STUDIES ON CERTAIN ASPECTS OF TAXONOMY AND GENETICS OF SOME AIR-BREATHING FISHES OF NORTH-EASTERN INDIA

ABSTRACT

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The live fishes comprise about 15% of the total marketable surplus of inland fisheries which seems to originate as captured fishery, either from wild water or from culture pond, naturally occurring with carps. Since it is an unorganised capture fishery, there is no authentic data regarding production.

However, the culture of air-breathing fishes could certainly constitute a substantial second line of production in terms of fish protein from the inland water and could help to step up the nutritional effort which is comparatively very low in India. Keeping this fact in mind, in recent years, the air-breathing fishes have caught the imagination of fishery scientists, in view of their popular demand, their nutritive value and recuperative importance and also for the need to utilize the swamps which cannot be easily made suitable for carp culture. The swamps with diverse water condition can be easily utilized by hardy fishes with air-breathing nature, thus these fishes could provide considerable scope to play an important role in the rural economy and hence it becomes imperative to organize planned effort to render these swamp production. On the other hand, while considering the development and standardization of the fishery management techniques of the air-breathing fishes, many gaps in the information were experienced in the field of biology, ecology and genetics, and therefore it is necessary to undertake the study of certain aspects of biology, systematics and genetics of these fishes. The present investigation is a part of such studies which involves a particular group of air-breathing fishes, the 'Channids' or murrels.

The murrels or the snake-headed fishes are represented by

only one genus Channa (= Ophiocephalus), comprising of six species. They have a homogenous distribution in tropical and subtropical region of the world and at least five species viz. Channa striatus, Channa barca, Channa punctata, Channa stewartii and Channa orientalis, are readily available in North-Eastern India. All the representatives are very much alike in colour and shape and therefore are often difficult to distinguish when they are of the same size. We have undertaken in our laboratory a detailed study on the biology and genetics of this group and keeping this in view, the present work has been carried out and the findings have been presented in three chapters of this thesis.

The first chapter presents the results of morphometric analysis and meristic studies of these five species while the second chapter deals with the chromosome analysis and the third chapter has been devoted to electrophoretic investigations on certain proteins.

I - Morphometric analysis and Meristic counts :

As far as the present study is concerned, a fairly successful working key for the field identification of the different species has been provided from the point of view of morphotaxonomy. All together twentynine morphological parameters have been studied. Though certain amount of intra-species variations are observed, measurements and counts of different body parameters show considerable amount of distinctiveness among different species. Biometric indices for fifteen body parameters have been carried out for all the five species and compared. This study, thus provides a balanced key to identify the different species, irrespective of size, form

and colour. Regression equations for ten body parameters have also been worked out for all the five species studied.

II - Cytogenetical Investigation :

All the five species of Channa have been subjected to chromosome analysis. The 2n numbers of different species are found to be as follows :-

C. striatus	2n=40 (8m + 6st + 26t), NF 54
C. barca	2n=38 (6m + 6sm + 4st + 22t), NF 54
C. punctata Var. A	2n=34 (16m + 14sm + 4t), NF 64
C. punctata Var. B	2n=32 (16m + 16sm), NF 64
C. stewartii	2n=66 (12m + 6sm + 6st + 42t), NF 90
C. orientalis	2n=76 (2m + 6sm + 68t), NF 84

The most interesting finding is the existence of two chromosomal races of C. punctata having 2n number as 34 and 32 respectively, which could not be detected by morphological studies. Moreover, it has been observed that all the species are markedly different from one another at their karyotypic level. Comparison made with the earlier works reveals that certain species (eg. C. orientalis) show quite a good amount of differences in their total chromosome complements. However, basing on the present finding, a hypothetical line of karyotypic speciation has also been presented. It has been suggested that species with more number of acrocentric chromosomes are nearer to the primitive teleosts while species with more number of bi-armed chromosomes are comparatively more advanced in the line of karyotypic evolution. But the karyotypes of C. stewartii and C. orientalis do not show any direct relationship with the karyotypes of C. striatus, C.barca or C.punctata.

III - Electrophoretic Investigations :

Characterization of different Channa species has also been tried through electrophoretic investigation of soluble tissue proteins and serum proteins along with two enzyme systems- Esterases and Lactate dehydrogenase. It has been observed that the pattern of distribution of tissue and serum proteins in all the five species are species specific as well as tissue specific, even through certain homologous bands could be detected among different species. Use of esterases results in unequivocal assignment to species because of species-specific banding pattern. To characterise the nature of esterases, inhibition experiments with different esterase activity inhibitors such as urea, $CuSO_4$, Eserine sulphate, Diisopropylflurophosphate and heat, have also been performed and eight zones of esterase activity could be identified for all the five species. Lactate dehydrogenase isoenzymes show an unique distribution in all the five species studied. LDH A_4 is found to be more negatively charged than LDH B_4 and migrates furthest towards the cathode. LDH E_4 isoenzyme is present in all the species. The overall distribution and banding pattern of LDH is also medicative of the distinctiveness of the genus.

As a follow up of the present work we suggest the study of banding pattern of the karyotype to provide further insight into the karyotypic evolution within this group. We would also like to suggest further application of biochemical techniques involving a large number of enzymes and statistically significant number of individuals to find out the genetic distance between the members which we believe will have the last word in unravelling the phylogenetic relationship of this group of fishes.