Morphological and molecular characterization of the benthic dinoflagellate *Amphidinium* from coastal waters of Mexico
Supplementary Material
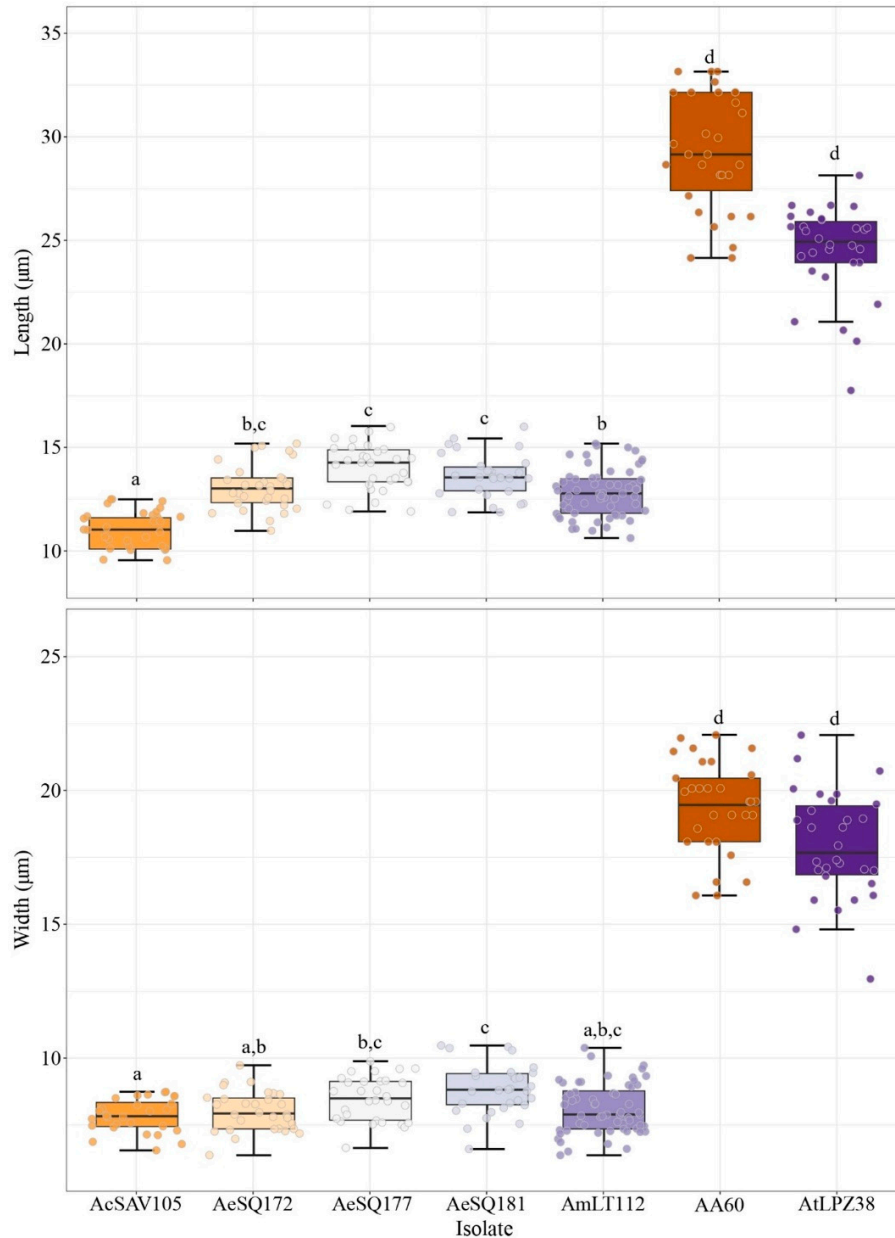

Figure S1. Comparison of morphometric characteristics of cultured *Amphidinium* species from Mexican coastal waters (*n*=30 for each isolate). *A. carterae* = AcSAV105; *A.* cf. *carterae* = AeSQ172, AeSQ177, and AeSQ181; *A. massartii* = AmLT112; *A. operculatum* = AA60; *A. theodorei* = AtLPZ38). The line inside the boxes indicates the median, the whiskers represent the highest and lowest value excluding outliers, and the transparent points represent the underlying distribution of the data. Different letters (a,b,c,d) above the boxes indicate significant differences at 0.05% error.

Molecular Phylogeny of the large ribosomal subunit (LSU) gene for the *Amphidinium* genus

The phylogenetic analysis for the large ribosomal subunit of *Amphidinium* species included 54 sequences and 1466 nucleotide positions. The nucleotide substitution model that best fitted the data was the Tamura Nei model. Two trees were obtained, one for the maximum likelihood (ML) method and another for the maximum parsimony (MP) method. The tree for the ML method is presented in the Figure S2 (next page), where tree branches represent the estimated genetic distances. For the MP method, the consensus tree topology is presented in Figure S3.
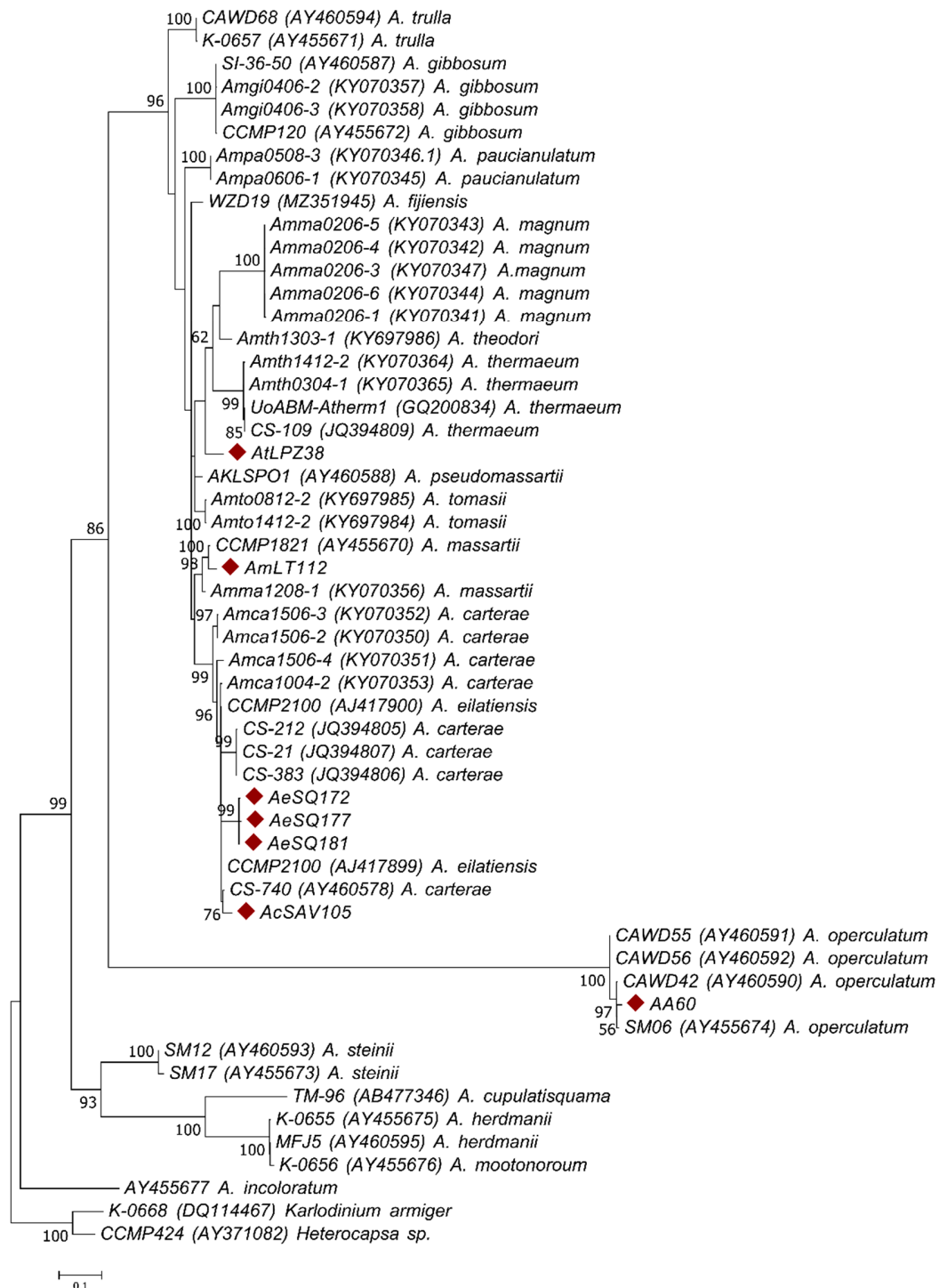
Figure S2. Maximum-likelihood tree for large ribosomal subunit (LSU) gene sequences of *Amphidinium* species. Sequences obtained in the present study are marked with diamond shapes. The percentage of trees in which the associated taxa clustered together (after 2000 bootstrap replicates) is shown next to the branches. A discrete Gamma distribution was used to model evolutionary rate differences among sites (+G, parameter = 0.8832). Sequence labels include the strain name, GenBank accession number, and species name.
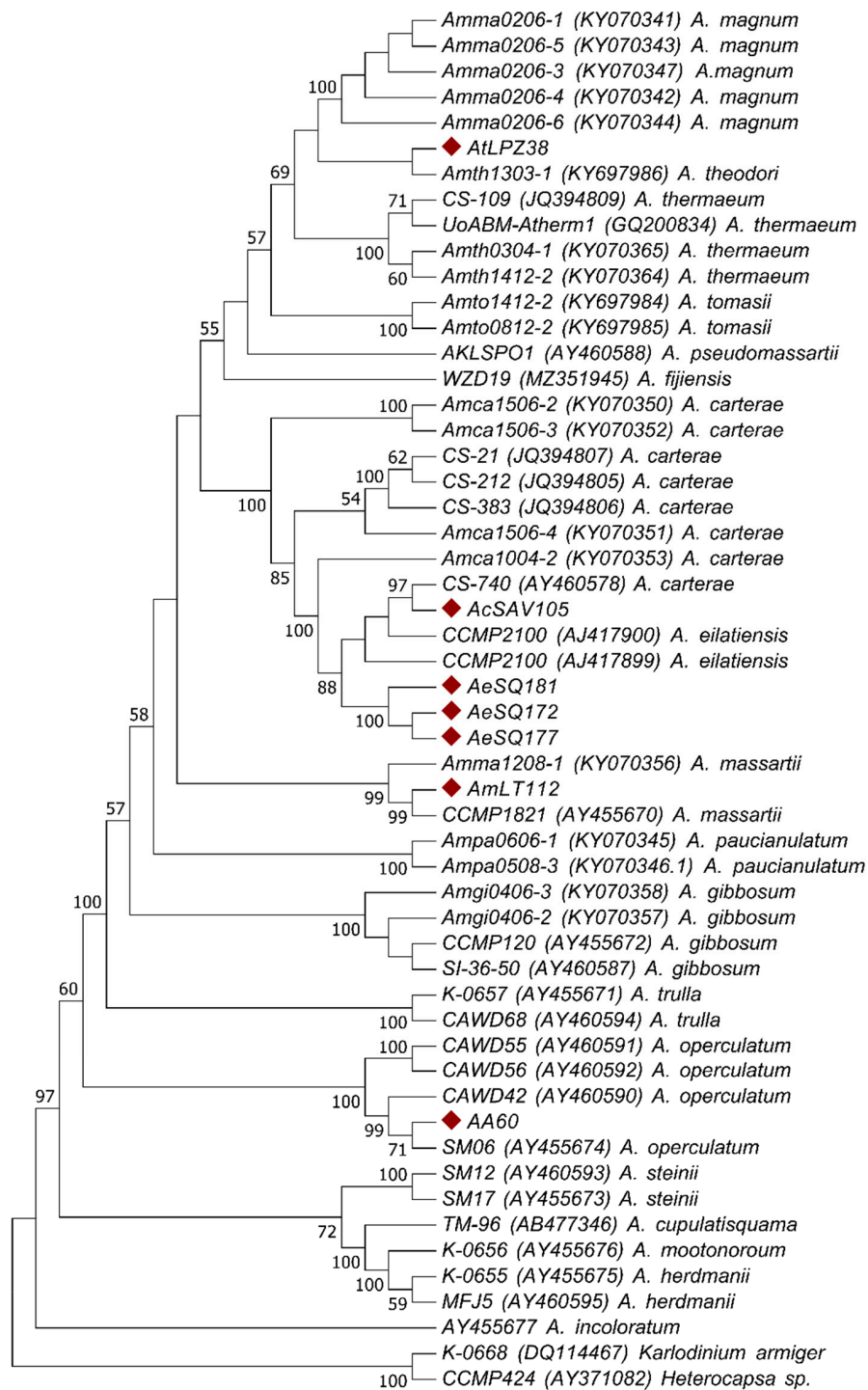
Figure S3. Maximum-parsimony consensus tree for large ribosomal subunit (LSU) gene sequences of *Amphidinium* species. Sequences obtained in the present study are marked with diamond shapes. The percentage of trees in which the associated taxa clustered together (after 2000 bootstrap replicates) is shown next to the branches. Sequence labels include the strain name, GenBank accession number, and species name.

Molecular phylogeny of the ITS1-5.8 S rRNA-ITS2 region for the *Amphidinium* genus

The phylogenetic analysis for the ITS1 to ITS2 region of *Amphidinium* species included 39 sequences and 710 nucleotide positions. The nucleotide substitution model that best fitted the data was the Kimura 2-parameter model. Two trees were obtained, one for the maximum likelihood (ML) method and another for the maximum parsimony (MP) method. The tree for the ML method is presented in the Figure S4, where tree branches represent the estimated genetic distances. For the MP method, the consensus tree topology is presented in Figure S5.
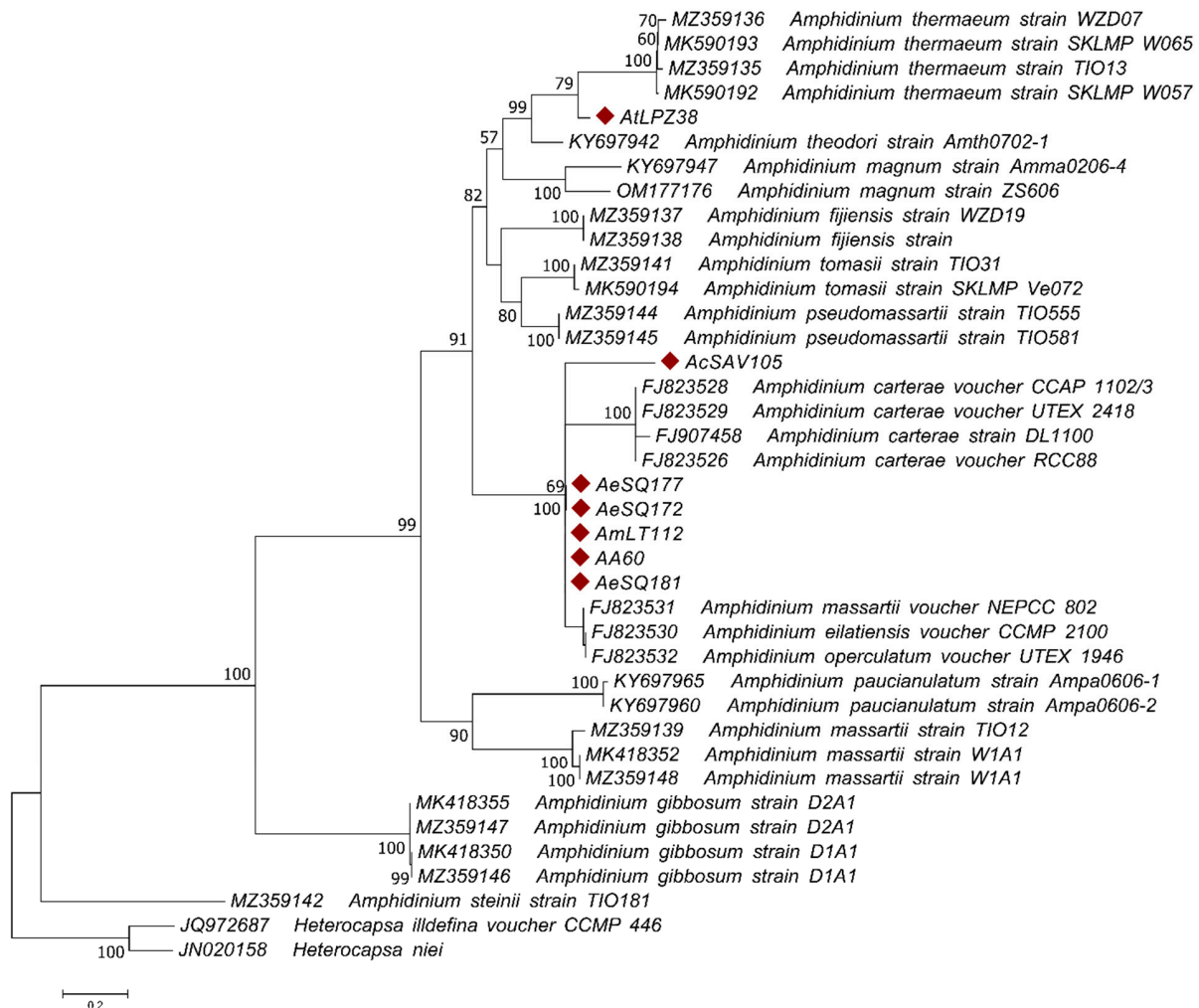

Figure S4. Maximum-likelihood tree for the ITS1-5.8 S rRNA-ITS2 region of *Amphidinium* species. Sequences obtained in the present study are marked with diamond shapes. The percentage of trees in which the associated taxa clustered together (after 2000 bootstrap replicates) is shown next to the branches. A discrete Gamma distribution was used to model evolutionary rate differences among sites (+G, parameter = 2.1612). Sequence labels include the GenBank accession number, and species name, and the strain name.
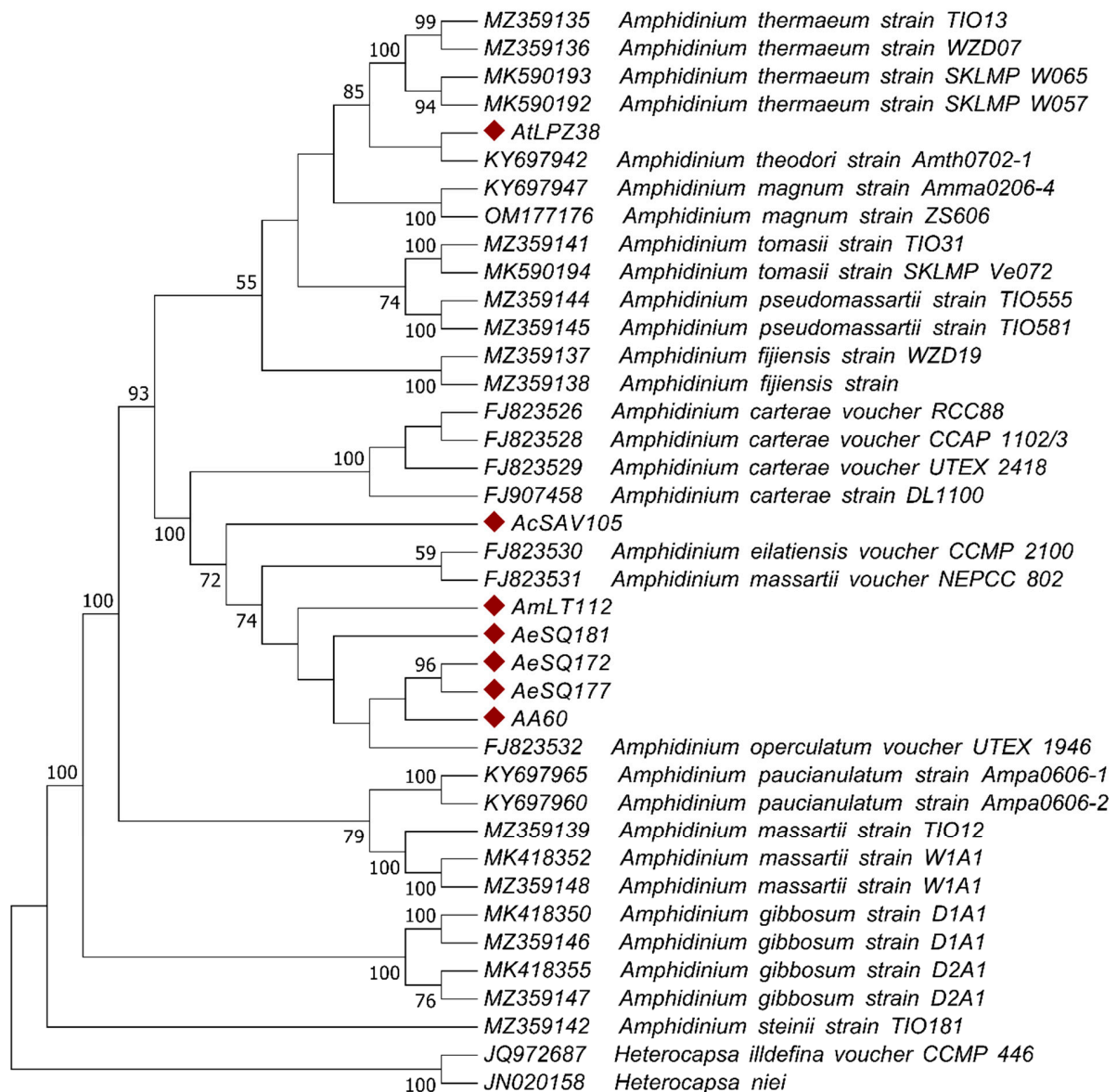
Figure S5. Maximum-parsimony consensus tree for the ITS1-5.8 S rRNA-ITS2 region of *Amphidinium* species. Sequences obtained in the present study are marked with diamond shapes. The percentage of trees in which the associated taxa clustered together (after 2000 bootstrap replicates) is shown next to the branches. Sequence labels include the GenBank accession number, and species name, and strain name.

*Discussion on these results is found in the main manuscript.