

# Molecular phylogeny and systematics of the genus *Adeonella* (Bryozoa, Cheilostomatida) from False Bay, South Africa

Mabalabala O <sup>[1]</sup>, Boonzaaier-Davids MK <sup>[2]</sup> <sup>[3]</sup>, Puckree-Padua C <sup>[1]</sup>, Kara J <sup>[1]</sup>

<sup>[1]</sup> Department of Conservation and Marine Sciences, Cape Peninsula University of Technology,

<sup>[2]</sup> Department of Forestry, Fisheries and the Environment, Cape Town & <sup>[3]</sup> Iziko Museums of South Africa.

\*Corresponding author: [onikamabalabala@gmail.com](mailto:onikamabalabala@gmail.com) and [219159335@mycput.ac.za](mailto:219159335@mycput.ac.za).

## INTRODUCTION & AIM

The use of molecular techniques in studying bryozoans in South Africa is still in its early stages, offering significant research potential. Bryozoans are crucial bioindicators of changing environments, and new molecular trees provide insights into phylogenetic relationships and evolution patterns (Nikulina et al., 2007; Lukhtanov, 2019). *Adeonella* is a large genus that comprises of 58 known extant- and fossil species globally, with the most species distributed throughout the Indo-West Pacific realm, the Mediterranean and South Atlantic Ocean (Hayward, 1988; Amui, 2005; Rosso & Novosel, 2010). More than 60% of adeonellids are considered endemic to South Africa's coastline, but owing to high morphological plasticity and polyphyletic relationships within this group (Hayward, 1988; Orr et al. 2019), molecular techniques are necessary to distinguish between species.

## METHODS



Figure 1: Samples sites in False Bay: Bordjesrif, Buffel's Bay, Millers Point, Dalebrook, A-Frame, Strand, and Gordon's Bay.



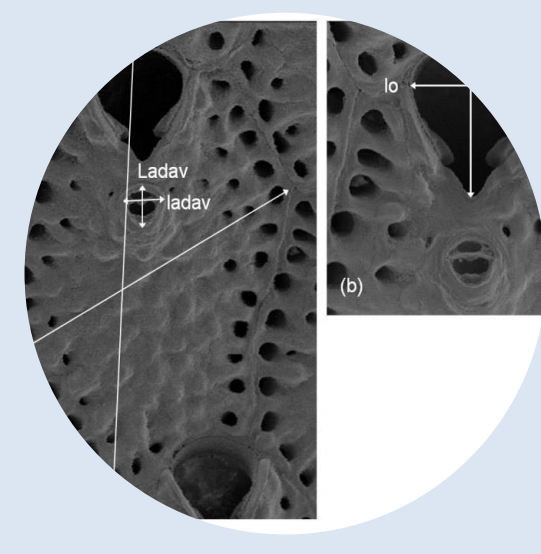
1. Light microscope for initial rapid morpho-species identification



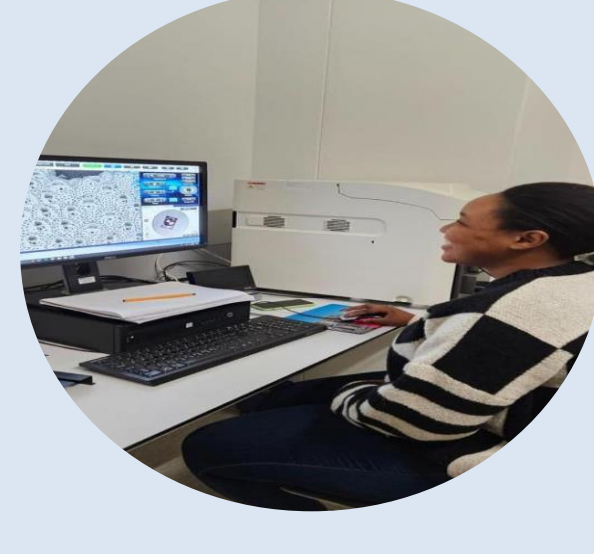
2. Bleaching of specimen to expose skeletal features



3. Sonic water bath (5 min) to remove excess organic matter



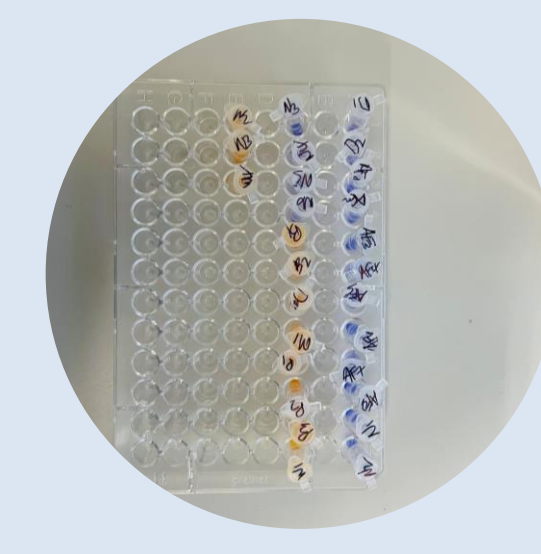
6. Statistical measurements collected from SEM images



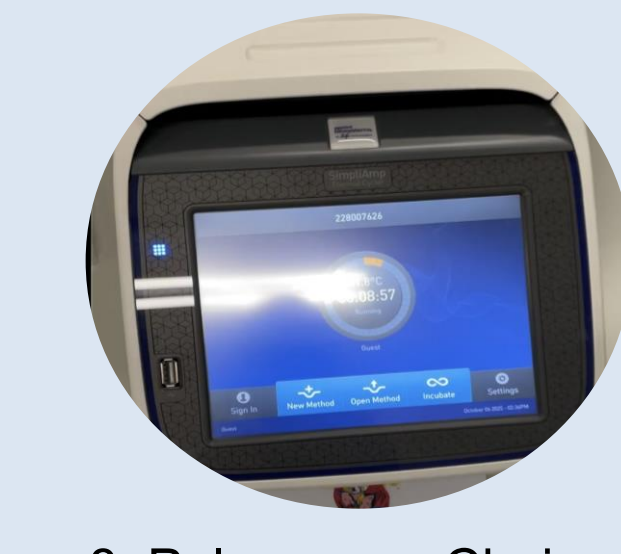
5. SEM imaging taking place



4. Specimen mounted on to stubs for SEM imaging.



7. Adeonellid samples ready for PCR



8. Polymerase Chain Reaction taking place.

## RESULTS & DISCUSSION

Across 13 sites (Fig. 1), 27 adeonellid samples were collected from False Bay and Algoa Bay, with most coming from subtidal habitats (22) and fewer from intertidal zones (5). Five species (*A. pluscula*, *A. conspicua*, *A. guttata* and *L. jellyae* and an unnamed *Adeonella* sp.) were identified, three of these species are considered endemic to South Africa (Fig.1,3,5). Interestingly, all four known species identified in this study were found in both False Bay and Algoa Bay, which are approximately 600 km apart, and potentially due to larval transportation via the Agulhas current that flows southward. DNA extraction and PCR were conducted. Poor sequences were produced; however, troubleshooting is underway to ensure quality sequences.

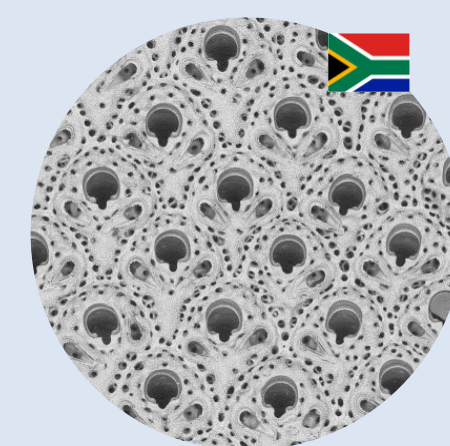


Figure 1. *Laminopora jellyae*, Levinson, 1909.

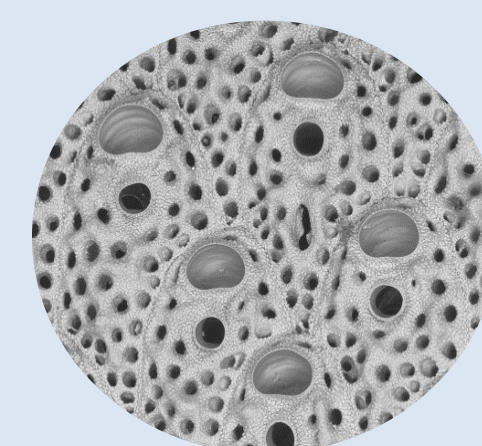


Figure 2. *Adeonella pluscula*, Hayward, 1988



Figure 3. *Adeonella guttata*, Hayward, 1988

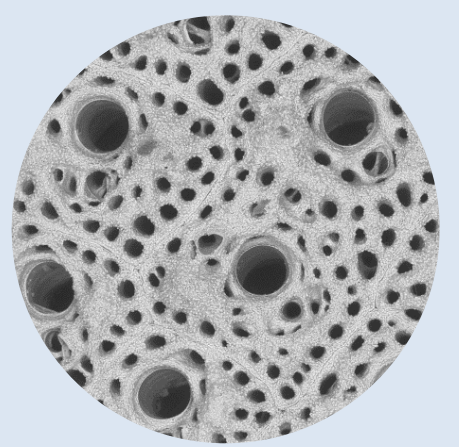


Figure 4. Unnamed *Adeonella* sp.

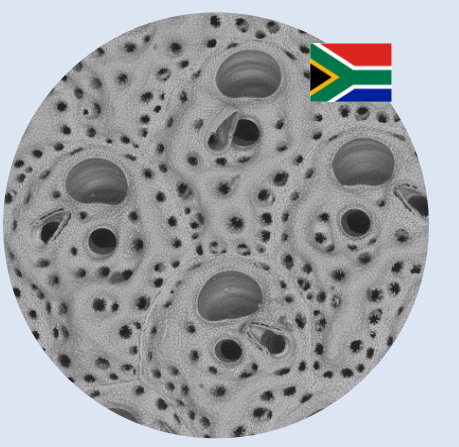


Figure 5. *Adeonella conspicua*, Hayward & Cook, 1983

The study was focused on False Bay (22 samples), but additional adeonellid samples from Algoa Bay (5 samples) allowed us to compare species between the two regions and broaden our barcode reference collection. Large-scale genetic barcoding of bryozoans in South Africa is lacking, with only a small fraction of species barcoded. To better understand phylogenetic relationships, there is a need for broad movement toward the integration of morphological and molecular data (Orr et al., 2019). In our ongoing research, we will expand our sampling efforts in False Bay to collect additional adeonellid samples, while also utilizing previously collected samples to perform genetic barcoding to distinguish between these cryptic species

## CONCLUSION

Few studies in South Africa focus on understanding the evolutionary changes of bryozoans using both taxonomic and molecular data. Integrating these data types will help with providing a better understanding of phylogenetic relationships among species within the same taxa. In conclusion, this study encourages extensive sampling efforts to fully understand the endemism of bryozoans within False Bay and along the Southern African coastline

## REFERENCES

- Amui, A. M. (2005). Adeonellas from the Gulf of Aden including one new species. *Zootaxa*, 52(1012), 45–52. <https://doi.org/10.11646/zootaxa.1012.1>.
- Bock, P. E. (1831). Class Anthozoa Ehrenberg, 1834. In: Zhang, Z.-Q. (Ed.) Animal biodiversity: An outline of higher-level classification and survey of taxonomic richness. *Zootaxa*, 3148(1), 19. <https://doi.org/10.11646/zootaxa.3148.1.5>
- Boonzaaier-Davids, M. K., Florence, W. K., & Gibbons, M. J. (2020). Novel taxa of cheilostomata bryozoa discovered in the historical backlogs of the iziko south african museum. *Zootaxa*, 4820(1), 105–133. <https://doi.org/10.11646/zootaxa.4820.1.5>.
- Boonzaaier, M. K. (2016). *Diversity and Zoogeography of South African Bryozoa* Melissa Kay Boonzaaier Thesis Unvepresented for the Degree of Doctor of Philosophy Department of Biodiversity and Conservation Biology The rsity of the Western Cape DECLARATION. June.
- Lukhtanov, V. A. (2019). Species Delimitation and Analysis of Cryptic Species Diversity in the XXI Century. *Entomological Review*, 99(4), 463–472. <https://doi.org/10.1134/S0013873819040055>.
- Nikulina, E. A., Hanel, R., & Schäfer, P. (2007). Cryptic speciation and paraphyly in the cosmopolitan bryozoan *Electra pilosa*-Impact of the Tethys closing on species evolution. *Molecular Phylogenetics and Evolution*, 45(3), 765–776. <https://doi.org/10.1016/j.ympev.2007.07.016>.
- Orr, R. J. S., Haugen, M. N., Berning, B., Bock, P., Cumming, R. L., Florence, W. K., Hirose, M., Di Martino, E., Ramsfjell, M. H., Sannum, M. M., Smith, A. M., Vieira, L. M., Waeschenbach, A., & Liow, L. H. (2019). A genome-skimmed phylogeny of a widespread bryozoan family, Adeonidae. *BMC Evolutionary Biology*, 19(1), 1–10. <https://doi.org/10.1186/s12862-019-1563-4>