

Genetic consequences of introducing allopatric lineages of Bluestiped Snapper (*Lutjanus kasmira*) to Hawaii

Michelle Gaither¹, Brian Bowen¹, Rob Toonen¹, Serge Planes², Vanessa Messmer², John Earle³, Ross Robertson⁴
¹Hawaii Institute of Marine Biology, Honolulu, Hawaii; ²Universite de Perpigna, Perpignan Cedex, France; ³Bishop Museum, Honolulu, Hawaii; ⁴Smithsonian Tropical Research Institute, Panama



Abstract

A half century ago the State of Hawaii began a remarkable, if unintentional, experiment on the population genetics of introduced species, by releasing 2431 Bluestriped Snappers (*Lutjanus kasmira*) from the Marquesas Islands in 1958 and 728 conspecifics from the Society Islands in 1961. By 1992 *L. kasmira* had spread across the entire archipelago. Genetic surveys of the source populations reveal diagnostic differences in the mtDNA control region ($d = 3.8\%$; $\Phi_{ST} = 0.734$, $P < 0.001$) and significant allele frequency differences at nuclear DNA loci ($F_{ST} = 0.49$; $P < 0.001$). These findings, which indicate that source populations have been isolated for approximately half a million years, set the stage for a survey of the Hawaiian Archipelago ($N = 385$) to determine the success of these introductions in terms of genetic diversity and breeding behavior. Both Marquesas and Society mtDNA lineages were detected at each survey site across the Hawaiian Archipelago, at about the same proportion or slightly less than the original 3.4:1 introduction ratio. Nuclear allele frequencies and parentage tests demonstrate that the two source populations are freely interbreeding. The introduction of 2431 Marquesas founders produced only a slight reduction in mtDNA diversity (17%), while the 728 Society founders produced a greater reduction in haplotype diversity (41%). We find no evidence of genetic bottlenecks between islands of the Hawaiian Archipelago, as expected under a stepping-stone model of colonization, from the initial introduction site. This species rapidly colonized across 2000 km without loss of genetic diversity, illustrating the consequences of introducing highly-dispersive marine species.

Introduction

The Bluestriped Snapper, *Lutjanus kasmira*, is a wide spread and highly dispersive reef fish. A range wide genetic survey showed little population subdivision across its Indo-Pacific range (Figs 1&2; Gaither et al. 2010a). An exception to this pattern is the highly divergent population at the Marquesas (Fig 1, black shading). This population shares no mitochondrial haplotypes and shows strong shifts in nuclear allele frequencies (data not shown) with all other Indo-Pacific populations.

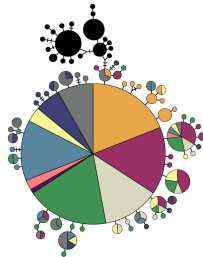


Fig 1. Statistical parsimony network constructed using TCS 2.21 for 336 cytochrome *b* sequences (Gaither et al. 2010a).

- Between 1958 and 1961 2,431 *L. kasmira* from the Marquesas and 728 from the Society Islands (Moorea) were introduced to the Island of Oahu (Fig 2).
- L. kasmira* spread quickly through the archipelago reaching Midway Atoll by 1992.
- We capitalized on the genetic distinctiveness of the two source populations to determine the relative success of these two introductions.

Methods

A total of 385 *Lutjanus kasmira* were collected from 10 locations across the Hawaiian Archipelago (Fig 3). We amplified 575 bp of the mitochondrial control region, 215 bp of the third intron in the gonadotropin-releasing hormone, 650 bp of intron 5 of the Growth Hormone gene, and 395 bp of the Adenine Nucleotide Transporter Translocase intron (Gaither et al. 2010b).

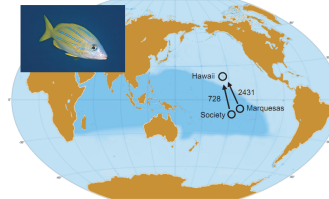


Fig 2. Map of the Indo-Pacific. The number of fish introduced from each source population is shown. Blue shading represents natural range. (Photo credit: Keoki Stender)

Results

- Individuals from both source populations became established in Hawaii and their descendants have colonized each of the atolls and Islands sampled (Fig 3).
- The ratio of Marquesan to Society haplotypes (Fig 3) is roughly the same at each sample location with only the Island of Hawaii being significantly different than the introduction ratio of 3.4:1.0.

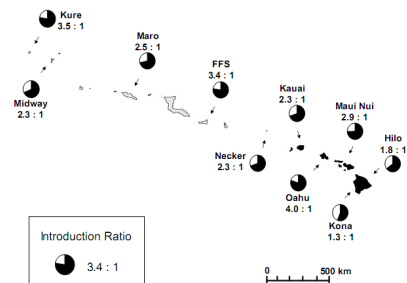


Fig 3. Map of the Hawaiian archipelago. Pie charts show the ratio of *L. kasmira* in either the Marquesas (black) or Society (white) lineage (Gaither et al. 2010b)

Literature Cited:

Gaither, M., Toonen, R., Robertson, R., Bowen, B. (2010a). *Journal of Biogeography*, 10, 133-147.
 Gaither, M., Bowen, B., Toonen, R., Planes, S., Messmer, V., Earle, J., Robertson, R. (2010b). *Molecular Ecology*, 19, 1107-1121.

Results

- When compared to the source populations, we found evidence of a slight but significant decrease (17%) in haplotypes from the Marquesas lineage and a greater decrease (41%) from the Society lineage in Hawaii (Table 1).
- There was no loss of genetic diversity as the fish colonized the archipelago.
- Overall genetic structure within the archipelago was not significant ($\Phi_{ST} = 0.003$, $P = 0.276$; $F_{ST} = 0.001$, $P = 0.293$).
- Parentage tests indicate that the two genetic lineages are freely interbreeding in Hawaii.

Population	N	N _h	H	% lost	P-value
Marquesas Lineage					
Source	50	47			
All Hawaii	270	142	39.0 ± 2.50	17.0%	< 0.001
Society Lineage					
Source	49	31			
All Hawaii	115	30	18.3 ± 2.06	41.0%	< 0.001

Table 1. Results of rarefaction analyses. Number of specimens (N), number of haplotypes (N_h), and mean number of haplotypes (H) (± standard deviation) estimated from 10,000 random subsamples of the Hawaiian lineages are listed (Gaither et al. 2010b).

Discussion

- Fish from both the Marquesas and Society Islands became established in Hawaii and colonized the archipelago with roughly equal success.
- The lack of genetic structure in Hawaii and the maintenance of genetic diversity throughout the Islands indicate that this species spread through the Islands quickly and in large numbers
- After approximately 500,000 years of separation these two lineages are freely interbreeding in Hawaii.
- These data invoke the hypothesis that species that show low levels of population structure over wide biogeographic ranges will prove to be the most successful invaders. Work is ongoing in our lab to test this hypothesis.

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