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Research Article

Trans-Pacific rafting in tsunami associated debris by the Japanese yellowtail jack, *Seriola aureovittata* Temminck & Schlegel, 1845 (Pisces, Carangidae)

Matthew T. Craig[1,*], James Burke[2], Kevin Clifford[2], Evonne Mochon-Collura[2], John W. Chapman[3] and John R. Hyde[1]

[1]*NOAA, National Marine Fisheries Service, Southwest Fisheries Science Center, 8901 La Jolla Shores Dr., La Jolla, CA 92037, USA*
[2]*Oregon Coast Aquarium, 2820 SE Ferry Slip Rd., Newport, OR 97365, USA*
[3]*Department of Fisheries and Wildlife, Oregon State University, Hatfield Marine Science Center, 2030 SE Marine Science Dr., Newport, Oregon, USA*

Author e-mails: matthew.craig@noaa.gov (MTC), jim.burke@aquarium.org (JB), Kevin.Clifford@aquarium.org (KC), evonne.mochon-collura@aquarium.org (EMC), john.chapman@oregonstate.edu (JWC), john.hyde@noaa.gov (JRH)

**Corresponding author*

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Abstract

The devastating tsunami of March 2011 on the Pacific coast of Japan produced abundant marine debris which drifted across the Pacific Ocean to North America. Here we document rafting of the Japanese yellowtail jack *Seriola aureovittata* Temminck & Schlegel, 1845 (Carangidae) across the North Pacific inside a tsunami-generated derelict vessel. Long-distance transport of rafted fish may be an infrequent but potentially consequential mechanism for the introduction of invasive fish, especially given the increasing volumes of debris in the world's oceans.

Key words: dispersal, North Pacific, invasive species, *Seriola lalandi, Seriola dorsalis*

Introduction

On March 11, 2011 the Great East Japan Earthquake produced a devastating tsunami largely concentrated on the Tohoku coast of the island of Honshu. The tsunami produced abundant marine debris (Carlton et al. 2017), a large fraction of which supported Japanese species, and which crossed the Pacific Ocean to North America and the Hawaiian Islands.

In April 2015 the upright bow section of a derelict vessel, 8 m long and 4 m wide (Figure 1), lacking specific identification (but later determined to be of Japanese origin, see below), was encountered in the open ocean 8 km west of Seal Rock off the coast of central Oregon, USA. Within the vessel's middle compartments were two fish species that aroused curiosity. One was a single specimen of the Asian barred knifejaw *Oplegnathus fasciatus* (Temminck &

Figure 1. Photograph of JTMD-BF-356 at the time of discovery off the coast of Seal Rock, Oregon, USA. Photograph by John Chapman.

Figure 2. Japanese yellowtail jacks, *Seriola aureovittata*, within the hold of a Japanese derelict fishing vessel, 9 April 2013, and after capture. Photograph of fish in the well by James Burke. Photograph of fish after capture by Caren Braby.

Schlegel, 1844). The other was a group of 21 large fish in the family Carangidae tentatively identified as yellowtail jacks, *Seriola* sp. (Figure 2).

Along with these fishes, the biofouling assemblage on the vessel included the Japanese oyster *Crassostrea gigas* (Thunberg, 1794), the Japanese barnacle *Megabalanus rosa* (Pilsbry, 1907), the mussel *Mytilus galloprovincialis* Lamarck, 1799, and other Japanese invertebrates. This faunal assemblage was in concert with the biota found on other Japanese Tsunami Marine Debris (JTMD) items from the Tohoku coast that had been intercepted between 2012 and 2015 in the Pacific Northwest. Subsequently, genetic studies of the green alga *Ulva* from the vessel's biofouling indicated that it was a member of the *Ulva pertusa* Kjellman, 1898 / *U. australis* Areschoug, 1854-complex, with a unique haplotype signature associated with populations in Tohoku's Iwate Prefecture (Ta et al. 2018; G. Hansen, Hatfield Marine Sciences Center, Oregon State University, Newport, USA, *pers. comm.*). This vessel was registered as JTMD-BF-356 in the JTMD database (Carlton et al. 2017).

Seriola is a genus of primarily coastal pelagic fishes with species occurring globally in all but polar

regions. The yellowtail jack (*Seriola lalandi* Valenciennes, 1833, *sensu lato*) was long thought to be a single cosmopolitan species, albeit with a disjunct distribution. However, yellowtail jacks (also known as yellowtail amberjacks) are now known to be a complex of at least three morphologically similar but genetically distinct species: *S. aureovittata* Temminck & Schlegel, 1845 (in the Western Pacific), *S. dorsalis* (Gill, 1863) (in the Eastern Pacific), and *S. lalandi* (in the southern hemisphere) (Martinez-Takeshita et al. 2015). All three species are important components of coastal ecosystems and are favored for recreational fishing. With the rise of aquaculture, *Seriola* species have also become a cost-effective culture species. Among all sectors of the fishery, both cultured and wild, the estimated global market value of *Seriola* is more than $1 billion USD (FAO 2002).

Given the broad distribution of yellowtail jacks across the Pacific Ocean, the species of *Seriola* in question, and thus the origin of these fish, were uncertain. In order to test the hypothesis that the fish were of Japanese origin and had successfully sustained trans-Pacific transport, genetic data were gathered from eight of the fish and compared to previously published results showing distinct genetic signals for Japanese and North American Pacific coast yellowtail jack, *S. aureovittata* and *S. dorsalis*, respectively (Martinez-Takeshita et al. 2015; Purcell et al. 2015).

Materials and methods

The 21 fish were retrieved from the vessel and taken to the Oregon Coast Aquarium (OCA) in Newport. Also retrieved were invertebrate biofouling samples (noted earlier), as well as samples of dense swarms of the small (< 10 mm in length) gammarid amphipod *Jassa marmorata* Holmes, 1905, which were found in the vessel's middle compartments.

The fish (which appeared to be emaciated), ranging in size from 42–52 cm total length, were placed in quarantine and examined for external parasites prior to display. During quarantine, fin clips were taken from each individual and stored in 100% ethanol and sent to the NOAA National Marine Fisheries Service Southwest Fisheries Science Center for analysis. Genomic DNA was isolated using a Qiagen DNeasy kit following manufacturer's instructions. PCR was used to amplify a portion of COI gene using the M13-tailed primers FF2d (5'-TTCTCCACCAACCA CAARGAYATYGG-3') and FR1d (5'-CACCT CAGGGTGTCCGAARAAYCARAA-3') (Ivanova et al. 2007), as well as a portion of the nuclear peroxisomal enoyl-CoA hydratase/L-3-hydroxyacyl-CoA dehydrogenase (EHHADH) gene using the M13-tailed primers Seriola-EHHADH-F (5'-TGTA AAACGACGGCCAGTACCACCTGGCCTCTCAA ACTC-3') and Seriola-EHHADH-R (5'-CAGGAA ACAGCTATGACGCAGCTATTCCATCCTCCAA GATGC-3') (Martinez-Takeshita et al. 2015). Both the mitochondrial COI and nuclear EHHADH genes were shown to successfully distinguish *Seriola* spp. by Martinez-Takeshita et al. (2015). Thermal cycling parameters were as follows: 94 °C for 2 min followed by 35 cycles of 94 °C for 30 s, 55 °C for 60 s, 72 °C for 60 s (COI) or 35 cycles of 94 °C for 30 s, 68 °C for 60 s, 72 °C for 60 s (EHHADH), and a final extension step of 72 °C for 5 min. PCR products for all genes were enzymatically cleaned using Exonuclease I and Shrimp Alkaline Phosphatase digestion (ExoSAP). BigDye v3.1 (Applied Biosystems) dye terminator cycle sequencing was carried out following manufacturer's protocols using universal M13 primers (M13F [-21]: 5'-TGTAAAACGACGGCCAGT-3' and M13R [-27]: 5'-CAGGAAACAGCTATGAC-3').

Additional COI sequence data were downloaded from GenBank for comparative analysis, representing each unique haplotype or genotype found in Martinez-Takeshita et al. (2015) (COI: KM877615–KM877656, EHHADH: KM877657–KM877698) and aligned with data generated in this study using the program Clustal X (Thompson et al. 1997) under default settings. These data included individuals collected from the Southern Hemisphere (South Africa, Chile, and New Zealand), the Western Pacific Ocean (Japan), and the Eastern Pacific Ocean (USA and Baja California, Mexico). Datasets were reduced to unique haplotypes/genotypes, and a similarity matrix was created using Kimura 2-p distances (chosen based on simplicity of data set). These distances were used to generate a phylogram using the Neighbor-joining algorithm as implemented in MEGA v.7.0.9 (Kumar et al. 2015) and rooted with sequences from the congener *S. rivoliana* (GenBank accession number COI: KP733847.1; EHHADH: KP733847.1).

Results

We resolved 655 base pairs of the mitochondrial COI gene (8 specimens; GenBank: MF069448–MF069455) and 564 bases of the nuclear EHHADH gene (7 specimens; GenBank: MF0609456–MF069462). All specimens associated with JTMD-BF-356 had identical COI and EHHADH sequences; in the latter, none were heterozygous. The Neighbor-Joining algorithm produced nearly identical topology for both trees and both showed three clusters corresponding to *S. aureovittata*, *S. dorsalis*, and *S. lalandi* (Figure 3). All samples from the current study clustered with those from the Western Pacific *S. aureovittata*.

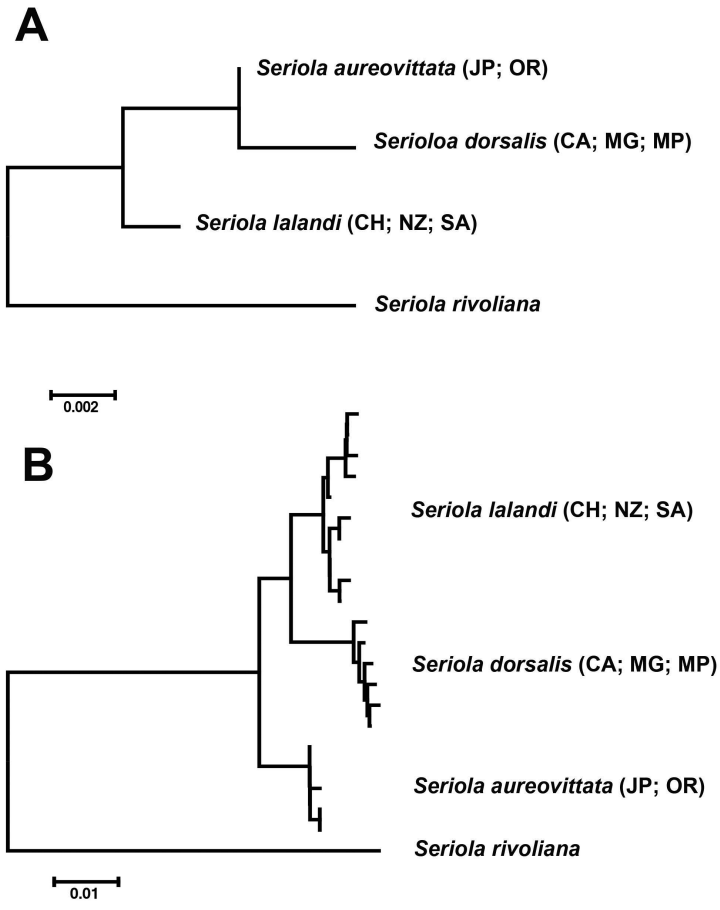

Figure 3. A. Neighbor-Joining phylogram based on Kimura-2 parameter distances of 564 base pairs of the nuclear EEHADH gene for yellowtail jacks, *Seriola* spp. **B.** Neighbor-Joining phylogram based on Kimura-2 parameter distances of 655 base pairs of the nuclear EEHADH gene for yellowtail jacks, *Seriola* spp. In both phylograms the yellowtail jacks associated with vessel JTMD-BF-356 cluster with the Japanese yellowtail jack, *Seriola aureovittata*, indicating that they are the same. Scale bar is substitutions/site. CA = California, U.S.A, CH = Chile, JP = Japan, MG = Mexico (Gulf of California), MP = Mexico (Pacific), NZ = New Zealand, OR = Oregon, SA = South Africa.

Most of the yellowtail jacks bore skin and gill notectoparasitic monogene flatworm parasites. The skin flukes resembled *Benedenia seriolae* (Yamaguti, 1934) Meserve, 1938, widely reported from *Seriola* populations in the Pacific Ocean. The skin flukes were controlled in an initial treatment but high mortality continued. Necropsies of the dead fish revealed gill flukes resembling *Heteraxine heterocerca* (Goto, 1894) Yamaguti, 1938 or *Zeuxapta seriolae* (Meserve, 1938) that were controlled by a second treatment method.

The size of the fish corresponded to the 12–17 month old fishes under normal ocean growth conditions (Shiraishi et al. 2010). In captivity in the OCA, offered food required adjustments over the fish's first 20 days in quarantine. The fish swam toward all larger food offered, but were unable to open their mouths sufficiently wide to bite. The diets were therefore changed to small foods, including krill, until the fish were capable of opening their jaws wide enough for feeding more on standard size food objects.

Discussion

Genetic identity and fish history

Both genes examined in this study confirm that the yellowtail jacks within the hold of the "Seal Rock boat", JTMD-BF-356, were the Japanese yellowtail jack, *Seriola aureovittata*. This finding is thus in concert with earlier determinations, based on invertebrate and algal biofouling, that this vessel originated from the coast of Japan.

The physical condition of the vessel (whose construction indicated that it was likely a live seafood transport vessel) suggested that it had been wreckage on the seafloor for some length of time after March 2011 (J.W. Chapman, *unpublished observations*) and then floated free, after which point the yellowtail and barred knifejaw became trapped in the vessel. A delayed post-tsunami departure of the vessel from Japan would explain the younger age (1–2 years) of the fish, compared to the age of the tsunami event (4 years prior to the vessel's arrival in Oregon).

The inability of the fish to initially feed on larger food items may be related to their having likely relied for food for many months on the small gammarid amphipod *Jassa marmorata,* a prey item not requiring wide jaw gapes. Wave wash over the decks surrounding the compartments was sufficient to permit the growth of a thick cover of the seaweed *Ulva* that also harbored dense populations of the amphipod *Jassa*. These deck populations of amphipods were likely washed into the middle compartments, providing food for the fish.

Implications of transoceanic fish rafting

While generally perceived as a coastal pelagic species, yellowtail jacks are also often found as both juveniles and adults associated with drifting seaweeds and other floating objects a considerable distance from shore (Safran 1990; Safran and Omori 1990; Hobday 2000). Purcell et al. (2015) noted two individuals from southern California in their study that appeared to be hybrids between the Japanese and California yellowtail jacks (*S. aureovittata* and *S. dorsalis*, respectively). This finding was difficult to interpret, as trans-Pacific dispersal seemed unlikely given that the genetic architecture of each species is quite distinct and pervasive genetic connectivity appears to be essentially absent (Martinez-Takeshita et al. 2015; Purcell et al. 2015). The discovery of Western Pacific yellowtail jack in the Eastern Pacific, albeit inside a derelict rafted vessel, suggests that, although rare, long-distance rafting events of *Seriola* may be possible.

While long-distance rafting of sedentary organisms has been invoked many times in marine biogeography, it is also important to consider the implications of rafting for fishes in general, in addition to crevicolous species such as blennies and gobies intimately tied to the substrate. With the growing volumes of marine debris in the world's oceans, fishes accompanying long-distant transport of masses of flotsam and other materials, acting as fish aggregating devices, may increase, and provide an infrequent, but potentially not inconsequential, mechanism for the introduction of non-native fish.

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