

Genetic Differentiation between Members of a Species Complex (*Retropinna* spp.)

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Abstract : Population connectivity plays an important role in the conservation and recovery of declining species. It affects genetic diversity, adaptive potential and resilience of species in nature. Loss of genetic variation can affect populations by limiting their ability to persist in stressful environmental conditions. Generally, freshwater fishes show higher levels of genetic structuring and subdivision among populations than those inhabiting estuarine or marine environments due to the presence of artificial (e.g. dams) and natural (e.g. mountain ranges) barriers to dispersal in freshwater ecosystems. The Australian smelt (*Retropinnidae*: *Retropinna* spp.) is a common freshwater fish species which is widely distributed throughout coastal and inland drainages in South - eastern Australia. These fish are found in a number of habitats from headwaters to lowland sites. They form large shoals in the mid to upper water column and inhabit deep slow - flowing pools as well as shallow fast flowing riffle-runs. Previously, Australian smelt consisted of two described taxa (*Retropinna semoni* and *Retropinna tasmanica*), but recently a complex of five or more species has been recognized based on an analysis of allozyme variation. In many area, they spend their entire life cycle within freshwater. Although most populations of the species are thought to be non-diadromous, it is still unclear whether individuals within coastal populations of Australian *Retropinna* exhibit diadromous migrations or whether fish collected from marine/estuarine environments are vagrants that have strayed out of the freshwater reaches. In this current study, the population structure and genetic differentiation of Australian smelt fish were investigated among eight rivers of South-East Queensland (SEQ), Australia. 11 microsatellite loci were used to examine genetic variation within and among populations. Genetic diversity was very high. Number of alleles ranged from three to twenty. Expected heterozygosity averaged across loci ranged from 0.572 to 0.852. There was a high degree of genetic differentiation among rivers ($F_{ST} = 0.23$), although low levels of genetic differentiation among populations within rivers. These extremely high levels of genetic differentiation suggest that the all smelt in SEQ complete their life history within freshwater, or, if they go to the estuary, they do not migrate to sea. This hypothesis is being tested further with a micro-chemical analysis of their otoliths.

Keywords : diadromous, genetic diversity, microsatellite, otolith

Conference Title : ICMEEG 2017 : International Conference on Molecular Ecology and Evolutionary Genetics

Conference Location : Prague, Czechia

Conference Dates : July 09-10, 2017