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**Comparison of nutrient retention efficiency between vertical-flow and floating treatment wetland mesocosms with and without biodegradable plastic**

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**Short title:** Nutrient retention efficiency in wetland mesocosms with and without biodegradable plastic

20 **ABSTRACT**

21 Treatment wetlands are ecological systems that are engineered to improve polluted water quality  
22 through macrophyte, soil, and microbial remediation and are used commonly for urban and  
23 agricultural runoff treatment. However, constructed wetlands used for marine aquaculture  
24 effluent treatments are understudied when compared to their freshwater counterpart. We  
25 compared the nutrient retention and the microbial communities of two types of constructed  
26 wetland mesocosms, a vertical-flow treatment wetland (VFTW) and floating treatment wetland  
27 (FTW) in subtropical south Florida. To enhance nutrient retention efficiency, we implemented  
28 biodegradable plastic (polycaprolactone), as an external carbon source and monitored the  
29 performance of VFTW and FTW for the treatment of marine aquaculture effluent.  
30 Polycaprolactone surface were covered by various cyanobacterial genera including *Oscillatoria*,  
31 *Leptolyngbya*, *Brasilonema*, and *Trichormus* and some plastic-degrading bacteria such as  
32 *Pseudomonas*. The presence of a biodegradable plastic in FTW improved the overall  
33 performance of nitrogen removal (nitrite plus nitrate) by 14% through denitrification. The pattern  
34 of nutrient removal between two treatment wetland mesocosms were significantly different ( $p <$   
35  $0.01$ ), with over 87-91% retention of total nitrogen in VFTW and no retention in FTW, the latter  
36 due to poor retention of nitrite plus nitrate and production of organic nitrogen from the system  
37 not present in inflow waters. Total phosphorus was retained in both mesocosm types, with higher  
38 retention (74-81%) in the VFTW than in the FTW (17-40%). The nutrient retention in VFTW  
39 was higher overall compared with FTW mesocosms regardless of biodegradable plastic presence.

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44 **Keywords:** biodegradable plastic, vertical-flow treatment wetland, floating treatment wetland,  
45 aquaculture, microbial community

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## 60 **1. INTRODUCTION**

61 Wetland construction or wetland restoration has been effective in water quality  
62 enhancement through nutrient reductions from agricultural and urban runoff (Fink and Mitsch,  
63 2004; Nahlik and Mitsch, 2006; Mitsch et al., 2012, 2015; Griffiths and Mitsch, 2017).  
64 Treatment wetlands are ecological systems that are engineered to treat polluted water through  
65 macrophyte, soil, and microbial remediation and have some varieties (Vymazal, 2007). Vertical-  
66 flow treatment wetlands (VFTWs) are fed inflows intermittently or continuously with a relatively  
67 short hydraulic residence time (Stottmeister et al., 2003; De Lange et al., 2013) and effective for  
68 solids removal from the water column and nutrient cycling by means of phytoremediation and  
69 microbial processes (e.g. denitrification and nitrification) (Fuchs et al., 2011; De Lange et al.,  
70 2013).

71 A floating treatment wetland (FTW) is a relatively new phytoremediation technique to  
72 reduce the impact of excess nutrient loading within the waterbody itself. FTWs consist of aquatic  
73 or terrestrial plants grown hydroponically on a floating mat directly in the open water of the  
74 system allowing for direct treatment of eutrophic waters (Hubbard et al., 2004; Vymazal, 2007;  
75 Headley and Tanner, 2011; Zhao et al., 2012; Olguín et al., 2017; Pavlineri et al., 2017). The  
76 plant roots are exposed directly to the water column instead of buried in a sand or gravel  
77 substrate allowing for nutrients to be absorbed hydroponically, reducing the nutrient load  
78 internally (Zhou and Wang, 2010; Headley and Tanner, 2011; White and Cousins, 2013). The  
79 development of an extensive root system along with microbial biofilm formation provide for the  
80 main nutrient removal pathway in this type of wetland system (Headley and Tanner, 2011).  
81 FTWs have been shown to be effective at treatment of high nutrient wastewaters (e.g.  
82 stormwater, sewage, agriculture) (Headley and Tanner, 2011; Yeh et al., 2015; Chen et al.,

83 2016). Plant roots have a greater surface area exposure in the water column, which allow for  
84 greater bacterial colonization and unique rhizosphere microbial functions (Zhao et al., 2012;  
85 White and Cousins, 2013; Urakawa et al., 2017). These two wetland designs (VFTW and FTW)  
86 have been proven to be effective for agriculture and storm water treatments (Faulwetter et al.,  
87 2011; Zhang et al., 2013b; Liu et al., 2016; Fu et al., 2017; Urakawa et al., 2017).

88         Since treatment wetlands have been specifically designed for wastewater treatment  
89 removing high nutrients and suspended solids (Turcios and Papenbrock, 2014; Mitsch and  
90 Gosselink, 2015), it is possible to apply treatment wetlands to remediate aquaculture wastewater  
91 as a cost-effective approach (Brown et al., 1999; Lin et al., 2010; Liang et al., 2017). One of the  
92 most common treatment wetlands for aquaculture effluent is characterized as subsurface flow  
93 construction, which has a sand or gravel substrate, where water flows either vertically (vertical-  
94 flow) or horizontally (horizontal-flow), and treated water is either reused in a closed system or  
95 discharged in an open system (Konnerup et al., 2011; Mitsch and Gosselink, 2015).  
96 Enhancement of aquaculture wastewater treatment capacity could be possible through the  
97 addition of various external carbon sources such as methanol, glucose, starch, and cellulose (Wu  
98 et al., 2014). Several studies aimed to explore different denitrification activity with external  
99 carbon in constructed wetlands, use of periphyton as a producer of organic carbon (Sirivedhin  
100 and Gray, 2006), and addition of different sugars (e.g. glucose and fructose) to wetland influents  
101 (Lin et al., 2002; Lu et al., 2009).

102         Using biodegradable plastic as an external carbon source in treatment wetlands is a new  
103 approach and two benchtop scale wetland microcosms were previously designed with the use of  
104 a cornstarch/polycaprolactone blend (Shen et al., 2015) and poly-3-hydroxybutyrate-co-3-  
105 hydroxyvalerate/polyacetic acid (PHBV/PLA) (Yang et al., 2018). However, no application has

106 been made in a medium scale outdoor treatment wetland and understanding the microbial  
107 community composition in a treatment wetland with biodegradable plastic is the next question to  
108 improve the performance of nutrient removal.

109 In this study, we evaluated nutrient retention efficiency between vertical-flow and  
110 floating treatment wetland mesocosms with and without biodegradable plastic  
111 (polycaprolactone) for treatment of marine aquaculture effluent to enhance nutrient cycling (e.g.  
112 denitrification). Likewise, determining how microbial community composition could change  
113 with the addition of a biodegradable plastic and how microbial community composition differs  
114 between vertical-flow and floating treatment wetland mesocosms was concurrently studied for a  
115 better understanding of microbial community composition of these two treatment wetland  
116 systems.

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## 118 **2. MATERIALS AND METHODS**

### 119 *2.1 Vertical-flow treatment wetland construction*

120 In May 2016, the experimental units were constructed at the Everglades Wetland  
121 Research Park of Florida Gulf Coast University (26°06.452'N, 81°46.334'W) in two rows of  
122 four wetland mesocosms (1.33 m x 0.47 m x 0.61 m polyethylene tubs) with one row modeling  
123 vertical-flow treatment wetlands (VFTW) and one row modeling floating treatment wetlands  
124 (FTW) in a batch system (**Fig. 1**). Vertical-flow constructed mesocosms were filled with a 10 cm  
125 layer of gravel followed by an approximate 30 cm of sand fill according to methods outlined in  
126 Ahn et al. (2001) and Ahn and Mitsch (2002) (**Fig. 1**). Cordgrass (*Spartina patens*) was collected  
127 from a nearby 23-ha restored brackish marsh (5 ppt) at the Naples Botanical Garden

128 (26°06.181'N, 81°46.534'W) (Zhang et al., 2017a) and planted in August 2016. Salinity was  
129 gradually increased from 0 to 5 ppt to acclimate plants for 10 months prior to starting the  
130 experiment. Two mesocosms were incorporated with a 1 cm layer of polycaprolactone beads (3.5  
131 mm in diameter, IC3D, TechTack Moldable plastic) buried at a depth of 9 cm (1.82 kg) within  
132 the upper substrate layer prior to effluent feeding to mesocosms to allow for settling of the  
133 plastics, which are buoyant in water, as upper substrate layer was no longer densely packed after  
134 burial. Two other mesocosms were used as a control without biodegradable plastic incorporation.  
135 A nutrient removal experiment was conducted during June 2017.

## 136 2.2 Floating treatment wetland construction

137 Four floating mat treatment mesocosms were filled with lake water pumped up from an  
138 adjacent lake. Each mat had 18 plantings (9 cm diameter) spaced 25 cm apart from the center of  
139 each hole (**Fig. 1**). Seven-cm cordgrass (*S. patens*) plants were placed in aerator pots seated  
140 within the floating mats. Artificial saltwater (Instant Ocean) was used to adjust salinity to be 5  
141 ppt. A recirculating bioreactor system was equipped in all four floating treatment wetlands: two  
142 mesocosms had bioreactors with polycaprolactone (PCL) plastic beads as a reactor medium with  
143 two mesocosms having empty bioreactors used as control. The recirculating bioreactor setup  
144 consisted of 250 mL biodegradable beads (472 g) in AQUAMAXX bioreactors (1 L volume)  
145 connected with a filter pump (Cobalt MJ-1200) and a flow nozzle controlled to a flowrate at 1 L  
146 min<sup>-1</sup>.

## 147 2.3 Upstream tank setup

148 A 560-liter upstream tank (dimensions 1.00 x 0.8 x 0.7 m<sup>3</sup>) housed 10 Pinfish (*Lagodon*  
149 *rhomboides*) used to generate the brackish aquaculture wastewater (**Fig. 2**). A filtration system

150 consisted of a canister filter with ultraviolet sterilizer lamp (55.9 cm h x 35.6 cm d, Red Sea  
151 brand) and a 3.8 L bioreactor (NextReef, MR1 XL) with polypropylene plastic fill (2.54 cm Bio  
152 Barrels, Pentair) and filtration pump (Maxi-jet Pro Powerhead, Pentair). The brackish  
153 aquaculture wastewater was fed manually once a week for one month prior to starting the  
154 experiment and then every six days after start for two months to both systems. Average inflow  
155 parameters such as temperature, salinity, DO, and nutrient concentration are shown in **Table 1**.

#### 156 *2.4 Water sampling and chemical analysis*

157 Water samples were collected in 250 mL autoclaved polypropylene sampling bottles  
158 (ThermoScientific Nalgene) from the outflow pipe of mesocosms (**Fig. 1**) and stored at -20°C  
159 until analysis. The hydraulic loading rate of the vertical-flow systems were set to be 3.03 L day<sup>-1</sup>  
160 (48.4 cm day<sup>-1</sup>), manually fed to the system from the upstream tank, which allowed for a  
161 complete flow-through of three days to the outflow pipe. The hydraulic loading rate (HLR) was  
162 determined according to Mitsch and Gosselink (2015) using the following equation,  $q = 100Q /$   
163  $A$ , where  $q =$  (HLR), (cm day<sup>-1</sup>),  $Q =$  inflow rate, m<sup>3</sup> day<sup>-1</sup>, and  $A =$  wetland surface area, (m<sup>2</sup>).  
164 Water quality parameters such as water temperature, pH, salinity, and dissolved oxygen (DO)  
165 were measured in the FTW mesocosms using a YSI Pro Plus meter. Turbidity was determined  
166 using a Trilogy fluorometer with a turbidity module (Turner Design). Ammonia concentration  
167 was colorimetrically conducted using a Spectronic Genesys 20 spectrophotometer (Thermo  
168 Scientific) using a standard sodium salicylate method. Nutrients in water samples were  
169 colorimetrically determined using a SmartChem Autoanalyzer to measure nitrate-nitrite nitrogen  
170 and Total Kjeldahl nitrogen (TKN) according to EPA guidelines 353.1 and 351.2 respectively  
171 (USEPA, 1993b, a). Total nitrogen was determined from the combined TKN and nitrate-nitrite



172 concentrations. Total phosphorus (TP) concentration was determined according to the EPA  
173 guideline 365.1 (USEPA, 1993c).

#### 174 *2.5 Plant tissue samples*

175 Aboveground plant tissue samples (9 cm<sup>2</sup>) were randomly collected from all mesocosms  
176 at the start and end of the experiment. Changes in plant stem height were measured for an  
177 estimate of daily growth rate over each system period.

#### 178 *2.6 Microscopy*

179 Water samples were collected from the outflow pipes of each mesocosm and fixed with  
180 formalin (2% final concentration [vol/vol]). Cells were stained with 4', 6-diamidino-2-  
181 phenylindole (DAPI), then part of the fixed water samples (0.8 mL) were filtered onto black  
182 0.22- $\mu$ m polycarbonate isopore membrane filters (GTBP, MilliporeSigma) with a standard hand  
183 vacuum pump operation. An anti-bleaching agent was used as the mounting medium (AF1;  
184 Citifluor). Cells were observed under 600x magnification using an Olympus BX51  
185 epifluorescence microscope system. For each filter, more than 10 random fields were viewed to  
186 determine cell numbers.

#### 187 *2.7 Sample collection for microbial analysis*

188 Biodegradable plastics were collected in clean 50 mL plastic centrifuge tubes from those  
189 embedded in the VFTW mesocosms and bioreactors on the FTW mesocosms. Root samples were  
190 collected using sterilized scissors and stored in 50 mL centrifuge tubes, consisting of a mixture  
191 of 0 - 15 cm depth segments from two distinct locations within each mesocosm. Soil samples  
192 were collected from two distinct locations in each vertical-flow mesocosm at a depth of 5 cm.  
193 The collected soil samples were vortexed for homogenization after initial collection. Water

194 samples (250 mL) collected from all FTW mesocosms were filtered using 0.2  $\mu\text{m}$  cellulose  
195 nitrate membrane filters (47 mm diameter, Fischer Scientific Nalgene Analytical Test Filter) for  
196 further DNA extraction. All samples were stored at  $-20^{\circ}\text{C}$  for DNA extraction.

### 197 *2.8 High throughput sequencing*

198 DNA samples were extracted from biofilm on PCL beads, root, soil, and water filter  
199 using the MagAttract PowerSoil DNA KF kit (Qiagen) according to the manufacturer's  
200 instructions. Extracted DNA was eluted into 100  $\mu\text{L}$  EB solution. Archaeal and bacterial 16S  
201 rRNA genes were amplified using the primer set, 515yF (5'GTGYCAGCMGCCGCGGTAA)  
202 and 926pfR (5'CCGYCAATTYMTTTRAGTTT) (Parada et al., 2016) tagged with the Illumina  
203 i5 forward (TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG) and i7 reverse  
204 (GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG) sequencing primer. Each PCR  
205 reaction contained 25  $\mu\text{L}$  reactions with Qiagen HotStar Taq master mix, equal amount of  
206 forward and reverse primers (5  $\mu\text{M}$  each), and 1  $\mu\text{L}$  of DNA template (1 to 20 ng). Thermal  
207 cycling consisted of an initial denaturation at  $95^{\circ}\text{C}$  for 5 min, followed by 35 cycles of  $94^{\circ}\text{C}$  for  
208 30 sec, annealing at  $54^{\circ}\text{C}$  for 40 sec, and extension at  $72^{\circ}\text{C}$  for 1 min, with a final extension of  
209 10 min at  $72^{\circ}\text{C}$ . PCR product from the first stage was then transferred to a second PCR based on  
210 qualitatively determined concentrations with primers for the second PCR based on the Illumina  
211 Nextera PCR primers forward (AATGATACGGCGACCACCGAGATCTACAC-[i5 index]-  
212 TCGTCGGCAGCGTC) and reverse (CAAGCAGAAGACGGCATAACGAGAT-[i7 index]-  
213 GTCTCGTGGGCTCGG). The second stage amplification was run with the same as the first  
214 except for 10 cycles instead of 35 cycles. Amplicons were visualized with eGels (Life  
215 Technologies), products were pooled equimolar with each size selected quantified using the

216 Quibit 2.0 fluorometer (Life Technologies). Amplicons were then loaded on an Illumina MiSeq  
217 (Illumina) 2 x 300 flow cell at 10 pM (RTL Genomics).

218 For analysis, FASTQ formatted files were merged using the PEAR Illumina paired-end  
219 read merger (Zhang et al., 2013a). Prefix dereplication was completed using the algorithm of  
220 USEARCH (Edgar et al., 2011). Clustering at a 3% divergence level was conducted using the  
221 USEARCH (Edgar et al., 2011). Operational taxonomic unit (OTU) selection was performed  
222 using UPARSE-OTU algorithm (Edgar, 2013). Chimera checking was completed using  
223 UCHIME (Edgar, 2010) and detected chimera sequences were removed. Representative OTUs  
224 were used to determine taxonomic information through a basic local alignment search tool  
225 (BLAST) at National Center for Biotechnology Information (NCBI), and MG-RAST (Meyer et  
226 al., 2008). The high-throughput sequence datasets were deposited in GenBank under BioProject  
227 number PRJNA496041.

## 228 *2.9 Data analysis*

229 The significant differences were determined when  $p < 0.05$ . Tukey-Kramer method was  
230 employed in conjunction with a one-way analysis of variance (ANOVA) using JMP data analysis  
231 software (SAS Institute) according to Lehman (2005) for testing statistical differences among  
232 multiple mesocosm settings. Student's t-test was also implemented to determine if two sets of  
233 data were significantly different from each other. All statistics (one-way ANOVA, Tukey-  
234 Kramer, and Student's t-test) were completed using two-tailed and unpaired data analyses. Data  
235 were presented by mean  $\pm$  standard deviation unless otherwise noted. General statistics of high-  
236 throughput sequence data were performed using MG-RAST (Meyer et al., 2008). Diversity index  
237 calculations (Shannon index, Menhinick's richness and Pielou's evenness indices) were  
238 implemented using Microsoft Excel.

239

## 240 **3. RESULTS AND DISCUSSION**

### 241 *3.1 Physical parameters*

242 Average rainfall over the experimental period was  $7.6 \pm 0.9$  mm day<sup>-1</sup> measured using  
243 the real-time hydrologic, water quality monitoring, and meteorological field station at the  
244 Everglades Wetland Research Park (Zhang et al., 2017a), which was less than the calculated  
245 HLR  $48.4$  cm day<sup>-1</sup>, with an average rain gauge depth of  $1.2 \pm 1.3$  cm. Physical parameters were  
246 measured for FTW mesocosms with an average water temperature of  $29.9^{\circ}\text{C}$ , salinity of  $5.1$  ppt,  
247 pH of  $7.95$ , and DO of  $3.2$  mg L<sup>-1</sup>. Turbidity (NTU, nephelometric turbidity unit) was high in the  
248 VFTW mesocosms ( $23.5 \pm 3.0$  NTU and  $47.0 \pm 7.3$  NTU with and without biodegradable plastic,  
249 respectively) and low in the FTW mesocosms ( $1.71 \pm 0.1$  NTU and  $2.26 \pm 0.2$  NTU) due to the  
250 impact of soil.

### 251 *3.2 Effect of biodegradable plastics for nutrient removal*

252 Total nitrogen retention was significantly different ( $p < 0.001$ ,  $n = 8$ , one-way ANOVA)  
253 and higher in the vertical-flow system (**Table 2**). TN retention performance in our vertical-flow  
254 system (86.9-90%) was consistent with other saline aquaculture effluent treatment wetland  
255 systems with a mean removal efficiency of 98% TN (Brown et al., 1999), and 98.2% TDIN  
256 (Webb et al., 2012) (**Table 3**). On the contrary, TN retention was not observed in FTW  
257 mesocosms over the experimental period as outflow concentrations exceeded the inflow  
258 concentration of effluent (**Table 2**), leading to a negative retention rate, consistent with a  
259 previous aquaculture wastewater treatment study showing outflow concentration of TKN  
260 exceeded feed water TKN (Lin et al., 2010). However, the presence of PCL significantly

261 increased the TN retention, even though a negative retention occurred in this system, a greater  
262 negative TN retention was observed without the use of PCL beads in our control condition ( $p <$   
263  $0.0001$ , Tukey-Kramer pairwise). This finding was not identified in the VFTW system (**Table 2**).  
264 A comparison study in China found that floating treatment systems had a lower TN removal  
265 efficiency compared with vertical-flow systems (Zhang et al., 2015). Newly constructed or  
266 newly restored wetlands are found to have a low C:N ratio, therefore the addition of an external  
267 carbon can enhance denitrification in these wetland systems (Bachand and Horne, 1999), as  
268 evidenced in the FTW system in our study. Overall, these lines of evidence indicate the strict  
269 carbon limitation in the FTW than the other treatment wetland systems (Zhang et al., 2015).

270 Inflow TN was composed of over 98% inorganic nitrogen, mainly in the form of nitrate  
271 and nitrite (**Table 1**). In the VFTW system nitrate plus nitrite ratio decreased to be 17.6% in the  
272 control and 16.2% with embedded PCL, along with a decrease of the TN:TP ratio from 8.9 to 4.7  
273 and 4.5 respectively, indicating microbial nitrogen removal processes (i.e. denitrification or  
274 DNRA [dissimilatory nitrate reduction to ammonium]) (**Fig. 3a**). Our ammonia measurements  
275 showed the depletion of ammonia from 9.2% in inflow to 7.1% in the control and 5.7% with  
276 embedded PCL, with an increase in organic nitrogen to 75.3% and 78.2%, respectively. Based on  
277 these findings we concluded that denitrification, not DNRA, was the major process in the  
278 removal of nitrate plus nitrite pool in the VFTW. In the FTW system nitrate plus nitrite ratio  
279 decreased from 94.2% to be 40.5% in the FTW control and 10.7% in FTW with PCL condition,  
280 with an increased removal efficiency with presence of PCL (**Fig. 3a**). Additionally, we found a  
281 decrease of ammonia in outflow water from 5.8% to 3.2% in control and 4.3% with PCL  
282 conditions. Organic nitrogen increased to 56.3% in control and 85.0% in FTW mesocosms with  
283 embedded PCL, a greater proportion of organic nitrogen with presence of PCL. Aquaculture

284 effluent contains low organic nitrogen and phosphorus in the water column with 7-32% of  
285 nitrogen found in suspended solids (Turcios and Papenbrock, 2014). As previously discussed,  
286 TN retention was not observed in FTW mesocosms due to the production of organic nitrogen  
287 from the system not present in inflow waters leading to the negative retention of TN as  
288 production of nitrogen occurred. However, there was a decrease in inorganic nitrogen  
289 concentrations with greater decreases observed with the presence of PCL, suggesting the use of  
290 PCL as a carbon source for denitrification (**Fig. 3a**). In contrast with the VFTW system, the  
291 TN:TP ratio in outflow water increased from 13.2 to 27 in control and 17 with PCL medium  
292 supporting our finding of greater nitrogen concentration found without presence of PCL in the  
293 FTW system (**Fig. 3b**). The accumulation of organic nitrogen within the FTW system was  
294 attributed to the release of organic nitrogen from plant pot soil within the floating mats which  
295 was supported by the anomaly of water column microbial community dominated by soil bacteria,  
296 which will be discussed further in later sections. The production of organic nitrogen in wetlands  
297 can also partially be attributed to nitrogen-fixing bacteria which fix N<sub>2</sub> from the atmosphere  
298 leading to production of organic nitrogen reducing the overall nitrogen removal efficiency  
299 (Mitsch and Gosselink, 2015; Zhang et al., 2017b).

300 TP retention was significantly higher in the VFTW system than for the FTW system ( $p <$   
301  $0.0032$ ,  $t$ -test), however, no significance was found with the presence of PCL in both mesocosm  
302 systems (**Table 2**). The TP retention in the VFTW mesocosms had a mean retention of 74 -  
303 81.1%, which was lower than similar studies, 99% (Brown et al., 1999) and 88% (Lymbery et  
304 al., 2006) (**Table 3**). Zhang et al. (2015) found TP removal efficiency ranged from 26-70% and  
305 was more variable than nitrogen in constructed wetland systems. The mean TP retention in the

306 FTW system was 17.4-39.5%, consistent with findings by Lin et al. (2010) with 2-18% removal  
307 and Pavlineri et al. (2017) of 18.2% removal efficiency, with an increase over time (**Table 3**).

### 308 *3.3 Growth of Spartina in vertical-flow and floating treatment systems*

309 Change in plant height ranged from 1.7 to 17.3 mm day<sup>-1</sup> with the highest growth rate  
310 occurring in the FTW mesocosms with PCL medium (**Fig. 4**). Even though there seemed to be an  
311 increased growth rate associated with use of PCL medium in the FTW system, the range of  
312 measurements overlapped when looking at mean growth rate. Due to a low number of replicates  
313 in this study ( $n = 2$ ), no statistical comparison was made.

### 314 *3.4 Bacterial abundance*

315 Total bacterial abundance of wetland water columns generally range from 10<sup>5</sup> to 10<sup>6</sup> cells  
316 mL<sup>-1</sup> (Urakawa and Bernhard, 2017), which was similar with our findings. No significant  
317 differences were found in the outflow bacterial abundance with the following distribution;  
318 VFTW control ( $3.7 \times 10^6 \pm 1.8 \times 10^6$  cells mL<sup>-1</sup>), VFTW with embedded PCL ( $3.5 \times 10^6 \pm 1.7 \times$   
319  $10^6$  cells mL<sup>-1</sup>), FTW control ( $1.0 \times 10^6 \pm 6.3 \times 10^5$  cells mL<sup>-1</sup>), and FTW with PCL medium ( $3.2$   
320  $\times 10^6 \pm 2.2 \times 10^6$  cells mL<sup>-1</sup>).

### 321 *3.5 High-throughput sequencing of 16S rRNA gene*

#### 322 *3.5.1 Taxonomic overview of dominant phyla*

323 A total of 86,547 sequences were analyzed and resulted in 2346 operational taxonomic  
324 units (OTUs) (**Table 4**). Shannon index indicated significant differences between sample means  
325 ( $p = 0.02$ , one-way ANOVA) with the lowest diversity in water samples and the highest diversity  
326 in root samples. There were significant differences found between VFTW root and FTW water  
327 samples ( $p = 0.03$ , Tukey-pairwise). The highest diversity found in soil samples was consistent

328 with previous reports (Urakawa and Bernhard, 2017). The taxonomic analysis identified 29 phyla  
329 from all samples: 12-21 collected from PCL plastic biofilm, 15-24 in root samples, 17-20 in soil  
330 samples, and 8-11 in water samples. No statistical difference was found in PCL biofilm samples  
331 ( $p = 0.06$ ,  $t$ -test) and soil samples ( $p = 0.5$ ,  $t$ -test). Root samples were significantly different ( $p =$   
332  $0.03$ ,  $n = 2$ , one-way ANOVA) between VFTW control and FTW with PCL ( $p = 0.03$ , Tukey-  
333 pairwise). Water samples in floating treatment system conditions having PCL bioreactor medium  
334 were significantly lower than the control samples ( $p = 0.0002$ ,  $t$ -test).

335 The three predominant phylum present in all samples were *Proteobacteria* (2-44%),  
336 *Cyanobacteria* (0.04-51%) and *Bacteroidetes* (0.02-30%) (**Fig. 5**). These results were consistent  
337 with previous studies of wetland microbial communities (Bai et al., 2014; Liu et al., 2016;  
338 Urakawa and Bernhard, 2017). Members of *Proteobacteria* are important in wetlands because of  
339 their strong involvement in biogeochemical cycling (Liu et al., 2016) and they dominated in a  
340 majority of samples except for water column samples from FTW. The two most abundant phyla  
341 in the water column samples were *Firmicutes* (59-90%) and *Actinobacteria* (6-17%) (**Fig. 5**).  
342 Unexpectedly, the most dominant member of *Firmicutes* was identified as *Bacillus* (57-88%),  
343 this trend agreed between four samples assuring good reproducibility of the method used. We  
344 attributed this finding to the presence of soil within plant pots (**Fig. 2**). *Bacillus* is recognized as  
345 a representative degrader of biodegradable plastics. For example, *Bacillus pumilus*, isolated from  
346 a freshwater pond and river were shown to degrade poly (ε-caprolactone) hydrolytically (Tezuka  
347 et al., 2004). However, presence of *Bacillus* was found regardless of PCL medium indicating that  
348 *Bacillus* was not directly enriched by the biodegradable plastics (**Table 5**).

349 Soil microbial communities in VFTW were dominated by *Proteobacteria* (40-85%),  
350 *Cyanobacteria* (5-40%), *Bacteroidetes* (2-10%), and *Planctomycetes* (2-7%) (**Fig. 5**). The soil



351 was covered with approximately 5-10 cm of water layer (**Fig. 2**). *Cyanobacteria* is a typical  
352 phylum found in freshwater sediment and water column communities (Paerl, 2014; Urakawa and  
353 Bernhard, 2017; Paerl, 2018). Thus, the observed microbial community might resemble a typical  
354 freshwater sediment community rather than a typical soil community (Zhang et al., 2013b). A  
355 steep oxic-anoxic gradient contributes to maintain high microbial diversity and functionally  
356 diverse organisms (Urakawa et al., 2017). Our results supported this finding by having the  
357 highest diversity found in soil samples of our wetland.

### 358 3.5.2 Comparison of rhizosphere communities in soil and water

359 In wetland plants, the rhizosphere acts as an interface between the surface of roots and  
360 the surrounding soil, which transports oxygen and other minerals to the roots which results in  
361 unique microbial communities distinct from surrounding soil and water column in a case of  
362 floating macrophytes (Mitsch and Gosselink, 2015; Urakawa et al., 2017).

363 The nitrogen cycle plays an important role in wetland plant metabolisms through the  
364 transformation of nitrogen species (i.e. ammonia and nitrate). *Mesorhizobium* and *Rhizobium* are  
365 essential diazotrophs and plant growth-promoting rhizosphere bacteria found in wetland systems  
366 (Zhang et al., 2013b; Urakawa et al., 2017). *Mesorhizobium* was identified in root, soil, water,  
367 and PCL biofilm samples while *Rhizobium* was identified only in vertical-flow root samples  
368 (**Table 5**). Nitrogen-fixing bacteria were more abundant in the VFTW than FTW mesocosms.  
369 The only nitrifying bacterium identified was *Nitrospira*, in root, soil, and VFTW PCL biofilm  
370 samples.

371 Methanogenesis is an important process in wetlands through which methane is naturally  
372 produced by methanogens and methane oxidation occurs from methanotrophic bacteria to

373 convert methane to carbon dioxide (Mitsch and Gosselink, 2015). Archaea are important  
374 methanogens in wetland sediments contributing to methane production (Madigan et al., 2012;  
375 Urakawa and Bernhard, 2017), three genera of methanogenic archaea found were  
376 *Methanobacterium*, *Methanoregula*, and *Methanosarcina*. Six methanotrophic genera were also  
377 found, *Methylocystis*, *Methylobacter*, *Methylococcus*, *Methylosoma*, *Methylocella* and  
378 *Hyphomicrobium*. These methanogens and methanotrophs were more abundant in the VFTW  
379 than in the FTW mesocosms (**Table 5**). *Hyphomicrobium* belonging to *Alphaproteobacteria* and  
380 *Methylibium* belonging to *Betaproteobacteria* were the two most abundant facultative  
381 methylotrophic genera and widely distributed in our constructed wetland systems, which  
382 supported a previous wetland study (Zhang et al., 2013b). *Methylocella* was the most widespread  
383 methanotroph found in this study. Coexistence of methanogens and methane oxidizers suggests  
384 the existence of the methane cycle and the skewed relative abundance of these microorganisms  
385 indicated more imperative role of this process in the vertical-flow system than in the floating  
386 wetland system.

387 Sulfate-reducing bacteria (SRB) were the predominant sulfur cycling microorganisms  
388 found in root samples and PCL biofilm. Although SRB were found in both systems, the vertical-  
389 flow system contained a greater diversity of organisms (i.e. *Desulfobulbus*, *Desulfatitalea*,  
390 *Desulfobacterium*, *Desulfonema*, *Desulfocapsa*, *Desulfopila*, *Desulfomicrobium*, and  
391 *Desulfovibrio*) than were found in the floating treatment system (i.e. *Desulfovibrio* and  
392 *Desulfobulbus*) (**Table 5**). The floating treatment system contained very minor amount of SRB in  
393 contrast to Urakawa et al (2017) which found a very rich SRB community in floating treatment  
394 rhizosphere. SRB communities in rhizosphere and soil in a *Phragmites australis* planted wetland

395 (Zhang et al., 2013b) and wetland soils (Faulwetter et al., 2009; Wang et al., 2012) were very  
396 diverse and consistent with our findings.

### 397 *3.5.3 Denitrification in vertical-flow and floating treatment systems*

398 Denitrification is the main nitrogen removal process in treatment wetland systems as  
399 discussed previously and paired with nitrification, a process in which nitrate is produced from  
400 ammonium, can fully remove nitrogen microbially from wastewater systems (Faulwetter et al.,  
401 2009). Predominant denitrifiers found in our study were *Bacillus* in water column samples,  
402 *Nitratireductor*, a marine denitrifier (Labbè et al., 2004) represented in all samples in minor  
403 amount, and *Pseudomonas* (0.2%) in soil samples with embedded biodegradable plastics (**Table**  
404 **5**). *Pseudomonas* has been found to degrade plastic particles in an urban river environment  
405 (McCormick et al., 2014), soil environments (Emadian et al., 2017), and the deep-sea (Sekiguchi  
406 et al., 2011). The presence of *Pseudomonas* only in soil samples with PCL may indicate the  
407 possibility of PCL use as a substratum or degradability, as indicated by similar findings of  
408 *Pseudomonas* on plastic pot biofilm from a floating treatment wetland (Urakawa et al., 2017).  
409 These findings support our observation of increased denitrification activity in the VFTW and  
410 FTW construction with the presence of PCL.

### 411 *3.5.4 PCL degradation in a vertical-flow and floating treatment constructed wetland*

412 The most abundant genera found in PCL biofilm samples collected from VFTW sediment  
413 were identified as *Oscillatoria* (7%) and *Leptolyngbya* (6%) and from FTW bioreactors were  
414 *Brasilonema* (8%) and *Trichormus* (9%) belonging to the phylum *Cyanobacteria* (**Table 5**).  
415 Additionally, *Leptolyngbya* was identified in VFTW sediment with embedded PCL. The  
416 localization of *Cyanobacteria* in VFTW plastics was attributed to a partial exposure of plastics to

417 the surface (**Fig. 2**). We identified many *Cyanobacteria* within our study in presence of PCL  
418 plastic, consistent with previous marine plastic debris research (Bryant et al., 2016; Debroas et  
419 al., 2017; Quero and Luna, 2017). *Cyanobacteria* were identified as the key species in the  
420 microbial network which is formed on the surface of plastics (Debroas et al., 2017). However,  
421 none of these studies confirmed if *Cyanobacteria* are actively involved in the biodegradation of  
422 the plastics (Debroas et al., 2017; Quero and Luna, 2017). Bryant et al. (2016) and Debroas et al.  
423 (2017) identified *Leptolyngbya* on the surface of plastics collected from the surface water of the  
424 North Atlantic. It should be noted that *Cyanobacteria* are able to synthesize  
425 polyhydroxybutyrate, an intracellular storage compound and bioplastic, under photoautotrophic  
426 or chemoheterotrophic conditions (Balaji et al., 2013; Singh et al., 2017). Additionally, several  
427 genera can synthesize polyhydroxyalkanoate (PHA) and contain PHA biosynthesis genes (e.g.  
428 *Oscillatoria limosa*, *Anabaena cylindrica*, *Synechococcus* spp.), these findings can lead to the  
429 speculation they are also able to degrade these bioplastic storage compounds for intracellular use.

### 430 *3.6 Economic impact of plastic-embedded constructed wetlands*

431 As previously discussed, constructed wetlands are beneficial in terms of nutrient  
432 retention. Our approach will potentially enhance the performance of nutrient retention processes  
433 and increase the value of constructed wetlands. We used 1 kg m<sup>-2</sup> of PCL within the VFTW  
434 system. If we assume to construct a 1 ha vertical-flow wetland embedded with PCL  
435 biodegradable plastics, it would cost approximately \$56,500 only considering the price of  
436 plastics. Boley et al. (2000) estimated the consumption of plastic substrate per kg N-NO<sub>3</sub><sup>-</sup> and  
437 cost of denitrification per kg N-NO<sub>3</sub><sup>-</sup> in a study of an aquaculture bioreactor system with an  
438 approximate 0.64 kg of N-NO<sub>3</sub><sup>-</sup> removal by PCL per kg. A study by Batson et al. (2012)  
439 estimated the nitrogen removal from a constructed riparian wetland as 0.0164 kg m<sup>-2</sup> yr<sup>-1</sup>.

440 Therefore, if we assume all embedded PCL is used for denitrification, the constructed wetland  
441 has at least a 39 times performance increase than regular constructed wetlands to remove  
442 nitrogen, suggesting a great potential for use in cityscape and other high-priced areas. In the  
443 future, we anticipate that the use of biodegradable plastics will increase due to the current plastic  
444 pollution problems. A part of used biodegradable plastics can be embedded in soil and used as a  
445 carbon source by wetland microbes. In this scenario, the cost of used biodegradable plastics can  
446 be negligible. Our study showed the potential use of this system however, much longer-term  
447 monitoring and more expanded field experiments are required in the future applications.

448

#### 449 **4. CONCLUSIONS**

450 Wetlands play a vital role in water purification and nutrient cycling which can be utilized  
451 to treat agricultural runoff and aquaculture discharges in a sustainable fashion (Headley and  
452 Tanner, 2011; Mitsch and Gosselink, 2015). Comparison of wetland construction performance in  
453 this study between a vertical-flow treatment wetland and a floating treatment wetland showed  
454 there was an increased nutrient retention for both TN and TP with a vertical-flow system. The  
455 use of a biodegradable plastic, PCL, was utilized as a novel approach in this study as an external  
456 carbon source to enhance microbial activity. PCL was shown to increase the TN nutrient  
457 retention in the FTW system, however, this system exhibited a negative retention during our  
458 study period due to the release of organic nitrogen from soil in plant pots, which was inferred  
459 from the dominance of *Firmicutes* (59-90%) (e.g. *Bacillus*) in the water column of FTW.  
460 Presence of PCL in the FTW system allowed for a greater production of organic nitrogen and a  
461 greater removal of inorganic nitrogen, suggesting PCL enhanced nitrogen cycling within this  
462 system. Microbial community composition was shown to be altered with the presence of PCL,

463 community selection for cyanobacterial genera and other bioplastic-degrading microorganisms  
464 was found from high-throughput sequencing analysis. Further long-term studies are needed at  
465 this point to have a greater understanding of microbial plastic degradation and associated nutrient  
466 cycling in constructed wetland systems. A general cost analysis of utilizing a biodegradable  
467 plastic for enhanced microbial activity and nutrient removal was conducted, it was seen that the  
468 upfront cost is high, however, compared to the potential N-NO<sub>3</sub><sup>-</sup> removal efficiency in the system  
469 this cost is negligible over time. We believe that the potential for use of a biodegradable plastic  
470 to enhance nutrient removal within a constructed wetland can be a promising approach in  
471 wetland engineering for increased nutrient cycling efficiency.

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693

694 **Figure Legends**

695

696 **Fig. 1. Design of two wetland systems** **a)** Overview of experimental setup **b)** schematic of  
697 vertical-flow treatment wetland (VFTW) mesocosm and **c)** schematic for floating  
698 treatment wetland (FTW) mesocosm. **b)** and **c)** schematic denoting length (1.33 m) x  
699 width (0.47 m) x height (0.61 m) with different design depth and width of mesocosms  
700 with PCL, polycaprolactone, identical design was used for controls without PCL aspect.

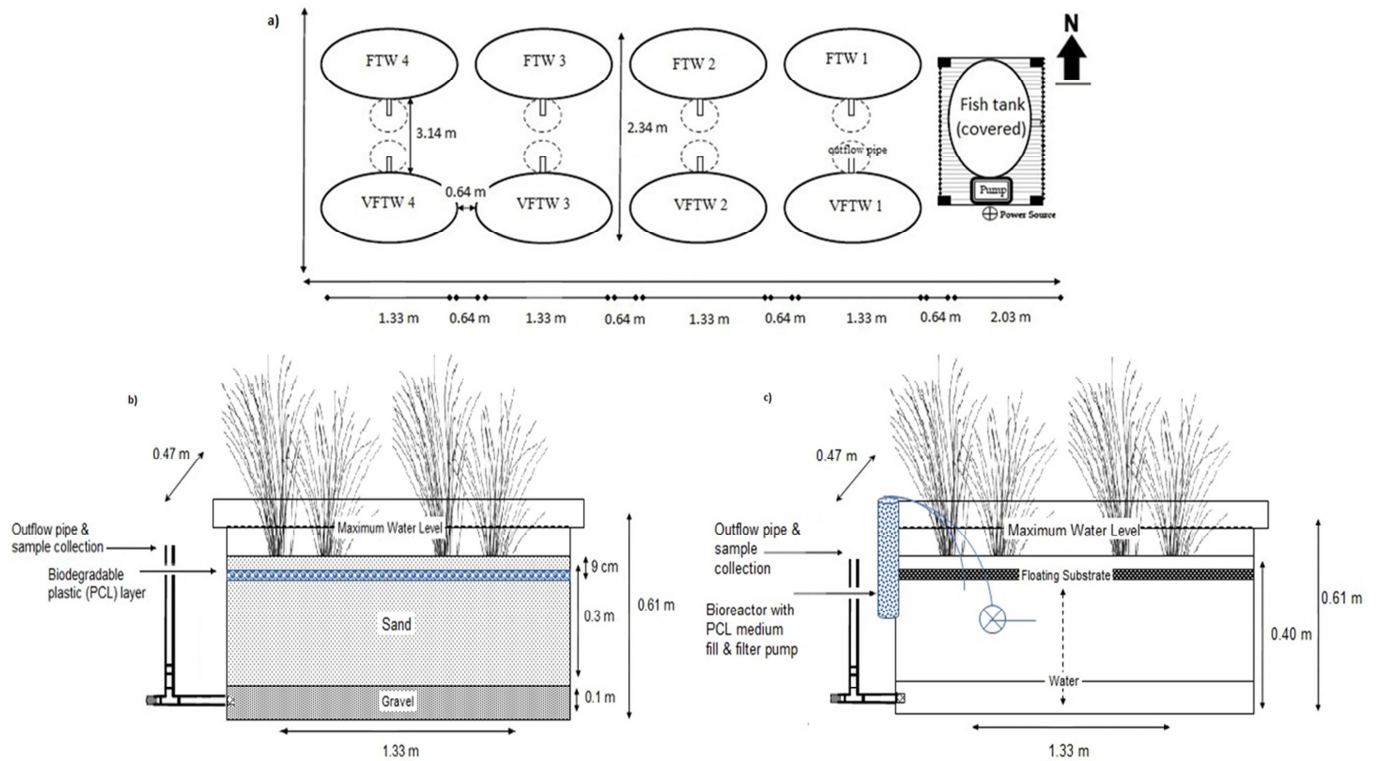
701 **Fig. 2. Mesocosms used in this study.** **a)** Overview of VFTW mesocosms in setup, **b)** *Spartina*  
702 *patens* location within mesocosm relative to edge of tub, **c)** VFTW mesocosm containing  
703 PCL plastic beads which had the ability to float when flooded, **d)** overview of FTW  
704 mesocosm with bioreactor setup (rear row), **e)** FTW mesocosm containing PCL plastic as  
705 reactor medium, **f)** configuration of floating mat with 18 planting holes, **g)** view of  
706 aerator pot and plant root, and **h)** overview setup of upstream aquaculture tank with  
707 double filtration system that housed Pinfish (*Lagodon rhomboides*).

708 **Fig. 3. Change in inflow and outflow nutrient concentrations.** **a)** percent composition of  
709 nitrogen in inflow and outflow and **b)** TN:TP ratio change over time, with (-) denoting  
710 control and (+) presence of PCL in construction. A solid horizontal line indicates mg-  
711 based Redfield ratio between N and P (8.9).

712 **Fig. 4. Change in stem height of *Spartina patens*.** Measured in mm day<sup>-1</sup> with the same naming  
713 scheme as previous. Data are shown as mean ± range (*n* = 2).

714 **Fig. 5. Relative bacterial and archaeal abundance at the phylum level.** Percent relative  
715 abundance distribution after normalization to 10,000 reads per sample. *Proteobacteria*

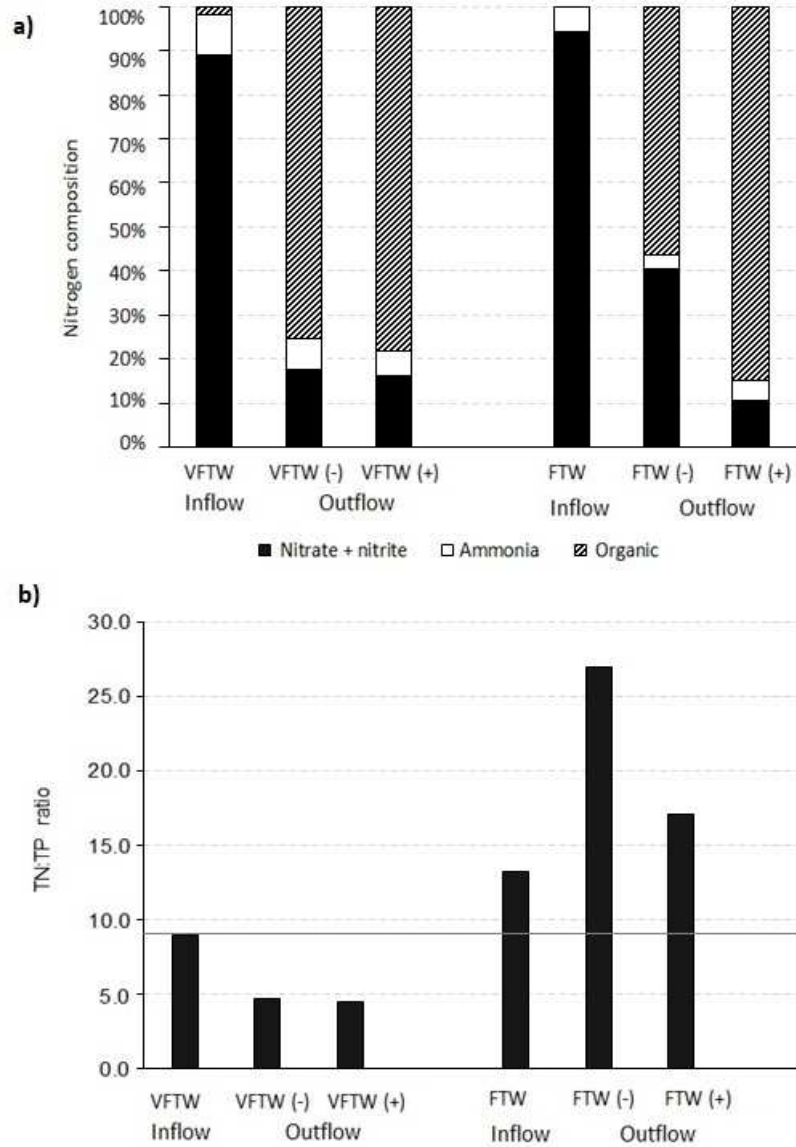
716 are shown at the class level. Sample naming uses 1 and 2 showing replication and (-) and  
717 (+) denoting presence of PCL.



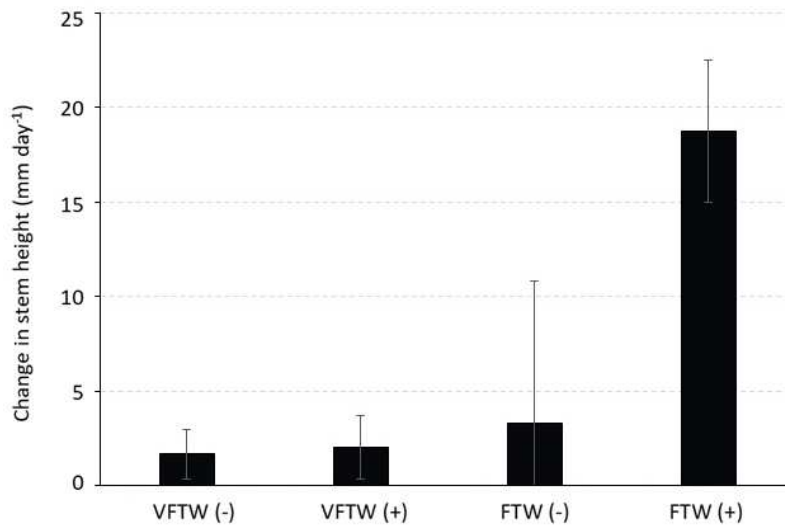
**Figure 1 Design of two wetland systems. a)** Overview of experimental setup **b)** schematic of vertical-flow treatment wetland (VFTW) mesocosm and **c)** schematic for floating treatment wetland (FTW) mesocosm. **b)** and **c)** schematic denoting length (1.33 m) x width (0.47 m) x height (0.61 m) with different design depth and width of mesocosms with PCL, polycaprolactone, identical design was used for controls without PCL aspect.



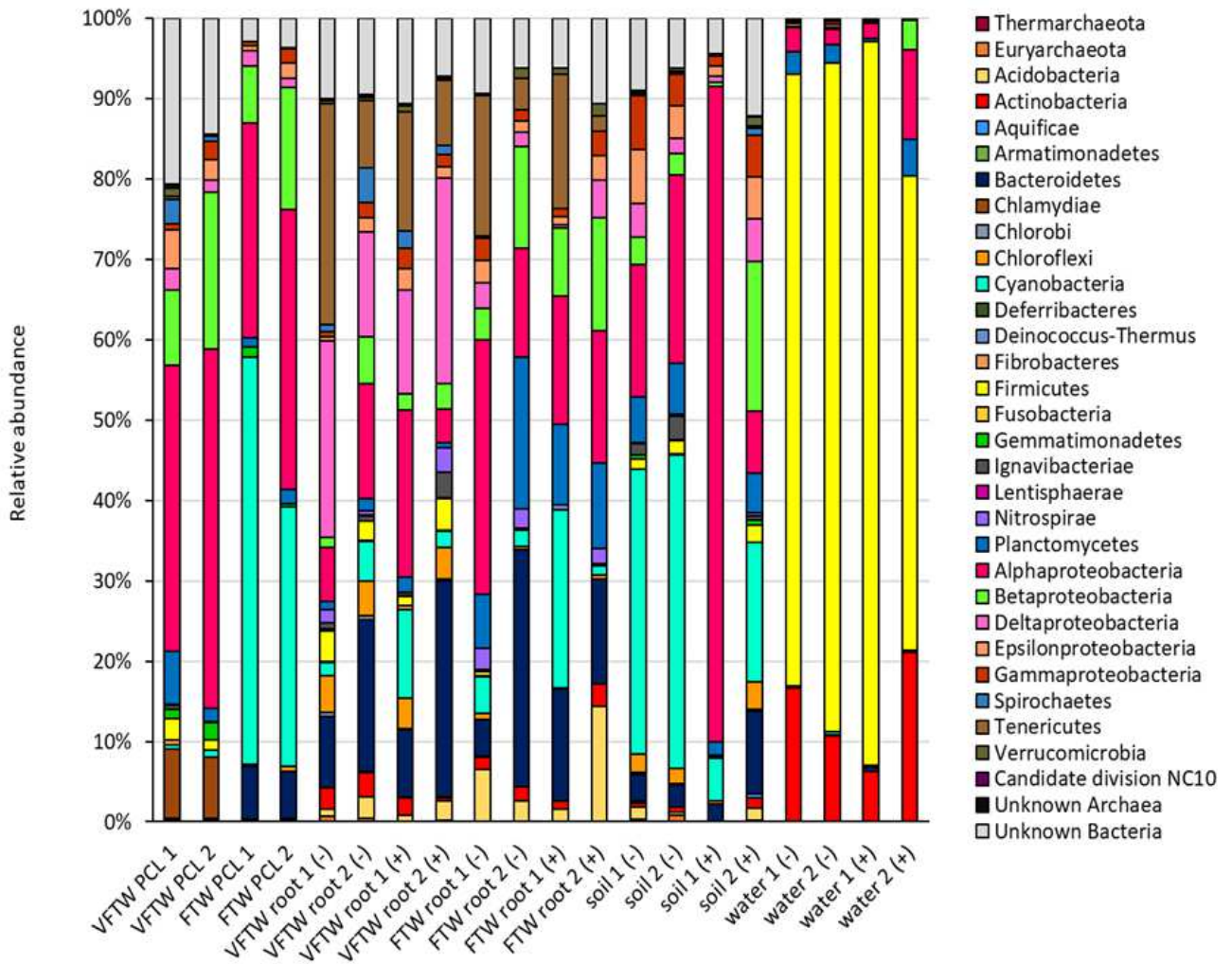
**Figure 2 Mesocosms used in this study.** **a)** Overview of VFTW mesocosms in setup, **b)** *Spartina patens* location within mesocosm relative to edge of tub, **c)** VFTW mesocosm containing PCL plastic beads which had the ability to float when flooded, **d)** overview of FTW mesocosm with bioreactor setup (rear row), **e)** FTW mesocosm containing PCL plastic as reactor medium, **f)** configuration of floating mat with 18 planting holes, **g)** view of aerator pot and plant root, and **h)** overview setup of upstream aquaculture tank with double filtration system that housed Pinfish (*Lagodon rhomboides*).



**Figure 3 Change in inflow and outflow nutrient concentrations.** a) percent composition of nitrogen in inflow and outflow and b) TN:TP ratio change over time, with (-) denoting control and (+) presence of PCL in construction. A solid horizontal line indicates mg-based Redfield ratio between N and P (8.9).



**Figure 4 Change in stem height of *Spartina patens*.** Measured in mm day<sup>-1</sup> over the month testing period with (-) denoting control and (+) presence of PCL in construction. Data are shown as mean  $\pm$  range ( $n = 2$ ).



**Figure 5 Relative bacterial and archaeal abundance at the phylum level.** Percent relative abundance distribution after normalization to 10,000 reads per sample. *Proteobacteria* are shown at the class level. Sample naming uses 1 and 2 showing replication and (-) and (+) denoting presence of PCL.



**Table 1 Inflow water quality parameters.**

Wetland type	NO <sub>3</sub> -NO <sub>2</sub> (mg L <sup>-1</sup> )	NH <sub>4</sub> <sup>+</sup> (mg L <sup>-1</sup> )	Organic N (mg L <sup>-1</sup> )	TN (mg L <sup>-1</sup> )	TP (mg L <sup>-1</sup> )	DO (mg L <sup>-1</sup> )	Salinity (ppt)	Temp (°C)
FTW	4.35 ± 0.82	0.27 ± 0.08	0.0 ± 0.0	4.62 ± 1.10	0.35 ± 0.20	7.04 ± 0.27	16.2 ± 0.84	29.8 ± 4.25
VFTW	15.8 ± 3.34	1.64 ± 0.31	0.31 ± 0.50	17.8 ± 0.31	1.99 ± 0.41	6.60 ± 0.16	16.6 ± 0.40	29.5 ± 1.05

Data are mean ± standard error of upstream tank effluent before loading to the FTW system ( $n = 4$ ) and the VFTW system ( $n = 4$ ) mesocosms.

**Table 2 Nutrient flux of two constructed wetland systems.**

Wetland	PCL	TN (mg m <sup>-2</sup> day <sup>-1</sup> )				TP (mg m <sup>-2</sup> day <sup>-1</sup> )			
		Inflow	Outflow	Removal efficiency	Reduction (%)	Inflow	Outflow	Removal efficiency	Reduction (%)
VFTW	(-)		8.63 ± 0.26	77.41 ± 0.45 <sup>a</sup>	90.0		1.82 ± 0.09	7.82 ± 0.11 <sup>a</sup>	81.1
	(+)	86.04 ± 0.19	11.29 ± 0.53	74.75 ± 0.72 <sup>b</sup>	86.9	9.64 ± 0.02	2.51 ± 0.19	7.13 ± 0.63 <sup>a</sup>	74.0
FTW	(-)		27.48 ± 0.59	(-5.09) ± 0.72 <sup>c</sup>	0		1.01 ± 0.06	0.66 ± 0.1 <sup>b</sup>	39.5
	(+)	22.39 ± 0.13	23.95 ± 0.65	(-1.56) ± 0.78 <sup>d</sup>	0	1.67 ± 0.04	1.38 ± 0.05	0.29 ± 0.09 <sup>b</sup>	17.4

\*Data are mean ± standard error ( $n = 8$ ) for all experimental conditions with percent retention quantified from  $((\text{inflow concentration} - \text{outflow concentration}) / (\text{inflow concentration})) \times 100$  (Olguín et al., 2017).

The letter next to the monthly retention denotes statistical significance from completing, one-way ANOVA for TN, and significance shown for TP retention,  $t$ -test.

**Table 3 Removal efficiency of various constructed wetlands for aquaculture effluent treatment.**

Study	Scale	Construction type	Plant species used	Removal efficiency (%)*	Salinity (ppt)	Temperature (°C)	Location
Brown et al., 1999	Mesocosm	Subsurface flow	<i>Suaeda eseroa</i> , <i>Salicornia bigelovii</i> , <i>Altriplex barclayana</i>	TN:98, TIN:94, TP:99	10	22.6 - 37.4	Tucson, AZ USA
Lymbery et al., 2006	Mesocosm	Horizontal subsurface flow	<i>Juncus kraussii</i>	TN:69, TP:88	6.6 - 24.8	N/A	Australia
Li et al., 2007	Pilot-scale	Vertical - flow	<i>Canna indica</i> , <i>Typha latifolia</i> , <i>Acorus calamus</i> , <i>Arave sisalana</i>	TN:54.6 TP:80.1	0	23.6 - 24.0	China
Zhang et al., 2010	Pilot-scale	Vertical - downflow vertical - upflow hybrid	<i>Canna indica</i> , <i>Typha latifolia</i> , <i>Acorus calamus</i>	TN:48, TP:17	N/A Freshwater	N/A	China
Webb et al., 2012	Pilot-scale	Subsurface flow	<i>Salicornia europaea</i>	TDIN:98.2, DIP:36 - 89	22	23.1	North Wales, UK
Lin et al., 2003	Pilot-scale	Free water surface – subsurface flow hybrid	<i>Phragmites australis</i>	TIN:68.2, PO4-P:5.4	N/A <i>Litopenaeus vannamei</i> culture	23.5	Taiwan
Lin et al., 2010	Pilot-scale	Floating macrophyte – subsurface flow hybrid	<i>Eichhornia crassipes</i> , <i>Pistia stratiotes</i> , <i>Typha angustifolia</i> , <i>Phragmites communis</i> , <i>Canna generalis</i> , <i>Cyperus alternifolius</i>	TN:0 - 18, TP:2 - 18	0	N/A	Taiwan
De Stefani et al., 2011	in-stream	Floating treatment wetland	<i>Chrysopogon zizanioides</i> , <i>Typha latifolia</i> , <i>Sparganium erectum</i>	TN:13 - 29, TP:65	N/A Freshwater	10.0 - 14.0	Italy
Li and Li, 2009	Pilot-scale	Floating treatment wetland	<i>Ipomenea aquatica</i>	TN:30.6, TP:18.2	N/A Freshwater	24.4	China
This study	Mesocosm	Vertical - flow	<i>Spartina patens</i>	TN: 86.9 - 90.7 TP: 74 - 81.1	7.4	28.8	FL, USA
	Mesocosm	Floating treatment wetland	<i>Spartina patens</i>	TN: 0 TP: 17.4 - 39.5	5.1	29.9	FL, USA

\*Removal efficiencies are denoted TN (total nitrogen), TIN (total inorganic nitrogen), TDIN (total dissolved inorganic nitrogen), TP (total phosphorous), DIP (dissolved inorganic phosphorous), and phosphate. Temperature is denoted as air temperature for subsurface flow and water temperature for floating treatment systems. N/A shows data not measured.

**Table 4 Summary of DNA sequencing and diversity indices.**

Samples	PCL presence	Sequences	OTU	Mean sequence length	Pielou evenness	Menhinick richness index	Shannon index
PCL Biofilm							
VFTW <sub>1</sub>		21,519	776	411 ± 19	0.42	2.53	2.32
VFTW <sub>2</sub>		13,069	504	412 ± 6	0.41	2.04	2.18
FTW <sub>1</sub>		13,118	211	411 ± 2	0.62	1.09	2.91
FTW <sub>2</sub>		13,496	278	412 ± 8	0.53	1.35	2.62
Root							
VFTW <sub>1</sub>	(-)	22,640	622	412 ± 8	0.39	2.5	2.14
VFTW <sub>2</sub>	(-)	23,988	871	411 ± 13	0.48	2.98	2.73
VFTW <sub>1</sub>	(+)	23,930	764	412 ± 6	0.48	2.53	2.14
VFTW <sub>2</sub>	(+)	11,796	525	411 ± 15	0.48	1.93	2.43
FTW <sub>1</sub>	(-)	27,026	472	411 ± 6	0.47	1.86	2.46
FTW <sub>2</sub>	(-)	19,676	316	411 ± 6	0.51	1.33	2.48
FTW <sub>1</sub>	(+)	15,924	194	411 ± 4	0.48	0.89	2.14
FTW <sub>2</sub>	(+)	17,078	355	411 ± 3	0.48	1.56	2.43
Soil							
VFTW <sub>1</sub>	(-)	18,851	646	412 ± 8	0.6	2.26	3.23
VFTW <sub>2</sub>	(-)	17,544	529	412 ± 8	0.6	2.15	3.24
VFTW <sub>1</sub>	(+)	20,381	208	411 ± 14	0.29	1.04	1.37
VFTW <sub>2</sub>	(+)	22,693	827	412 ± 8	0.55	2.57	3.07
Water							
FTW <sub>1</sub>	(-)	20,580	143	412 ± 5	0.29	0.75	1.24
FTW <sub>2</sub>	(-)	21,014	135	412 ± 4	0.22	0.76	0.95
FTW <sub>1</sub>	(+)	25,287	113	412 ± 4	0.17	0.64	0.69
FTW <sub>2</sub>	(+)	26,658	128	412 ± 3	0.35	0.71	1.5

Diversity indices were calculated after normalization to 10,000 reads per sample. Samples 1 and 2 denote replicates and (-) and (+) denotes presence of PCL in construction when applicable.

**Table 5 Functional groups at the genus level.**

		PCL biofilm		Roots				Soil		Water	
		VFTW	FTW	VFTW (+)	VFTW (-)	FTW (+)	FTW (-)	VFTW (+)	VFTW (-)	FTW (+)	FTW (-)
<b>Nitrogen - fixing bacteria</b>											
<i>Alphaproteobacteria</i>	<i>Nitrospirillum</i>	77	1	15	9	0	0	20	2	0	0
	<i>Rhizobium</i>	1	0	33	4	0	0	4	3	0	0
	<i>Bradyrhizobium</i>	0	0	11	5	4	0	0	0	1	0
	<i>Mesorhizobium</i>	83	15	7	9	20	6	12	13	2	4
	<i>Azospirillum</i>	9	0	5	0	0	0	8	0	0	0
<i>Betaproteobacteria</i>	<i>Azohydromonas</i>	18	2	8	1	4	11	15	51	0	0
	<i>Azonexus</i>	2	0	13	4	0	0	1	1	0	0
	<i>Derxia</i>	39	0	10	14	0	0	7	115	0	0
<i>Cyanobacteria</i>	<i>Anabaena</i>	12	0	0	0	0	0	6	0	0	0
	<i>Nostoc</i>	79	115	43	19	2	1	1063	92	0	2
	<i>Calothrix</i>	84	6	9	30	0	0	51	30	0	0
	<i>Cylindrospermum</i>	36	0	79	36	0	0	526	56	0	0
<b>Nitrifying bacteria</b>											
<i>Nitrospira</i>	<i>Nitrospira</i>	1	0	1	0	265	88	0	8	0	0
<i>Gammaproteobacteria</i>	<i>Nitrosococcus</i>	5	1	23	59	114	63	14	21	0	0
<b>Denitrifying bacteria</b>											
<i>Bacilli</i>	<i>Bacillus</i>	3	0	7	6	0	0	26	24	7589	7245
<i>Alphaproteobacteria</i>	<i>Nitrateductor</i>	3	1	24	16	4	1	51	7	0	0
<i>Gammaproteobacteria</i>	<i>Pseudomonas</i>	27	2	4	0	1	0	0	19	0	0
<b>Sulfate-reducing bacteria</b>											
<i>Deltaproteobacteria</i>	<i>Desulfobulbus</i>	25	1	29	140	0	2	1	22	0	0
	<i>Desulfatitalea</i>	302	0	0	76	0	0	0	0	0	0
	<i>Desulfobacterium</i>	0	0	0	19	0	0	0	0	0	0
	<i>Desulfonema</i>	28	0	5	11	0	0	0	0	0	0
	<i>Desulfocapsa</i>	24	0	59	69	0	0	4	3	0	0
	<i>Desulfopila</i>	1	0	11	9	0	0	2	0	0	0
	<i>Desulfomicrobium</i>	11	0	5	12	0	0	15	6	0	0
	<i>Desulfovibrio</i>	40	24	137	138	6	7	44	12	0	0
<b>Sulfur-oxidizing bacteria</b>											
<i>Chlorobia</i>	<i>Chlorobium</i>	9	0	13	8	0	0	4	2	0	0
<i>Betaproteobacteria</i>	<i>Thiobacillus</i>	74	4	15	11	73	99	17	40	1	1
	<i>Thiobacter</i>	2	0	5	1	0	0	0	1	0	0
<i>Gammaproteobacteria</i>	<i>Thiothrix</i>	0	2	0	0	1	32	0	0	0	0
<b>Methanogenic archaea</b>											
<i>Methanobacteria</i>	<i>Methanobacterium</i>	19	0	43	13	0	0	51	11	0	0
<i>Methanomicrobia</i>	<i>Methanoregula</i>	0	0	3	0	0	0	0	0	0	0
	<i>Methanosarcina</i>	1	0	2	0	0	0	2	0	0	0

**Methanotrophic bacteria**

<i>Alphaproteobacteria</i>	<i>Methylocystis</i>	0	0	7	0	0	0	0	0	0	0
	<i>Methylobacter</i>	0	0	0	0	0	2	0	0	0	0
	<i>Methylocella</i>	0	3	0	1	26	41	0	0	0	2
<i>Gamma</i> proteobacteria	<i>Methylococcus</i>	0	0	4	0	0	0	0	0	0	0
	<i>Methylosoma</i>	0	0	0	0	9	3	0	0	0	0

**Methylotrophic bacteria**

<i>Alphaproteobacteria</i>	<i>Methylobacterium</i>	0	0	1	1	5	8	0	0	0	0
	<i>Methylobacillus</i>	0	0	5	5	0	0	0	2	0	0
	<i>Hyphomicrobium</i>	4	3	16	6	89	80	14	8	8	9
<i>Beta</i> proteobacteria	<i>Methylophilus</i>	0	0	0	0	15	4	0	0	0	0
	<i>Methylibium</i>	200	5	13	53	7	4	171	550	0	0

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Shown are average bacterial and archaeal relative abundance of sample distribution ( $n = 2$ ) after normalization to 10,000 reads per sample. *Cyanobacteria* are shown at the phylum level as class level was unidentified.