Supplementary Information: Draft Genome Sequences of Three Filamentous Cyanobacteria Isolated from Brackish Habitats

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Supplementary Figures S1 to S5

Supplementary Table S1

Figure S1: De Bruijn graph visualisation of assembled reads from the culture of Halomicronema sp. CCY15110. Nodes are coloured on a graduated scale according to sequencing depth of \geq 83.36 (green) and \leq 10.84 (red). Matches to known cyanobacterial genes are annotated with black text.



Figure S2: De Bruijn graph visualisation of assembled reads from the culture of Leptolyngbya sp. CCY15150. Nodes are coloured on a graduated scale according to sequencing depth of \geq 65.3 (green) and \leq 16.08 (red). Matches to known cyanobacterial genes are annotated with black text.



Figure S3: De Bruijn graph visualisation of assembled reads from the culture of Spirulina sp. CCY15215. Nodes are coloured on a graduated scale according to sequencing depth of \geq 55.86 (green) and \leq 16.93 (red). Matches to known cyanobacterial genes are annotated with black text.



Figure S4: Maximum likelihood phylogeny of cyanobacteria, generated in IQ-TREE v1.6.7 (23) from an alignment of 139 proteins (53,242 amino acid positions), 165 rRNA (1,717 nucleotide positions) and LSU rRNA (3,117 nucleotide positions). Node labels represent UFBoot support values (25). Branch lengths represent the number of substitutions per site, with the scale bar representing an average of 0.2 substitutions per site.



100 P. marinus.str.AS9601 100 Prochlorococcus.sp.RS0 100 P. marinus.str.MIT9301 P. marinus.str.MIT9202 P.sp. MIT0801 P.marinus.str.NATL1A Is subsp.marinus.str.CCMP1375

Figure S5: 16S SSU rRNA phylogeny of cyanobacteria, generated with maximum likelihood methodology implemented in IQ-TREE v1.6.1 (23) from an alignment of 1,717 nucleotide positions. Node labels represent UFBoot support values (25) less than 95, whereas node circles represent UFBoot support values higher than 95. Branch lengths represent the number of substitutions per site, with the scale bar representing an average of 0.2 substitutions per site. Draft genomes sequenced in this study are highlighted in red text with red arrows.



Table S1: Query sequences used for BlastP for compatible solutes

Compatible Solute	Enzyme	NCBI Accession Number	Source strain
Sucrose	SpsA (<i>Sll0045</i>)	AGF53073.1	Synechocystis sp. PCC 6803
	SpsA (<i>Alr3370</i>)	WP_044521731.1	Nostoc sp. PCC 7120
	SpsA (<i>All4376</i>)	WP_010998513.1	Nostoc sp. PCC 7120
	Spp	AGF52107.1	Synechocystis sp. PCC 6803
Trehalose	TreY	WP_010994344.1	Nostoc sp. PCC 7120
	TreZ	WP_044520508.1	Nostoc sp. PCC 7120
Glucosylglycerol	GgpS	AGF52040.1	Synechocystis sp. PCC 6803
	GgpP	AGF53289.1	Synechocystis sp. PCC 6803
Glucosylglycerate	GpgS	ACB00008.1	Synechococcus sp. PCC 7002
	GpgP	AAP99773.1	Prochlorococcus marinus
Glycine betaine	GSMT	WP_015227493.1	Halothece sp. PCC 7418
	DMT	WP_015227494.1	Halothece sp. PCC 7418