

Using ocean models and genetics, the Moana Project helped to [investigate the connectivity of scampi](#) (*Metanephrops challengeri*; Figure 1). Scampi are endemic to Aotearoa New Zealand and are fished by commercial bottom trawling over extensive areas of the continental shelf below 100 m depth, including around offshore islands.

The scampi fishery is divided into 10 spatial management areas (Figure 1). Two of the management areas are of greatest fisheries importance; SCI_3 and SCI_6A together account for 54% of the total allowable commercial catch for the species. Typically, the species is found in higher densities on deep sea seafloor plateaus. Despite intensive commercial fishing, relatively little is known about their biology and stock structure.

What little we know at present indicates that the distance scampi larvae is dispersed is likely limited because of the short time larvae spend in the water column (typically less than 11 days), and their very poor swimming abilities throughout the larval stages. Juveniles and adults of scampi live in burrows in soft sediment and emerge to scavenge for food near their burrows, which means they likely do not move great distances.

There are major gaps in our knowledge of the biology of scampi, so we set out to improve the understanding of larval dispersal and wild population connectivity to benefit current fisheries management strategies.

Combining ocean models and genetic analysis we estimated scampi population connectivity. We used the Moana hydrodynamic ocean model to track scampi larvae trajectories among five well-dispersed fishery locations (Figure 1).

The model showed that larvae settle close to their starting location by the end of their time drifting in the water column (Figure 2).

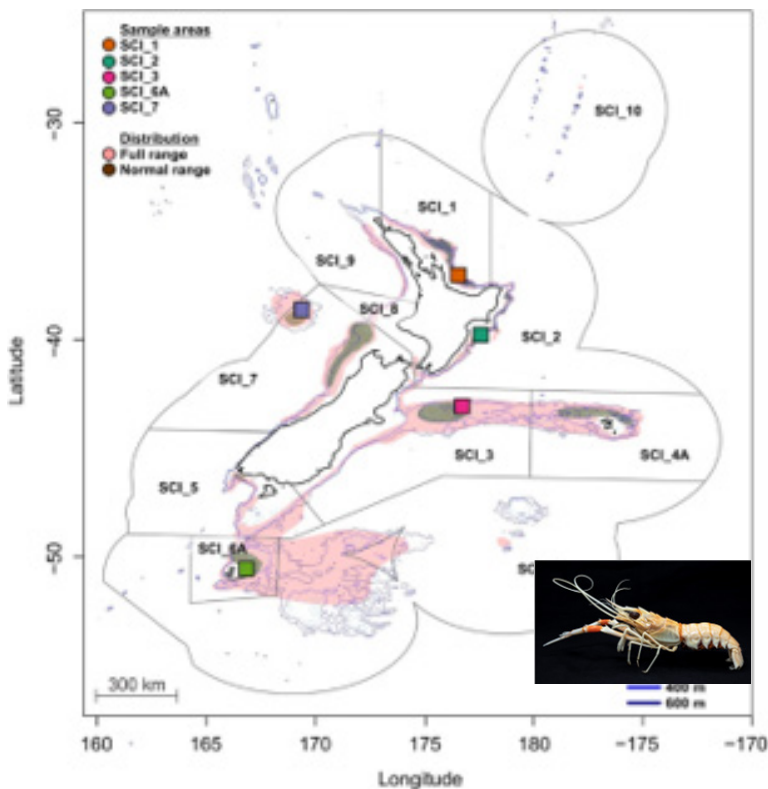


Figure 1. Scampi were collected from five commercial fishery management areas (SCIs shown on map). Map shows the sampling area within each management area (coloured square) and the approximate normal (90% distribution) and full scampi range. The normal distribution is targeted by commercial fisheries and heavily fished.

Scampi photo: Charlotte Johnson, University of Auckland.



The transit time to reach the other sample locations shows that multiple successive generations occurring at intermediate locations (stepping stones) are needed for the connectivity between widely dispersed locations.

Both genetics and hydrodynamic modelling show dispersal around New Zealand aligning with major currents, with an overall eastward dispersal of larvae (Figure 2).

The model highlights the strong connectivity among eastern sampling locations (SCI_1-3) and explains the low genetic differentiation detected there. Together, modelling and genetic evidence indicates directional migration among stocks and revealed source-sink dynamics.

Source-sink dynamics are key ecological features with important implications for fisheries stock recruitment/management as connectivity

influences both sustainability and yield. A source is a population in which the net export of individuals or genetic material is greater than the net import, while the reverse is a sink.

The two management areas (SCI_3 and SCI_6A) of greatest fisheries importance showed contrasting differences in population connectivity. SCI_6A was identified as a source population while SCI_3 was identified as the main sink, providing important ecological information for fisheries management.

Overall, this complementary approach illustrates how ocean currents influence connectivity between populations, highlighting the value of using a transdisciplinary approach to inform conservation and fishery management.

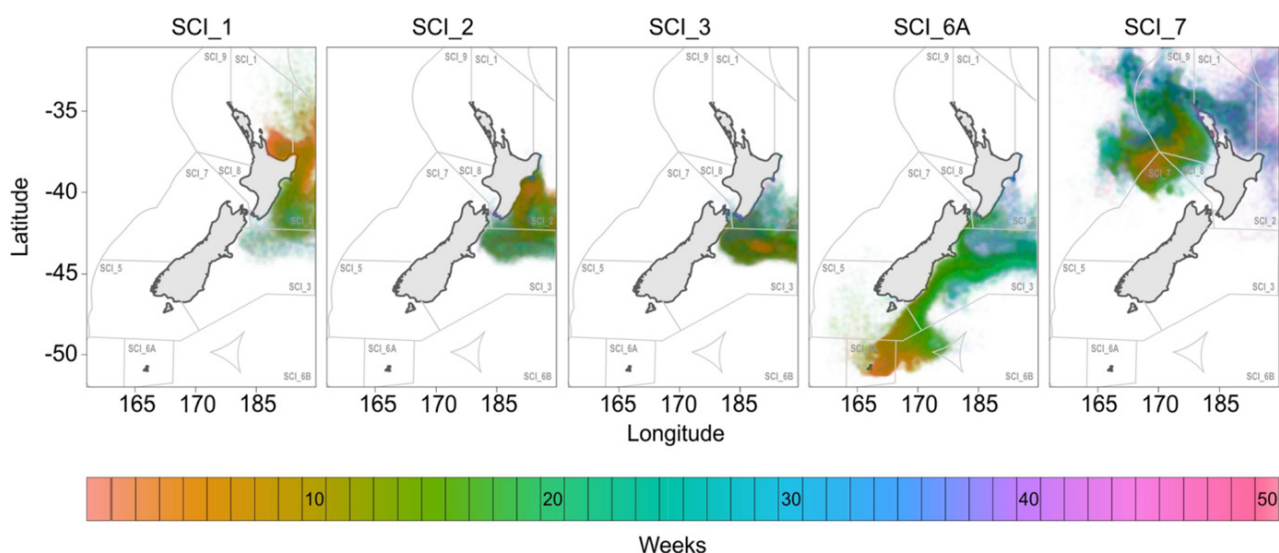


Figure 2. To simulate scampi larval dispersal, we modelled positions of particles in New Zealand waters up to approximately one year after being released from the five scampi fishery management areas (SCI_1, SCI_2, SCI_3, SCI_6A and SCI_7). Plotted is a random selection of 20,000 particles that were released divided equally per SCI, and their movement captured.