

Table 2. Summary of SSU rRNA gene sequences analyzed from bacterial, cyanobacterial and eukaryotic-specific gene libraries and the associated diversity indices.

	Clone libraries	No. of clones analyzed	No. of OTUs	Ace	Chao1	Chao1 95% confidence interval	singletons	Coverage (%)
Bacteria	AQ1 Library 1	84	56	198	169	104/323	43	49
	AQ1 Library 2	192	93	243	215	153/339	61	68
	AQ1 total (1+2)	276	126	423	313	228/468	87	68
	AQ2 Library 1	65	42	181	147	81/328	33	49
	AQ2 Library 2	200	57	82	74	63/103	30	85
	AQ2 total (1+2)	265	86	149	134	108/190	48	82
	AL31 Library 2	199	53	119	131	82/260	31	84
	AL67 Library 2	202	31	43	42	34/73	12	94
	AL52 Library 1	44	17	39	35	21/92	11	75
	AL52 Library 2	196	67	137	113	88/171	39	80
	AL52 total (1+2)	240	74	137	122	95/180	41	83
	Cyanobacteria	AQ1 Library 1	53	9	10	12	9/34	3
AQ1 Library 2		108	7	7	7	/	0	100
AQ1 total (1+2)		161	16	16	16	/	1	99
AQ2 Library 1		49	13	20	21	15/56	5	90
AQ2 Library 2		101	19	30	28	20/64	8	92
AQ2 total (1+2)		150	22	29	36	25/89	8	95
AL31 Library 2		63	8	11	9	8/23	3	95
AL67 Library 2		62	6	8	6	6/14	1	98
AL52 Library 1		39	5	5	5	/	1	97
AL52 Library 2		61	8	10	9	7/22	3	95
AL52 total (1+2)		100	11	21	26	14/79	6	94
Eukaryotes		AQ1	95	21	32	28	22/53	9
	AQ1 b	76	22	24	23	22/31	4	95
	AQ1 w	69	19	74	31	21/74	12	83
	AQ2	117	23	30	27	23/45	7	94
	AQ2 b	83	16	16	16	16/19	2	98
	AQ2 w	72	11	20	21	13/63	5	93
	AL31	48	1	0	1	1/1	0	100
	AL67	38	1	0	1	1/1	0	100
	AL52	38	5	7	6	6/14	2	95

AQ1b and AQ2b refer to aquarium wall-attached biofilm samples; AQ1w and AQ2w refer to plankton samples.
doi:10.1371/journal.pone.0028767.t002

At a finer phylogenetic scale, we detected 38 cyanobacterial OTUs (including 4 diatom chloroplast sequences): 9 OTUs only in lake samples, 17 only in aquaria, and the remaining 12 were shared (Figure 4). OTU diversity was thus larger in aquaria microbialites compared to field microbialites. Oscillatoriales were the most diverse group with 16 OTUs, including 3 of the most abundant ones. These affiliated to the genus *Leptolyngbya* and were also detected in AL31 and AL67. Pleurocapsales were the second most diverse group with 5 OTUs. One of them (CyanoOTU35) accounted for 69% of all cyanobacterial sequences in the 14 m-deep sample AL52 (Figure 4). This phylotype was also present in the other lake samples and in AQ1, though in lower proportions. Its high abundance in deep samples was corroborated by DGGE analyses, corresponding to one of the most intense bands in deep sample fingerprints (band J in samples AL58, AL55 and AL52, Figure S2 and Table 3).

In addition to Pleurocapsales, the Acaryochlorales OTU CyanoOTU23 was relatively abundant at 14 m, in agreement

with the low-light-intensity adaptation characteristic of Acaryochlorales [47]. We also detected 5 Chroococcales OTUs, one of them (CyanoOTU32) particularly abundant at 8 m (AL58 sample) as shown by DGGE analyses (band I in Figure S2 and Table 3). Finally, we identified 3 very divergent OTUs belonging to the deep-branching Gloeobacterales. Among them, CyanoOTU02, identified in field sample AL31 (0.5 m), represented 18% and 20% of AQ1 and AQ2 cyanobacterial sequences.

Other bacterial taxa with photosynthetic members

Apart from cyanobacteria, we identified phylotypes of other bacterial phyla that comprise phototrophic, in addition to heterotrophic, members: Alphaproteobacteria, Gammaproteobacteria and Chloroflexi. With ~30% of field sample clones, Alphaproteobacteria was the second most abundant group after Cyanobacteria (Figure 3). Their relative abundance was constant with depth. They were also extremely diverse, with 68 OTUs: 35