Marine metaphylogeographic structure across the North Central Pacific

Taylor D. Ely[1], Donald R. Kobayashi[2], Amy L. Moran[3], Johanna L.K. Wren[2], Peter B. Marko[3]
[1]School of Life Sciences, University of Hawai'i at Mānoa; [2]Pacific Islands Fisheries Science Center, National Marine Fisheries Service;
[3]Oregon Institute of Marine Biology, University of Oregon

Questions

Are patterns of species and haplotype composition concordant across the North Central Pacific (NCP)? How are marine communities in Hawai'i connected to the rest of the NCP?

Background

- Hawai'i is extremely geographically isolated (Fig. 1), with no direct current to Hawai'i
- Biogeography and population genetics of fish suggest strong links with Johnston Atoll and potentially the Line Islands and Japan
- Comparing patterns across multiple taxa can offer clues about the processes connecting or isolating island communities

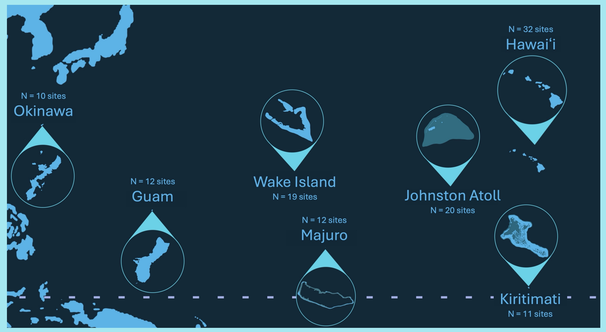


Figure 1. Sampling locations. Hawai'i includes 4 islands: Big Island, Maui, O'ahu, and Kaua'i.

- Accurate haplotype frequencies can be determined from eDNA seawater samples (Fig. 2)

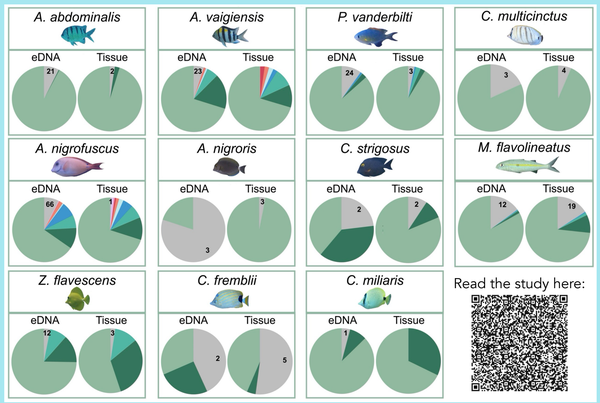
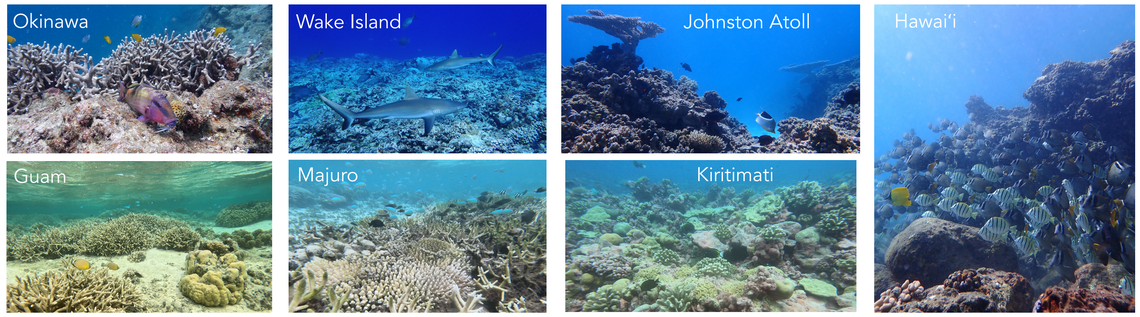


Figure 2. Species haplotype frequencies. eDNA-derived and tissue-derived haplotype frequencies. Haplotypes not shared between the two methods were pooled in grey area with counts of unique haplotypes.



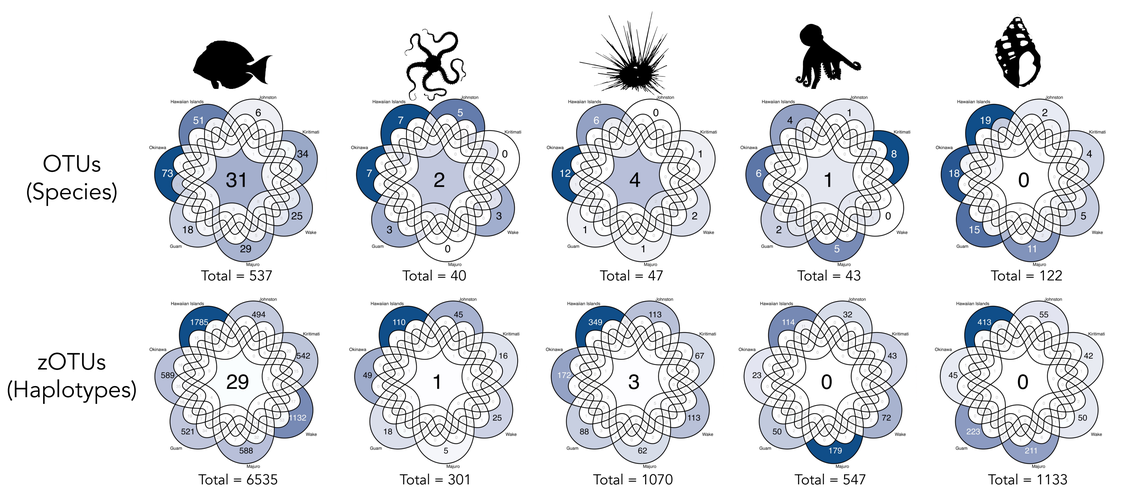


Figure 3. Patterns of shared and unique OTUs (top) and zOTUs (bottom). Darker blue indicates more OTUs or zOTUs shared. The center numbers are OTUs/zOTUs shared everywhere, while the outer numbers are those unique to each region.

Haplotype composition reveals geographic patterns that species composition may miss

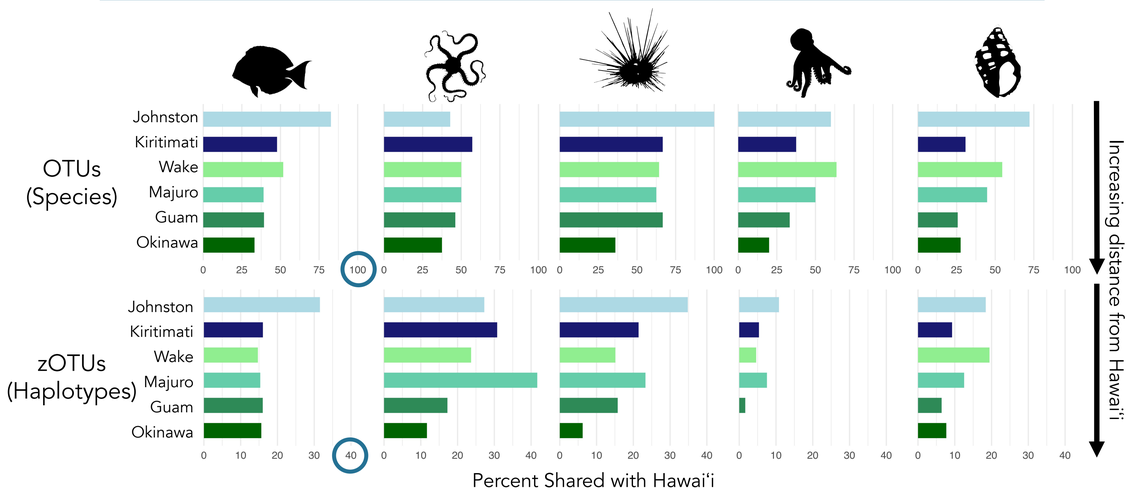


Figure 4. Percent OTUs (top) or zOTUs (bottom) shared with Hawai'i. Ordered by increasing geographic distance from Hawai'i.

Methods

Collected 8 seawater samples, 2 L each, at 8 – 20 sites per island (Fig. 1)

Sequenced 230 – 312 bp of cytb or COI using 5 primer pairs targeting: [1,2] custom

Converted eDNA read counts per sample to a scaled by reads proxy (0 – 4 "individuals" per sample) for haplotype frequencies within species

Findings

- Moderate overlap in species composition across regions, indicating widespread colonization and persistence, except for gastropods (🐚) (Fig. 3 top)
- Most haplotypes are unique to each region, indicating low connectivity (Fig. 3 bottom)
- Johnston Atoll: most similar to Hawai'i, except for echinoderms 1 (🕷) (Figs. 4 & 5)
- General trend of increasing dissimilarity with distance from Hawai'i for biodiversity (Fig. 4 top) but not for phylogenetics (Figs. 4 bottom & 5)

	Hawaii	Johnston	Kiritimati	Wake	Majuro	Guam	Okinawa
Hawaii		0.013 (49)	0.083 (35)	0.049 (53)	0.044 (39)	0.083 (36)	0.083 (22)
Johnston	0.031 (49)		0.084 (22)	0.070 (38)	0.037 (23)	0.110 (24)	0.052 (15)
Kiritimati	0.174 (35)	0.183 (22)		0.024 (33)	0.030 (29)	0.047 (24)	0.045 (14)
Wake	0.138 (53)	0.164 (38)	0.073 (33)		0.030 (32)	0.030 (30)	0.028 (19)
Majuro	0.106 (39)	0.103 (23)	0.087 (29)	0.077 (32)		0.029 (46)	0.027 (23)
Guam	0.213 (36)	0.191 (24)	0.156 (24)	0.069 (30)	0.088 (46)		0.022 (22)
Okinawa	0.186 (22)	0.157 (15)	0.160 (14)	0.091 (19)	0.128 (23)	0.141 (22)	

Φ_{ST} 0.20 0.15 0.10 0.05

Figure 5. Mean (below diagonal) and median (above diagonal) pairwise Φ_{ST} values across OTUs. Darker blue indicates higher Φ_{ST} values. Sample size (number of OTUs) is in parentheses.

Summary

Contrasting patterns of species and haplotype composition are the result of processes operating at different timescales: species distributions reflect colonization and persistence, whereas haplotype distributions are driven by recent dispersal. Our data suggest that Hawaiian marine fauna are both isolated and differentiated from the NCP except for Johnston.

References: [1] L14912-CYB - Minamoto, T., H. Yamanaka, T. Takahara, et al. 2012. Limnology 13:193–197; [2] H15149 - Burgener, M., and P. Hübner. 1998. Eur. Food Res. Technol. 207:261–263.

Email: tely@hawaii.edu