

Table S2. Ratios of metabolite abundance in R1 of the elongation zone between water-stressed and well-watered primary roots of cotton and maize.

Sub Pathway	Metabolite	Cotton	Maize
		Region 1	Region 1
Amines and poly- amines	5-methylthioadenosine (MTA)	1.56	NS
	nicotianamine	0.51	0.56
	putrescine	0.37	NS
	<i>N</i> -acetylputrescine	NS	0.72
Aromatic amino acid metabolism (PEP derived)	3-(4-hydroxyphenyl)lactate	4.06	NS
	tryptamine	4.97	1.97
	tyramine	3.41	6.89
	tyrosine	1.35	NS
	phenylalanine	0.72	NS
	3-methoxytyrosine	0.58	NS
	quinate	0.51	NS
	kynurenate	0.48	NS
	tryptophan	NS	1.55
	phenylpyruvate	NS	0.39
	<i>N</i> -methylphenylalanine		26.44
	O-methyl tyrosine		0.55
	phenyllactate (PLA)		0.23
Aspartate family (OAA derived)	2-hydroxyadipate	2.43	NS
	<i>N</i> -methylpipercolate	3.92	3.44
	<i>N</i> -acetyl- β -alanine	3.09	0.65
	methionine	3.08	NS
	S-adenosylmethionine (SAM)	2.59	NS
	lysine	2.29	NS
	homoserine lactone	2.07	NS
	methionine sulfoxide	1.93	0.3
	alanine	1.84	NS
	<i>N</i> -acetylalanine	0.72	NS
	aspartate	0.48	0.74
	S-adenosylhomocysteine (SAH)	0.43	NS
	asparagine	NS	3.87
	6-oxopiperidine-2-carboxylic acid	NS	2.11
	allo-threonine	NS	1.83
	<i>N</i> 6-carboxymethyllysine	NS	1.75
	threonine	NS	1.53
	S-methylmethionine	NS	0.8
	<i>N</i> -acetylaspargate (NAA)	NS	0.21
	<i>N</i> -acetylaspargine	NS	0.11

	<i>N</i> -formylmethionine	NS	0.5
	<i>N</i> -acetylthreonine		2.07
	N6-carboxyethyllysine		1.64
	2-piperidinone		1.19
	<i>N</i> -6-trimethyllysine		0.7
Branched Chain Amino Acids (OAA derived)	allo-isoleucine		0.56
BCAA-isoleucine catabolism	2-methylglutarate	2.58	1.7
Branched Chain Amino Acids (pyruvate derived)	methylsuccinate	5.31	1.47
	leucine	1.82	NS
	α -hydroxyisovalerate	1.78	2.34
	2,3-dihydroxyisovalerate	0.58	NS
	2-isopropylmalate	0.46	NS
	3-methyl-2-oxobutyrate	NS	6.85
	3-hydroxyisobutyrate	NS	0.56
	4-methyl-2-oxopentanoate	NS	0.4
	<i>N</i> -methylleucine		6.95
	3-hydroxy-2-ethylpropionate		1.55
	levulinate (4-oxovalerate)		0.54
	norvaline		0.5
Glutamate family (alpha-ketoglutarate derived)	pyroglutamine	12.16	NS
	stachydrine	6.68	NS
	<i>N</i> -acetylproline	4.65	1.75
	1-methylhistidine	4.54	NS
	trans-4-hydroxyproline	3.89	3.47
	3-methylhistidine	1.94	NS
	carboxyethyl-GABA	1.92	0.41
	homocitrulline	1.64	0.67
	<i>N</i> - δ -acetylornithine	0.82	NS
	glutamate	0.72	0.71
	<i>N</i> -acetylglutamate	0.64	0.49
	<i>N</i> -monomethylarginine	0.6	NS
	4-guanidinobutanoate	0.72	NS
	<i>N</i> -acetylarginine	0.58	NS
	<i>N</i> -methylglutamate	NS	1.64
	arginine	NS	1.47
	ornithine	NS	0.67
	dimethylarginine (SDMA + ADMA)	NS	0.52
	<i>N</i> -acetylglutamine	NS	0.28
	4-acetamidobutanoate	NS	0.58
	1,3-diaminopropane		0.53

	4-hydroxy-2-oxoglutaric acid		0.17
Glutathione metabolism	ophthalmate	4.42	NS
	γ-glutamylmethionine	3.83	NS
	γ-glutamylleucine	2.5	NS
	glutathione, reduced (GSH)	0.71	41.38
	glutathione, oxidized (GSSG)	0.68	6.4
	cysteine-glutathione disulfide	0.58	NS
	γ-glutamylglutamate	0.53	NS
	γ-glutamyltryptophan	NS	2.52
	γ-glutamylglycine	NS	1.67
	γ-glutamylthreonine	NS	1.87
	γ-glutamylglutamine	NS	0.47
	4-hydroxy-nonenal-glutathione		11.72
	norophthalmate		1.64
Serine family (phosphoglycerate derived)	betaine	4.2	NS
	serine	1.76	2.58
	<i>N</i> -acetylserine	0.55	0.53
	<i>N</i> -acetyltaurine	0.82	2.15
	cysteine	NS	1.7
	sulfate	NS	1.22
	O-acetylserine		0.53
	homocysteine		0.39
Amino sugar and nucleotide sugar	arabonate	1.65	NS
	UDP- <i>N</i> -acetylglucosamine	0.67	0.7
	ribose	0.62	NS
	UDP- <i>N</i> -acetylgalactosamine	0.68	NS
	<i>N</i> -acetylglucosamine 6-phosphate	0.67	3.05
	ribulose	NS	0.48
	ribonate	NS	0.41
	xylulose		0.62
	maltol		0.5
	xylitol		0.74
C5 branched dibasic acid metabolism	itaconate (methylenesuccinate)		0.46
Calvin cycle and pentose phosphate	ribose 5-phosphate		0.61
	ribose 1-phosphate		0.52
Glycolysis	pyruvate	1.94	0.53
	lactate	1.92	NS
	glucuronate	0.6	NS

	glucose 6-phosphate	0.59	NS
Inositol metabolism	inositol 1-phosphate (I1P)	0.41	NS
Photorespiration	oxalate (ethanedioate)	0.84	NS
Sucrose, glucose, fructose metabolism	galactinol	5.08	
	galactonate	1.61	NS
	mannose-6-phosphate	0.67	NS
	mannitol	0.73	NS
	3-deoxyoctulosonate	0.73	NS
	maltotriose	NS	1.43
	galactose 1-phosphate	NS	0.64
	methyl glucopyranoside ($\alpha + \beta$)	NS	0.55
	1-kestose		3.78
	sucrose-6-phosphate		2.34
	erythrose		2.16
	glucoheptose		0.29
TCA cycle	citrate	0.43	0.38
	aconitate	0.31	0.63
	isocitrate	0.24	NS
	succinate	0.75	0.5
	α -ketoglutarate	NS	3.57
	malate	NS	0.67
	maleate	NS	0.41
Carnitine metabolism	deoxycarnitine	11.05	NS
Ascorbate metabolism	gulonate	NS	0.64
CoA metabolism	phosphopantetheine		4.59
Nicotinate and nicotinamide metabolism	trigonelline (N'-methylnicotinate)	2.32	0.39
	nicotinate ribonucleoside	0.75	0.43
	nicotinamide adenine dinucleotide (NAD ⁺)	0.62	0.76
	nicotinate	0.42	NS
	nicotinamide ribonucleotide (NMN)	NS	0.67
	nicotinamide	NS	0.35
	nicotinamide riboside	NS	0.27
Oxidative phosphorylation	methylphosphate	0.68	NS

Riboflavin and FAD metabolism	flavin adenine dinucleotide (FAD)	0.51	0.35
	flavin mononucleotide (FMN)	0.4	NS
Thiamine metabolism	thiamin (Vitamin B1)	0.52	NS
Vitamin B metabolism (B6 or B12)	pyridoxine (Vitamin B6)	0.67	NS
	pyridoxal	0.55	0.59
Choline metabolism	2-dimethylaminoethanol		0.1
Fatty acid, Amino	2-aminoheptanoate	3.45	NS
Fatty acid, Dicarboxylate	pimelate (heptanedioate)	7	0.61
	glutarate (pentanedioate)	3.06	NS
	malonate	2.03	1.66
	adipate	1.48	0.65
	azelate (nonanedioate)	0.81	NS
	suberate (octanedioate)	0.71	NS
	ethylmalonate		0.46
	dodecanedioate		0.33
Free fatty acid	3-hydroxybutyrate (BHBA)	0.79	NS
	linolenate [α or γ ; (18:3n3 or 6)]	0.41	NS
	2-hydroxypalmitate	NS	0.57
	arachidate (20:0)	NS	0.53
	2-hydroxystearate	NS	0.5
	eicosenoate (20:1)	NS	0.33
	palmitate (16:0)	NS	0.75
	oleate (18:1n9)		0.57
	heptanoate (7:0)		0.33
Phospholipids	choline	0.8	NS
	1-palmitoyl-GPE (16:0)	0.71	NS
	1-linoleoyl-GPE (18:2)	0.69	NS
	1-oleoyl-GPE (18:1)	0.6	0.57
	ethanolamine	0.56	NS
	1-palmitoyl-GPA (16:0)	0.54	NS
	1-oleoyl-GPA (18:1)	0.47	0.32
	1-palmitoyl-GPG (16:0)	0.62	NS
	1-oleoyl-GPG (18:1)	0.48	0.34
	1-linoleoyl-GPI (18:2)	0.44	0.26
	glycerophosphoethanolamine	NS	31.92
	glycerophosphoglycerol	NS	27.39
	glycerophosphoinositol	NS	6.62

	glycerol 3-phosphate	NS	6.5
	1-palmitoyl-2-oleoyl-GPC (16:0/18:1)	NS	2.59
	1-palmitoyl-2-linoleoyl-GPC (16:0/18:2)	NS	2.39
	glycerol	NS	1.25
	1-oleoyl-2-linoleoyl-GPI (18:1/18:2)	NS	0.47
	1-palmitoyl-2-oleoyl-GPE (16:0/18:1)	NS	0.36
	1-oleoyl-GPI (18:1)	NS	0.21
	1-palmitoylglycerol (16:0)	NS	0.43
	1-palmitoyl-2-arachidonoyl-GPC (16:0/20:4)		3.81
	2-palmitoylglycerol (16:0)		0.41
	1-oleoylglycerol (18:1)		0.45
Sphingolipid	sphingosine	0.52	0.11
	sphinganine	NS	0.18
Sterols	stigmasterol	1.68	0.44
	campesterol	NS	0.57
	3-hydroxy-3-methylglutarate	NS	0.57
	fucosterol	NS	0.5
Purine metabolism	adenosine 3'-monophosphate (3'-AMP)	9.39	0.36
	guanosine 3'-monophosphate (3'-GMP)	3.94	NS
	adenosine-2',3'-cyclic monophosphate	2.78	NS
	inosine 5'-monophosphate (IMP)	2.32	0.6
	adenosine 2'-monophosphate (2'-AMP)	1.55	NS
	N6-carbamoylthreonyladenosine	0.76	NS
	adenosine 5'-monophosphate (AMP)	0.61	NS
	guanosine 5'- monophosphate (5'-GMP)	0.49	1.51
	N6-succinyladenosine	0.49	NS
	guanosine	0.47	0.62
	N2-methylguanosine	0.44	NS
	N1-methyladenosine	0.35	NS
	N6-methyladenosine	0.3	NS
	xanthine	0.24	NS
	adenine	0.24	NS
	2'-deoxyinosine	0.21	NS
	2'-deoxyguanosine	0.12	0.61
	2'-deoxyadenosine	0.11	0.64
	2'-deoxyadenosine 5'-monophosphate	0.11	NS
	2'-deoxyguanosine 5'-monophosphate (dGMP)	0.11	NS
	guanine	0.67	NS
	7-methylguanosine	0.58	NS
	N1-methylguanosine	0.49	NS
	allantoin	NS	3.04
	N2,N2-dimethylguanosine	NS	2.94

	allantoic acid	NS	0.5
	inosine	NS	0.27
	2'-O-methyladenosine	NS	0.63
	urate	NS	0.27
	2'-deoxyadenosine 3'-monophosphate		0.45
	2'-deoxyguanosine 3'-monophosphate		0.45
Pyrimidine metabolism	β-alanine	3.03	3.6
	uridine 2'-monophosphate (2'-UMP)	0.61	NS
	cytidine 3'-monophosphate (3'-CMP)	0.59	NS
	uridine	0.53	0.56
	orotate	0.52	0.22
	uracil	0.47	NS
	pseudouridine	0.41	NS
	cytidine 5'-monophosphate (5'-CMP)	0.32	0.56
	5-methylcytidine	0.25	NS
	5-methyluridine (ribothymidine)	0.2	NS
	5-methyl-2'-deoxycytidine	0.18	0.46
	thymidine	0.17	0.66
	thymidine 5'-monophosphate	0.15	NS
	2'-deoxycytidine 5'-monophosphate	0.14	0.63
	2'-deoxycytidine	0.1	0.42
	3-ureidopropionate	0.65	NS
	cytidine	NS	0.51
	cytosine	NS	0.11
	3-aminoisobutyrate		1.86
	thymidine 3'-monophosphate		0.36
	ectoine		0.07
Dipeptide	cys-gly, oxidized	2.54	4.85
	glutaminylleucine	1.28	NS
	leucylglycine	1.65	NS
	alanylleucine	NS	0.7
	threonylphenylalanine	NS	0.68
	phenylalanylalanine	NS	0.46
	leucylglutamine	NS	0.61
	leucylphenylalanine/isoleucylphenylalanine		0.36
Benzenoids	hydroquinone β-D-glucopyranoside	0.62	NS
Fatty acid and sugar derivatives	galactarate (mucic acid)	NS	0.6
Phenylpropanoids	ferulate	1.76	NS
	4-hydroxycinnamate	0.53	2.15

	vanillate	NS	1.85
	3,4-dimethoxycinnamic acid		4.74
	coniferyl aldehyde		1.4
Terpenoids	mevalonate		0.53
	mevalonolactone		0.29
Chemicals	succinimide		0.2

In the water stress treatments, vermiculite water potentials were -1.0 MPa (cotton) and -1.6 MPa (maize), which resulted in equivalent root tip water potentials in the two species (Figure 2). The fold changes are the averages of comparisons of the water-stressed treatment to well-watered developmental and temporal controls. Yellow and blue cells indicate significant increases or decreases in abundance, respectively (darker shades, $p < 0.05$ in all comparisons; lighter shades, $0.05 < p < 0.10$ in at least one comparison). White cells indicate non-significant (NS) changes in at least one comparison. Gray cells indicate that the metabolite was not detected. No minimum cutoff value was applied to the fold changes.