
**EVOLUTIONARY GENETICS OF BARRAMUNDI
(*LATES CALCARIFER*) IN THE AUSTRALIAN REGION**

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I declare that this thesis is my own account of my research and contains as its main content work which has not previously been submitted for a degree at any tertiary institution.

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“It’s not that evolutionary significance starts at a certain point. Your mother probably thinks you’re an evolutionarily significant unit.”

-Waples, 1991

ABSTRACT

Barramundi (*Lates calcarifer*) is a centropomid teleost with a wide distribution across the Indo Pacific. In Australia, barramundi are native to the tropical zone from Exmouth Gulf in Western Australia, across the northern part of the continent, to the Mary River in Queensland. Barramundi are protandrous hermaphrodites, and are euryhaline, with a catadromous life history. Barramundi are a valuable Australian resource, with important commercial and recreational fisheries and aquaculture production to the value of \$11 million dollars per year. Recent declines in the availability of the fish in some rivers has led to an interest in the possibility of restocking rivers with barramundi from other areas.

Determining the genetic structure of barramundi populations in Australia is important for understanding biogeographic history, and appropriate management practices for both aquaculture and recreational and commercial fishing. Previous studies have concentrated on the east coast of Australia, and have largely ignored the western populations. In this study, I obtained DNA data from barramundi populations across the Australian range of the species, as well as populations from Papua New Guinea and Indonesia. The aims of this study were to use the genetic data to determine: 1. if populations in Western Australia show genetic differences between geographic regions 2. if these populations show an ancestral split from populations in the east of Australia and 3. the ancestral origins of Australian barramundi.

Previous studies of DNA data from barramundi have discovered an east/west split occurring at the Torres Strait that was assumed to be caused by the closing of the strait during lowered sea levels. However, these studies suffered from a bias in sampling area, concentrating either on the eastern half of the range of barramundi, or on the western tip of the range. Data from these studies were combined and reanalyzed. Two major clades were discovered, with considerable biogeographic structuring, but their geographic locations did not coincide with the reported vicariance event at the Torres Strait. Instead, historical divisions among freshwater drainage systems appeared to have driven the evolutionary history of barramundi in Australia.

In order to investigate these historical divisions further, a 290 bp section of the mitochondrial DNA control region was sequenced in 284 barramundi from seven populations across the Australian geographic range of the species and from one population in Papua New Guinea and one population in Indonesia. Analyses of molecular variance within and among populations showed significant geographic structuring, based on biogeographical provinces and drainage divisions. Nested clade analyses indicated that these geographical associations were the result of restricted gene flow, range expansion, and past fragmentation events. I hypothesise that the Ord River area in the west of the continent was the ancestral source population for the rest of the species' range across Australia, with Indonesia being the most likely origin of this source. Populations of barramundi from the Pilbara region are genetically distinct and geographically isolated, with strong evidence of an ancestral divide along geographical barriers to dispersal. There is a strong association between Papua New Guinea and Australia, although further

investigations using the cytochrome b region of mitochondrial DNA indicated a more ancestral divide between the two than is currently evident, which could reflect an ancient geographical divide between the two, or could be evidence of a secondary migration route to Australia.

For a more detailed study of evolutionary processes acting on populations of barramundi in Western Australia, allelic diversity was examined at five microsatellite loci. All loci were polymorphic and genotypic frequencies conformed to Hardy-Weinberg expectations, with no significant linkage between loci evident in any population. Measures of within population diversity were significantly related to latitude, suggesting southerly migration from a northern source population. The Ord River was the most genetically diverse population, and the most likely ancestral migration source to the area, with diversity decreasing down the west coast. Although there were significant differences among populations, the nuclear microsatellite data do not indicate the same degree of genetic structuring as is evident in the mitochondrial data. This may be a consequence of rapid evolutionary change at microsatellite loci, with past separations or population differences masked by recombination and back mutation of the microsatellite alleles. However, the nature of nuclear and mitochondrial inheritance may also indicate life history differences between the sexes, where significant genetic contribution to gene flow by males and limited female gene flow may lead to preservation of maternally inherited population substructure.

The principal findings from this study are:

- There is no genetic evidence for an east/west division of barramundi populations in Australia, as suggested by previous research.
- Despite barramundi's catadromous life history, and ability to disperse through marine waters, the present genetic structure indicates a division principally among river drainages. From a population genetic viewpoint, the species can be regarded as freshwater, rather than marine.
- The most likely origin of barramundi in Australia is the Ord River region, with Indonesia as the route of migration.
- Differences in the population structure demonstrated by nuclear and mitochondrial data indicate possible life history differences between the sexes.
- Barramundi populations in different biogeographical provinces may have been substantially isolated over a long period of time, and may therefore represent independently evolving populations. This has important implications for fishery management and translocation issues for restocking rivers.

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