Supporting information

Methods

Sediment Chemistry- To quantify soil moisture fraction (proportion of water in wet soil), a subsample (~5 g) was dried at 105 °C for 72 hours. We then estimated % organic matter by combusting the subsample at 550 °C for four hours. Another subset of dried sediment was pulverized using a ball mill and analyzed for % C and % N content using a Costech ECS 4010 (Valencia, CA, USA). We used soil slurries (1:5 ratio of soil to deionized water) to determine electrical conductivity (EC) and pH with an Orion Conductivity Cell and an Orion Star A215 pH Conductivity Meter Orion with Ross Ultra pH/ATC Triode. We extracted soil-water ammonium (NH_4^+-N) with 2M KCl (soil:KCl = 1:10), filtered extracts using 110 mm Whatman paper (adapted from Keeney & Nelson, 1982), and analyzed them on a SmartChem®200 discrete analyzer (Westco Scientific Instruments, Brookfield, CT, USA). NH_4^+ concentrations were omitted from analyses as only four of 89 samples were above detection limit (1.58 ppm).

Carbon Mineralization- Carbon mineralization rates were measured as headspace-accumulated CO_2 during a 24-hour period utilizing a Picarro G2201-*i* gas analyzer and two, 16-port distribution manifolds (Johnson, 2018). We created soil slurries by adding ~50 g of sieved soil with 100 mL of deionized water to 196 mL glass canning jars, allowed them to come to room temperature, and connected them to the gas analyzer; headspace gas concentrations were measured every two hours over a 24-hour period. We calculated gas flux rate as the linear change in concentration over time and corrected for temperature, pressure, and chamber volume, using the ideal gas law.

Denitrification Potential and N_2O Yield – Rates of denitrification potential were measured using denitrification enzyme activity assays (DEA) and acetylene inhibition technique (Groffman et al., 1999). We subsampled 10 g of homogenized soil and made slurries using 20 mL of DEA solution in 125-mL glass flasks. Each g of wet soil received 3.6 mg KNO_3, 2.5 mg glucose, and 0.625 mg chloramphenicol to remove carbon and nitrogen limitations and prevent synthesis of new microbial enzymes. We used N_2 to induce anoxia and subsequently replaced 10 mL of headspace gas with acetylene to inhibit the reduction of N_2O. We drew discrete headspace gas samples 0, 30, 60, and 90 minutes. N_2O concentrations were measured with a Clarus 580 gas chromatograph with an electron capture detector, delivered with a TurboMatrix 40 Trap Headspace Autosampler (PerkinElmer, Shelton, USA). To estimate rates of net N_2O production, we used the same method but without acetylene inhibition to allow N_2O reduction to N_2. N_2O yield was calculated as the ratio between N_2O production and denitrification potential.

Microbial Communities-

At the Connecticut Agricultural Experiment Station, a ~0.5 g subsample was aseptically transferred to a power bead tube (MO BIO Power Soil Kit, Carlsbad, CA) and DNA was extracted using the supplied protocols. The extractions were then processed at the University of Connecticut's Microbial Analysis, Resources, and Services unit of the Center for Open Research Resources and Equipment for PCR reactions and sequencing. Bacterial 16S rRNA genes were amplified using 30 ng of extracted DNA. The V4 region was amplified using primers 515F and 806R with Illumina adapters and dual indices (8 basepair golay on 3' (Caporaso et al., 2012), and 8 basepair on the 5' (Kozich et al., 2013)). Samples were amplified in triplicate using GoTaq (Promega) with the addition of 10 µg BSA (New England BioLabs). The PCR reaction was

incubated at 95 ˚C for 3.5 minutes, then 30 cycles of 30 s at 95.0 °C, 30 s at 50.0 °C and 90 s at 72.0 °C, followed by final extension as 72.0 °C for 10 minutes. PCR products were pooled for quantification and visualization using the QIAxcel DNA Fast Analysis (Qiagen). PCR products were normalized based on the concentration of DNA from 250-400 bp then pooled using the QIAgility liquid handling robot. The pooled PCR products were cleaned using the Mag-Bind RxnPure Plus (Omega Bio-tek) according to the manufacturer's protocol. The cleaned pool was sequenced on the MiSeq platform using v2 2 x 250 chemistry (Illumina, Inc).

Paired sequences were assembled into contigs using the make.contigs command with default parameters in the mothur software package, only retaining contigs of at least 253 bases. Each contig was further screened to remove any sequences with any ambiguous nucleotide calls or homopolymers of $\geq$ 7 bases. Potential chimeric sequences were removed from the dataset with the mothur utilization of vsearch. Sequences were clustered into operational taxonomic units (OTUs) with the OptiClust algorithm in mothur. For analyses of diversity and composition, an OTU definition of $\geq$ 97 % sequence identity was used. Taxonomic assignment of sequences was performed with the mothur utilization of classify.seqs against the SILVA 132 ribosomal database (Quast et al., 2013).

Literature Cited

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Supporting Information: Tables

Table 2. Soil and biogeochemical rates averaged across species (*S. alterniflora*, *S. patens*, *P. australis*) and SLR treatments (± 1 SE). No significant differences were observed across treatments.

	Species Treatment			**SLR Treatment**		
	S. alterniflora	***S. patens***	***P. australis***	**0 cm**	**+7.5 cm**	**+15 cm**
EC (mS cm^{-1})	4.79 (0.30)	5.31 (0.36)	5.00 (0.32)	5.19 (0.32)	5.07 (0.30)	4.85 (0.36)
Soil Moisture Fraction	0.61 (0.03)	0.62 (0.10)	0.58 (0.03)	0.58 (0.02)	0.63 (0.03)	0.59 (0.03)
pH	6.17 (0.09)	5.96 (0.09)	5.87 (0.08)	5.9 (0.11)	6.07 (0.08)	6.02 (0.08)
% Organic Matter	16.66 (1.51)	18.02 (1.90)	14.76 (1.21)	16.10 (1.47)	17.32 (1.91)	16.01 (1.36)
% C	11.18 (0.83)	10.52 (0.61)	10.82 (3.83)	11.04 (0.95)	11.44 (0.87)	10.04 (0.58)
% N	0.57 (0.07)	0.49 (0.05)	0.48 (0.08)	0.50 (0.08)	0.56 (0.07)	0.45 (0.05)
Denitrification potential (w/o acetylene) (ng-N hr-1 g dry soil-1)	102.05 (30)	132.36 (39)	75.80 (23)	71.54 (21)	135.65 (44)	103.01 (72)
Denitrification potential (w/ acetylene) (ng-N hr^{-1} g dry $soil^{-1}$)	771.65 (241)	423.43 (152)	350.41 (140)	561.11 (238)	433.92 (139)	550.45 (178)

Table 3. ANOVA results for biomass and biogeochemical fluxes. No interactions (Species*SLR) were detected. NS: $P \geq 0.10$, *: $P \leq 0.05$, **: $P \leq 0.01$, ***: $P \leq 0.001$

Response	Treatment	*df*	F-value	p-value
Aboveground Biomass	Species	2	11.83	***
	SLR	2	1.26	NS
Log (Belowground Biomass)	Species	2	0.73	NS
	SLR	2	0.53	NS
NEE	Species	2	12.73	***
	SLR	2	19.04	***
ER	Species	2	7.6	**
	SLR	2	0.71	NS
Carbon Mineralization	Species	2	4.85	*
	SLR	2	2.31	NS
Sqrt (Denitrification potential w/o acetylene)	Species	2	1.01	NS
	SLR	2	0.81	NS
Sqrt (Denitrification potential with acetylene)	Species	2	1.35	NS
	SLR	2	0.10	NS
N_2O Yield	Species	2	0.53	NS
	SLR	2	0.48	NS

Table 4. Sediment bacterial richness (number of operational taxonomic units (OTUs)) and diversity (Shannon's diversity index, inverse Simpson index) did not differ among plant species, sampling date, or SLR treatment. Mean values (± 1 SE) for each treatment combination and sampling campaign.

Species	**Date**	**SLR Treatment**	**Number of OTU's**	**Shannon**	**InvSimpson**
S. alterniflora	June	0 cm	748 (± 225)	6.0 (±0.7)	270 (±184)
		7.5 cm	864 (±92)	6.4 (±0.3)	348 (±160)
		15 cm	828 (±131)	6.2 (±0.4)	242 (±178)
	September	0 cm	816 (±144)	6.2 (±0.4)	268 (±188)
		7.5 cm	930 (±63)	6.5 (±0.1)	421 (±112)
		15 cm	902 (±70)	6.5 (±0.2)	455 (±134)
S. patens	June	0 cm	589 (±68)	5.6 (±0.3)	107 (±78)
		7.5 cm	745 (±229)	5.9 (±0.9)	214 (±158)
		15 cm	704 (±176)	5.9 (±0.7)	221 (±192)
	September	0 cm	797 (±68)	6.3 (±0.2)	275 (±106)
		7.5 cm	798 (±249)	5.9 (±1.1)	269 (±223)
		15 cm	939 (±32)	6.5 (±0.1)	334 (±108)
P. australis	June	0 cm	756 (±182)	6.0 (±0.5)	241 (±221)
		7.5 cm	825 (±168)	6.2 (±0.5)	291 (±171
		15 cm	661 (±222)	5.7 (±0.8)	194 (±177)
	September	0 cm	693 (±168)	5.8 (±0.5)	116 (±51)
		7.5 cm	904 (±31)	6.5 (±0.01)	429 (±62)
		15 cm	831 (±198)	6.3 (±0.4)	342 (±147)