Extremely high genetic differentiation between two populations of the river goby, *Glossogobius callidus* (Smith, 1937)

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Abstract

Two populations, an estuarine and freshwater population, of *Glossogobius callidus* were studied using protein gel electrophoresis to compare the extent of genetic variation and differentiation within and between them. Thirty protein coding loci were resolved of which eleven loci were polymorphic. The Nhlabane Estuary population displayed higher expected heterozygosity (H_E = 0.066) than the freshwater population (H_E = 0.025). Rogers' and Nei's genetic distance values as well as genetic heterogeneity estimates (F_{ST} values) indicate a high degree of genetic differentiation between the two populations. The possible reasons for the low variability and the extensive differentiation are discussed.

Introduction

In Southern Africa, the Gobiidae represents a speciose family of 51 genera comprising 107 species (Smith and Heemstra, 1986). The family is found primarily in inshore marine habitats although some species are commonly found in estuaries, coastal lakes and freshwater habitats (Skelton, 1994).

The river goby, *G. callidus* (Smith, 1937), exhibits extensive salinity tolerance as it may be found in estuarine as well as freshwater habitats. This species may also penetrate considerably far inland, especially at the northern limits of its distributional range. Thus, it is evident that estuarine and freshwater populations of *G. callidus* are exposed to widely different environments and therefore selection pressures which, in turn, might favour localised genetic adaptation and ultimately genetic divergence. Furthermore, it has been suggested that specific activities of allozymes may also be affected by salinity (Koehn and Siebenaller, 1981). These are only some of the factors that may influence the genetic structure of estuarine and freshwater populations of the river goby.

The long-term adaptability of populations, and therefore species, is dependent upon a base of genetic variation by means of which to respond to environmental or biotic occurrences (Meffe, 1990). Any management programme involving the river goby will therefore benefit from an understanding of the extent of genetic variation of this species and the preservation of this variation for future adaptation. The need for knowledge regarding the genetic structure of the river goby becomes even more evident when one considers its potential as an ornamental aquarium fish as well as its importance in the fishing industry as a source of protein for subsistence fishermen and/or as bait for the larger game fish species. In light of the above, the genetic structure of an estuarine and a freshwater population of the river goby was examined as part of a broader study on the genetic structure of Southern African gobies.

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Materials and methods

A seine net was used to sample a total of 57 and 49 individuals from the Phalaborwa Barrage (24°03' S, 31°08' E) in the Olifants River system and the Nhlabane Estuary (28°38' S, 32°16' E) in KwaZulu-Natal respectively (Fig. 1). Voucher specimens of both populations were deposited in the JLB Smith Institute for Ichthyology. Catalogue numbers are as follows: Phalaborwa Barrage (RUSI 57805) and Nhlabane Estuary (RUSI 57806). After capture, the specimens were transported alive to the laboratory where they were frozen in liquid nitrogen (-196°C) and stored at -40°C to await electrophoresis. Immediately prior to electrophoresis, the samples were thawed and the head, tail, fins, scales and all internal organs were removed from each specimen. Approximately 0.5 g of the remaining tissue was mixed with 1 mℓ distilled water and homogenised using a glass rod. Extracts were absorbed directly onto Whatman Nr. 3 filter paper wicks.

Horizontal starch gel electrophoresis (13% gels), employing three buffer systems, was used to separate the proteins. The following buffer systems were used:

A - a continuous Tris, citric acid (pH 6.9) buffer system (Whitt, 1970);
B - a continuous Tris, boric acid, EDTA buffer (pH 8.6) as described by Markert and Faulhaber (1965);
C - a discontinuous Tris, citric acid (gel pH 8.7), lithium hydroxide, boric acid (electrode pH 8.0) buffer system (Ridgway et al. 1970).

Electrophoresis was carried out at a constant current of 50 mA for 4 to 5 h. Following electrophoresis, enzymes were visualised using the histochemical methods of Harris and Hopkinson (1976) and Hillis and Moritz (1990). Interpretation of gel-banding patterns was as described by Grant (1989). The locus nomenclature described by Shaklee et al. (1990) was used.

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), average observed (H_O) and expected (H_E) heterozygosity per locus. Both H_O and H_E estimates were determined to facilitate