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The deep-sea ecosystem is increasingly subject to destructive industries such as bottom trawling and deep-sea mining. Taonga ('treasure' in Te Reo Māori) species like kekeno and hoki depend on the deep-sea ecosystem. Ensuring that future generations will benefit from these taonga requires conservation (Eero et al., 2021). Yet many facets of deep-sea biology remain understudied, hindering effective conservation efforts. The food web biology of deep-sea squids is one such poorly studied area and their environmental importance will substantially increase as global squid populations fill the void left behind by over harvested fish (Doubleday et al., 2016). My research focuses on the dietary ecology of 3 poorly described deep-sea squid species sampled from local waters: the Angolan flying squid, the southern flying squid, and the hooked squid. To achieve this, I am analysing the squids' gut contents via morphological prey identification and DNA barcoding of prey tissues. This only provides a snapshot of the squids' most recent meals, but longer-term comparative data can be obtained through stable isotope analysis. Squid beaks are chitinous structures that are formed in layers over their lives and stable isotope values of carbon and nitrogen are indices for habitat and food ladder placement (Boecklen et al., 2011). By sub-sampling the beaks and measuring their stable isotope values, squids' habitat and dietary changes can be reliably quantified throughout their lives. Multivariate analysis of variance of identified prey items and stable isotope data will provide further insight into how prey influence the movement of nutrients in the waters of New Zealand. In this presentation, I will showcase that using multiple, complementary methods, we can robustly model the dietary and habitat preferences of these poorly studied yet increasingly important species.

Keywords

Food-web ecology; conservation; stable isotope analysis; cephalopod biology

References

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