

Ocean currents predict fine scale genetic structure and source-sink dynamics in a marine invertebrate coastal fishery

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Estimates of connectivity are vital for understanding population dynamics and for the delimitation of spatial management areas. However, understanding connectivity in the marine environment is still a major challenge because the relative contributions of environmental factors influencing the exchange of individuals amongst subpopulations are difficult to assess. This study combined population genetics with hydrodynamic modelling (Regional Oceanographic Modelling System - ROMS) to assess the spatial and temporal exchange of individuals amongst subpopulations of the endemic New Zealand scallop, *Pecten novaezelandiae*, within the commercial Coromandel fishery area. Small but significant genetic differentiation was revealed amongst subpopulations, suggesting that the Coromandel fishery does not form a single panmictic unit, but that it supports a model of source-sink population dynamics. Highly variable levels of self-recruitment were observed in the different subpopulations and variability in ocean currents estimated from ROMS strongly reflected the genetic structure of populations. Connectivity as assessed by ROMS was a significant explanatory variable of genetic differentiation when accounting for the spatial dependency between locations. Results imply that exploitation strategies should be spatially and temporally adjusted to ensure sustainable scallop fisheries in the future, for example by setting annual catch limits for each subpopulation in relation to its likely role in supporting recruitment. This study highlights the importance of combining different methods for a better prediction of spatial dynamics of populations, and the role that such an approach may play in the management of marine resources.

Keywords: marine connectivity; gene flow; source-sink dynamics; regional ocean modelling system; scallop; New Zealand; fisheries management