

Supplementary figure legends

Figure S1. Distribution of module sizes for well-watered (blue) and drought (red) modules of *P. amilis* (A) and *P. oleracea* (B). Histograms of node degree for genes in *P. amilis* (C) and *P. oleracea* (D) photosynthetic gene networks.

Figure S2. Transcripts per million (TPM) normalized abundance of all *P. amilis* gene families discussed in the text. Gene model and name are shown above each plot, and black and red lines indicate median well-watered and drought abundance of all biological replicates, respectively; error bars show interquartile range. Significant differences in expression between well-watered and drought conditions are shown in the upper right corner of each plot; 'NS' = non-significant, '*' = $q < 0.05$, '**' = $q < 0.01$, '****' = $q < 0.001$.

Figure S3. Transcripts per million (TPM) normalized abundance of all *P. oleracea* gene families discussed in the text. Gene model and name are shown above each plot, and black and red lines indicate median well-watered and drought abundance of all biological replicates, respectively; error bars show interquartile range. Significant differences in expression between well-watered and drought conditions are shown in the upper right corner of each plot; 'NS' = non-significant, '*' = $q < 0.05$, '**' = $q < 0.01$, '****' = $q < 0.001$.

Figure S4. Preservation of C₄ PGNs in *P. amilis* (A) and *P. oleracea* (B). Orange edges represent correlations among genes shared between species, while black edges are unique to each respective species.

Figure S5. Subnetworks induced by common genes of *P. amilis* (A) and *P. oleracea* (B) well-watered C₄ PGNs. Orange edges represent correlations among genes shared between species, while black edges are unique to each respective species. Colors of gene boxes indicate functional categories.

Figure S6. Hypothesized major carbon fluxes of C₄+CAM in *P. oleracea* when well-watered (A) and droughted (B). Red, blue, and purple lines indicate NAD-specific, NADP-specific, and shared reactions, respectively, and grey lines show novel, possible pathways for malate that are unique to C₄+CAM photosynthesis. Line thicknesses are indicative of relative fluxes through pathways. ALAAT, alanine aminotransferase; ASP, aspartate aminotransferase; BCA, beta carbonic anhydrase; CBC, Calvin-Benson Cycle; NAD-MDH, NAD-dependent malate dehydrogenase; NADP-MDH, NADP-dependent malate dehydrogenase; NAD-ME, NAD-dependent malic enzyme; NADP-ME, NADP-dependent malic enzyme;

PEP, phosphoenolpyruvate; PEPC, PEP carboxylase; PPDK, pyruvate, phosphate dikinase; OAA, oxaloacetate.

Supplementary tables

Table S1. Photosynthetic gene network summary statistics

Network	Nodes (genes)	Edges	Average degree	Median degree	Density *
<i>P. amilis</i> well-watered	387	10,103	52.2119	34	0.1352
<i>P. amilis</i> drought	405	9,620	47.5062	46.0	0.1175
<i>P. oleracea</i> well-watered	369	5,508	29.8537	17	0.0811
<i>P. oleracea</i> drought	467	13,743	58.8565	49.0	0.1263

* Density for an undirected graph was calculated by $2m/n(n-1)$, where m is the number of edges and n is the number of nodes.

Table S2. Motifs enriched in the 5'UTRs of genes preserved in the *P. amilis* C₄ modules

Motif name	JASPAR matrix ID	Consensus sequence	Associated TF	<i>Arabidopsis</i> ortholog
KAN4	MA1028.1	GAATATTC	KANADI 4 (KAN4)/AERRANT TESTA SHAPE (ATS)	AT5G42630
OJ1058_F05.8	MA1033.1	MCACGTGK	N/A	N/A
bZIP68	MA0968.1	HNACGTGKM	bZIP transcription factor 68 (BZIP68)	AT1G32150

ERF122	MA1261.1	HDDHTRCGGCKGHGG	Ethylene-responsive transcription factor (ERF112)	AT5G67000
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Supplementary data files

1. *Portulaca amilis* photosynthesis related gene annotations with functional categorizations and module assignments
2. *Portulaca oleracea* photosynthesis related gene annotations with functional categorizations and module assignments
3. Orthogroup assignments
4. Orthogroup gene trees