



Conference Abstract

# eDNA reveals estuarine benthic community response to nutrient enrichment - evidence from an *in-situ* experiment

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Received: 02 Mar 2021 | Published: 02 Mar 2021

Citation: Clark DE, Pilditch CA, Ellis JI, Borja A, Atalah J, Pearman J, Zaiko A (2021) eDNA reveals estuarine benthic community response to nutrient enrichment – evidence from an *in-situ* experiment. ARPHA Conference Abstracts 4: e65403. <https://doi.org/10.3897/aca.4.e65403>

## Abstract

Nutrient loading is a major threat to estuaries and coastal environments worldwide, therefore, it is critical that we have good monitoring tools to detect early signs of degradation in these ecologically important and vulnerable ecosystems. We carried out a seven-month manipulative experiment in two estuaries to assess the effects of nutrient loading on benthic communities. Environmental DNA metabarcoding was used to examine the response of eukaryotic (18S rRNA), diatom (rbcL), and bacterial (16S rRNA) communities to two levels of nutrient enrichment (150 and 600 g N m<sup>-2</sup>). Multivariate analyses demonstrated consistent changes in eukaryotic, diatom, and bacterial communities in response to enrichment, despite differing environmental conditions between sites (Fig. 1). These patterns aligned with changes in macrofaunal communities identified using traditional morphological techniques, confirming concordance between disturbance indicators detected by eDNA and current monitoring approaches. Clear shifts in eukaryotic and bacterial indicator taxa were seen in response to nutrient loading while changes in diatom communities were more subtle. Community changes were discernable

between nutrient levels, suggesting that estuary health assessment tools could be developed to detect early signs of degradation. Existing eDNA-based biotic indices (microgAMBI and mtMBI) were able to detect these community shifts, suggesting transferability of these indices to other regions and systems. This work represents a first step towards the development of molecular-based estuary monitoring tools, which could provide a more holistic and sensitive approach to ecosystem health assessment with faster turn-around times and lower costs.

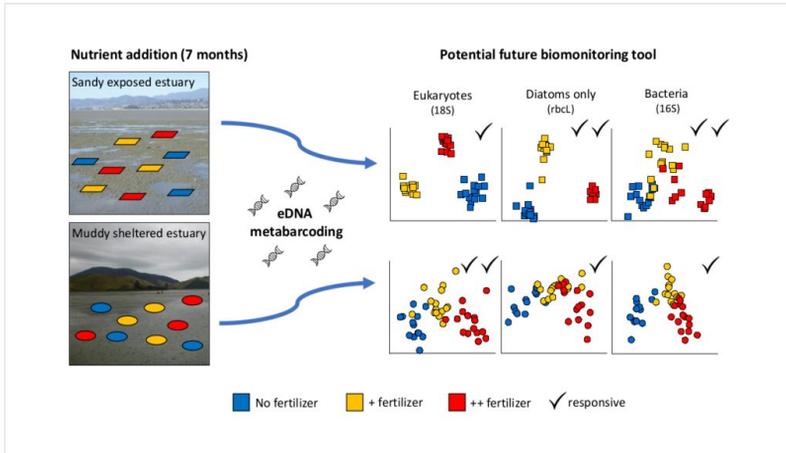


Figure 1. [doi](#)

Graphical summary of experiment

## Keywords

environmental monitoring, bacteria 16S, diatoms rbcl, eukaryotes 18S, high-throughput sequencing

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## Presented at

1st DNAQUA International Conference (March 9-11, 2021)

## Acknowledgements

This research was supported by the New Zealand Sustainable Seas National Science Challenge (Tipping Points Project), Nelson City Council, the Cawthron Institute's Internal

Investment Fund, and the New Zealand Coastal Society. Special thanks to Rebecca Gladstone-Gallagher, Anna Berthelsen, Shaun Bryant, Chris Cornelisen, Lisa Floerl, Simon Madill, Emma Newcombe, Holly Bennett, Sorrel O'Connell-Milne, Yuriy Malakhov, Jamie McAuley and Lais Miura for help in the field and Laura Biessy for assistance with laboratory work. We also thank Te Tau Ihu iwi for supporting our research in these two estuaries. Gretchen Rasch provided constructive comments on a draft version of the manuscript.