IJCRT.ORG

ISSN: 2320-2882



INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

A Study of Karyotypes and NOR Phenotypes in Two Species of *Mystus* (Bagridae, Osteichthyes)

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Abstract

Nucleolus organizer regions (NORs) were studied in the mitotic chromosomes of two species of fish genus *Mystus* (Bagridae), Ag-staining in these Siluriform *M. cavassius* exhibited large NORs on single chromosome pair. A clear heteromorphism with respect to size also observed in this species. *M. seenghala* revealed small NORs of equal size on single chromosome pair. Small NORs located in a single chromosome pair are considered as the fundamental and primitive NOR distribution pattern, and large NORs as the derived type. Therefore, it appears that *M. cavassius* have an advanced status on the evolutionary scale.

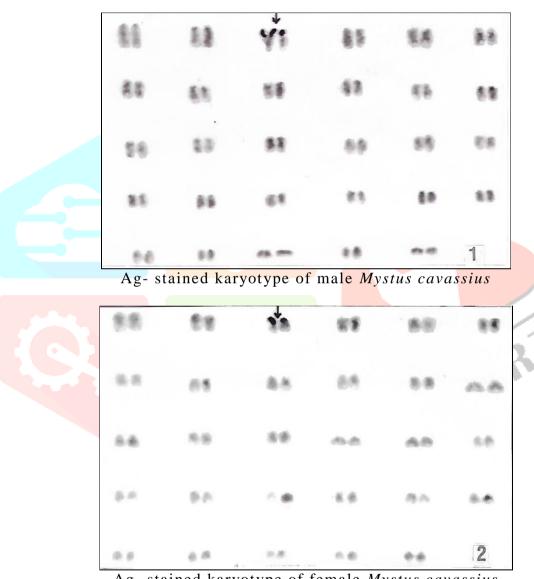
Key words: NORs, catfishes, karyotype.

Introduction: Fishes enjoy a very special position with respect to their economic importance. Therefore, analyses of all the aspects of these animals are quite desirable. More necessary however, could be their genetic assessment which forms a necessary component of any programme envisaging improvement of the existing fish stock. At present, a considerable amount of information on the fish chromosomes has accumulated and more data are continuously pouring in from various laboratories around the world. Although two hundred or so species of Indian fishes have been worked out cytogenetically yet most of them remain unanalyzed by different types of banding technique. However, few reports are there (Barat and Khuda Bukhsh,1986; Barat *e.t al.*, 1990; Das and Khuda-Bukhsh, 2003; Khuda-Bukhsh and Chakarbarti, 1999; Rishi and Thind, 1994; Rishi et al., 1995; Sharma *et. al.* 1986; Thind, 2022; Tripathy and Das,1980; Neeru, 2014; Neeru *et. al.* 2018; Verma *et al.* 2020).

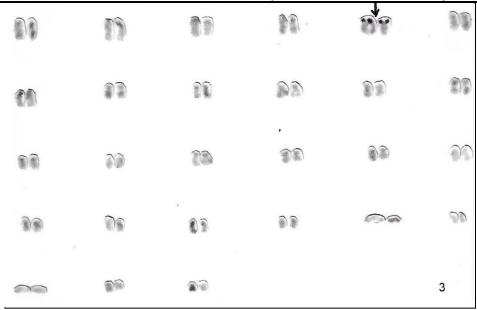
As of now thirteen species of the genus *Mystus* have been worked out cytogenetically by different workers. But noticeable difference have been observed in the data of various workers pertaining to the same species. The reason of this may be inaccurate identification of fish or obsolete methodology. Moreover, the possibility of the presence of sibling species in these Bagrids cannot be ruled out (Le Grande, 1981). Distribution of nucleolus organizer regions (NORs) is an important parameter revealing structural details of karyotypes in a species. Silver staining of NORs shows the nucleolus components positively stained and it serves to identify transcriptionally active NORs at intra-specific level may reveal the extent of NOR variation which may be useful in determining phylogenetic relationships. Taking the above views into consideration, two species of genus *Mystus* have been analyzed presently for karyotypic details and NOR distribution. **Materials and Methods**: Male and female specimens of both species of genus *Mystus* were collected from nature. M. cavassius was collected from village pond near Kurukshetra. *M. seenghala* was captured from Satluj- Ymuna Link canal near Kurukshetra. In each case, the fishes were immediately used for chromosome

preparation. Both in vivo and in vitro treatment of colchicine was given. Slides were prepared from the gill epithelium, spleen and kidney tissue. The usual colchicine -hypotonic- acetic alcohol- air drying technique was used for chromosomal preparations. For NOR analysis, one step method of Howell and Black (1980) was made use of.

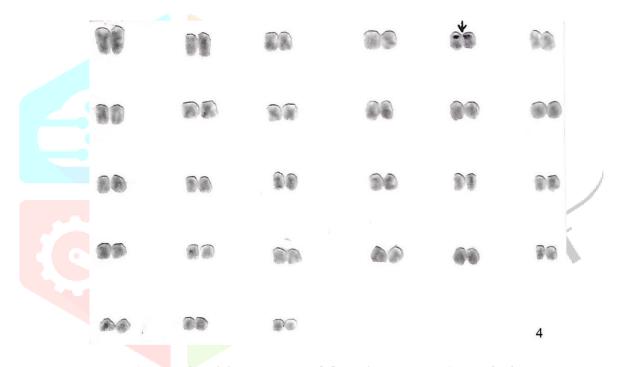
Results: The karyotypic data revealed 58 chromosomes in *M. cavassius* classified as 18 metacentric, 10 submetacentric 2 sub-telocentric and 28 telocentric chromosomes, with FN value 86 in both sexes. Ag-NOR staining revealed only a single pair of NOR- bearing homologues placed at third position in the karyotype. A clear heteromorphism with respect to size of NORs has been observed in M. cavassius (Fig. 1,2). Karyotype of M. seenghala revealed 54 chromosomes out of which 28 metacentric, 12 submetacentric, 4 sub telocentric and 10 telocentric with FN value 94. Ag-NOR staining has revealed small, similar sized NORs only on 5th pair of homologues in both the sexes (Fig. 4,5).



Ag- stained karyotype of female Mystus cavassius



Ag- stained karyotype of male Mystus seenghala



Ag- stained karyotype of female Mystus Seenghala

Discussion: The genus *Mystus* is the best worked out genus of the family Bagridae. Most fish species have small NORs present on a single chromosome pair. This usual condition can be taken as fundamental and original. Takai and Ojima (1986) suggest that fishes with a small amount of DNA have small amount of r-DNA and therefore small NORs. But accidental translocations, duplications and other aberrations, taking place during evolution, could increase the amount of r-DNA and produce large NORs. Thus small NORs located in a single chromosome pair are considered as the fundamental and primitive NOR distribution pattern, and large NORs as derived type (Takai and Ojima, 1986). In the presently analyzed fishes *M. seenghala* have reveled NORs of small size but *M. cavassius* have shown large NORs. Therefore, it appears that *M.cavassius* has an advanced status on the evolutionary scale.

Although the NORs are generally of equal size on the two homologues, a pronounced heteromorphism of NORs is also not uncommon in fishes. Presently, this inequality in size of NORs between two homologous members have been observed in *M. cavassius*. the polymorphism may be due to the variable distribution and/or activity of ribosomal cistrones (Takai and Ojima, 1986; Foresti et al., 1989). Therefore, heteromorphism may either be functional as well as it may even be structural. The issue can be settled by further research at molecular level.

Conclusion: It is clear from the Figures 1-4 NOR-bearing chromosomes in the presently analyzed species are of various forms and sizes, but sites of NORs are mostly terminal (on short arm). The diversity of NOR-bearing chromosomes has probably resulted by way of translocation of NOR sequences from one pair of chromosomes to another. But the difference in the sites of NORs on the chromosomes are dependent upon inversion. This variety of Nor phenotypes can, therefore, be of great use in systematics of any group of fishes.

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