

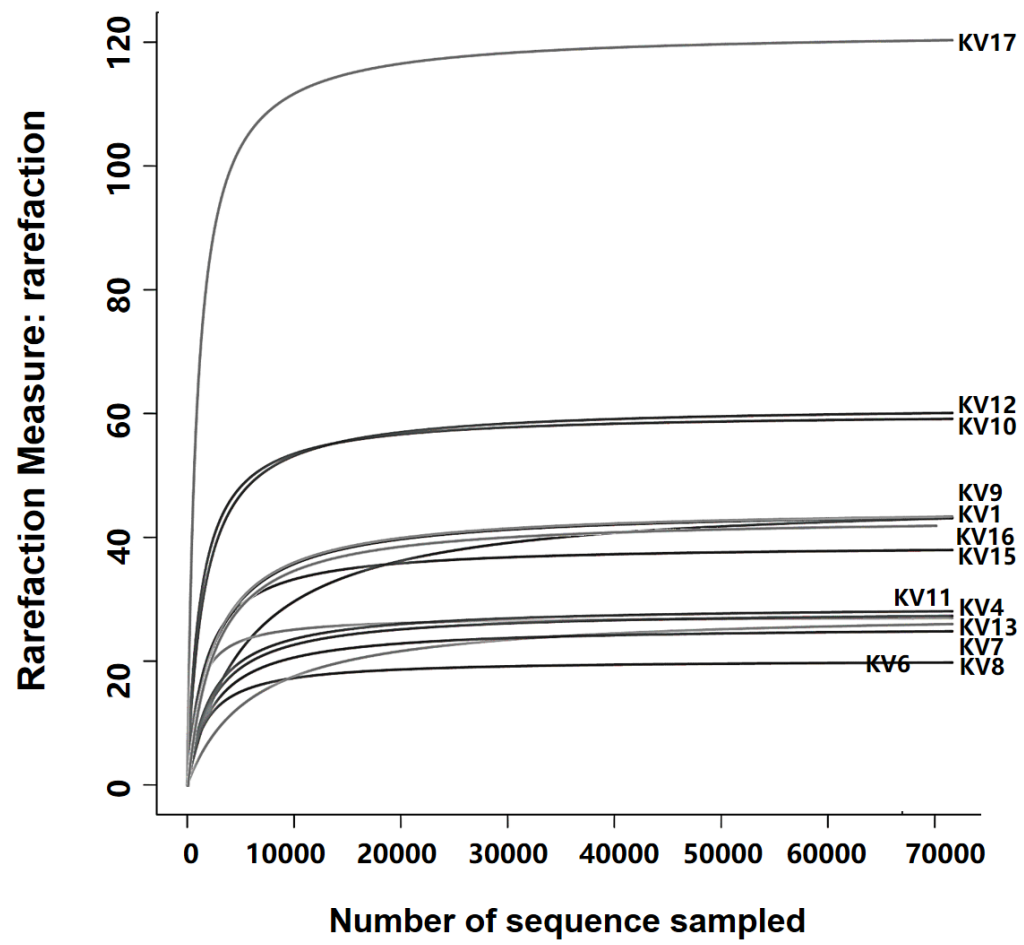
Supplementary Figures

Supplementary Figure S1. Rarefaction curves of the 13 samples.

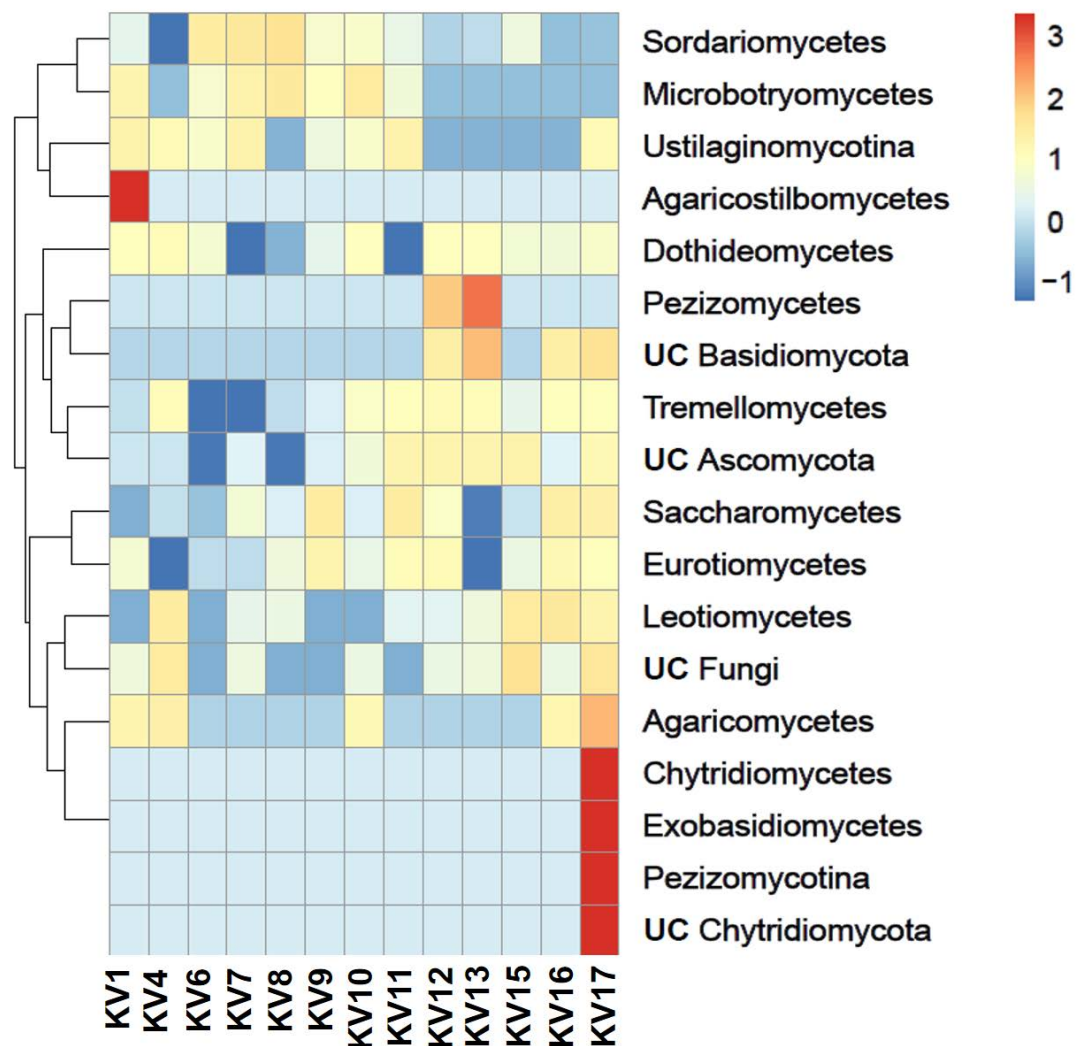
Supplementary Figure S2. Heatmap analysis of the whole fungal communities living with *Karlodinium veneficum* at class level.

Supplementary Figure S3. Phylogenetic tree derived from Maximum Likelihood analysis based on ITS sequences of representative fungal ASVs feature sequences obtained in this study.

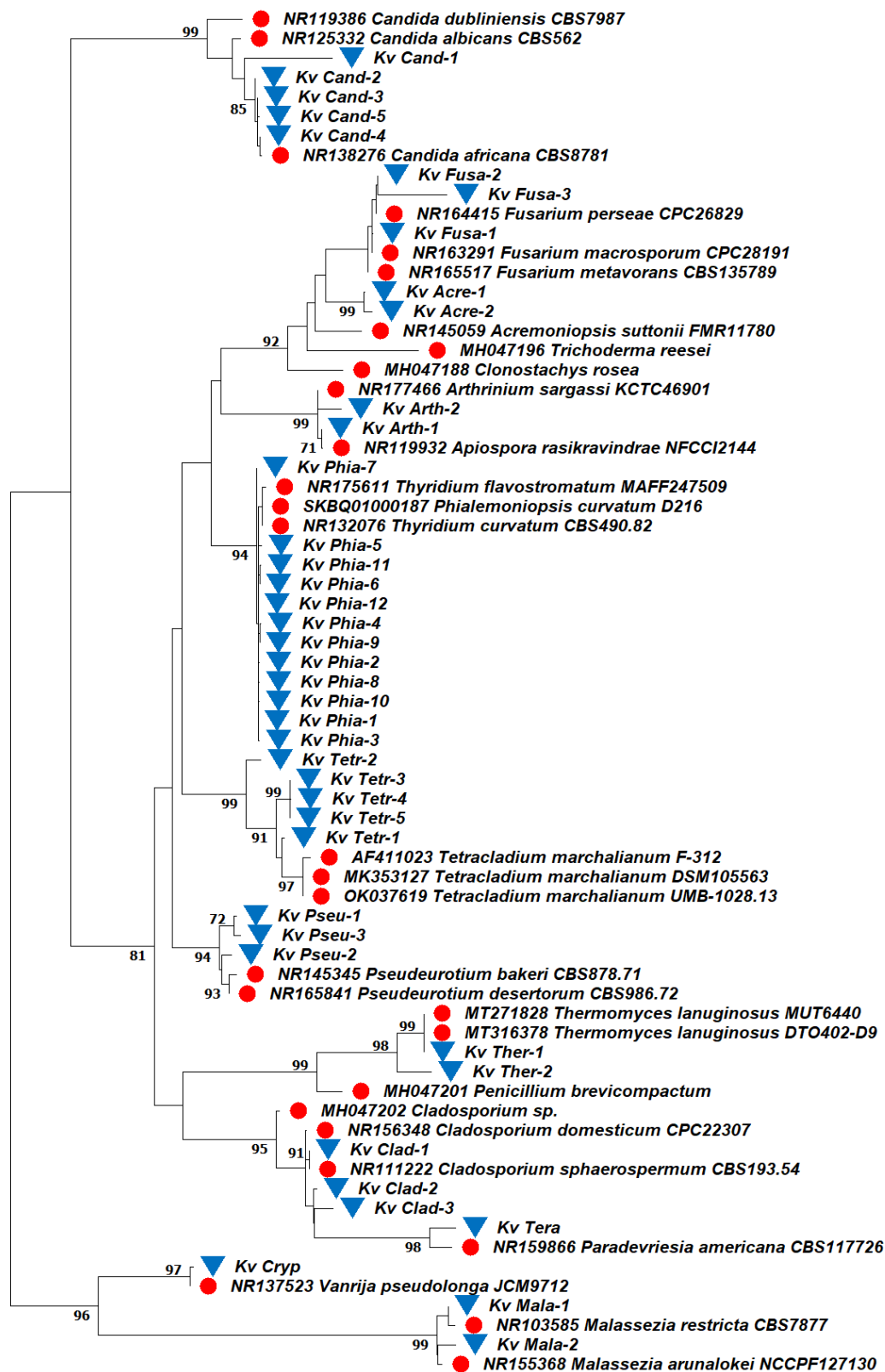
Supplementary Figure S4. The phylogenetic relationships of the 13 *Karlodinium veneficum* investigated in this work.



Supplementary Figure S1. Rarefaction curves of the 13 samples.



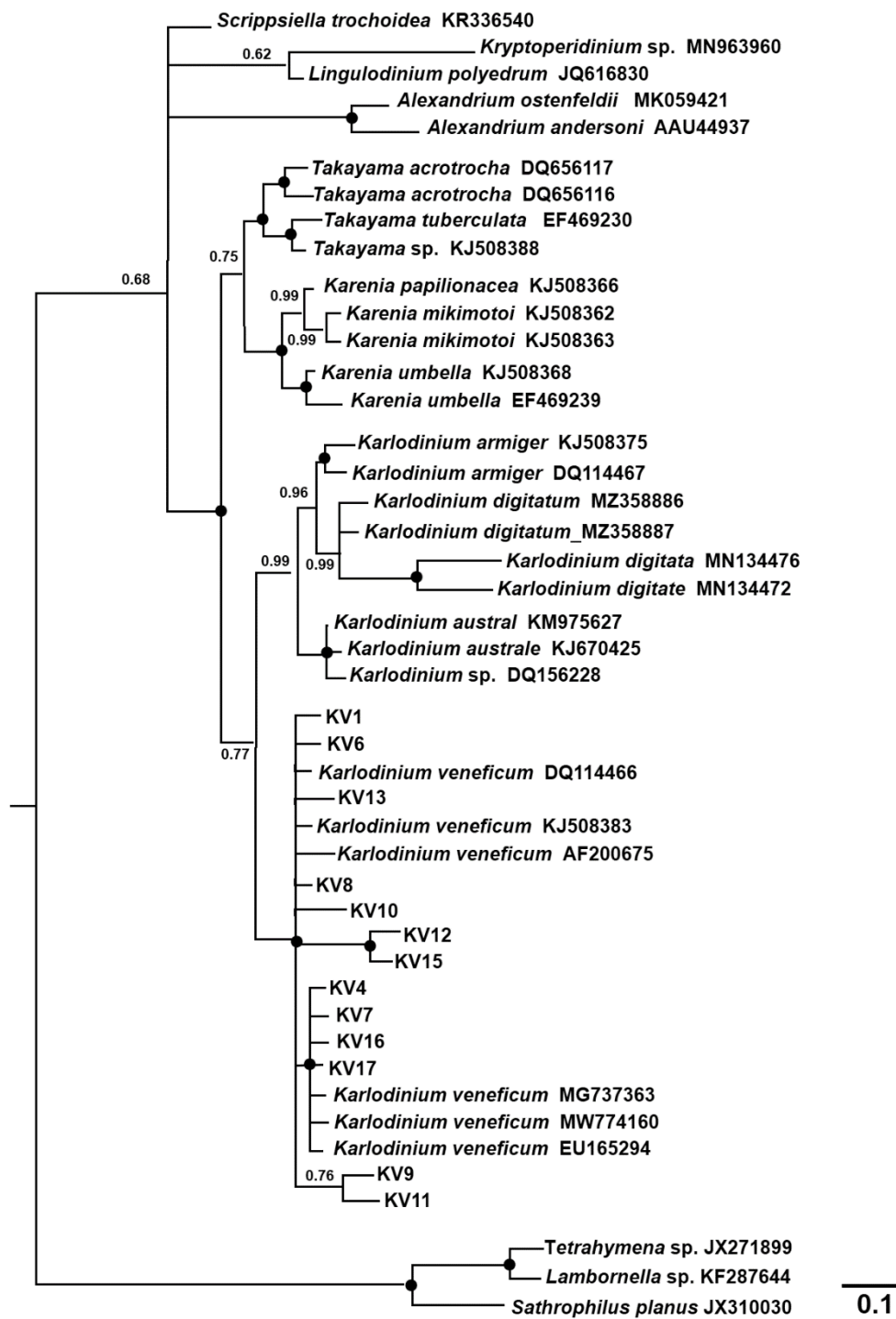
Supplementary Figure S2. Heatmap analysis of the whole fungal communities living with *Karlodinium veneficum* at class level. UC: unclassified.



Supplementary Figure S3. Phylogenetic tree derived from Maximum Likelihood analysis based on 208-bp of 5.8S-ITS2 DNA sequence data. Analysis was performed in MEGA X (Kumar et al., 2018), using General Time Reversible (Nei and Kumar, 2000) and gamma-distribution rate variation (GTR+G model) with 1000 bootstrap replicates. The analysis involved 70 nucleotide sequences, including representative fungal ASVs feature sequences obtained in this study (● with Kv prefix), and the reference fungal strain sequences retrieved from GenBank (▼ with accession number). ML bootstrap support (BS) values are shown at the nodes (BS > 70 %). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The scale bar indicates the nucleotide substitutions per position.

References;

- Kumar, S.; Stecher, G.; Li, M.; Knyaz, C.; Tamura, K. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution* **2018**, *35*, 1547-1549.
- Nei, M.; Kumar, S. Molecular Evolution and Phylogenetics. **2000**, Oxford University Press, New York.



Supplementary Figure S4. The phylogenetic relationships of the 13 *Karlodinium veneficum* investigated in this work. Phylogenetic reconstruction was inferred from partial LSU rRNA gene sequences using the Bayesian-Inference (BI) method as described in Deng et al. (2019, 2021). Numbers at the nodes represent BI posterior probabilities. Black circles (●) indicate maximal support (1.00). GenBank accession number of each sequence is noted following the species name. All branches are drawn to scale.

References;

- Deng, Y.Y.; Li, F.T.; Hu, Z.X.; Yue, C.X.; Tang, Y.Z. The implication inferred from the expression of small heat-shock protein genes in dinoflagellate resting cysts buried in marine sediment. *Diversity* **2021**, *13*, 471.
- Deng, Y.Y.; Hu, Z.X.; Chai, Z.Y.; Tang, Y.Z. Cloning and comparative studies of proliferating cell nuclear antigen (PCNA) genes for nine dinoflagellates. *Journal of Applied Phycology* **2019**, *31*, 2969-2979.