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**Interspecific root interactions enhance photosynthesis and biomass of intercropped millet and peanut plants**

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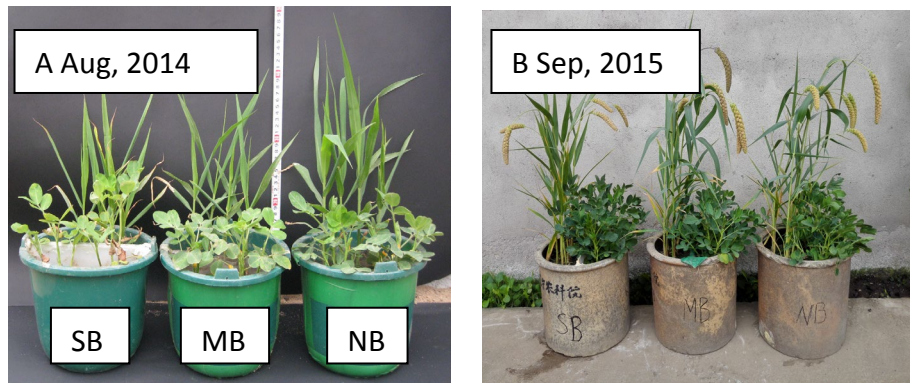
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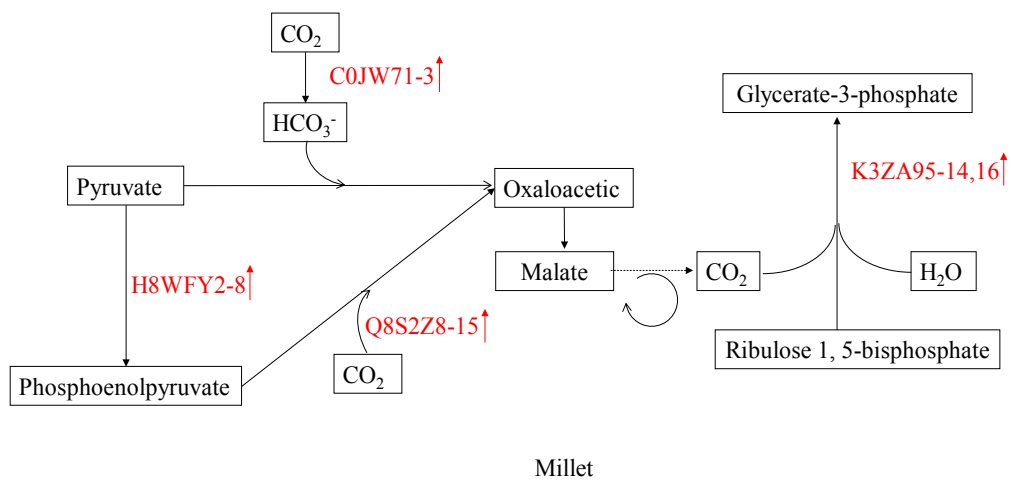
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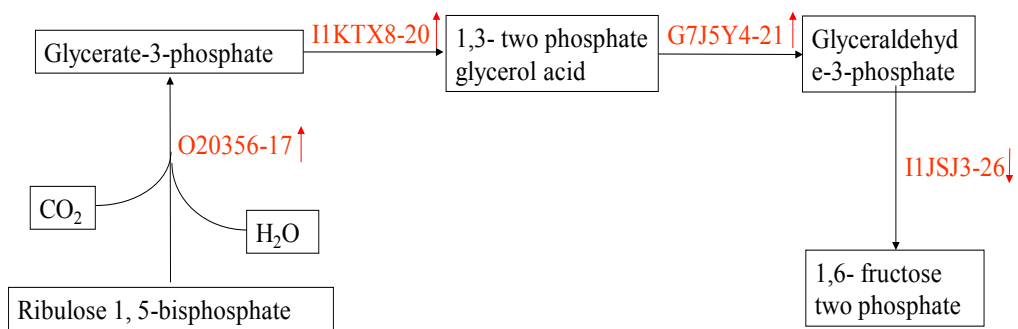
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**Fig. S1.** Response of millet and peanut plants to each of three different root-interaction treatments: (1) no root interactions, (2) partial root interactions, and (3) full root interactions in 2014 (A), and in 2015 (B).



**Fig. S2.** Metabolic pathway of differentially expressed proteins in millet affected by interspecific root interactions in millet/peanut intercropping. The upward arrows indicate up regulated expressed proteins.



Peanut

**Fig. S3.** Metabolic pathway of differentially expressed protein in peanut affected by interspecific root interaction in millet/peanut intercropping. The upward arrows indicate up regulated expressed proteins.

**Table S1. Identification of mass spectrometric for differentially expressed protein spots in millet leaves of three root partition patterns**

Spot ID	Accession No.	Protein name	Score	Taxonomy	MW(kDa)	PI	Coverage%	Match peptides	Accumulated level	
									Partial/No root interactions	Full/No root interactions
Carbon metabolism										
	3C0JW71	Chloroplast beta-carbonic anhydrase	33.6	<i>Pennisetum americanum</i>	27.1	8.75	13.6	2	1.09±0.34	1.50±0.37
	11P93805	Phosphoglucomutase, cytoplasmic 2	200	<i>Zea mays</i>	63.0	5.71	30.2	8	1.55±0.44	2.31±0.19
	14K3ZA95	Ribulose biphosphate carboxylase small chain Putative C4	120	<i>Setaria italica</i>	19.1	8.53	37.5	6	1.33±0.38	1.66±0.19
	15Q8S2Z8	phosphoenolpyruvate carboxylase	899	<i>Setaria italica</i>	110	6.23	38.8	24	3.23±0.89	1.58±0.03
	16X4YSW6	Ribulose bisphosphate carboxylase large chain	114	<i>Setaria italica</i>	52.6	6.54	18.1	8	3.66±1.82	1.50±0.14
	1K3XV32	Uncharacterized protein	278	<i>Setaria italica</i>	110	6.34	37.7	21	2.10±0.18	1.64±0.36
Energy metabolism										
	8H8WFY2	Pyruvate or thophosphate	153	<i>Digitaria</i>	91.9	5.00	8.06	4	2.30±0.64	1.80±0.09

	dikinase	<i>sanguinalis</i>								
12B4FH62	NAD-dependent epimerase/dehydratase	48.2	<i>Zea mays</i>	31.8	9.09	14.1	4	0.78±0.41	0.83±0.28	
13K3ZZV7	Nucleoside diphosphate kinase	103	<i>Setaria italica</i>	12.9	5.83	77.4	5	1.59±0.24	1.51±0.32	
2K3Z8Z2	Uncharacterized protein	50.9	<i>Setaria italica</i>	28.7	8.84	20.5	4	0.68±0.26	1.03±0.33	
6K3Z3X1	Uncharacterized protein	26.4	<i>Setaria italica</i>	88.7	5.00	7.36	4	1.05±0.122	1.59±0.22	
9K3YQW5	Uncharacterized protein	186	<i>Setaria italica</i>	68.4	5.39	41.1	16	0.38±0.16	0.58±0.04	
10K3YQW5	Uncharacterized protein	225	<i>Setaria italica</i>	68.4	5.39	52.5	22	0.38±0.23	0.57±0.07	
7K3Z2D6	Uncharacterized protein	48.5	<i>Setaria italica</i>	24.0	7.44	21.3	3	1.98±0.39	1.99±0.34	
Amino acid metabolism										
5K3Z414	Uncharacterized protein	150	<i>Setaria italica</i>	84.4	6.04	33.5	19	0.82±0.28	0.65±0.31	
unclassified										
	3-beta hydroxysteroid									
4B6TV09	dehydrogenase/isomerase family protein	62.8	<i>Zea mays</i>	32.6	7.81	13.4	2	0.74±0.24	0.70±0.19	

The value  $\geq 1.5$  or  $\leq 0.67$  indicates significantly up-regulated or down-regulated expression of proteins

**Table S2. Identification of mass spectrometric for differentially expressed protein spots in peanut leaves of three root partition patterns**

Spot ID	Accession No.	Protein name	Score	Taxonomy	MW(kDa)	PI	M	CV	Accumulated level	
									Partial/No root interactions	Full/No root interactions
Carbon metabolism										
17O20356		Ribulose 1,5-bisphosphate carboxylase-oxygenase large subunit	19.4	<i>Arachis hypogaea</i>	51.5	6.64	3	7.10	1.19±0.48	1.92±0.71
18E9KT56		Light harvesting complex from photosystem I type b	27.3	<i>Oxytropis arctobia</i>	10.2	5.81	2	16.7	2.59±1.43	2.67±1.32
19H9AGI0		Ribulose bisphosphate carboxylase large chain	50.9	<i>Trifolium dubium</i>	19.8	7.93	2	11.1	2.95±0.90	5.54±2.09
20I1KTX8		Phosphoglycerate kinase	317	<i>Glycine max</i>	50.2	8.13	9	25.4	2.16±0.91	1.80±0.39
21G7J5Y4		Glyceraldehyde-3-phosphate dehydrogenase	211	<i>Medicago truncatula</i>	47.9	7.20	7	27.7	2.06±0.71	2.59±0.28
22I1KTX8		Phosphoglycerate kinase	108	<i>Glycine max</i>	50.2	8.13	5	16.7	3.20±0.11	3.04±0.93
23I1N5Q8		Carbonic anhydrase	157	<i>Glycine max</i>	28.1	6.54	3	12.4	4.28±0.23	3.61±0.26
24P27520		Chlorophyll a-b binding protein 215, chloroplastic	47.9	<i>Pisum sativum</i>	28.9	5.67	4	26.4	6.04±3.55	6.23±5.73

	Ribulose 1,5-bisphosphate								
25O20356	carboxylase-oxygenase large subunit	46.4	<i>Arachis hypogaea</i>	51.5	6.64	3	12.5	10.8±4.13	3.39±2.15
2611JSJ3	Fructose-bisphosphate aldolase	328	<i>Glycine max</i>	42.5	6.79	6	17.7	0.46±0.09	0.17±0.02
27F8UX79	Glyceraldehyde-3-phosphate dehydrogenase	39.2	<i>Arachis hypogaea</i>	43.2	8.27	3	12.4	2.14±0.18	2.32±0.62
Amino acid and protein metabolism									
28B4UWD5	Proteasome subunit alpha type	31.1	<i>Arachis hypogaea</i>	15.0	9.17	2	22.6	1.79±0.75	1.97±0.79
29G7J013	Alanine glyoxylate aminotransferase	100	<i>Medicago truncatula</i>	43.9	7.11	2	6.98	2.17±0.90	2.26±0.01
30B4UW54	GroES-like protein	191	<i>Arachis hypogaea</i>	21.2	8.78	6	44.1	0.65±0.07	1.01±0.09
31C6TJS6	Putative uncharacterized protein	20.8	<i>Glycine max</i>	26.4	8.65	2	9.16	13.4±3.58	4.92±2.28
32B4UW54	GroES-like protein	272	<i>Arachis hypogaea</i>	21.2	8.78	8	51.5	0.33±0.01	0.25±0.03
Unclassified									
33D5K110	Actin-like protein	38.8	<i>Tachigali</i>	13.6	4.70	2	26.2	1.08±0.136	1.99±0.55



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		<i>melinonii</i>							
34E3NYT1	Harpin binding protein	115 <i>Arachis diogoi</i>	18.0	7.27	2	21.8	2.82±0.784	2.52±0.60	
		<i>Vigna</i>							
35F5C0D3	2-cys-peroxiredoxin	27.9 <i>unguiculata</i>	22.1	5.06	3	23.1	1.64±0.363	1.86±0.27	

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The value  $\geq 1.5$  or  $\leq 0.67$  indicates significantly up-regulated or down-regulated expression of proteins