Inter- and intraspecific allozyme comparisons of mormyrids (Pisces, Mormyridae) from South Africa and Namibia, with reference to an undescribed species

FH van der Bank*

Research Unit for Aquatic and Terrestrial Ecosystems, Rand Afrikaans University, PO Box 524, Auckland Park 2006, South Africa

Abstract

Allozyme comparisons of allopatric populations *of Marcusenius macrolepidotus* and *Petrocephalus catostoma* (from the eastern Caprivi, Namibia, and the Kruger National Park, South Africa) showed little differentiation between the populations of the former species mentioned, but distinct differences between the two populations of *P. catosloma* studied. Three continuous and two discontinuous buffer systems were used, and gene products of 26 protein coding loci were examined by horizontal starch gel-electrophoresis. Fixed allele differences between *M. macrolepidotus* and P. *catostoma* were obtained at 13 of these loci. Allele frequency differences were found between ullopatric populations of the former species, whereas distinct allozyme differences were found at seven of the loci studied in the latter species. This, together with the mean genetic distance value of 0.311, suggests the existence of an undescribed *P. catostoma* species from the Sabie River system. The unbiased genetic distance value among the *M. macrolepidotus* populations studied was 0.023, and it averaged 0.927 between the confamilial genera *Marcusenius* and *Petrocephalus*.

Introduction

There are 18 genera and approximately 200 species in the family Mormyridae in Africa (Skelton, 1993). These fishes have large brains, relative to body mass, comparable to those of humans. They use their electric sense for location and communication, they are popular with aquarists and they are a favourite bait among anglers forcatching tigerfish. These fishes can also be trained by rewarding them with treats for executing the appropriate action upon receiving a previously tape-recorded electric organ discharge, and some mormyrids have been utilised to monitor changes in water quality (Van der Bank and Kramer, 1996).

Van der Bank and Van der Bank (1995) recommended that representatives of certain mormyrid genera should be analysed electrophoretically and compared, especially populations which show differences in electric organ discharge waveforms. Examples of populations that should be studied are *Marcusenius macrolepidotus* (Peters, 1852) from the Sabie and Zambezi River systems, *Pollimyrus castelnaui* (Boulenger, 1911) from the Zambezi and Kwando River systems, and *Hippopotamyrus ansorgii* (Boulenger, 1905) from the Zambezi River. It is possible that different races or species are involved because Kramer and Skelton (1995) observed distinct differences in electric organ discharge (EOD) waveforms between *M. macrolepidotus* from the Sabie River (South Africa) and from the Zambezi River (Namibia). More species than previously recognised might exist because **EODs** are species-specific (Van der Bank and Kramer, 1996). Kramer(1996) indicated sexual dimorphism in *M. macrolepidotus* (i.e. two distinct forms of **EOD** were present), and a statistically significant difference exists in **EOD** waveforms, correlating with age and sex in *Petrocephalus catostoma* (Giinther, 1866) from Namibia. The **EODs** of/', *catostoma* from the Sabie River have not been studied before.

An electrophoretical analysis of such populations should provide a better understanding of the genetic divergence and biogeography of the snoutfishes. The purpose of this study is to use allozyme comparisons, of allopatric populations of *M. macrolepidotus* and *P. catostoma,* as an aid to taxonomy and systematics.

Materials and methods

Electrophoretic data for five *M. macrolepidotus* and four *P. catostoma* individuals from the Upper Zambezi River(17°29'S, 24°26'E) were compared with those of 15 and 8 individuals, respectively, from the Sabie River in the Kruger National Park (25°07'S, 31°53'E). The fish were sampled within a 10 km stretch of the rivers in the area indicated by the co-ordinates. Tissue extracts were prepared and analysed by starch gel electrophoresis (12% gels) using buffers, standard electrophoretic procedures, method of interpretation of gel-banding patterns and locus nomenclature as referred to by Van der Bank and Van der Bank (1995) and Van der Bank and Kramer (1996). Statistical analysis of allozyme data was executed using BIOSYS-1 (Swofford and Selander, 1981).

Results

Locus abbreviations, enzyme commission numbers, and monomorphic loci are listed in Table 1. Allele products at the following loci were monomorphic: **AK, CK-A, PEPA-1, PER, PROT-2** and **sSOD.** Allele frequencies for polymorphic loci are presented in Table 2. Allozyme phenotypes of putative heterozygotes were congruent with those expected on the basis of the quaternary structure of the enzyme (Ward, 1977). Thus heterozygotes at **GAPDH** and **LDH** were five-banded, triple-banded at **ADH, G3PDH, GPI** and **MDH,** as expected for dimeric enzymes, and heterozygotes at the monomeric enzymes **AAT, CK** and **EST** were double-banded. Zymograms of **GPI, LDH** and **MDH,**

* (011) 489-2911; fax (011) 498-2191; e-mail fhvdb@rau3.rau.ac.za

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