

The following supplement accompanies the article

A global estimate of genetic and geographic differentiation in macromedusae—implications for identifying the causes of jellyfish blooms

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Supplement 3. Additional figures S1–S4 and text

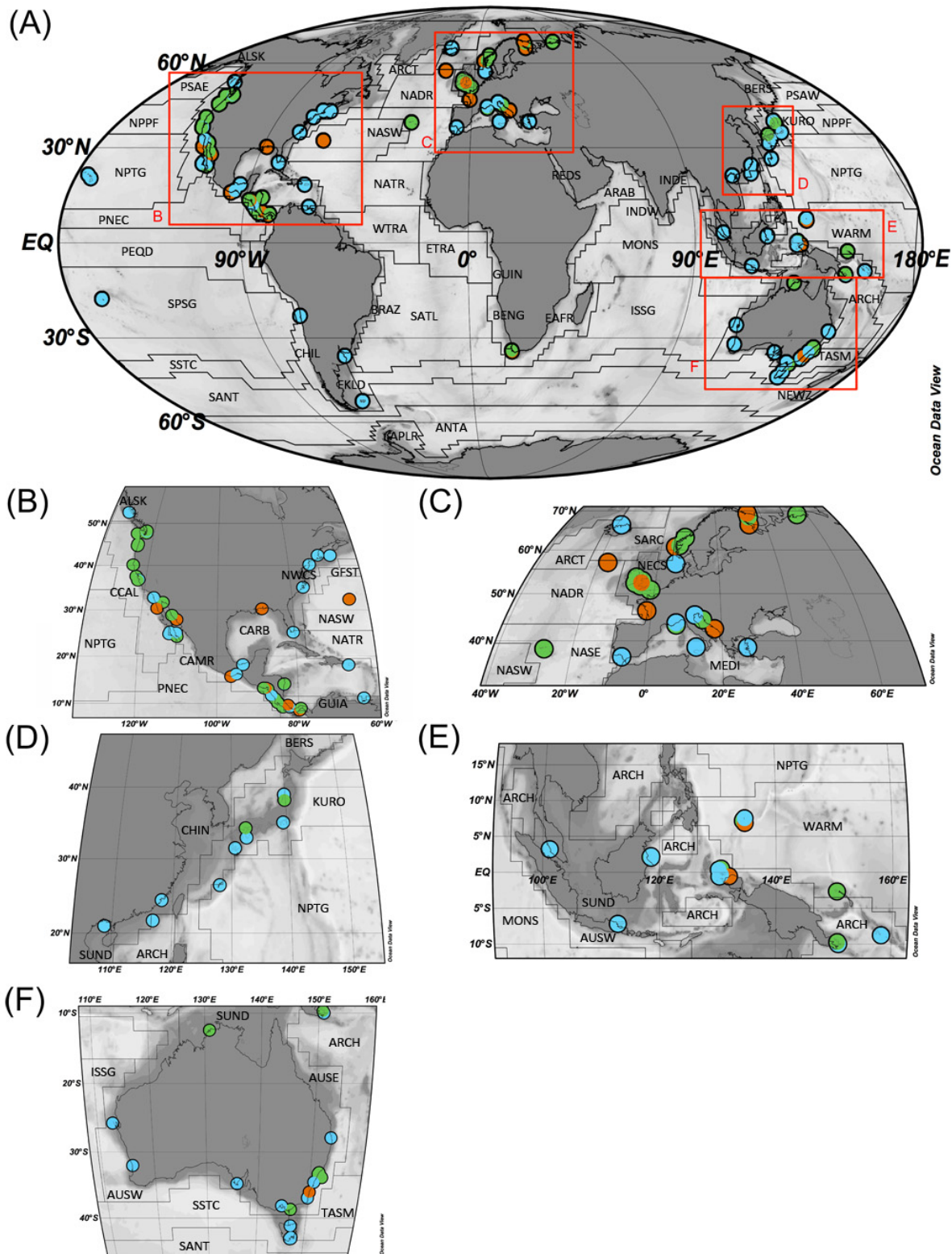


Figure S1. Maps showing Longhurst biogeographical provinces (LBP) boundaries (solid black lines) with corresponding LBP codes (based on Longhurst 2007) and sampling locations used for the within-LBP (green), between-LBP (blue), and both within- and between-LBP (orange) analyses. The global map (A) for all sampling locations includes map insets: (B) Alaska, North America, tropical eastern Pacific, and Caribbean; (C) Europe, Russia, Mediterranean Sea; (D) China coast and Japan; (E) Indo-Pacific; (F) Australia. Maps were made in ODV v4.7.4 (Schlitzer 2015) using a Mollweide equal area projection.

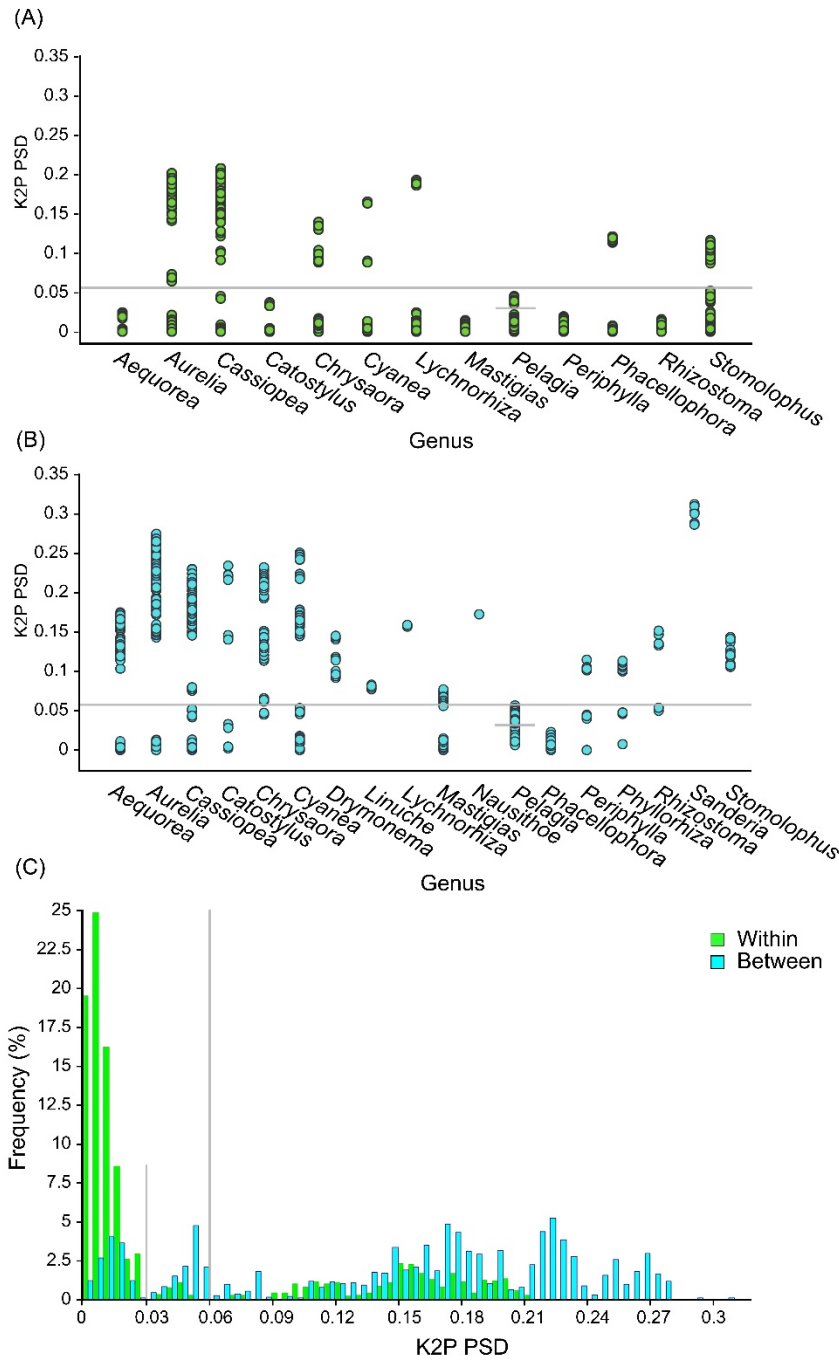


Figure S2. Distribution of pairwise Kimura 2-Parameter (K2P) pairwise sequence distances (PSD) for cytochrome *c* oxidase subunit I (COI) plotted for Longhurst biogeographical provinces (LBP) by genus for (A) within-LBP comparisons and (B) between-LBP comparisons. (C) The frequency distribution of COI PSD values for within- (green) and between- (blue) analyses. In all panels, long grey lines show PSD=0.06 (species delimitation in this study) and short grey lines show PSD=0.03, (possible species delimitation for *Pelagia* according to Gómez Daglio and Dawson (2017)). The x-axis only extends to 0.315, but a small percentage (<0.04%) of comparisons yield PSDs > 0.315.

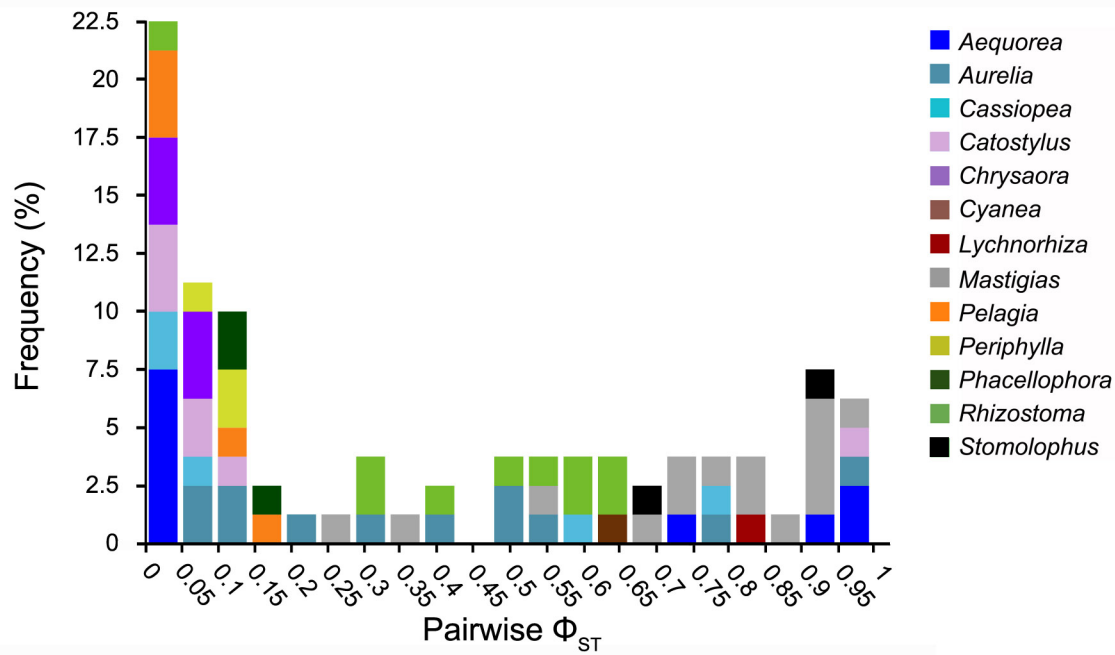


Figure S3. Frequency distribution of pairwise Φ_{ST} values for comparisons of congeneric macro-medusae within Longhurst biogeographical provinces (LBP). Percentages are all calculated relative to the entire within-LBP analysis (n=120 sample-by-sample comparison). Genera that are absent from this figure but present in the between-LBP analysis (Fig. 2B, Tables S6 and S10 in Supplement 1) were available from only one location or had sample-sample PSD values >0.06.

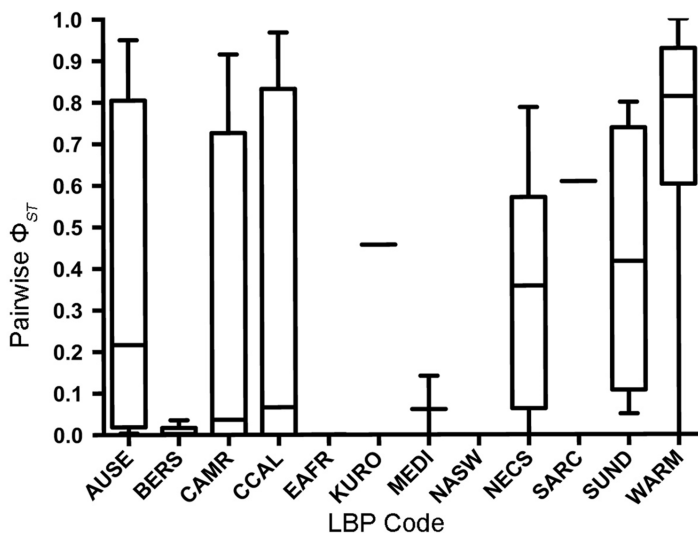


Figure S4. Pairwise Φ_{ST} values for all taxa and numbers of location-by-location comparisons (n=80) within 12 Longhurst biogeographical provinces (LBP) included in the within-LBP analysis. The names of the LBP are listed in alphabetical order by code: AUSE-East Australian Coastal Province (n=4), BERS- N. Pacific Epicontinental Province (n=6), CAMR-Central American Coastal Province (n=10), CCAL-California Upwelling Coastal (n=13), EAFR-E. Africa Coastal (n=1), KURO-Kuroshio Current Province (n=1), MEDI-Mediterranean Sea & Black Sea (n=3), NASW-N.W. Atlantic Subtropical Gyral Province (n=1), NECS-N.E. Atlantic Shelves Province (n=19), SARC-Atlantic Subarctic Province (n=1), SUND-Sunda-Arafura Shelves Province (n=4), and WARM-W. Pacific Warm Pool Province (n=17). For more information on latitude, longitude, oceanic region, and included genera of LBPs see Tables S1 and S3 (both in Supplement 1). LBPs

with $n=1$ have the single pairwise Φ_{ST} value presented as the median. EAFR and NASW each had a single sample-sample comparison, Φ_{ST} value=0. Horizontal line: median, boxes: 25th and 75th percentile, whiskers: range.

Other text for supplementary documentation:

FROM RESULTS:

Longhurst's Biogeographical Provinces (LBP) Analyses

Within-LBP Analyses

Considering mean K2P pairwise sequence distances (PSDs) calculated between samples within Longhurst biogeographical provinces (LBP), values ranged between 0 and 0.2 ($n=5736$ total individual comparisons or 213 sample-sample comparisons including self-comparisons, mean $SD=0.057$; Figure S2A, S2C, and Table S8 in Supplement 1). Summing proportional K2P PSDs (referred to PSDs for the remainder of this document) percentages by genus and within-LBP sampling, we found 25.1% of PSDs were ≥ 0.06 ($n=1458$ individual comparisons). Seven of the thirteen sampled genera (53.8%) contained multiple species within a single LBP, but not necessarily within the same sample location (Figure S2A, S2C, and Table S8): *Aurelia*, *Cassiopea*, *Chrysaora*, *Cyanea*, *Lychnorhiza*, *Phacellophora*, and *Stomolophus*. Thirteen of the thirteen sampled genera for the within-LBP analysis (100%) had PSD values < 0.06 between locations within a single LBP: *Aequorea*, *Aurelia*, *Cassiopea*, *Catostylus*, *Chrysaora*, *Cyanea*, *Lychnorhiza*, *Mastigias*, *Pelagia*, *Periphylla*, *Phacellophora*, *Rhizostoma*, and *Stomolophus*.

For the within-LBP analysis, pairwise Φ_{ST} estimates ($n=80$ LBP sample-sample comparisons) ranged between -0.07 (corrected to 0) and 1 (mean $SD=0.364$; Figure S3; Tables S5 and S9, both found in Supplement 1). Of the 80 sample-sample comparisons, 32.5% had $\Phi_{ST} < 0.05$, 15% had $0.05 \leq \Phi_{ST} < 0.2$, and 52.5% had $\Phi_{ST} \geq 0.2$ (Figure S3, Table S5, S8–S10). Molecularly-identified species (found within seven genera: *Aequorea*, *Aurelia*, *Cyanea*, *Lychnorhiza*, *Phacellophora*, *Rhizostoma*, and *Stomolophus*) specimen-specimen and sample-sample comparisons with PSDs ≥ 0.06 were excluded from the pairwise Φ_{ST} estimate within-LME analysis resulting in the $n=80$. Prior to removal, aforementioned genera exhibited pairwise PSD ≥ 0.06 in 33.8% (41 instances) of potential sample-sample comparisons (out of 121 instances; Table S8). Excluded values can be found in Table S8. Proportional percent frequency of $\Phi_{ST} \geq 0.2$ scaled by the within-LME analysis ($n=80$ sample-sample comparisons) and to the percentage of comparisons per taxon showed that *Aequorea* ($n=10$; 40%), *Aurelia* ($n=12$; 58.3%), *Mastigias* ($n=15$; 100%), *Rhizostoma* ($n=10$; 90%), and *Stomolophus* ($n=2$; 100) had the highest proportion of sample-sample comparison $\Phi_{ST} \geq 0.2$ (N.B. *Cyanea* and *Lychnorhiza* because they only had $n=1$ each; Figure S3). Comparing the within-LBP variation among regions showed that there is considerable geographic variation in terms of mean, median, maximum, and minimum pairwise Φ_{ST} values (Figure S4). Of the LBPs with multiple locations per genus considered (3+), LBP codes AUSE, CAMR, CCAL, and WARM had highest maximum genetic differentiation (Figure S4, Table S9); LBPs AUSE, KURO, NECS, SARC, SUND, and WARM had median Φ_{ST} values > 0.2 , though KURO and SARC data sets comprised of only one sample-sample comparison each. Lastly, BERS, EAFR, MEDI, and NASW exhibited the lowest pairwise Φ_{ST} median values ($\Phi_{ST} < 0.2$). EAFR and NASW data sets included only one sample-sample comparison each, $\Phi_{ST}=0$. The remaining LBPs (BERS and MEDI) had Φ_{ST} means and medians < 0.2 (Figure S4 and Tables S5–S6, S8). LBPs ARCH, BPLR, CCAL, SUND, and WARM had instances of sympatry where congeneric individuals from the same location had K2P PSD values ≥ 0.6 (Table S10). The genera that exhibited instances of sympatry using the cut-off of PSD = 0.06 were *Cassiopea*, and *Cyanea* (Table S10).

Between-LBP Analyses

Among LBP comparisons (n=2601 total pairwise individual comparisons or 289 LBP-LBP pairs, including self-comparisons) showed mean PSD values ranging between 0 and 0.3 with a mean of 0.147 (mean SD=0.08; Figure S2B and Table S8). Summing proportional PSDs percentages by genus and between-LBP sampling, 23.9% of PSD values were < 0.06, i.e. twelve of the eighteen sampled genera (66.7%) contained a single species across two or more LBPs (Figure S2B, S2C, and Table S8): *Aequorea*, *Aurelia*, *Cassiopea*, *Catostylus*, *Chrysaora*, *Cyanea*, *Mastigias*, *Pelagia*, *Periphylla*, *Phacellophora*, *Phyllorhiza*, and *Rhizostoma*. The remaining 76.1% of all between-LBP comparisons yielded PSD values ≥ 0.6 (Figure S2 and Table S8), i.e. sixteen of the eighteen sampled genera exhibited different species in different LBPs: *Aequorea*, *Aurelia*, *Cassiopea*, *Catostylus*, *Chrysaora*, *Cyanea*, *Drymonema*, *Linuche*, *Lychnorhiza*, *Mastigias*, *Nausithoe*, *Phacellophora*, *Phyllorhiza*, *Rhizostoma*, *Sanderia*, and *Stomolophus*.