

# Allozyme differences between populations of chubbyhead barb (*Barbus anoplus* Weber, 1897) and Marico barb (*B. motebensis* Steindacher, 1894)

JS Engelbrecht\* and FH van der Bank

Department of Zoology, Rand Afrikaans University, POBox524, Auckland Park, 2006, South Africa

## Abstract

Starch gel-electrophoresis was used to assess genetic differences between two morphologically similar barb species. Two population samples of each species were analysed and polymorphism was detected, in one or both species, at 10 of the 30 protein coding loci examined. Relative mobility differences of alleles among the four populations were found at 20 of these loci (56.7%). We conclude that the extent of genetic differences between the two species supports the present taxonomic status of these species, which were previously thought to be synonymous. The genetic differences between the species and populations are of conservation importance and can be used to study possible migration routes and the evolution of the species.

## Introduction

*Barbus anoplus* was initially described from the Buffels River (Gouritz River System) in the Cape and is the most widely distributed fish species south of the Limpopo River (Jubb, 1967; 1968). This species is mostly limited to altitudes above 900 m in Kwazulu-Natal and the former Transvaal and it is often the only species present in these river sections (Crass, 1964; Gaigher, 1973). Morphologically, this species resembles *B. motebensis* which is endemic to the former Transvaal and occurs in the upper catchments of some Limpopo River tributaries (Fig. 1). The distribution maps of Skelton (1993) and distribution records (former

Transvaal Nature Conservation) suggest that the distribution of these two species may overlap in the Steelpoort River catchment (Fig. 1) According to Jubb (1968), *B. motebensis* differs from *B. anoplus* in having a lower caudal peduncle scale count and the

breeding males of the former species exhibit numerous conical tubercles on the snout, forehead and the lower jaw. Both Gaigher (1969; 1973; 1976) and Groenewald (1958) experienced difficulties in separating *B. anoplus* from *B. motebensis* and suggested that the two species are synonymous. In the present study the genetic variation within and between four geographically isolated populations was investigated to determine whether *B. anoplus* and *B. motebensis* represent one or more species and to what extent the various populations differ from each other.

\* To whom all correspondence should be addressed.

Present address: Mpumalanga Parks Board, Private Bag X 1088, Lydenburg, 1120, South Africa  
(01323) 2395; fax (01323) 2732; e-mail:

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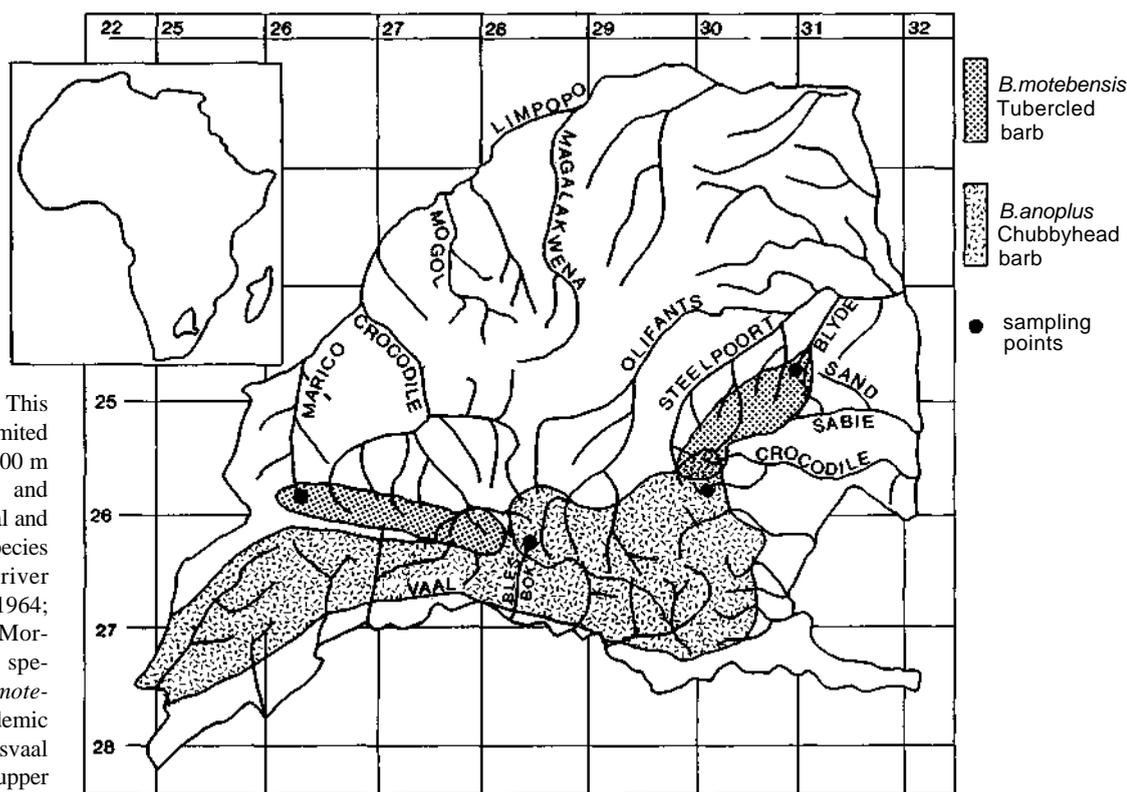


Figure 1  
Map of the former Transvaal depicting the distribution of *Barbus motebensis*, *B. anoplus* and sampling sites