Table S1. 16S rRNA gene similarity (p-distance) matrix comparing *Salileptolyngbya* strains*.

1	*S. insularis*	LEGE 181150 PQ454229																									
2	*S. insularis*	LEGE 181187 PQ454231	100,00																								
3	*S. insularis*	LEGE 181149 PQ515100	100,00	100,00																							
4	*S. insularis*	LEGE 181190 PQ454230	100,00	100,00	100,00																						
5	*S. insularis*	LEGE 181212 PQ454232	100,00	100,00	100,00	100,00																					
6	*S. insularis*	LEGE 181158 PQ515097	99,68	99,68	99,68	99,68	99,68																				
7	*S. insularis*	LEGE 181198 PQ515098	99,60	99,60	99,60	99,60	99,60	99,84																			
8	*S. insularis*	LEGE 181205 PQ515099	99,76	99,76	99,76	99,76	99,76	99,92	99,84																		
9	*S. insularis*	LEGE 181184 PQ515094	99,44	99,44	99,44	99,44	99,44	99,60	99,52	99,68																	
10	*S. insularis*	*Salileptolyngbyai insularis* ALCB132760 MW024863	99,36	99,36	99,36	99,36	99,36	99,52	99,52	99,52	99,68																
11	*Salilepolyngbya* sp. (Clade A)	LEGE 181194 PQ515101	97,48	97,48	97,48	97,48	97,48	97,56	97,56	97,48	97,48	97,48															
12	*Salilepolyngbya* sp. (Clade A)	LEGE 171504 PV275272	97,97	97,97	97,97	97,97	97,97	98,30	98,30	98,22	98,22	98,14	99,28														
13	*Salilepolyngbya* sp. (Clade A)	LEGE 181219 PQ515093	98,79	98,79	98,79	98,79	98,79	99,11	98,95	99,03	99,03	98,95	98,46	99,20													
14	*Salilepolyngbya* sp.	LEGE 181216 PQ515092	94,75	94,75	94,75	94,75	94,75	94,75	94,83	94,84	95,18	94,92	94,76	94,49	94,84												
15	*Salilepolyngbya* sp. (Clade B)	Leptolyngbya sp HBC8 EU249119	96,22	96,22	96,22	96,22	96,22	96,39	96,30	96,47	96,47	96,30	96,31	96,39	96,89	94,68											
16	*Salilepolyngbya* sp. (Clade B)	Leptolyngbya WR6 MH666137	95,97	95,97	95,97	95,97	95,97	96,13	96,14	96,13	96,14	96,14	96,56	96,56	96,64	94,08	98,79										
17	*Salilepolyngbya* sp.	Leptolyngbya CCAP1442 HE975019	96,05	96,05	96,05	96,05	96,05	95,97	95,97	95,97	96,14	96,31	96,65	96,31	96,39	94,60	96,90	97,48									
18	*S. diazotrophica*	*Salileptolyngbya diazotrophicum* SCSIO43686 MF614799	95,97	95,97	95,97	95,97	95,97	96,05	95,97	96,14	96,48	96,14	96,31	95,89	96,31	95,37	96,81	97,31	97,39								
19	*Salilepolyngbya* sp. (Clade C)	LEGE 181195 PQ515095	97,72	97,72	97,72	97,72	97,72	97,89	97,80	97,97	98,13	97,80	96,72	96,98	97,48	95,02	96,13	96,05	95,88	96,30							
20	*Salilepolyngbya* sp. (Clade C)	LEGE 181217 PQ515096	97,56	97,56	97,56	97,56	97,56	97,72	97,72	97,72	97,89	97,72	96,72	96,81	97,31	95,02	96,05	96,30	96,14	96,38	99,76						
21	*Salilepolyngbya* sp. (Clade C)	LEGE 181222 PQ454228	97,56	97,56	97,56	97,56	97,56	97,72	97,72	97,72	97,89	97,72	96,72	96,81	97,31	95,02	96,05	96,30	96,14	96,38	99,76	100,00					
22	*S. caboverdiana* sp. nov.	LEGE 181209 PQ4542270	97,97	97,97	97,97	97,97	97,97	97,97	97,97	97,97	97,64	97,81	97,06	97,06	97,89	94,66	96,47	96,22	96,47	96,80	97,72	97,89	97,89				

*The number of base substitutions per site from between sequences are shown. Analyses were conducted using the Maximum Composite Likelihood model [1]. This analysis involved 22 nucleotide sequences. All positions containing gaps and missing data were eliminated (complete deletion option). There were a total of 1250 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [2]

1. Tamura K., Nei M., and Kumar S. (2004). Prospects for inferring very large phylogenies by using the neighbor-joining method. Proceedings of the National Academy of Sciences (USA) 101:11030-11035.

2. Tamura K., Stecher G., and Kumar S. (2021). MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution https://doi.org/10.1093/molbev/msab120.

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