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Supplementary Material

Understanding the molecular events underpinning cultivar differences in the physiological performance and heat tolerance of cotton (*Gossypium hirsutum*)

Nicola S. Cottee^{A,D}, Iain W. Wilson^B, Daniel K. Y. Tan^C and Michael P. Bange^A

^ACSIRO Plant Industry, Locked Bag 59, Narrabri, NSW 2390, Australia.

^BCSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia.

^CFaculty of Agriculture and Environment, The University of Sydney, Sydney, NSW 2006, Australia.

^DCorresponding author. Email: nicola.cottee@csiro.au

Table S1. Number of genes for MapMan assigned statistically significantly ($P \leq 0.05$) altered functional bins

Functional bin	No. genes up-regulated	No. genes down-regulated	P-value
Abiotic heat stress	149	53	$<1 \times 10^{-20}$
Abiotic stress	273	153	6×10^{-12}
Secondary metabolism	180	279	8×10^{-12}
Stress	377	257	8×10^{-08}
Transport	476	395	1×10^{-07}
Lignin biosynthesis	15	57	2×10^{-07}
Phenylpropanoid metabolism	41	94	2×10^{-07}
TCA cycle /organic transformation	46	99	5×10^{-07}
Flavonoid metabolism	39	74	1×10^{-05}
Cell wall precursor synthesis	20	52	3×10^{-05}
RNA	1404	1031	1×10^{-04}
S-assimilation	2	22	1×10^{-04}
Metabolite transport at the envelope membrane	6	31	2×10^{-04}
Cell vesicle transport	42	86	5×10^{-04}
Glycolysis	45	83	6×10^{-04}
TCA cycle	29	56	7×10^{-04}
Organic acid transformation (TCA cycle)	11	34	7×10^{-04}
Citrate lyase transformation (TCA cycle)	1	12	0.001
Dihydroflavonol metabolism	18	38	0.001
Methionine synthesis	10	38	0.002
Chloroplast/mitochondrial - plastid ribosomal protein synthesis	49	16	0.003
RNA regulation of transcription	1123	805	0.003
Regulation of NAC domain transcription factor family	45	13	0.004
UXS cell wall precursor synthesis.	2	17	0.004
Protein folding	48	20	0.005
Amino acid synthesis	147	177	0.005
ATPase transport	28	52	0.010
Exotic lipid metabolism	49	81	0.012
Ethylene.signal transduction	4	13	0.017
Chalcones (flavanoid) metabolism	4	13	0.018
C1-metabolism	18	38	0.018
Chloroplast/mitochondrial - plastid ribosomal protein synthesis	23	5	0.021
Oxidative Phosphate Pathway	18	36	0.029
Ascorbate and glutathione metabolism	37	64	0.029
Amino acid metabolism	294	329	0.037
Ethylene metabolism	84	43	0.037
Homocysteine metabolism	0	7	0.038
Major carbohydrate synthesis	22	43	0.045
APR assimilation (S-assimilation)	0	6	0.045
Calvin cycle glyceraldehyde-3-phosphate dehydrogenase metabolism	0	12	0.045
Histone synthesis	47	25	0.045

Table S2. Sequences for primers used

GenBank accession	UniGene	Gene description	Forward	Reverse
AI731438	–	Mitochondrial uncoupling protein	TACCATTCTTTGGACACTGC	GGCGATGTAAACCAGCAACTA
CO124594	–	Ribonuclease H-like protein	GACCAAAACATCCACAGCATT	GGAAGTTGAAAGCGCAGATAA
CO072814	Gra.3235	Rubisco subunit binding protein	GGTGGTGCTGCATTAGTTCAT	CTTCCATTCTGCATTTTGAG
CO492249	Ghi.24465	β -tubulin housekeeping	AGAACATGATGTGTGCTGC	AGCTGTGAACTGCTCACTC
DN800322	Ghi.10785	PSII oxygen-evolving protein	CTCAGAAACAGGCAGTCCAAG	TGTGTTTGT TTTTGGCTTTCC
DT048069	Ghi.3704	Glycerol-3-phosphate dehydrogenase	GGCAGAAGAGCCTGAAAACT	ATCATAACCCTTCCCCTTGATG
DT048453	Ghi.4752	Oxioeductase / sphingolipid delta-4 desaturase	ATACGTTGGTCACGATTCAGG	GGTGAGCATTGTGAGTCCATT
DT049115	Ghi.8379	<i>Gossypium hirsutum</i> low molecular weight heat shock protein (LMWHSP6)	CCAACAGTCACATCGTTTCT	GATCTCCACCTTACCTCCTC
DT465471	Ghi.3468	Serine-type endopeptidase	CAATGGCTTTTACAGGGTTGA	ATTTCACCTCATTGGTCTCC
DT467180	Ghi.5136	<i>Gossypium hirsutum</i> low molecular weight heat shock protein (LMWHSP3)	GAGTGAATTTGCAACCGAAAA	CCGTATCGTCAGAAAGATCCA
DT545357	Ghi.9821	Mitochondrion-localized small HSP	AAAAACGGTGTGCTCAAAGTG	CCAAAGAAAACCCACTTAGCC
DV850132	Ghi.10747	Ethylene responsive element binding factor	AAACGACTCCGATTTGGCTAT	CTAAAGCTTGAGCTCCTGCAA
DW499824	Ghi.13891	Phosphofructo-1-kinase	GTCTTGTGAATGGAAGGCAGA	TCGTTTGAGGATTCTTCATGG

Table S3. Expression ratios (log₂) for heat map (Error! Reference source not found.)

Genbank Accession	Unigene ID	Sicala 45				Sicot 53				Description
		0.5 h	1 h	3 h	7 h	0.5 h	1 h	3 h	7 h	
DT545357	Ghi.9821	4.77	3.54	5.59	2.37	3.67	2.81	5.54	3.04	Mitochondrion-localised small HSP 23.6
DT467180	Ghi.5136	4.8	3.25	4.21	1.29	3.06	3.07	4.03	3.26	Low molecular weight HSP 3
DT049115	Ghi.8379	3.77	2.25	2.65	-0.19	2.49	2	2.48	1.08	Low molecular weight HSP 6
CO124594	-	2.1	0.67	1.16	-0.01	3.43	2.97	2.62	2.26	Ribonuclease H-like superfamily protein
CO072814	Gra.3235	1.2	2.21	2.53	0.04	0.94	2.22	3.19	0.59	Rubisco subunit binding-protein
DT048069	Ghi.3704	-0.08	1.72	2.23	0.33	0.18	0.64	0.49	0.6	Glycerol-3-phosphate dehydrogenase (NAD ⁺)
DT465471	Ghi.3468	-0.43	-0.56	1.43	-2.7	-0.66	-0.37	0.11	0.64	Serine-type endopeptidase activity
DN800322	Ghi.10785	0.34	0.6	0.33	-1.46	0.58	1.91	0.04	-1.37	Photosystem II oxygen-evolving enhancer protein
DV850132	Ghi.10747	0.18	1.38	-1.32	-1.5	-1.44	0.61	-0.11	-1.03	Ethylene responsive element binding factor
DT048453	Ghi.4752	-0.14	-1.99	-1.55	-0.83	-2.08	-1.56	-1.76	-0.98	Oxidoreductase/ sphingolipid delta-4 desaturase
DW499824	Ghi.13891	-0.46	-1.06	-1.4	-2.2	-0.15	-0.37	-1.3	-1.66	Pyrophosphate-dependent phosphofructo-1-kinase
AI731438	-	-0.72	-0.72	-1.28	-1.47	-0.72	-0.26	-1.31	-1.23	Mitochondrial uncoupling protein (complex IV)