

UV-B를 처리한 *Miscanthus*의 cDNA library로부터  
기능성 유전자의 발현 및 분류

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Expression and Classification of functional genes from a cDNA Library of  
*Miscanthus sinensis* treated with UV-B

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**Objectives**

We present the digital gene expression profiles for 1000 *Miscanthus* genes across all tissues. We focused on the classification of expressed sequence tags (ESTs) from an enriched cDNA library of *Miscanthus* leaves and stems exposed to UV-B irradiation.

**Materials and Methods**

- Plant Material: *Miscanthus* were grown in a growth chamber at 25 ± 3°C under a photo cycle of 16 h dark/8 h light (600 - 700 μmol photons m<sup>-2</sup>s<sup>-1</sup>) and then treated with UV-B for 48h. Whole *Miscanthus* plants were used as the plant material for cDNA library construction.

- cDNA Sequencing and Sequence Analysis: Database searches were performed using BLASTX software with default parameters. Homologies with E values of ≤10<sup>-5</sup> were divided into known functions, putative functions, and unknown functions; the other unigenes (no hit or an E value >10<sup>-5</sup>) were classified as non-significant matches. Unigenes matching proteins with known functions were categorized manually according to a BLASTN and BLASTX program searches at the homepage of the NCBI database. Individual gene expression levels were examined based on the redundancy of cDNA clones found in each contig comprising more than 10 ESTs.

**Results**

- Sequencing and grouping of ESTs: . In this library, 72 contigs clustered from 1000 clones and 755 singletons were formed. The set of contigs and singletons resulted in 947 assembled sequences that represented the putative transcripts found in *Miscanthus* leaves.

- Annotation and classification of known functional genes: Examination of the initial BLASTX matches showed that these could be categorized into three categories: 36% of unigenes matched to proteins with known function in the public databases; 55% of unigenes matched to proteins with unknown functions; and 9% of unigenes matched to proteins with no hit in the NCBI database.

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Putative function	E-value		E-value
(E)-beta-carotophyllene synthase	1.00E-120		
26S proteasome AAA-ATPase subunit RPT6a	3.00E-24		
26S proteasome ATPase subunit	1.00E-105		
2-on-2 hemoglobin	1.00E-52		
60S ribosomal protein L17	7.00E-75		
Abscisic acid 8-hydroxylase 1	5.00E-10		
Acetyltransferase, GNAT family protein	6.00E-87		
Acyl carrier protein 2, chloroplast	2.00E-46		
Adenylylhomocysteinease	4.00E-71		
Alanine-glyoxylate aminotransferase 2, mitochondrial	1.00E-101		
Alcohol dehydrogenase 2	1.00E-129		
Armadillo/beta-catenin repeat family protein	1.00E-99		
ASF/SF2-like pre-mRNA splicing factor SRF52	3.00E-22		
Ascorbate peroxidase	1.00E-118		
Aspartate aminotransferase	2.00E-23	Putative 1-deoxy-D-xylose 5-phosphate reductoisomerase	3.00E-76
ATP sulfurylase	1.00E-140	Putative 3-beta hydroxysteroid dehydrogenase isomerase (NAD dependent epimerase (dehydratase family protein))	3.00E-57
ATP synthase delta chain, chloroplast	3.00E-78	Putative 3-hydroxyisobutyryl-coenzyme A hydrolase	1.00E-125
ATP synthase gamma chain, mitochondrial	5.00E-74	Putative 5-alpha-taxadienol-10-beta-hydroxylase	1.00E-86
ATP synthase subunit gamma, chloroplast	4.00E-78	Putative 5-formyltetrahydrofolate cycloligase	3.00E-82
ATPase, AAA family protein	1.00E-123	Putative 60S ribosomal protein L37	1.00E-42
Edfunctional aminoacyl-tRNA synthetase	1.00E-146	Putative 60S ribosomal protein L38	3.00E-30
Edfunctional phosphopantetheine adenylyl transferase dephospho CoA kinase-like protein	8.00E-79	Putative acetylornithine aminotransferase	5.00E-65
Bundle sheath cell specific protein 1	2.00E-35	Putative aconitate hydratase, cytoplasmic	1.00E-101
BZIP transcription factor	9.00E-12	Putative alcohol dehydrogenase 1	1.00E-121
Calcineurin B-like protein 10	1.00E-84	Putative alpha-soluble NSF attachment protein	1.00E-15
Calmodulin-like protein	2.00E-59	Putative beta-1,3-glucanase	1.00E-76
CAX-interacting protein 4 (CAXIP4)-like	6.00E-17	Putative C4 phosphoenolpyruvate carboxylase	9.00E-91
Cellulose synthase-1	1.00E-104	Putative C4 phosphoenolpyruvate carboxylase	1.00E-123
Chlorophyll a-b-binding apoprotein CP26	1.00E-134	Putative clathrin coat assembly protein APL17	3.00E-60
Chlorophyll a-b-binding protein 1E-21, chloroplast	2.00E-17	Putative collagen (PHD-finger family protein)	1.00E-63
Chlorophyll a-b-binding protein M9, chloroplast	2.00E-71	Putative cytochrome P450	1.00E-112
Chloroplast ferredoxin 1 (Putative uncharacterized protein)	3.00E-32	Putative DegP2 protease	1.00E-165
Cyclin-T1-1	7.00E-31	Putative dehydratase deaminase	3.00E-85
Cytochrome P450 family protein	1.00E-23	Putative disease resistance protein II	3.00E-43
Cytochrome P450-like	2.00E-91	Putative ER6 protein	1.00E-55
DNA-directed RNA polymerase	5.00E-94	Putative esterase	1.00E-110
DnaJ-related protein ZMD11	1.00E-136	Putative exoribonuclease (3' exoribonuclease family, domain 1 containing protein)	1.00E-120
DnaK-type molecular chaperone hsp70-like	1.00E-127	Putative gag-pol polyprotein	5.00E-95
DREB 1A (Transcription factor DREB1A)	0.073	Putative glucosyl transferase	3.00E-24
Elongation factor 1-alpha	1.00E-150	Putative iron inhibited ABC transporter 2	1.00E-121
Enolase	1.00E-117	Putative ketol-acid reductoisomerase	1.00E-122
Ethylene-responsive factor-like transcription factor ERF1a	3.00E-50	Putative leucine zipper protein	2.00E-08
Eukaryotic translation initiation factor 5A	6.00E-86	Putative leucine-rich repeat protein (BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1)	1.00E-101
Ferredoxin-NADP reductase	1.00E-112	Putative LMW heat shock protein	1.00E-17
Ferritin-1, chloroplast	7.00E-99	Putative MAPK delta-1 protein kinase	5.00E-47
Filamentation temperature-sensitive H 2A	7.00E-51	Putative mitochondrial energy transfer protein	8.00E-63
Glutathione S-transferase 4	1.00E-104	Putative Mob1-like protein (Mps one binder kinase activator-like 1A)	1.00E-113
Glutathione S-transferase GST 17	1.00E-103	Putative NADPH-dependent retinol dehydrogenase reductase	1.00E-99
Glutathione S-transferase GST 22	5.00E-82	Putative N-ethylmaleimide sensitive fusion protein	1.00E-143
Glutathione S-transferase GST 30	3.00E-67	Putative nuclear protein p30	1.00E-59
Glutathione S-transferase GST 42	4.00E-21	Putative nucleic acid binding protein	3.00E-76
Glutathione transferase	3.00E-78	Putative Oxygen-evolving enhancer protein 3-2, chloroplast	1.00E-38
Glutathione transferase	1.00E-71	Putative phosphate transport protein, mitochondrial	9.00E-62
Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast	1.00E-146	Putative phosphoenolpyruvate carboxylase	1.00E-55
Glycine-rich RNA-binding protein	3.00E-40	Putative phosphoglucomutase	1.00E-132
GspE2	1.00E-111	Putative phospholipase D-like protein	1.00E-60
H0103C06.6 protein	1.00E-128	Putative photosystem I antenna protein	1.00E-120
Haloacid dehalogenase-like hydrolase family protein	1.00E-104	Putative Phytoalexin receptor	5.00E-68
Heat shock cognate 70 kDa protein	1.00E-155	Putative PrMCS	4.00E-96
Heat shock protein 26	5.00E-92	Putative receptor-like protein kinase (Protein kinase domain containing protein)	3.00E-23
Histidine-containing phosphotransfer protein	7.00E-54	Putative RGH1A	7.00E-69
Histone H3	3.00E-69	Putative ribosomal protein S15(40S ribosomal protein S15)	2.00E-40
Hydrolase, carbon-nitrogen family protein	1.00E-102	Putative RING finger 1	6.00E-92
Hydroperoxide lyase	2.00E-86	Putative ripening regulated protein DDTFR18	2.00E-19
Hydroxyproline-rich glycoprotein family protein	5.00E-60	Putative RRM-containing protein	5.00E-49
Indole-3-glycerol phosphate lyase	3.00E-10	Putative Ser/Thr kinase	6.00E-81
Isochorismate lyase-like	2.00E-72	Putative SET-domain transcriptional regulator	1.00E-110
Leucine Rich Repeat family protein	3.00E-37	Putative tetrahalo-phosphatase	3.00E-46
Leucine Rich Repeat family protein	2.00E-35	Putative tRNA-glutamine synthetase	5.00E-97
LHCII type III chlorophyll a/b binding protein	1.00E-86	Putative UDP-glucose dehydrogenase (UDP-glucose 6-dehydrogenase)	4.00E-53
Lipase class 3 protein-like	9.00E-21	Putative UOS1	1.00E-110
Lipoxygenase 1	2.00E-05	Rab7 OS=Penicillium americanum	1.00E-110
Lipoxygenase	7.00E-89	Receptor-like protein kinase ARK1	1.00E-98
Maf-like protein	2.00E-52	Rhamnose biosynthetic enzyme 1	1.00E-66
Malate dehydrogenase	1.00E-121	Ribosomal protein L35A	6.00E-38
Metallothionein	2.00E-12	Ribosomal protein S21-like protein	2.00E-16
Metallothionein-like protein	1.00E-11	Ribosomal protein of RPS6-2	1.00E-101
Methionine synthase protein	1.00E-168	RING zinc finger protein-like	1.00E-36
Methylenetetrahydrofolate reductase 1	1.00E-114	RING zinc finger protein-like	1.00E-16
Mitochondrial aldehyde dehydrogenase	1.00E-111	RNA-binding protein	0.001
Mitochondrial uncoupling protein 4	4.00E-66	Sedobryulose-1,7-bisphosphatase	1.00E-108
Mitogen activated protein kinase 6	1.00E-12	Serine threonine protein kinase	1.00E-133
Monosaccharide transport protein 1	2.00E-65	Serine threonine-protein phosphatase PP1	1.00E-116
Multidrug resistance associated protein MRP2	6.00E-80	SIR2-like histone deacetylase	3.00E-92
Multidrug resistance-associated protein MRP1	1.00E-109	Small GTP binding protein Rab2A	1.00E-105
NADP-specific isocitrate dehydrogenase	1.00E-126	Terpene synthase 2	4.00E-93
NBS-LRR resistance-like protein	6.00E-50	Transcription elongation factor	9.00E-42
NBS-LRR type R protein, Nbs1-PI2	4.00E-05	Tropinone reductase 1	3.00E-86
NOD26-like major intrinsic protein	1.00E-125	U1 snRNP	4.00E-90
Non-specific lipid-transfer protein 1	3.00E-40	UDP-glucose 6-dehydrogenase	1.00E-127
Non-specific lipid-transfer protein	4.00E-36	UDP-glucose-4-epimerase	1.00E-124
OS/NBSa0085110.10 protein	3.00E-39	Vacuolar H+-ATPase c subunit	1.00E-57
Pepidyl-prolyl cis-trans isomerase	9.00E-40	V-ATPase subunit c	4.00E-38
Phosphoenolpyruvate carboxylase 2	2.00E-31	VIP3 protein	3.00E-60
Pre-mRNA splicing factor ATP-dependent RNA helicase	1.00E-101	YDG SRA domain containing protein	1.00E-130
Proteasome subunit beta type	4.00E-53	Zinc finger protein-like	1.00E-125
PSI type III chlorophyll a/b-binding protein	4.00E-19		