Ecosystem biomonitoring with eDNA: Metabarcoding across the tree of life in a tropical marine environment

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eDNA Analysis Methods

• Environmental Shotgun Sequencing (ESS)
  • Randomly sequences fragmented DNA directly from environmental sample
  • Cost prohibitive
  • Hasn’t been widely used for eukaryotes

• DNA Metabarcoding
  • PCR Amplification of target genes on bulk DNA extracts + next-generation sequencing (NGS)
  • Potential PCR bias
eDNA Method Survey

- Focused on single tropical reef site (Coral Bay in west Australia)
  - Renowned for marine biodiversity
- Explored utility of eDNA methodologies to assess eukaryotic diversity on ecosystem level
- Validated extent to which metabarcoding can inform on marine biodiversity
- Determined capacity for eDNA analysis from seawater
ESS from seawater

• Analyzed over 23 million sequences from 9L of filtered seawater
Tree of Life (ToL) Metabarcoding
ToL metabarcoding cont’d
ESS vs ToL metabarcoding

• ToL metabarcoding required less sequencing effort
• Greater percentage of metabarcoding sequences passed quality filtering (79% vs 14%)
• Metabarcoding gave a broader eDNA snapshot (prokaryotes + eukaryotes)
Conclusion

- For methodologies explored:
  - Required minimal equipment
  - Rapid procedure
  - Non-invasive
  - Can be conducted autonomously

- Metabarcoding
  - Proved to be superior to ESS
  - Viably assessed eukaryotic diversity from eDNA seawater samples

- eDNA analyses have great potential for future marine biomonitoring programs