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Supplementary Material

RESEARCH ARTICLE

Meta-Analysis of Expression of the Stress Tolerance Associated Genes and Uncover their *Cis*-Regulatory Elements in Rice (*Oryza sativa* L.)

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SUPPLEMENTARY TABLES

Supplementary Table 1. Summary of information associated with gene expression experiments used for meta-analysis.

Number of experiments	Title	Summary	Design
1	Differential expression for salt and drought stress	Leaf samples were used. We exposed young seedlings to NaCl and drought.	Expression study in 24 hrs salt and drought conditions. Salt-sensitive and salt-tolerant strains of rice exposed to NaCl or control conditions. Drought-sensitive and drought-tolerant strains of rice exposed to drought or control conditions [53].
2	Expression data of 8 rice accessions under cold stress in seedling stage	The 8 accessions from China Core Collection include 4 cold tolerance accessions, 3 sensitivity accessions and 1 intermediate type accession. We used microarrays to detail variation of the gene expression after cold treatment and screen more cold-response genes in rice.	In order to getting more understanding of gene expression after cold treatment in rice seedling stage, we applied 8 accessions by cold stress screening in this Affymetrix microarrays, and each accession include 3 time-points samples: (1) before the cold treatment; (2) 6 hours after the cold treatment; (3) 24 hours after the cold treatment [47].
3	Genome-wide Gene Expression Profiling of Salinity Responsiveness in Rice	Under salinity condition, the number of differentially expressed genes (DEGs) in 177-103 was more than that in IR64, and most of up-regulated DEGs in 177-103 are response to stress. But in IR64, most of up-regulated DEGs are transcription related genes. The DEGs under salinity showed very strong tissue specificity, the number of DEGs in leaf was more than that in root. A lot of genes differentially expressed by exogenous ABA treatment under salinity condition, such as Leaf senescence protein, 1-deoxy-D-xylulose 5-phosphate synthase 2 precursor and Protein of unknown function DUF26 were induced by ABA and contributed to salinity tolerance.	In this study, the gene expression patterns across two organs including leaves and roots at seedling stage were characterized under control, salinity, salinity+ABA treatments by using the Affymetrix rice microarray platform based on a salinity tolerant rice line derived from IR64 [50].
4	Transcriptome profiling for drought tolerant and susceptible cultivars of indica rice	In this study, we have analyzed the transciptomes of two contrasting cultivars, i.e. Dagad deshi (tolerant) and IR20 (susceptible), under control and stress conditions to elucidate the differences in their responses to drought stress using Affymetrix microarray platform.	Hydroponically grown seven-day-old seedlings of Dagad deshi and IR20 were subjected to drought stress by placing them on 3 mm Whatmann sheets under light for 3 h and 6 h at 28±1oC. For control samples, seedlings were kept in RGM (root growth medium) for 6 h at 28±1oC. RNA extracted from each sample was hybridized on rice Affymetrix microarrays. Three biological replicates of each sample were used for microarray analysis. Overall, eighteen samples were analyzed representing control, 3 h and 6 h of dehydration stress for each cultivar (Dagad deshi and IR20) [48].

(Table 1) cont.....

Number of experiments	Title	Summary	Design
5	A resource for systems analysis of transcriptional modules involved in drought response in rice	Here we present drought transcriptomes of rice in three developmental stages and gain insights into the processes and regulatory mechanisms involved in common and stage specific drought responses.	Total RNA was isolated from the rice seedlings, vegetative (V4) and reproductive (R4) tissues of both control and stress treated plants for hybridization on Affymetrix microarrays. Two independent replicates for seedling and reproductive stages, and three replicates for vegetative stages were generated, for both control and stress samples. For drought treatments, plants were gradually subjected to field drought conditions in order to reach 50% field capacity (FC) by regulating water supply, whereas control plants were maintained at 100% FC [52].
6	Expression data from rice varieties IRAT109 and ZS97 for drought stress treatment in flag leaves	Comparative transcriptional profiling of two contrasting rice genotypes, IRAT109 (drought-resistant japonica cultivar) and ZS97 (drought-sensitive indica cultivar), under drought stress during the reproductive stage	Four samples with RWC in the range of 94–95% (no stress, D0), 83–88% (slight drought in which leaves were slightly rolled, D1), 74–78% (moderate drought in which about half of each leaf was rolled, D2), and 65–69% (severe drought in which all leaves were completely rolled, D3) were collected for expression profiling analysis using an Affymetrix GeneChip [51].
7	Expression data for heat shock in rice seedlings	In this study, we have analyzed the expression profiles of rice genes under control and heat shock conditions using microarray technology to identify the genes differentially expressed.	14-day-old light-grown rice seedlings grown under controlled conditions and those subjected to heat shock were used for RNA extraction and hybridization on Affymetrix microarrays. Three technical replicates of each sample were used for microarray analysis. For heat shock treatment, the seedlings were kept in a chamber at 42-degree C. The seedlings kept at 28-30 degree C, served as control (Seedling) [46].
8	Expression data for stress treatment in rice seedlings	In this study, we have analyzed the expression profiles of rice genes under control and abiotic stress conditions using microarray technology to identify the genes differentially expressed during various abiotic stresses.	Seven-day-old light-grown rice seedlings grown under controlled conditions and those subjected to various abiotic stress conditions were used for RNA extraction and hybridization on Affymetrix microarrays. Three biological replicates of each sample were used for microarray analysis. For salt treatment (SS), the rice seedlings were transferred to a beaker containing 200 mM NaCl solution for 3 h. For desiccation (DS), rice seedlings were dried for 3 h between folds of tissue paper at 28±1 degree C, in a culture room. For cold treatment (CS), the seedlings were kept at 4±1 degree C for 3 h. The seedlings kept in water for 3 h, at 28±1 degree C, served as control (Seedling) [49].
9	Coordinated regulation of photosynthesis in rice, increases yield and tolerance to environmental stress.	To study the regulation of photosynthesis, we developed a rice gene regulatory network and identified a transcription factor HYR (HIGHER YIELD RICE) associated to PCM, which on expression in rice enhances photosynthesis under multiple environmental conditions, determining a morpho-physiological program leading to higher grain yield (GY) under normal, drought and high temperature stress conditions. We show HYR is a master regulator, directly activating photosynthesis genes, cascades of transcription factors and other downstream genes involved in PCM and yield stability under drought and high temperature environmental stress conditions. To assess the role of increased HYR expression in rice, whole-genome microarrays were used to generate gene expression profiles of rice cultivar Nipponbare transformed with an overexpression construct of the HYR gene (Loc_Os03g02650) under control of the CaMV 35S promoter, along with control wild-type (WT) lines.	Two biological replicate samples each from the HYR and WT-control lines were profiled using rice whole-genome microarrays [45].