

# **An Integration of Transcriptomic Data and Modular Gene Co-Expression Network Analysis Uncovers Drought Stress-Related Hub Genes in Transgenic Rice Overexpressing *OsAbp57***

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**Table S1** Primers used in this study for qPCR validation.

Gene	Sequence (5'-3')	Annealing temperature (°C)	Amplicon (bp)
Os07g0513000 ( <i>ATPF1G</i> )	F: GCTCGACATGCTCAGATCAAAGGG R: TCGACTTGGTCGAGTTGTTCGTC	60	65
BG10SGA005667- TA ( <i>GS</i> )	F: AGGACCCATTTCAGGAAGGGAAAC R: CGTGTAGCAATCGCACATGACAG	58	101
Os06g0136600 ( <i>Enolase 5</i> )	F: TGATGGCAAGCCATAGGAGTGG R: ACAGACCAACTGAGAGGTCAGC	60	66
Os04g0178300 ( <i>OsCPS4</i> )	F: TGAGTTGAATGGCCTTAGAAGGTG R: TGTGGATCAGTCCCTCCAAACC	60	69
Os12g0115700 ( <i>CHI</i> )	F: TTCAGGCCCTAGTTTCTGCTCCTG R: CTCCTCATCCTCGTACTTGTCCAC	60	143
Os10g0567400 ( <i>OsCAOI</i> )	F: TCAGGTGTTGCTCCAGAAAGGG R: GCACCGCATACACCTTGATTCCTC	60	60
<i>U6</i> <i>snRNA</i> (Control)	F: TACAGATAAGATTAGCATGGCCCC R: GGACCATTTCTCGATTTGTACGTG	54	60
<i>UBQ 5</i> (Control)	F: CGCAAGTACAACCAGGACAA R: TGGTTGCTGTGACCACACTT	60	69

**Table S2** List of over-represented biological processes in modules (M1 – M12) determined by hypergeometric test.

Module	Function	GeneRatio	BgRatio	pvalue	p.adjust	qvalue
M1	translation	35/668	42/1117	0.00079947	0.01286598	0.01046515
M1	protein folding	17/668	18/1117	0.00116963	0.01286598	0.01046515
M1	carbohydrate metabolic process	62/668	88/1117	0.02091087	0.14883784	0.12106427
M1	protein phosphorylation	99/668	147/1117	0.02706143	0.14883784	0.12106427
M1	regulation of transcription, DNA-templated	60/668	87/1117	0.04302967	0.18933054	0.15400092
M1	microtubule-based movement	17/668	22/1117	0.06777138	0.24849507	0.20212518
M1	photosynthesis	10/668	12/1117	0.08023445	0.25216542	0.20511063
M1	fatty acid biosynthetic process	13/668	18/1117	0.20188003	0.55517009	0.45157376
M1	DNA replication	10/668	14/1117	0.27278253	0.66680173	0.54237461
M1	cell redox homeostasis	6/668	10/1117	0.62858881	0.99997637	0.81337791
M1	signal transduction	7/668	13/1117	0.76784265	0.99997637	0.81337791
M1	lipid metabolic process	10/668	20/1117	0.87071886	0.99997637	0.81337791
M1	proteolysis	26/668	51/1117	0.92709526	0.99997637	0.81337791
M1	response to stress	6/668	14/1117	0.94102112	0.99997637	0.81337791
M1	metabolic process	35/668	70/1117	0.96721119	0.99997637	0.81337791
M1	defense response	4/668	11/1117	0.9704252	0.99997637	0.81337791
M1	transport	16/668	36/1117	0.98047621	0.99997637	0.81337791
M1	drug transmembrane transport	8/668	21/1117	0.98779528	0.99997637	0.81337791
M1	biosynthetic process	6/668	17/1117	0.98942986	0.99997637	0.81337791
M1	response to oxidative stress	20/668	46/1117	0.9925469	0.99997637	0.81337791
M1	metal ion transport	6/668	18/1117	0.99430334	0.99997637	0.81337791
M1	transmembrane transport	38/668	94/1117	0.99997637	0.99997637	0.81337791
M2	transmembrane transport	35/235	94/1117	0.00011875	0.00237507	0.00212507
M2	metal ion transport	9/235	18/1117	0.00567252	0.05672518	0.05075411
M2	biosynthetic process	7/235	17/1117	0.04696954	0.3009903	0.26930711
M2	defense response	5/235	11/1117	0.06019806	0.3009903	0.26930711
M2	metabolic process	20/235	70/1117	0.07737964	0.30951855	0.27693765
M2	proteolysis	15/235	51/1117	0.09549052	0.31830173	0.28479629
M2	cell redox homeostasis	4/235	10/1117	0.13892581	0.37956202	0.33960813

M2	response to stress	5/235	14/1117	0.15182481	0.37956202	0.33960813
M2	drug transmembrane transport	6/235	21/1117	0.26853268	0.5967393	0.53392463
M2	response to oxidative stress	11/235	46/1117	0.36949385	0.73898771	0.66119953
M2	lipid metabolic process	5/235	20/1117	0.41585897	0.75610722	0.67651699
M2	signal transduction	3/235	13/1117	0.53692694	0.89062718	0.79687695
M2	DNA replication	3/235	14/1117	0.59131191	0.89062718	0.79687695
M2	transport	7/235	36/1117	0.66064089	0.89062718	0.79687695
M2	regulation of transcription, DNA-templated	17/235	87/1117	0.68312612	0.89062718	0.79687695
M2	microtubule-based movement	4/235	22/1117	0.71250174	0.89062718	0.79687695
M2	carbohydrate metabolic process	14/235	88/1117	0.91766299	0.99507604	0.8903312
M2	photosynthesis	1/235	12/1117	0.94217786	0.99507604	0.8903312
M2	translation	5/235	42/1117	0.96076135	0.99507604	0.8903312
M2	protein phosphorylation	20/235	147/1117	0.99507604	0.99507604	0.8903312
M3	drug transmembrane transport	5/71	21/1117	0.00823589	0.08457617	0.07630933
M3	transmembrane transport	12/71	94/1117	0.01208231	0.08457617	0.07630933
M3	biosynthetic process	3/71	17/1117	0.08807491	0.41101623	0.37084172
M3	lipid metabolic process	3/71	20/1117	0.12906811	0.41803707	0.3771763
M3	metabolic process	7/71	70/1117	0.14929895	0.41803707	0.3771763
M3	response to oxidative stress	4/71	46/1117	0.33435762	0.78016779	0.70391079
M3	transport	3/71	36/1117	0.40431999	0.80863997	0.72959998
M3	signal transduction	1/71	13/1117	0.57621447	0.88612307	0.79950954
M3	fatty acid biosynthetic process	1/71	18/1117	0.69623955	0.88612307	0.79950954
M3	metal ion transport	1/71	18/1117	0.69623955	0.88612307	0.79950954
M3	protein folding	1/71	18/1117	0.69623955	0.88612307	0.79950954
M3	carbohydrate metabolic process	4/71	88/1117	0.8290833	0.96726385	0.87271926
M3	protein phosphorylation	6/71	147/1117	0.92555207	0.98070088	0.8848429
M3	regulation of transcription, DNA-templated	2/71	87/1117	0.98070088	0.98070088	0.8848429
M4	transport	4/34	36/1117	0.02113418	0.23247596	0.20021853
M4	response to oxidative stress	4/34	46/1117	0.04719581	0.25957693	0.22355908
M4	protein phosphorylation	7/34	147/1117	0.14817965	0.54332539	0.46793575
M4	proteolysis	3/34	51/1117	0.19964207	0.54901568	0.47283647
M4	defense response	1/34	11/1117	0.28935538	0.63658184	0.5482523

M4	fatty acid biosynthetic process	1/34	18/1117	0.42922164	0.63801033	0.54948258
M4	metal ion transport	1/34	18/1117	0.42922164	0.63801033	0.54948258
M4	lipid metabolic process	1/34	20/1117	0.46400751	0.63801033	0.54948258
M4	carbohydrate metabolic process	2/34	88/1117	0.7646258	0.93454264	0.80486926
M4	metabolic process	1/34	70/1117	0.89297436	0.93920877	0.80888794
M4	regulation of transcription, DNA-templated	1/34	87/1117	0.93920877	0.93920877	0.80888794
M5	drug transmembrane transport	2/32	21/1117	0.11911406	0.656219	0.656219
M5	proteolysis	3/32	51/1117	0.17607005	0.656219	0.656219
M5	defense response	1/32	11/1117	0.27471702	0.656219	0.656219
M5	photosynthesis	1/32	12/1117	0.2957017	0.656219	0.656219
M5	signal transduction	1/32	13/1117	0.31609766	0.656219	0.656219
M5	response to stress	1/32	14/1117	0.33592092	0.656219	0.656219
M5	response to oxidative stress	2/32	46/1117	0.38325965	0.656219	0.656219
M5	fatty acid biosynthetic process	1/32	18/1117	0.40979227	0.656219	0.656219
M5	regulation of transcription, DNA-templated	3/32	87/1117	0.46095301	0.656219	0.656219
M5	carbohydrate metabolic process	3/32	88/1117	0.46872786	0.656219	0.656219
M5	metabolic process	2/32	70/1117	0.6080474	0.7638386	0.7638386
M5	transport	1/32	36/1117	0.6547188	0.7638386	0.7638386
M5	transmembrane transport	2/32	94/1117	0.76783826	0.81544773	0.81544773
M5	protein phosphorylation	3/32	147/1117	0.81544773	0.81544773	0.81544773
M6	transport	4/18	36/1117	0.00201825	0.01614597	0.01487129
M6	transmembrane transport	3/18	94/1117	0.18795856	0.68063858	0.62690395
M6	metal ion transport	1/18	18/1117	0.25523947	0.68063858	0.62690395
M6	translation	1/18	42/1117	0.50106262	0.77438072	0.7132454
M6	proteolysis	1/18	51/1117	0.57165297	0.77438072	0.7132454
M6	metabolic process	1/18	70/1117	0.69092596	0.77438072	0.7132454
M6	regulation of transcription, DNA-templated	1/18	87/1117	0.77036773	0.77438072	0.7132454
M6	carbohydrate metabolic process	1/18	88/1117	0.77438072	0.77438072	0.7132454
M7	response to oxidative stress	2/13	46/1117	0.09700394	0.28660525	0.28660525
M7	response to stress	1/13	14/1117	0.15198688	0.28660525	0.28660525
M7	biosynthetic process	1/13	17/1117	0.18164561	0.28660525	0.28660525
M7	metabolic process	2/13	70/1117	0.19359814	0.28660525	0.28660525

M7	protein phosphorylation	3/13	147/1117	0.23883771	0.28660525	0.28660525
M7	carbohydrate metabolic process	1/13	88/1117	0.65794596	0.65794596	0.65794596
M8	transmembrane transport	2/6	94/1117	0.08408382	0.30625592	0.30625592
M8	transport	1/6	36/1117	0.17881643	0.30625592	0.30625592
M8	response to oxidative stress	1/6	46/1117	0.22345531	0.30625592	0.30625592
M8	proteolysis	1/6	51/1117	0.24500474	0.30625592	0.30625592
M8	protein phosphorylation	1/6	147/1117	0.57201908	0.57201908	0.57201908
M9	transmembrane transport	1/11	94/1117	0.23514772	0.71546557	0.71546557
M9	translation	1/11	42/1117	0.3452623	0.71546557	0.71546557
M9	proteolysis	1/11	51/1117	0.40335685	0.71546557	0.71546557
M9	regulation of transcription, DNA-templated	1/11	87/1117	0.59186256	0.71546557	0.71546557
M9	carbohydrate metabolic process	1/11	88/1117	0.59622131	0.71546557	0.71546557
M9	protein phosphorylation	1/11	147/1117	0.78979577	0.78979577	0.78979577
M10	fatty acid biosynthetic process	1/8	18/1117	0.12223746	0.44265627	0.44265627
M10	microtubule-based movement	1/8	22/1117	0.14755209	0.44265627	0.44265627
M10	response to oxidative stress	1/8	46/1117	0.28645618	0.57291235	0.57291235
M10	metabolic process	1/8	70/1117	0.40513717	0.57406418	0.57406418
M10	regulation of transcription, DNA-templated	1/8	87/1117	0.47838682	0.57406418	0.57406418
M10	protein phosphorylation	1/8	147/1117	0.67782585	0.67782585	0.67782585
M11	DNA replication	1/14	14/1117	0.16274067	0.55330953	0.55330953
M11	response to stress	1/14	14/1117	0.16274067	0.55330953	0.55330953
M11	lipid metabolic process	1/14	20/1117	0.2246496	0.55330953	0.55330953
M11	protein phosphorylation	3/14	147/1117	0.27665477	0.55330953	0.55330953
M11	response to oxidative stress	1/14	46/1117	0.44693535	0.64295308	0.64295308
M11	proteolysis	1/14	51/1117	0.48221481	0.64295308	0.64295308
M11	metabolic process	1/14	70/1117	0.5980947	0.68087349	0.68087349
M11	regulation of transcription, DNA-templated	1/14	87/1117	0.68087349	0.68087349	0.68087349
M12	protein phosphorylation	3/6	147/1117	0.03304658	0.0930752	0.06531593
M12	signal transduction	1/6	13/1117	0.06797728	0.0930752	0.06531593
M12	fatty acid biosynthetic process	1/6	18/1117	0.0930752	0.0930752	0.06531593