Supplementary Information

Diversity and Community Composition of Labyrinthulomycetes Protists in the Coastal Zone of Hainan Island, South China Sea

Jing Song[1], Xiuping Liu[1], Ningdong Xie[1], Jiaqian Li[1], Xianhua Liu[1], Biswarup Sen [1,*] and Guangyi Wang [1,2,3,4,*]

[1]Center for Marine Environmental Ecology, School of Environmental Science and Engineering, Tianjin University, Tianjin 300072, China;

[2]Frontiers Science Center for Synthetic Biology, Tianjin University, Tianjin 300072, China

[3]Key Laboratory of Systems Bioengineering (MOE), Tianjin University, Tianjin 300072, China

[4]Center for Biosafety Research and Strategy, Tianjin University, Tianjin 300072, China

*Correspondence:

bsen@tju.edu.cn (B.S.); gywang@tju.edu.cn (G.W.)

Table S1. Spearman's rank correlation coefficients and p values between the abundance of LP and environmental factors

	Depth	**Temp**	**Sal**	**Chl-α**	**NH_4^+**	**SiO_3^{2-}**	**PO_4^{3-}**	**NO_3^-**	**NO_2^-**	**TP**	**TN**
Coefficient (ρ)	0.05	-0.16	0.22	0.24	-0.20	-0.35	-0.02	-0.18	-0.32	-0.16	0.44
P value	0.86	0.52	0.39	0.35	0.42	0.13	0.95	0.48	0.20	0.53	0.07

Table S2. Taxonomy of shared ASVs and their relative abundance

ID	**Taxonomy**	**Relative abundance (%)**
ASV1	d__Eukaryota; p__Labyrinthulomycetes; c__Labyrinthulomycetes; o__Labyrinthulomycetes; f__Thraustochytriaceae; g__Aplanochytrium	39.97
ASV2	d__Eukaryota; p__Labyrinthulomycetes	9.30
ASV10	d__Eukaryota; p__Labyrinthulomycetes; c__uncultured; o__uncultured; f__uncultured; g__uncultured	2.06

Note: d = domain; p = phylum; c = class; o = order; f = family; g = genus.

Table S3. Properties of the interaction network between Labyrinthulomycetes and Bacteria in the surface seawater.

	p_Laby	*Aplanochytrium*	f_Laby	*Ulkenia*	*Aurantiochytrium*
Degree	11	9	4	4	3
Positive	90.91%	11.11%	25%	66.67%	0
Negative	9.09%	88.89%	75%	33.33%	100%

Table S4. Properties of the interaction network between Labyrinthulomycetes and Bacteria in the bottom seawater

	Aplanochytrium	f_Laby	*Aurantiochytrium*	p_Laby	o_Laby	*Ulkenia*
Degree	18	11	11	8	8	8
Positive	16.67%	36.36%	100%	75%	37.5%	50%
Negative	83.33%	63.64%	0	25%	62.5%	50%

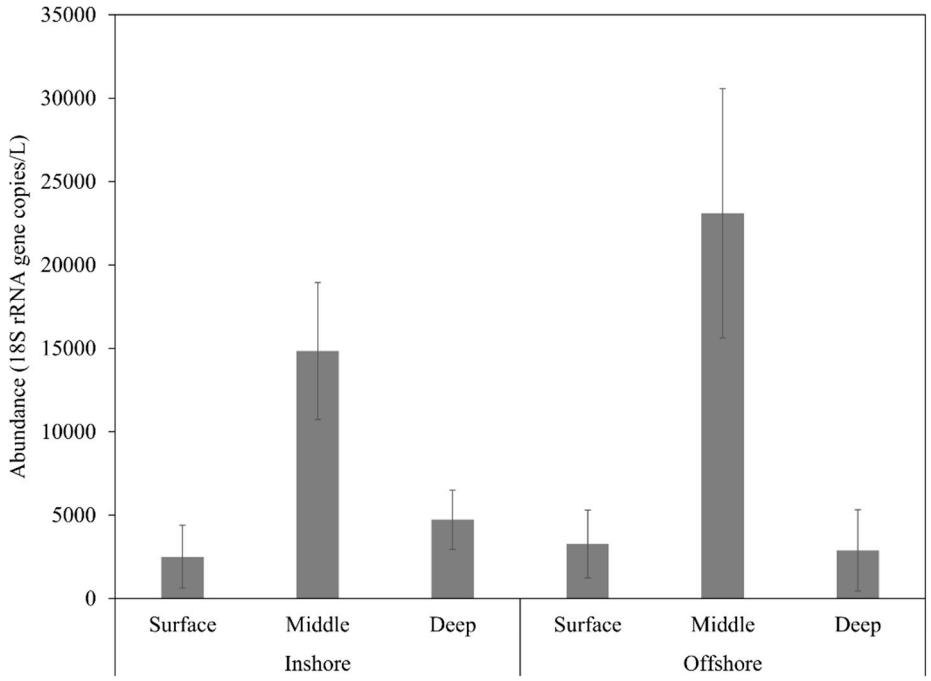

Figure S1. Abundance of Labyrinthulomycetes protists at different depths in the inshore and offshore habitats. The data represent the mean ± S.E of three stations.

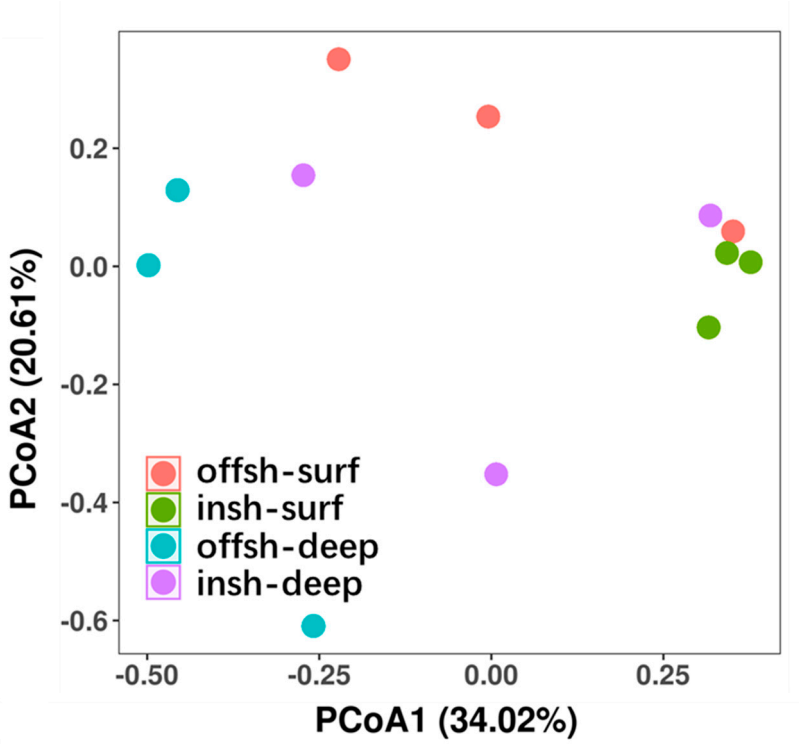

Figure S2. Principal coordinate analysis (PCoA) based on Bray-Curtis similarities among the communities of Labyrinthulomycetes. Labels "offsh-surf", "insh-surf", "offsh-deep" and "insh-deep" represent offshore surface water, inshore surface water, offshore deep water and inshore deep water, respectively.

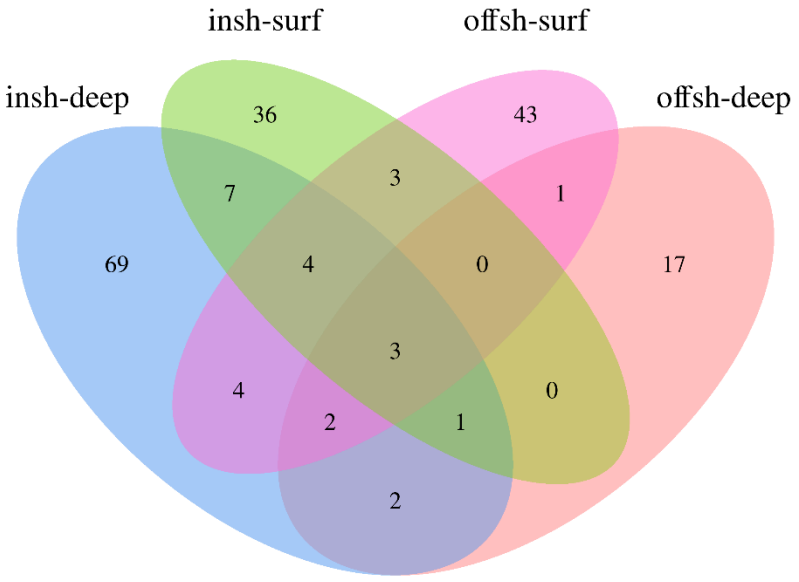

Figure S3. Venn diagram showing the unique and common ASV numbers of different habitats. Labels "insh-deep", "insh-surf", "offsh-surf" and "offsh-deep" represent inshore deep water, inshore surface water, offshore surface water, and offshore deep water, respectively.

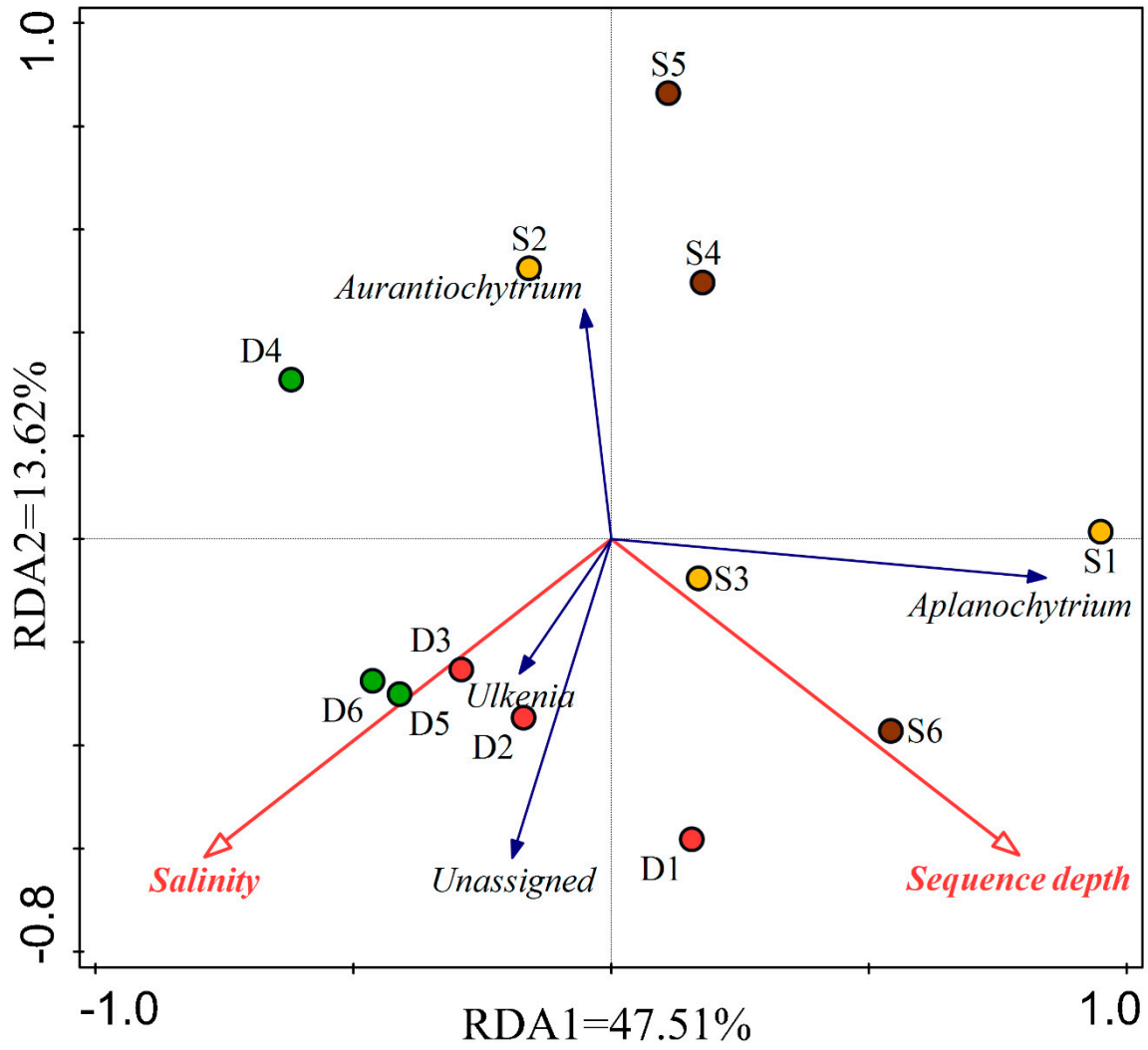

Figure S4. Redundancy analysis (RDA) based on the level of the genus Labyrinthulomycetes. In simple effects and condition effects, only salinity (“salt”) was significantly associated. The term "abundance" refers to the sequencing depth of each station.