Population genetic structure of the ornate (*Cyclodina ornata*) and copper (*C. aenea*) on Great Barrier Island: Applications to the endangered chevron skinks (*Oligosoma homalonotum*).

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Chevron skinks (*Oligosoma homalonotum*) are a Class Vulnerable (VU D2) by the IUCN. Currently found only on Great Barrier and Little Barrier Islands, this highly cryptic skink species has a low capture rate in the wild, thus making genetic study of the population very challenging. Two more abundant skink species, *Cyclodina* ornata and *C. aenea*, occupy similar habitats to *O. homalonotum*. The purpose of this study is to look at the population genetic structure of subpopulations from selected sites of all three skink species relative to geographic distances between them, and to investigate the use of the two more common species as possible genetic surrogates for the endangered *O. homalonotum*.

A minimum of ten tissue samples (tips of tails) from *C. ornata* and *C. aenea* were collected at selected sites on Great Barrier Island. Tissue samples from stored chevron skink specimens were also collected. All *C. ornata*, *C. aenea* and only current *O. homalonotum* tissue samples will be tested with microsatellite analysis using primers originally developed for the grand skink (*O. grande*). The population genetic structure of each species will be determined by comparing the genetic diversity within and between selected areas. The relative connectivity of populations will be estimated by determining levels of gene flow. All *O. homalonotum* samples will also be used in the mitochondrial DNA (mtDNA) analysis to investigate both contemporary and historical phylogeographic patterns within this species.

The outcomes of this study will 1) elucidate population genetic structure of all three skink species; 2) identify the appropriate species to be used as a genetic surrogate for *O. homalonotum*; and 3) produce recommendations for the Chevron Recovery Plan.