ABSTRACT

Consquidering Populations: Genetic Markers to Inform Sustainable Harvest of Arrow Squid

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Two species of arrow squid (Nototodarus gouldi and N. sloanii) comprise the largest commercial squid fishery in Aotearoa, New Zealand. This trawl fishery spans nearly the entirety of Aotearoa's exclusive economic zone (EEZ). It is of substantial economic and sustenance value for people, with an average total annual value of 140 million dollars and a catch of ~30,500 tonnes (Statistics New Zealand, 2020). In addition to economic value, Aotearoa's arrow squids are also of high ecological importance as prey items, being consumed by many species including the endangered pakake, New Zealand sea lion (Phocarctos hookeri) (Meynier et al., 2010). Although these two species are generally found in distinct geographic areas, the Ministry for Primary Industries (MPI) manages both species under a shared Total Allowable Commercial Catch (TACC) limit.

By looking at both single nucleotide polymorphisms (SNPs) and simple sequence repeats (SSRs) as genetic markers, this study will be the first to investigate population structure in Aotearoa's arrow squids. SNPs and SSRs will be sequenced from specimens of both species throughout their range. This data will be used to generate haplotype maps, calculate observed and expected heterozygosity, analyse genetic clustering, and determine population differentiation. These tools will be used to investigate diversity and the presence or absence of sub and meta-population dynamics. These findings will be communicated to inform sustainable fisheries management of arrow squids. Comparisons will also be made between the utility of SNPs and SSRs as population genetic markers for arrow squids, another first in cephalopod research.

References

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