

# Biogeography and Evolution of South Pacific Topshells (Gastropoda, Trochidae) and their Trematode Parasites

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## ABSTRACT

We have used the DNA sequences of Pacific topshells, belonging to the genera *Diloma*, *Melagraphia* and *Austrocochlea*, to ascertain how this group became established over a large area of the Pacific. Phylogenetic analyses of three genes revealed that Pacific topshell species belong to three major clades. The first two clades, including the most basal clade, consisted solely of Australian *Austrocochlea* species. The third clade contained the remainder of the Pacific species, representing all three genera, collected from sites in Australia, New Zealand, Chile, Samoa and Japan. Studying these molecular phylogenies, in conjunction with information available on the fossil record of this group and their life history, allowed us to explain how their Pacific wide dispersal evolved. Our results suggest that there were initially two dispersal events from Australia: a northeastward dispersal to an area stretching from Samoa to Japan and an eastward dispersal to New Zealand. From New Zealand there were subsequent dispersals to Chile and there is also tentative evidence to suggest a back dispersal from New Zealand to Australia. Owing to the short-lived nature of the topshell larvae, trans-oceanic larval dispersal is unlikely. Dispersal most probably occurred by rafting of adults on a suitable platform such as macroalgae, indeed kelp is the natural habitat of several topshell species. Our molecular phylogenies imply that, rather than being a random, unlikely event, adult rafting in ocean currents has occurred repeatedly throughout the evolutionary history of topshells, and has resulted in their Pacific-wide distribution. We have also employed molecular techniques to gain understanding of the biogeography and evolution of the parasites, which have been found to infect six Australasian topshell species. Phylogenetic relationships amongst these parasites were inferred based upon two gene sequences. Our molecular phylogeny separated the single parasitic morphotype into three clearly defined clades (which are almost certainly separate biological species): (i) those infecting two species of *Austrocochlea* from Tasmania, (ii) those infecting *Diloma subrostrata* in Otago and Southland, New Zealand and (iii) those infecting all the parasitised New Zealand topshells (*Melagraphia aethiops*, *D. subrostrata*, *Diloma nigerrima* and *Diloma arida*) throughout the country. This last group comprised two subclades, one infecting only *D. subrostrata* and one infecting the other three species. Three *D. subrostrata* populations were infected by genetically distinct parasites, yet sympatric populations of the other snail species were not necessarily infected. This study is the first to reveal cryptic digenean species in a single population of a molluscan first-intermediate host. Using molecular techniques, in conjunction with more traditional techniques, such as fossil record and morphological analyses, allowed us to gain insight into topshell and trematode evolution and biogeography.

**Keywords and phrases:** *Austrocochlea*, *Diloma*, *Melagraphia*, molecular phylogeny, parasite, rafting, topshell.

