

Table S7. Control information from other 5 cultures of microalgae examined for fungal presence with same high-throughput gene amplicon sequencing targeted at rDNA ITS region. All these 5 cultures and the 13 *Karlodinium veneticum* cultures examined in this study were cultivated and processed in the same protocols in our laboratory.

Samples	Genus/species	Origin/ Isolation date	Accession No. ¹	<i>Thyridium</i> ²	<i>Pseudeurotium</i>	<i>Candida</i>
KD	<i>Karlodinium decipens</i>	Jiaozhou Bay, Shandong Province (Yellow Sea, China), 2019	PRJNA892752	Y ³	N	N
PF	<i>Pselodinium fusus</i>	Jiaozhou Bay, Shandong Province (Yellow Sea, China), 2019	PRJNA892740	N	N	Y
BB	<i>Biecheleria brevisulcata</i>	Ningde, Fujian Province (East China Sea), 2018	PRJNA892739	N	N	N
AA	<i>Aureococcus anophagefferens</i>	USA, 1986 ⁴	PRJNA892281	Y	N	Y
AS	<i>Akashiwo sanguinea</i>	Northport Bay, New York, USA, 2011	PRJNA892755	N	N	N

¹ The accession number of the high-throughput gene amplicon sequencing data for rDNA ITS region of the sample in the NCBI Short Read Archive (SRA) database.

² *Thyridium*: formerly as *Phialemoniopsis* (Sugita and Tanaka, 2022, MycoKeys, 86, 147) and *Phialemonium* (Perdomo et al. 2013, Mycologia, 105, 398-421).

³ Y/N: the fungal genus has been/ has not been detected in the sample.

⁴ The culture of *Aureococcus anophagefferens* strain CCMP1984 (CCMP, Culture Collection of Marine Phytoplankton) was obtained from Stony Brook University and cultured in our laboratory since 2013.