

Size-based spatiotemporal dynamics of striped marlin movement in the Pacific Ocean: first observations

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Abstract

Striped marlin, *Kajikia audax*, have been in overfished condition in the western and central North Pacific, and overfishing is still occurring, prompting an urgent need to devise conservation and management measures based on the best, current knowledge on biology and ecology of this species. Movement data is crucial information for the understanding and determination of stock structure, mixing, and ecological relationships of striped marlin. This paper attempts to distill the results available from genetic and tagging studies, and characterize movement patterns from complementary approaches. Broadly speaking, recent genetic and tagging results are in agreement and support the presence of three genetic populations (North, Western South and Eastern Central) in the Pacific Ocean. Furthermore, mixing do occur between distinct populations, and in particular, movement between North Pacific and Western South Pacific could reach 19% or higher. We postulate mixing may be widespread in space and time, and may be observable with better sampling and tagging technologies. Limitations of what genetic and tagging studies were explained in details, and suggestions for future research and funding were explored. Finally, we introduce an approach to utilize fisheries data, namely size information in fisheries logbooks, and be combined with movement insights derived from genetics and tagging and generalize the spatiotemporal dynamics on movement for striped marlin.

1. Introduction

Differential body sizes are well documented in striped marlin across the Pacific Ocean, in which individuals of >90 kg whole weight are mostly found in the Southern Hemisphere off Australia and New Zealand (Domeier, 2006; Kopf et al., 2011). Analyses of fisheries logbook have shown variability in catch patterns over seasons and decades (Ijima, 2017; 2019; Sculley, 2019), but size structure has not been considered in the same spatiotemporal context. By tracking changes in the movement of different size classes of striped marlin, much like the seminal work by Squire and Suzuki (1990), we have the potential to follow how fish of various genetic populations, fishery stocks, and ages move around the

Pacific, and when they are recruited to the fishery, especially in light of recent information from genetics and tagging. Materials presented here represent a selected review of movement information derived from available genetic and tagging results. Although far from comprehensive, together these results provide a framework to incorporate traditional fisheries-dependent data like weight-at-catch, and build a case for size-based spatiotemporal dynamics of striped marlin movement in the Pacific Ocean.

2. Genetics

Striped marlin in the Pacific Ocean have at least three genetic populations, identified via whole genome analyses (Mamoozadeh et al., 2020). A pan-North Pacific population (NPO) consists of fish sampled off Japan, Taiwan, Hawaii and California; an Eastern Pacific population (ECPO) with fish off Baja California, Ecuador and Peru, and lastly, a Western South Pacific population (WSPO) composed of fish sampled off New Zealand and the east coast of Australia. These populations are consistently identified by genetic studies published to date (McDowell and Graves, 2008; Purcell and Edmands, 2011; Mamoozadeh et al., 2020).

However, identification of additional genetic units appears inconclusive. For example, a second North Pacific unit, NPO2 (Mamoozadeh et al., 2020) was suggested to be composed of only Hawaii-sampled fish but was later attributed to be an artifact of inadequate sampling (J. L. Martinez, unpublished data). Earlier genetic results derived from microsatellites (Purcell and Edmands, 2011) also pointed to a Hawaii-only unit involving only adult fish of over >29 kg or 143 cm eye fork length (EFL). With each genetic study analyzing only its own set of samples collected from disparate locations and dates, it is especially difficult to reconcile any discrepancies in stock identification among various studies. Moreover, most existing genetic studies only resolve sample collection location at a regional level, for example, “Hawaii” can broadly mean any sample collected from a vessel offloading their catch at the port of Honolulu. Where and when a fish was caught, and sometimes length and/ weight or other biological metadata, is often unavailable, and not considered by a typical genetic study. Theoretically, modern genomic approaches are highly sensitive and powerful enough to

distinguish genetic differences in pelagic fishes with a sample size of <30 from each location (Pecoraro et al., 2018), and specific sampling requirements are not needed to account for kinship or relatedness (Anderson et al., 2019), as well as, seasonal and inter-annual variations. However, no studies to date has discussed or laid out the potential limitations or pitfalls from their experimental design and methods in sample collection.

To experiment with a more intensive genetic profiling of striped marlin during the spawning season, we conducted opportunistic sampling of 148 fish landed at United Fish Agency's Honolulu Fish Auction, Hawaii, USA between June 30 and August 3, 2017. Each sampled fish was noted of its head-and-gutted weight, later converted whole weight (Ito, 2019), and finally, to eye fork length (Hsu et al., 2019). Approximate location of where a fish was caught was resolved at a 5°-grid and 2-week fishing window to protect the intellectual property and identity of longline operators. After performing all the necessary quality control on sequenced DNAs, 55 Hawaii-landed striped marlin were analyzed in conjunction with 67 and 57 individuals caught off East Australia and New Zealand, respectively (Evans et al., 2021). Based on the best mixture model, landed fish were assigned to two genetic groups: Australia, New Zealand and Hawaii (AU-NZ-HI) comprising the first group ($n = 19$), and a second ($n = 36$) as Hawaii (HI) alone (Evans et al., 2021). Notably, 17 (89%) individuals assigned to AU-NZ-HI were sampled prior to July 11, while 26 (72%) HI fish were sampled afterward (Table 1). In addition, individuals assigned to AU-NZ-HI (172 ± 12 cm EFL) were significantly (Student's t-test, $p < 0.0001$) larger than those of HI (145 ± 9 cm EFL). Striped marlin from both genetic groups mixed in an area centered at 27.5 °N, 150 °W, between June and mid-July, where longline vessels also concentrated. The centroid of fishing activities then shifted south to 17.5 °N, 157 °W after July 11.

A north-south size stratification in striped marlin around Hawaii is consistent with the longline quarterly catch distribution (Sculley 2019). Individuals from the WSPO population spending time near Hawaii has also be previously noted for 4 out of 21 samples (19%) in Mamoozadeh et al. (2020). Ongoing analyses of genetic materials collected in 2019 Q4 by observers on Hawaii-based longliners

pointed to a strong southern representation, contributing as many as 66% of the sampled striped marlin during that quarter (J. L. Martinez, unpublished data). It is therefore necessary to consider that mixing of striped marlin of different origins, at least in the Central North Pacific, is not an isolated episode, and will be more frequently observed as sampling efforts increase. These first results open the possibility for a number of movement scenarios, including fish of multiple genetic origins present on fishing grounds, and/ sex or size partitioning of habitats around the Hawaiian Islands and beyond, potential ontogenetic shifts in movement, and age-specific movements. Shifts in movement may also occur at a shorter time step than a season (or quarter in assessment), and can also be offset to different calendar months for northern and southern populations.

3. Tagging

Tagging results have traditionally failed to replicate patterns of connectivity among genetic populations of striped marlin in the Pacific Ocean. Almost all earlier conventional and electronic tag releases were conducted by recreational fishermen or off charter vessels (Ortiz et al., 2003; Domeier, 2006), and consequently biasing tag recoveries and data returned towards coastal areas where striped marlin are known to aggregate, and the most accessible to fishers. Electronic tagging, with very few exceptions, can only follow striped marlin for at most, up to eight months at liberty (Domeier, 2006), which is inadequate for delineating seasonal or other longer-term migratory patterns. It is then, unsurprising that striped marlin are traditionally characterized as localized to their regional coastal hotspots, and large-scale movements are rare (Bromhead et al., 2004).

This has all changed since 2017 with the successful deployment of popup satellite archival tags (PSATs) off Hawaii-based longline vessels (Lam et al., 2019). The first documented trans-equatorial, trans-Pacific movement of a 150-cm EFL fish (PG01) showed connectivity between the Central North Pacific and Oceania (Figure 1), which complements genetic results on mixing described in the previous section. Without the genetic evidence, PG01's crossing to the Southern Hemisphere would have been considered as a singular episode or an outlier. When the yearlong journey of PG01 is broken down into monthly legs,

the fastest travel speed was observed in January, during which it was travelling to the east of American Samoa, speeding past the West Pacific Warm Pool (Wyrtki, 1989). This particular location is situated within a broad area in the West Pacific that has a very low catch-per-unit effort (CPUE) for striped marlin, i.e., the empty portion of the horseshoe-like (\supset) catch distribution (Bromhead et al., 2004). Avoidance of this same part of the West Pacific has previously been identified for five Argos satellite-tracked striped marlin off New Zealand (Sippel et al., 2011), all of which abruptly reversed travel directions once they reached 20-21 °S. Albeit a small number of tracked individuals, they showed observed CPUE patterns could be an emergent feature from the collective fish movement preferences.

Other examples of longer-term tracks from the Central North, and East Pacific off California (Figure 2), together with long-distance conventional tag recoveries (Figure 3), combined to provide new evidence in support of a wider connectivity in the North Pacific, showing possible east-west movement pathways for the pan-North Pacific population, NPO, and potential aggregation hotspots over broad latitudes within 130-145 °W. Striped marlin congregating in this longitude band, where white sharks are also known to aggregate (Nasby-Lucas et al., 2009), could be attracted by high abundances in prey items that include squid (Shimose et al., 2010).

Elsewhere in the East Pacific, none of the 46 PSAT-tagged fish off Baja California, Mexico ventured north of 31 °N, i.e., did not reach waters off San Diego, California, USA (Lam et al., 2015). This contrasts with fish tagged up north, off Los Angeles, California with PSATs and conventional tags (Figure 3) that did travel south to Mexico, arriving usually during late fall and winter. A recent breakthrough in positioning ten archival-tagged striped marlin (Domeier et al., 2019) has provided the first, long-term tracking for up to 7.7 years, yielding a total of 7300+ daily positions (Lam et al. in prep). Reconstructed tracks revealed tagged striped marlin remained in the East Pacific throughout 2008 to 2016, and confined mostly to the east of 120 °W, a pattern consistent with a distinct genetic population, ECPO. Seasonal north-south migrations were prominent, and inter-annual and individual variations were also observed. Trans-equatorial

movements were documented for the first time for striped marlin in the East Pacific, as were extended occupancy of >1 year in pelagic waters. All these diversity in movement point to the fact that striped marlin display migratory plasticity in both hemispheres of the Pacific Ocean. It is fair to say we are only beginning to observe new patterns with the recent improvements in tracking capability, but our ability to determine mechanistic causality remains extremely limited by the poor understanding of basic biology and ecological linkages from climate systems to prey species dynamics.

When a growing number of longer-term tracks are collectively evaluated, they can show when and where mixing could occur, and offer spatiotemporal details (daily resolution; spatial accuracy from 500 m to 100 km) that are unavailable through genetic or chemical approaches. However, longer-term tagging results are still expensive to obtain and hard to achieve, so it is essential to use the new insights we have gained from tagging so far to search for related patterns in complementary datasets that have a long time series and broad spatial coverage, such as the logbooks of pelagic longline fleets.

4. Next steps: fisheries data

Weight, catch and effort information will be obtained from the Japanese offshore and distant water logbooks between 1994 and 2020 for the entire Pacific Ocean. The collection of logbook records is detailed previously (Ijima, 2017;2019), and elsewhere in working papers of the current meeting (ISC/21/BILLWG-02/01 & ISC/21/BILLWG-02/04). Analyses are ongoing; therefore we briefly describe the approach we will employ here in hopes of getting inputs from the ISC Billfish Working Group:

1. Summary statistics on CPUE, number of fish caught, and semi-dressed weights are obtained at an aggregated monthly time step, and 5°-grid, Pacific wide.
2. Semi-dress weight is binned into 10-kg size categories. No fish of less than 10 kg was present in the logbook records.
3. Ranges of a given size category are converted to those of eye-fork lengths following Ijima (2019).

4. EFLs are then used to approximate ages for the various size categories (Kopf et al., 2011; Shimose and Yokawa, 2019; Kanaiwa et al., 2020); with the smallest category, 10-20 kg corresponds to ~100-135 cm EFL or roughly, 6-12 months old.
5. Year-of-young (YOY) striped marlin will be one of the main focuses of subsequent analyses. We will attempt to backtrack 6-12 months old individuals on possible origins of their birth (Shimose and Yokawa, 2019), in relation to known reproductive schedules, spawning grounds and places where larvae were sampled.
6. Other sizes of interest will relate to the length at 50% maturity for adults sampled across different Pacific locations, and identify possible mature adult movements.
7. Spatial changes in size distribution are then analyzed with respect to time steps longer than monthly to cover temporal breaks or longer scales resulting from gear modifications to climatic oscillations etc.
8. Reconcile spatiotemporal patterns in size with tagging and genetic results, and life history requirements.

5. Limitations and data needs

One key motivation for this work is the apparent mismatch in movement patterns deduced from genetics and observed from tagging. It is therefore necessary to understand that our main sources for the derivation of striped marlin movement: genetics, tagging and fisheries data, are available at different spatiotemporal resolutions, and each of them carries inherent limitations that may often be overlooked. We therefore want to highlight some of the issues or assumptions with each source, and identify data gaps that regional fisheries management organizations should invest in addressing.

Genetics

Genetic approaches are ideal for identifying the origin of birth for a pelagic fish at any time point in its life, much like the “nationality” of a genetically sampled fish. , Imprinting, an additional process that has to occur shortly after birth, is required to chemically coded olfactory signals (e.g., salmon; Bett et al., 2016), magnetic intensity or inclination (e.g., eel; Durif et al., 2021) or other unique

information relevant to the birthplace to enable an animal to use such inputs for the eventual navigation back to the same geographical location. Without an explicit knowledge on this imprinting process has taken place, birth origin, also referred to as spawning site fidelity, alone does not dictate how an individual fish or schooling fish would move and migrate. Rather, movement is more likely an emergent feature of an individual's behavior in fulfilling its life history needs from foraging to reproduction (Lowerre-Barbieri et al., 2017), and collectively, life history choices and preferences could become barriers to connectivity that may be associated with physical or oceanographic features. Therefore, genetic results will still require fundamental knowledge on the biology and ecology of a species for a fuller interpretation of identified patterns in movement. Equally important, assumptions used in population modeling should be grounded by a species' biology.

Genomic approaches, in particular next-generation sequencing, are promising on many levels, but in reality, single nucleotide polymorphism (SNP) libraries or panels are often proprietary and cannot be transferred across studies. Without a concerted effort to share or open-source screened SNPs, genetic studies will remain non-reproducible, and/ its applications be monopolized to a small number of laboratories and investigators. Such situations are far from ideal and, they represent roadblocks to the wider applications of genetic stock identification and elucidation of pelagic species movement.

Tagging

The benefits of tagging to stock assessment and management are discussed in details elsewhere (Sippel et al., 2015), but it is necessary to reiterate, financial reality often constraints the quantity of tagging that can be carried out (Lutcavage et al., 2014). Through our review of tagging data, the West Pacific, especially in vast open-ocean areas from Japan and/ Taiwan to Hawaii, is severely lacking in tagging data. Investments should be made to fill this huge gap, and could be wisely spent on tag deployments by observers on longline vessels. Similarly, tagging in the South East Pacific from Ecuador to the south of Peru will need to be stepped up. However, in both locations, it is unclear if any economic resources would be available in the near or medium future. Coordination among

principal investigators deploying tags should also be encouraged, which can increase the likelihood of physical tag recoveries or sharing fish handling techniques or tagging know-hows to improve tag retention. Researchers can explore any overlap in deployment schedule even when tagging efforts may be regionally localized. Such measures may present a “get around” to the limited duration of tracking, before technological breakthroughs deliver tagging equipment that is capable of routine tracking of animals for over 2 years (Lutcavage et al., 2014).

Fisheries data

Our choice to begin with the Japanese longline logbook data for the determination of size-based movement dynamics is based of its decadal series and broad spatial coverage. Inclusion of other logbook data from a different gear or fleet will be highly beneficial and complementary. Given we are in an early stage in the analysis, a more complete set of recommendations will be made in future reporting.

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Table 1 Assignment results of genetically sampled striped marlin in relation to the approximate location of fishing activities (5° grid cell), sampling date on the auction floor and size classes in 10-cm eye fork length (converted from dressed weight) intervals. Two genetic groups were identified: 1) Australia-New Zealand-Hawaii (**AU-NZ-HI**), and 2) Hawaii only (**HI**) by population modeling. Not all sampled fish were successfully genotyped (**Unavailable**) but sampling dates and size information are retained for completeness.

<i>Centroid of fishing activities</i>	150 °W 27.5 °N				157 °W 17.5 °N				2017	
	27-Jun	30-Jun	5-Jul	10-Jul	12-Jul	14-Jul	2-Aug	3-Aug		
<i>Assignment</i>										
(eye fork length 10-cm bin)										
AU-NZ-HI	8	3	2	4		1		1	19	
150			1	2			1		4	
160	3		1	2					6	
170	2	2						1	5	
180	2								2	
190	1	1							2	
HI	2		5	3	4	9	10	3	36	
120				1		1			2	
130					1	2	4	1	8	
140			1	2	2	3	3	1	12	
150	2		4		1	3	3	1	14	
Unavailable	6	9	15	26	11	15	8	3	93	
120				1	1	1			3	
130	1	1	1	3	1	2	7	2	18	
140		2	2	8	3	4	1	1	21	
150	3	2	7	9	3	5			29	
160	1	2	5	5	3	3			19	
180	1	2							3	
Grand Total	16	12	22	33	15	25	18	7	148	

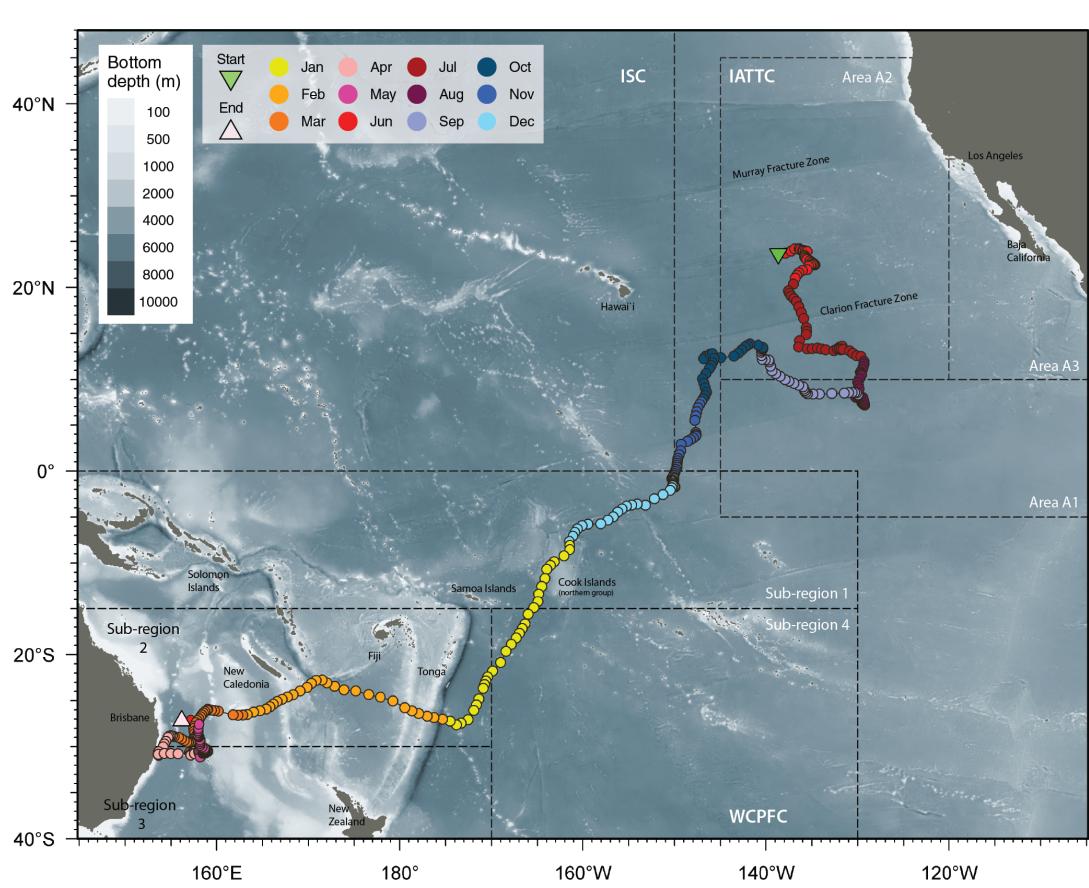


Figure 1 Yearlong track for striped marlin PG01 (150 cm EFL).

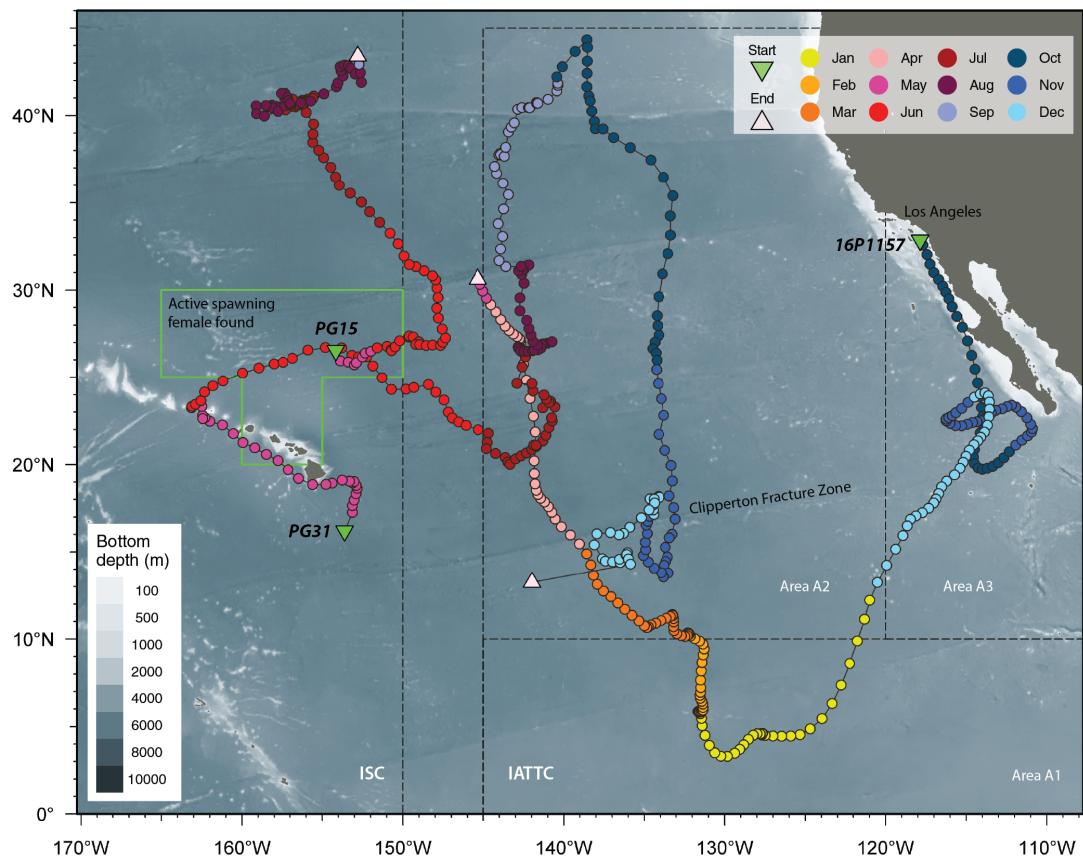


Figure 2 Movement trajectories of striped marlin PG15 (154 cm EFL), PG31 (157 cm EFL) and 16P1157 (151 cm EFL) with reference to the extent of a spawning ground (green box; Humphreys and Brodziak, 2019).

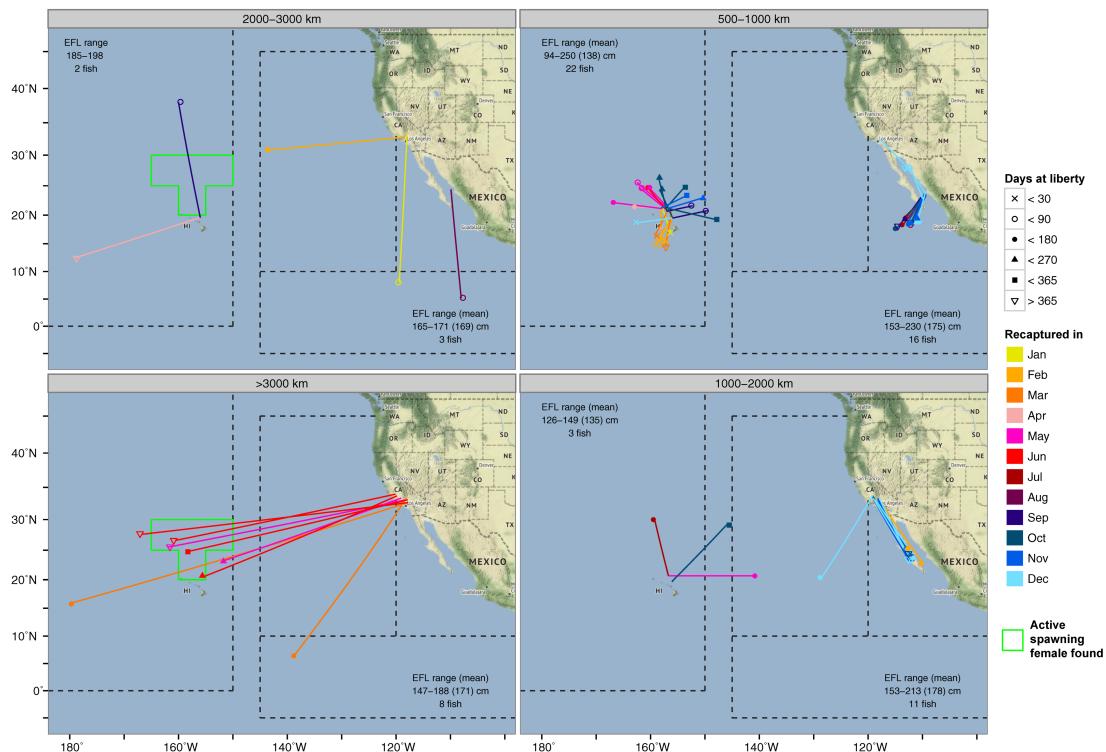


Figure 3 Long-distance (>500 km) conventional tag recaptures of striped marlin from NOAA Southwest Fisheries Science Center Cooperative Billfish Tagging Program. The month in which a tag was recaptured is color-coded. Icons at the recapture location indicate the number of days post-release. The extent of an area with active spawners (Humphreys and Brodziak, 2019) during the spawning season is outlined in green, and displayed for recaptures >2000 km. The number of tag recaptures and eye fork length statistics are indicated in each subplot