frontiers | Frontiers in Marine Science

TYPE Brief Research Report
PUBLISHED 08 January 2025
DOI 10.3389/fmars.2024.1482873

OPEN ACCESS

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RECEIVED 18 August 2024
ACCEPTED 13 December 2024
PUBLISHED 08 January 2025

CITATION
Mowatt-Larssen T, Thys TM, Hildering J, Caldera EJ, Biesack EE, McDowell JR and Nyegaard M (2025) Hook, line, and social media: crowd-sourced images reveal size and species patterns of ocean sunfishes (Tetraodontiformes, Molidae) from California to Alaska. *Front. Mar. Sci.* 11:1482873. doi: 10.3389/fmars.2024.1482873

Hook, line, and social media: crowd-sourced images reveal size and species patterns of ocean sunfishes (Tetraodontiformes, Molidae) from California to Alaska

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Taxonomic confusion and limited data have impeded species-level biogeographic analyses of the world's largest bony fishes, ocean sunfishes (Molidae; 'molids'), in many ecosystems. However, recent advances in molid taxonomy and the emergence of photo-based community-science platforms provide an opportunity to revisit species-level biogeography. In this study, we use crowd-sourced images of 1,213 ocean sunfishes to determine if molid morphology visible in citizen-science images permits reliable species determination. From the ensuing data, we describe patterns in molid size structure and species composition from 1,178 molids observed in the Alaska and California Current Systems (ACS and CCS, respectively). Molids <1 m total length (TL) were commonly reported in the CCS, particularly off the central coast of California, suggesting this area may function as a molid nursery. Molids >1 m TL were more commonly observed in both the CCS and cooler ACS, which suggests larger molids occupy a larger thermal range (ontogenetic habitat expansion) than smaller individuals. Overall, *Mola mola* was the most frequently observed species in both the ACS and CCS; however, the persistent occurrence of *Mola tecta* in both current systems suggests a range extension for this otherwise Southern Hemisphere species. The species identity of six *M. tecta* specimens from California and Alaska were verified with genetic analysis. Finally, two *Mola alexandrini* confirmed in the southern portion of the CCS represent the first records of this species in the Northeast Pacific Ocean.

KEYWORDS

citizen science, species identification, ontogenetic habitat shift, range extension, hoodwinker sunfish, molid identification guide, Cytochrome c oxydase subunit 1

1 Introduction

Ocean sunfishes (Molidae; 'molids') are charismatic teleost megafauna known for their unusual appearance, high fecundity and large adult size, including the record for heaviest bony fish. Currently, one small (<75 cm total length, TL) and four large species (>2.4 m TL) are recognized across three genera: slender sunfish *Ranzania laevis* (Pennant 1776), sharptail sunfish *Masturus lanceolatus* (Liénard 1840), ocean sunfish *Mola mola* (Linnaeus 1758), giant sunfish *Mola alexandrini* (Ranzani 1834) *sensu* Sawai et al. (2018) and Sawai and Nyegaard (2023), and the recently described hoodwinker sunfish *Mola tecta* Nyegaard et al., 2017. Although molids occur circumglobally in tropical to cold-temperate marine ecosystems, a legacy of taxonomic confusion and misidentification has confounded knowledge of species-level biogeography (Fraser-Brunner, 1951; Phillips et al., 2017; Nyegaard et al., 2018a, b; Sawai et al., 2018; Caldera et al., 2020; Sawai et al., 2020). Recent advances in phylogenetic, taxonomic, and morphological understanding of the genus *Mola* (Sawai et al., 2018; Nyegaard et al., 2018b; Sawai et al., 2020) and the emergence of online community-science platforms (e.g., www.inaturalist.org) provide an opportunity to revisit species-level biogeographic patterns using crowd-sourced media.

The ocean sunfish, *M. mola*, has long been known to occur in the Alaska and California Current Systems (ACS and CCS, respectively). There is evidence of a prehistoric fishery for *M. mola* in southern California (Porcasi and Andrews, 2001), and, despite not being targeted commercially in the ACS or CCS, *M. mola* was reported to comprise 14-61% of the total catch in the large-mesh California drift gillnet fishery (set to phase out in 2027) (Cartamil and Lowe, 2004; Thys et al., 2015; Hahlbeck et al., 2017). In the southern CCS, small juvenile *M. mola* school seasonally along the California coast (Thys unpublished data, www.oceansunfish.org), foraging on energy-rich benthic prey (e.g., Nakamura and Sato, 2014; Phillips et al., 2020). As they grow, they become semi-solitary and exhibit vertical excursions to forage on gelatinous zooplankton (e.g., Nakamura and Sato, 2014; Phillips et al., 2020). Larger subadult and adult *M. mola* are commonly observed near the coast of California and can be seen year-round in Monterey Bay (Thys pers obs). However, some individuals migrate seasonally in the southern portion of the CCS, moving southward into Mexican waters during fall and winter (Thys et al., 2015). Although little is known about molids in the ACS, *M. mola* has been reported as far north as Alaska and in substantial numbers in Queen Charlotte Sound in British Columbia, Canada, during summer (Thys and Williams, 2013). Before 2019, no other *Mola* species had been known to occur in the CCS and ACS.

The hoodwinker sunfish, *M. tecta*, first described in 2017, was initially confirmed off New Zealand, Southeast Australia, South Africa, and Chile, with a single putative record from the Northern Hemisphere (Dutch coast, 1889) (Nyegaard et al., 2018b). Accordingly, *M. tecta*'s core distribution was described as the temperate Southern Hemisphere with specimens later confirmed in Peru's cold Humboldt Current (Mangel et al., 2019; Caldera et al., 2020). However, in 2019, a *M. tecta* specimen was stranded in Santa Barbara, California (US01 in Supplementary Table 1), and additional verifiable reports of *M. tecta* from the Northeast Pacific Ocean emerged from ensuing media attention. These observations raise several questions, including: How common is *M. tecta* in the Northeast Pacific Ocean, and should this ecosystem be considered a range extension?

In this study, we leveraged crowd-sourced molid media and tissue samples from the ACS and CCS to genetically confirm the occurrence of *M. tecta* in these ecosystems; explore if molid species can be consistently distinguished based on morphological characteristics visible in images and videos; and describe broad spatial patterns in molid size structure and species composition from the ACS and CCS.

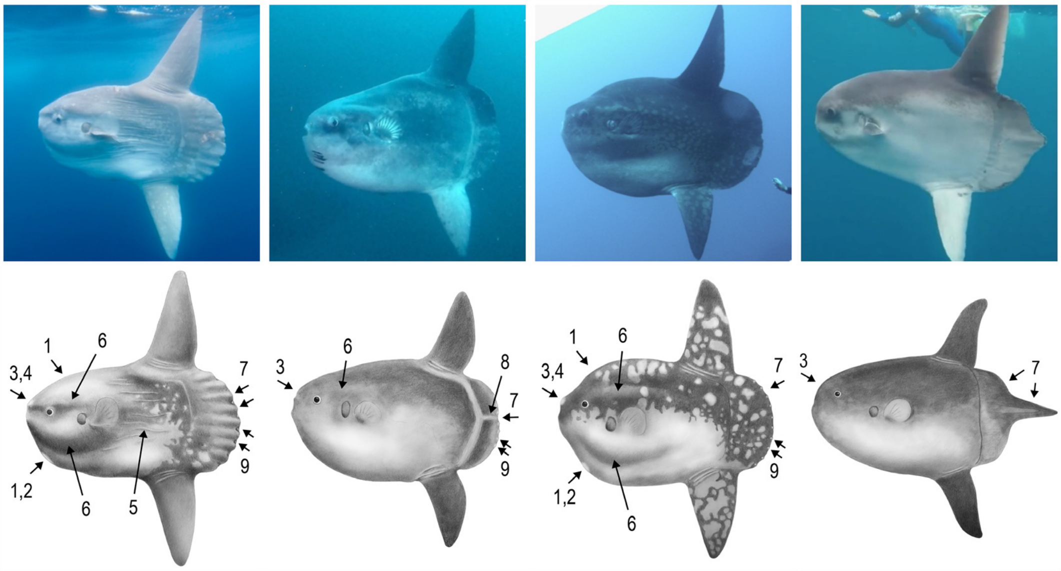
2 Methods

2.1 Media collection

Media (photos, videos) of molids from the ACS and CCS, along with metadata, were compiled from several sources, including iNaturalist (www.inaturalist.org), public outreach campaigns, the authors' private networks, and in collaboration with several ocean-focused organizations (e.g., Marine Education and Research Society, oceansunfish.org, Coastal Observation and Seabird Survey Team, JellyWatch, NOAA, and various museum collections). Crowd-sourced media comprised sightings from beach strandings, museum records, and live sightings from vessels, divers, snorkelers, and remotely operated vehicles. Most data (68%) originated from direct submissions to iNaturalist or the Marine Education and Research Society. Sighting metadata was verified with observers whenever possible (date, location/locality, molid size, and observation notes) except for records from iNaturalist, where observer-reported metadata was assumed correct. Each observation, including accompanying metadata, was reviewed before being included in the analysis. Only observations with an identifiable photo or video, and where date and location could be reasonably inferred, were considered. Duplicate observations, observations of captive fish, observations from other ecosystems, and observations without photo or video were excluded from the analysis. When observers did not provide GPS coordinates but provided a detailed description of the locality, coordinates were estimated within 10 km of landmarks referenced in the submission using Google Earth. Each record was also annotated with the observation type [at surface (seen from above water); at/near surface (seen from below water); at depth (seen from below water); stranded, on fishing boat (caught), in collection].

2.2 Size and species determination

The size of each molid was subjectively gauged by a Molidae researcher (MN) as <1 m TL or >1 m TL based on 1) relative size to other objects in the images, 2) the aspect ratio (height to width) of dorsal and anal fins, which decreases with increasing molid size (Watanabe and Sato, 2008; Watanabe and Davenport, 2020), and 3) the degree of body bulkiness, which increases with molid size.



		Mola mola	*Mola tecta*	*Mola alexandrini*	*Masturus lanceolatus*
1	Head bump, chin bump	Variable; develop with size in some individuals[a]	Absent	Pronounced; develop with size	Absent
2	Chin ossicle	Present	Absent	Present	Absent
3	Snout	Rounded or protruding	Rounded	Rounded or protruding	Rounded
4	Snout ossicle	Present	Absent	Present	Absent
5	Body skin wrinkles	Lengthwise, develop with size	Absent	Absent	Absent
6	Lateral ridges	Dorso- and ventro-lateral ridges develop with size	Short dorso-lateral keel	Dorso- and ventro-lateral ridges develop with size	Absent
7	Clavus margin	Wavy in some individuals[a], ossifies with size	Rounded with small median indent	Rounded (slightly wavy in some individuals)	Rounded with median projection of varying length
8	Smooth band back fold	Usually absent, faint when present	Present, defined	Usually absent, faint when present	Absent
9	Clavus ossicles	Large, usually triangular in shape; usually 8 – 9	Small, elongated; usually 5 – 7	Large, usually round; usually 8 – 15	Usually none, max 4 at tip of projection (rare)
ns	Paraxial ossicles[b]	United	Separate	Separate	Absent
ns	Body scales[c,d]	Dot shaped, ragged tips, close set	Dot shaped, rounded tips, sparse set	Rectangular in larger fish[e]	Small, dot shaped, ragged tips, close set

[a]Generally more pronounced in Atlantic than Pacific M. mola; [b]Only visible in dried/decayed carcasses; [c]Only visible on high-resolution, close-up images; [d]Note, scale shapes vary across the fish, use body scales posterior of the pectoral fin for ID; [e]Confirmed in individuals >162.5 cm TL; ns: not shown in figure.

FIGURE 1
Summary of key taxonomic characters in large-bodied molids (Molidae) used for species determination in this study (Sawai et al., 2018, 2020; Nyegaard et al., 2018b; Sawai, 2021). Note that nearly all illustrated characters emerge/develop with size and depicted fish are c 1.5 m total length. Images by Travis Wheeland (*M. mola*), Paul E. Festa (*M. tecta*), Marianne Nyegaard (*M. alexandrini*), Adi Huang (*Masturus lanceolatus*), illustrations by Cata & Co.

Molid species determination was based on all visible taxonomic characteristics following Sawai et al. (2018, 2020) and Sawai (2021) (Figure 1). We holistically assessed all visible characters, because single characters are typically insufficient to determine to species. For example, the presence of a smooth band back-fold, or an indent in a smooth clavus margin (see Figure 1), does not, in isolation, identify *M. tecta* because *M. mola* and *M. alexandrini* may have faint back-folds (Sawai et al., 2018; Nyegaard et al., 2018b) and an indent in the clavus margin could be due to injury or malformation. Further, the presence or absence of morphological characters was considered relative to molid size, as nearly all characters develop with growth. Each molid observation was independently determined to the lowest possible taxon by two identifiers – a Molidae researcher with ten years of experience (MN) and a fish ecologist trained using the guide in Figure 1 (TML). Where determinations differed, a third Molidae researcher (TMT) independently identified the observation. Determinations differing in taxonomic level (e.g., *M. mola* versus *Mola* sp.) were resolved using the majority ID (2/3 of identifiers). Direct species- or genus-level conflicts (e.g., *M. mola* vs *M. tecta*) would have been resolved by reverting to the lowest agreed taxon (in this case, *Mola* sp.); however, no such conflicts occurred.

Spatial distributions of size and species data were plotted as hexagonal heatmaps in R (Villanueva and Chen, 2019), where a latitudinal boundary between the ACS and CCS was defined at 43°N (Auad et al., 2011). The frequencies of <1 m TL and >1 m TL molids, and *M. tecta* >1 m TL relative to all other molids >1 m TL in each current system were compared using Pearson's chi-squared test for count data with Yates' continuity correction ($\alpha = 0.01$) in R (version 4.3.1) using the function chisq.test().

2.3 Genetic analyses

Tissue samples from six stranded (dead) molids, identified as *M. tecta* from photos, were opportunistically collected by local scientists and members of the public (California: n=4, Alaska: n=2). Tissue was preserved in 70% ethanol, RNA*Later*® or dimethyl sulfoxide (DMSO) for transport to labs. All DNA extractions proceeded using Qiagen DNeasy Blood and Tissue Kits, following the manufacturer's protocol. The Cytochrome *c* subunit 1 (CO1) locus was amplified and sequenced as described in Supplementary Table 1. All sequences were submitted to GenBank [Accession numbers PQ636871 - PQ636876].

To verify the species identity of the sampled molids, the COI sequences were pooled with all CO1 sequences labeled *Mola* spp. or *Ma. lanceolatus* in NCBI (n=61). The sequences were aligned with Clustal W in Unipro UGENE v50.0 using default settings and trimmed to equal lengths (616 base pairs), except 7 shorter sequences (511 – 611 bp). Phylogenetic relationships were inferred using the PhyML (Maximum Likelihood; ML) analysis on the T-rex server (Boc et al., 2012; http://www.trex.uqam.ca). Following Nyegaard et al. (2018b) for Molidae COI model selection, the HKY85 model was used with optimized equilibrium frequencies, estimated tv/ts ratio, gamma distribution parameter, and four substitution rate categories, with the mean used for the middle of each rate class. Branch support was estimated with 1,000 bootstraps. The resulting phylogenetic tree was visualized in TreeViewer v2.2.0 (Bianchini and Sánchez-Baracaldo, 2024) as a rooted tree with *Ma. lanceolatus* as the outgroup.

To confirm the species identity of the sampled molids, we compared the tree topology with the analysis in Nyegaard et al. (2018b), which included an assessment of likely mislabeled Molidae sequences in NCBI. Finally, we determined which species group(s) our novel sequences clustered with.

3 Results

3.1 Size and species determination

Media from 1,213 molids (representing 1,000 observations) in the ACS and CCS were examined to determine species identities. Species determination by two independent identifiers resulted in 1,152 agreements (95.0%) and 61 disagreements (5.0%). All disagreements occurred due to differences in taxonomic level (e.g., *M. mola* vs. *Mola* sp.), with no direct, species-level conflicts (e.g., *M. mola* vs. *M. tecta*). Most disagreements (72.1%; n=44) occurred between determinations of *M. mola* versus *Mola* sp. Resolving determination disagreements with input from the third identifier resulted in an additional twenty-nine species-level identifications (all *M. mola*), twenty-six genus-level identifications (all *Mola* sp.), one family-level identification (Molidae), and three instances of unverifiable organisms (undetermined; removed from the dataset). In total, 471 specimens were identified to species level (423 *M. mola*, 45 *M. tecta*, 2 *M. alexandrini*, 1 *R. laevis*), 648 specimens identified as *Mola* sp., and 83 specimens identified as large-bodied Molidae (*Mola* spp. or *Ma. lanceolatus*). As our study focused on large-bodied molids, the small-bodied *R. laevis* was removed from the dataset.

The subset of observations for which a location and a size estimate were available (n=1,178 specimens) consisted of nearly equal numbers of molids <1 m TL (n=586) and >1 m TL (n=592) (Figure 2A). While most of the molids >1 m TL (62.3%; n=369) were determined to species, the vast majority (77.6%; n=455) of molids <1 m TL could only be determined to genus (*Mola* sp.; Figure 2A) often due to insufficient development of taxonomic characters. All identified molids <1 m TL were determined to be *M. mola*. In both size groups, molids determined to family were consistent with *Mola* spp. but were insufficiently visible in the images to definitively exclude *Ma. lanceolatus*.

3.2 Observation types

Across the dataset, most observation types were of molids basking or swimming at the sea surface (seen from above water) (59.7%, n=703) or stranded on beaches (25.7%, n=303). However, this differed between size categories; most >1 m TL molids were observed at the sea surface, while most <1 m TL molids were observed either at the sea surface or stranded on beaches (Figures 2B, C).

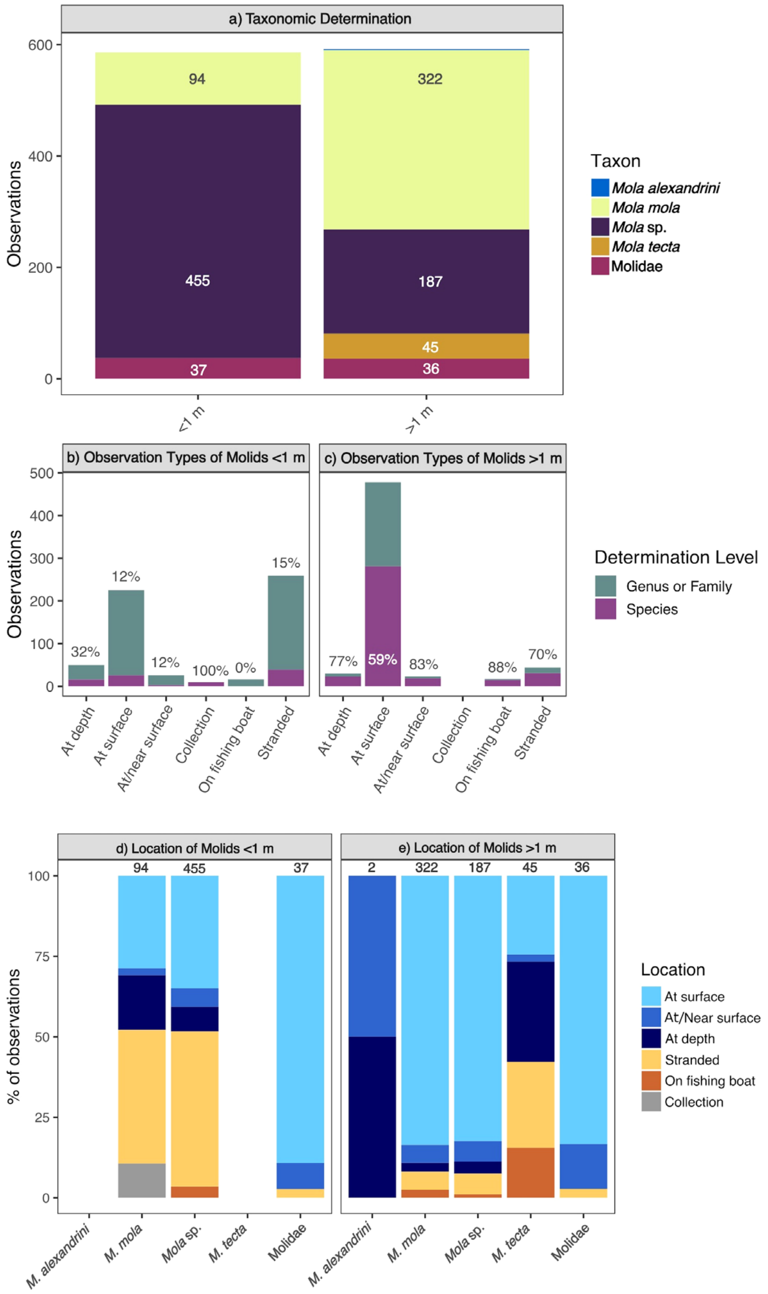


FIGURE 2

(A) Final taxonomic determinations (n=1,178), based on three identifiers, by molid size category (<1 and >1 m total length). **(B, C)** Taxon determination level (species or genus/family) of molid observations by size and observation type. Percentages above the bars indicate the percent of specimens identified to species for each category. **(D, E)** Molid observation type (n=1,178) by taxon and size category. Numbers above the bars denote the number of specimens for each taxon and size group. Observation types are: at surface (seen from above water); at/near surface (seen from below water); at depth (seen from below water); stranded, on fishing boat (caught), in collection.

Across observation types, most molids <1 m TL could not be determined to species, except for specimens accessioned in museum collections (100% success) (Figure 2B). In contrast, most molids >1 m TL types could be determined to species across all observation types (Figure 2C).

The taxa- and size categories comprised different proportions of observation types (Figures 2D, E). Both Molidae <1 m TL and >1 m TL mainly comprised observations at the sea surface. The *M. mola* and *Mola* sp. <1 m TL observations were mainly of stranded specimens and specimens at the sea surface (Figure 2D). The *M. Mola* and *Mola* sp. >1 m TL observations were mainly from the the sea surface, with similar proportions of observations from other observation categories (Figure 2E). In contrast, relatively few *M. tecta* observations were made at the sea surface, with comparatively higher proportions of underwater observations, strandings, and fishing boat captures (Figure 2E).

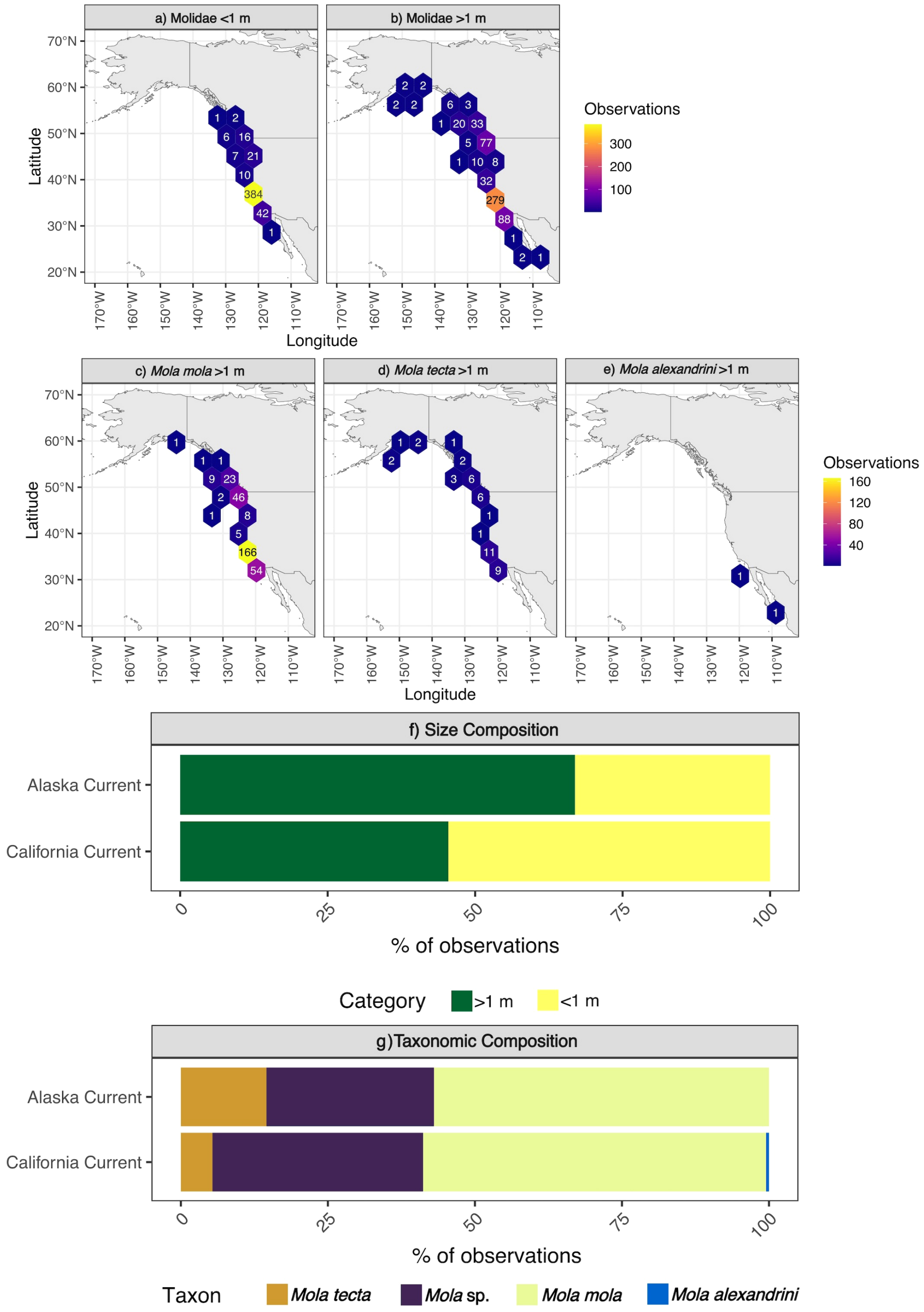


FIGURE 3
Spatial distribution of crowd-sourced observations of **(A)** Molids <1 m in total length (TL) (n=490), and **(B)** Molids >1 m TL (n=575) along the Northeast Pacific coastline of North America. Distribution of crowd-sourced observations of **(C)** *Mola mola* >1 *m* TL (n=317), **(D)** *Mola tecta* >1 *m* TL (n=45), and **(E)** *Mola alexandrini* >1 *m* TL (n=2). Within each panel, hexagons represent the same area (of geographic space). Size **(F)** and species **(G)** composition of molids from crowd-sourced observations across Alaska and California Current Systems.

3.3 Species and size composition

Molids were observed from southern California to Kodiak Island in Alaska, with most sightings from the California coast for both size groups (Figures 3A, B). *Mola mola* and *M. tecta* observations had overlapping distributions from southern California to Alaska, with most sightings along the California coast for both species (Figures 3C, D). *Mola alexandrini* was only observed twice, and both times near the California-Mexico border (Figure 3E). A single *R. laevis* was observed in the southern California Current [iNaturalist observation 1472850 – removed from the final dataset]. Observed molids in the ACS comprised a significantly higher proportion of >1 m TL individuals compared with the CCS [X^2 (1, N = 1185) = 37.27, p< 0.01] (Figure 3F). Similar numbers of *M. tecta* (n=24 and n=21) were

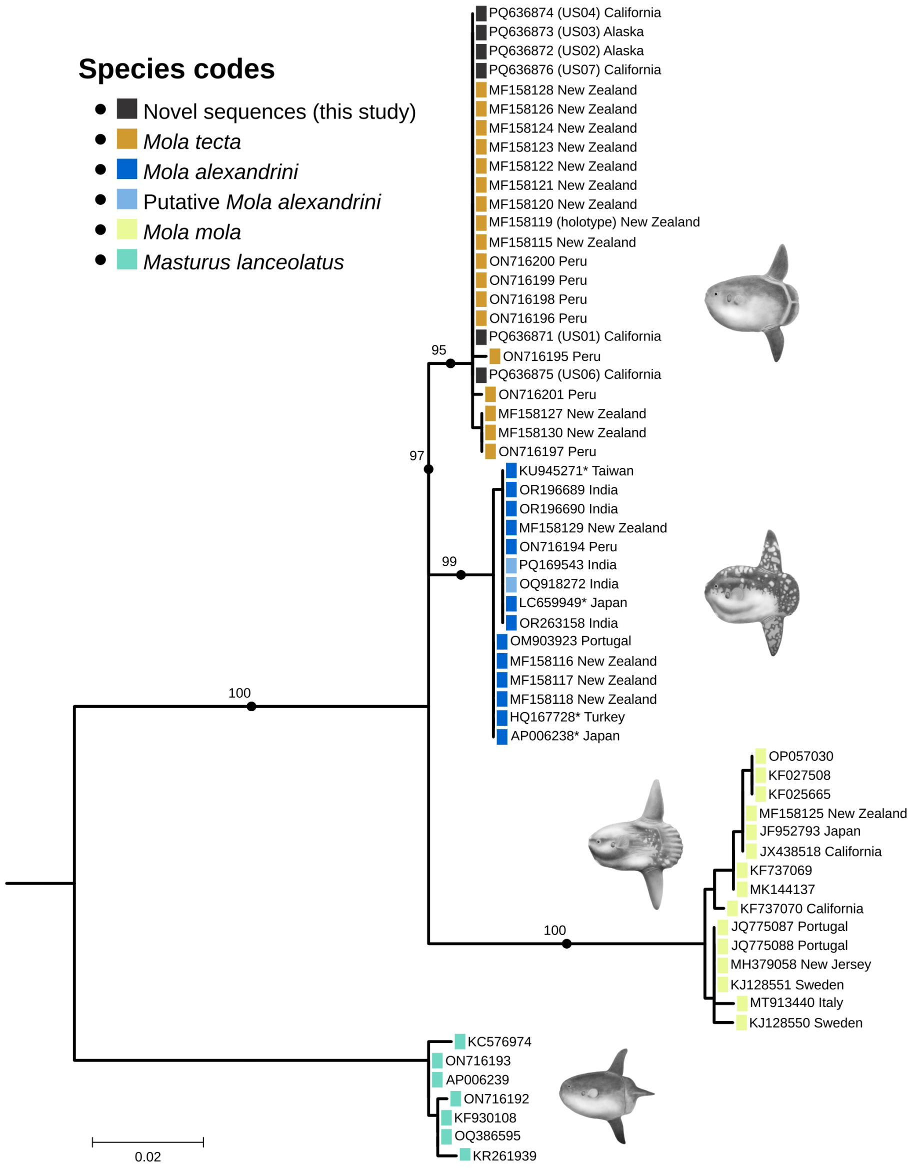


FIGURE 4
Phylogenetic relationships inferred by maximum likelihood (ML), based on the CO1 locus from six novel molid sequences (this study), pooled with *Mola* spp. and *Masturus lanceolatus* sequences from NCBI (n=61). All ML bootstrap values >70 are shown numerically above black dots. The scale bar represents nucleotide substitution. *Denotes sequences resolved in Nyegaard et al. (2018b) or in this study as *M. alexandrini* despite being labelled otherwise in NCBI. Putative *M. alexandrini* are labeled *M. mola* in NCBI, presumably in error (see text).

reported in both current systems; however, *M. tecta* (all >1 m TL) contributed a significantly higher proportion of total molids >1 m TL in the ACS (15.8%) than in the CCS (5.3%) [X^2 (1, N = 594) = 11.92, p< 0.001] (Figure 3G).

3.4 Genetic analyses

DNA from all six samples was successfully amplified and sequenced. The ML phylogenetic tree closely resembled that of Nyegaard et al. (2018), with four major clades with high branch support (95 – 100). Three of these clades consisted of NCBI sequences labeled either *Ma. Lanceolatus, M. tecta*, or *M. mola*, respectively (Figure 4). The fourth was a mixed species cluster of NCBI sequences labeled *M. mola* and *M. alexandrini*. These findings were similar to those of Nyegaard et al. (2018b), where three "*M. mola*" sequences were found to be mislabeled *M. alexandrini.* Our mixed cluster included an additional three, newer "*M. mola*" sequences, with one of these (LC659949) being *M. alexandrini* (A. Yamada pers com Nov 2024). The remaining two sequences (OQ918272, PQ169543) are likely cases of mistaken identity, related to the recent redescription of *M. alexandrini* (Sawai et al., 2018), the historic taxonomic confusion in Molidae, and the lack of updated Molidae field guides. Regardless, all novel sequences from this study clustered with known *M. tecta* sequences, including the holotype (Nyegaard et al., 2018b), confirming the visual identification of the sampled fish.

4 Discussion

4.1 Media-based species determination

Morphological species characteristics were sufficiently visible in most crowd-sourced media for species determination of molids >1 m TL, revealing two species (*M. alexandrini* and *M. tecta*) not previously reported from the Alaska or California Current Systems. Opportunistic genetic analyses corroborated the species identity of a subset of stranded *M. tecta* (n=6) identified visually from photographs.

Our holistic, media-based approach to molid species determination was remarkably consistent among identifiers (no direct determination conflicts; 95% were exact matches among two identifiers). However, as anticipated, our strategy was ineffective with molids <1 m TL (excluding *R. laevis*), as their diagnostic morphological characteristics had not yet developed or were not visible in crowd-sourced media. Therefore, a media-based approach to molid biogeography is currently most informative for larger molids and less so, without supportive methods, for smaller molids.

4.2 Ontogenetic changes in habitat

Our results suggest that molids exhibit ontogenetic shifts in habitat use in the Alaska and California Current Systems. Molids <1 m TL were frequently reported from the central California coast and comprised over half of all observations in the CCS. These findings align with the known seasonal influx of small molids (approx 30 – 50 cm TL; Thys pers obs; Gotshall, 1961) along the Californian coast, where they strand along beaches and are preyed upon by California sea lions (Thys, 1994). Conversely, larger molids (>1 m TL) dominated observations in the ACS. Larger molids have higher thermal inertia and utilize a broader depth range than smaller individuals (e.g., Nakamura and Sato, 2014), so the significantly higher proportion of larger molids in the colder ACS suggests these molids occupy a wider thermal range across geographic space, too. Our results are consistent with opportunistic spring and summer ship-board surveys in Queen Charlotte Sound, British Columbia, where reported molids were nearly all >1 m TL (Thys and Williams, 2013). These findings suggest that California's southern and central coast may function as a nursery for small molids, with larger individuals being more broadly distributed in the northern CCS and ACS.

4.3 Species composition

Our study revealed extensive geographic overlap of *M. mola* and *M. tecta* in the ACS and CCS. Overlapping distributions of large-bodied molid species have also been reported in other ocean ecosystems (e.g., Yoshita et al., 2009; Nyegaard et al., 2018a; also, see observations on www.inaturalist.org). However, niche partitioning between sympatric molid species is poorly understood (Arostegui et al., 2020), with recent research finding similar trophic niches and narrow diets for the close relatives *M. mola* and *M. alexandrini* in Taiwanese waters (Chang et al., 2024).

In our study, species composition analysis revealed that while *M. mola* was the most observed species within both current systems, the proportion of reported *M. tecta* (all >1 m TL) relative to other molids >1 m TL was significantly higher in the ACS compared with the CCS. This difference could potentially reflect differing thermal optima between the two species (e.g., Nyegaard et al., 2018a; Arostegui et al., 2020), or niche partitioning in habitat, diet, or foraging between the two species (e.g., Chang et al., 2024). However, little is known about the diet and horizontal and vertical movements of *M. tecta*. For example, while biotelemetry studies across several ocean ecosystems have reported seasonal latitudinal migrations and repeated deep-water excursions for *M. mola* (e.g., Dewar et al., 2010; Thys et al., 2015; review in Sousa et al., 2020), no research has been conducted on the movements of *M. tecta*. The E/V *Nautilus'* ROV *Hercules* observation off Santa Barbara in July 2017 – included in this study – represents this species' deepest confirmed record (71-74 m).

4.4 Observation types and molid behavior

Gathering crowd-sourced media of molids is inexpensive (albeit time-consuming), however, the diverse means of data collection and variable data quality has implications for species determination. For molids <1 m TL, the species determination success was low for all observation types, except the 'collection' category, where detailed images were available. For >1 m TL molids, the species determination success was high and similar across observation types. Of these, the least successful observation type was 'at sea surface, seen from above water', mainly due to numerous images showing only a dorsal fin.

Pooling observations from different observation types could potentially lead to bias if behavioral differences between molid species lead to differing probabilities of human detection. For example, several observations in this study (n=5) confirm *M. tecta* bask at the ocean's surface (like *M. mola* - Abe and Sekiguchi, 2012; Nakamura et al., 2015); however, it is unknown if *M. tecta* and *M. mola* spend similar time basking with equal likelihood of being observed by vessels. In our study, the smaller proportion of *M. tecta* observations from the sea surface compared with >1 m TL *M. mola* could indicate this may be the case. Similarly, while observations (n=4) confirm *M. tecta* solicit cleaner fish interactions on California reefs (like *M. mola* - Hobson, 1971; Vasco-Rodrigues and Cabrera, 2015), it is unknown if both species spend similar amounts of time at cleaning stations with equal likelihood of being observed by SCUBA divers. Any such differences could potentially introduce bias in a dataset like ours, originating from many sources (whale-watching vessels, SCUBA divers, beachcombers, etc.). This could further be exacerbated by the varying observational footprints in space and time, including the disparity in observational effort in the CCS (with large population centers) and the ACS (in general, sparsely populated, especially in the northern region).

In conclusion, the diverse means of data collection employed in this study and uncertainty in species-specific molid behaviors create challenges for directly comparing species commonality in the two current systems. Further research is needed to establish if *M. tecta* is proportionally more common among molids in the ACS than the CCS; two current systems that could be valuable comparative study areas to investigate niche partitioning between two morphologically similar species.

4.5 Range extension

Mola tecta is considered a temperate species (Nyegaard et al., 2018b), with no current observations in tropical waters. While warm equatorial waters may form a thermal barrier for continuous *M. tecta* distribution between the Northeast and Southeast Pacific Oceans basins (i.e., between California and Peru), trans-equatorial movements could potentially occur through isothermal submergence as has been suggested for other species (e.g., Møller et al., 2003) or become more frequent during cool phases of climate oscillations (e.g., La Niña) when equatorial surface water temperatures drop (e.g., see ENSO-linked Humbolt squid range expansion - Zeidberg and Robison, 2007). While further research is needed to understand *M. tecta*'s distribution, the large number of confirmed *M. tecta* from the Northeast Pacific Ocean (n=45) provides compelling evidence for a species range extension in the CCS and ACS. Genetic research could help elucidate this species' connectivity across its Pacific Ocean distribution.

Key aspects of *M. tecta*'s reproductive biology remain unknown, including the location of spawning grounds. It is worth noting that all sampled individuals in this study were female. Examination of the ovary of a 205 cm TL *M. tecta* stranded in Santa Barbara, California (US01 in Supplementary Table 1) revealed signs of secondary oocyte recruitment but no indications of prior spawning (Forsgren et al., 2020). The size at maturity is unknown for *M. tecta*, so it is unclear if this is unusual. It is also unclear whether the CCS functions as a nursery area for this species, like *M. mola*. All confirmed *M. tecta* observations were of relatively large fish (all estimated at >1 m TL; size estimates provided by observers ranged from 1.2–2.2 m), however, we cannot dismiss the possibility that smaller *M. tecta* occur in the Northeast Pacific Ocean.

4.6 Conclusion

The use of crowd-sourced observations to study large marine animals presents both exciting opportunities and notable limitations. Overall, we report that media crowdsourcing is a practical, noninvasive, complementary tool to genetic analysis to elucidate species-level molid biogeography, with potential to compile much larger datasets than genetic sampling alone. By mobilizing large numbers of community scientists (in this case, hundreds of observers), we were able to expand the temporal and spatial range of molid data, which would be cost-prohibitive and logistically challenging for traditional monitoring approaches. This approach can be particularly useful for understanding the distribution and habitat use of data-deficient species that are frequently observed by humans. However, key challenges include ensuring data consistency and accuracy (data quality varies), temporal and spatial observation biases (uneven observer density and interspecific behavioral differences), difficulty quantifying or standardizing effort across diverse data sources (e.g., divers, whale-watching vessels, beachcombing), and the loss of 'absence data' collected in traditional scientific surveys (which can be useful in predictive models of species range).

Media-based datasets and emerging technologies (e.g., artificial intelligence) have exciting promise for numerous applications, including molid species determinations and recognition of individuals; these technologies could be used to generate large datasets and investigate environmental perturbations on molid strandings, mortality, behavior and site fidelity (e.g., Nyegaard et al., 2023). However, the approach currently has limitations; our crowd-sourced data collection suggests that the central coast of California may function as a nursery for young molids. These small molids, in general, cannot be identified to species from crowd-sourced media alone because they haven't yet developed clear diagnostic morphological characters. Developing a molid field guide (to include subadult molids) is vital to help identify key habitats for molids' early life stages and assess conservation status (Thys et al., 2020; Phillips et al., 2023).

Finally, although we find that *M. mola* is the most frequently observed species in the ACS and CCS, we also report – for the first time – the occurrence of *M. alexandrini* (in the southern portion of the CCS) and *M. tecta* (from southern CCS to central ACS).

Data availability statement

The novel DNA sequences presented in this study can be found at National Center for Biotechnology Information (https://ncbi.nlm.nih.gov), accession numbers PQ636871 - PQ636876. The name of the repository and accession numbers can also be found in the article and Supplementary Material. The raw media-based data supporting the conclusions of this article will be made available by the authors, without undue reservation.

Ethics statement

Ethical approval was not required for the study involving animals in accordance with the local legislation and institutional requirements because all tissue samples were obtained from fish, which had stranded and died naturally prior to sampling.

Author contributions

TM-L: Data curation, Formal analysis, Methodology, Visualization, Writing – original draft, Writing – review & editing. TMT: Data curation, Investigation, Writing – review & editing. JH: Investigation, Resources, Writing – review & editing. EJC: Investigation, Resources, Writing – review & editing. EEB: Investigation, Resources, Writing – review & editing. JRM: Investigation, Resources, Writing – review & editing. MN: Conceptualization, Data curation, Formal analysis, Methodology, Resources, Validation, Visualization, Writing – review & editing.

Funding

The author(s) declare financial support was received for the research, authorship, and/or publication of this article. A project GoFundMe campaign covered costs of Molidae illustrations and FileMakerPro software to curate crowd-sourced observations.

William & Mary Libraries APC Support Fund covered the publishing charge. Genetic analysis and sequencing were covered in-kind by the laboratories.

Acknowledgments

We are grateful to the many members of the public who supported our GoFundMe campaign and/or provided molid observations to iNaturalist (www.inaturalist.org), www.oceansunfish.org, via the data collection campaign of the Marine Education and Research Society, or directly to the authors. We are also grateful for assistance in sampling stranded molids, obtaining larger image datasets, local knowledge, and for permission to use media during the outreach campaign: Cheryl Applebaum, Wendy Ranney Armstrong (Orca Adventure Lodge), Daniel Bianchetta (Big Sur Photo), Jeremy Botz (Alaska Dept of Fish and Game), Jason Bradley (Bradley Print Services), Blue Ocean Productions, Allison Bronson (Humboldt State University), Catalina Sea Camp, Jeff Cole, Chad Chrighton, Louisa Clarke and Natasha Dickinson (Fisheries and Oceans Canada), Bryan Curtis, Matt Drake (Fisheries and Oceans Canada), Jean-Louis Delezenne, Doug Engel, John Evans, Ralph Foster (South Australian Museum), Paul Furnarni, Erika Grebeldinger, Will Greenough, Kirk Hargreaves, Michael Howard (Monterey Bay Aquarium), Jacqueline Huard (University of British Columbia), Karen Johnson (Unusual Marine Life of Alaska), Howard Jones, Jackie Lindsey and Julia Parrish (COASST), Jake Pattison, Nick LeBeouf (SD Expeditions), Michelle McCune, Mark McGrouther (Australian Museum), Steve Moffitt (Alaska Dept of Fish and Game, retired), Cheryl Morgan and Jamal Moss (NOAA), Jim Murphy (NOAA, retired), Erik Obrien (Southwest Alaska Municipal Conference), Anthony Norton, Joe Orisi (NOAA), Kenley Prober, J.R. Rardon (Strait Shooter Photography), Michael Regular, Richard Schwarz, Frank Soldano Jr., Kellen Shoemaker, John Vonderlin, Keller Wattum (Deckled Aviation), Jennifer Weber and crew (Solomon Gulch Fish Hatchery), Patrick Webster (Monterey Bay Aquarium), S Yin and Desray Reeb, Colleen Young (California Dept of Fish and Wildlife), and several Monterey SCUBA divers, including Wei Wei Gao, Morton Jonus chat, Don Mueller, Joe Platko, Jr Sosky, Lauren Wilson. A special thank you to Jessica Nielsen (Coal and Oil Point Reserve) and Thomas Turner (University of California Santa Barbara), who found and assisted in the species verification of the *Mola tecta* found in Santa Barbara in 2019.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fmars.2024.1482873/full#supplementary-material

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