Novel chytrid lineages dominate fungal sequences in diverse marine and freshwater habitats									
André M. Comeau, Warwick F. Vincent, Louis Bernier & Connie Lovejoy									

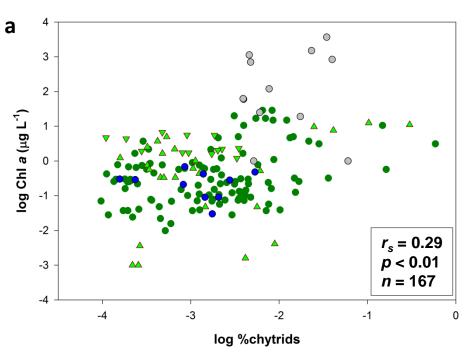


Figure S1. Biotic and abiotic parameters correlated to proportions of total fungi or Chytridiomycota-like sequences. Weak, but significant, positive correlations are present between proportions of chytrids and either chlorophyll a (a) or proportions of diatoms (b) for all sample types together. Note that data on chlorophyll a was not available for Lake Tahoe. A slightly stronger, but negative, correlation was seen between total fungi

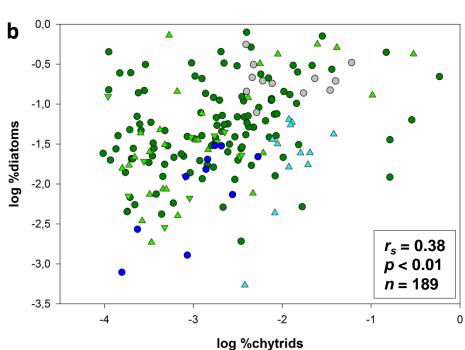
Arctic SWAtlantic SW

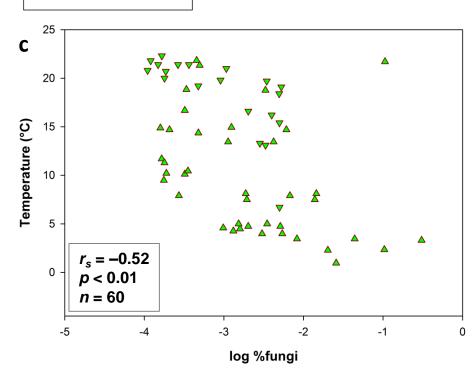
Lagoon SWArctic FW

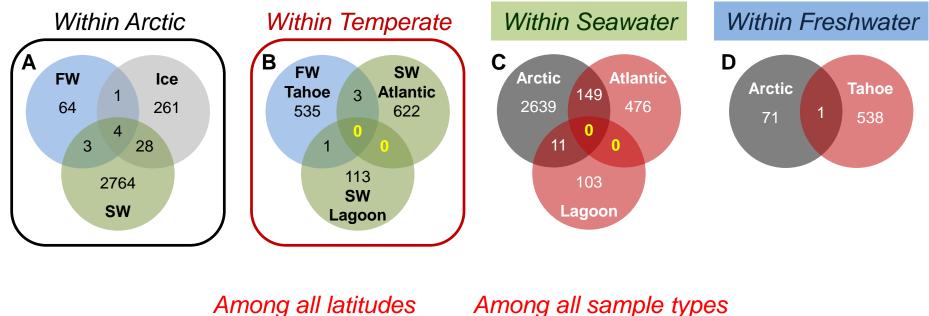
△ Lake Tahoe FW

Arctic ICE

in temperate locations only and temperature (**c**). Listed are Spearman's *r* values along with the *p* values and sample sizes (*n*) for each plot. FW, freshwater; SW, seawater.







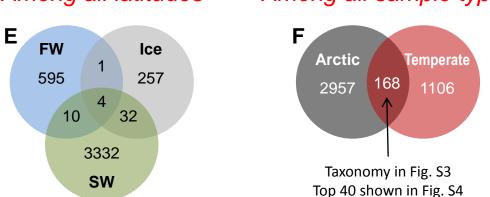


Figure S2. Numbers of shared OTUs (98% identity) between the various sample types. Color-coding for sample types matches Fig. 3 and case numbers (A-F) are referred to in Fig. S3. FW, freshwater; SW, seawater.

		# shared OTUs	Clone CFL161DB09	Crypto-Rozella	Asco-Epicoccum	Asco-Mycochaetophora	Asco-Aureobasidium	Asco-Cladosporium	Asco-Cordyceps	Asco-Engyodontium	Asco-Eurotium	Asco-Meyerozyma	Asco-Mycosphaeralla	Asco-Nectria	Asco-Sarocladium	Basidio-Leucosporidium	Basidio-Sporisorium	Unclassified
	Universal FW+Ice+SW	4	1	-	_	_	2	_	_	_	_	_	_	_	_	_	1	
Case A	Shared FW+Ice	1	_	_	_	_	1	_	_	_	_	_	_	_	_	_	_	_
Case A	Shared Ice+SW	28	24	_	1	_	_	_	_	_	_	_	1	_	1	1	_	_
	Shared SW+FW	3	1	_	_	_	_	_	_	_	_	_	_	_	1	_	_	1
	Universal Tahoe+Atlantic+Lagoon	_	_	_	-	_	-	-	_	_	_	_	_	_	_	_	_	_
Case B	Shared Tahoe+Atlantic	3	_	_	_	_	1	1	_	_	_	_	1	_	_	_	_	_
Case D	Shared Atlantic+Lagoon	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_
	Shared Lagoon+Tahoe	1	_	_	_	_	1	_	_	_	_	_	_	_	_	_	_	_
	Universal Arctic+Atlantic+Lagoon	_	_	_	-	-	-	-	_	-	-	-	-	_	_	-	-	_
Case C	Shared Arctic+Atlantic	149	105	11	2	4	5	2	1	2	2	1	1	1	6	2	2	2
Case C	Shared Atlantic+Lagoon	_	-	_	-	_	-	-	_	_	-	_	_	_	_	_	-	_
	Shared Lagoon+Arctic	11	6	_	_	_	3	1	_	_	_	_	_	_	_	1	_	_
Case D	Universal Arctic+Tahoe	1	_	_	_	_	_	_	_	_	_	_	_	_	_	_	_	1
	Universal FW+Ice+SW	4	1	_	-	_	2	-	-	_	_	_	_	-	-	_	1	_
Case E	Shared FW+Ice	1	-	_	-	_	1	-	-	_	-	_	_	-	-	_	-	_
Oude L	Shared Ice+SW	32	27	_	1	1	1	_	_	_	_	_	_	_	1	1	_	_
	Shared SW+FW	10	1	_	_	_	4	1	_	_	_	_	2	_	1	_	_	1
Case F	Universal Arctic+Temperate	168	114	11	2	4	11	3	1	2	2	1	2	1	6	3	2	3

Figure S3. Taxonomic identities of the shared OTUs (98% identity) between the various sample types. Color-coding for taxa matches Fig. 3 and case numbers (A-F) refer to Fig. S2. Asco, Ascomycota; Basidio, Basidiomycota; Crypto, Cryptomycota; FW, freshwater; SW, seawater.

Figure S4. Top 40 OTUs. Distribution of sequences within the top 40 shared OTUs (98% identity) showing vastly different profiles between Arctic and Temperate samples.

