

Supplementary Material for the Manuscript: Large-scale cloning and analysis of genes preferentially expressed in elongating cotton fibers, Ji et al.

Summary of cDNA Array Data from Differential Screen and Expression Pattern of the Cotton Fiber Development-Related ESTs

This table summarizes the cDNA array comparison between 10 dpa upland cotton fiber and 10 dpa *fl* mutant ovule, and the expression pattern analysis during early cotton fiber development (0, 5, 10, 20 dpa). A clone is included in this list if its expression ratio of wild-type to mutant greater than 2. For each cDNA, a Clone ID is given, which can be used to retrieve the nucleotide sequence and other information at <http://cottonfiber.cbi.pku.edu.cn>.

Clone No.	Annotation	Ratio ^a	Relative expression level ^b			
			0dpa	5dpa	10dpa	20dpa
Type I Highly expressed around 5 dpa						
P2B03	tRNA-Ile gene	4.2	0.04	12	12	0
P2E06	Lipid transfer protein 11	3	0.21	9	7.5	6.9
P2F07	Acyltransferase homolog	16	0.36	6.8	4.8	1.4
P2G03	Plasma-membrane H ⁺ ATPase	2.3	0.01	2	0.5	0
P2H05	Sodium channel α -subunit	6.1	1.94	1.5	1.1	-2.3
P2H09	Endo-1,4- β -mannosidase	29	0.05	4	0.4	0
P2H10	Enolase	2.6	0.09	1.2	-1.1	-1.8
P3B05	Cinnamyl-alcohol dehydrogenase	5.6	0.04	10	9.8	5.5
P3G12	Unknown	7.3	0.05	1	-1	-1.5
P3H08	Unknown	97	0.04	0.5	-0.7	-1
Type II Highly expressed around 10dpa						
P1A09	Unknown	3.6	0	0	0.5	-10
P1B01	Proline-rich protein 1	160	0.6	7.4	35	20
P1B02	Proline-rich protein 2	100	0.56	7.6	32	19
P1B03	Proline-rich protein 3	116	0.68	8.1	32	19
P1B04	Proline-rich protein 4	2	0.09	55	240	149
P1B06	Proline-rich protein 5	32	0.05	94	256	92
P1B08	Proline-rich protein 6	190	0.93	5.9	22	13
P1B10	Arabinogalactan protein 2	30	0.03	43	400	347
P1B11	Arabinogalactan protein 3	12	0.06	34	203	195
P1B12	Arabinogalactan protein 4	14	0.03	70	423	380
P1C01	Arabinogalactan protein 5	21	0.09	26	178	121
P1C05	Proline-rich extensin	3.4	0.22	4.4	13	10
P1C06	Unknown	3.7	0.27	3.3	7.8	3.3
P1C08	Expansin 1	51	0	0	0.1	-2
P1C10	Expansin 3	13	1.08	5.4	20	12
P1C11	Expansin 4	11	1.02	5.7	22	13
P1C12	Expansin 5	5.2	0.1	29	120	75
P1D01	Xyloglucan endotransglycosylase	3.2	0.15	20	99	73
P1F01	Auxin binding protein	8.5	0.32	13	59	25
P1F02	Annexin	2.3	1.41	3.9	11	8.8
P1F07	P-glycoprotein	2.8	0.21	1.9	2.4	0.3
P1D05	α -tubulin 2	4.4	1.55	3.2	13	8.7

P1D08	α -tubulin 4	2.6	0.02	0	13	7.5
P1D11	β -tubulin 7	7	0.01	3	20	34
P1F04	Histone H2B1	10	3.13	1.7	3.6	2.8
P1F11	Phosphoserine aminotransferase	2.9	0.27	5.1	9.9	8.7
P1F12	Serine/glycine hydroxymethyltransferase	2.2	0.08	2.1	11	5.8
P1G01	β -alanine-pyruvate aminotransferase	7.8	0.09	2.3	5.1	0.6
P1G05	Homeodomain protein	4.2	2.07	1.9	5.8	5.4
P1H05	DNA-binding cnd41-like protein 1	5.4	0.02	10	29	26
P1H06	DNA-binding cnd41-like protein 2	9.4	0.46	12	45	21
P1H07	Putative chloroplast DNA-binding protein	15	0.02	17	42	33
P1H10	Unknown	5.3	0.08	17	253	144
P1H12	Unknown	2.3	0.66	4.5	23	18
P2A03	Ribosomal protein small subunit 4e	3	0.82	1	3	1.6
P2A06	Ribosomal protein S18	32	0.95	5.9	22	14
P2A10	60S ribosomal protein L21	2.8	1.26	2.1	4.9	3.9
P2B05	Unknown	3.2	3.33	1.6	3.5	2.6
P2B06	Unknown	5.6	0.03	7.7	22	18
P2B10	Subtilisin-like proteinase	8	0	0.02	18	3.5
P2B11	Unknown	18	0.11	18	50	19
P2B12	Putative serine proteinase	2.5	1.74	2.6	11	5.7
P2C02	70 kDa heat shock protein 1	2	0.13	2.1	15	6.2
P2C03	70 kDa heat shock protein 2	2.8	0.02	1	5.5	0
P2C04	70 kDa heat shock protein 3	4.7	0.03	129	160	91
P2C05	15kDa heat shock protein	5	0.05	10	15	9.4
P2C07	18 kDa class I heat shock protein	4.3	0.07	18	33	26
P2C09	Cyclophilin	2.2	0.17	4.6	5.5	4.8
P2C10	26S proteasome AAA-ATPase subunit	172	0.03	28	106	84
P2D04	Putative importin	3.3	0.02	128	186	98
P2D05	Putative peptide transporter PTR2-B	3.3	0.03	8.3	43	25
P2D06	Lipid transfer protein 1	93	0.75	7.6	27	18
P2D07	Lipid transfer protein 2	57	1.02	5.5	22	13
P2D08	Lipid transfer protein 3	34	1.16	5	19	12
P2D09	Lipid transfer protein 4	45	1.53	3.7	14	8.9
P2D10	Lipid transfer protein 5	25	1.38	4.1	16	9.8
P2D12	Lipid transfer protein 6	37	0.28	12	80	48
P2E01	Lipid transfer protein 7	33	0.13	6.5	21	7.2
P2E02	Lipid transfer protein 8	2.7	0.39	12	30	22
P2E03	Lipid transfer protein 9	37	0.05	5.6	26	14
P2E05	Lipid transfer protein 12	24	1.5	3.9	15	9.1
P2E07	β -ketoacyl CoA synthase 1	39	0.04	12	75	59
P2E08	β -ketoacyl CoA synthase 2	45	0	0.2	5	5
P2E09	β -ketoacyl CoA synthase 3	24	0	0.2	7	6.1
P2E11	β -ketoacyl CoA synthase 4	31	0.04	11	89	51
P2F01	VLCFA condensing enzyme	39	0.12	1.7	5.8	0.8
P2F03	LCFA ^c elongation enzyme 1	91	0.02	66	175	57
P2F04	LCFA elongation enzyme 2	47	0	2	1.4	-1.5
P2F05	Putative fatty acid elongase	3.3	0.15	7.4	13	11

P2F02	Arabidopsis FIDDLEHEAD homology	74	0.05	16	57	24
P2E12	Alu I-fragment-like protein	5.8	0.3	4.3	56	23
P2F11	Aquaporin	2.2	1.94	3	12	7
P2G01	V-ATPase catalytic subunit	146	0.01	97	996	746
P2G02	Vacuolar H ⁺ -ATPase subunit E	2.4	0.83	4.8	11	9.6
P2G07	Unknown	35	0.05	19	81	80
P2G08	Putative ABC transporter	3.4	0.18	13	52	25
P2G12	Unknown	3.3	0	0.1	7.3	5.9
P1A03	Acid invertase	16	0	0	0.5	2
P2H11	Fructose-bisphosphate aldolase	71	0.06	14	19	13
P3A03	Quinone oxidoreductase	7.5	0.25	6.1	24	17
P3A05	Cytochrome P450-like protein 1	14	0.03	94	280	177
P3A07	Cytochrome P450-like protein 2	2.9	0.09	32	99	62
P3A08	Cytochrome-c oxidase chain III	2.5	0.03	0.7	4.3	0
P3B01	NADH:ubiquinone oxidoreductase	2.2	0.41	3.3	11	6.7
P3B02	Unknown	40	0.23	19	93	53
P3B03	Unknown	12	0.36	8.3	24	11
P3B04	Putative oxidoreductase	22	0.2	7.6	34	14
P3B06	Aldehyde dehydrogenase	4.2	0.08	2.5	4	2.3
P3B08	PDI-like protein	2.6	0.08	1.3	6.9	3.6
P3C03	Cycloartenol synthase	4	0.77	5.2	26	17
P3C04	Anthocyanidin synthase	2.3	0.95	2.1	2.1	1.3
P3C06	Putative calmodulin	2	0.36	2.6	7.1	4.4
P3C08	Unknown	14	0.51	8.7	39	26
P3C09	Unknown	10	1.5	2.8	13	8.9
P3C12	Leucine-rich repeat protein kinase	3.3	0.56	2.6	11	5.3
P3D03	MAP kinase-like protein	53	0.51	10	51	25
P3D04	Unknown	3.9	0.24	1.5	5.5	4.5
P3D06	Unknown	2.4	0.4	7.3	23	21
P3D07	Unknown	10	0.16	2.7	12	6.3
P3D10	Peroxidase	20	0.03	4	26	12
P3D11	Dehydration-induced protein RD22-like	20	1.15	4.9	19	11
P3E01	Elicitor-like protein	5.1	0.65	2.9	7.5	4.5
P3E02	Nitrate-induced NOI protein	2.7	0.21	3.5	15	8
P3E07	En/Spm-like transposase	27	3.33	1.7	4.4	3
P3E08	Unknown	67	0.17	26	123	44
P3E09	Mutator-like transposase	2.8	0.02	0	6.5	4.5
P3E04	E6-like protein 1	42	0.99	5.7	22	14
P3E11	Salicylic acid-induced fragment 1 protein	3.1	1.5	3.8	15	9
P3E12	Acid phosphatase	9.2	0.2	12	22	5.2
P3F02	(+)- δ -cadinene synthase	48	0.25	2.5	2.8	2.2
P3F03	16S ribosomal RNA gene	2.9	3.16	1.8	6.3	4
P3F06	Fibroblasts of periodontal ligament	3.6	0.04	46	171	92
P3F07	Mago Nashi-like protein	2.2	0.75	4	20	11
P3F10	Arabidopsis PUR α -1 like protein	2.4	0.35	6.3	23	18
P3F11	Unknown	25	0.12	5.5	23	19
P3F12	Ripening-related protein	2.8	1.27	2.9	4.9	2.3

P3G05	Unknown	∞	0.02	42	260	160
P3G09	Unknown	45	0.08	7	43	27
P3H02	Unknown	188	0.04	26	288	210
P3H03	Unknown	4.9	0.68	4.2	29	18
P3H07	Unknown	13	0.04	27	35	14
Type III Expression reaching plateau around 10-20dpa						
P1B09	Arabinogalactan protein 1	7.3	0.07	21	163	166
P1C03	Extensin-like protein	9.5	0.16	3.7	4.1	4.6
P1E04	β-tubulin 9	8.9	0.19	3.7	71	71
P2C08	Unknown	3.7	0.03	29	174	179
P2E04	Lipid transfer protein 10	6	0.15	9.2	29	32
P2F09	Anther-specific proline-rich protein	2.8	0.22	2.2	3.6	4
P2G06	Putative transmembrane transporter	137	0.12	13	29	32
P3A02	Pyruvate kinase	2.1	0.24	4.7	17	16
P3E03	Unknown	14	0.18	2.6	8.4	8.7
P3E05	E6-like protein 1	3.7	0.1	19	54	55
P3C01	Chalcone synthase	3.8	0	0.02	12	12
Type IV With increasing expression levels even at 20dpa						
P1C09	Expansin 2	94	0.08	13	17	30
P1D02	Endo-xyloglucan transferase homolog	2	0.03	1	5.7	13
P1D12	β-tubulin 8	19	0.01	4	59	305
P1E01	β-tubulin 5	6.7	0.06	1.5	7.8	11
P1E02	β-tubulin 4	6.1	0.15	5.5	22	33
P1E03	β-tubulin L	11	0.22	4.1	46	58
P1E05	Profilin	41	0.01	21	26	67
P1E06	α-subunit of F-actin capping protein	4.6	0.05	2.6	8.4	19
P1E07	Kinesin-like calmodulin binding protein	11	0.01	5	330	606
P1E08	Kinesin heavy chain	2.9	0.03	1	5.3	18
P1F09	Methionine synthase	2.6	0.03	-1.5	6.7	9.3
P1H02	Unknown	50	0.27	4.4	8.2	10
P1H03	Putative RING zinc finger protein	56	0.02	20	53	73
P2A05	Putative 40S ribosomal protein S17	2.6	0.27	4.3	7.5	11
P2A08	Unknown	3.4	0	0	0.01	20
P2A09	60S ribosomal protein L17	2.1	0.37	2.5	3.7	4.6
P2B07	Cysteine proteinase isoform III	3.3	0.39	5.2	9.9	14
P2B08	Cysteine proteinase	4.1	0.03	14	26	46
P2D01	Putative serine carboxypeptidase	2.3	0.1	6.8	8	11
P2F06	Fatty acid elongase	∞	0	0.01	1	19
P2F08	Lipase/hydrolase-like protein	17	0.01	14	8	36
P2G05	Transmembrane transporter homolog	6.1	0.21	3.7	1.1	4.5
P2G10	Unknown	28	0.16	2.2	11	16
P2H01	Unknown	4	0.06	6.8	1.5	6.7
P2H03	Unknown	3.6	0.01	9	7	19
P2H04	Unknown	∞	0	0.07	2.1	12
P2H06	β-galactosidase	4.7	0.02	4	10	39
P2H07	Unknown	3.1	0.08	2	3.8	5
P3D05	WD-40 repeat protein homolog	2.3	0.11	3.5	11	14

P3F05	FbLate-2 gene		7.1		0.05		7.6		195		272
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^a Differential expression ratio of 10 dpa fiber cDNA to that of 10 dpa *fl* mutant ovule.

^b Values in red are the volume values acquired from the array analysis. If the value at 0 dpa is zero, the value at 5 dpa is shown, and so on. Other values in black represent the fold of increase or decrease (preceded with “-” signs) relative to values obtained at 0 dpa or at the earliest date that produced a positive volume value.

^c LCFA, long-chain fatty acid.



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