Supporting information

Table S1 Accession numbers of sequences used

Species	Accession number	Congener	Synonym
Acorus calamus	JF953049.1		
Amborella trichopoda	AF465284.1		
Butomus umbellatus	JN894389.1		
Iris wilsonii	JF954173.1	*Iris sanguinea*	
Lythrum salicaria	MF350260.1		
Pontederia cordata	KJ747577.1		
Polygonum lapathifolium	MG221002.1		*Persicaria lapathifolia*
Sagittaria trifolia	JF956183.1		
Typha minima	KJ841034.1	*Typha latifolia*	

Table S2 Letter-based representation of the results of pairwise PERMANOVA of *Alternanthera philoxeroides*

Group	C1	C2	C3	C4	C5	C6	C7	C8	8-species mixture
Biomass per individual	a	ab	b	ab	b	ab	b	b	c
Root-shoot ratio	a	bc	b	ad	ad	acd	ad	ad	d

Groups C1-C8 are the 1-species recipient communities grown with *A. philoxeroides*. The resident species in each of the groups are: C1, *Lythrum salicaria*; C2, *Iris wilsonii*; C3, *Acorus calamus*; C4, *Typha minima*; C5, *Pontederia cordata*; C6, *Polygonum lapathifolium*; C7, *Sagittaria trifolia*; C8, *Butomus umbellatus*. The 8-species mixture has all of the eight resident species grown with *A. philoxeroides*. Groups in each line marked without the same letter differ significantly (threshold is $P < 0.05$). P-values for multiple comparison were adjusted using "fdr" method.

Table S3 Results of pairwise PERMANOVA for effects of SR levels on *Alternanthera philoxeroides* growth traits

Comparison	Total mass	Root mass	Stem mass	Leaf mass	Stem length	Number of nodes	SLA	Number of leaves
1 - 2	1.378	1.121	1.322	1.403	2.446*	1.795	0.727	1.796
1 - 4	1.525	1.742	1.570	1.042	1.297	0.946	1.967	0.571
2 - 4	0.198	0.839	0.280	0.234	1.536	0.932	2.082	1.303

See Fig. 6 for data. Values are *F*-values (d.f. = 1, 23 for SR level 1; d.f. = 1, 7 for SR level 2 and 4). *, $P = 0.01–0.05$; **, $P = 0.001–0.01$; ***, $P < 0.001$. SLA, specific leaf area.

P-values for multiple comparison were adjusted using “fdr” method.

Table S4 Results of pairwise PERMANOVA for effects of SR levels on community indicators

Comparison	Diversity index	Evenness index	RDI	Total biomass
1 - 2	2.160*	0.255	1.241	0.332
1 - 4	3.867***	0.127	2.138	1.563
2 - 4	1.759	0.313	1.222	0.993

See Fig. 7 for data. Values are *F*-values (d.f. = 1, 23 for SR level 1; d.f. = 1, 7 for SR level 2 and 4). *, $P = 0.01–0.05$; **, $P = 0.001–0.01$; ***, $P < 0.001$. RDI, relative dominance index. P-values for multiple comparison were adjusted using "fdr" method.

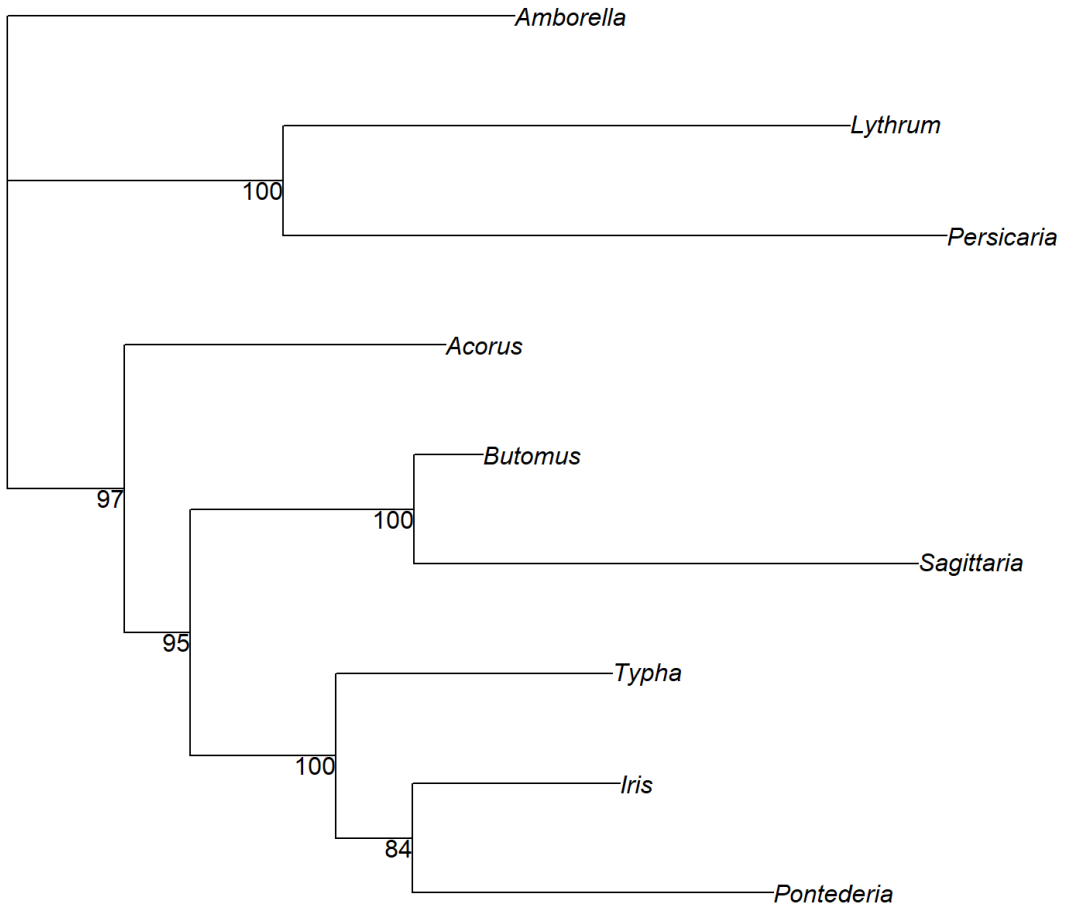

Figure S1: Phylogenitic relationship among the resident species using molecular phylogenetic analysis by Maximum Likelihood method.

The evolutionary history was inferred by using the Maximum Likelihood method based on the General Time Reversible model. The tree with the highest log likelihood (-3409.16) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying the Maximum Parsimony method. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.5031)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 9

nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were a total of 596 positions in the final dataset. Evolutionary analyses were conducted using RAxML.

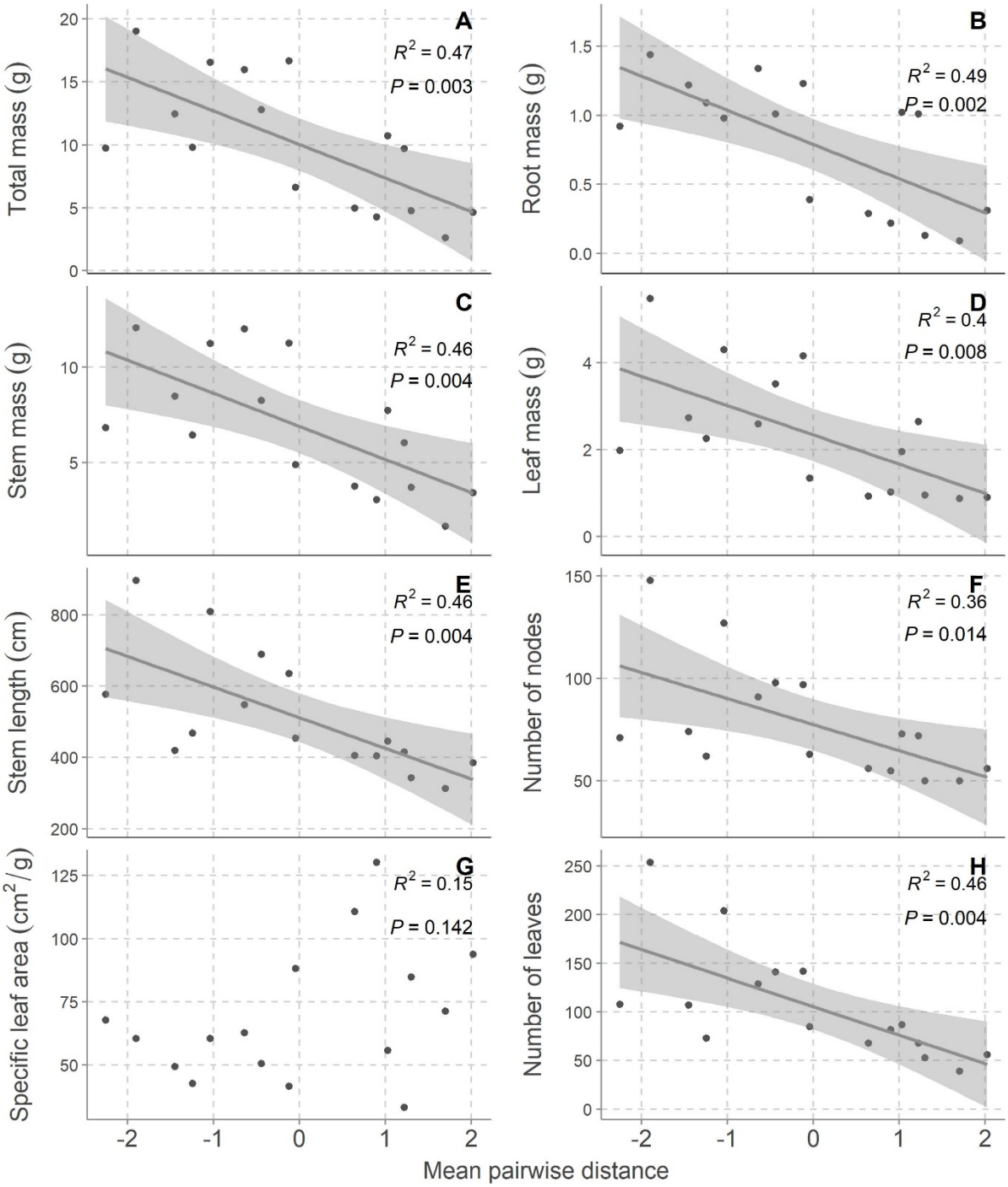

Fig. S2: Linear relationships betewen MPD and *Alternanthera philoxeroides* growth traits, with species combination as a random effect.