Supplementary Material for:

Emersion-Associated Responses of an Intertidal Coral and Its Suitability for Transplantation to Ecologically Engineer Seawalls

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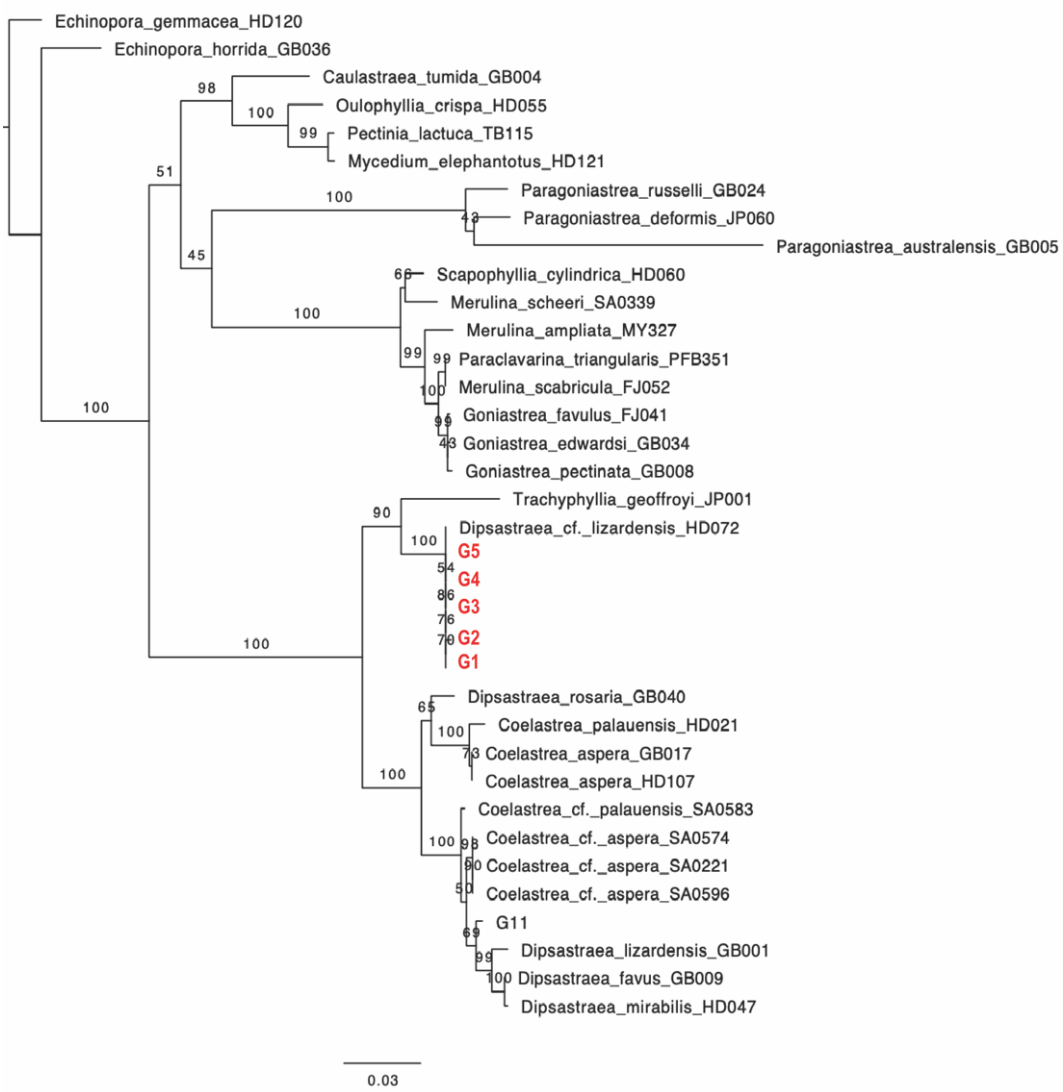
1. Species identification

Genomic DNA (gDNA) from six *Dipsastraea* samples were extracted using ReliaPrepTM gDNA tissue miniprep (Promega, Wisconsin, USA) following the manufacturer's protocol. Polymerase chain reaction ((PCR), Labcycler Gradient and Thermoblock 96, Sensoquest, Germany) was performed to amplify the mitochondrial intergenic region (MNC1f: 5'-GAGCTGGGCTTCTTTAGAGTG-3', MNC1r: 5'-GTGAGACTCGAACTCACTTTTC-3') [44,77]. Each PCR reaction (25.0 µl volume) consisted of 12.5 µl of GoTaq Green Master Mix (Promega, Wisconsin, USA), 1.0 µl of each forward and reverse primer (10 µM), 8.5 µl of water and 2.0 µl of diluted gDNA. PCR reaction steps were (1) denaturation: 95 °C 45 s (2) annealing: start at 55 °C, increasing in increments of 1 °C to annealing temperature (60 °C) for 45 s (3) extension: 72 °C for 5 min, repeated for 30 cycles. Gel electrophoresis was performed to verify the amplification. Amplified products were purified using SureClean Plus (Biolene Inc., London, UK) according to the manufacturer's protocol. Sequencing of the purified DNA products was performed with the dye terminator method on an Applied Biosystems 3130XL Genetic Analyzer.

DNA sequences obtained here were combined with those in [44] that have been reduced to species level (see [78]) and compiled in Mesquite 3.6 [79]. Alignments were carried out using the E-INS-i option under default parameters in MAFFT 7.205 [80–82]. The max-imum likelihood phylogeny under the GTRGAMMA model was inferred using RAxML 8.0.9 [83,84] and 100 random starting trees, with 1000 bootstrap replicates.



Supplementary Figure S1. Maximum likelihood tree of coral species under the family Merulinidae based on the mitochondrial intergenic region (iGR), showing five tagged colonies (G1-G5, in red) clustered under *Dipsastraea* cf. *lizardensis*.

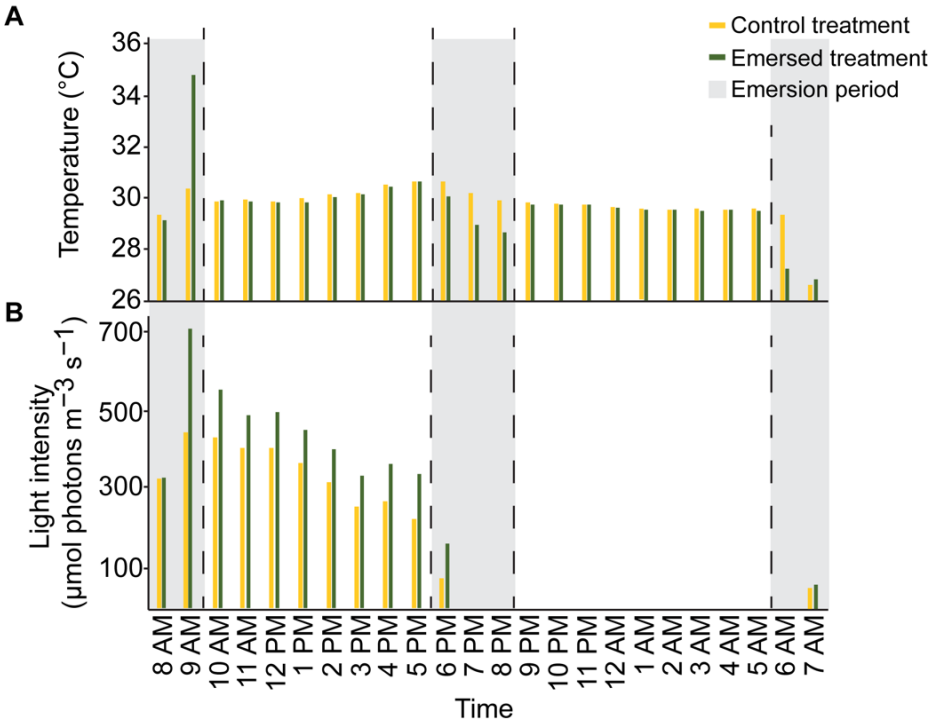
2. Genotyping

Genomic DNA (gDNA) from five confirmed *Dipsastraea* cf. *lizardensis* colonies (i.e., G1-G5, Supplementary Figure S1) were extracted using Qiagen DNeasy Blood and Tissue Kit following the manufacturer's protocol. The internal transcribed spacer 2 (*ITS2)* was amplified using coral-specific (forward) primer A18S: 5′ – GATCGAACGGTTTAGTGGG – 3′ [85] and universal (reverse) primer "ITS-4: 5' – TCCTCCGCT TATTGATATGC – 3' [86]. Downstream processes (i.e., gel electrophoresis, amplicon cleanup and Sanger sequencing) followed the same procedures described above. Sequences were aligned and pairwise distances of the samples were obtained using the Geneious software package (http://www.geneious.com (accessed on 1 October 2021)) to determine that distinct genotypes were present.

Out of the five colonies, only G1, G3 and G4 were successfully sequenced, and these were found to be genetically distinct. The average pairwise similarity between the three genotypes was 97.87 ± 0.41 %. (Supplementary Table S1). The sequence qualities for G2 and G5 were poor (~20%) and thus uninformative.

Supplementary Table S1. Genetic identity matches between pairs of genotypes.

	G1	G3	G4
G1	-	97.54%	97.39%
G3	97.54%	-	98.69%
G4	97.39%	98.69%	-



Supplementary Figure S2. Temperature (**A**), light intensity (**B**) and estimated emersion period profile.

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