An estimate of the amount of genetic variation in a population of the Bulldog *Marcusenius macrolepidotus* (Mormyridae)

FH van der Bank[1]* and M van der Bank[2]

[1]Research Unit for Aquatic and Terrestrial Ecosystems, Rand Afrikaans University, PO Box 524, Auckland Park 2006, South Africa
department of Botany, University of the Witwatersrand, Johannesburg 2050, South Africa

Abstract

As far as could be ascertained, this is the first account of allozyme variation in mormyrids, Five (3 continuous and 2 discontinuous) buffer systems were used and 29 enzymes and proteins were stained for, of which 26 revealed interpretable results. Gene products of 52 protein coding loci in Af. *macrolepidotus* were examined by horizontal starch gel electrophoresis and genetic variation was observed at 21 (40.4%) of these loci. The percentage of polymorphic loci, the mean number of alleles per locus and the average heterozygosity per locus were 30.8% (0,95 criterion), 1.44 (±0.08) and 0.09 (±0.02) respectively. Genetic variation is comparable to values obtained for other freshwater fish species from the Zambezi River.

Introduction

Representatives of the family Mormyridae, of which there are 18 genera and approximately 200 species in Africa (Skelton, 1993), have large brains comparable (relative to body mass) to those of humans. These fishes use their electric sense for location and communication and have been shown to be both electrogenic and electroreceptive (Lissmann, 1958; Kramer, 1990; 1994). *Marcusenius macrolepidotus* (Peters, 1852) is popular with aquarists, is a favourite bait among anglers for catching tigerfish, and some mormyrids have been utilised to monitor changes in water quality (Geller, 1984; Kunze and Wetzstein, 1988; Kunze, 1989). Mormyrids can also be trained by rewarding them with treats for executing the appropriate action when a previously tape-recorded electric organ discharge was sent (Kramer, 1979; Graff and Kramer, 1992). Despite the peculiarities and applications of mormyrids, no information is available on genetic variation in these fishes. We estimated the amount, distribution and pattern of genetic variability in *M. macrolepidotus* from the Zambezi River.

Materials and methods

Muscle and liver samples from 50 *M. macrolepidotus,* collected from the Upper Zambezi River near Katima Mulilo (24°26'S, 17°29'E), were stored in liquid nitrogen and transported to the laboratory. Tissue extracts were prepared and analysed by starch ge) electrophoresis (12% gels) following procedures, method of interpretation of gel banding patterns and locus nomenclature of Van der Bank et al. (1992). Statistical analysis of allozyme data was done using **BIOSYS-1** (Swofford and Selander, 1981).

The following buffer systems were used: HC - a continuous histidine, citrate buffer, pH 6.5, (Kephart, 1990); **MF-**a continuous Tris, boric acid, EDTA buffer, pH 8.6, (Markert and Fauihaber, 1965);P- a discontinuous Tris, citric acid (gel 8.7), NaOH, boric acid (electrode pH 8.2) buffer (Poulik, 1957); RW - a discontinuous Tris, citric acid, (gel pH 8.7), lithium hydroxide, boric acid (electrode pH 8.0) buffer (Ridgway et al., 1970); and TC - a continuous Tris, citric acid (pH 6.9) buffer system (Whitt, 1970).

* To whom all correspondence should be addressed.
(011)489-2911; [F] (011) 489-2191; e-mail fhvdb@rau3.rau.ac.za
Received 6 December 1994; accepted in revised form 3 May 1995.

Results

Locus abbreviations, enzyme commission numbers, tissues and buffers giving the best results in M. *macrolepidotus* are listed in Table 1. Thirty-one of the 52 loci (59.6%) were monomorphic (Table 1). Products of the following loci migrated cathodally:AK-3, **ADH, FH-2, GAPDH-3, GPD-2, SORD-2, IDH-2, LDH-3, MDH-2, ME-2, PER-2** and **SKDH-2.** We also stained for aspartate aminotransferase (E.C. 2.6.1.1), dihydrolipoamide dehydrogenase (E.C. 1.8.1.4) and purine-nucleoside phosphorylase (E.C. 2.4.2.1) which, together with **GAPDH-1, HK-2, SORD-1** and **SKDH-1,** did not show sufficient activity or resolution for satisfactory scoring.

Table 2 presents allele frequencies, coefficients for heterozygosity deficiency or excess (D), Chi-square (X^2) values and degrees of freedom for all the polymorphic loci, as well as individual heterozygosity values *(h).* Loci where significant $(P<0.05)$ deviations of alleles from expected Hardy-Weinberg proportions occurred are also listed in Table 2. Allozyme phenotypes of putative heterozygotes were congruent with those expected on the basis of the quaternary structure ofthe enzyme (Ward, 1977). Thus heterozygotes at **GAPDH** and **LDH** were five-banded, triple banded at **ADH, GPD, GPI, IDH, MDH** and **SOD,** as expected fordimeric enzymes, and heterozygotes at the monomeric enzymes **AK, EST, SORD, PEP, MNR, ME, MPI** and **PGM** were double banded.

Of the 52 protein coding loci which provided interpretable results in *M, macrolepidotus,* 40.4% were polymorphic. Genotypic frequencies at nine loci **(ADH, EST-4, GAPDH-3, GPD-2, SORD-2, LDH-3, MDH-1** and **SOD)** in *M. macrolepidotus* closely approximated Hardy-Weinberg expectations (Table 2). Deficiencies of heterozygotes occurred at all of the other loci, except at **PEP-S3** (Table 2). The number of alleles at the **GPD-1 andMDH-1** loci were three whereas two alleles were present at all of the other polymorphic protein coding loci studied. The mean number of alleles per locus was 1.44 (±0.08), *h* values ranged from 0.039 to 0.500, and the average heterozygosity per locus (H) was 9.2% (±0.02).

Discussion

Deviations of allele frequencies from expected Hardy-Weinberg proportions occurred at the **AK-2, CK-2,** EST-3, **GPD-1,**