# Allozyme variation in *Chiloglanis paratus* and *C. pretoriae* (Pisces, Mochokidae) from the Limpopo River system, Southern Africa

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## Abstract

The gene products of 32 protein coding loci in two populations of *Chiloglanis paratus* and one population of *C. pretoriae* were examined by horizontal starch-gel electrophoresis. Genetic variability estimates were low in all three populations. The percentage of polymorphic loci using the 95% criterion ranged from 6.3% to 9.4% and observed ($H_O$) and expected heterozygosity ($H_E$) values for the three populations ranged from $H_O$ = 0.022 to 0.031 and $H_E$ = 0.025 to 0.036 respectively. Fixed allele mobility differences between the two species were observed at 17 loci and deviations of genotypes from Hardy-Weinberg expectations occurred at six loci. Genetic distance and Wright's fixation index estimates were consistent with values expected for conspecific populations but indicated extensive genetic differentiation between the congeneric species.

## Introduction

The genus *Chiloglanis* comprises 34 species of which eight occur in Southern Africa. Members of the genus, commonly known as suckermouths, are small catlets adapted for life in fast flowing rocky streams or rapids and rocky stretches of rivers (Skelton, 1993). They are valuable in river management programmes as they are useful indicator species of pollution (Skelton, 1993). Furthermore, the suckermouths are popular aquarium fish.

Despite their popularity among aquarists and their importance in river conservation studies, there is no information available on the extent of genetic variation in suckermouths. A scientific approach to conservation and management of biotic resources requires a thorough understanding of the genetic structure of the species concerned. The applicability of allozyme electrophoresis for determining the genetic structure of populations is well documented (e.g. Grant et al., 1988; Van der Bank, 1996) and was the method of choice in the present study.

Two sympatric species comprising two populations of *C. paratus* and one population of *C. pretoriae* were analysed. Both species are endemic to Southern Africa and are superficially similar in appearance, distinguished by the presence of a serrated dorsal spine in *C. paratus* and a smooth dorsal spine in *C. pretoriae*. The purpose of this study was to provide information on the extent of genetic diversity and variability in *C. paratus* and *C. pretoriae* and to compare the data obtained with those for other freshwater fish species.

## Materials and methods

Specimens were collected by electro-narcosis at two localities in the Limpopo River system (Fig. 1). Population 1, *C. paratus* ($N$ = 50), was sampled at the confluence of the Shashe and Limpopo Rivers (22°14' S, 29°22' E) whereas Population 2, *C. paratus* ($N$ = 48), and Population 3, *C. pretoriae* ($N$ = 46), were collected at the Phalaborwa Barrage (24°03' S, 31°08' E) in the Olifants River. Voucher specimens of each population were deposited in the JLB Smith Institute for Ichthyology. The catalogue numbers are as follows: Population 1 (RUSI 57514), Population 2 (RUSI 57512) and Population 3 (RUSI 57513).

After capture, the specimens were frozen in liquid nitrogen (-196°C) for transportation purposes and then stored at -40°C in the laboratory to await electrophoresis. Prior to electrophoresis, approximately 0.5 g skeletal muscle tissue was mixed with 0.5 mℓ distilled water and homogenised using a glass rod. The samples were analysed by horizontal starch-gel electrophoresis using the experimental procedures, methods of interpretation of gel-banding patterns, locus nomenclature and statistical analysis as described and referred to in Engelbrecht and Mulder (1999). The buffer system of choice for separation of the proteins was a continuous Tris, boric acid, EDTA buffer (pH 8.6) as described by Markert and Faulhaber (1965). All allozyme data were analysed using the BIOSYS-1 programme of Swofford and Selander (1981). Genetic variability was assessed by calculating the percentage of polymorphic loci ($P_{0.95}$) and average observed ($H_O$) and expected heterozygosity ($H_E$) per locus. Deviations of allele frequencies from expected Hardy-Weinberg proportions for each locus were tested using the $X^2$-test for goodness-of-fit. Nei's (1972) genetic distance coefficients and fixation indices ($F_{ST}$) were calculated to determine the extent of genetic differentiation among the populations (Wright, 1978).

## Results

Locus abbreviations, enzyme commission numbers and polymorphic loci are listed in Table 1. Eighteen enzyme systems coded by 32 loci were analysed of which 21 loci (66%) were monomorphic. Allele frequencies for polymorphic loci are presented in Table 2. Fixed allele mobility differences between the two species were observed at **AAT-2**, **CK-1**, **EST-1**, **EST-2**, **GPDH-1**, **GPI-2, IDH-1**, **IDDH-1, LDH-1**, **MPI-1**, **PEP-LT- 1**, **PGDH-1**, **PROT-1, PROT-2, PROT-3, PROT-4** and **SOD-1**. A zymogram of the **GPI** protein coding loci showing allele mobility differences for these enzymes between the three populations are presented in

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