

*Mychal W. Ivancich, Rafi Shaik and Wusirika Ramakrishna**

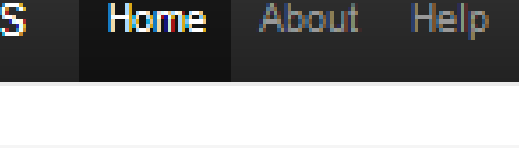


❑ Although many of the existing tools and databases provide microarray data analysis services they are not specifically and extensively built for analysis of stress responses in plants.

❑ Stress responsive genes (SRGs) identified from meta-analysis of microarray studies are available online through a user friendly interface built using HTML5, PHP and JavaScript with MySQL backend at URL <http://srgps.bio.mtu.edu>

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Homepage of SRGPs

An online resource for comparative analysis of 'Stress Responsive Genes in Plants'.

Organism: ☒ Arabidopsis ☐ Rice

Stress: Database:

Query: Common: ☐

More information on this project can be found at the [About's section](#)

Graphs		Export Table																											
Search:																													
3892 Genes						Drought			Salinity			Bacteria			Fungi														
ProbelD	Locus	Annotation				FC	Pvalue	D.E	FC	Pvalue	D.E	FC	Pvalue	D.E	FC	Pvalue	D.E												
261564_at	AT1G01720	ATAF1; transcription activator/ transcription factor				0.3114	0.000000	Up	0.3934	0.000000	Up	-	-	-	-	-	-												
264837_at	AT1G03600	photosystem II family protein				1.4287	0.000100	Up	0.7166	0.000000	Up	-	-	-	-	-	-												
264580_at	AT1G05340	unknown protein				0.0875	0.000000	Up	0.1356	0.000000	Up	-	-	-	0.4432	0.000000	Up												
261192_at	AT1G05675	unknown protein				1.4123	0.000000	Up	0.5479	0.000000	Up	0.8958	0.000000	Up	0.8309	0.000000	Down												
260955_at	AT1G06000	UDP-glucuronosyl/UDP-glucosyl transferase family protein				0.9779	0.000000	Up	-	-	-	1.2309	0.000200	Up	1.1896	0.000000	Down												
262626_at	AT1G06430	FTH8; ATP-dependent peptidase/ATPase/ metallopeptidase/ zinc ion binding				0.6262	0.000400	Up	0.7748	0.000000	Up	-	-	-	-	-	-												
262635_at	AT1G06670	PDS1 (PHYCONE DESATURATION 1); 4-hydroxyphenyl/pyruvate dioxygenase				0.3330	0.000200	Up	0.3711	0.000000	Up	-	-	-	-	-	-												
262616_at	AT1G06620	2-oxoglutarate-dependent dioxygenase, putative				0.6429	0.000000	Up	0.8005	0.000000	Up	1.1530	0.000000	Up	-	-	-												
261077_at	AT1G07430	protein phosphatase 2C, putative / PP2C, putative				0.0859	0.000000	Up	0.1968	0.000000	Up	-	-	-	0.8429	0.000400	Down												
264662_at	AT1G08920	sugar transporter, putative				0.4454	0.000000	Up	0.4726	0.000000	Up	-	-	-	-	-	-												
264063_at	AT1G09970	LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase				0.0961	0.000000	Up	0.7873	0.000000	Up	1.2329	0.000000	Up	0.6183	0.000000	Up												
264436_at	AT1G10370	ERD9 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase				0.6317	0.000000	Up	0.7056	0.000000	Up	-	-	-	1.8351	0.000000	Down												
261826_at	AT1G11580	PMPCORA (METHYLESTERASE PCR A); enzyme inhibitor/ pectinesterase				1.0310	0.000000	Up	1.2796	0.000000	Down	1.2168	0.000200	Up	0.9782	0.000000	Down												

Figure 1 displays the expression of LOC_Os07g48200 across four conditions (Drought, Salinity, Bacteria, Fungi) for three samples (S1, S2, S3). The heatmap shows the log2 fold change values, with a color scale from -4.0 (blue) to 1.0 (red). The line graph shows the log2 fold change values for each sample across the four conditions. The gene LOC_Os07g48200 is highlighted with a red box in the heatmap and a red line in the line graph.

Gene = LOC_Os07g48200, Fold Change = -2.54

Legend: Drought (Yellow), Salinity (Light Blue), Bacteria (Red), Fungi (Green)

Search:

Organization = Rice, Stress = All, Database = GO, Query = undefined

GO term	Description	Number of Genes	FDR
GO 0004722	protein serine/threonine phosphatase activity	5	0.031
GO 0005056	iron ion binding	23	0.024
GO 0006869	lipid transport	7	0.048
GO 0006990	response to stress	25	0.048
GO 0008171	O-methyltransferase activity	5	0.031
GO 0009055	electron carrier activity	25	0.031
GO 0010876	lipid localization	7	0.048
GO 0016491	oxidoreductase activity	44	0.031
GO 0020037	heme binding	20	0.024
GO 0030528	transcription regulator activity	29	0.024
GO 046906	tetrapyrrole binding	20	0.024

SRGPs

Results

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Query Information: Organism = Rice, Stress = All, Database = microRNA, Query = Not specified, Exclusive = Yes

*IF EXCLUSIVE, LIST GENES THAT CHANGED EXCLUSIVELY WITHIN THE SPECIFIED STRESSES

*IF NO QUERY IS SPECIFIED IT RETURNS ALL GENES FOR THE SPECIFIED STRESS

Search:

55 miRNAs

miRNA ID	Drought	Salinity	Bacteria	Fungi	All
osa-miRf10319-akr	9	6	13	2	1
osa-miRf11270-akr	8	3	4	3	1
osa-miRf12007-akr	8	2	3	3	1
osa-miRf10830-akr	7	5	8	6	1
osa-miRf11218-akr	7	5	4	4	1
osa-miRf11624-akr	7	4	7	3	1

Genes			Salinity		
ProbeID	Locus	Annotation	FC	Pvalue	D.E
<input type="checkbox"/> Os.18734.1.S1_at	LOC_Os03g01700	expressed protein	1.8665	0.000000	Down
<input type="checkbox"/> Os.34767.2.S1_s_at	LOC_Os03g12530	cation efflux family protein, putative, expressed	1.9810	0.000000	Down
<input type="checkbox"/> Os.47914.1.S1_at	LOC_Os06g11210	12-oxophytodienoate reductase, putative, expressed	1.0583	0.000000	Down
<input type="checkbox"/> Os.11914.1.S1_at	LOC_Os06g11240	12-oxophytodienoate reductase, putative, expressed	0.8974	0.000100	Down
<input type="checkbox"/> Os.18665.1.S1_at	LOC_Os08g13699	expressed protein	1.1885	0.000000	Down
<input type="checkbox"/> OsAflx.30196.1.S1_at	LOC_Os09g39070	thiol protease SEN102 precursor, putative, expressed	2.0952	0.000000	Down

- ❑ Expand to other model plant and agronomically important crop species