KARYOTYPES OF *GYMNARCHUS NILOTICUS* CUVIER AND *POLLIMYRUS PETRICOLUS* DAGET (*OSTEOGLOSSIFORMES*) FROM OLUWA RIVER, ONDO STATE, NIGERIA

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ABSTRACT

The karyotypes of *Gymnarchus niloticus* Cuvier and *Pollimyrus petricolus* Daget from Oluwa River, Okitipupa, Ondo State were investigated to determine their diploid numbers and characteristics. This was with a view to assessing the chromosomal pattern and evolution of karyotypes in the order Osteoglossiformes.

Mitotic cells obtained from kidney and gill tissues of *G. niloticus* and *P. petricolus* were arrested at metaphase stage by injecting the specimens intraperitoneally with 0.05% colchicines. Hypotonic treatment was in 0.075 M potassium chloride, while prepared slides were stained with 8% Giemsa in 6.8 pH phosphate buffer. The slides were viewed under a binocular light microscope (Leical Gallen III model), and the pictures of cells with good metaphase spread obtained using a digital camera (AmScope MT version 3.0.0.1) mounted on the microscope. Chromosome arms were measured from enlarged computer prints of the best metaphase spread. Karyotyping was made from photo prints of the digital photographs and idiogram plotted using Microsoft Office Excel.

G. niloticus had a karyotype of 2n = 54; 24m+20sm+10sta (FN = 98), while a karyotype of 2n = 48; 10m+18sm+20sta (FN = 76) was recorded for *P. petricolus*. A tetraploid cell (4n = 96) was found in *P. petricolus*.

This study concluded that the karyotype obtained for *G. niloticus*, provided a cytogenetic basis for the separation of *G. niloticus* from the family Mormyridae into a separate family, the Gymnarchidae.

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CHAPTER ONE

INTRODUCTION

Fishes consist of 62 orders, 515 families, and 27,977 extant species making them the most diverse of all vertebrate groups (Arai, 2011). Ichthyfauna constitute more than 48% of all vertebrates and have succeeded at occupying almost all the available niches in the aquatic ecosystems (Helfman *et al*., 2009). Restricted gene flow occasioned by geographical barriers and distance contribute to reproductive isolation in the aquatic environment, and consequently genetic population structuring (Chen *et al*., 2009). It is these genetically differentiated populations that form the basis of species microevolution and divergence.

However, the degree of species diversity of fishes is difficult to explain on the basis of geographical isolation alone. There are increasing evidences that rearrangements involving changes in number and structure of chromosomes play significant role in speciation events (Brun and Galetti, 1997; Miya *et al*.; 2003; Galetti *et al*., 2006; Azevedo *et al*., 2007). This underscores the importance of chromosomal studies to evolutionary biology.

Cytogenetic data have diverse application. They have been used to resolve questions relating to species identification, taxonomy, cryptic reproductive isolation and hybridization in nature (Margarido *et al*., 2007). Cytogenetical data are also highly valuable in the study of ploidy level and in predicting the success of hybridization programmes in cultured species. It has in addition proved to be a useful tool in identification of sex chromosomes, and also in the variations in the number and types of sex chromosomes (Margarido *et al*., 2007; Janko *et al*., 2007) and phylogeny (Pardo *et al*., 2001; Santos *et al*., 2009).

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In most vertebrate groups, karyotype and genome size in combination with data from mitochondria and nuclear gene sequences have contributed to the resolution of questions relating to systematics and evolution (Arai, 2011). Although DNA sequence data have contributed significantly to resolving the issues mentioned above, a more useful approach is one that involves analyses of morphometrics, molecular phylogenetic, genome size and comparative karyology data, rather than utilizing data from only one or a few of these sources (Arai, 2011).

The use of cytogenetic information in complementing other sources of data aimed at addressing the above questions has been very limited in fishes. To date, karyotypic data are available only for about 3,425 species representing 12.24% of extant fishes with 216 families of the actinopterygians lacking karyotype information (Arai, 2011). The reason for the dearth of information on fish karyotypes is because work on fish cytogenetics is very challenging. Many fish species are difficult to keep alive more than a few hours outside their natural environment, which makes it difficult to study the karyotypes of fishes that are difficult to collect alive and those from remote locations. Even obtaining fresh material provides no assurance that reliable chromosome number can be obtained easily, because fish chromosomes are usually small and numerous (Arai, 2011).

In Nigeria, works on fish chromosomes include Clufeagba *et al*. (1999); Awodiran *et al*. (2000); Eyo (2005) and Majolagbe *et al*. (2011); which were carried out on the genera *Clarias* and *Heterobranchus*, and on the Tilapias (Aluko *et al*., 1995). This is probably due to the growing importance of these groups of fish in aquaculture. Lack of appropriate techniques for obtaining fish chromosomes might also have contributed to this situation. Most workers obtain metaphase chromosomes from fish embryos or hatchlings, a technique that limits the fish species

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from which metaphase chromosomes can be obtained to those that can be artificially propagated.

The alternative method of obtaining metaphase chromosomes from fish

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