

## **Influence of scale on biomass growth and nutrient removal in an algal-bacterial leachate treatment system**

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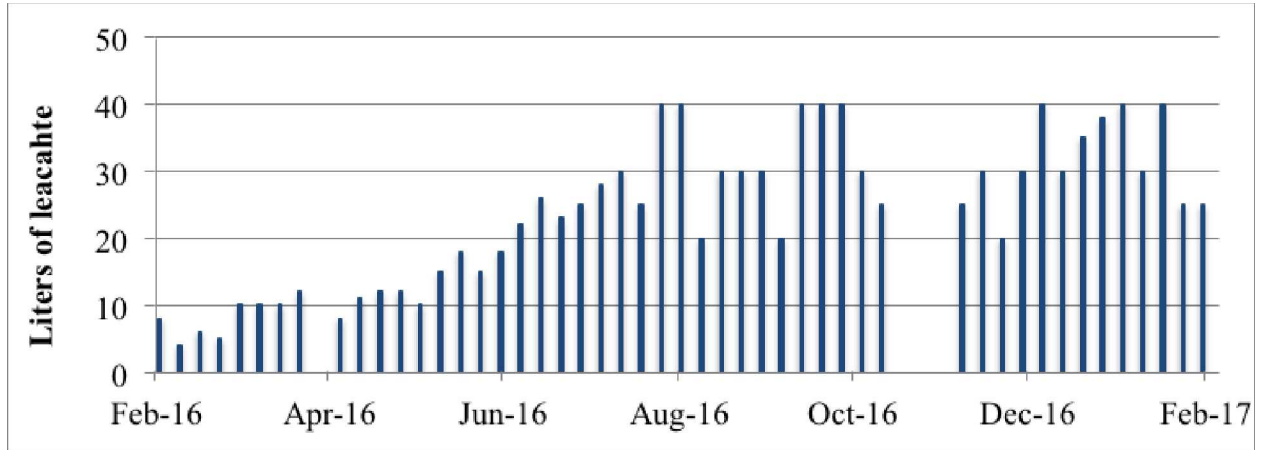
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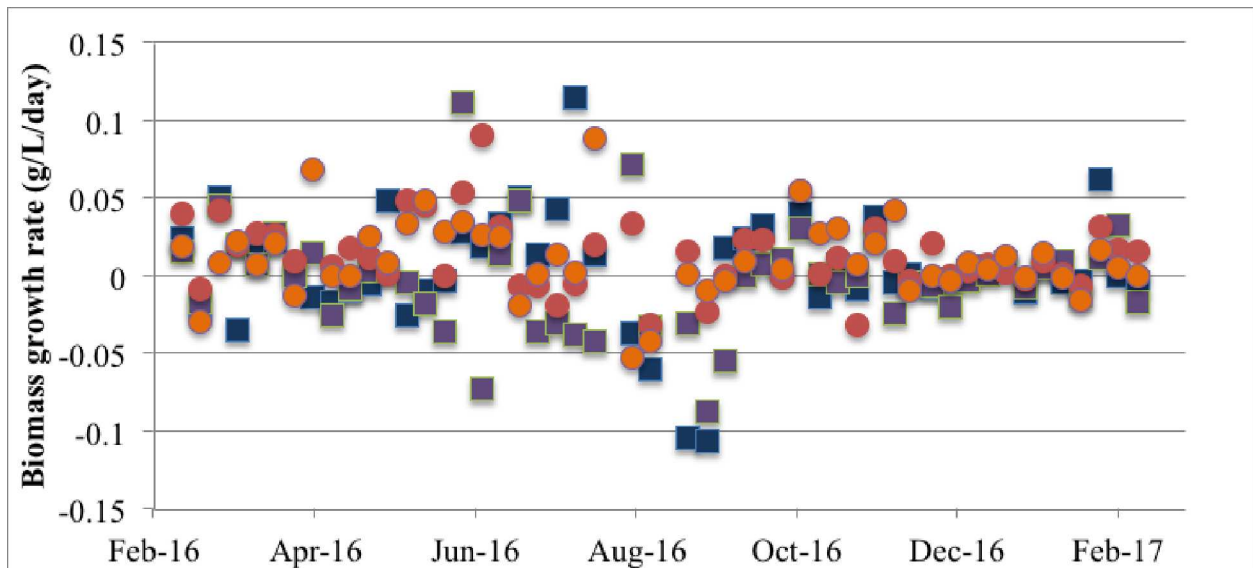
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*Figure S1:* Weekly leachate additions  
Liters of leachate added to the system each week.



*Figure S2:* Biomass growth rates from mid- and large- scale vessels.  
The biomass growth rates over the yearlong study are shown here. Rates from large-scale vessels are shown in red and orange circles. Rates from mid-scale vessels are shown in blue and purple squares.

**Table S1:** Chemical components of leachate at each collection time.

	Feb. '16	Mar. '16	Apr. '16	Jun. '16	Jul. '16	Sept. '16	Jan. '17
pH	6.48	7.09	7.37	7.22	7.56	7.42	7.18
BOD5 (mg/L)	113	124	243	800	166	145	68.3
COD (mg/L)	1750	1240	2280	2990	1440	1760	1380
Ammonia (mgN/L)	795	463	320	796	657	719	935
TOC (mg/L)	413	333	472	710	44	433	389

**Table S2:** MG-RAST identification information and quality control statistics

<b>Sequencing Technology</b>	<b>Illumina HiSeq 2500</b>
Project Name	p_reactor
Metagenome Name	CSJP002A
MG-RAST Metagenome ID	4632721.3
Upload: bp Count	5,660,327,312
Upload: Sequences Count	19,747,725
Upload: Mean Sequence Length (bp)	286 ± 68
Upload: Mean GC (%)	50 ± 17
Artificial Duplicate Reads: Sequence Count	542,165
Post QC: bp Count (bp)	3,941,990,331
Post QC: Sequences Count	17,512,059
Post QC: Mean Sequence Length (bp)	225 ± 91
Post QC: Mean GC percent (%)	49 ± 17
Processed: Predicted Protein Features	9,565,213
Processed: Predicted rRNA Features	218,346
Alignment: Identified Protein Features	3,456,150
Alignment: Identified rRNA Features	4,116
Annotation: Identified Functional Categories	2,718,901

**Table S3:** Ranges of initial conditions at each scale

	<b>Initial Ammonia (mgN/L)</b>	<b>Initial Total N (mgN/L)</b>	<b>Initial Biomass (mg/L)</b>
Large –Scale (1000L)	0.2-101.2	10.0-113.6	140-1780
Mid-Scale (100L)	0.4-161	8.12-187.8	100-1650
Small-scale (0.25L)	3-109.2	12.8-119.1	40-1130

Table S4: Domain-level relative abundance

Domain	Relative Abundance	
	RefSeq	M5nr
Archaea	0.38%	0.32%
Bacteria	92.83%	90.70%
Eukaryota	6.69%	8.66%
Viruses	0.07%	0.07%
other sequences	0.03%	0.25%

Table S5: Phylum-Level Relative Abundance (top 10 most abundant)

Phylum	Relative Abundance
Proteobacteria	68.37%
Bacteroidetes	14.36%
Actinobacteria	2.24%
Chordata	1.88%
Planctomycetes	1.71%
Firmicutes	1.43%
Arthropoda	1.36%
Cyanobacteria	1.21%
Chlorophyta	0.81%
Verrucomicrobia	0.73%
<b>Total (Top 10)</b>	<b>94.09%</b>

Table S6: Relative abundance of taxa falling within Chlorophyta using RefSeq annotations

Genus and Species	Relative Abundance	
	Overall	Within Chlorophyta
Bryopsis hypnoides	0.0005%	0.0632%
Chlamydomonas moewusii	0.0001%	0.0119%
Chlamydomonas reinhardtii	0.2564%	31.8145%
Chlorella vulgaris	0.0086%	1.0688%
Dunaliella salina	0.0000%	0.0012%
Floydiella terrestris	0.0030%	0.3682%
Leptosira terrestris	0.0011%	0.1394%
Micromonas pusilla	0.0139%	1.7194%
Micromonas sp. RCC299	0.0176%	2.1889%
Monomastix sp. OKE-1	0.0004%	0.0465%
Nephroselmis olivacea	0.0034%	0.4230%
Oedogonium cardiacum	0.0046%	0.5708%
Oltmannsiellopsis viridis	0.0002%	0.0274%
Ostreococcus 'lucimarinus'	0.0589%	7.3042%
Ostreococcus tauri	0.0143%	1.7695%
Parachlorella kessleri	0.0043%	0.5291%
Pedinomonas minor	0.0002%	0.0203%
Prototheca wickerhamii	0.0023%	0.2848%
Pseudendoclonium akinetum	0.0001%	0.0131%
Pycnococcus provasolii	0.0002%	0.0191%
Pyramimonas parkeae	0.0014%	0.1740%
Scenedesmus obliquus	0.2047%	25.4039%
Stigeoclonium helveticum	0.0005%	0.0596%
Volvox carteri	0.2094%	25.9795%
<b>Total</b>	<b>0.8059%</b>	<b>100.0000%</b>

Table S7: Relative abundance of taxa falling within Cyanobacteria using RefSeq annotations

Genus and Species	Relative Abundance	
	Overall	Within Cyanobacteria
Acaryochloris marina	0.0348%	2.8809%
Anabaena azollae	0.0053%	0.4425%
Anabaena variabilis	0.0806%	6.6652%
Arthrospira maxima	0.0124%	1.0281%
Arthrospira platensis	0.0050%	0.4155%
Crocospaera watsonii	0.0226%	1.8735%
cyanobacterium UCYN-A	0.0018%	0.1478%
Cyanobium sp. PCC 7001	0.0056%	0.4632%
Cyanothece sp. ATCC 51142	0.0256%	2.1166%
Cyanothece sp. CCY0110	0.0221%	1.8290%
Cyanothece sp. PCC 7424	0.0384%	3.1781%
Cyanothece sp. PCC 7425	0.0470%	3.8884%
Cyanothece sp. PCC 7822	0.0605%	5.0095%
Cyanothece sp. PCC 8801	0.0107%	0.8835%
Cyanothece sp. PCC 8802	0.0251%	2.0777%
Cylindrospermopsis raciborskii	0.0055%	0.4537%
Gloeobacter violaceus	0.0768%	6.3522%
Lyngbya sp. PCC 8106	0.0236%	1.9553%
Microcoleus chthonoplastes	0.0301%	2.4876%
Microcystis aeruginosa	0.0384%	3.1749%
Nodularia spumigena	0.0147%	1.2188%
Nostoc punctiforme	0.0835%	6.9107%
Nostoc sp. PCC 7120	0.0632%	5.2303%
Nostoc sp. PCC 7524	0.0000%	0.0008%
Oscillatoria sp. PCC 6506	0.0208%	1.7217%
Prochlorococcus marinus	0.0236%	1.9529%
Raphidiopsis brookii	0.0043%	0.3575%
Synechococcus elongatus	0.0643%	5.3169%
Synechococcus sp. BL107	0.0012%	0.1025%
Synechococcus sp. CC9311	0.0057%	0.4727%
Synechococcus sp. CC9605	0.0070%	0.5824%
Synechococcus sp. CC9902	0.0040%	0.3345%
Synechococcus sp. JA-2-3B'a(2-13)	0.0218%	1.8052%
Synechococcus sp. JA-3-3Ab	0.0204%	1.6868%
Synechococcus sp. PCC 7002	0.0193%	1.5970%
Synechococcus sp. PCC 7335	0.0402%	3.3275%
Synechococcus sp. RCC307	0.0069%	0.5681%
Synechococcus sp. RS9916	0.0018%	0.1478%

Synechococcus sp. RS9917	0.0056%	0.4632%
Synechococcus sp. WH 5701	0.0063%	0.5236%
Synechococcus sp. WH 7803	0.0048%	0.3981%
Synechococcus sp. WH 7805	0.0045%	0.3710%
Synechococcus sp. WH 8102	0.0138%	1.1425%
Synechococcus sp. WH 8109	0.0008%	0.0683%
Synechocystis sp. PCC 6803	0.1351%	11.1781%
Thermosynechococcus elongatus	0.0258%	2.1349%
Trichodesmium erythraeum	0.0370%	3.0629%
<b>Total</b>	<b>1.2086%</b>	<b>100.0000%</b>

*Table S8: Relative abundance of nitrifying and anammox bacteria (Genus-level)\**

<b>Genus</b>	<b>Relative Abundance</b>	
	<b>RefSeq</b>	<b>M5nr</b>
<b>Ammonia-oxidizing bacteria</b>		
<i>Nitrosomonas</i>	9.61%	9.19%
<i>Nitrosococcus</i>	0.48%	0.41%
<i>Nitrospira</i>	2.25%	2.48%
<b>Total</b>	<b>12.33%</b>	<b>12.08%</b>
<b>Nitrite-oxidizing bacteria</b>		
<i>Nitrobacter</i>	0.73%	0.60%
<i>Nitrospina</i>	-	-
<i>Nitrococcus</i>	0.13%	0.13%
<i>Nitrospira</i>	0.08%	0.07%
<b>Total</b>	<b>0.94%</b>	<b>0.81%</b>
<b>Anammox Bacteria</b>		
Candidatus Brocadia	-	-
Candidatus Kuenenia	-	0.02%
Candidatus Anammoxoglobus	-	-
Candidatus Jettenia	-	-
Candidatus Scalindua	-	-
<b>Total</b>	<b>0.00%</b>	<b>0.02%</b>
<b>Grand Total</b>	<b>13.28%</b>	<b>12.91%</b>
* Dashes indicate that no reads were annotated for this genus		

Table S 9: Non standardized  $\beta$  values of regression

<u>Dependent variable</u>	<u>Model Components</u>	<u>Non-standardized B value</u>
Ammonia Removal Rate	Initial ammonia concentration	0.131
	Average DO	-0.274
	Maximum pH	2.059
	Minimum pH	-0.939
	Constant	-10.653
Total N Removal Rate	Initial ammonia concentration	0.115
	Maximum pH	2.822
	Minimum water temperature	-0.15
	Weekly avg daylight hrs	0.615
	Constant	-25.026
Biomass Growth Rate	Initial biomass concentration	-0.082
	Avg. weekly daylight hrs	0.008
	Max water temperature	0.001
	Minimum DO	-0.003
	Constant	-0.099