

Which home for coelacanth?

SIR — In 1938, the first living coelacanth (*Latimeria chalumnae*) was trawled off the sandy estuary of the Chalumna River on the east coast of South Africa at a depth of 75 m. All 200 catches since then have come from the Comores, northwest of Madagascar. In August 1991, a gravid female was trawled during the day at a depth of 40–45 m off Quelimane, Mozambique (Fig. 1). This raised the question of whether other coelacanth populations exist along the African mainland or whether coelacanths caught off the African coast are strays.

Our submersible survey at Grande Comore and Anjouan reveals that *Latimeria* is a bottom-oriented drift hunter inhabiting the relatively calm waters of the rocky slopes at around 200 m depth. Being inactive during the day, it retreats to the still waters of lava caves¹. By contrast with the Comorean habitats, the South African and Mozambique locations are exposed to the current, have flat, sandy bottoms and are shallow, seeming unsuitable for coelacanths.

To test the assumption that the Mozambique coelacanth does not belong to the Comorean population, we compared mitochondrial DNA sequences from the most rapidly evolving part of the control region as well as band-sharing frequencies of multilocus DNA fingerprints of several individuals from the Comores and of the Mozambique specimen. Only two different sequences were obtained, varying by one transition at one position in 261 base pairs of the control region among 16 individuals of the Comores. The Mozambique sequence was identical to one of them. This result strongly suggests that the Mozambique and the Comorean coelacanths belong to the same population.

We used DNA multilocus fingerprint-

ing to exclude very recent population differentiation. DNA samples of sufficiently high molecular mass (>30 kb) were digested with *Hinf*I, *Hae*III and *Alu*I, separated on 0.8% agarose gels and hybridized to a panel of simple repeat oligonucleotide probes (see ref. 2). Several of these yielded a uniform multilocus hybridization pattern whereas others produced uninformative smear signals using *Latimeria* DNA as target. Most informative with respect to individualization were (CT)₄ (CA)₅ and (CA)₈ among more than 20 simple repeat probes tested.

Five different individuals from Grande Comore were compared with late-term pups of the gravid female from Mozambique. Determination of the band-sharing index revealed a high similarity of the fingerprints from the Comorean fish, showing a close relationship and low genetic variability comparable to that in close-bred stocks of laboratory fish³. The Mozambique samples are as similar to each of the Grande Comore fish as they are to each other (Fig. 2).

If a separate population of coelacanths exists at the East African coast, we would have expected substantially different fingerprint patterns from the Comorean population. Thus, mitochondrial as well as nuclear markers indicate that the Mozambique coelacanth originated in the Comorean population. An alternative explanation would be that there is an African coastal population in continuous genetic contact with the Comores. But this seems very unlikely.

The Comores are isolated volcanic seamounts surrounded by depths of more than 3,000 m. Coelacanths are adapted to temperate waters of the twilight zone¹. Therefore, benthic migrations through cold waters of the deep sea are extremely unlikely and so the animals could have migrated only by passive drift through the pelagic. However, during almost 200 dives, we never found coelacanths in open waters; drifting in the pelagic zone must be extremely rare. Therefore we believe that the Mozambique coelacanth is a stray originating from the Comores. The Comorean archipelago is exposed to the strong southwest-flowing Mozambique current⁴ which could have transported the fish (Fig. 1).

Although we have not yet been able to obtain

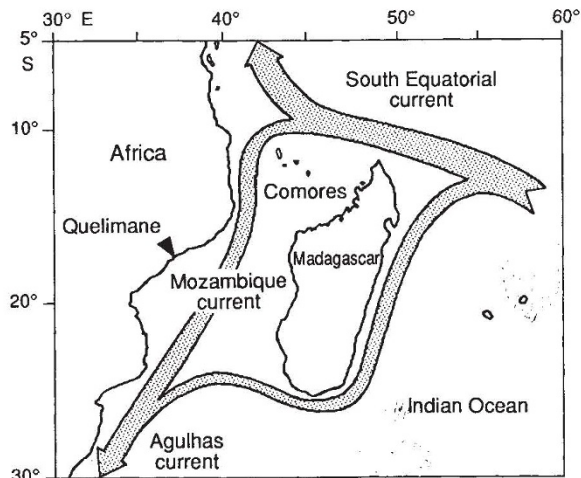


FIG. 1 Classical model of current distribution in the Mozambique Channel⁴. Arrowhead, location of the second coelacanth catch outside the Comores, at Quelimane.

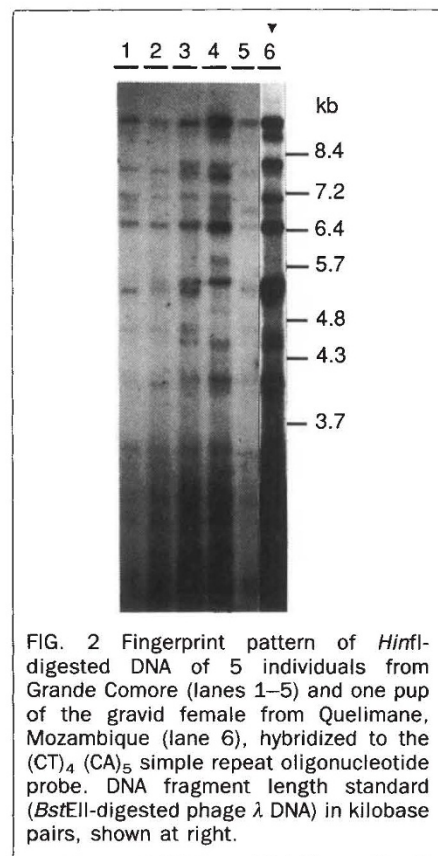


FIG. 2 Fingerprint pattern of *Hinf*I-digested DNA of 5 individuals from Grande Comore (lanes 1–5) and one pup of the gravid female from Quelimane, Mozambique (lane 6), hybridized to the (CT)₄ (CA)₅ simple repeat oligonucleotide probe. DNA fragment length standard (*Bst*EII-digested phage λ DNA) in kilobase pairs, shown at right.

polymerase chain reaction amplifications of the formalin-fixed South African coelacanth, this specimen could also have been a stray. This has already been suggested by J. L. B. Smith, the discoverer of the living coelacanth. The South African location is exposed to the Agulhas current, in part a continuation of the Mozambique current. Therefore the South African coelacanth could also have been derived from the Comores, although we cannot exclude an origin from the east coast of Madagascar.

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