Table S1 Cyanobacterial OTU affiliation obtained by alignment of 16S rDNA sequences with NCBI BLAST tool, Genbank Databases, and sequences from strains isolated from Lake Dziani Dzaha [18].

OTU number	NCBI affiliation	Genbank affiliation	Identity (%)	PMC reference strains	Identity (%)
1	*Arthrospira*	*Arthrospira platensis*	99%	*Arthrospira fusiformis*	99%
10	Unknown	*Leptolyngbya*	≤ 95%	*Leptolyngbya*	≤ 95%
23	*Lyngbya*	*Microcoleus / Geitlerinema*	99%	*Sodalinema komarekii*	99%
60	*Synechococcus*	*Synechococcus*	99%	*Spirulina subsalsa*	≤ 90%
105	*Xenococcus*	*Xenococcus*	98%	*Spirulina subsalsa*	≤ 92%
450	*filamentous cyanobacterium LLi71*	*filamentous cyanobacterium LLi71*	99%	*Leptolyngbya*	≤ 94%
339	*Oscillatoriales cyanobacterium*	*Leptolyngbya*	97%	*Leptolyngbya*	≤ 93%
365	*Oscillatoriales cyanobacterium*	*Leptolyngbya*	97%	*Leptolyngbya*	≤ 93%