

Classifying symbiotic relationships: Corals and Polynoidae of the South Orkney Islands Southern Shelf MPA

Antarctic Science Bursary 2016 - Madeleine Brasier

Overview

In 2016 I was invited to help sample the benthic habitats of the South Orkney Islands Southern Shelf Marine Protected Area (MPA) with the British Antarctic Survey as a polychaete (worm) taxonomist. During this expedition we collected an abundance of polynoid scale worms living on deep-sea corals. To date the taxonomy and ecology of similar species has been described from surveys and laboratory observations on the northern species (Roberts, 2005). Using preserved polynoid material collected on the South Orkney expedition in a collaboration between the Natural History Museum, British Antarctic Survey and the University of Liverpool, we were awarded an Antarctic Science Bursary to:

- Use DNA barcoding to identify the polynoid symbionts to a species level and assess genetic diversity within the MPA
- Use bulk and stable compound specific stable isotope analysis to measure $\delta^{15}\text{N}$ signatures and determine the trophic traits of the polynoid symbionts
- By comparison to the trophic traits of free-living Antarctic polychaetes (previously collected by the candidate) describe the symbiotic relationship between the polynoids and their host corals



Polynoid morphotypes collected from corals within and around the South Orkney Islands Southern Shelf MPA. Scale bar = 5 mm.

Preliminary results

Comparison of our DNA barcodes to publicly available sequences on GenBank showed that our polynoids were closely related to symbiotic polynoids in the South West Indian Ocean (Serpetti et al. 2016). In previous studies of Antarctic polychaetes we recorded an abundance of cryptic species i.e. species which are morphologically identical but genetically distinct (Brasier et al. 2016). However, the genetic diversity of the polynoids was indicative of potentially polymorphic species, species that are morphologically different but genetically similar, a trait that has been recorded in other polynoids (Nygren et al. 2012).

Analysis of $\delta^{15}\text{N}$ signatures from bulk tissue and “trophic” amino acids, those that are enriched in ^{15}N with increasing trophic level and thus providing information about trophic position, found significant differences between the trophic traits of the two morphotypes. In comparison to free-living polynoids which are normally regarded as predator scavenger species, we found distinct differences in the trophic signatures when compared to the symbionts.

By combining these results with information about host species and $\delta^{15}\text{N}$ signatures of “source” amino acids, those that are not enriched in ^{15}N with increasing trophic level and thus providing information about the base of the foodweb, we are beginning to describe their symbiotic relationship.

Impact

The genetic data collected in this project will add to a body of data investigating the evolution and diversity of Antarctic benthos, which is important for understanding and monitoring how these environments may change in the future.

The compound specific stable isotope analysis used in this project is still relatively new to deep-sea biological investigations but has the potential to utilise previously collected material for functional ecological studies. To date the preliminary results have been presented at SCAR Biology 2017 in Leuven, Belgium, where they were well received and gained interest for future symbiotic analyses.

Additionally, our project contributed to our understanding of the ecological value of benthic communities and Vulnerable Marine Ecosystem Taxa within the South Orkney MPA (Brasier et al. 2018) which is up for review by the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) next year.

Next steps

Upon finalising our compound specific stable isotope data, our manuscript will be submitted to Antarctic Science. Our genetics and isotope data will be submitted to GenBank and the SCAR Southern Ocean Diet and Energetics database (SO-DIET) respectively, to be available for future diversity, food web and ecosystem studies.

Acknowledgements

I would like to thank Dr Huw Griffiths and Dr Susie Grant for inviting myself and Dr Helena Wiklund ‘the worm team’ on their research expedition and to all the scientists on board that helped with proposal writing at sea. Thanks are also due to *Antarctic Science* for enabling this opportunity to utilise collected material providing an additional chapter to my PhD thesis and hopefully, a well-received publication.

References

- Brasier, M. J., Wiklund, H., Neal, L., Linse, K., Ruhl, H., Jeffreys, R. M. & Glover, A. G. 2016. DNA barcoding uncovers cryptic diversity in 50% of deep-sea Antarctic polychaetes *Royal Society Open Sciences*, 11, 160432.
- Brasier, M.J., Grant, S.M., Trathan, P.N., Allcock, L., Ashford, O., Blagbrough, H., Brandt, A., Danis, B., Downey, R., Eléaume, M.P. et al. 2018. Benthic biodiversity in the South Orkney Islands Southern Shelf Marine Protected Area. *Biodiversity*, 1-15.
- Nygren, A., Norlinder, E., Panova, M. & Pleijel, F. 2011. Colour polymorphism in the polychaete *Harmothoe imbricata* (Linnaeus, 1767). *Marine Biological Research*, 7, 54-62.
- Roberts, J. M. 2005. Reef-aggregating behaviours by symbiotic eunicid polychaetes from cold-water corals: do worms assemble reefs? *Journal of the Marine Biological Association UK*, 85, 813-819.
- Serpetti, N., Taylor, M., Brennan, D., Green, D., Rogers, A., Paterson, G. & Narayanaswamy, B. 2016. Ecological adaptations and commensal evolution of the Polynoidae (Polychaeta) in the Southwest Indian Ocean Ridge: A phylogenetic approach. *Deep Sea Research Part II: Topical Studies in Oceanography*, 137, 273-281.