

Using ocean models and genetics, the Moana Project is investigating the connectivity of important kaimoana species, including the blackfoot pāua (*Haliotis iris*).



The blackfoot pāua, *Haliotis iris*, off Kaikōura. Photo by Daniel Crossett, Cawthron Institute.

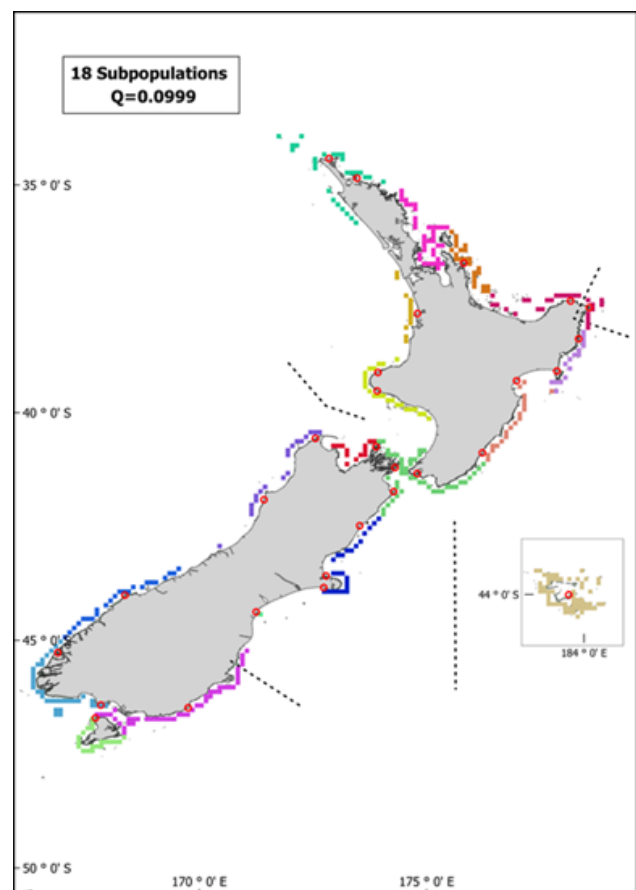
Blackfoot pāua are endemic to Aotearoa New Zealand and support a large commercial and recreational fishery. Wild stocks of many abalone species around the world have collapsed and their cautionary tales show why it is necessary to carefully manage the resource to maintain sustainable exploitation. Major gaps in our knowledge of the biology of blackfoot pāua remain and improved understanding of larval dispersal and wild population connectivity would benefit current management strategies.

Using models to simulate the dispersal of pāua larvae between populations

Combining ocean models and genetic analysis we estimated blackfoot pāua population connectivity. We used the numerical ocean model to track pāua larvae trajectories between 464 populations over 24 years (1993-2017). To validate the model estimates, we used results from previously published genetic studies.

Maps of connectivity and population structure

The model shows that larvae settle close to their starting location, most often within the first 10km. However, all the populations remain well-connected through stepping-stones except at the Chatham Islands, which are isolated from other pāua populations due to their remoteness.



Estimated pāua population structure based on biophysical modelling. The overall population can be divided into 18 subpopulations (colour coded on the map) with high levels of connectivity and, potentially, inter-dependent dynamics. Dashed lines represent previously identified barriers to gene flow using genetic samples taken at 27 locations (red dots on the map).



Within mainland New Zealand, we identified three separate areas where local populations are very well inter-connected: the Cook Strait, the Bay of Plenty, and adjacent to Stewart Island. Estimates of connectivity match the results from the larval dispersal model for the genetic similarities from sampling sites around the country.

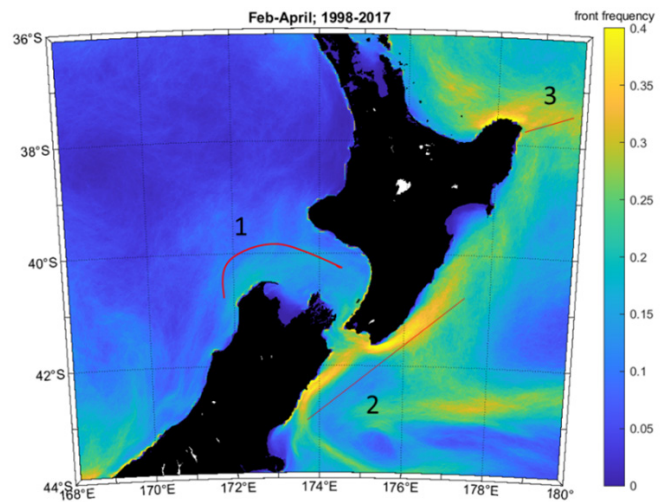
Mapping the demographic structure based on estimated connectivity, we grouped the pāua into 18 subpopulations (figure above), matching most of the barriers to gene flow identified in previous studies (dashed lines on figure).

Impact of fronts on population structure

An analysis of the oceanic fronts around Cook Strait and East Cape helps us understand the population structure. We found three recurring fronts over a period of 10 years. The first front wraps around the top of the South Island and prevents larvae spawned in PAU7 from reaching Taranaki populations, creating the barrier observed in the genetic study.

The second front helps larvae transition from PAU3 (Kaikōura) to PAU2 on the North Island. The third front corresponds to the weak barrier identified at East Cape.

In conclusion, we mapped the connectivity between pāua populations in Aotearoa New Zealand and validated the model estimates with previously published genetic dataset.



Fronts responsible for the population structure in the Cook Strait and East Cape labelled 1-3. Pāua larval trajectories are constrained by these oceanic fronts. e.g. front 1 in the Cook Strait that prevents larvae from reaching the populations in Taranaki.

We found that the population is composed of 18 subpopulations and is strongly influenced by the presence of recurring oceanic fronts and the distance between suitable reefs.

The subpopulation structure, created by the larval exchanges, must be considered when managing the fishing effort to maximise the resilience of populations and ease recovery from local disturbances.

Although the division of the Quota Management Areas separate areas following the main genetic structure identified between Chatham Island and the main islands, unfortunately it does not align well with the metapopulation structure identified in our research.