Allozyme variation in the river sardine, *Mesobola brevianalis* (Pisces, Cyprinidae)

GD Engelbrecht* and PFS Mulder
Department of Physiology, University of the North, Private Bag X1106, Sovenga 0727, South Africa

Abstract

A population of *Mesobola brevianalis* was examined for genetic variation using horizontal starch gel electrophoresis. Gene products of 27 protein coding loci were consistently resolved and revealed polymorphism at five loci. Observed genotype frequencies at three loci, **CK-1**, **HK-1** and **PGDH-1**, deviated significantly from Hardy-Weinberg expectations. Genetic variability estimates were congruent with those obtained for fish in general. Possible reasons for the low variability values obtained are discussed in relation to natural and anthropogenic influences in the river system. The results are of value for conservation authorities as well as for aquarists concerned with commercial production of the species.

Introduction

Members of the genus *Mesobola*, commonly referred to as neobolins, are relatively small, shoaling species which prefer the upper stratum of open water in rivers and dams. The genus, which comprises four species, is endemic to Africa. A single species, the river sardine (*M. brevianalis*), occurs in Southern Africa (Bell-Cross and Minshull, 1988; Skelton, 1993).

In terms of commercial potential, the river sardine must be one of the most underestimated fish species in Southern Africa. According to Bell-Cross and Minshull (1988), it is invaluable in dam management where it is introduced as fodder for large game fish and other predatory fish such as tigerfish (*Hydrocynus vittatus*), bass (*Micropterus* spp.), nembwe (*Serranochromis robustus*) and silver catfish (*Schilbe intermedius*). This species is also harvested to some extent by subsistence fishermen and is used as bait for predatory fish by anglers. Furthermore, the river sardine is also popular amongst ornamental fish aquarists. Despite these attributes, the river sardine seldom features in large-scale commercial aquacultural ventures.

Information regarding the genetic variation occurring in the river sardine is a basic prerequisite for further fundamental and applied research designed to develop a basis for successful management of this species. Such an understanding of detectable genetic variation will also be important for the establishment of proposed aquaculture ventures involving the species. The present study aims to provide objective information regarding the genetic structure of the potentially commercially important river sardine, using allozyme electrophoresis.

Materials and methods

Sixty individuals were collected with a seine net and by electronarcosis from the Phalaborwa Barrage (24°03' S, 31°08' E) in the Olifants River, Limpopo River system. 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 buffer systems used, electrophoretic procedures, histochemical staining techniques and interpretation of gel-banding patterns are as described in Engelbrecht et al. (1997).

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 using the 95% criterion ($P_{0.95}$) and average observed (H_O) and expected (H_E) heterozygosity per locus. Both H_O and H_E estimates were determined to facilitate comparison with other studies. All polymorphic loci were tested by chi-square (X^2) analysis for goodness-of-fit to Hardy-Weinberg proportions.

Results

The products of 27 protein coding loci were detected and provided interpretable results for population analysis. The names of the proteins examined, locus abbreviations, enzyme commission (E.C.) numbers, and buffer systems giving the best results are presented in Table 1. Twenty-two of the 27 loci (81%) were monomorphic. All polymorphic loci displayed allozyme banding patterns consistent with that expected from the known quaternary structure of the proteins (Ward, 1977). Allele frequencies for polymorphic loci, X^2 values of loci which deviated significantly from expected Hardy-Weinberg proportions, $P_{0.95}$, H_O and H_E estimates for the two populations are presented in Table 2.

Observed genotype frequencies deviated significantly from expected Hardy-Weinberg proportions at three loci, **CK-1**, **HK-1** and **PGDH-1**. These deviations were associated with a deficit of heterozygotes at all three the above-mentioned loci (Table 2). The percentage of polymorphic loci ($P_{0.95}$) was calculated at 14.8%. Estimates of observed and expected heterozygosity were H_O = 0.011 and H_E = 0.025 respectively.

Discussion

Successful management of a species depends on data regarding the genetic structure of populations. The data obtained may be used in management plans by conservation authorities as well as by

* To whom all correspondence should be addressed
☎ (015) 268-2269; fax (015) 268-2209; e-mail engelbrecht@unin.unorth.ac.za
Received 10 June 1998; accepted in revised form 2 February 1999.