-specific polymorphism was done by Slecttitova *et al.* (1992) in European white fish and peled fishes of family coregonidea that as well showed polymorphism.

Variability in species is present (among populations and also between individuals within a population) in response to survive and successfully react to the environmental changes [32].

Conclusion

There is a reduction in the genetic resources of natural fish populations due to over utilization of fish stocks, pollution and human intervention. Conservation of this fragile genetic diversity is extremely important to maintain ecological balance. Genetic variability is an important attribute of the species, since those with higher levels of variation are most likely to present high additive genetic variance for productive traits. The species with more genetic variability perform better (growth), are viable, have high fecundities and resistant to environmental stress ^[7]. Moreover, an efficient use of any biological resources requires a thorough knowledge of the amount and distribution of genetic variability within the species under consideration. The advent of biotechnology has greatly accelerated the progress of studies on the population structure of the species. Genetically variant species have proven valuable for aquaculture and fisheries management, identification of stocks, breeding programme, restoration of ecology and estimation of genetic contributions in stock. The merits of genetic methods for delineating stock structure have been discussed by many researchers [6, 29, 35, 47]. The advantages of genetic methods include (1) they allow the direct examination through statistical testing of the null hypothesis of a single panmictic population ^[11] (2) they are applicable to any species, available in nature (3) natural genetic variation provides the markers necessary for GSI studies, eliminating costs and assumptions of tagging (4) genetic markers are unaffected by environmental factors (unlike other characters like meristic and morphometric) and (5) genetic markers can be used transgenerationally (e.g., to investigate interbreeding between hatchery and naturally produced individuals and the relative reproductive success of hatchery animals.

Consistent information and research work on genetic variability are crucial for improving yield of fish. Studies can help identify proteins and enzymes in fish that are responsible for increasing the meat yield and also in the treatment of various fish diseases. Moreover, variations in an organism's protein may reflect physiological adaptations to an ecological niche and environment ^[26].

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