In Hawai‘i, *Acropora cytherea* (Dana, 1846) is essentially restricted to the central portion of the archipelago in the Northwestern Hawaiian Islands (NWHI), although it was present in the Main Hawaiian Islands (MHI) in the fossil record (Grigg 1981). Recently however, two relatively young (<5 years) colonies were first documented (Kenyon 2007) from Kaua‘i in the MHI (Fig. 1). Grigg (1981) proposed Johnson Atoll was the origin of the recent Hawaiian *Acropora* fauna, and computer simulations predict larval transport corridors linking Johnston Atoll with both French Frigate Shoals and Kaua‘i (Kobayashi 2006). Alternatively, these newly discovered colonies could be a southerly range expansion from the large NWHI population, or originate from another source not previously considered.

To test these alternative hypotheses regarding the source population, samples were collected from one of these juvenile *A. cytherea* colonies on Kaua‘i (23.12N, 159.61W), 51 colonies at French Frigate Shoals (23.75N, 166.15W), 57 at Johnston Atoll (16.73N, 169.53W) and 25 at Kingman Reef (6.38N, 162.42W) in the Northern Line Islands; sites separated from Kaua‘i by roughly 700 km, 1200 km, and 1750 km, respectively. These sites represent the closest emergent coral reef habitat to the MHI on which *A. cf cytherea* corals are known to exist. Samples were identified by Jean Kenyon and Jim Maragos, and genotyped for each of seven microsatellite loci as outlined in Concepcion et al. (2010). Pairwise $F_{ST}$ values among the possible source sites ranged from a low of 0.016 (FFS to JO) to a high of 0.06 (FFS to KI). Comparison of these sites with Kwajalein Atoll (8.72N, 167.73E) gives pairwise $F_{ST}$ values on the order of 0.15, suggesting that the more proximate sites are the more likely sources of these colonists. Pairwise $F_{ST}$ values among these sites are certainly on the low end of the range recommended for confident assignment to source populations (reviewed by Manel et al. 2005), but equivalent to those used in some successful applications of this approach (e.g., Guillemaud et al. 2010). An assignment test was then performed and probabilities of assignment to a reference population were computed with 100,000 iterations of a Monte Carlo resampling algorithm as implemented in GENECLASS2 (Piry et al. 2004).

Surprisingly, the population with the highest probability of assignment (99.9%) was the Kingman Reef in the Line Islands, followed distantly by French Frigate Shoals (78.5%) and Johnston Atoll (75.2%). None of the populations could be positively excluded as possible sources, which is consistent with the relatively low pairwise $F_{ST}$ values among these populations, but it is striking that the highest likelihood of assignment is to the most distant population, which has not
previously been considered as a possible source of recruitment to the Hawaiian Archipelago. Similar results linking Kingman Reef to the MHI have recently been reported for echinoderms (Skillings et al. 2011). While these data are not able to identify the source population conclusively, they provide preliminary evidence that the recent colonization of Kaua‘i by juvenile *Acropora* may have come from outside the Hawaiian Archipelago. Together with the data from echinoderms, these data suggest the possible presence of an overlooked larval transport corridor connecting the Hawaiian Archipelago with the Northern Line Islands that is worthy of further investigation.

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**References**


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