

Supplementary Materials: Salt Shock Responses of *Microcystis* Revealed through Physiological, Transcript, and Metabolomic Analyses

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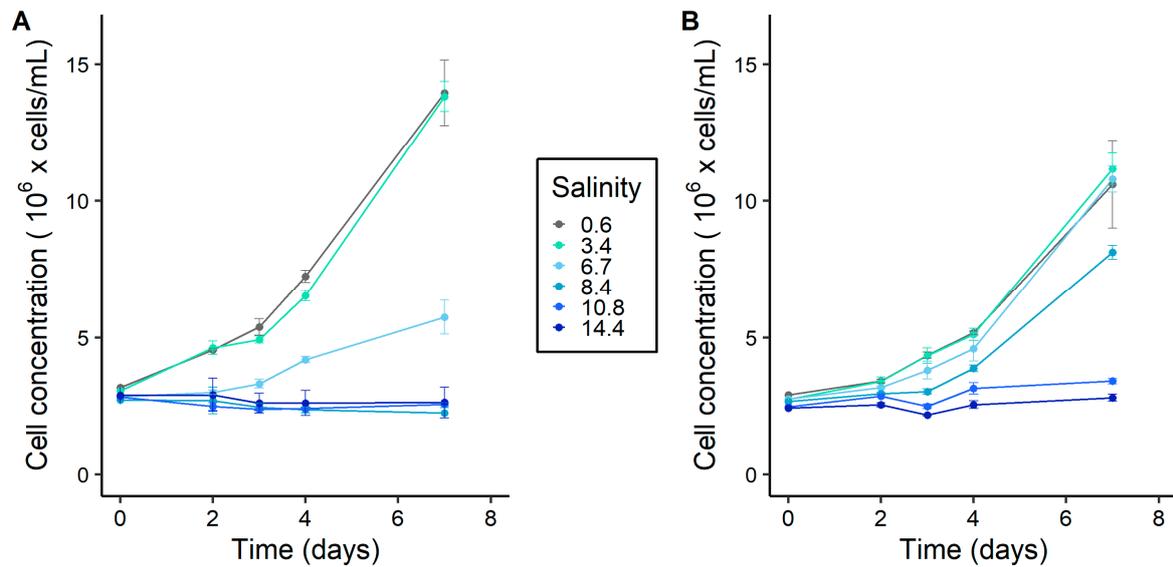


Figure S1. Cell concentrations over time after salt treatments for *Microcystis aeruginosa* PCC 7820 (freshwater) (A) and PCC 7806 (brackish water) (B). Triplicates of culture are represented as mean and error bars represent the standard deviation.

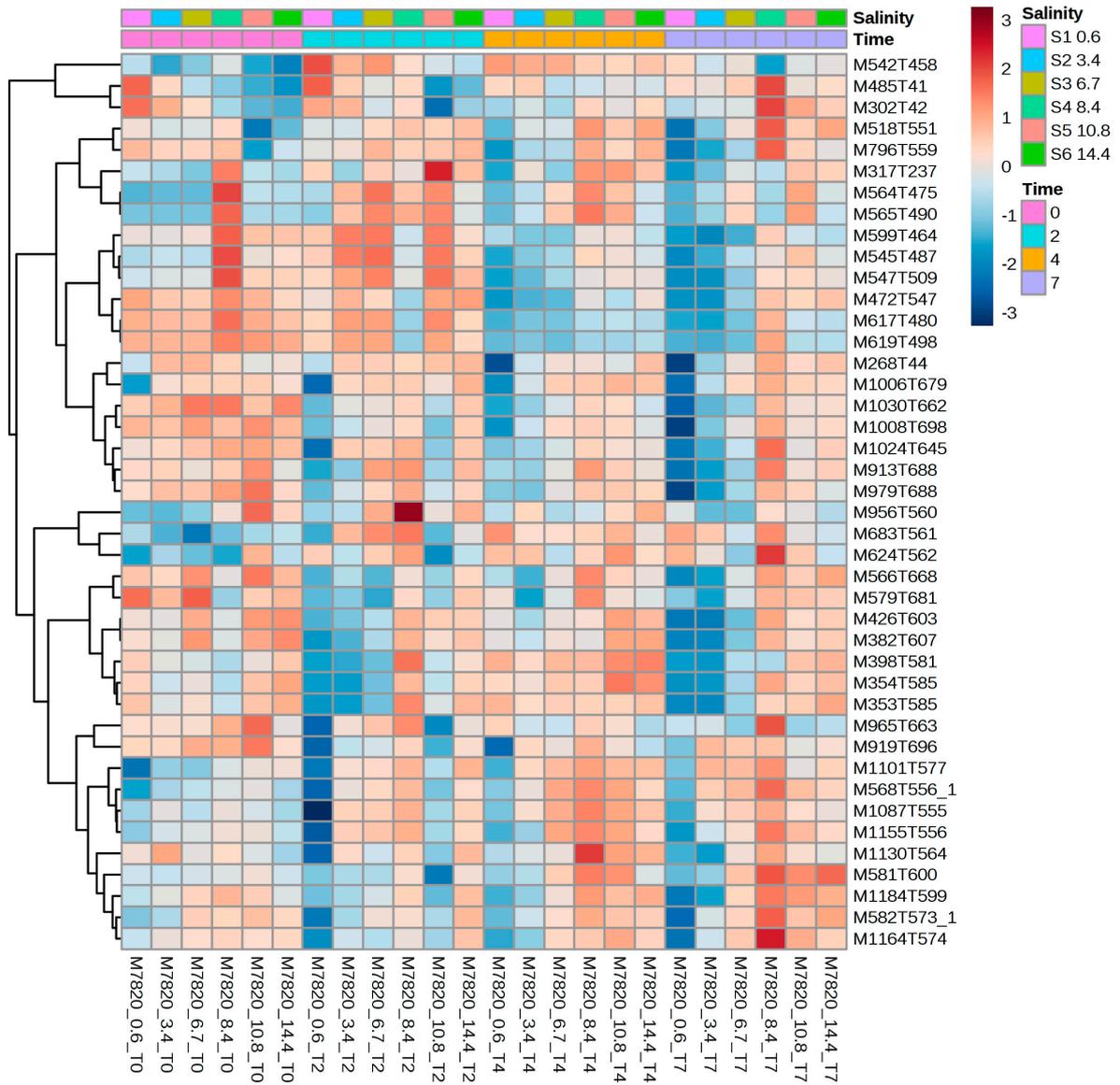


Figure S2. Heatmap of significantly time-affected metabolites of *M. aeruginosa* PCC 7820 (freshwater). Data represented are means of triplicate. (M: mass; T: retention time, time in days) and corresponded to features with a relatively lower (blue) and higher (red) area.

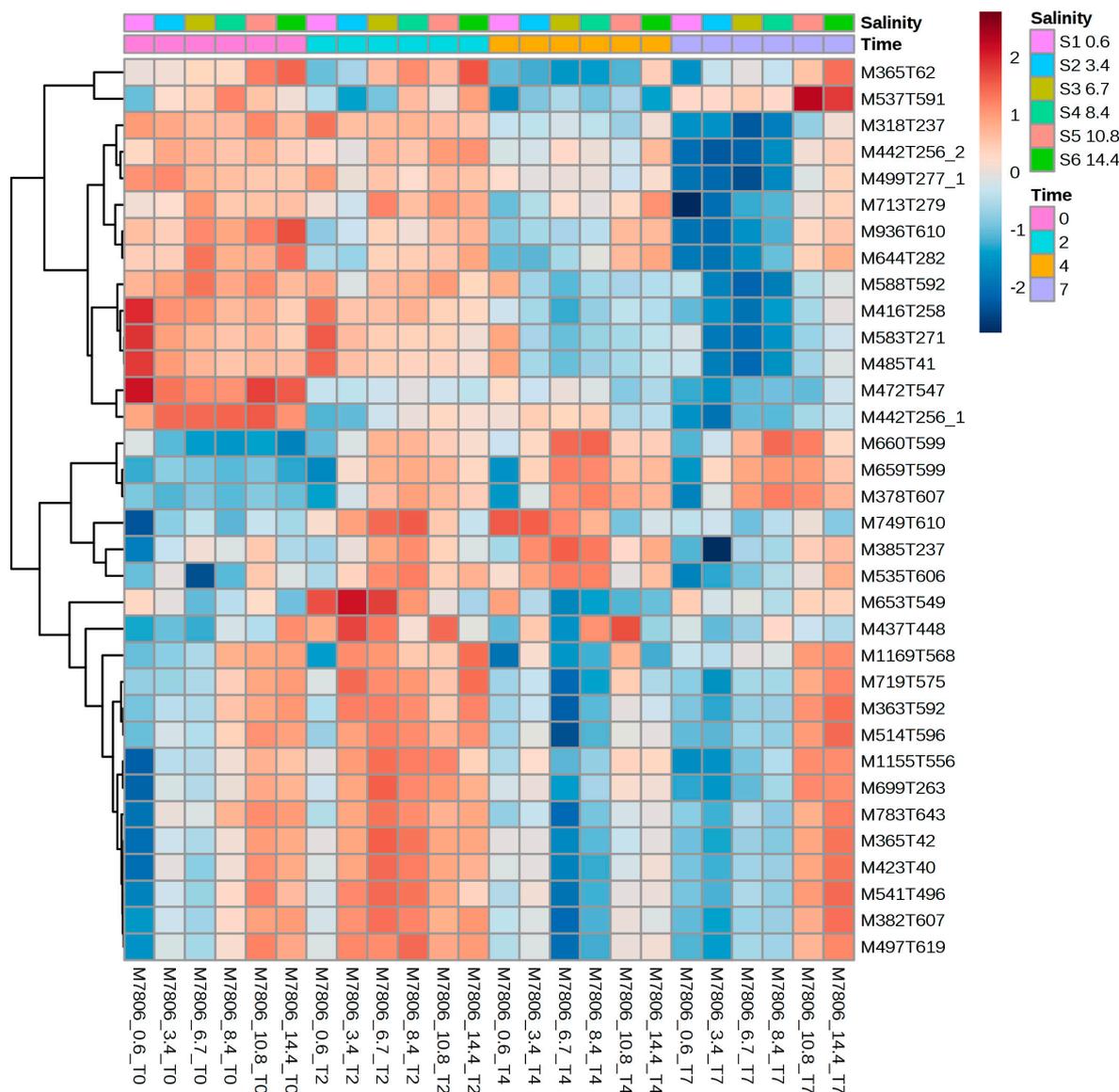


Figure S3. Heatmap of significantly time-affected metabolites of *M. aeruginosa* PCC 7806 (brackish water). Data represented are means of triplicate. (M: mass; T: retention time, time in days) and corresponded to features with a relatively lower (blue) and higher (red) area. Sucrose was extracted in ethanol then evaporated and rehydrated. In order to have a sufficient amount of cells to extract, the cell pellets obtained from the triplicate of cultures were pooled before the extraction (for the salinity 0.6, 6.7, and 10.8). After derivatization, the sucrose was analyzed by gas chromatography coupled to a flame ionization detector (GC-FID) as described by Adams et al. (1999) [73]. Analyses were conducted on a GC system (model HP-6890, Hewlett-Packard) equipped with a CP8008 precolumn (Ret Gap, 2.5 m × 0.32 mm, Agilent Technologies) and a CP-Sil 5 CB capillary column (60 m × 0.32 mm, 0.25 μm, Agilent). Flow rates for air and H₂ for the FID were 400 and 40 mL/min, respectively. Sucrose CAS [57-50-1] (Sigma-Aldrich) was used as standard and myo-inositol as internal standard to determine concentrations.

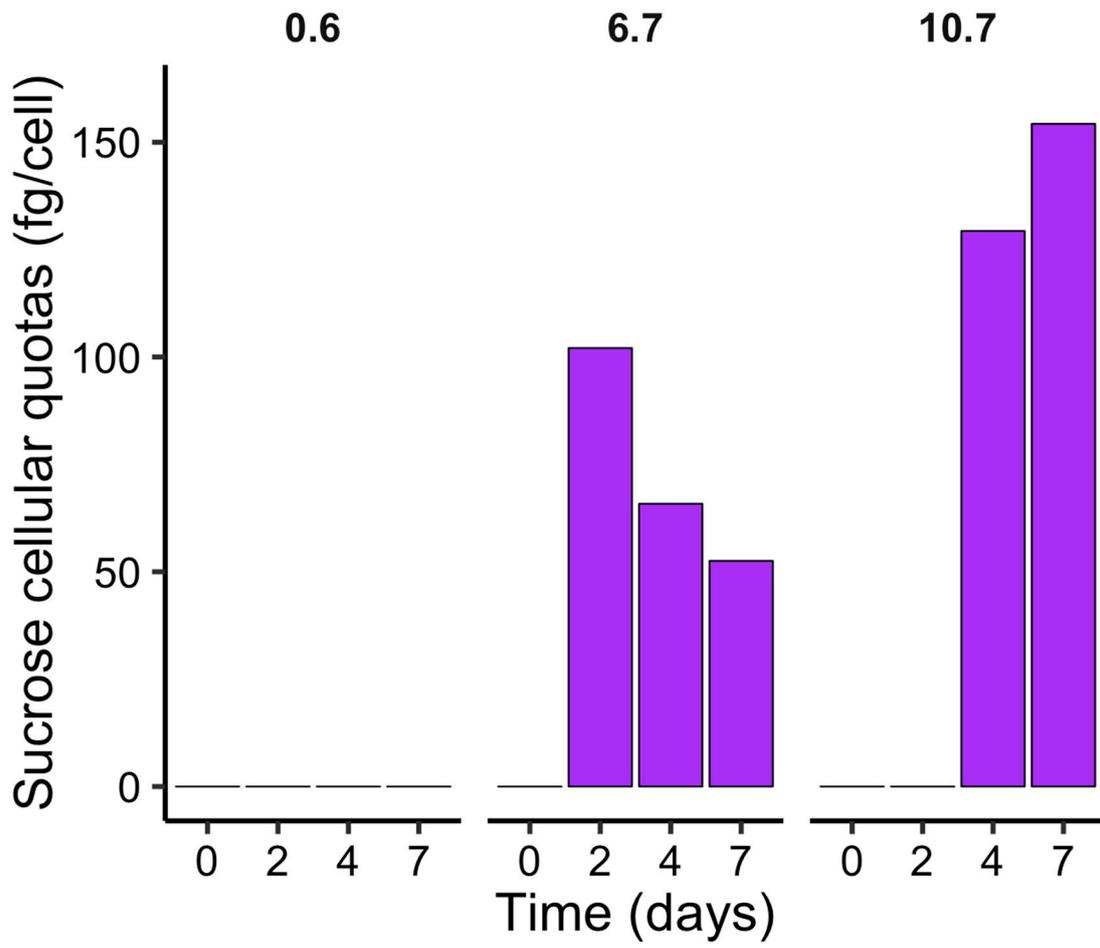


Figure S4. Sucrose cellular quotas over time and salinities for *M. aeruginosa* PCC 7806 (brackish water).

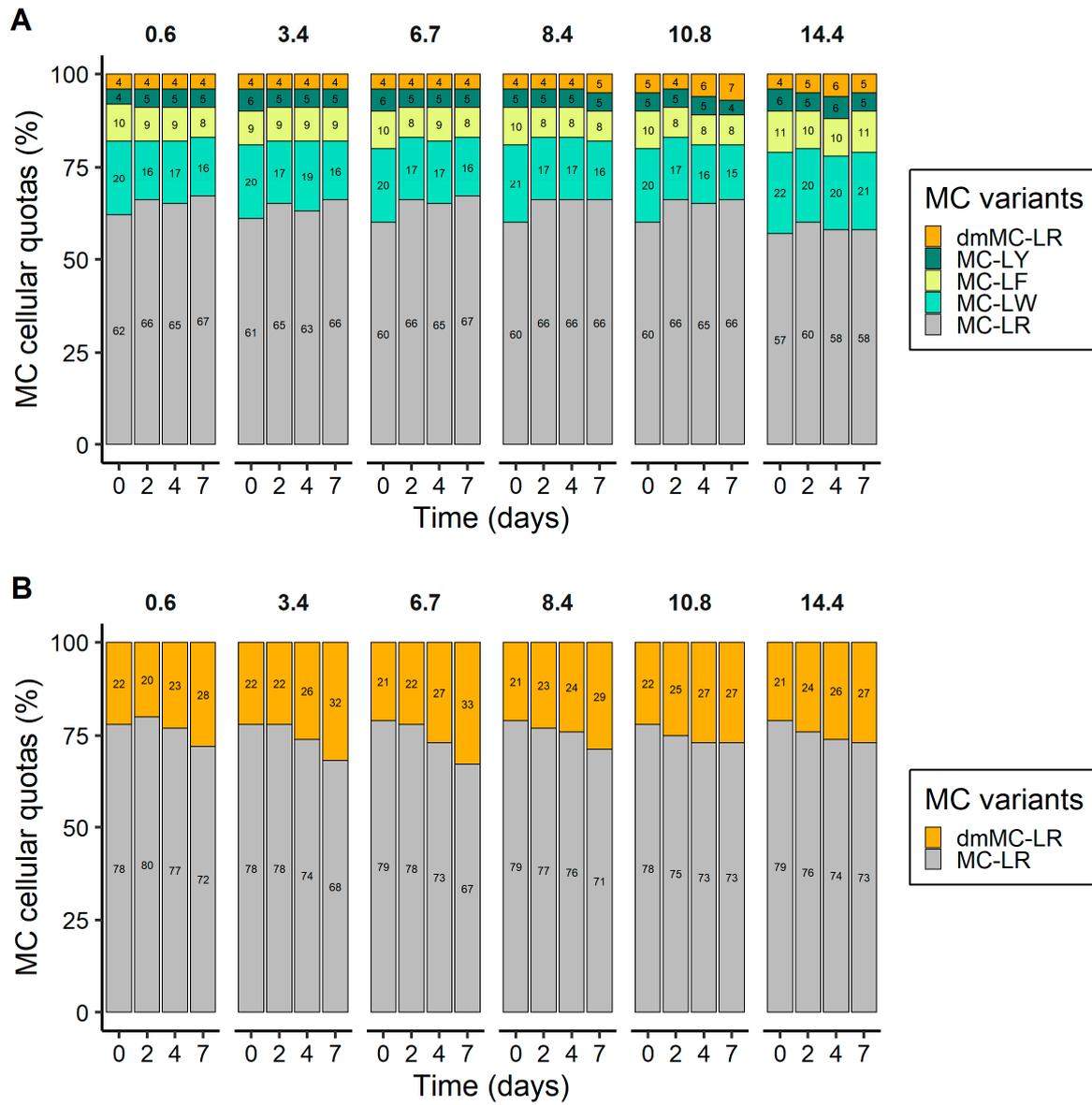


Figure S5. MC cellular quotas over time and salinities expressed as the percentage of each variant relative to the total amount of MCs per cell for *M. aeruginosa* PCC 7820 (freshwater) (A) and PCC 7806 (brackish water) (B).

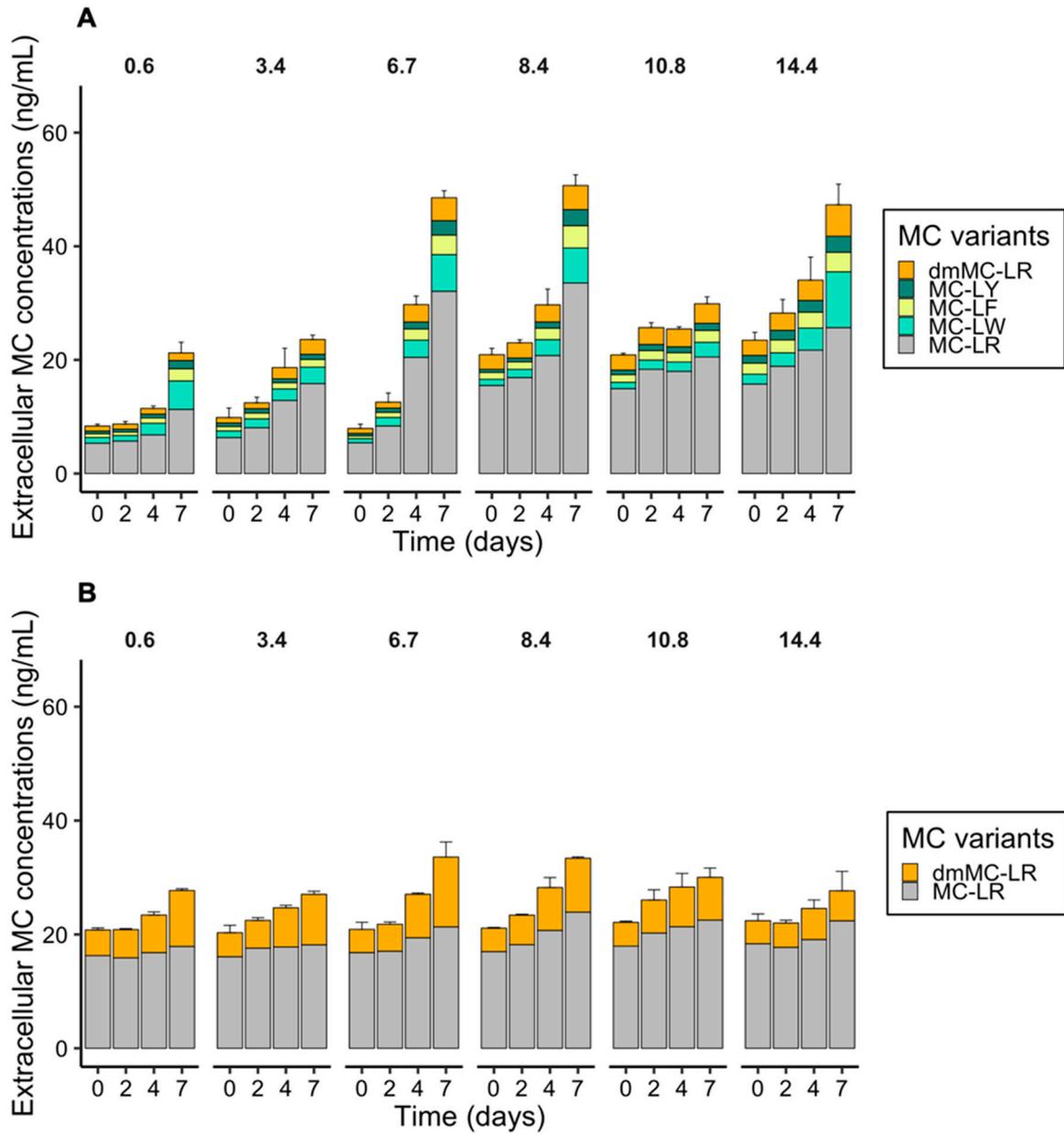


Figure S6. Extracellular MC quotas over time and salinities for *M. aeruginosa* PCC 7820 (freshwater) (A) and PCC 7806 (brackish water) (B) Error bars represent the standard deviations ($n = 3$).

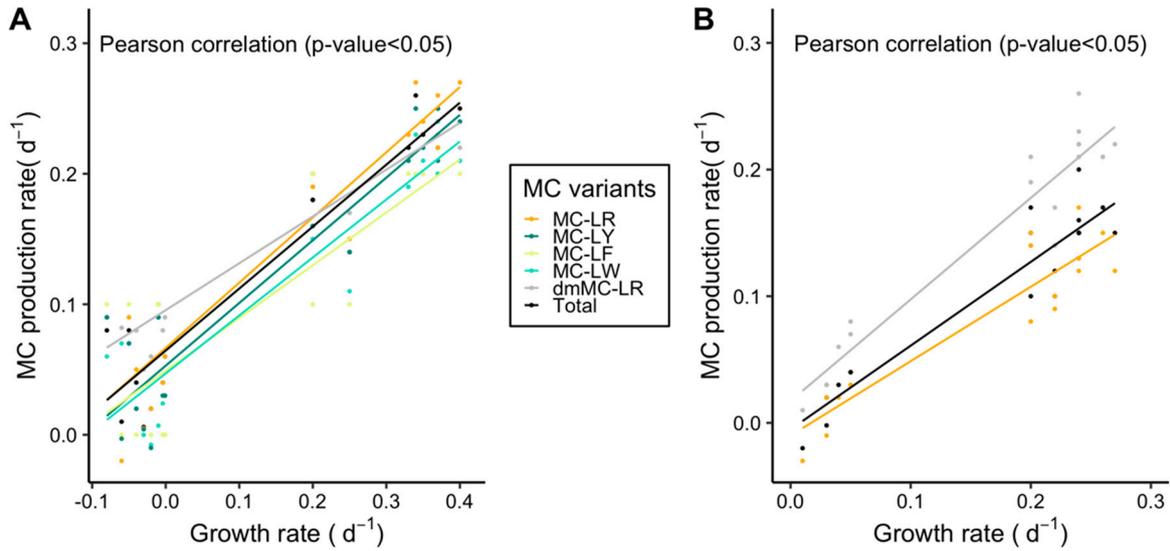


Figure S7. Linear regression between growth rates and MC production rates for *M. aeruginosa* PCC 7820 (freshwater) (A) and PCC 7806 (brackish water) (B). For both strains and all variants, the Pearson correlation was significant with $p < 0.05$. The “Total” regression curve indicates the linear regression when all the MC variants were pooled to calculate the MC production rate.

Table S1. Primer sequences used for RT-qPCR reactions.

Primer	Forward Sequence (5' – 3')	Reverse Sequence (5' – 3')	Design
<i>rnpB</i>	TACCTCAAGCGGTCCTAA	CTGATACCTGATAACTGATTGGG	[61]
<i>sod</i>	AGAAGCATCACCAGCAACCT	GCCTTAGAGCCTTGCATCAC	This study
<i>groEL</i>	CTGGACCCAAAGGTCGTAA	CCGCTACATCGTTGGTTTT	This study
<i>psaA</i>	CGGATTCCTCACCTTCAA	TTCGAGGATTCCTTCATGC	This study
<i>psbC</i>	TCTTCGGCTGTACTCGGTT	GCACCACAACCCAAGAGAAT	This study
<i>spsA</i>	ATCATTCCCTTGCTGCAATC	GCAGATTTTCTGCCTCTTGG	This study
<i>sppA</i>	GTGGGCGATAGTCTGGCTAC	CCGACGGAGGTAATCCAGTA	This study