

Supplemental materials

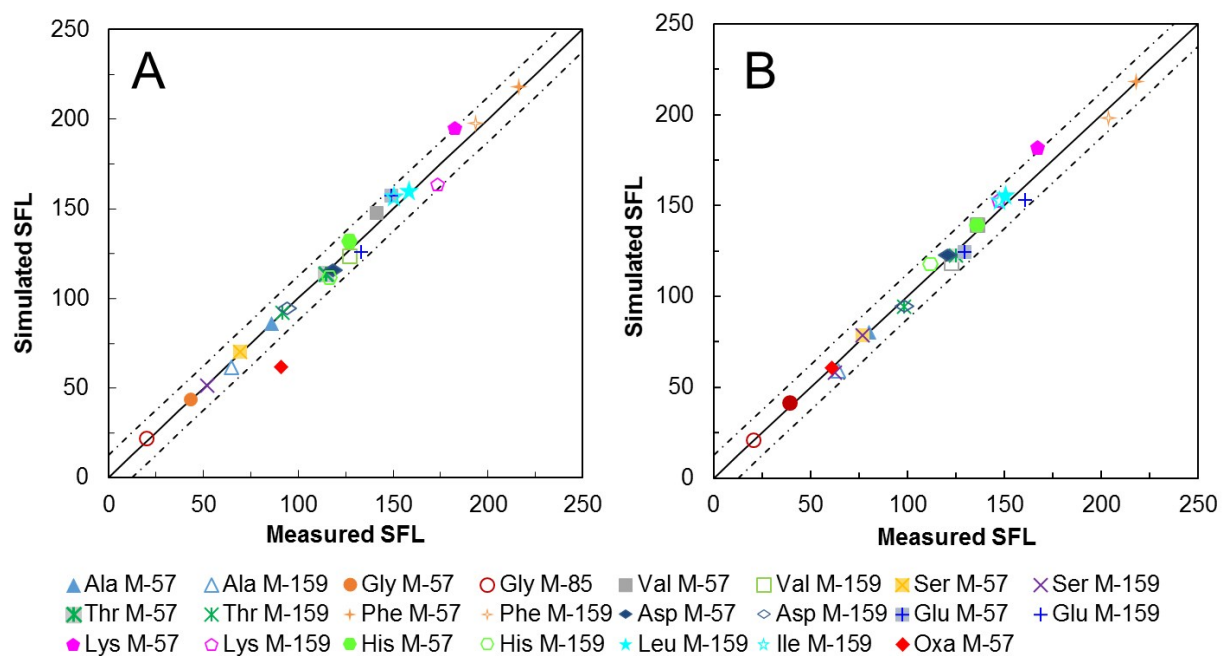


Figure. S1 Simulated isotopic labeled pattern fitting based on SFL calculation. (A) Low nitrogen condition (LN); (B) High nitrogen condition (HN)

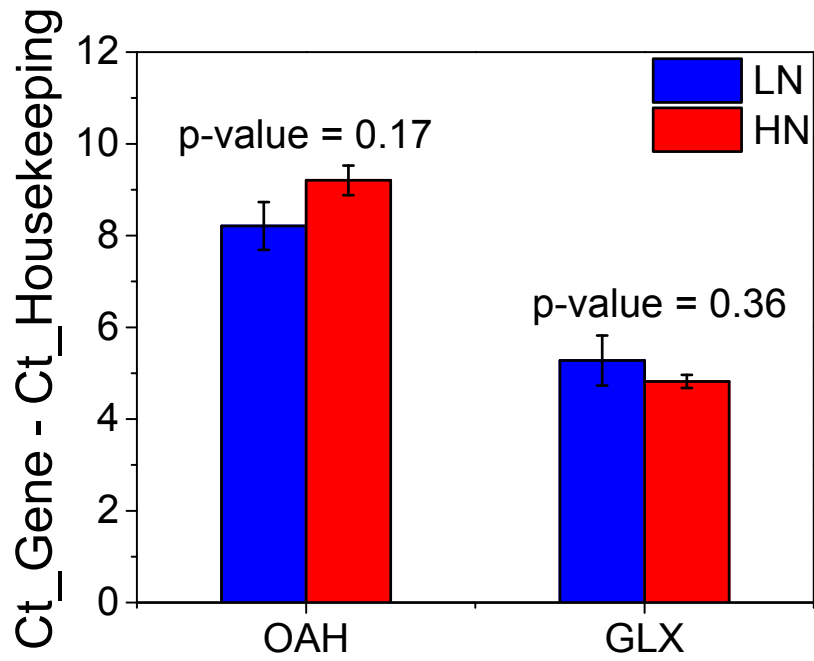


Figure. S2 qPCR results (Δ Ct, defined as the difference between Ct of target gene, i.e., Ct_Gene and Ct of housekeeping gene, i.e., Ct_Housekeeping) for genes encoding cytosolic oxaloacetate acetylhydrolase (OAH) and peroxisomal glyoxylate dehydrogenase (GLX) under LN and HN conditions.

Table S1. Metabolic flux distribution and central metabolic model.

No.	Reactions	Relative flux (LN)	^a STDEV	Relative flux (HN)	^a STDEV
1	GLC <-> G6P	100.0	0.0	100.0	0.0
2	G6P <-> F6P	36.7	2.2	41.5	0.8
3	F6P <-> DHAP + G3P	76.6	1.3	79.3	1.5
4	DHAP <-> G3P	76.6	1.3	79.3	1.5
5	G3P <-> PEP	167.3	0.1	163.3	0.1
6	PEP <-> PYRCYT	166.6	0.9	160.8	2.0
7	G6P <-> CO2 + P5P	60.1	5.3	56.7	0.9
8	P5P + P5P <-> S7P + G3P	20.0	1.7	18.9	0.3
9	S7P + G3P <-> F6P + E4P	20.0	1.7	18.9	0.3
10	P5P + E4P <-> F6P + G3P	19.9	1.8	18.9	0.3
11	PYRCYT <-> ACA + CO2	14.9	8.2	0.0	0.0
12	ACA <-> ETH	0.0	0.0	0.0	0.0
13	ACA <-> ACE	24.9	8.2	0.1	0.1
14	OAACYT <-> OXA + ACE	0.1	0.0	9.0	0.8
15	G3P <-> GLYC	5.5	4.3	1.8	0.1
16	ACE <-> ACCOACYT	24.7	8.0	0.0	0.0
17	PYRCYT + CO2 <-> OAACYT	96.4	7.3	52.8	0.9
18	PYRMIT <-> ACCOAMIT + CO2	98.8	5.3	125.8	0.5
19	OAAMIT + ACCOAMIT <-> ICIT	108.8	2.1	125.0	0.3
20	ICIT <-> AKG + CO2	99.5	2.3	124.8	0.3
21	ICIT <-> GLOX + SUC	9.2	0.2	0.2	0.0
22	GLOX <-> OXA	9.2	0.2	0.2	0.1
23	AKG <-> SUC + CO2	89.6	2.3	114.9	0.3
24	SUC <-> FUM	98.8	2.1	115.0	0.3
25	FUM + FUM <-> OAAMIT + OAAMIT	50.2	0.4	121.5	4.9
26	OAAMIT <-> FUM	1.6	1.3	127.9	10.1
27	GLOX + ACCOAMIT <-> OAAMIT	0.1	0.0	0.0	0.0
28	OAAMIT <-> OAACYT	-68.9	9.5	-28.3	0.1
29	ACCOACYT <-> ACCOAMIT	19.8	3.2	0.0	0.0
30	PYRCYT <-> PYRMIT	49.6	4.2	108.0	1.1
31	G3P <-> SER	0.0	0.0	11.8	2.5
32	SER <-> GLY + C1	0.0	0.0	9.5	0.2
33	OAACYT <-> THR	19.9	0.0	6.2	0.4
34	THR <-> GLY + ACA	10.0	0.0	0.1	0.1
35	OAAMIT <-> PYRMIT + CO2	59.1	9.5	18.3	0.2
36	G6P <-> G6POUT	3.2	3.1	1.8	1.8
37	P5P <-> P5POUT	0.2	0.2	0.0	0.0
38	E4P <-> E4POUT	0.1	0.1	0.0	0.0
39	G3P <-> G3POUT	0.2	0.2	0.6	0.5
40	PEP <-> PEPOUT	0.8	0.7	2.5	1.9
41	PYRMIT <-> PYRMITOUT	9.9	0.0	0.5	0.5

42	PYRCYT <-> PYRCYTOUT	5.6	4.3	0.0	0.0
43	OAACYT <-> OAACYTOUT	7.5	2.1	9.3	0.7
44	AKG <-> AKGOUT	9.9	0.0	10.0	0.0
45	ACCOACYT <-> ACCOACYTOUT	4.8	4.8	0.0	0.0
46	ACCOAMIT <-> ACCOAMITOUT	9.8	0.1	0.8	0.7
47	SER <-> SEROUT	0.0	0.0	2.3	2.3
48	GLY <-> GLYOUT	10.0	0.0	9.6	0.2
49	C1 <-> C1OUT	0.0	0.0	9.5	0.2
50	THR <-> THROUT	9.9	0.0	6.1	0.5
51	ETH <-> ETHOUT	0.0	0.0	0.0	0.0
52	ACE <-> ACEOUT	0.3	0.3	9.1	0.8
53	GLYC <-> GLYCOUT	5.5	4.3	1.8	0.1
54	CO2 <-> CO2OUT	325.6	1.5	387.7	0.2
55	OXA <-> OXAOUT	9.3	0.2	9.2	0.8

^a Standard deviation

BLAST results of oxalate biosynthesis enzymes in *G. trabeum*

Table S2. BLAST results of *G. trabeum* from *Fomitopsis palustris*

Enzyme	Score	Expected	Identities	Gaps	Strand
Oxaloacetate acetylhydrolase (fpOAH)	722 bits(800)	0.0	711/918(77%)	0/918(0%)	Plus/Plus
Glyoxylate dehydrogenase (fpGLOXDH1)	385 bits(426)	2e-106	920/1373(67%)	45/1373(3%)	Plus/Plus

>gi|472338812|dbj|AB690578.1| Fomitopsis palustris FpOAH mRNA for oxaloacetate acetylhydrolase, complete cds

Gloeophyllum trabeum ATCC 11539 Phosphoenolpyruvate/pyruvate domain-containing protein partial mRNA

Sequence ID: ref|XM_007867946.1| Length: 1008 Number of Matches: 1

>gi|225636765|dbj|AB079662.1| Fomitopsis palustris FPGLOXDH1 mRNA for glyoxylate dehydrogenase, complete cds

Gloeophyllum trabeum ATCC 11539 hypothetical protein mRNA

Sequence ID: ref|XM_007868156.1| Length: 1750 Number of Matches: 1