Marine Community Genetics: A Test of eDNA in the Hawaiian Islands

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Question

Can environmental DNA (eDNA) methods **recover accurate haplotype frequencies** for population genetics analyses?

Here, we evaluate whether community-level **eDNA can substitute** for traditional tissue-based datasets in **population genetics**

Background

No prior tests of eDNA for population-level genetic variation across marine communities

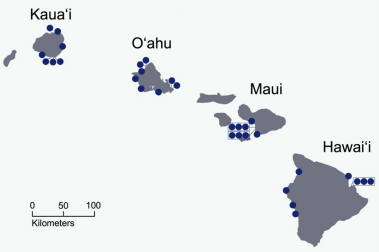
"Universal" primers boost species coverage allowing for large comparative studies

eDNA is mixed DNA from multiple individuals
- **Unknown number** of individuals/sample

Population structure analyses require haplotype **detections and frequencies**

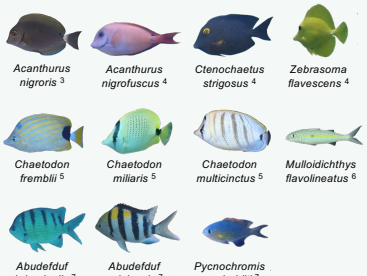
Methods

Collected 8 water samples, 2L each, from 8 nearshore reefs on each island

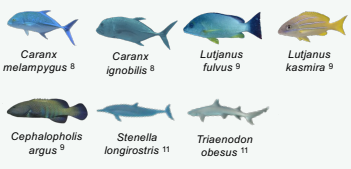


Sequenced 234 bp of cytochrome b[1,2]

Compared eDNA-derived metrics to previous tissue-derived metrics shortened to 234 bp of cytb for 11 species:



Additional 7 species for comparing to entire, ~600 bp, sequence derived from tissue:



Converted eDNA read counts to proxies for haplotype frequencies
- Presence-absence (0 or 1)
- Scaled by read counts (0 - 4)
- Read counts (no proxy)

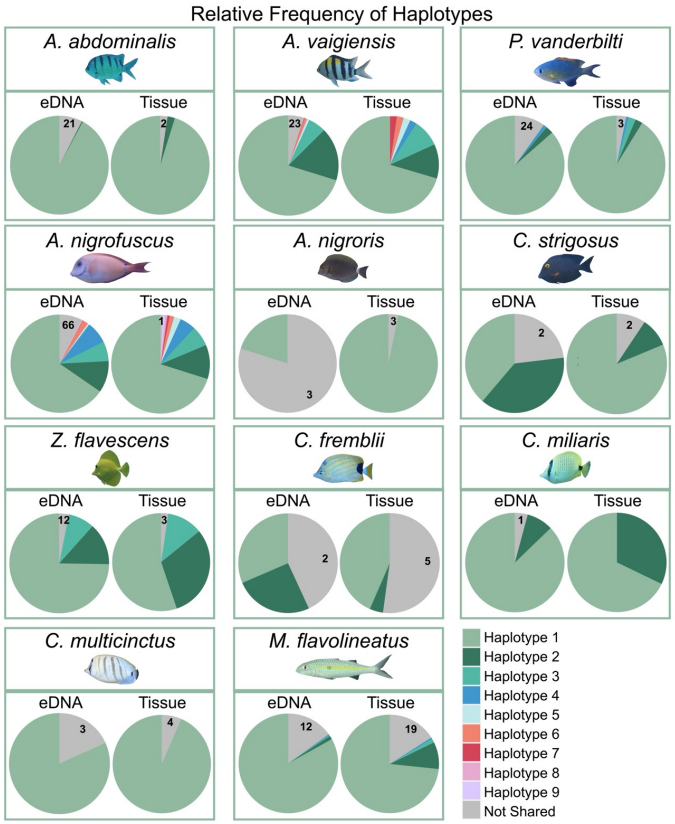


Figure 1. Species haplotype frequencies. eDNA-derived frequencies shown using raw-reads proxies and tissue-derived haplotypes have been shortened to the same amplicon as eDNA for direct comparison. Haplotypes not shared between the two methods were pooled, with pooled counts of unique haplotypes in the grey area.

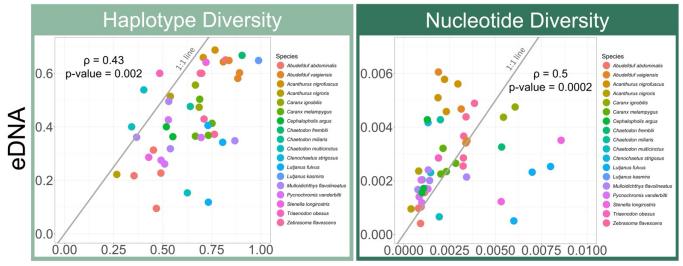


Figure 2. Descriptive mtDNA diversity Spearman's rank correlations. Correlations (ρ) between eDNA data using scaled-by-reads proxies and tissue data for each of the four islands of each species.

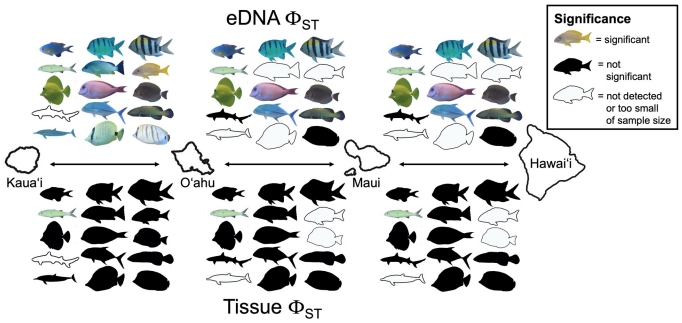


Figure 3. Cross-channel differentiation. Presence and absence of significant pairwise Φ_{ST} values across each island channel for eDNA data (top) and tissue-based data (bottom). eDNA data used raw-reads proxies.

Scan for figures with different eDNA haplotype frequency proxies

Findings

Genetic Diversity

1. eDNA detected **similar haplotype frequencies** as tissue studies (Fig. 1)
   - More rare haplotypes detected with eDNA in abundant species (Fig. 1)
   - Excess haplotypes unlikely to all be sequencing errors given strict filtering

2. Haplotype and nucleotide diversity were **significantly correlated** (Fig. 2)
   - Tissue: longer regions → more haplotype diversity

Population Differentiation

1. **More genetic differentiation** with eDNA
   - More species with differentiation (Fig. 3)
   - Larger pairwise Φ_{ST} values (Fig. 4)

2. Raw reads proxies → most differentiation
   - True sample size unknown but **eDNA statistical power changes** with proxy
   - Raw reads proxies inflates sample size
   - Presence-absence proxies likely underestimates sample size

3. Rare species are **often undersampled** with eDNA (Fig. 4)

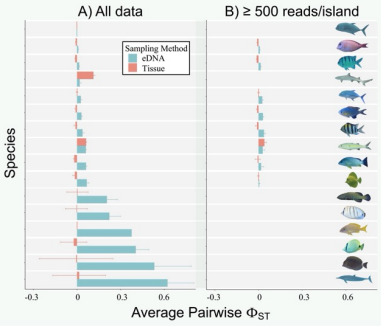


Figure 4. Genetic differentiation. Means pairwise Φ_{ST} estimates among islands were repeated for A) all data and B) a subset of islands with ≥ 500 reads. Error bars are standard error. eDNA data used raw-reads proxies.

Summary

eDNA recovered haplotype frequencies and patterns of genetic diversity similar to tissue studies for a marine vertebrate community.

Genetic diversity metrics were robust to sampling variation. Population genetic metrics were sensitive to low sampling of rare species and high gene flow of marine species.

Next Steps

Sampled North Central Pacific archipelagos

How are the Hawaiian Islands connected to the broader Pacific using biogeography, phylogeography, and population genetics?

Investigating marine metazoan communities:

Contact

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References:
[1] Minamoto, T., H. Yamanaka, T. Takahara, et al. . 2012. Limnology 13:193–197.; [2] Burgener, M., and P. Hübner. 1998. Eur. Food Res. Technol. 207:261–263.; [3] DiBattista, J. D., C. Wilcox, M. T. Craig, et al. 2011. J. Mar. Biol. 2011:1–17.; [4] Eble, J. A., R. J. Toonen, and B. W. Bowen. 2009. Mar. Biol. 156:689–698.; [5] Craig, M. T., J. A. Eble, and B. W. Bowen. 2010. J. Biogeogr. 37:2125–2136.; [6] Fernandez-Silva, I., J. E. Randall, R. R. Coleman, et al. 2015. J. Biogeogr. 42:2402–2413.; [7] Tenggardjaja, K. A., B. W. Bowen, and G. Bernardi. 2018. Mar. Biol. 165.; [8] Santos, S. R., Y. Xiang, and A. W. Tagawa. 2011. J. Hered. 102:47–54.; [9] Gaither, M. R., R. J. Toonen, and B. W. Bowen. 2012. Proc. R. Soc. B 279:3948–3957.; [10] Andrews, K. R., L. Karczmarski, W. W. L. Au, et al. 2010. Mol. Ecol. 19:732–748.; [11] Whitney, N. M., W. D. Robbins, J. K. Schultz, et al. 2012. J. Biogeogr. 39:1144–1156.