

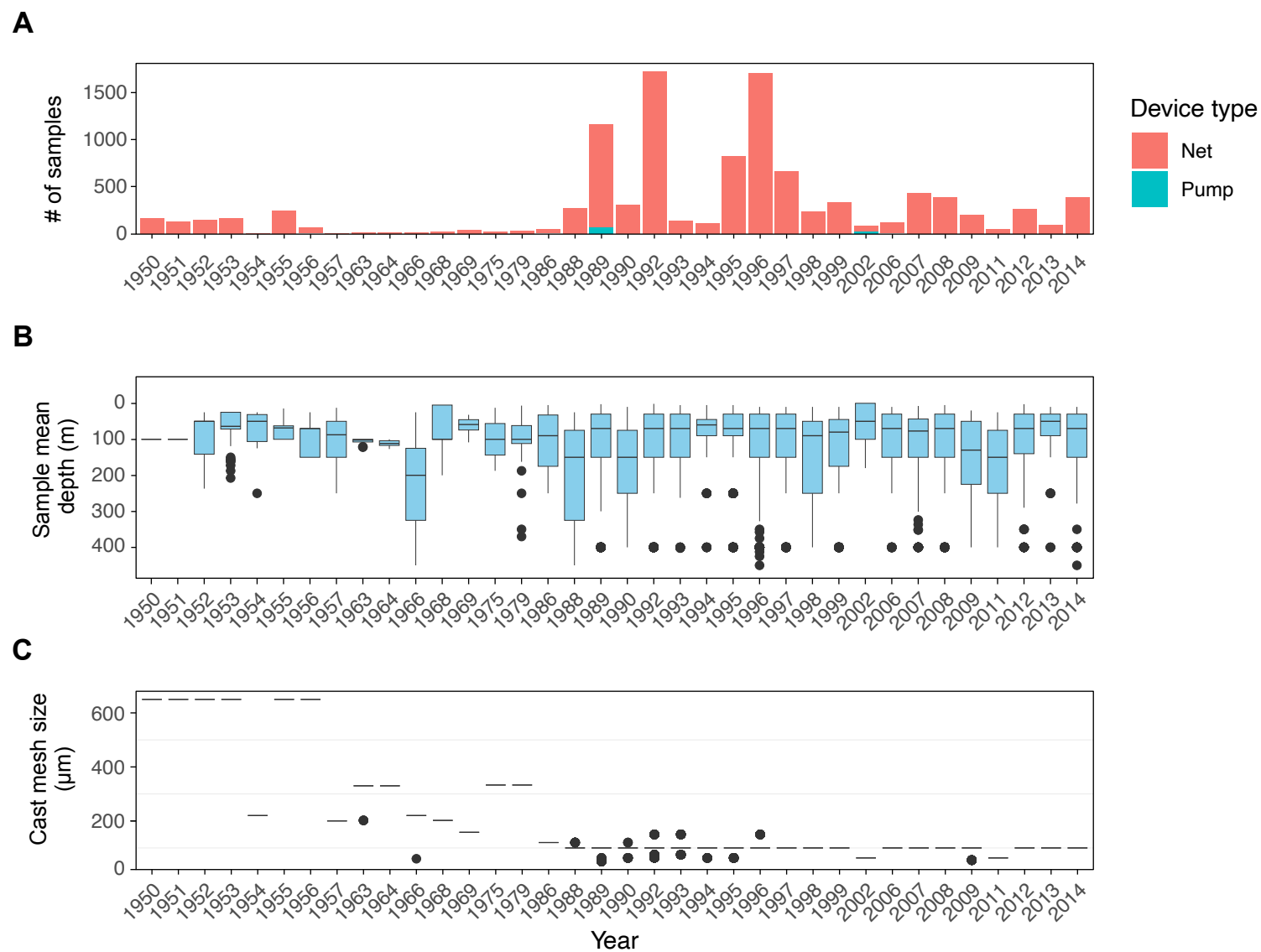


Fig. A1.1. Histograms of sample collection device type (A), average depth of collection (B), and cast mesh size (C) for each year for the final 10,632 samples used in modeling.

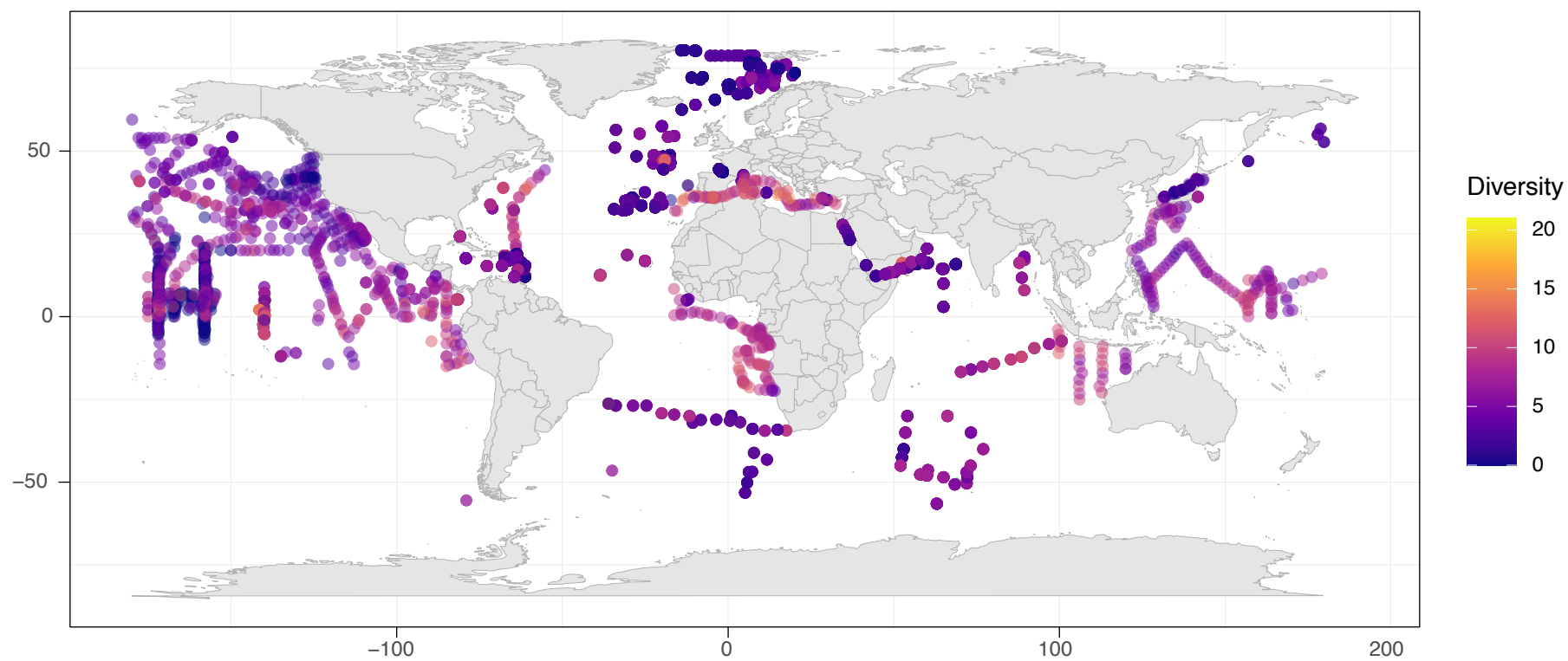
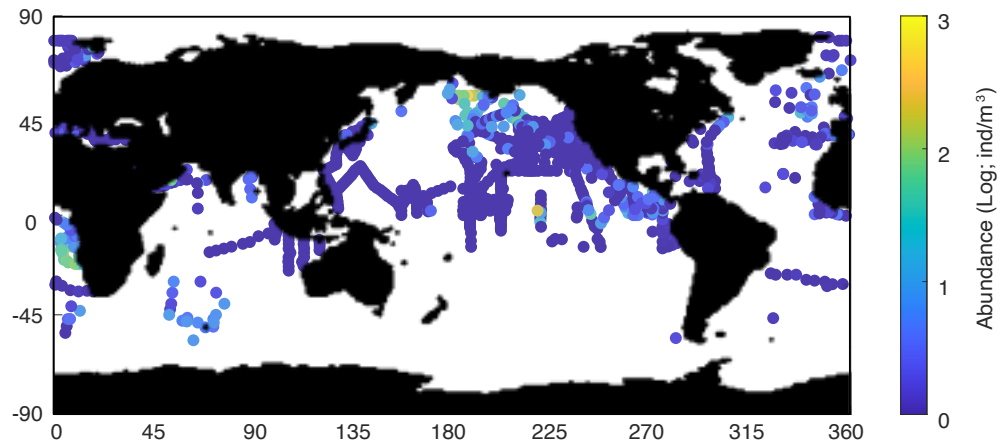
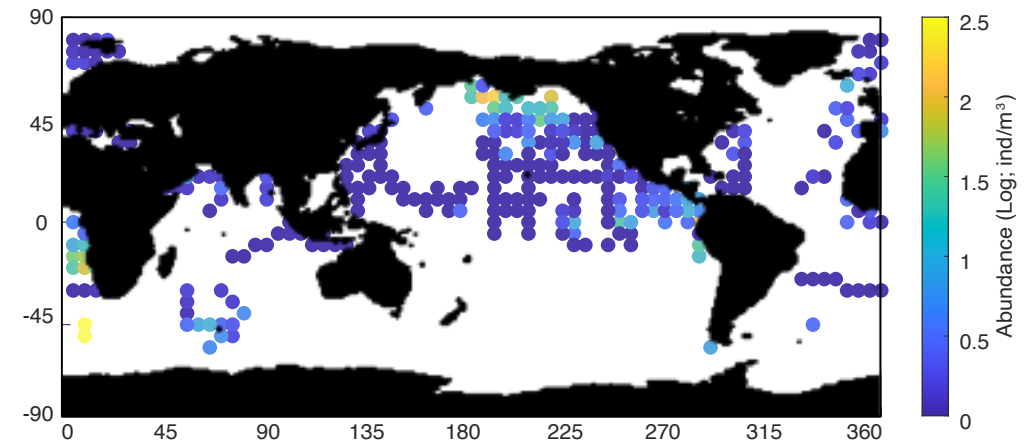


Fig. A1.2. Location and diversity (number of species out of 41 species) of the final subset of samples used in modeling (10,632 samples).

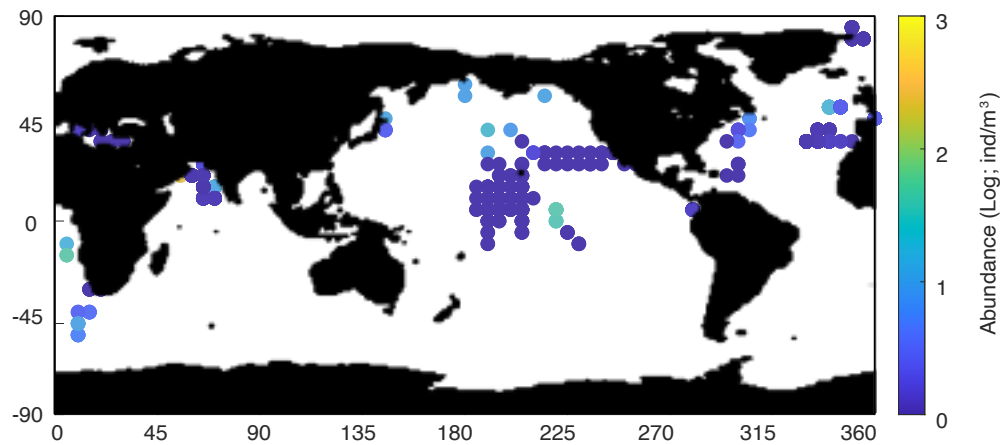
A



B



C



D

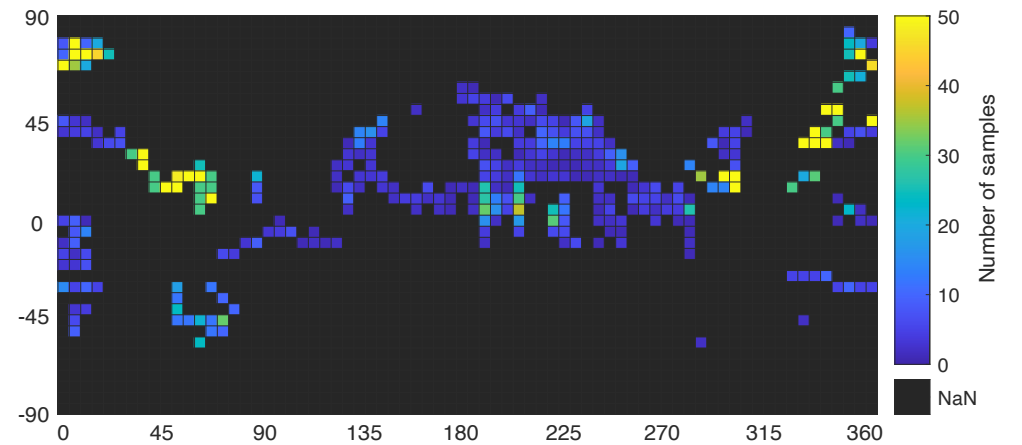


Fig. A2.1. Global maps of FORCIS log abundance data for *G. bulloides*. (A) Discrete samples for *G. bulloides* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure. (D) Heatmap of the number of samples in each 5°x5° latitude by longitude grid (same for all species)

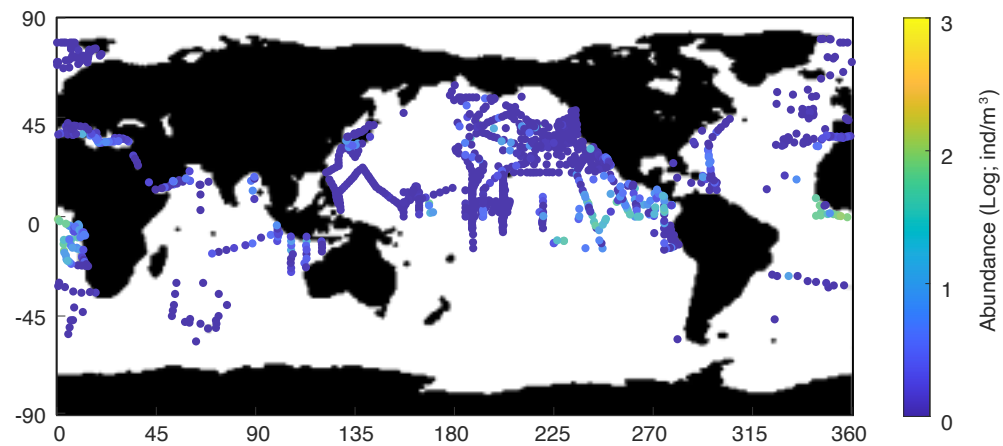
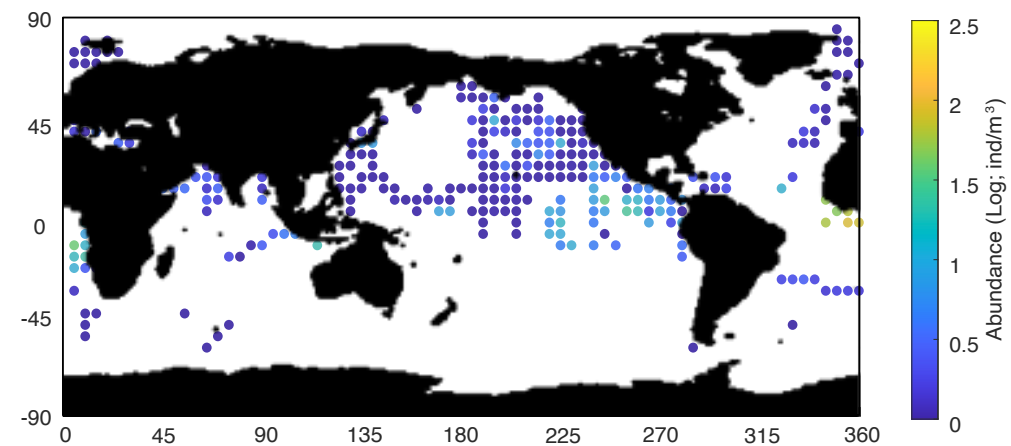
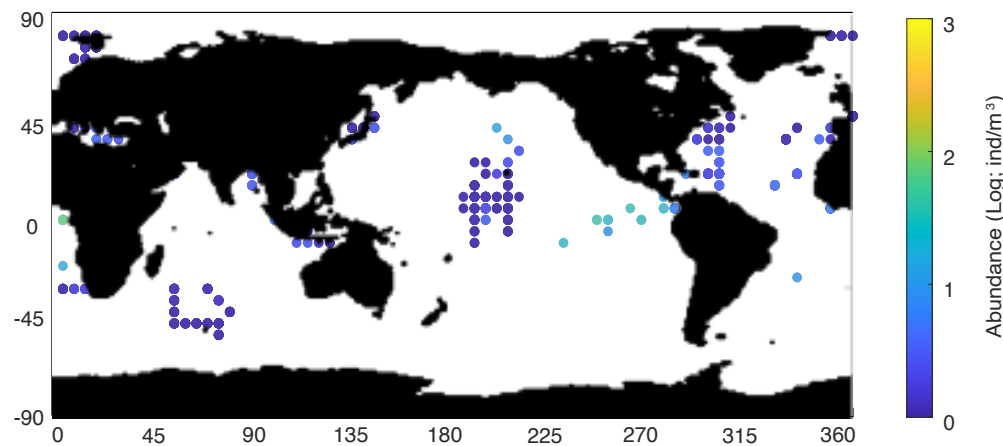
A**B****C**

Fig. A2.2. Global maps of FORCIS log abundance data for *G. ruber*. (A) Discrete samples for *G. ruber* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure.

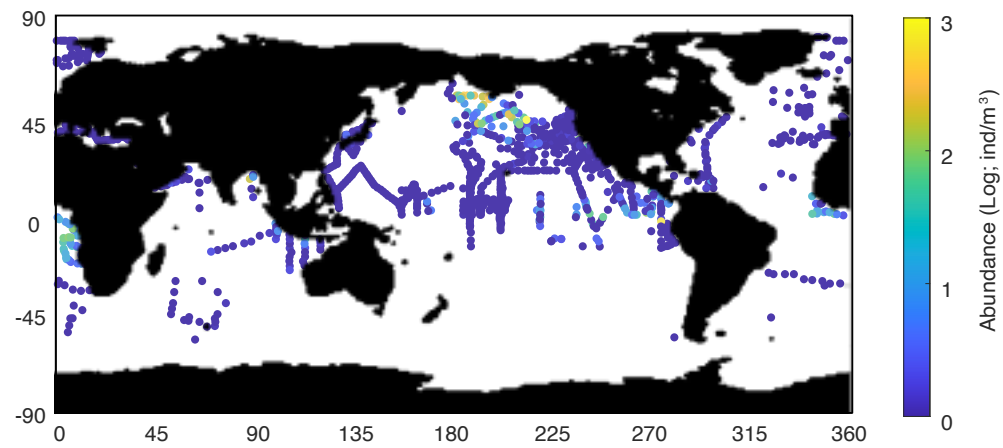
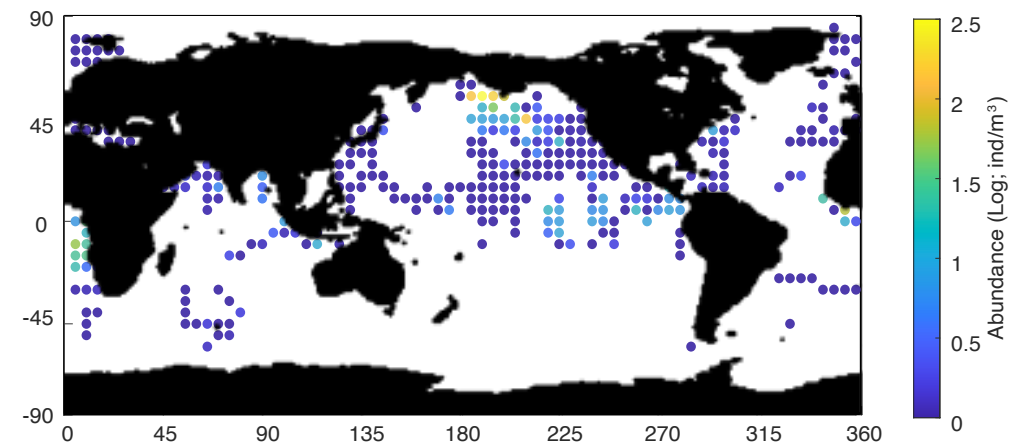
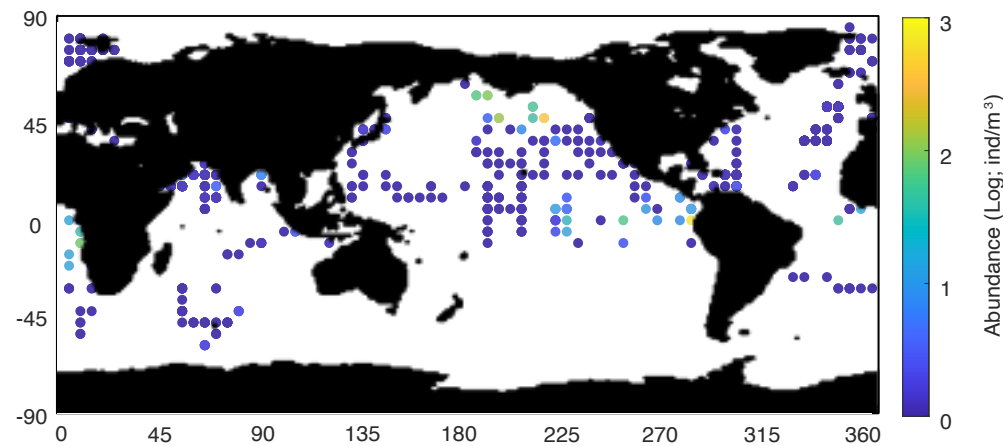
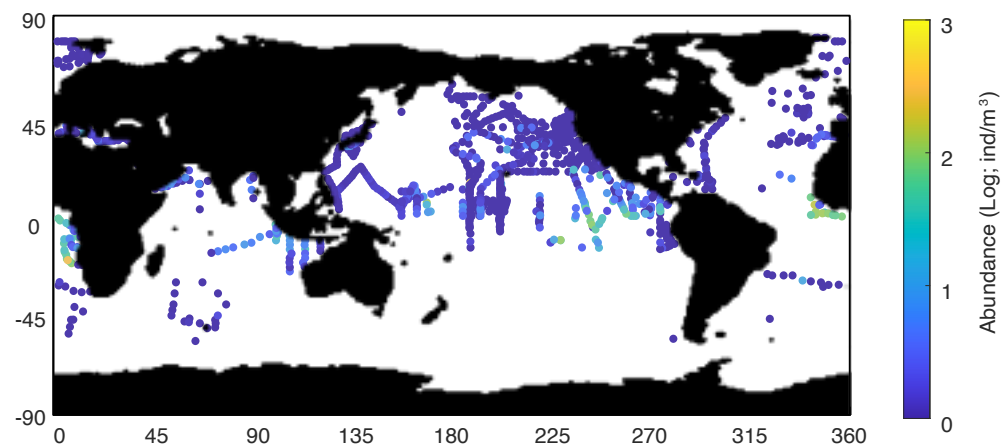
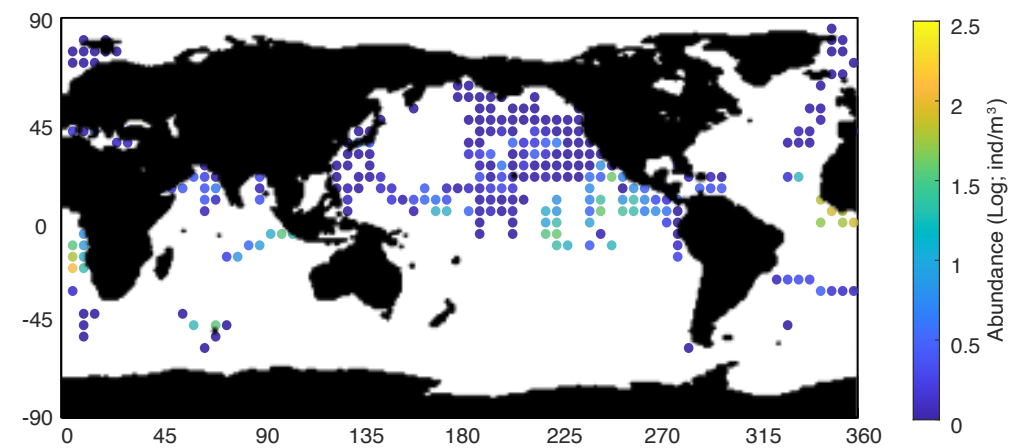
A**B****C**

Fig. A2.3. Global maps of FORCIS log abundance data for *N. dutertrei*. (A) Discrete samples for *N. dutertrei* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure.

A



B



C

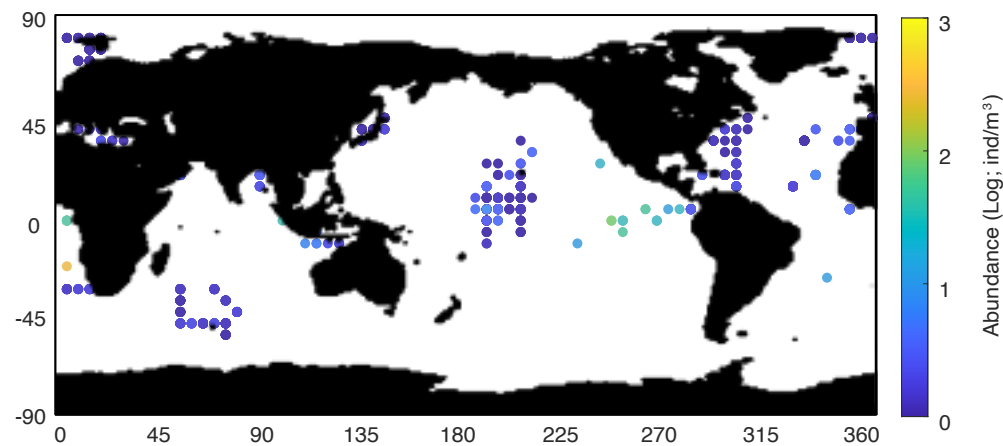


Fig. A2.4. Global maps of FORCIS log abundance data for *T. sacculifer*. (A) Discrete samples for *T. sacculifer* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure.

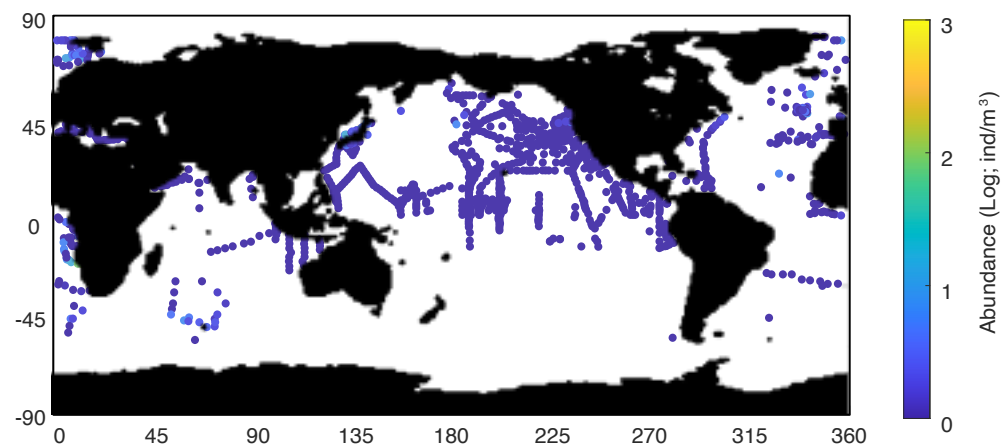
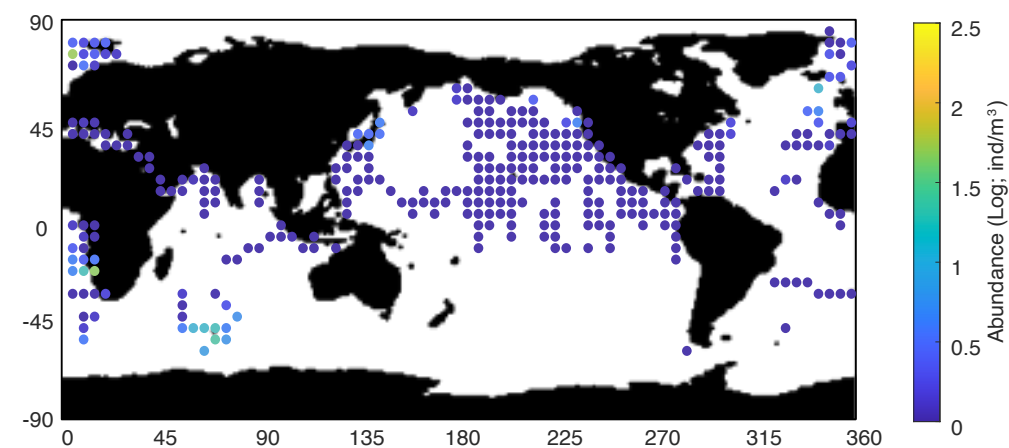
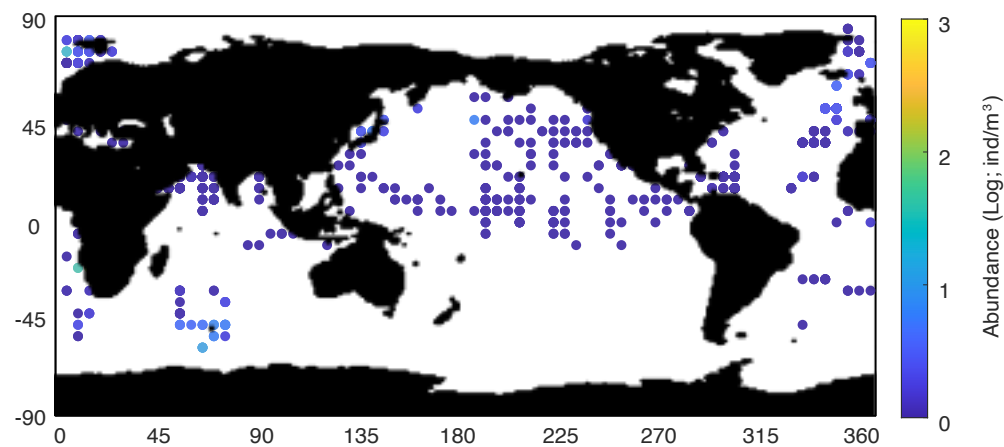
A**B****C**

Fig. A2.5. Global maps of FORCIS log abundance data for *N. incompta*. (A) Discrete samples for *N. incompta* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure.

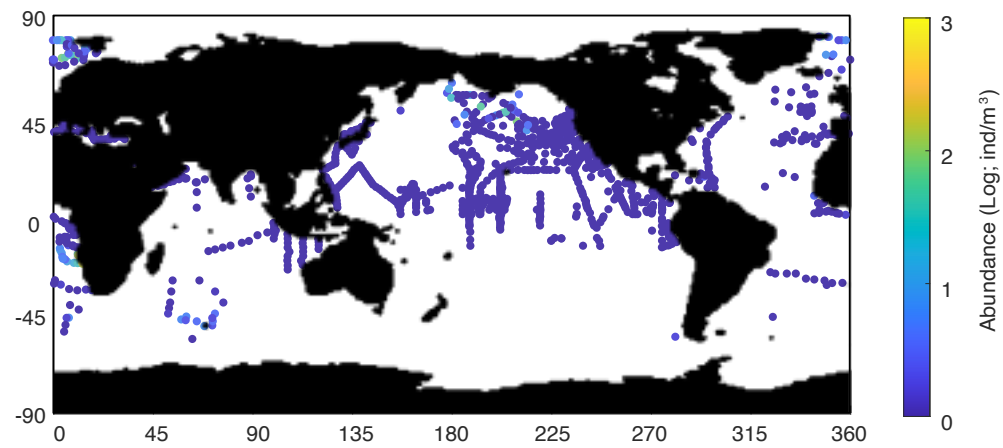
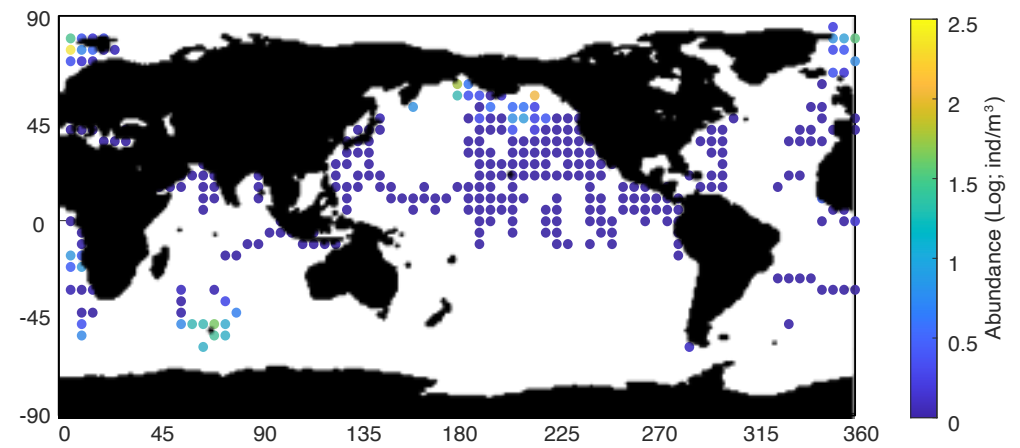
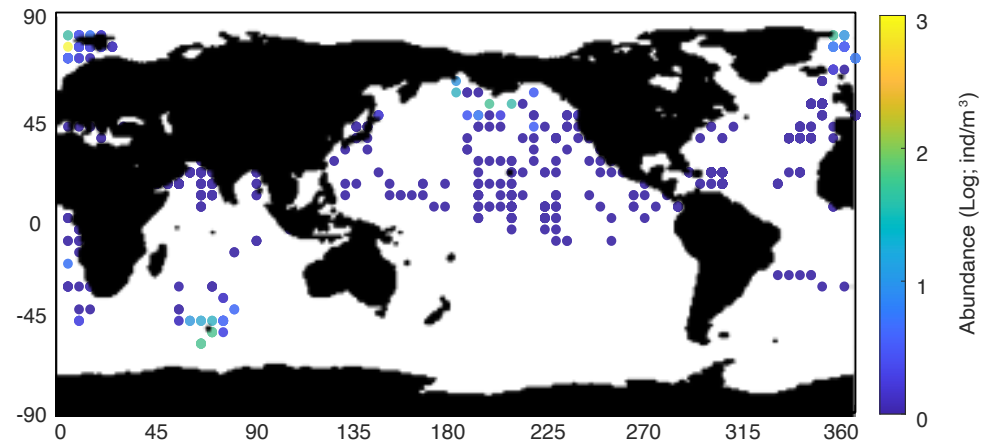
A**B****C****D**

Fig. A2.6. Global maps of FORCIS log abundance data for *N. pachyderma*. (A) Discrete samples for *N. pachyderma* from the FORCIS database. (B) Gridded training data with the average log abundance indicated by the colorbar. (C) Gridded validation data using the same gridding procedure.

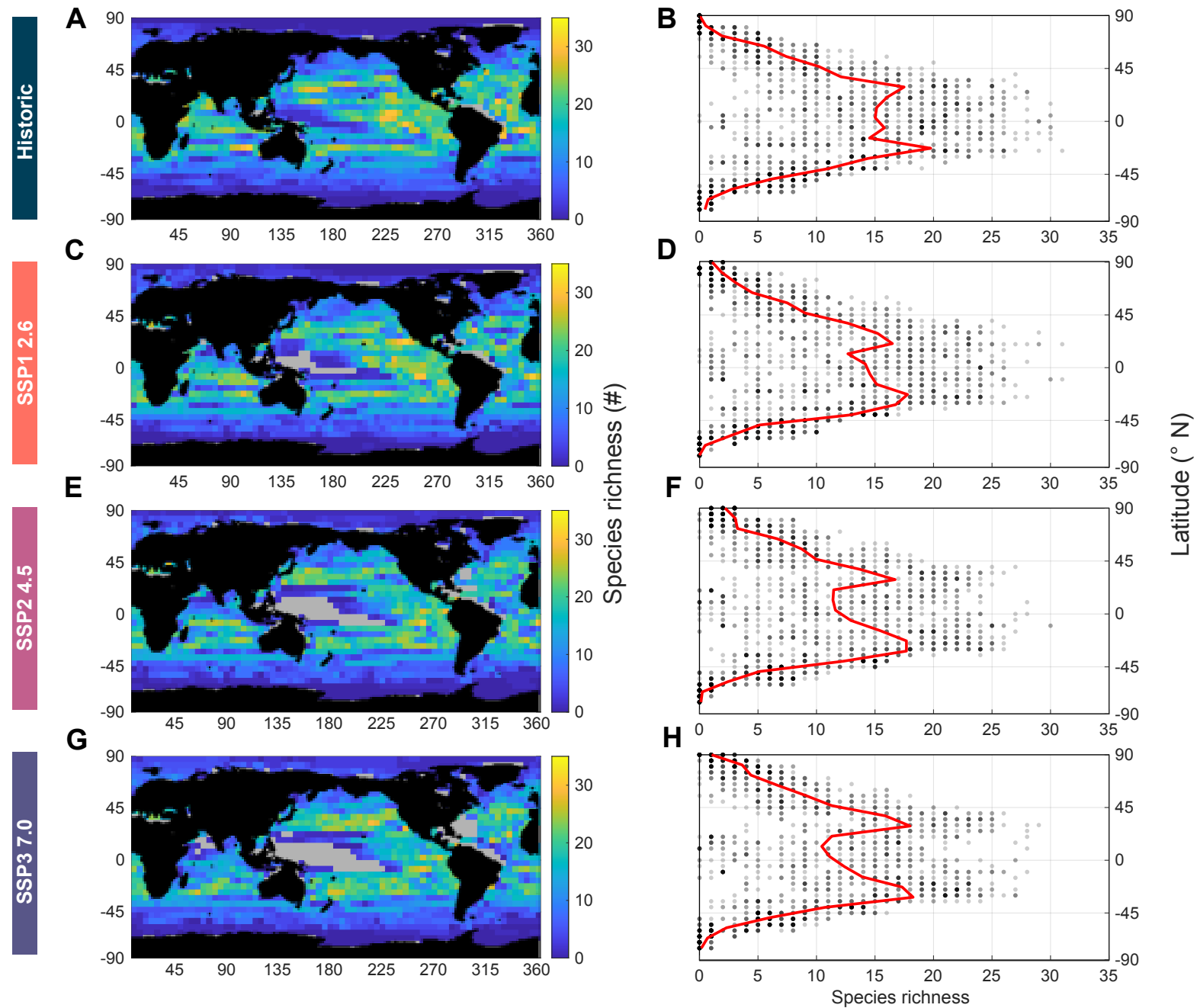


Fig. A3.1. ESM distribution maps for diversity using all 41 species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H). A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

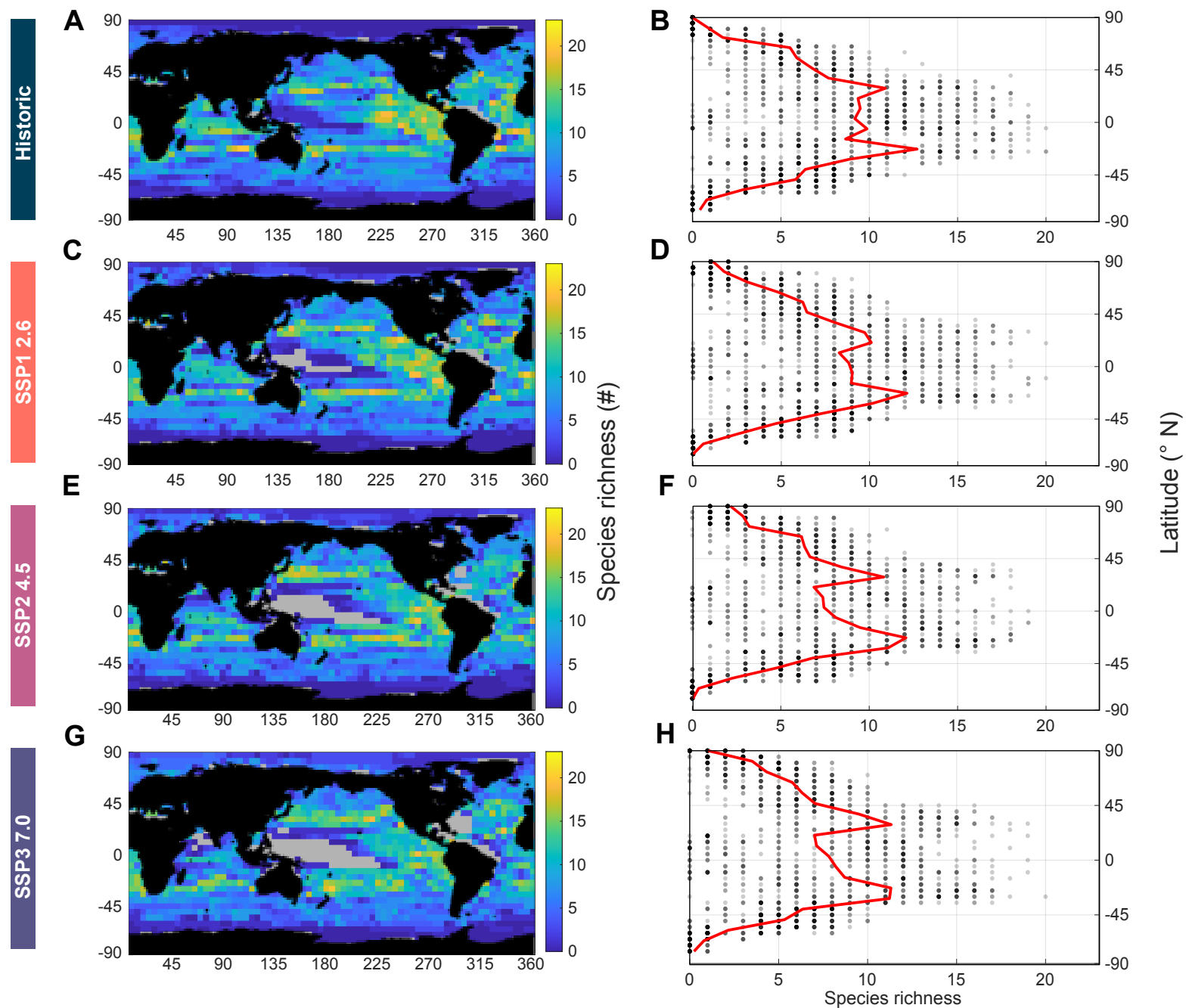


Fig. A3.2. ESM distribution maps for diversity using 26 major species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H).

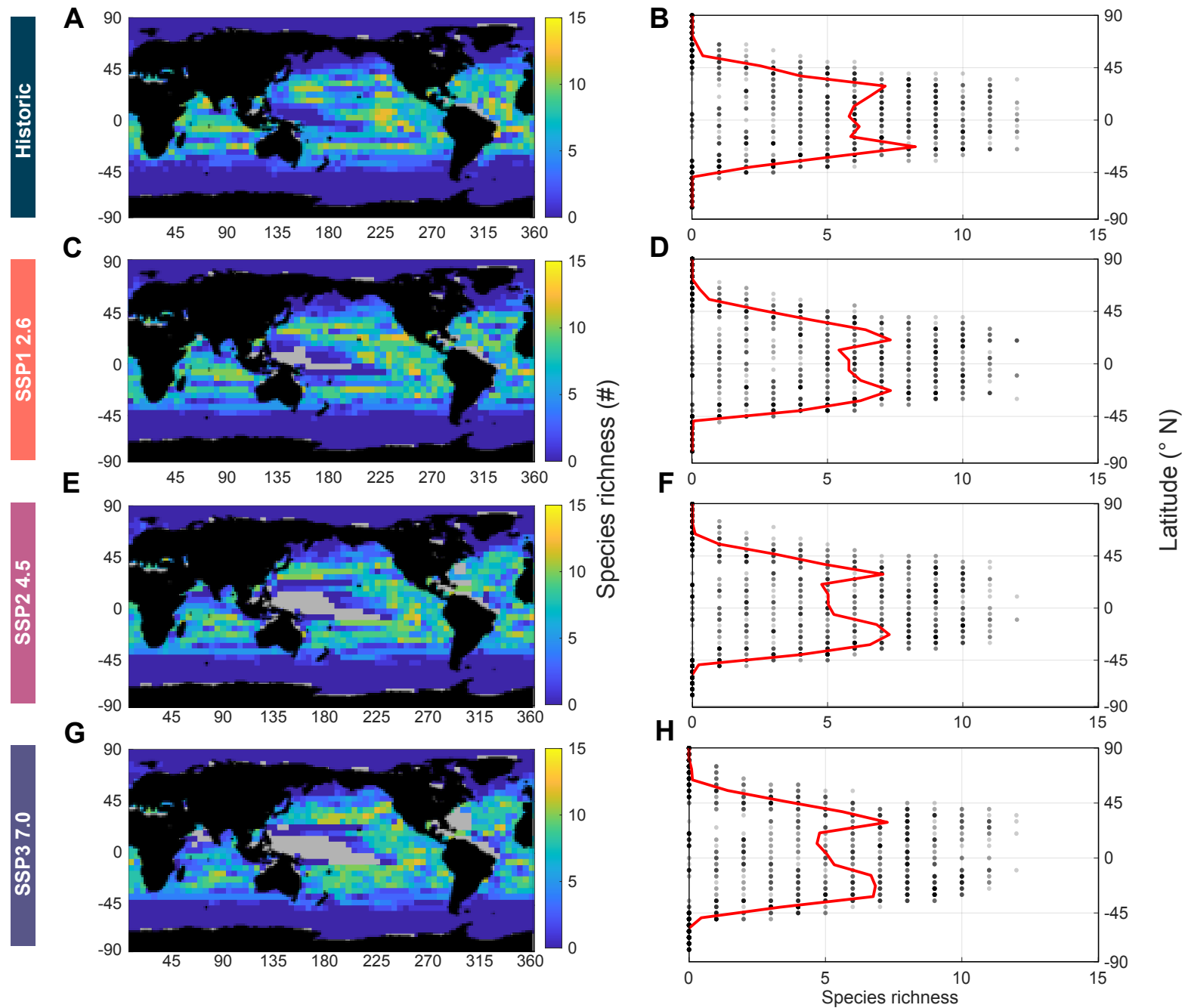


Fig. A3.3. ESM distribution maps for diversity using 12 symbiont-bearing species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H).

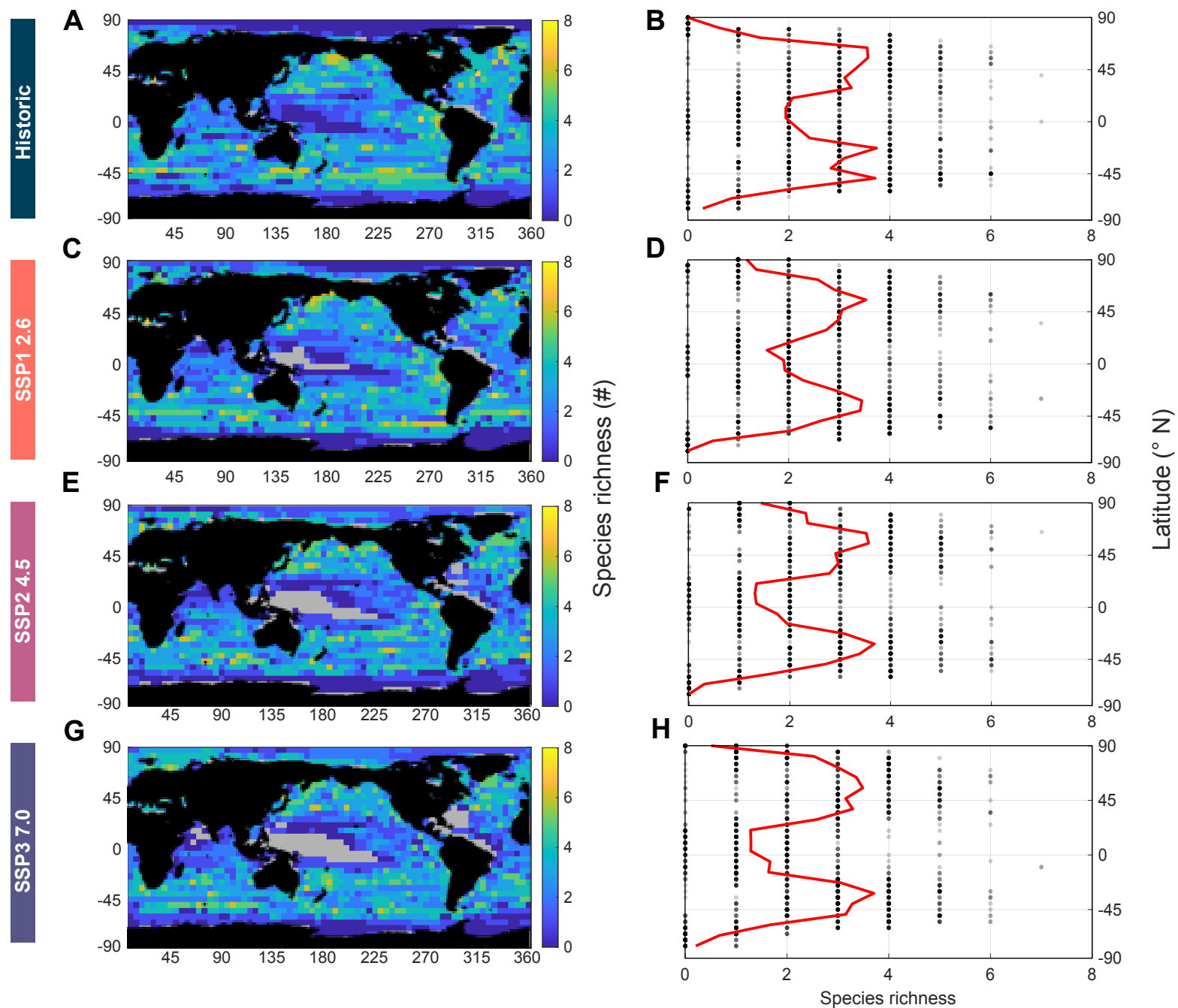


Fig. A3.4. ESM distribution maps for diversity using 10 symbiont-barren species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H).

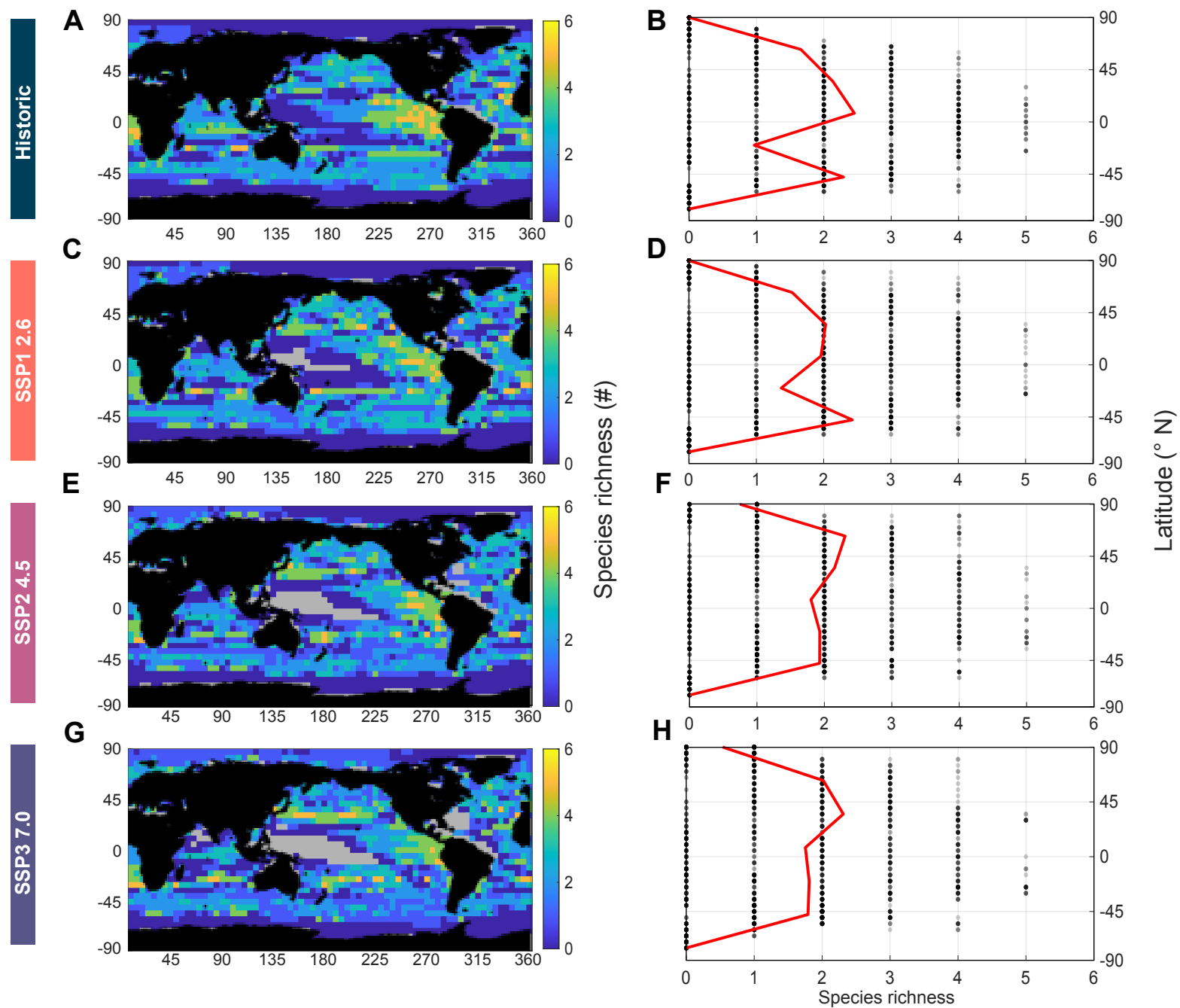


Fig. A3.5. ESM distribution maps for diversity using 6 facultatively symbiont-bearing species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H).

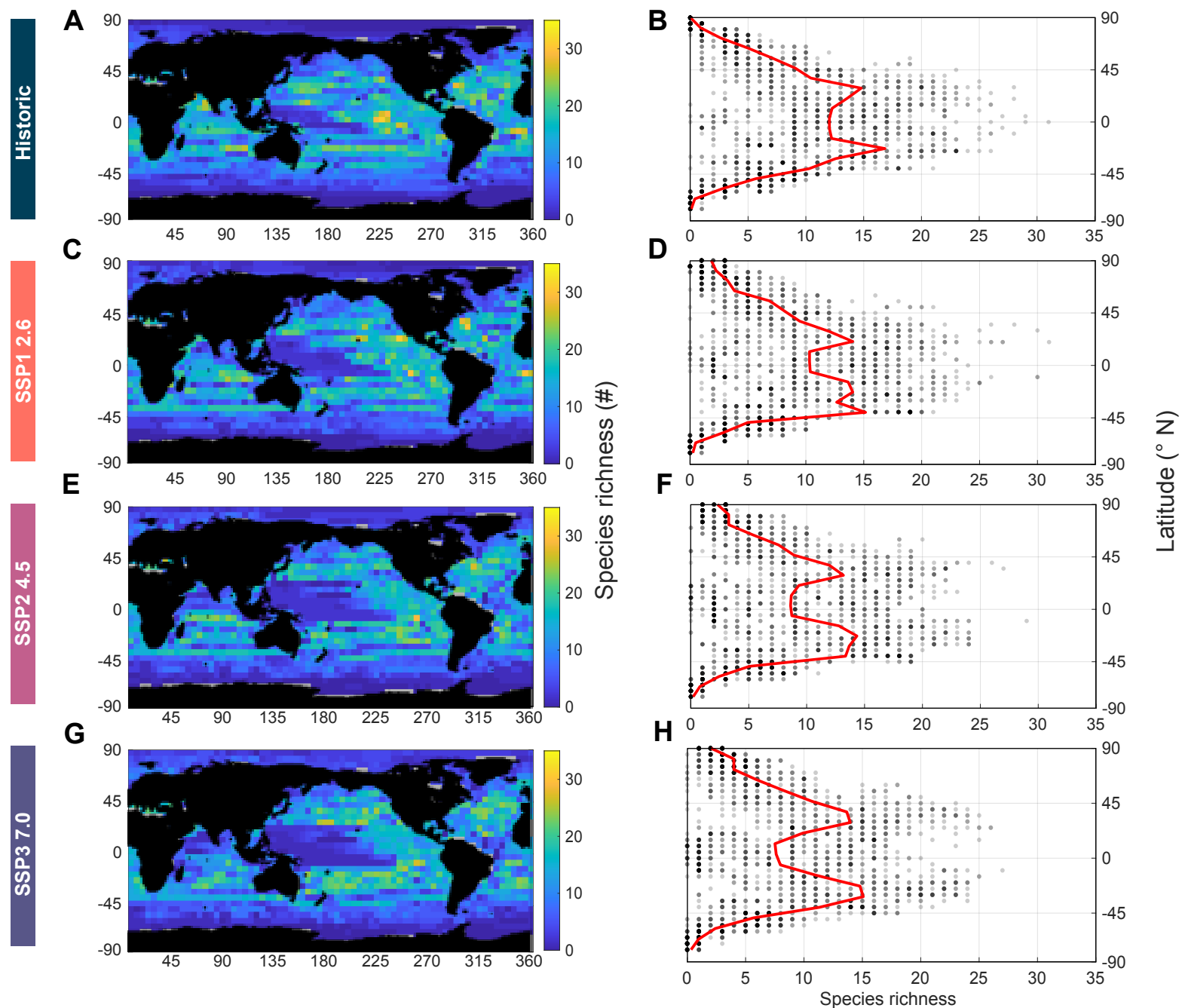


Fig. A3.6. GRNN distribution maps for diversity using all 41 species for the past (A) and future (C, E, and G) for different climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H). A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

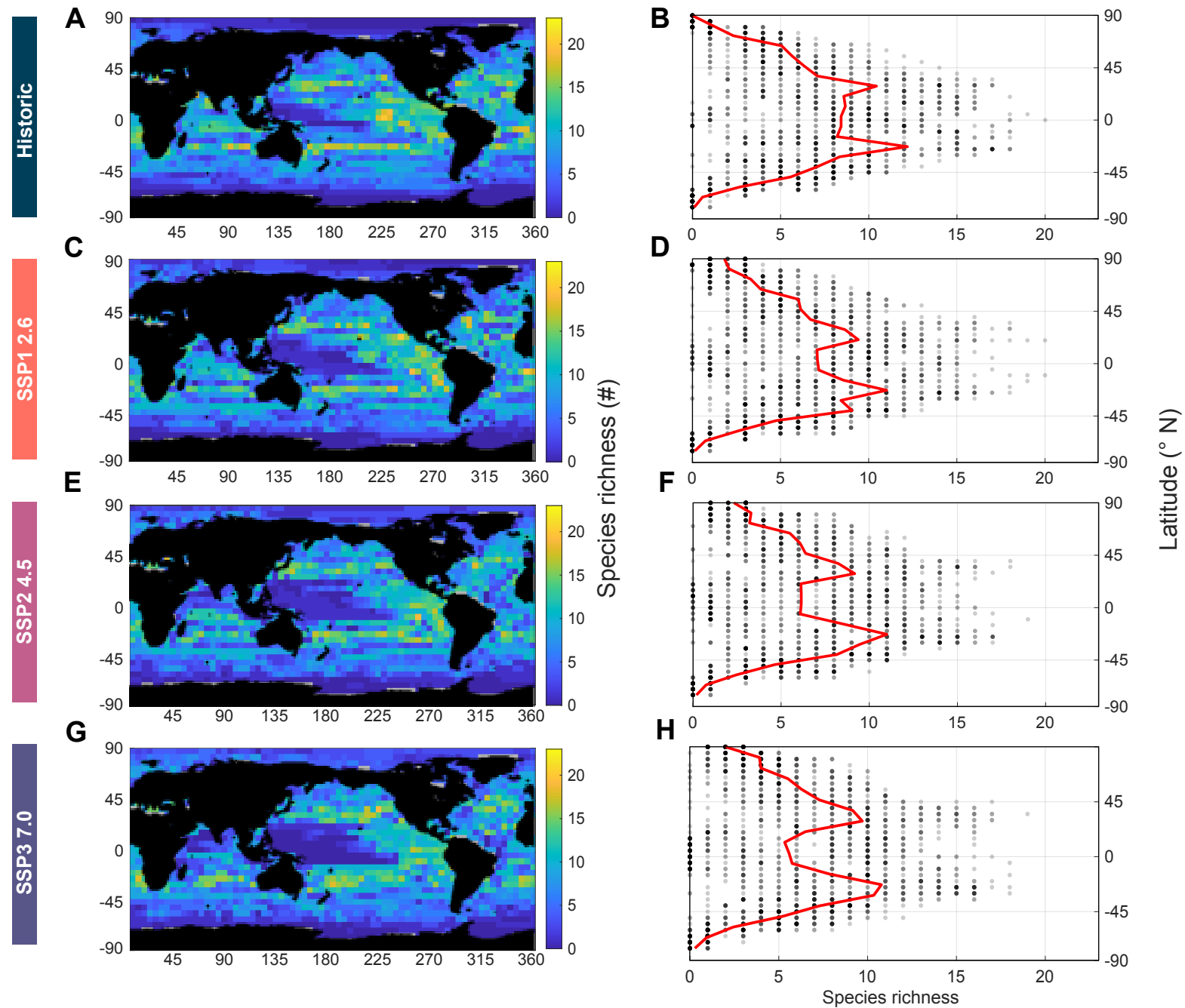


Fig. A3.7. GRNN distribution maps for diversity using 26 major species for the past (A) and future (C, E, and G) for each climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H). A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

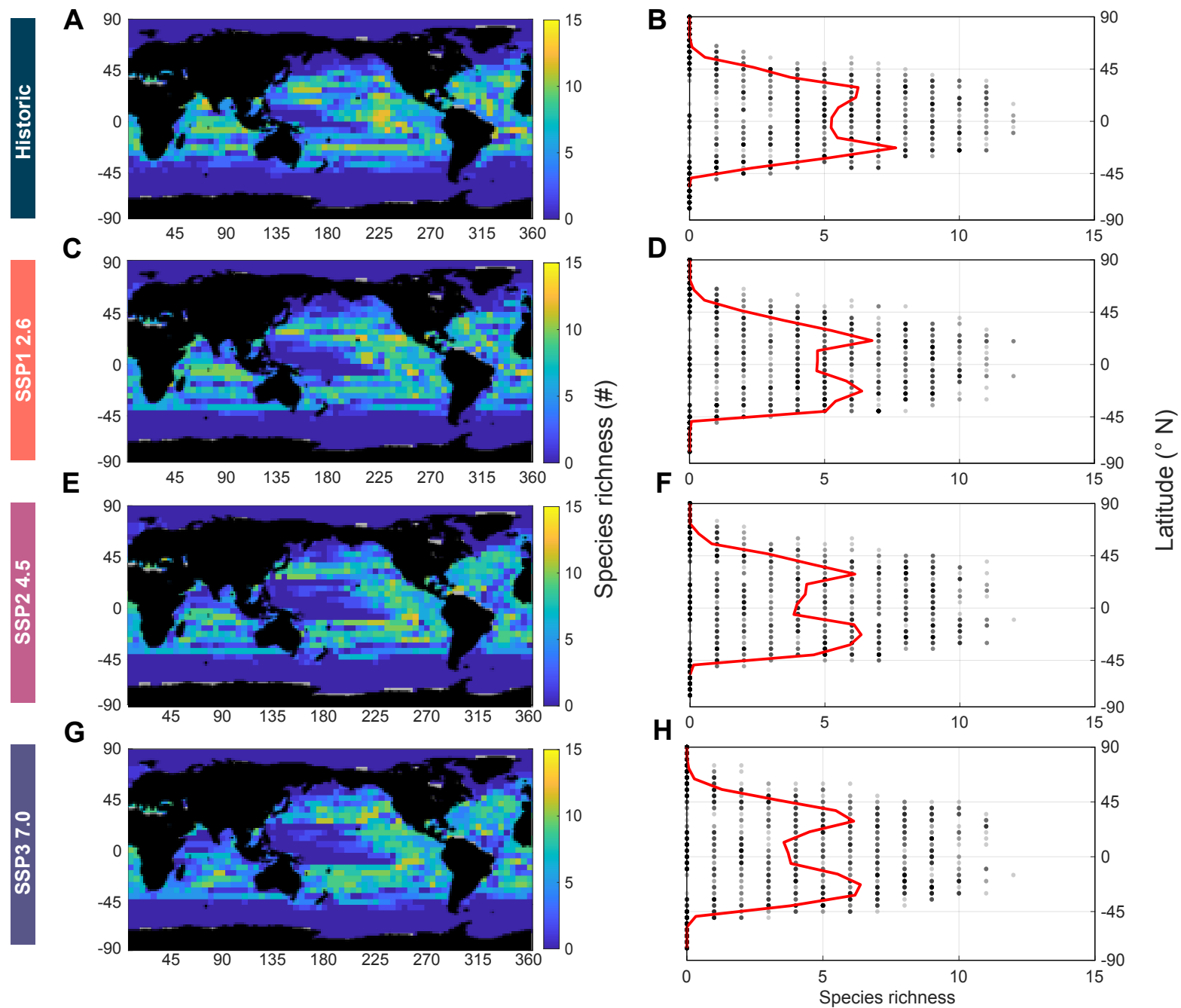


Fig. A3.8. GRNN distribution maps for diversity using 12 symbiont-bearing species for the past (A) and future (C, E, and G) for each climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H). A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

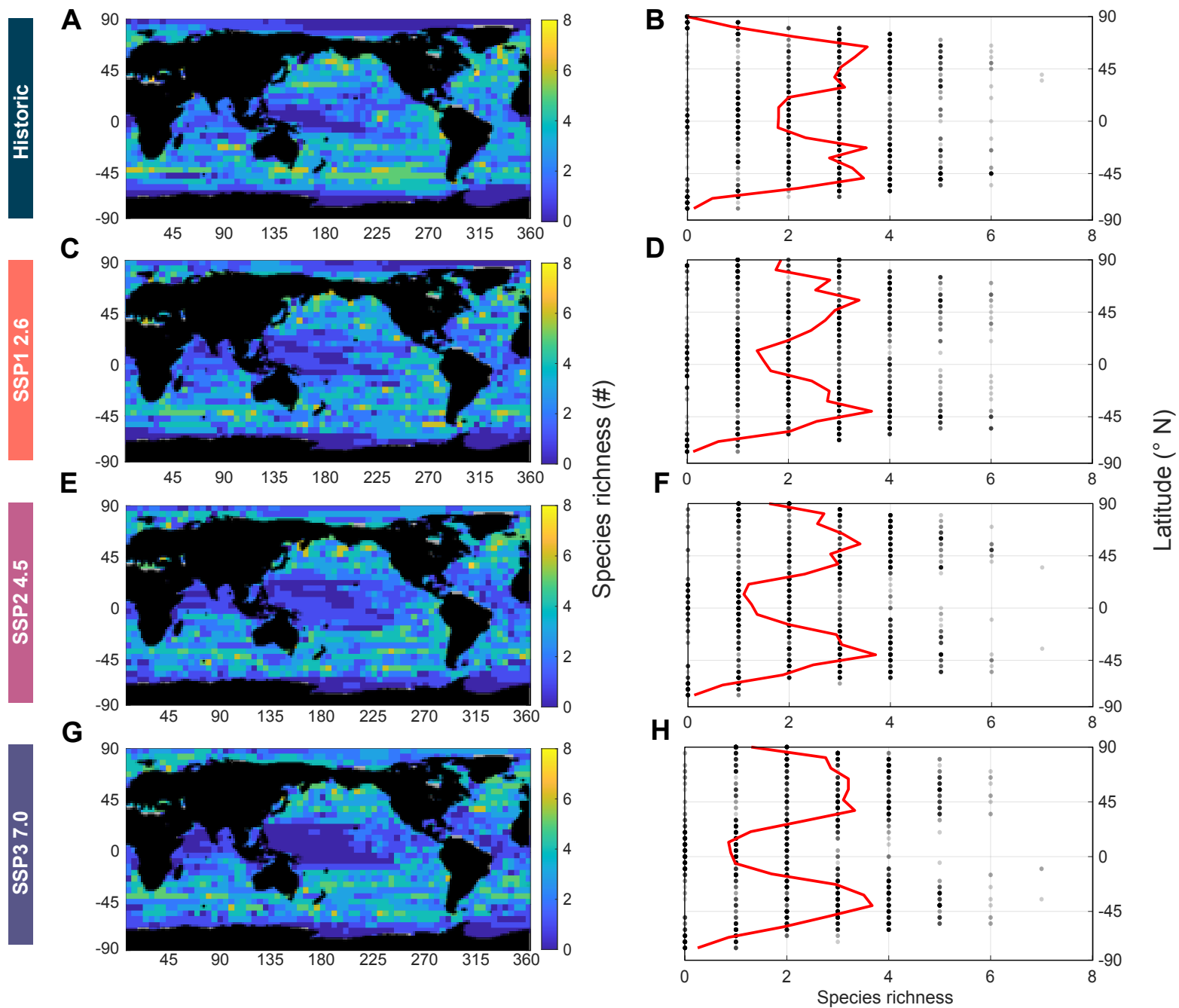


Fig. A3.9. GRNN distribution maps for diversity using 10 symbiont-barren species for the past (A) and future (C, E, and G) for each climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H).

A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

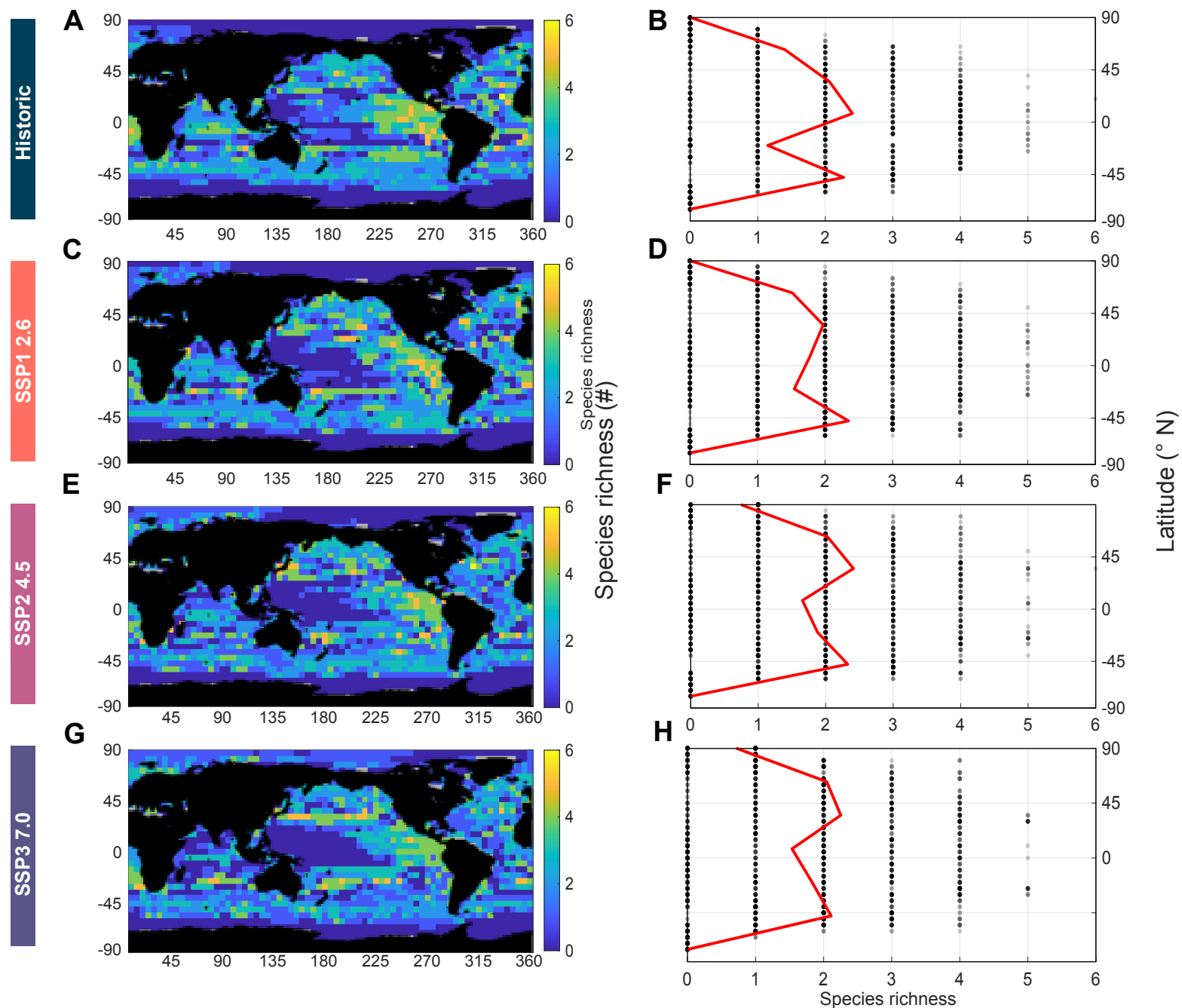


Fig. A3.10. GRNN distribution maps for diversity using 6 facultatively symbiont-bearing species for the past (A) and future (C, E, and G) for each climate scenario (SSP1-2.6: C; SSP2-4.5: E; SSP3-7.0: G) with associated latitudinal profiles (D, F, and H). A generalized additive model was fit to the values over each latitudinal degree and smoothed to create the latitudinal profiles.

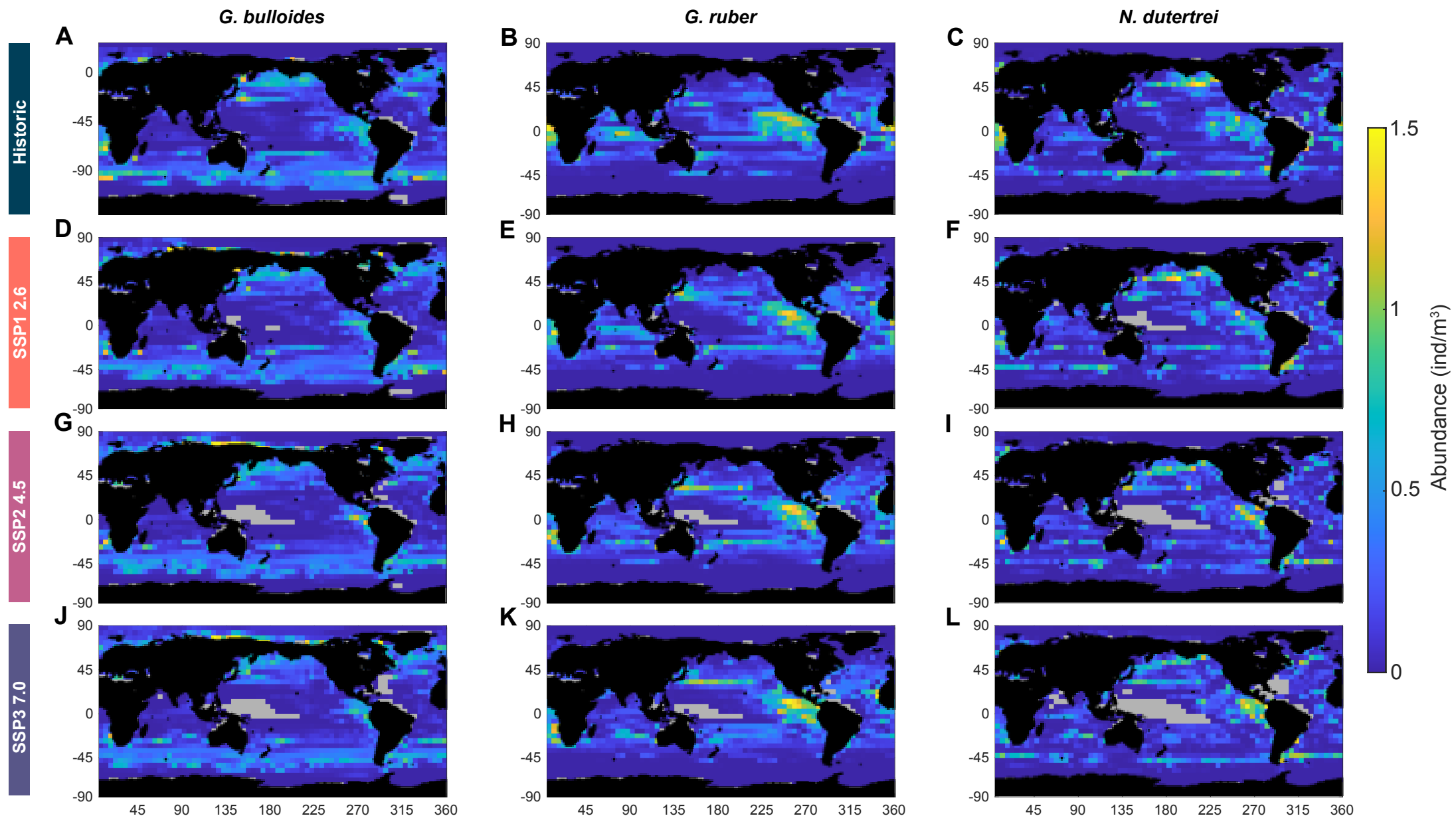


Fig. A4.1. ESM distribution maps for *G. bulloides* (A, D, G, J), *G. ruber* (B, E, H, K), and *N. dutertrei* (C, F, I, L) for the past and three scenarios with increasing forcing levels.

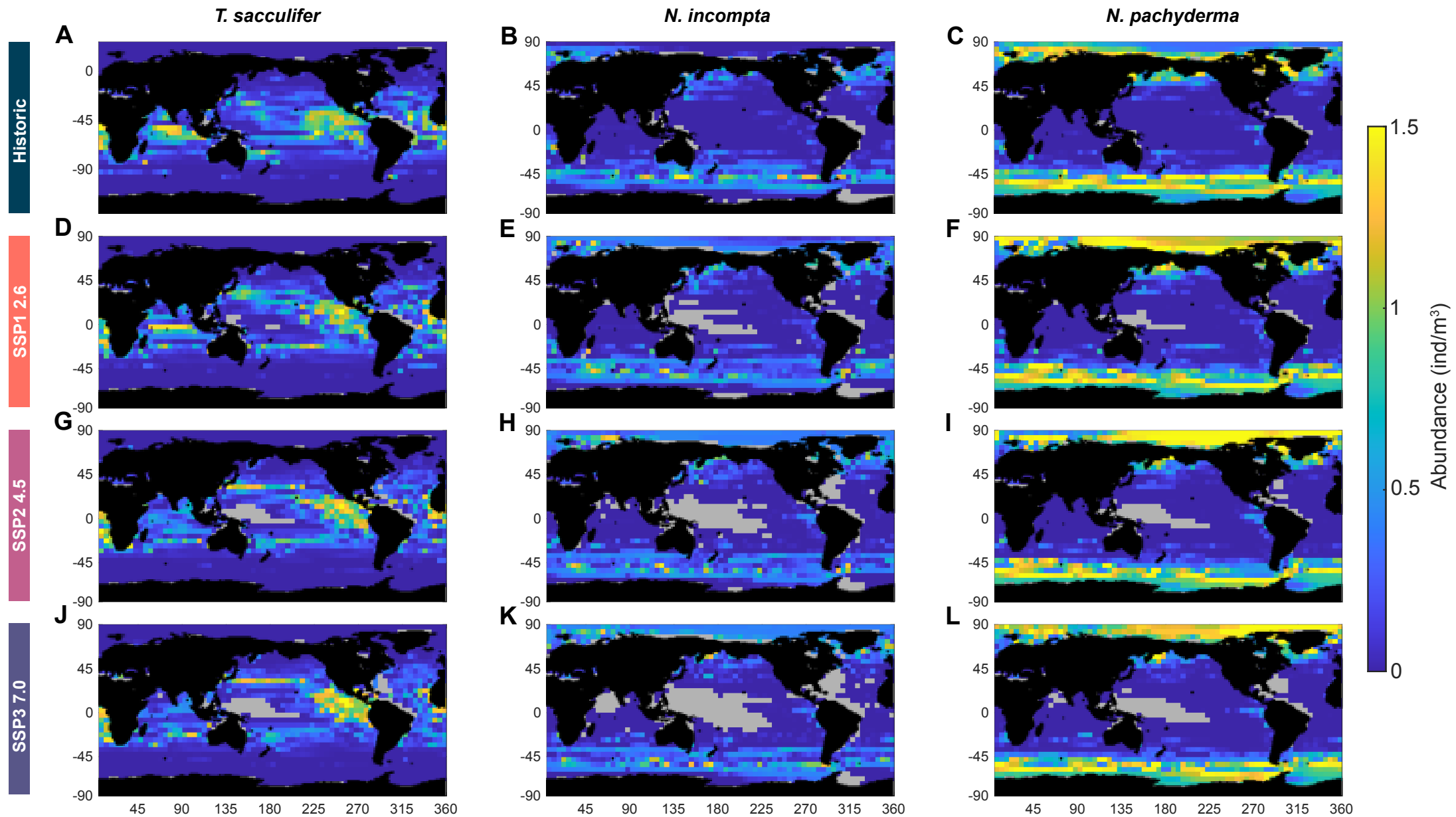


Fig. A4.2. ESM distribution maps for *T. sacculifer* (A, D, G, J), *N. incompta* (B, E, H, K), and *N. pachyderma* (C, F, I, L) for the past and three scenarios with increasing forcing levels.

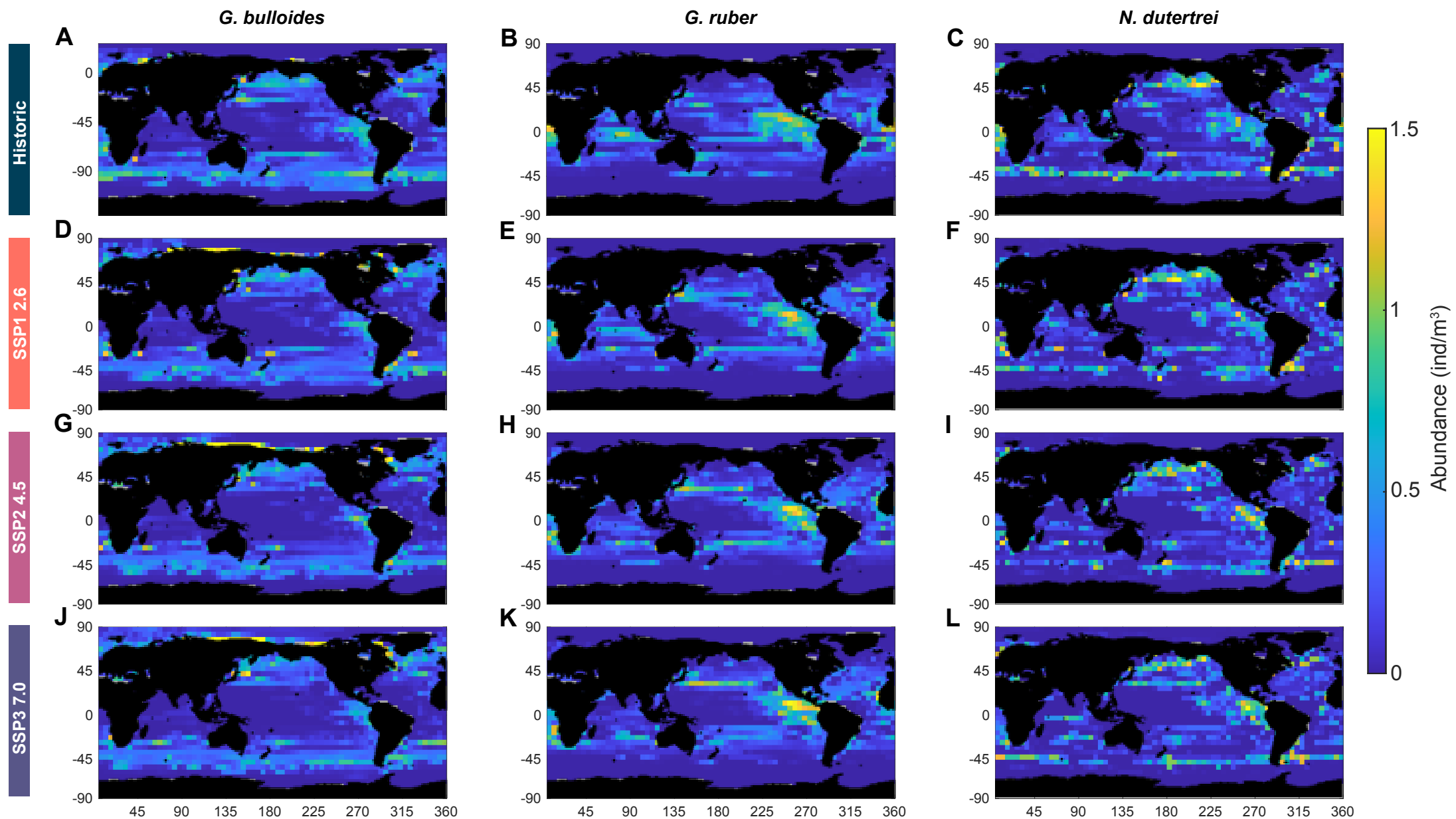


Fig. A5.1. GRNN distribution maps for *G. bulloides* (A, D, G, J), *G. ruber* (B, E, H, K), and *N. dutertrei* (C, F, I, L) for the past and three scenarios with increasing forcing levels.

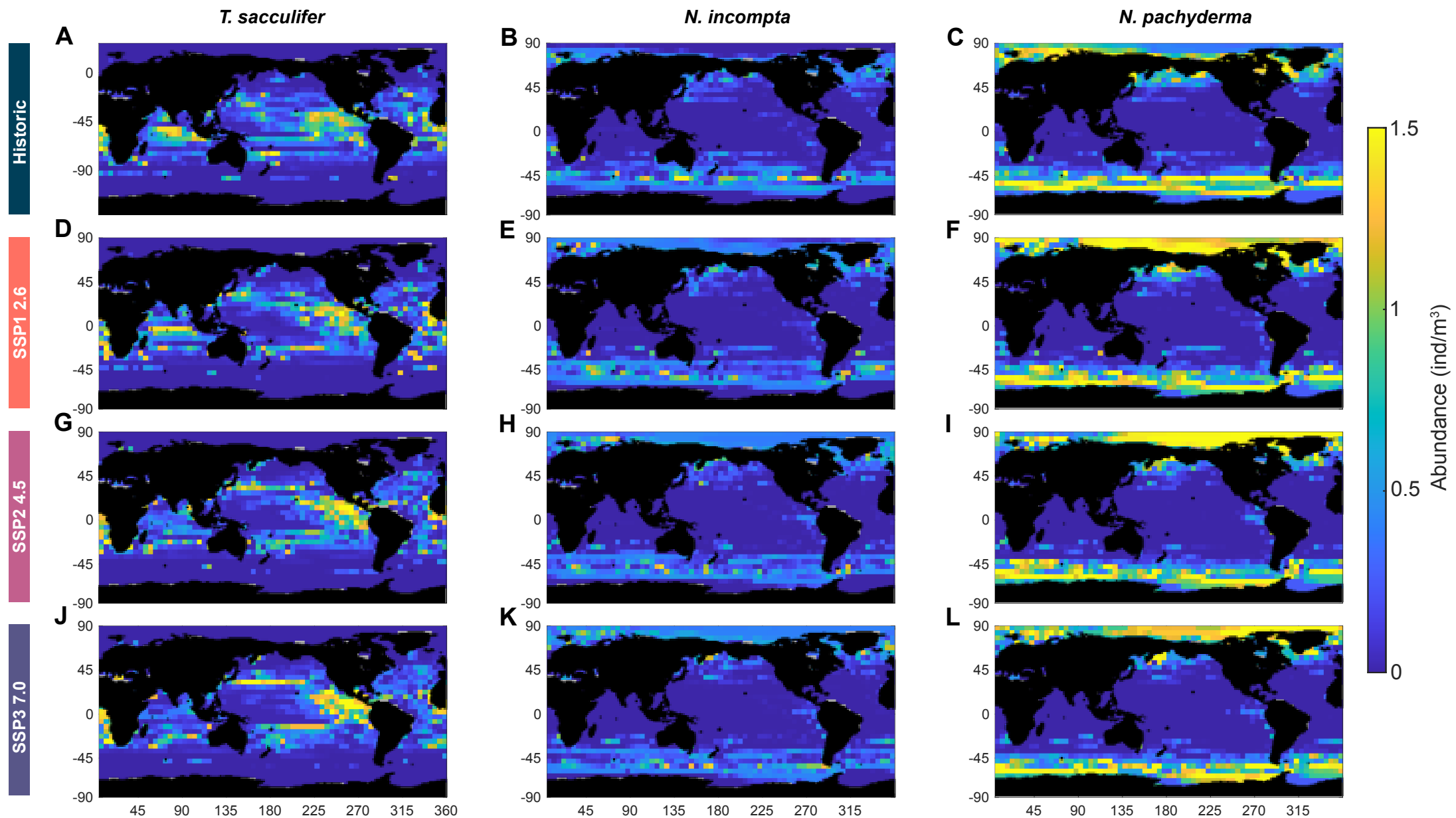


Fig. A5.2. GRNN distribution maps for *T. sacculifer* (A, D, G, J), *N. incompta* (B, E, H, K), and *N. pachyderma* (C, F, I, L) for the past and three scenarios with increasing forcing levels.

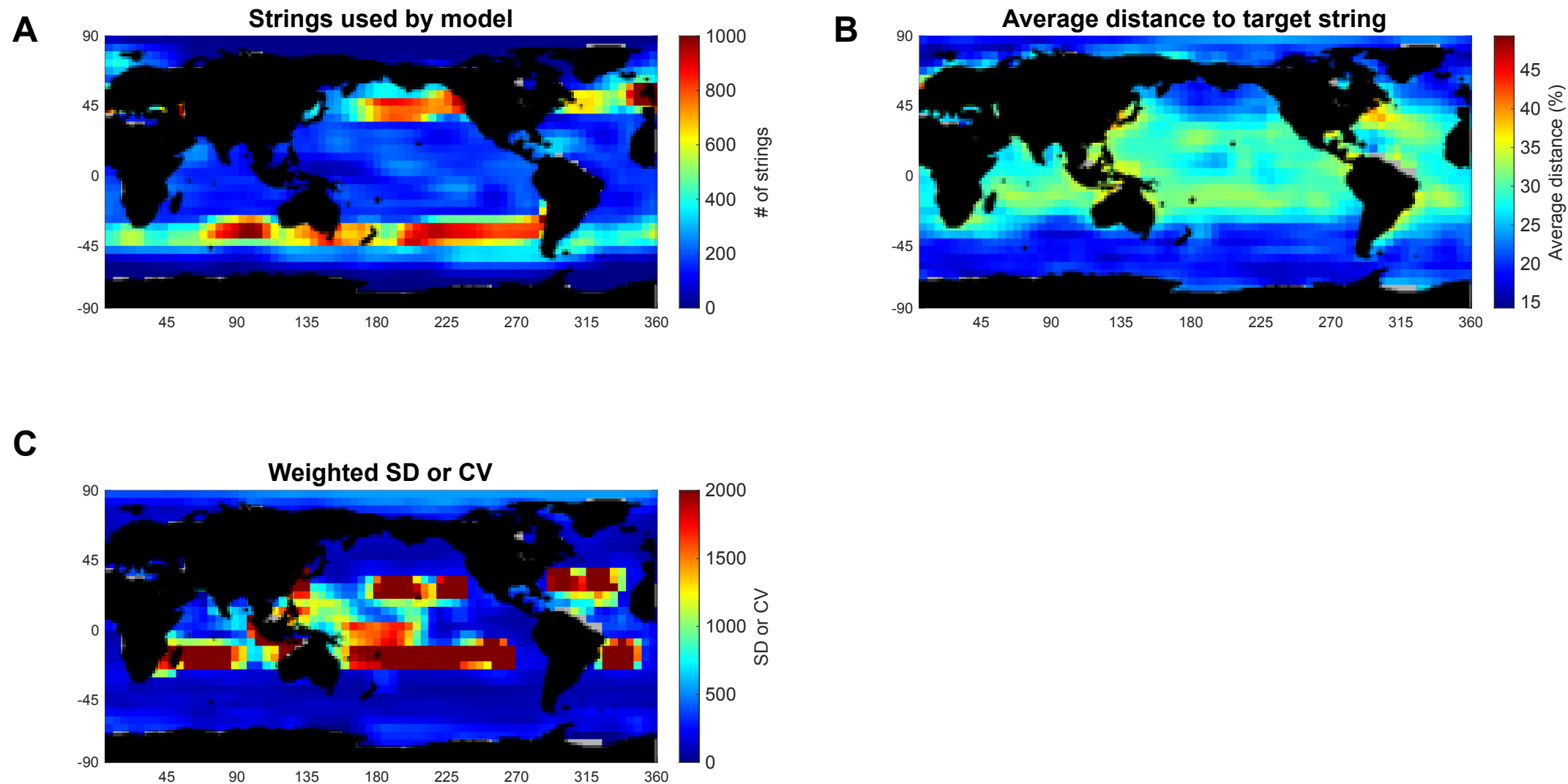


Fig. A6.1. ESM indicators of abundance estimate quality for *G. bulloides* for SSP2-4.5 ($d = 0.03$, $w = 1 \times 10^{15}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

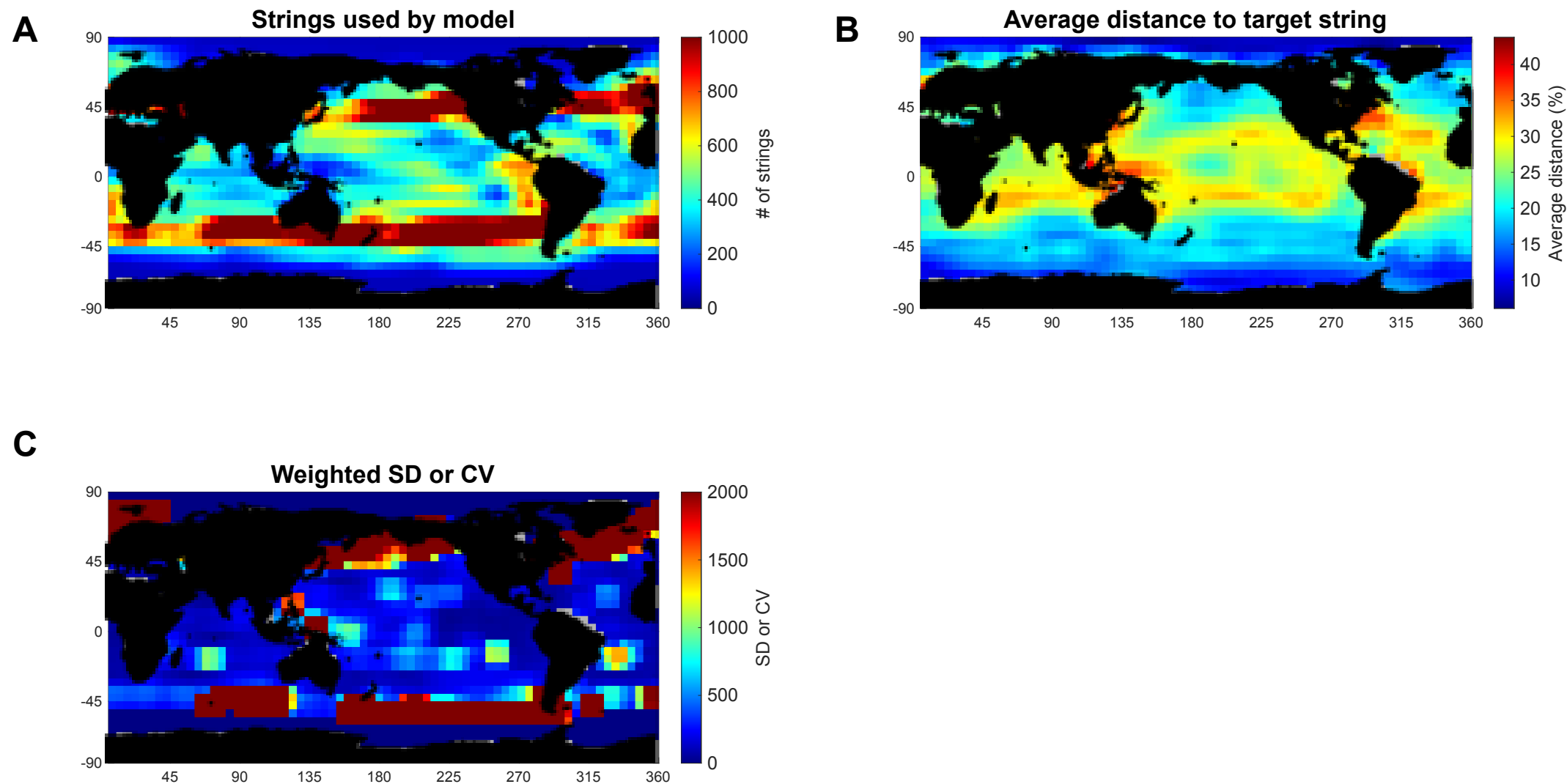


Fig. A6.2. ESM indicators of abundance estimate quality for *G. ruber* for SSP2-4.5 ($d = 0.04$, $w = 1 \times 10^{25}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

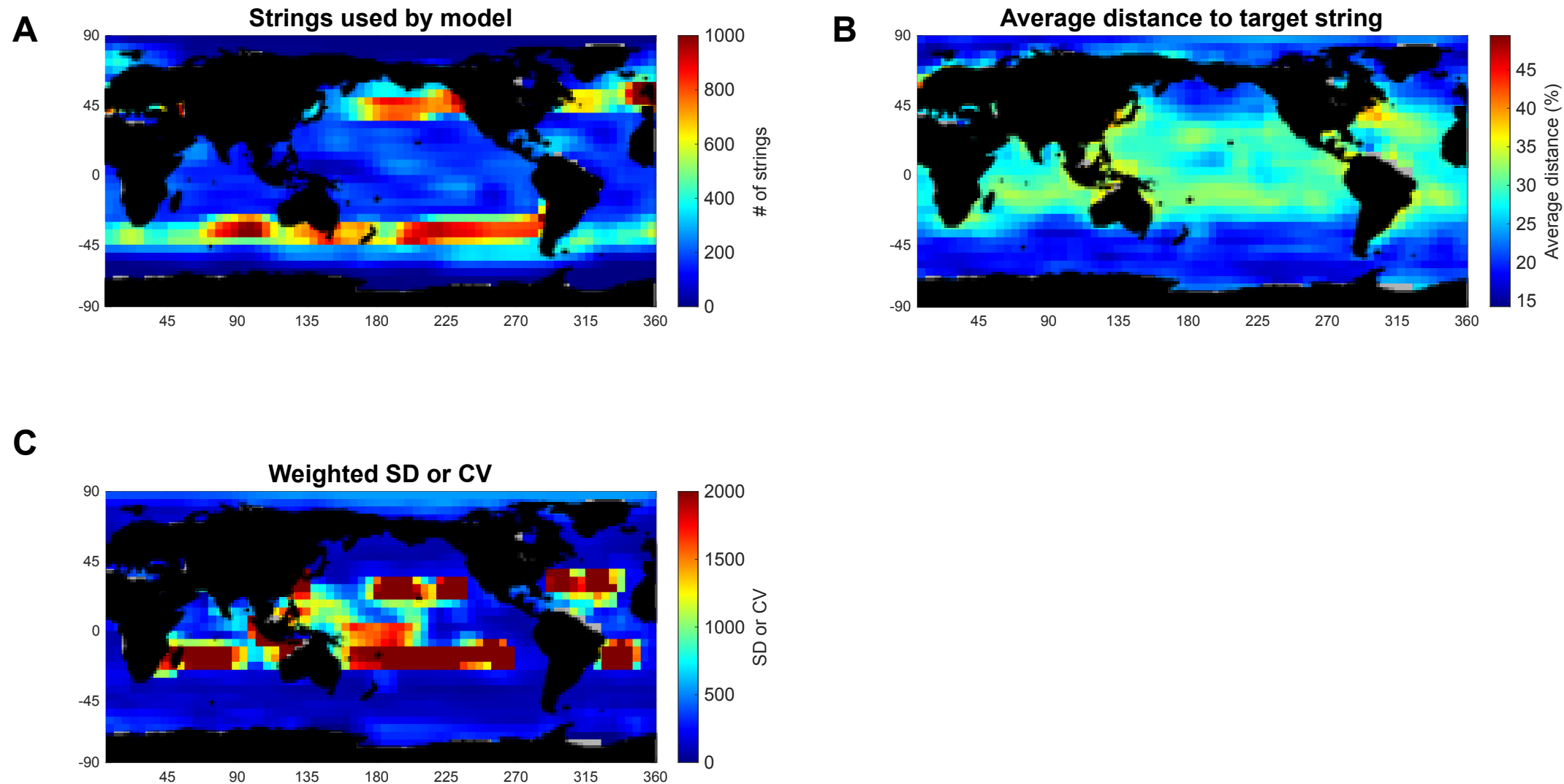


Fig. A6.3. ESM indicators of abundance estimate quality for *N. dutertrei* for SSP2-4.5 ($d = 0.02$, $w = 1 \times 10^{25}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

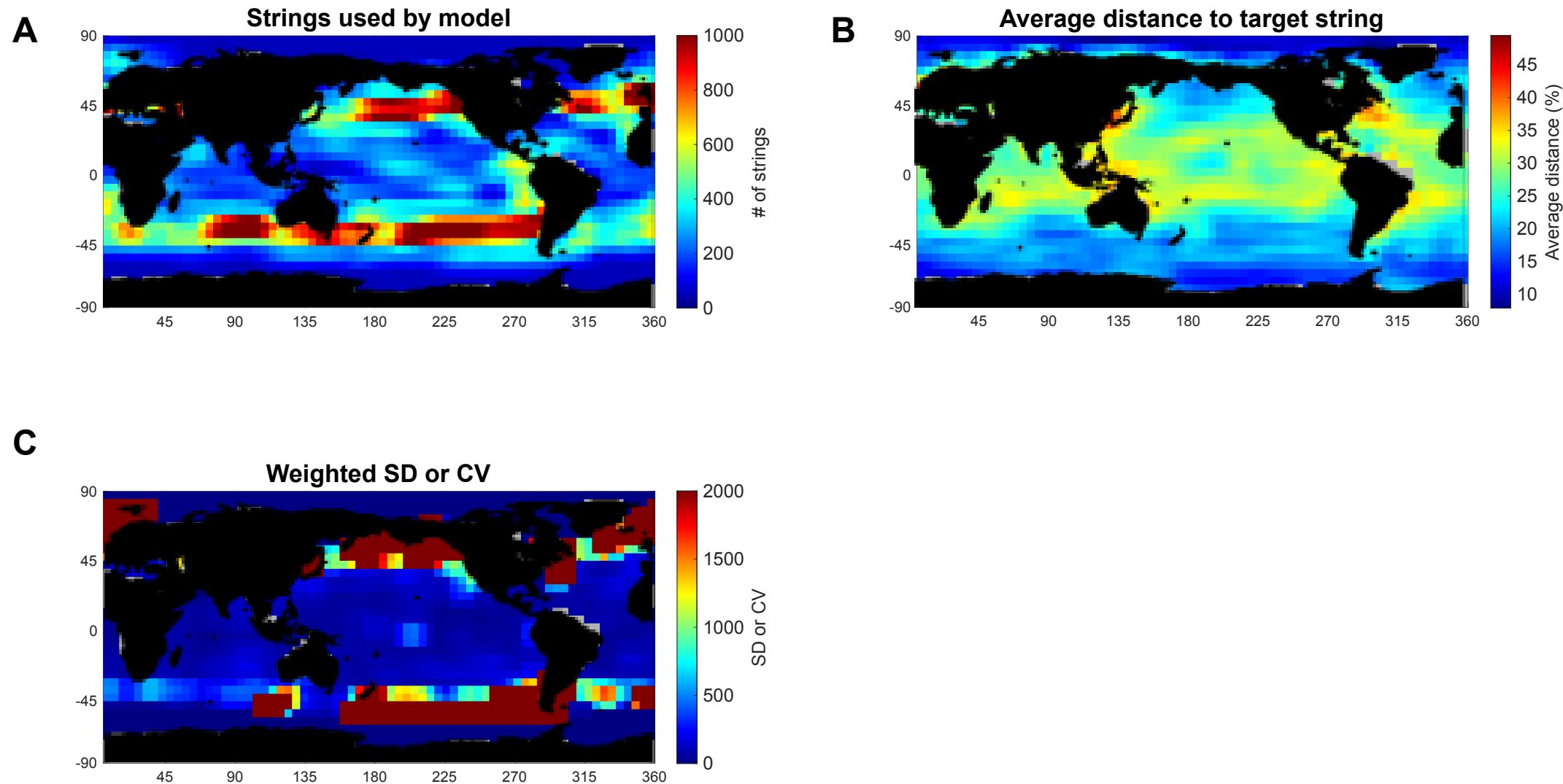


Fig. A6.4. ESM indicators of abundance estimate quality for *T. sacculifer* for SSP2-4.5 ($d = 0.03$, $w = 1 \times 10^{30}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

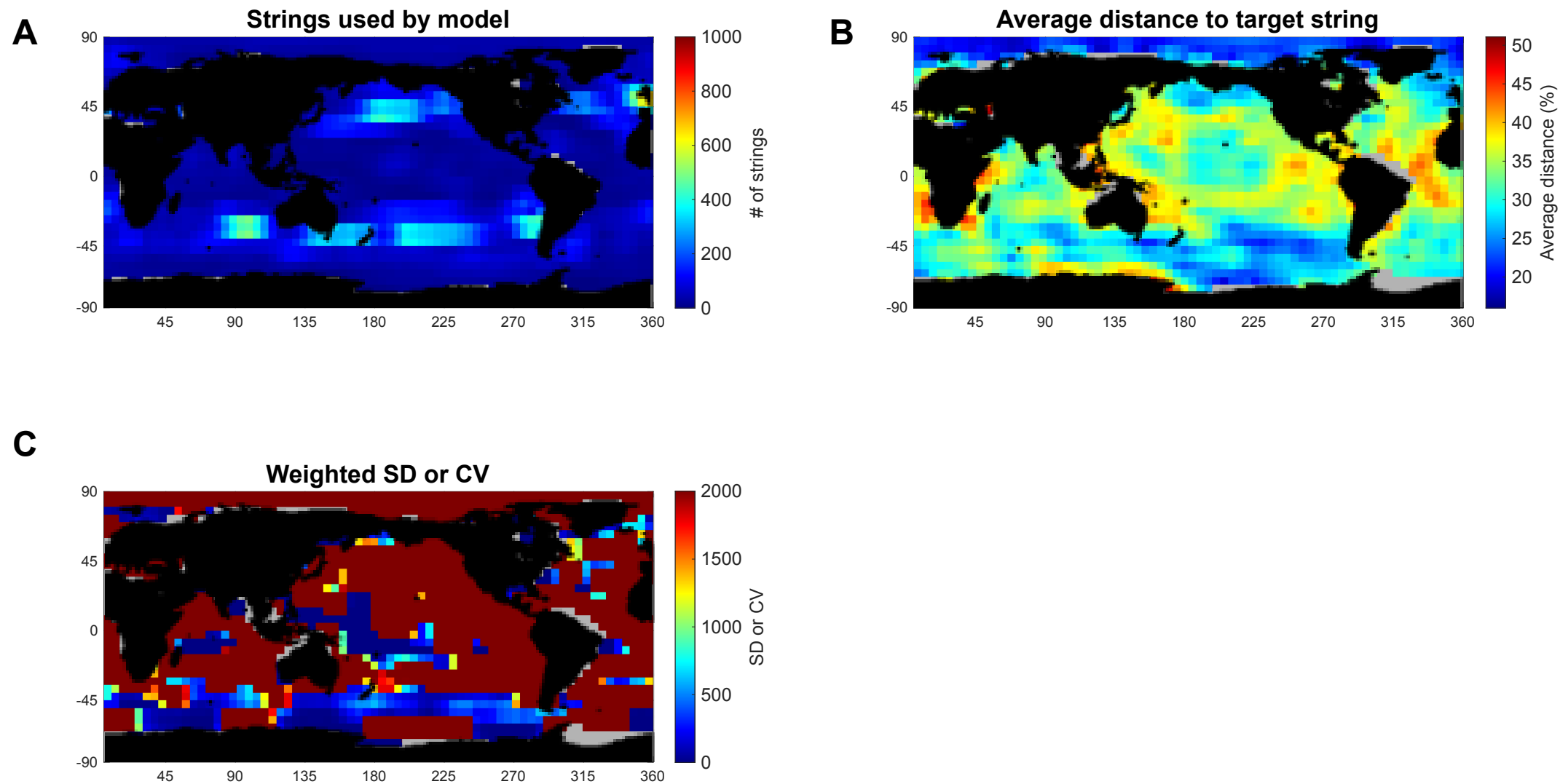


Fig. A6.5. ESM indicators of abundance estimate quality for *N. incompta* for SSP2-4.5 ($d = 0.01$, $w = 1 \times 10^{30}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

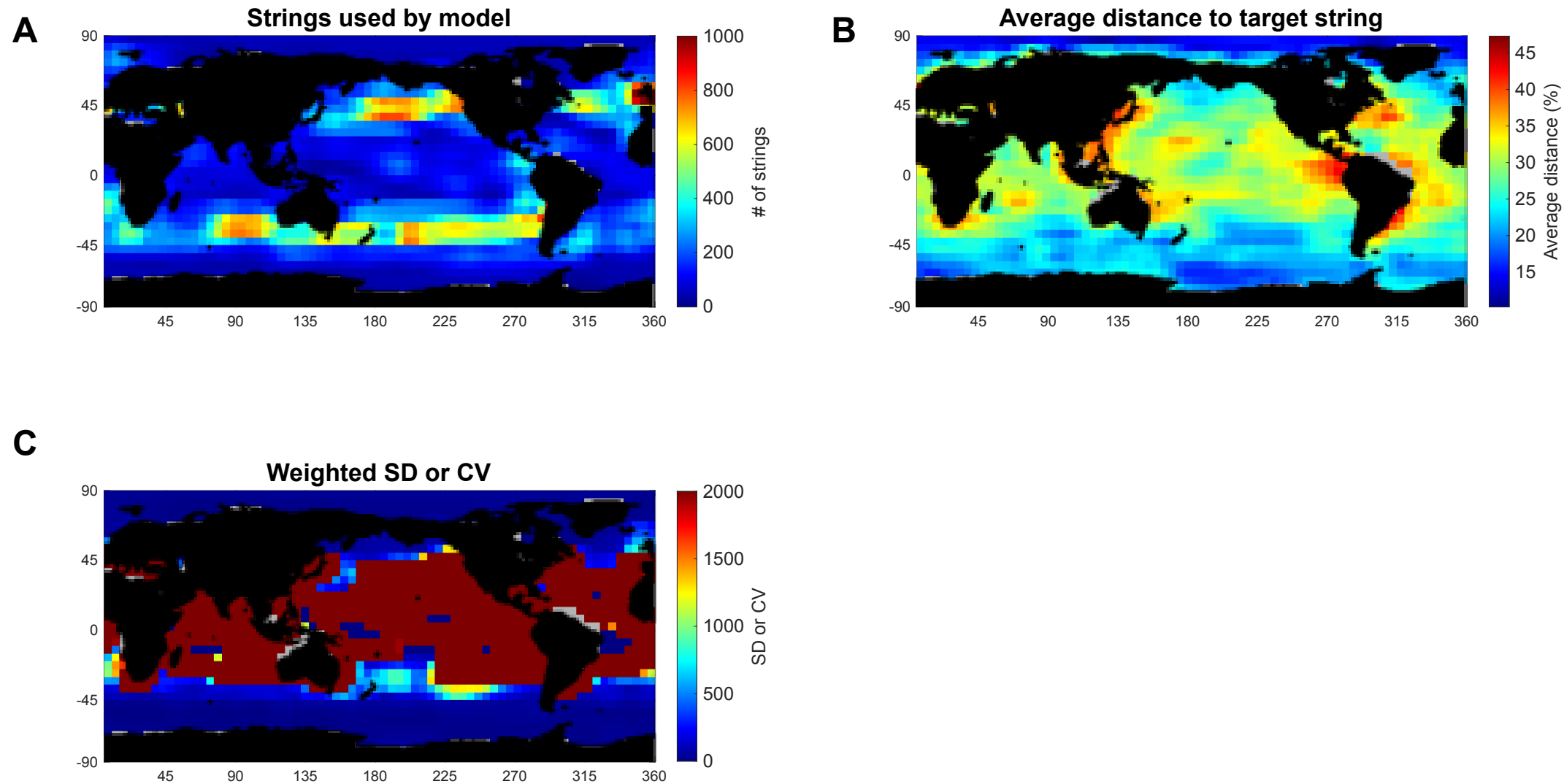


Fig. A6.6. ESM indicators of abundance estimate quality for *N. pachyderma* for SSP2-4.5 ($d = 0.02$, $w = 1 \times 10^{30}$). Each map gives the spatial distributions of the mean number of strings used by the model (A), mean distance to target string (B), and mean weighted coefficient of variation or standard deviation, depending on species abundance (if abundance is greater than 1, weighted CV is used) (C).

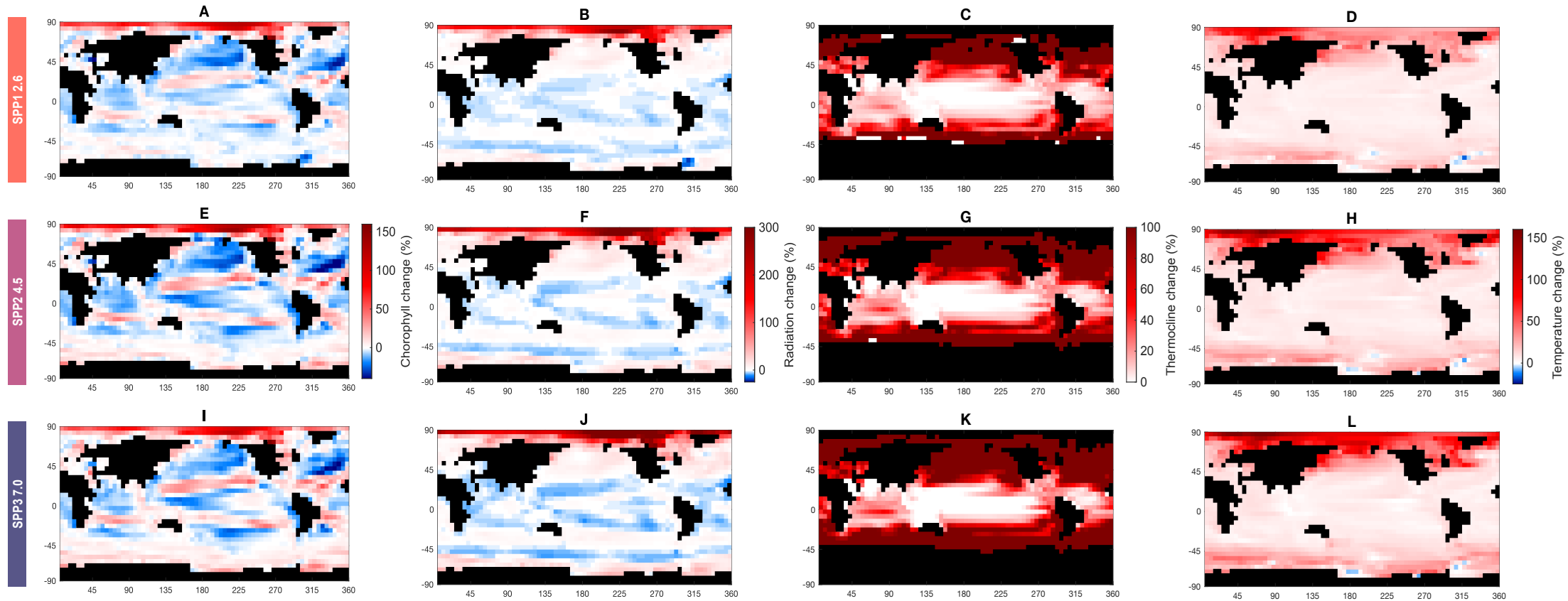
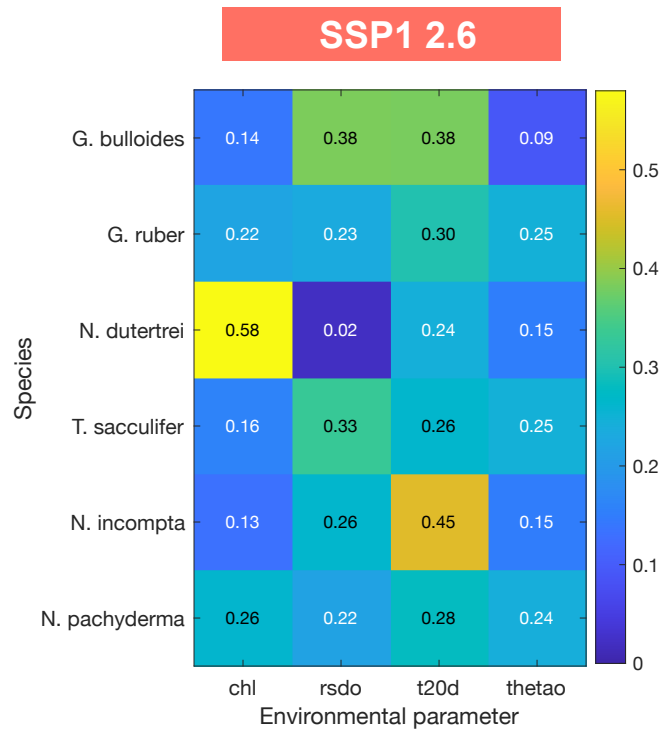
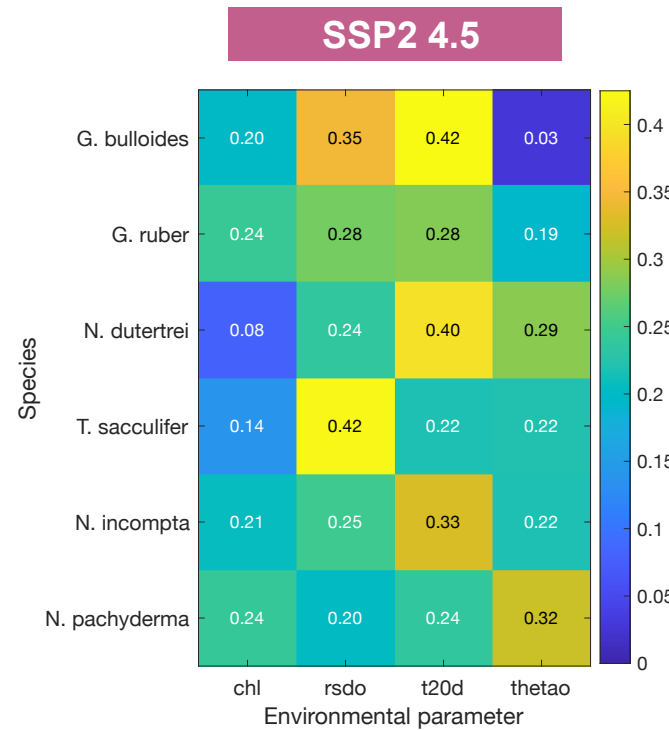


Fig. A7.1. Percent change between the historical (1941-2014) and the future (2070-2100) for the four normalized environmental parameters averaged over the top 100 meters for the SSP1-2.6 climate scenario (A-D). Percent change for the SSP2-4.5 climate scenario (E-H). Percent change for the SSP3-7.0 climate scenario (I-L).

A



B



C

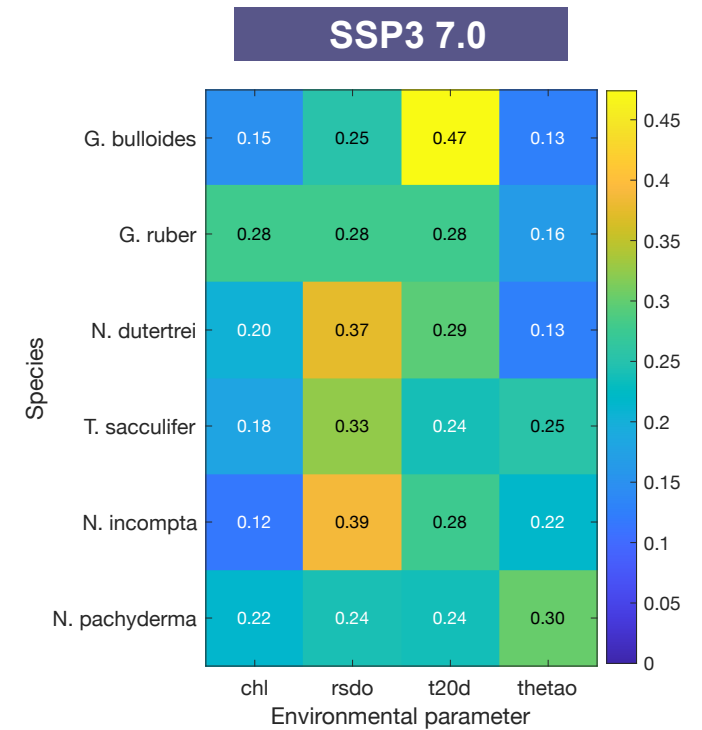
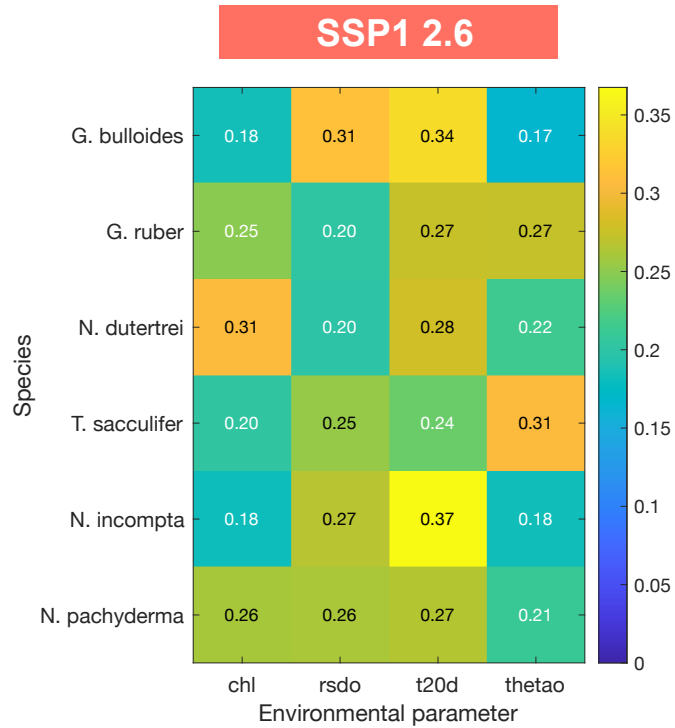


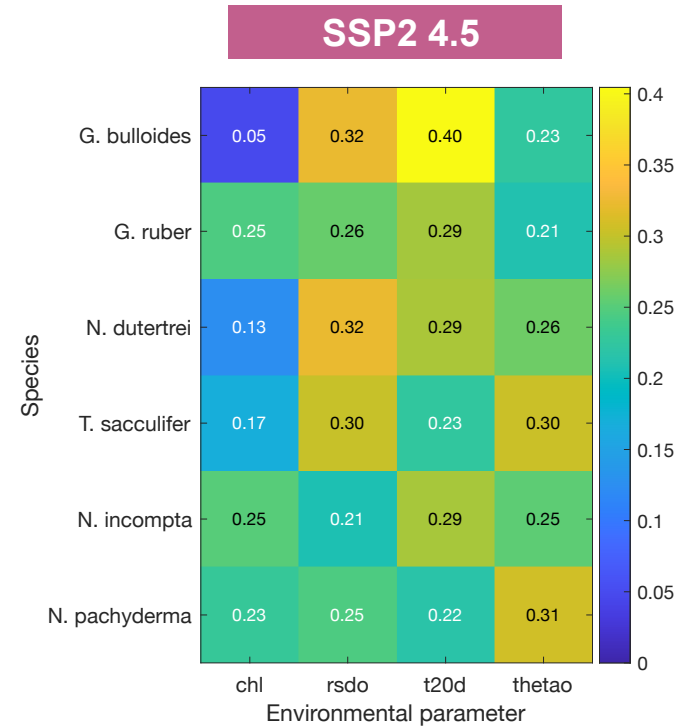
Fig. A7.2. Random Forest standardized feature importance analysis for the ESM abundance maps and environmental condition changes for chlorophyll, radiation, thermocline depth, and temperature for each species at each future SSP scenario (SSP1-2.6: A; SSP2-4.5: B; SSP3-7.0: C).

Across all SSP scenarios, chlorophyll is an important (proportion of importance > 0.25) environmental variable for two species (*N. dutertrei* and *N. pachyderma*), light is important for five species (*G. bulloides*, *G. ruber*, *N. dutertrei*, *T. sacculifer*, and *N. incompta*), thermocline depth is important for all six species, and temperature is important for three species (*N. dutertrei*, *T. sacculifer*, and *N. pachyderma*).

A



B



C

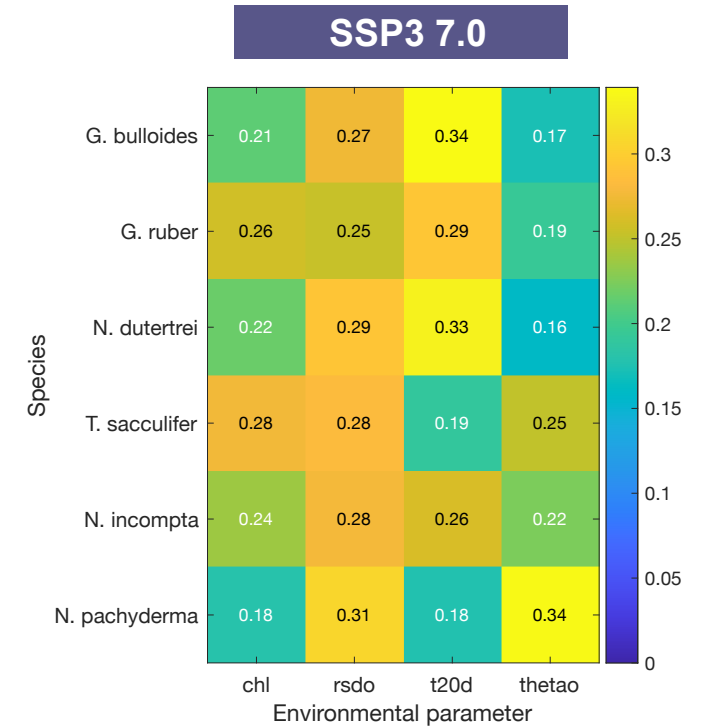


Fig. A7.3. Random Forest standardized feature importance analysis for the GRNN abundance maps and environmental condition changes for chlorophyll, radiation, thermocline depth, and temperature for each species at each future SSP scenario (SSP1-2.6: A; SSP2-4.5: B; SSP3-7.0: C).

Across all SSP scenarios, chlorophyll is an important (proportion of importance > 0.25) environmental variable for four species (*G. ruber*, *N. dutertrei*, *N. incompta*, and *N. pachyderma*), light is important for all six species, thermocline depth is important for five species (*G. bulloides*, *G. ruber*, *N. dutertrei*, *T. sacculifer*, and *N. incompta*), and temperature is important for five species (*G. ruber*, *N. dutertrei*, *T. sacculifer*, *N. incompta*, and *N. pachyderma*).