Quantification has long been an important issue in larval dispersal research. The Japanese anchovy (Engraulis japonicus) is one of the most ecologically and economically important small pelagic fish in the China Seas. However, a comprehensive and quantitative understanding of its larval dispersal patterns and underlying drivers has been lacking. This manuscript applies both 1D and 2D dispersal kernels to give a high spatiotemporal resolution, multi-factor, quantitative analysis of larval dispersal in Japanese anchovy across the China Seas, providing some new insights into the quantification of larval dispersal patterns. It also reveals the critical connectivity role of the Changjiang Estuary spawning ground, which is quite interesting and beyond expectations. However, I still have some concerns on the manuscript, and addressing them would, in my view, improve its quality.

Response: We sincerely thank the reviewer for reading and commenting on this manuscript. We have carefully considered all comments and addressed them point by point in the revised manuscript.

Main concerns:

1. *What is the meaning of connectivity matrix?*

Connectivity matrices have been used primarily for reef fish, where reef areas can function simultaneously as spawning grounds and nursery grounds. In this study, the y-axis of connectivity matrices represents spawning locations, but the x-axis represents settlement locations rather than nursery grounds. What, then, is the meaning of connectivity between a spawning location and a settlement location?

I suggest that the authors provide a more detailed explanation of the connectivity matrices, including their ecological interpretation and limitations.

Response: We agree that retaining the analysis could lead to over-interpretation, and therefore chose to remove it. Connectivity matrices have been widely applied to a variety of marine fish species, not only reef fishes. However, we agree that calculating connectivity among known spawning locations is of limited ecological relevance in our study. A more meaningful approach would be to quantify connectivity between spawning grounds and nursery areas. Because the nursery habitats of Japanese anchovy in the study region remain insufficiently defined, such an analysis cannot be conducted reliably with the available data.

Following the reviewer's suggestion, we have removed the connectivity matrix analysis from the manuscript, including Section 2.5 (Methods) and Section 3.3 (Results).

2. *Are Chinese stock and Japanese stocks connected through CJ ground?*

I do not think that the connectivity (dispersal rate) of larvae from the CJ spawning ground to the TWC and PS spawning grounds is sufficient to prove that the Chinese stock and the Japanese stock are connected. Although some larvae originating from CJ may reach the TWC region, larvae spawned at TWC may already have been advected further eastward by that time, resulting in limited spatial or temporal overlap between the two groups. Under such circumstances, the mere arrival of CJ larvae at TWC does not necessarily imply effective stock connectivity. Stronger evidence would come from demonstrating that larvae originating from CJ and TWC are transported to the same or nearby nursery habitats and overlap in space and time, thereby increasing the likelihood of mixing and subsequent recruitment into a common population. Such convergence of dispersal trajectories would provide a more convincing mechanism linking the two stocks.

I suggest that the authors discuss this point and greater caution should be exercised in both the wording and the conclusions of the manuscript, particularly when inferring stock connectivity from modeled dispersal pathways alone.

Response: We thank the reviewer for this suggestion. We have revised the discussion about connectivity between China Sea and Japanese Sea Stocks (Section 4.4) as follows:

> Whether Japanese anchovy populations from the China Seas and the Japan Sea spawning grounds belong to a single stock or represent distinct stocks remains unresolved. Using genetic analyses, Yu et al. (2002) reported that the Japanese anchovy populations from spawning grounds near northeastern Taiwan, in the Pacific Ocean, and near southwestern Taiwan, in the Taiwan Strait, were indeed separate stocks. In contrast, Yu et al. (2005) and Zheng et al. (2015) found no significant genetic differentiation among populations from the Yellow Sea and East China Sea. Furthermore, marginally significant genetic structure was detected between the Bohai Sea and Japan Sea populations, as well as between the North Yellow Sea and Japan Sea population (Zhang et al., 2020a).
>
> Results from the present larval dispersal study suggest that the CJ spawning ground may provide a potential pathway for larval exchange among regional populations. Larvae originating from CJ were transported not only to the central Yellow Sea, where they potentially overlap with larvae from other China Sea spawning grounds, but also to the northwest of Kyushu (TWC) and south of Kyushu (PS) in the Japan Sea. These results suggest the potential for larval exchange between the China Seas and Japan Sea regions. However, the arrival of CJ-derived larvae in TWC and PS alone is insufficient to demonstrate effective stock connectivity. Larvae spawned at TWC and PS may already have been transported elsewhere by the time CJ-derived larvae arrive, resulting in limited spatial and temporal overlap between the two groups. Consequently, the observed dispersal pathways indicate only the potential for connectivity, rather than direct evidence of population mixing or recruitment into a common stock. A more convincing

demonstration of stock connectivity would require showing that larvae originating from CJ, TWC, and PS converge in the same or adjacent nursery habitats and overlap in space and time, thereby increasing opportunities for mixing and recruitment into a shared population.

Minor suggestions:

3. L21: pattern, instead of patten.

Response: We have revised it.

4. L21: ranges from 44.53 to 150.56, replace "-" with "to".

Response: We have revised it.

5. L100: hydrodynamic model, instead of modal.

Response: We have revised it.

6. L128: you said "30 days" in L81, but why you used 30, 40, 50, 60 days here.

Response: Japanese anchovy larvae typically require approximately 30 days to grow to 20 mm in length, and therefore 30 days was used as the baseline scenario in our particle-tracking simulations. To further evaluate how dispersal patterns may vary with larval duration and to assess the sensitivity of our results to this parameter, we additionally simulated travel durations of 40, 50, and 60 days. These extended-duration scenarios were not intended to represent the typical larval period, but rather to examine the potential effects of prolonged transport on larval dispersal and connectivity.

7. L130: 15 times, instead of 15 days.

Response: We have revised it.

8. L131: The position of a particle stopped at the end…

Response: We have revised it.

9. L255-260: I think you need a Table S2 to give the values of modal dispersal distance, median-dispersal distance, and long-distance dispersal. It's hard to read these values from the figure.

Response: We think the reviewer is asking for the values of modal dispersal distance, median dispersal distance, and long-distance dispersal threshold. We have now added a Table S2 to provide the values of these metrics as follows:

Table S2. *Values of modal dispersal distance, median-dispersal distance, and long-distance dispersal threshold.*

	Modal dispersal distance (km)	**Median-dispersal distance (km)**	**Long-distance dispersal (km)**
From ZH	89.27	113.18	253.09
From BHB	93.12	110.96	233.69
From LZB	48.07	73.09	186.47
From YT	127.65	145.88	292.92
From SDI	150.56	177.53	369.65
From HZB	44.53	117.46	376.23
From CJ	131.23	196.02	494.69
All	77.31	128.37	344.03
April	76.39	104.92	250.22
May	93.74	128.97	307.97
June	109.29	162.91	410.61
July	86.52	145.22	391.36
August	53.10	108.85	320.57
30 days	63.68	98.97	255.82
40 days	79.45	121.71	311.91
50 days	92.20	141.79	364.23
60 days	101.5	158.77	411.89

10. L372: dispersal kernels, instead of dispersal kernel.

Response: We have revised it (the second line in Section 4.3).

11. L365: need a figure S2 to show the correlation between individual dispersal distances and PLD.

Response: We have added a figure S2 as below:

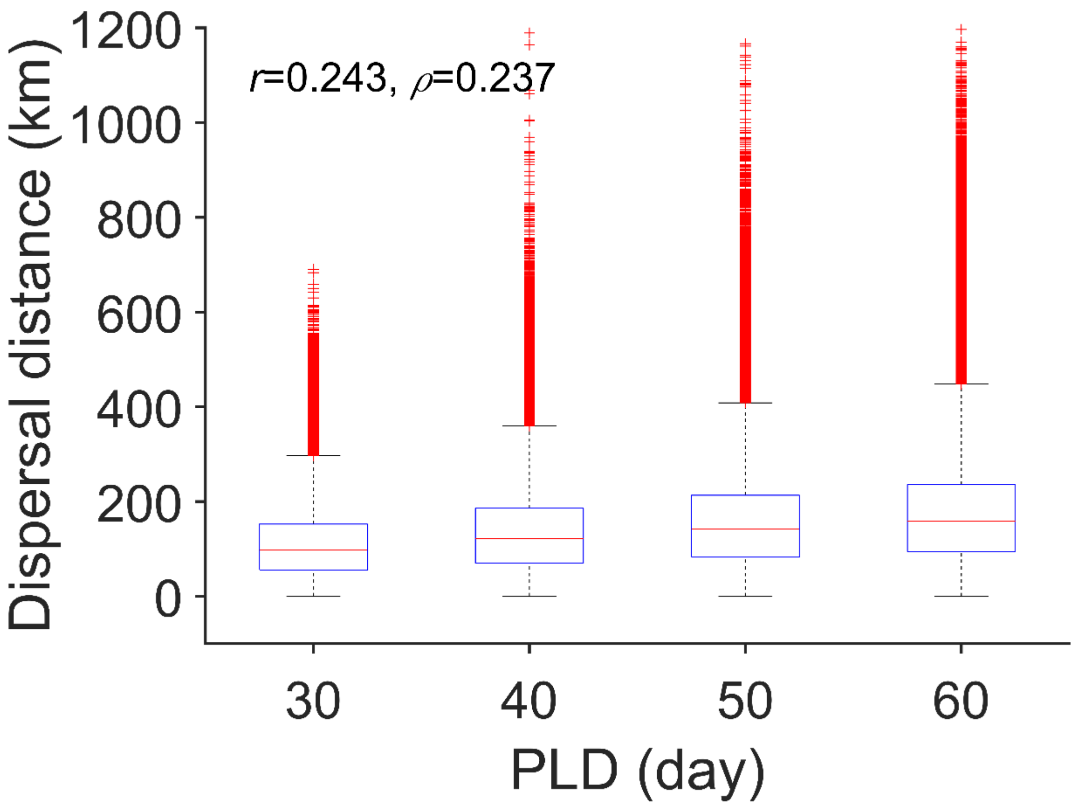

Figure S2. Box plots of dispersal linear distances showing a weak relationship between pelagic larval duration (PLD) and dispersal distance (Pearson's correlation: r=0.243; Spearman's correlation: ρ=0.237).

12. L366: The suggestion that PLD is not a reliable predictor of dispersal distance at the individual level, yet can capture broad average trends in dispersal potential, is interesting. Alvarez-Noriega et al. (2020), in their study "Global biogeography of marine dispersal potential," used PLD multiplied by average flow velocity to estimate mean dispersal distance and quantified the overall latitudinal gradient in larval dispersal distance. You could discuss this study to further contextualize or support your findings.

<u>Response:</u> We thank the reviewer for this helpful suggestion. We have incorporated a discussion of Alvarez-Noriega et al. (2020) into the manuscript. Specifically, we note that Alvarez-Noriega et al. (2020) assumed that larval dispersal distance is proportional to pelagic larval duration and estimated global latitudinal patterns in dispersal distance by multiplying PLD by local mean ocean current velocity. Our results provide additional context for this assumption by showing that, although PLD is a weak predictor of dispersal distance at the individual level, it remains useful for capturing broad-scale average trends in dispersal potential. This distinction helps reconcile the widespread use of PLD-based estimates in large-scale biogeographic studies with

the substantial variability in dispersal outcomes observed among individual larvae. We have revised the Section 4.2 as below:

> Previous studies have reported conflicting results on using PLD as a proxy for dispersal distance. Our results help reconcile these findings by showing that PLD can capture broad-scale average patterns of dispersal potential, but is a poor predictor of realized dispersal distance at the individual level. Shanks et al. (2003) and Shanks (2009) compiled independent, direct estimates of dispersal distance and compared them to propagule duration (a broader term encompassing PLD). Both studies found that, at a coarse scale, propagule duration was moderately correlated (R^2=0.6) with dispersal distance. Selkoe and Toonen (2011) further demonstrated a consistent, moderate fit between genetic proxies of dispersal (using either isolation-by-distance slope or global Wright's fixation index F_{ST}) and PLD. Similarly, Alvarez-Noriega et al. (2020) assumed that larval dispersal distance is proportional to PLD and thus computed the global latitudinal gradient in dispersal distance by multiplying PLD by local mean ocean current velocity. In contrast, D'aloia et al. (2015) observed that individual PLDs were not correlated with dispersal distance based on genetic parentage analysis. More recently, Shi et al. (2024) reported a very strong linear correlation (R^2=0.98) between PLD and travel distance (distance along transport trajectories), while only a moderate correlation (R^2=0.85) between PLD and linear distance.
>
> In this study, mean orthodromic distance from release location center to settlement center (d_m) increased with increasing PLD (Fig. 7), indicating that PLD captures average dispersal trends. However, the correlation between individual dispersal distance and PLD was weak (Pearson correlation = 0.243, Spearman correlation = 0.237; Fig. S2). These suggest that, PLD captures broad, average trends in dispersal potential, but it is not a reliable predictor of dispersal distance at the individual level. Longer PLD does not necessarily lead to a longer dispersal distance for individual larvae because larval trajectories are strongly influenced by topographic constraints on flow, and oscillatory flows, such as tides and seiches.

13. L402: as stated above, you can change the descriptions here, for example, we suggest that they may be connected through Changjiang spawning ground.

Response: We have revised the whole section 4.4.