**Electronic Supplemental Material 3\_Appendixes**

**Integrating laboratory experiments and biogeographic modelling approaches to understand sensitivity to ocean warming in rare and common marine annelids**

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**Appendix 1. Comparison between observed and modelled temperature data habitat suitability maps.**

Yearly average sea surface temperatures were extracted for the North Atlantic and Mediterranean regions using the World Ocean Atlas 2018 database (Locarnini et al. 2019) and for the Mediterranean Sea using the MEDAR/MEDATLAS database (Fichaut et al. 2003). Average values for each geographical cell on regular 0.5° x 0.5° grids were computed between Earth system models for each year and each decade. Then, using the fundamental niche obtained for each species (see main text for details), we retrieved the corresponding Habitat Suitability Index (HSI) averaged for each grid cell using bottom and surface temperatures. This way, we calculated HSI values for each species for the North Atlantic and Mediterranean regions and for the Mediterranean Sea using real temperature records. Since the studied species are associated with coastal environments, HSI values located in the open ocean domain were set at 0 following the biogeographical raster of Reygondeau et al. (2013) (see also Online Resource 1, Fig. S4-S5).

For each species, a Spearman correlation analysis was performed between HSI values calculated for the North Atlantic and Mediterranean region based on observed temperature data and those modelled for the reference period (1970–2000). Results show a significant correlation between the two datasets for each species considered (Online Resource 2, Table. S3).

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**Appendix 2. Phylogenetic reconstruction and phylogenetic signal estimation**

A maximum likelihood (ML) phylogeny was constructed using COI genes obtained from GenBank for the seven species of the genus *Ophryotrocha* considered in our study (accession numbers: *O. labronica* MK933740.1; *O. japonica* MK933739.1; *O. puerilis* MK933741.1; *O. adherens* MK933737.1; *O. diadema* MK933738.1; *O. robusta* MK933742.1; *O. hartmanni* EF464546.1) and for additional eight marine annelid species (accession numbers: *O. alborana* EF464540.1; *O. costlowi* JQ310757.1; *O. gracilis* EF464545.1; *O. notoglandulata* EF464542.1; *O. permanni* EF464535.1; *O. socialis* JQ310765.1; *Laeonereis culveri* MH235843.1; *Nothria conchylega* MG421891.1). The marine mollusc *Lottia gigantean* (accession numbers: AB238466.1) was used as outgroup.

Multiple sequence alignment was performed with MUSCLE (Edgar 2004) using the software MEGAX (Kumar et al. 2018) with default parameters, and then trimmed to the same length. 401 bp-long COI genes were then input in the IQ-TREE software (Nguyen et al. 2015) using the ultrafast bootstrap to obtained branch supports (Hoang et al. 2018). The R packages *ape* and *phytools* (RStudio Team 2020) were used to import and transform the resulting tree. The ‘drop.species’ function was used to remove the species that were not of interest to the present study. The inferred phylogeny (Online Resource 1, Fig. S6) did not show any cluster of the studied species based on their common, uncommon, or rare status.

Physiological thermal tolerance limits, survival, and total fecundity were measured from phylogenetically related species and, consequently, they could not be considered independent observations (Felsenstein 1985). Thus, we tested the association between *Ophryotrocha* species phylogeny and the measured traits at each of the three acclimation temperatures by estimating their phylogenetic signals using Pagel’s λ (Pagel 1999; Münkemüller et al. 2012). Pagel’s λ is a tree transformation that assesses the degree of phylogenetic signal within the trait by multiplying the internal branches of the tree by values ranging between 0 and 1. A λ of 1 indicates a Brownian Motion model, and the tree is returned with its branch lengths untransformed. A λ of 0 indicates no patterning as the tree is collapsed into a single large polytomy, i.e., a star phylogeny (Kamilar and Cooper 2013). Pagel’s λ values and their effect were obtained using the ‘phylosig’ function of the R package *phytool* (Revell 2012) and are shown in the Online Resource 2, Table S4.

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