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Identification of stress-responsive genes in an *indica* rice (*Oryza sativa* L.) using ESTs generated from drought-stressed seedlings

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Abstract

The impacts of drought on plant growth and development limit cereal crop production worldwide. Rice (*Oryza sativa*) productivity and production is severely affected due to recurrent droughts in almost all agroecological zones. With the advent of molecular and genomic technologies, emphasis is now placed on understanding the mechanisms of genetic control of the drought-stress response. In order to identify genes associated with water-stress response in rice, ESTs generated from a normalized cDNA library, constructed from drought-stressed leaf tissue of an *indica* cultivar, Nagina 22 were used. Analysis of 7794 cDNA sequences led to the identification of 5815 rice ESTs. Of these, 334 exhibited no significant sequence homology with any rice ESTs or full-length cDNAs in public databases, indicating that these transcripts are enriched during drought stress. Analysis of these 5815 ESTs led to the identification of 1677 unique sequences. To characterize this drought transcriptome further and to identify candidate genes associated with the drought-stress response, the rice data were compared with those for abiotic stress-induced sequences obtained from expression profiling studies in *Arabidopsis*, barley, maize, and rice. This comparative analysis identified 589 putative stress-responsive genes (SRGs) that are shared by these diverse plant species. Further, the identified leaf SRGs were compared to expression profiles for a drought-stressed rice panicle library to identify common sequences. Significantly, 125 genes were found to be expressed under drought stress in both tissues. The functional classification of these 125 genes showed that a majority of them are associated with cellular metabolism, signal transduction, and transcriptional regulation.

Key words: Abiotic stress, candidate genes, drought, stress-responsive genes, transcriptome.

Introduction

Rice, the world's most important cereal crop, is the primary source of food and calories for about half of mankind (Khush, 2005). In Asia, rice provides as much as 80% of the dietary calories in countries such as Bangladesh and Indonesia. Rice-growing areas span the tropics, subtropics, semi-arid tropics, and temperate regions of the world. The predominantly rice-growing areas in Asia (~130 million hectares) are often threatened by severe abiotic stresses, the most common being drought. These areas include irrigated and rainfed lowlands, which together account for more than 85% of total world rice production. Drought has become the most significant constraint to realizing the yield potential of rice across all agro-climatic zones. In some years, abiotic stresses cause crop losses by as much as 50% (Boyer, 1982; Bray *et al*., 2000) and drought alone may cause yield losses of as

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much as 15% (Dey *et al*., 1996). Drought spells across Asia have become more frequent and severe, leading to irregular and insufficient irrigation of the crop and depletion of groundwater resources leading to 100% yield losses in certain areas. Some genetic improvement of rice for water-limited environments has been achieved by crop breeding and improved crop husbandry. At least part of the reason for the slow progress in improving the genetic foundation of drought tolerance in rice has been a lack of sufficient genetic information about genes that govern this complex trait and its component secondary traits.

Insufficient water availability leads to a host of biochemical, physiological, and metabolic changes in rice. These changes, many apparently adaptive, include a host of biochemical pathways associated with signal perception, transduction, and regulation of gene expression in a temporal and spatial pattern. A significant number of genes, gene products, and pathways associated with drought response have been identified in rice using a variety of experimental approaches (Rabbani *et al*., 2003; Kawasaki *et al*., 2001; Matsumura *et al*., 1999; Gibbings *et al*., 2003; Gowda *et al*., 2004). Numerous laboratory water-stress experiments investigating dehydration-induced changes in rice gene expression have revealed several candidate genes that may be associated with drought tolerance. Molecular genetic analysis of drought tolerance through phenotyping and marker assisted selection (MAS) has identified several genomic regions, quantitative trait loci (QTLs), associated with drought tolerance.

With the near-completion of the rice genome sequence (Goff *et al*., 2002; Yu *et al*., 2002; IRGSP, 2005) and rapidly growing databases, complex traits like drought tolerance are now amenable to a detailed molecular analysis using genomic tools. The rice genome was variously estimated to have 37 000–60 000 genes (Goff *et al*., 2002; Yu *et al*., 2002, 2005; IRGSP, 2005). One reason for this variation in gene number estimation is a lack of supporting evidence from deep Expressed Sequence Tag (EST) coverage. Many ESTs have been generated for rice, and these have been valuable in confirming and cataloguing genes (Sasaki *et al*., 1994; Uchimiya *et al*., 1992; Umeda *et al*., 1994; Yamamoto and Sasaki, 1997; Reddy *et al*., 2002*a*; Markandeya *et al*., 2003; Zhang *et al*., 2005) and in deciphering the role of transcriptionally regulated genes in different tissues (Ewing *et al*., 1999). However, only a few studies have focused on the analysis of transcriptome profiles of rice seedlings subjected to abiotic stress (Umeda *et al*., 1994; Matsumura *et al*., 1999; Kawasaki *et al*., 2001) or drought (Babu *et al*., 2002; Markandeya *et al*., 2005). ESTs provide a direct approach for discovering genes associated with a stress response. This has been demonstrated in several plant systems (Michalek *et al*., 2002; Fernandes *et al*., 2002; Echenique *et al*., 2002; Reddy *et al*., 2002*a*; Markandeya *et al*., 2005). Rice has good EST coverage, in general, and a relatively large collection of ESTs generated from drought-stressed plants has been reported (Reddy *et al*., 2002*a*, b; Markandeya *et al*., 2003). These resources can be valuable for further expression studies using microarrays and in single nucleotide polymorphism (SNP) analysis for discovering specific alleles of target genes associated with the drought-stress response. Numerous putative drought-responsive genes have been uncovered by genome wide expression studies in rice (Rabbani *et al*., 2003; Gibbings *et al*., 2003; Gowda *et al*., 2004; Kawasaki *et al*., 2001; Matsumura *et al*., 1999, 2003). Most of these are dehydration-associated expression profiles of rice conducted under laboratory conditions, and therefore may not mimic true field drought responses. However, because the experiments were rigorously controlled and environmental variables kept at a minimum, these expression analyses provided uniquely valuable information.

The EST approach has been taken to identify genes associated with drought-stress response and tolerance in rice. A normalized cDNA library has been constructed from drought-stressed seedlings of *indica* rice cultivar, N22, and large-scale EST data sets have been generated (Reddy *et al*., 2002*a*) that have been deposited in GenBank (Reddy *et al*., 2002*b*; Markandeya *et al*., 2003). In the present study, more than 6000 additional ESTs are generated, allowing construction of an N22 unigene set of 1677 sequences. This unigene set was used in a comparative analysis of rice, *Arabidopsis*, maize, and barley for discovering shared genes for the plant drought response. The identification of 589 candidate shared genes for the plant drought response is reported here. Their predicted molecular functions and potential utility are discussed.

Materials and methods

Drought-stress treatment and cDNA library construction

A drought tolerant, deep-rooted *indica* rice genotype Nagina 22 was used for drought-stress induction under defined field capacity. Rice seedlings were grown in pots and maintained in a growth chamber simulating upland growth conditions. The seedlings were maintained at 32±1 ° C during the day and 20±1 ° C during the night in 60% relative humidity. The control plants were grown at 100% FC and 1-month-old plants grown at 70% FC were gradually subjected to drought stress in order to reach 50% FC by regulating the water supply. The physiological condition of plants at 50% FC was monitored by RWC and leaf samples were collected from the plants exhibiting 50–60% RWC. The drought-stress symptoms such as leaf rolling and basal leaf senescence were apparent at this stage in stress-induced plants, while control plants growing at 100% FC were observed to grow well showing 95% RWC. Total RNA isolation, cDNA synthesis, normalization, and the cDNA library construction technique were elaborately discussed in our previous report (Reddy *et al*., 2002*a*) wherein 1200 ESTs had been generated and deposited at NCBI (Reddy *et al*., 2002*b*).

cDNA cloning and EST sequencing

In the present study, this normalized cDNA library was used for further EST generation. Chemically competent *E. coli* (DH5α′) cells

were transformed with this library and individual colonies were selected randomly. Cultures from individual colonies were grown overnight and used in plasmid DNA preparation for sequencing, after column purification (Qiagen). The quality and concentration of the template plasmid DNA was checked on 1% agarose (USB Biochemicals) gels. Acceptable quality plasmid DNAs were used directly for sequencing. ESTs were generated from 3′ end single-pass sequencing of 6144 cDNA clones using M_{13} (−40) reverse primer 5′-CGCCGAGGTTTTCCCAGTCACGAC-3′ or M_{13} (−20) reverse primer 5′-GTAAAACGACGGCCAGTG-3′, on an automated capillary genetic analysis system (MegaBACE 500). DYEnamic ET terminator chemistry (Amersham Biosciences) was used for sequencing reaction set-up. Post-sequencing reaction clean-up and loading of samples onto the MegaBACE 500 were according to the manufacturer's instructions with adjustments to suit our conditions. The average run time was about 180 min at 6–7 kV.

Sequence repositories and software resources used in EST analysis

The EST sequences generated in the present study, as well as those reported earlier from the same library (Reddy *et al*., 2002*a*, *b*) and IR64 drought-stressed panicle ESTs (Bennett *et al*., 2002) were the primary data sources for the analyses performed. Standard sequence processing tools, Phred (Ewing and Green, 1998), Phrap and cross_match (Smith and Waterman 1981; Gotoh, 1982) were used with Codoncode InterPhace (http://www.codoncode.com). Homology searches in the NCBI database were carried out using network client software with the DNATools interface (http://www.crc.dk/dnatools).

Genome sequence data for *O. sativa* subsp. *japonica* cv. Nipponbare collected from TIGR (http://www.tigr.org/tdb/e2k1/osa1/) and draft sequence for *O. sativa* subsp. *indica* cv. 93–11 of the Beijing Genomics Institute (http://btn.genomics.org.cn/rice/) were used in the analysis. In addition, full-length cDNA sequences from Nipponbare (The Rice Full-Length cDNA Consortium, 2003) and full-length cDNA sequences of putative candidate genes derived from *Arabidopsis* expression profiling studies from The *Arabidopsis* Information Resource (www.arabidopsis.org) database were also employed. The nucleotide, protein, and EST databases at NCBI (http://www.ncbi.nlm.nih.gov) were utilized for homology searches using the BLAST program (Altschul *et al*., 1997).

Sequence processing and analysis

The low quality regions present at the beginning and end of each sequence were trimmed using a Phred 20 cutoff value. Vector screening was performed using the cross_match program with Codoncode InterPhace software. Sequences were edited for the removal of oligodT tracks and other contaminants. A batch file of ESTs having greater than 100 bp length of sequence reads were submitted to the NCBI dbEST division of GenBank. After the rice genome sequence was largely completed (IRGSP, 2005), all ESTs from this project were compared to the genomic sequence. All sequences that did not exhibit excellent nucleotide homology with the Nipponbare genomic sequence were removed from GenBank, with the assumption that they were most likely to be derived from microbial contaminants. Phrap and CAP3 (Huang and Madan, 1999) assembly algorithms were used to assemble the individual ESTs into clusters of sequences derived from the same transcript as tentative consensus sequences (TCs) and singletons representing unique transcripts.

Annotation

Homology searches were performed against non-redundant (nr) nucleotide and protein sequence databases using BLASTN 2.2.2 and BLASTX 2.2.2 versions of the BLAST programs (Altschul *et al*., 1997) through BLAST 2.0 network client software with the DNAtools interface (http://www.crc.dk/dnatools). The BLASTN program was used to identify rice EST hits and rice BAC/PAC clones in the non-redundant (nr) nucleotide sequence database, High Throughput Genomic Sequences (HTGS) division of GenBank and the Beijing WGS (whole genome shotgun contigs) draft sequence of the *indica* rice genome (Yu *et al*., 2002) in the NCBI database.

Identification of ESTs consistently associated with abiotic stress

The ESTs associated with stress responses were identified from multiple sources, based on the compiled list of stress-regulated genes documented in more than one plant species (http://stress-genomics.org/stress.fls/expression/expression.html). In addition, data from microarray expression profiles of possible candidate gene sequences comprising 650 from *Arabidopsis* (Seki *et al*., 2001, 2002*a*, *b*; Kreps *et al*., 2002), 150 from barley (Ozturk *et al*., 2002), and 100 from rice (Matsumura *et al*., 1999; Kawasaki *et al*., 2001; Rabbani *et al*., 2003) have been used. All stress-responsive gene sequences were retrieved from the above studies and a local database was constructed and utilized for BLAST analysis. These were compared to the EST data set using TBLASTX with *E*-value >$1e^{-20}$.

Results

Expressed sequence tag generation and analysis

A total of 7794 cDNA clones were sequenced from the 3′ end; of these 6694 readable sequences were obtained with a high quality index (Phred score >20). The sequencing strategy proved to be very efficient, with a success rate of ~85%. Our optimized sequencing efforts, through preparation of high-quality, uniform concentrations of sequencing templates and reduced dye chemistries, drastically reduced the costs of single-pass sequencing. The high-quality readable sequences were screened for vector contamination, highly redundant ribosomal RNA sequences, *E. coli* DNA contamination, and these clones were eliminated from further analysis. Low-quality sequence regions were trimmed and sequences less than 100 bp in length were excluded. The resulting 5815 sequences were submitted to the dbEST division of NCBI (GenBank accession numbers: BI305180 to BI306756; BU672765 to BU673915; and CB964418 to CB967504). Of these, 390 were found to have no homologues in the nearly-completed Nipponbare rice genome sequence (IRGSP, 2005). Although it is possible that some of these are from the few rice genes that have not yet been sequenced from Nipponbare, or even very rare genes that might be found in *indica* cultivar Nagina 22 and not in *japonica* cultivar Nipponbare (Bennetzen *et al*., 2004; Ma and Bennetzen, 2004), but it is probable that most or all of these are ESTs from microbial contaminants in our field-grown rice seedlings. For instance, 380 ESTs were removed prior to the submission of the 5815 sequences because it was clear they were viral sequences from Adenoviral type 2 encoding minor capsid protein VI (Table 1). Microbial

contamination is an unavoidable outcome of EST analysis on field-grown plants, but they can easily be excluded from data analysis, now that a full rice genome sequence is available (IRGSP, 2005). A summary of the EST data is provided in Table 1.

Construction and functional classification of a unigene set from EST data

Clustering of the 5815 ESTs allowed construction of a unigene set of 2067 unique gene expression products from our drought-stressed rice library. The assembly of sequences produced 1239 singletons and the remaining 4576 sequences were grouped into 828 contiguous sequences (contigs). Of these 2067, 390 were removed as microbial contaminants, leading to the identification of the 1677 N22 unigene set.

Sequence analysis of the N22 unigene set

The assembled N22 unigene set comprising 1677 unigenes have been annotated and functionally classified based on the GO database (Gene Ontology Consortium, 2001). Annotation of the assembled unigene set, through homology searches in the NCBI nr nucleotide and protein databases, revealed that 57% of the unigene set has hits with known putative functions, the remaining 43% of the unigene set comprised hits with no functional characterization and include expressed proteins, unknown proteins, hypothetical proteins, putative proteins, and predicted proteins. Among the functionally classified unigenes, the transcription factor class constitutes the third highest category of functionally classified unigenes, the first two being that of cellular metabolism and protein synthesis (Table 2). Among the ESTs identified, 334 did not show any homology to rice dbEST or rice cDNAs, but were localized onto the rice genome sequence (IRGSP, 2005). These constitute 19% of the total N22 unigene set. These novel ESTs provide expression evidence for the *in silico* predicted genes and will assist in their intron and exon annotation. As the ESTs in this study were from a cDNA library constructed from drought stress, these novel ESTs may mainly represent genes involved in the drought-stress response. The N22 unigene set was mapped onto rice genomic sequences, and the number of unigenes mapped onto each chromosome is given in Table 3.

Identification of putative abiotic stress-responsive genes

This additional coverage of the rice transcriptome with the drought-stressed leaf library resulted in the identification of potential stress-related genes. As these are from a normalized library constructed from drought-stressed seedling tissue, the profiles may provide clues in the identification of drought-stress responsive genes. The highly represented transcripts were further verified by annotation and comparison with those described in previous studies on the abiotic stress response in several plant species. Accordingly, the redundancy of the stress-responsive genes were considered for *in silico* northern analysis and expression profiles of these highly expressed genes are listed

Table 1. *Summary of EST generation and analysis*

Total number of readable sequences obtained	6694
Vector sequences	354
Viral contaminants (Adenovirus type 2)	380
Highly redundant ribosomal RNA sequence	224
Sequences between 50–75 bp	142
Mean average read length (bp)	483
Number of high quality sequences deposited in GenBank	5815
Unigenes identified by CAP3 assembly	2067
Number of unigenes found with no significant homology to the finished rice genome sequence (library contaminants)	390
Number of rice unigenes	1677
Number of unigenes which have no expressional evidence in rice (novel unigenes)	334

Table 2. *Functional classification of N22 unigene sequences*

Category	Number of sequences (%)	Number of novel sequences(%)
Cellular metabolism	229 (13.7)	25 (7.5)
Cell structure	51 (3.0)	6 (1.8)
Detoxification	56 (3.3)	8 (2.4)
Hormone response	17 (1.0)	4 (1.2)
Heat shock proteins	26 (1.5)	1 (0.3)
Osmotic protectants	38 (2.3)	4 (1.2)
Protein kinases and phosphatases	62 (3.7)	8 (2.4)
Pathogen response	31(1.9)	3 (0.9)
Photosynthesis	65 (3.9)	10 (3.0)
Protein synthesis	142 (8.5)	20 (6.0)
Signal transduction	49 (2.9)	9 (2.7)
Transcription factors	95 (5.7)	15 (4.5)
Transport	52 (3.1)	3 (0.9)
Protein degradation	40 (2.4)	5 (1.5)
Secondary metabolism	12 (0.78)	1 (0.3)
Unknown and unclassified	712 (42.5)	212 (63.5)
Total	1677	334

Table 3. *Distribution of unigene sequences in the rice genome*

Chromosome	Number of contigs	Percentage
1	258	15.4
2	209	12.5
3	233	13.9
4	147	8.8
5	138	8.2
6	138	8.2
7	118	7.0
8	112	6.7
9	84	5.0
10	78	4.7
11	74	4.4
12	88	5.3
Total	1677	100.0

in Table 4. Those ESTs that exhibit an abundance of 10 or more are considered here. Comparative *in silico* analysis of paralogues from multiple sources of rice (Matsumura *et al*., 1999; Kawasaki *et al*., 2001; Rabbani *et al*., 2003) and orthologues from other plants (Seki *et al*., 2001, 2002*a*; Kreps *et al*., 2002; Ozturk *et al*., 2002) led to the identification of 589 putative stress-responsive genes (SRGs). These are classified into 15 functional groups

Table 4. *Abundantly expressed stress-responsive genes in N22 seedlings*

N22 EST accession	Full-length cDNA accession	Abundance	Putative function	Identical accession in GenBank
BI305796	AK062796	101	Rice metallothionein	AB002820
BI306046	AK061611	64	Ribulose *bis*phosphate carboxylase, small subunit	L22155
BI306560	NF[a]	60	Heat shock protein 16.9C	L14444
BI305614	AK059196	55	Thioredoxin *h*	D26547
BI305481	AK058313	49	Metallothionein-like protein	AF001396
BI305617	AK058529	47	Metallothionein-like protein type 2	U57638
BI305566	AK106205	47	Rd22 (dehydration-responsive protein)	D10703
BI305843	AK060920	41	Triosephosphate isomerase	L04967
BI306132	NF	31	β-D-glucan exohydrolase	U46003
BI306388	NF	29	Jasmonate-induced protein	X98124
BI306379	AK104420	27	Peroxidase	M73234
BI305397	AK058788	25	Photosystem I PSI-K subunit	L12707
CB964951	AK065178	23	Hypothetical protein	NM_127785
BI306352	AK070414	23	Lipid transfer protein LPT IV	AF017361
BI305945	AK098931	20	No hit	
CB966658	AK109382	20	Quinone oxidoreductase-like protein	NM_121703
BI305557	NF	19	Ubiquinol–cytochrome *c* reductase	X79275
BI306687	NF	18	Cys2/His2 zinc-finger protein	X60700
BI306097	AK104005	18	Lipid transfer protein precursor	U29176
BI305750	AK065866	18	Chitinase	AB027426
CB967158	AK058918	17	Ribosomal protein l36e	AL132960
BI306475	AK070090	16	Calmodulin 1	AF042840
BI305543	AK073698	16	Malate dehydrogenase, NAD-dependent	X78800
BI305450	AK105037	15	Translation initiation factor SUI1	AF094774
BI305417	AK100321	15	Cytochrome P450	AY072297
BI305422	AK104176	15	Chlorophyll *a/b*-binding protein	U74295
BI305391	NF	14	3-oxoacyl-(acyl-carrier-protein) reductase, putative	AJ243091
BI306217	AK058741	13	Histone H4	M12277
BU673062	NF	13	Expressed protein	NM_129142
BI306338	AK106979	13	Hypothetical protein	AJ271079
BI305440	AK100908	13	UDP-glucuronic acid decarboxylase	AB079064
BI306390	AK105055	12	Photosystem II 10 kDa polypeptide psbr	U86018
CB966380	AK062463	12	Lipid transfer protein	U88090
BU673470	NF	12	Dehydration stress-induced protein	AF314810
BI305705	AK061000	12	Dof domain, zinc finger	AB028132
BI305703	U18404	11	Metallothionein-like protein	U18404
BI305752	AK111242	11	Glycosyl hydrolases family 16, putative	AF163820
BI305253	AK064960	11	Glyceraldehyde-3-phosphate dehydrogenase, type I	AF251217
CB966697	AK062882	11	AP2 domain transcription factor	NP_195167
BI306264	AK104987	11	Glutamine synthetase	X14245
BI305524	AK070516	11	Fructose-1,6-*bis*phosphatase	AB007193
BI306389	AK104912	11	Xyloglucan endo-1,4-β-D-glucanase	X93175
BI306059	AK066834	10	Osmyb1 transcription factor	D88617
BI305933	AK068686	10	Cell division protein ftsh-like protein	NM_111112
BI305835	AK066933	10	V-type H^+-translocating pyrophosphatase	D45384
BU672803	NF	10	Chitinase-B	AF402939
BI305595	AK064780	10	Heat shock protein 82	Z15018
BI305683	NF	10	Root-specific rcc3	L27208
BI306058	AK065962	10	Glutaredoxin	D86744
BI305598	AK068555	10	Ribulose *bis*phosphate carboxylase, small subunit	AF017364
BI306026	AK104719	10	Aldolase C-1	D50307
BU672976	AK065027	10	Disease resistance response protein	NM_123616
BI305650	AK065044	10	Exoglucanase precursor	U46003
BI305947	AK072166	10	Gigantea-like protein	AJ133787
BU673030	AK098982	10	Ribosomal protein S31	D38011
CB965712	AK067801	10	Phenylalanine ammonia-lyase	Z15085
BI306276	AK066771	10	Pathogenesis-related protein	U20347
BI306443	AK069446	10	Catalase	D26484

[a] NF indicates no significant similarity found in full-length cDNAs of rice.

(Fig. 1). Interestingly, the distribution of the 589 putative stress-responsive ESTs among the functional categories showed that transcription factors were particularly well represented. The list of abiotic stress-responsive genes identified from our ESTs, along with the source for paralogues or orthologues from rice and other plants, respectively, is given in supplementary Table S1 at *JXB* online. All of the identified SRGs were mapped to the rice genomic sequence (IRGSP, 2005) (Table 5).

Digital northerns

Apart from providing an efficient method for gene discovery, EST data sets can be used to provide low precision estimates of mRNA levels in a tissue through estimations of EST redundancy (Ohlrogge and Benning, 2000; Audic and Claverie, 1997). The EST library used in this study has relatively low redundancy because it was normalized (Reddy *et al*., 2002*a*), but still contains many more copies of some transcripts than others. The levels of redundancy among the contigs derived from the CAP3 assemblies have been studied. Of the 828 assembled sequences with more than one EST representation, the most highly represented transcripts were from metallothioneins, followed by transcripts involved in oxidative stress, novel genes, and expressed proteins with no known function. The *in silico* expression profiles are represented in Table 4.

Comparative analysis of expression profiles between leaf and panicle ESTs under drought stress

Whether the identified stress-responsive genes also appear in other tissue under drought stress, they were compared with panicle ESTs of an IR64 (*indica*) library made from drought-stressed plants. Surprisingly, only 280 genes were found in common between the two libraries. Among these, 125 genes were identified as predicted stress-responsive genes (Table 6). Functional classification of common drought-responsive genes showed that a majority

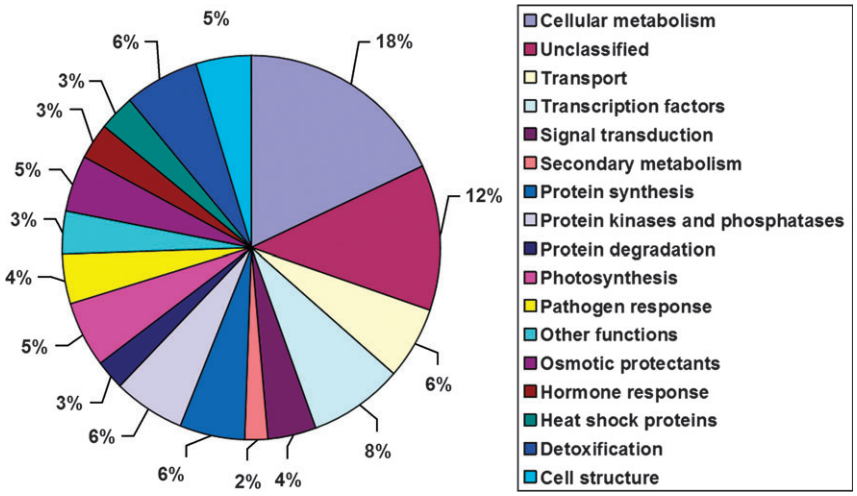

Fig. 1. Functional classification of 589 putative stress-responsive genes of rice.

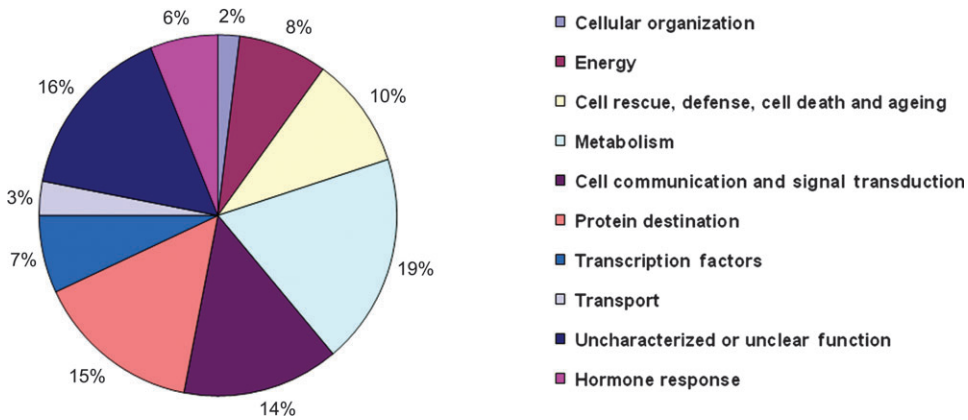

Fig. 2. Classification of 125 drought-stress responsive genes shared between leaf (N22) and panicle (IR64) tissues.

Table 5. *Distribution of putative stress-responsive genes (SRGs) in the rice genome*

Chromosome	SRGs
1	94
2	62
3	78
4	48
5	43
6	63
7	43
8	44
9	24
10	32
11	28
12	30
Total	589

of them (65%) are associated with metabolism, cellular communication and signal transduction, transcription factor, cellular defence, and protein destination categories (Fig. 2).

Discussion

In this study the utility of an EST-based approach for gene discovery in rice has been demonstrated. Nagina 22, an *indica* rice cultivar, was chosen for EST generation and gene discovery, based on its phenology and the utility of this genotype in developing drought-tolerance lines. Nagina 22 is adapted for upland conditions and possesses a constellation of morphological and physiological characters such as early maturity, heat tolerance, two-point root system, accumulation and mobilization of carbohydrates, high regeneration and recovery processes, all associated with drought tolerance mechanisms in plants. The extensive EST resources from N22 were used in characterizing the N22 drought-stress transcriptome and in identification of drought-stress responsive genes. A classification of the unigene set revealed a significant number of novel genes with unknown functions. Since these are specific to the drought-induced *indica* library and are not represented in other stress libraries of rice, most of them presumably are stress-responsive genes. Molecular functional classification of 1677 unigenes shows a large number of genes that are predicted to be involved in signal transduction and transcriptional regulation (Table 2). Of the 1677 N22 unigenes, 81% showed homologous sequences to existing rice expressed genes and the remaining 19% have no expressional evidence for rice EST or cDNAs in databases. These 19% constitute novel rice genes which have been uncovered in this study. Analysis of the N22 unigene set revealed that 57% of them have a candidate functional role assigned and the remaining 43% belong to genes which have expressional evidence, but no functional role assigned. This suggests that there are many functionally unclassified genes that need to be characterized to discover new pathways and mechanisms adapted by plants to cope with drought stress.

Analysis of the N22 unigene set revealed many putative candidate genes for stress response that can be major targets for engineered stress tolerance. Among these are the genes encoding proteins that are associated with an osmotic stress response such as osmoprotectant synthesis (BU673697, BU673025), the dehydration stress-induced proteins (BU673123, BU672787), and the dehydration-responsive proteins like RD22 (BU672774). Data in Table 4 shows that the EST data revealed a number of genes associated with sugar metabolism and antioxidant pathways, as well as osmolyte synthesis. Of the two isoforms of glutathione-*S*-transferases (GST) (BU673645), one shows sequence similarity with *Zea mays* GST (AF244678) and the other, *OsGSTZ1*, to that of rice (AF309381). Evidence for a protective function of intracellular reactive oxygen species scavenging systems by glutathione *S*-transferase and glutathione peroxidase has been obtained from transgenic experiments in maize (Roxas *et al*., 1997). Homologues of these genes were identified through our Nagina 22 EST analysis, and thus provide both orthologues and paralogues that may have evolved during duplications and acquired a new functional role in the due course of evolution. Several Nagina 22 ESTs were identified from genes that encode enzymes which break down H_2O_2 to water; catalase (BU673091, BU673392), ascorbate peroxidase (APX) (BU673288) showing homology to tomato APX (A3251882), and manganese superoxide dismutase (MnSOD) (BU673715) which is a homologue of rice MnSOD (L34039) seem to provide tolerance to oxidative stress. The over-expression of MnSOD in chloroplasts conferred tobacco paraquat tolerance (Tsang *et al*., 1991). In a field study McKersie *et al*. (1996) reported that transgenic alfalfa expressing MnSOD suffered reduced injury from water-deficit stress.

The most abundant class of Nagina 22 drought-stressed transcripts represent a group of genes that encode metallothioneins and metallothionein-like proteins, which help in metal detoxification. These are low molecular weight, cysteine-rich, soluble, and metal-binding proteins found in both plant and animal tissues. These proteins sequester toxic metal ions. Seven groups of metallothioneins were found showing different levels of sequence similarity to rice metallothioneins (BU672908, BU672800, BU672917, BU673120, BU673768, BU672968, and BU672982). Rice metallothioneins expression is reported to be markedly increased under H_2O_2, heat shock, abscisic acid, and salicylic acid in shoots (Zhou *et al*., 2005), indicating their functional role during oxidative stress. Promoter analysis revealed heat-shock elements motifs, besides many light-responsive elements. Since the genotype under study is a heat-tolerant cultivar, these could be the reasons for high transcript abundance under drought stress. Further characterization of these classes of genes is needed to elucidate

Table 6. *Comparison of stress-responsive ESTs from drought-stressed N22 leaf and IR64 panicle libraries*

N22 EST accession number (leaf)	Putative function	TIGR gene model	IR64 EST accession number (panicle)
	Cellular metabolism		
BU673346	Putative amine oxidase	11670.t05414	CA762096
BI306458	Ubiquinol–cytochrome *c* reductase	11669.t05537	CA766060
BI305797	Enolase	11669.t01296	CA759903
BU672850	Succinic semialdehyde dehydrogenase	11668.t00676	CA763533
BI306457	Cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPDH	11670.t03801	CB096682
CB964504	Trehalose-6-phosphate synthase	11682.t03982	CA765766
BI306315	Similar to ATP-citrate-lyase	11687.t04301	CA767579
CB967361	Aldolase	11667.t00188	CA765072
BI305193	Respiratory burst oxidase homologue	11687.t02970	CA760620
CB964609	Biotin synthase	11674.t04125	CA762191
BI306290	Ca^{2+} sensitive 3′(2′),5-diphosphonucleoside 3′(2′) phosphohydrolase	11686.t00729	CA759552
CB965408	Phosphoethanolamine methyltransferase	11667.t04614	CA762802
CB964525	Methionyl aminopeptidase-like protein	11673.t02294	CA759430
BI305434	Acyl-CoA:1-acylglycerol-3-phosphate acyltransferase	11667.t05351	CA762908
BI305360	Cytochrome P450	11667.t04030	CA763743
BI306288	Putative copper amine oxidase	11670.t03710	CA759334
BI305831	Sucrose synthase	11680.t00847	CA761643
BU673036	Putative phospholipid cytidylyltransferase	11687.t00205	CA766827
BI306060	GF14-c protein	11674.t03189	CA760002
BI305999	Expressed protein	11668.t04594	CA760466
	Structural proteins		
CB967019	Histone H3.2 protein	11669.t02534	CA761515
BI306497	Ubiquitin (mub1) gene	11667.t02054	CA763276
BU673900	Actin	11669.t04750	CA766273
	Defence		
BI306248	Thioredoxin *h*	11673.t00784	CA763750
BU673649	Glutathione *S*-transferase OsGSTZ1	11686.t00973	CA759451
BU673288	Ascorbate peroxidase (TL29)	11670.t04787	CA762991
CB966179	Phospholipid hydroperoxide glutathione peroxidase	11669.t02241	CA763032
CB967248	Glycolate oxidase	11673.t03998	CA764333
BI306655	Glyoxalase I	11674.t00825	CB096525
BI306573	Glutathione-dependent dehydroascorbate reductase precursor	11680.t01165	CA767174
BU673645	Glutathione *S*-transferase GST 13	11669.t00325	CA766885
	Pathogen response		
CB965601	Thaumatin-like protein	11680.t04523	CB097147
BU673639	Wound-inducive gene	11674.t02539	CB096245
BU672887	Sgt1	11667.t04013	CA759388
BI305746	Cyclophilin CYP5	11680.t04712	CA767313
	Hormone response		
BU673400	Indole-3-glycerol phosphate synthase	11670.t03633	CA763617
BI305739	Abscisic acid- and stress-inducible protein (Asr1)	11687.t00573	CA759579
BI306538	1-aminocyclopropane-1-carboxylate oxidase	11673.t02534	CA765577
BU673190	Putative IAA1 protein	11669.t04977	CA765289
BI306117	Elongation factor EF-2	11670.t00182	CA759898
BI305642	Phytochrome-associated protein	11667.t00846	CA759750
CB965518	Auxin-induced protein	11670.t02490	CA760053
	Heat shock proteins and osmotic protectants		
BI306480	High mobility group I/Y-2	11674.t03171	CA761966
BU673322	Luminal binding protein 2 precursor (BiP2)	11680.t01001	CB097040
BI306214	Chaperonin 21 precursor	11681.t02378	CA764694
BI305618	GrpE protein	11668.t03643	CA764945
BI306513	Mitochondrial chaperonin-60	11676.t02764	CA759723
BI306548	16.9 kDa heat shock protein	11667.t00335	CA761072
BI305213	Heat stress transcription factor Spl7	11668.t02914	CA760455
BI306657	Heat shock protein 82	11681.t02749	CA760049
BI306343	Glycine-rich protein	11680.t03864	CB096773
BI305248	Dehydrin	11687.t02337	CA766722
	Protein degradation		
BI306554	Serine carboxypeptidase	11687.t02109	CA764189
BI305677	Ubiquitin protein fused to a ribosomal protein	11669.t01168	CB097190
	Protein kinases and phosphatases		
BI306067	OsCDPK7	11670.t04657	CA765008
BI306714	Phosphoribulokinase	11668.t04309	CA764349
BI305348	Calcium-dependent protein kinase	11673.t03565	CA759704
BI306130	Protein kinase, putative	11669.t01452	CA762064
BI305344	Serine/threonine kinase	11669.t01890	CA762856

Table 6. (*Continued*)

N22 EST accession number (leaf)	Putative function	TIGR gene model	IR64 EST accession number (panicle)
CB967004	Protein kinase	11682.t03978	CA761897
BU672858	Mitogen-activated protein kinase homologue MMK2	11676.t03405	CA763089
BI305269	MAP3K-β-1 protein kinase	11669.t01408	CA760582
CB966430	Mitogen-activated protein kinase	11680.t00510	CA760368
BI305458	Nucleoside diphosphate kinase	11676.t03651	CB096334
BI305224	Contains similarity to protein phosphatase-2c~gene	11670.t03111	CB096996
CB964933	Protein phosphatase 2C-like protein	11669.t00343	CA766893
BI306327	Protein phosphatase 2C-like protein	11670.t05303	CA765327
	Photosynthesis		
BI306021	Chlorophyll *a*/*b*-binding protein	11673.t03477	CB097064
BU673906	Ribulose bisphosphate carboxylase/oxygenase	11686.t01663	CA767270
BU673889	Chloroplast apocytochrome b6 (petB)	11667.t05409	CA764607
BI305598	Small subunit of ribulose-1,5-*bis*phosphate carboxylase	11686.t01843	CB096380
BU672866	Putative chlorophyll synthase	11676.t03688	CA765915
BI305564	CP26, partial sequence	11687.t01243	CA760967
BI305247	Putative chloroplast RNA helicase VDL isoform 1	11667.t06958	CB097044
BI306736	Photosystem II D1 protein	11669.t01915	CB096561
BI305816	Photosystem I chain IV precursor	11673.t02296	CA765338
BI305763	Triosephosphate isomerase (Rictipi2) gene	11667.t00449	CA763752
	Protein synthesis		
CB967287	40S subunit ribosomal protein	11680.t00329	CA760617
BI306102	EF-1α	11669.t00701	CA759893
BI306120	EREBP-like protein	11669.t00750	CA766852
CB965835	*S*-ribonuclease binding protein SBP1	11668.t00276	CA759415
BI306102	EF-1α	11669.t00701	CA759893
BU673172	Elongation factor 1α	11669.t00701	CA759893
CB964857	No hit	11687.t00576	CB096917
BI306632	Ribosomal protein	11673.t03378	CB096625
BU673302	Translation initiation factor 4A	11669.t03349	CA763980
CB967086	RSZp22 splicing factor	11680.t00786	CA762148
BU673172	Elongation factor 1α	11669.t00701	CA759893
	Secondary metabolism		
BI306467	Putative strictosidine synthase-like	11669.t05057	CA763632
BI305578	γ-tocopherol methyltransferase	11668.t04338	CA759409
	Signal transduction		
BI305552	Small GTP-binding protein (Ran1)	11667.t03912	CA763744
BU673756	Signal recognition particle receptor α	11667.t06848	CA763094
BI305605	Vesicle soluble NSF attachment protein receptor	11669.t02342	CA759161
BI305572	Small GTP binding protein RACDP (RACD)	11668.t05480	CA763414
BU673747	Putative GTP-binding protein	11667.t00746	CA762975
	Transcription factors		
BU673061	Zinc finger protein	11670.t03862	CA765791
BI306209	RING finger protein	11682.t00608	CA761322
BU673870	HOS59	11680.t04149	CA760336
BU672942	Small zinc finger-like protein (TIM9)	11686.t03641	CA764474
BI305867	RING3-like bromodomain protein	11680.t00364	CA767235
BI305994	Similar to lipase	11667.t02472	CA764973
BI306221	Putative RING zinc finger protein	11676.t01170	CB096539
BI306016	Small nuclear ribonucleoprotein	11668.t00244	CA767531
	Transport		
BU673203	ABC transporter family protein	11668.t05262	CB096918
BI306386	Vacuolar H^+-ATPase (vatp-P1)	11687.t00590	CA763376
BU672768	Major intrinsic protein	11668.t01189	CA760846
BU673507	Vacuolar membrane ATPase subunit G	11670.t04784	CA767335
BI305935	DNA binding protein, putative	11670.t03474	CA760475
	Unclassified		
BI305711	Expressed protein	11681.t02973	CA765335
CB967067	Amino acid transporter family	11680.t04035	CA767198
BU673532	Unknown protein	11674.t02230	CA762677
BI306384	Expressed protein	11670.t03940	CA764882
BI306017	Unknown protein	11670.t05378	CA761712
BI306104	No hit	11681.t02166	CA761314
CB966166	Expressed protein	11667.t03957	CA765382
BI306086	Hypothetical protein	11682.t03722	CA767428
BI306484	Expressed protein	11669.t02872	CA766081
BI306324	Unknown protein	11667.t02941	CA767540
CB967400	Unknown protein	11669.t06006	CB096667

Table 6. (*Continued*)

N22 EST accession number (leaf)	Putative function	TIGR gene model	IR64 EST accession number (panicle)
BU673135	Unknown cold-induced protein	11682.t04051	CB096988
BI306518	Timing of CAB expression 1-like protein	11681.t03083	CA764459
BI306163	Early nodulin	11668.t01140	CA764447
CB967012	Pollen allergen-like protein	11670.t03620	CB096861
BU673348	Non-phototrophic hypocotyl 1b	11670.t02192	CA763992
BI306519	Putative pumilio/Mpt5 family RNA-binding protein	11668.t05346	CB096802
BI306073	Wound induced protein homologue	11667.t00305	CB096984

their role in the drought-stress response in rice. The other detoxifying proteins include thioredoxin (BU673762) showing homology to that of rice (AB053294), and the other showing homology to a gene in *Arabidopsis* (AY085055).

The stress-responsive gene sets also include those associated with water channels and transporters such as aquaporin (BU673363), an ABC transporter protein (BU673203), and an oligopeptide transporter protein (BU673275). The recently discovered aquaporins act as water channels and their transcript levels are shown to be influenced significantly by a wide variety of environmental stimuli (Weig *et al*., 1997). These are reported to be involved in water uptake and may function in metabolite or ion transport. These transport proteins are reported to show a 5-fold up-regulation under stress (Seki *et al*., 2002*a*).

Other important genes uncovered in Nagina 22 drought-stress ESTs include the membrane-stabilizing proteins and late embryogenic abundant proteins which enhance water-binding capacity, creating a protective environment for other proteins or structures, referred as dehydrins (BI305248). They play a major role in the sequestration of ions that are concentrated during cellular dehydration. Numerous genes involved in membrane stability and thermotolerance have been identified from the present EST collections. These include heat shock proteins (HSPs), which have been widely hypothesized to be a major factor in cell thermotolerance (Howarth and Ougham, 1993) and tolerance to other environmental assaults such as oxidative, chilling, salt, and heavy metal stresses. HSPs were also shown to regulate expression of other stress-inducible genes (Liu and Thiele, 1996).

Another group of genes uncovered include those encoding proteins involved in signal transduction and the regulation of gene expression. It is probable that these play a regulatory role in the plant stress response. These include protein kinases, protein phosphatases, transcription factors, and enzymes in phospholipid metabolism and other signaling molecules such as calmodulin-binding protein. Many kinases were observed in the collection (see supplementary Table S1 at *JXB* online), including mitogen activated protein kinases (MAPKs) (BU672858, BI305201), calcium-dependent protein kinase (BU673731), adenosine kinases, and adenylate kinases (BU673745, BU672936). In addition, the signalling molecule calmodulin (BU673090, BU672925, BU673775), a common participant in the MAPK signal transduction cascade, was found in the Nagina 22 EST libraries studied. The present EST analysis also revealed many more candidate signalling genes, such as MAP kinases and various transcription factors.

The identified transcription factors include proteins having typical DNA binding motifs such as bZIP, MYB, MYC, EREBP/AP2, and ZINC fingers. The role of various transcription factors in stress-responsive gene regulation has been investigated in plants, and several target genes and pathways have been identified (Thomashow, 1998; Park *et al*., 2001; Seki *et al*., 2001; Singh *et al*., 2002; Shinozaki *et al*., 2003). Overall, the normalized library proved to be a rich source of stress-responsive rice genes.

The EST data and analysis presented here are a first global overview of the transcripts that are expressed in *indica* rice under water stress. The annotation and comparative analysis of these ESTs have identified many genes associated with or having a potential role in drought-stress tolerance. These genes provide a starting point for understanding the nature of molecular mechanisms of a plant's response and tolerance to drought. EST analysis has uncovered numerous novel genes and transcriptional activators, the master switches that influence the expression of cascades of genes associated with a stress response.

Comparative analysis of SRGs of N22 (the present study) with IR64 panicle ESTs generated under drought-stress revealed that 125 (40%) of them are in common, demonstrating similar patterns of regulated pattern of gene expression between leaf and panicle tissues (Table 6). This pattern is largely similar to the one reported earlier (Tang *et al*., 2005). These genes are presumably associated with drought-stress response and tolerance during different growth stages of the rice plant. The remaining 60% of SRGs uncovered in this library could be genotype-specific or tissue-specific. However, whether these genes are actually genes involved in rice drought-tolerance cannot be definitely determined without further expression profiling, allele mining, QTL mapping, and reverse genetic experiments.

Identification of the genes in the rice genome has relied heavily on non-experimental methods such as *ab initio* gene prediction, sequence homology, and motif analysis. These efforts were limited by the insufficient ability of current gene-finding programs to identify and annotate genes from complex genomes effectively (Guigo *et al*., 2000; Mathe *et al*., 2002; Zhang *et al*., 2002; Bennetzen *et al*., 2004). So far, the identification of coding regions on a genome scale in rice has focused on EST and full-length cDNA analyses (Kikuchi *et al*., 2003). However, the available EST and cDNA resources do not comprehensively reveal all the genomic coding information as they are biased mostly toward highly expressed genes. Not surprisingly, exhaustive efforts to uncover the rice transcriptome have represented less than half of the predicted genes (Feng *et al*., 2002; Reddy *et al*., 2002; Sasaki *et al*., 2002; Yu *et al*., 2002; Markandeya *et al*., 2003, 2005; Zhao *et al*., 2004). Our EST data has aided in providing expression evidence for an additional 334 unigenes. Most EST sequencing projects have proven to be expensive due to high clone redundancy (Reddy *et al*., 2002*a*). In particular, transcript profiling under drought stress had not been carried out much in rice until our study to identify the drought transcriptome through large-scale EST generation. The EST resources of N22 have been found to be useful in the generation of high-density physical maps of stress-responsive genes in rice (Markandeya *et al*., 2005), to develop candidate gene molecular markers across selected cereals (Sivarama Prasad, 2005), including EST-PCRs (Chandrasekhar, 2005), and to identify SNPs (Lachagari *et al*., unpublished data). Further these ESTs are now being used as target probes in the fabrication of cDNA microarrays for expression profiling studies under field drought stress.

Supplementary data

Supplementary data are available at *JXB* online.

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