

Phragmites australis associates with belowground fungi communities characterized by high diversity and pathogen abundance

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Supplement

Table S1. Effects of community type, biotic context, abiotic conditions and distance on root and soil fungal composition, richness, antilogarithm of Shannon's entropy index, inverse of Simpson's concentration index and plant pathogen abundances. Final model variables for each model are included. The three primary comparisons correspond to our three hypotheses. Results of dbRDA permutation tests are displayed for effects of community type and biotic context on composition. ANOVA results from mixed effect linear models are displayed for diversity, richness, and pathogen abundance responses. P-values less than 0.1 are bold.

Comparison	Response (df)	Final Model Variables	F-value	P-value
(1) Monoculture vs Native Community Root	Composition	Community type	4.71	0.001
	Richness (1,146)	Community type	6.83	0.009
	Antilogarithm Shannon (1,146)	Community type	8.13	0.005
	Inverse Simpson (1,146)	Community type	14.16	0.0002
	Pathogen abundance (1,150)	Community type	22.03	<0.0001
		Nitrogen	8.43	0.004

Soil	Composition	Community type	2.64	0.001
		pH	1.60	0.011
	Richness (1,72)	Community type	6.07	0.02
		Nitrogen	8.94	0.004
		Salinity	14.72	0.0003
	Antilogarithm Shannon (1,72)	Community type	3.02	0.08
		Nitrogen	3.12	0.08
	Inverse Simpson (1,72)	Community type	9.47	0.0029
		Nitrogen	4.94	0.03
	Pathogen abundance (1,79)	Biotic context	5.02	0.003
(2) Monoculture center vs edge Root	Composition	Biotic context	1.64	0.006
	Richness (1,69)	Biotic context	0.73	0.39
		Carbon	5.03	0.03
	Antilogarithm Shannon (1,71)	Biotic context	1.85	0.18
		Carbon	1.83	0.18
	Inverse Simpson (1,69)	Biotic context	1.41	0.24
		Salinity	2.21	0.14
	Pathogen abundance (1,71)	Biotic context	7.88	0.006
		Nitrogen	4.02	0.048

Soil	Composition	Biotic context	1.81	0.001
		pH	2.02	0.001
	Richness (1,70)	Biotic context	0.27	0.61
		Nitrogen	5.92	0.02
		pH	5.57	0.02
	Antilogarithm Shannon (1,71)	Biotic context	1.67	0.21
		Nitrogen	3.69	0.06
	Inverse Simpson (1,70)	Biotic context	1.25	0.26
		Nitrogen	4.27	0.04
		Phosphorus	4.07	0.05
	Pathogen abundance (1,74)	Biotic context	2.42	0.12
(3) Native Community center vs edge Root	Composition	Biotic context	1.05	0.34
	Richness (1,69)	Biotic context	3.90	0.04
	Antilogarithm Shannon (1,69)	Biotic context	5.39	0.02
	Inverse Simpson (1,69)	Biotic context	0.43	0.51
		Salinity	3.45	0.07
	Pathogen abundance (1,72)	Biotic context	0.61	0.44

Soil	Composition	Biotic context	1.12	0.44
		pH	1.73	0.01
	Richness (1,70)	Biotic context	5.67	0.02
		Nitrogen	13.22	0.0005
		Salinity	13.22	0.0001
	Antilogarithm Shannon (1,70)	Biotic context	1.02	0.32
		Nitrogen	6.57	0.01
		Salinity	8.75	0.004
	Inverse Simpson (1,71)	Biotic context	5.25	0.02
		Nitrogen	5.89	0.02
	Pathogen abundance (1,75)	Biotic context	0.76	0.39

Table S2. Number of root samples per native species collected for each transect at each site.			
Site	Transect	Species	Count
Barataria Preserve	Native center	<i>Eleocharis sp.</i>	5
		<i>Schoenoplectus americanus</i>	1
	Native edge	<i>Eleocharis sp.</i>	5
		<i>Sacciolepis striata</i>	1
Turtle Cove Research Station	Native center	<i>Polygonum punctatum</i>	3
		<i>Eleocharis sp.</i>	2

		<i>Schoenoplectus americanus</i>	1
		<i>Spartina patens</i>	1
	Native edge	<i>Polygonum punctatum</i>	3
		<i>Paspalum dissectum</i>	2
		<i>Spartina patens</i>	2
Pearl River WMA	Native center	<i>Juncus roemarinus</i>	1
		<i>Schoenoplectus americanus</i>	3
		<i>Spartina patens</i>	3
	Native edge	<i>Schoenoplectus americanus</i>	2
		<i>Spartina patens</i>	5
Bayou Sauvage NWR	Native center	<i>Spartina patens</i>	7
	Native edge	<i>Spartina patens</i>	6
		<i>Ipomoea saggitata</i>	1
Fontainebleau State Park	Native center	<i>Spartina patens</i>	5
		<i>Schoenoplectus americanus</i>	1
	Native edge	<i>Spartina patens</i>	5
		<i>Schoenoplectus americanus</i>	2
Big Branch NWR	Native center	<i>Spartina patens</i>	6
		<i>Juncus roemarinus</i>	1
	Native edge	<i>Spartina patens</i>	5
		<i>Schoenoplectus americanus</i>	2

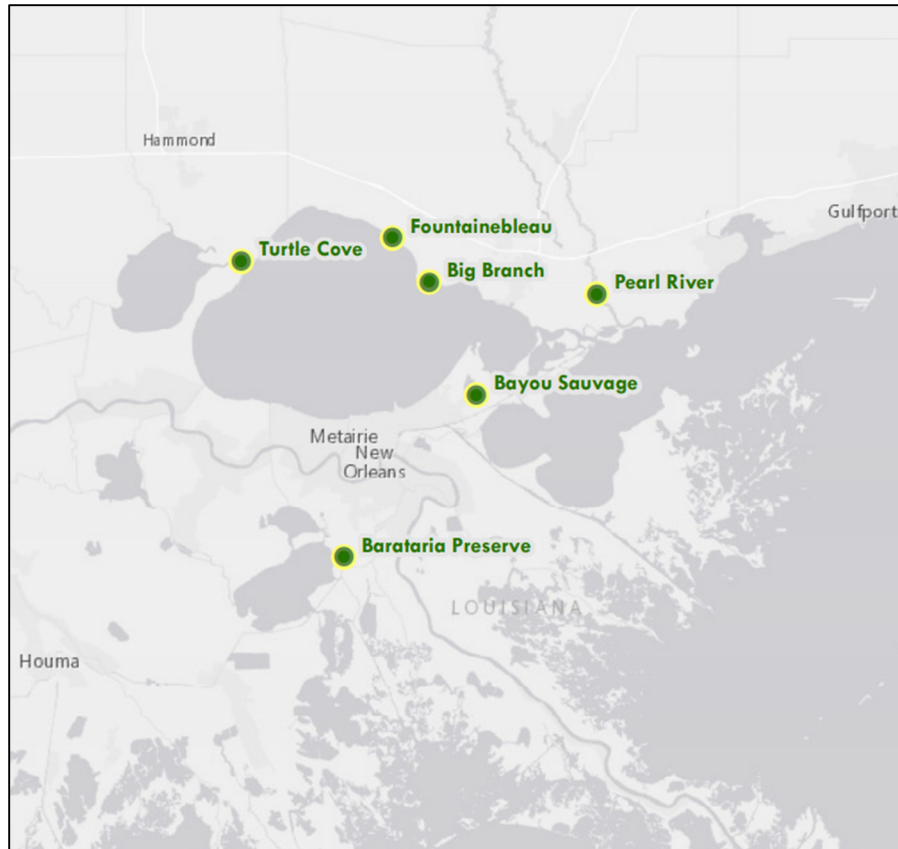


Figure S1. Map showing locations of the six *Phragmites australis* invaded field sites in Southern Louisiana.

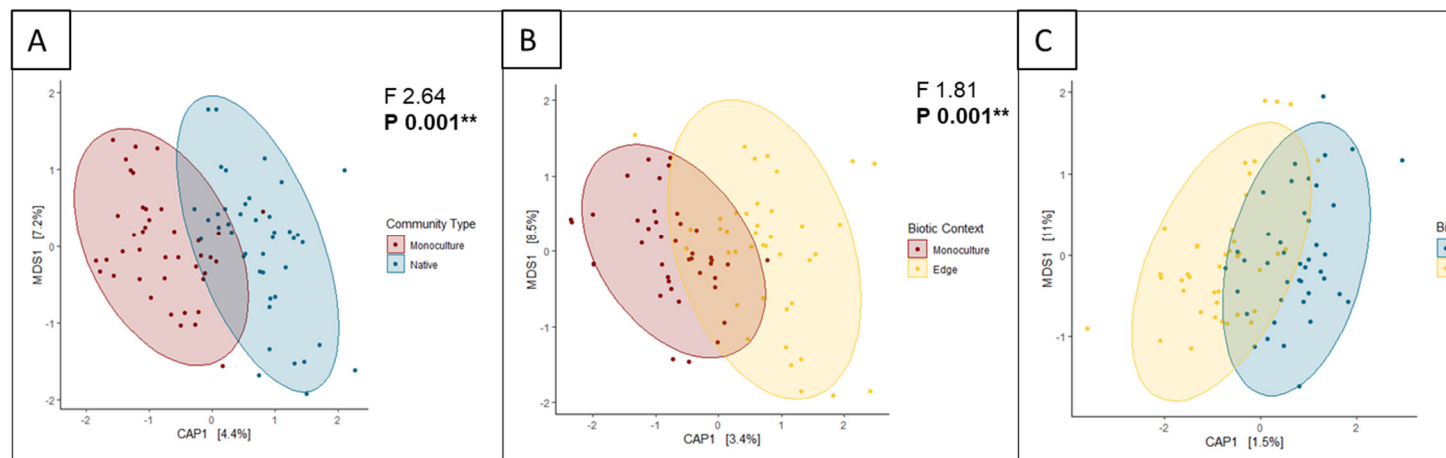


Figure S2. Constrained ordinations showing the effect of community type and biotic context on soil fungal composition. Each point represents an individual soil sample. Ellipses represent a 95% confident interval for each group. Soil fungal composition differed significantly between the monoculture and native community types (A). Soil fungal composition also differed between the center and edge biotic contexts within the monoculture community (B). There was no difference in soil fungal composition between the center and edge biotic contexts within the native community (C). P-values less than 0.1 are highlighted in bold and labeled with the following notation: + $P < 0.1$, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

