Transcriptome analysis of near-isogenic rice lines to identify expression signatures and gene combinations conferring tolerance to drought stress II

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Drought tolerant line: Aday Sel

NILs (backcrossing with IR64)

IR77298-14-1-2-**10**, IR77298-14-1-2-**13**, IR77298-5-6-**11**, IR77298-5-6-**18**

Physiological analysis: responses to the drought treatments
transpiration rate, biomass, root water uptake (field and green house)

Biological properties of NILs

Genotyping analysis: Fine genotyping chip analysis
SNP analysis (Cornell Univ)

The regions of introgression (INT)

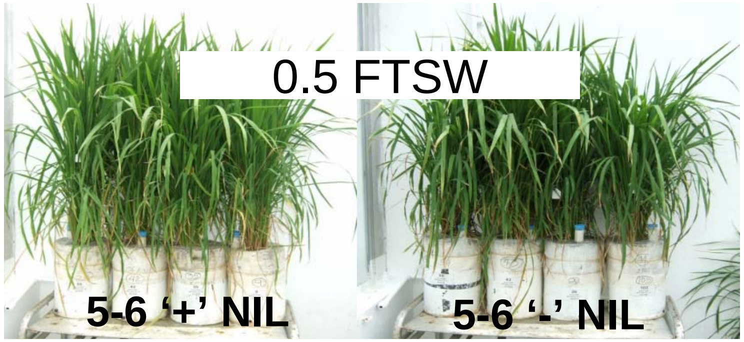
Gene expression (transcriptome) analysis by the 44K microarray system

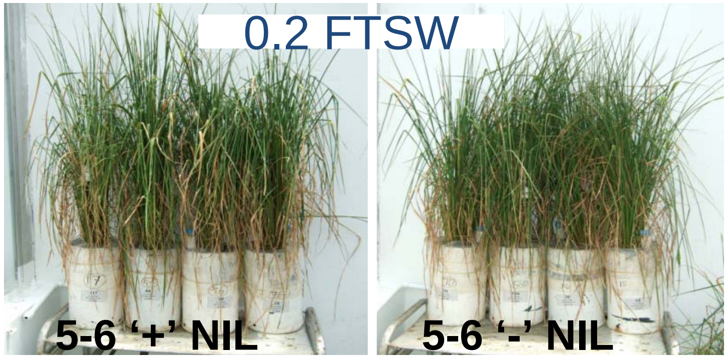
Global gene expression profiles
Pairwise differential expression genes in INT

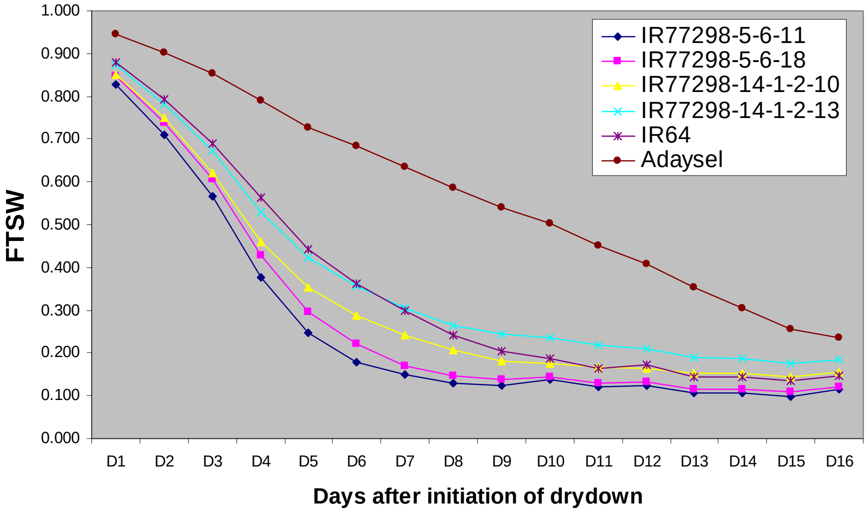
Molecular mechanism of drought tolerance

Transpiration rates of NILs

Direct dry down until the pot reaches targeted FTSW (0.2FTSW/0.5 FTSW), no water added back to the soil during dry down. Pots were maintained at targeted FTSW until harvesting







Graphical representation of progressive soil drying among different lines

- The IR77298-5-6 lines reached the targeted FTSW earlier than other lines which is mainly due to their higher biomass. Among these lines IR77298-5-6-18 reached the targeted FTSW later when compared to that of IR77298-5-6-11, which indicates that IR77298-5-6-18 showed lower transpiration rate.

Total biomass at 0.2 FTSW

Genotypes	Total Biomass	Total Transpiration
IR77298-14-1-2-10 (+QTL)	81.27 ± 8	3.44 ± 0.16
IR77298-14-1-2-13	59.4 ± 5	3.07 ± 0.27
IR77298-5-6-18 (+ QTL)	117.57 ± 10	4.58 ± 0.28
IR77298-5-6-11	103.46 ± 8	4.87 ± 0.28
Aday Sel	33.18 ± 2	2.59 ± 0.25
IR64	54.18 ± 7	3.6 ± 0.14
lsd @ 5%	26.47	0.68

- **The NILs IR77298-14-1-2-10 (+QTL) and IR77298-5-6-18 (+QTL) showed higher total biomass compared to IR77298-14-1-2-13 (-) and IR77298-5-6-11(-), respectively (though statistically not significant)**

- **Higher biomass in these NILs appeared to be due to higher tiller number and plant height.**

- **No significant difference between the NILs for total biomass under well watered condition**

Biomass under dry-down conditions of two pairs of NILs

IR77298-5-6 NILs at different FTSW levels

1.0 FTSW 0.5 FTSW 0.2 FTSW

IR77298-5-6-18 (+)

1.0 FTSW 0.5 FTSW 0.2 FTSW

IR77298-5-6-11 (-)

-Line IR77298-5-6-11 showed a higher reduction in biomass at 0.2 FTSW whereas IR77298-5-6-18 maintained almost equal biomass at 0.2FTSW when compared to other treatments

R77298-14-1-2 NILs at different FTSW levels

1.0 FTSW 0.5 FTSW 0.2 FTSW

IR77298-14-1-2-10

1.0 FTSW 0.5 FTSW 0.2 FTSW

IR77298-14-1-2-13

-Among the NILs IR77298-14-1-2-13 showed a higher reduction in biomass at 0.2 FTSW when compared to other treatments

- **In phytotron experiments, each pair of NILs showed differences in biomass under water stress.**
- **The trend of biomass reduction is similar to that observed under field conditions.**

Impa Somayanda, Venuprasad Ramaiah, Arvind Kumar, Rachid Serraj, IRRI

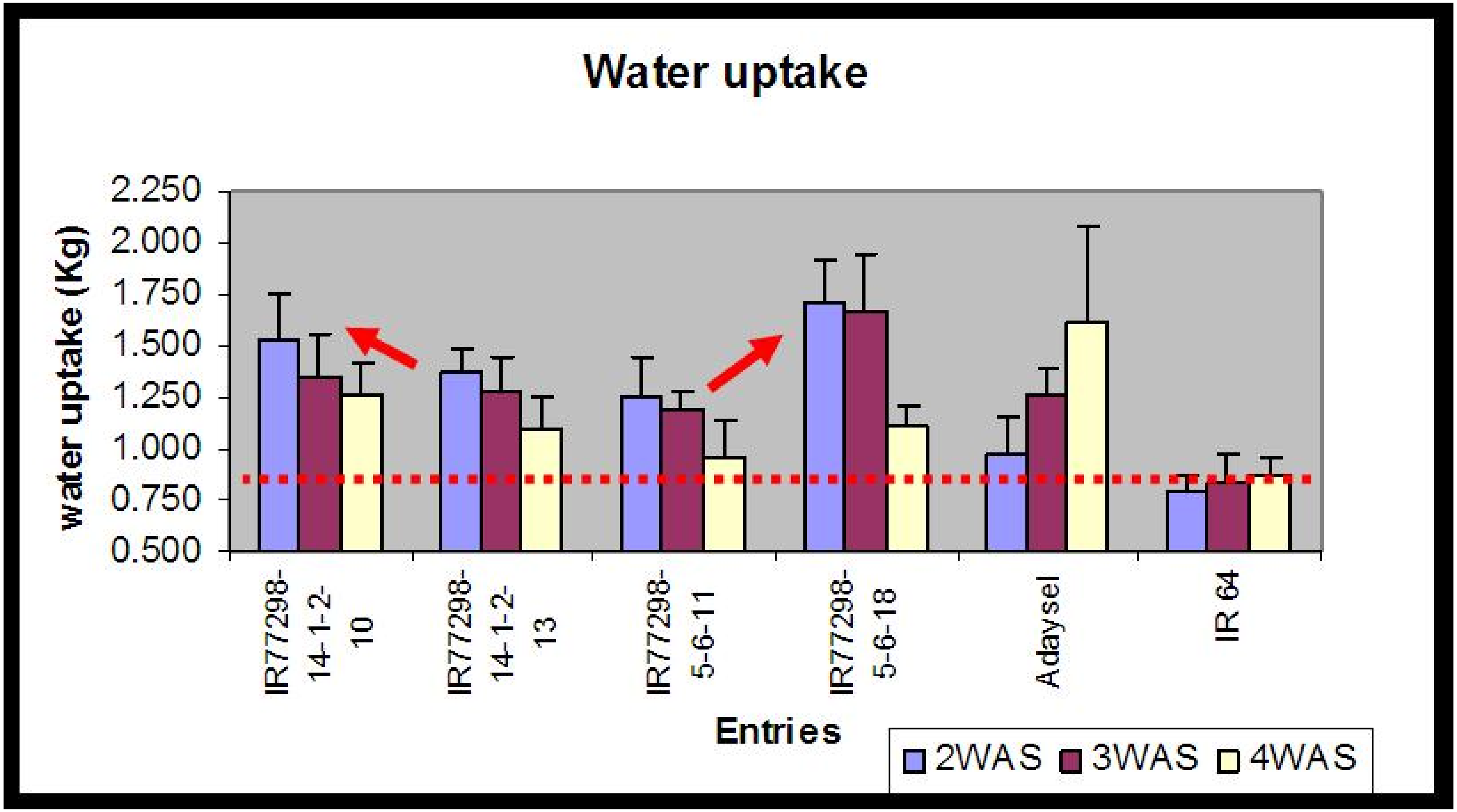
Comparative dynamics of water uptake under drought (Aday sel/IR64 NILs)

Control Treatment

Stress Treatment

Lowland soil
Top 20cm

Plant water uptake (kg/wk)



VRP Gowda & R Serraj

“18” showed higher water uptake than “11”. Difference between “10” and “13” is smaller than that of “18” and “11”.

Biological properties of NILs

Aday sel x IR64

Backcross (IR64 background)

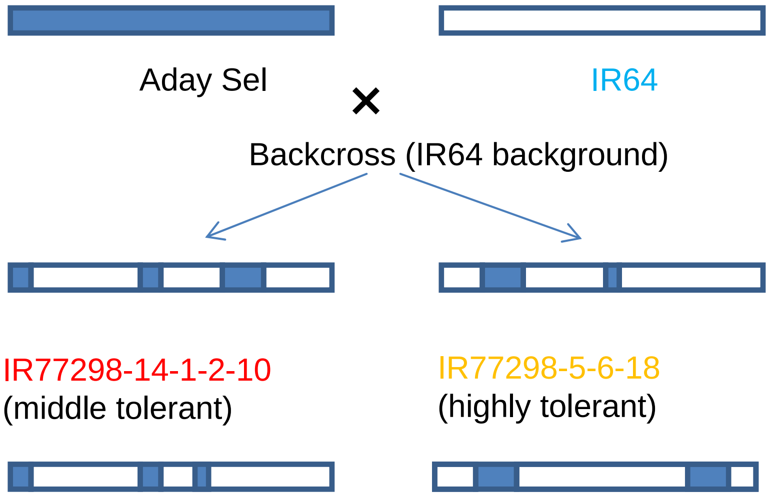
IR77298-14-1-2-10
(Drought tolerant)

IR77298-14-1-2-13
(Drought susceptible)

IR77298-5-6-18
(Highly drought tolerant)
Lower transpiration rate than 11.

IR77298-5-6-11
(Drought susceptible)
Difference of water uptake is higher than that between 10 and 13.

Genotyping and phenotyping data of NILs



Aday Sel × IR64

Backcross (IR64 background)

IR77298-14-1-2-10
(middle tolerant)

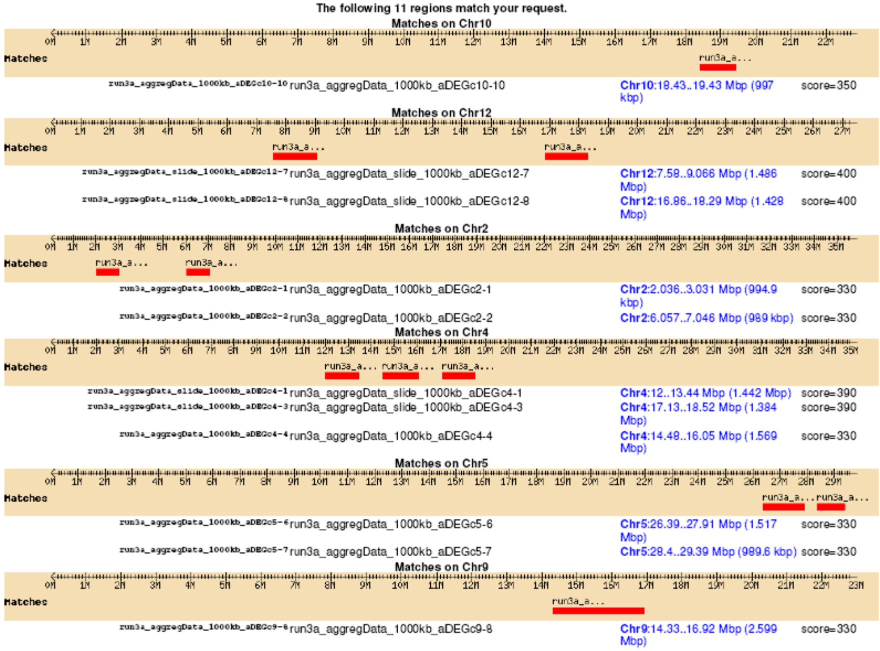
IR77298-5-6-18
(highly tolerant)

IR77298-14-1-2-13
(drought susceptible)

IR77298-5-6-11
(drought susceptible)

- **Sister-lines with contrasting performance to drought stress but no obvious polymorphism**

- **Chip data suggest 11 genomic regions that are different between two sister lines**



The following 11 regions match your request.

Matches on Chr10

run3a_aggregData_1000kb_aDEGc10-10 run3a_aggregData_1000kb_aDEGc10-10 Chr10:18.43..19.43 Mbp (997 kbp) score=350

Matches on Chr12

run3a_aggregData_slide_1000kb_aDEGc12-7 run3a_aggregData_slide_1000kb_aDEGc12-7 Chr12:7.58..9.066 Mbp (1.486 Mbp) score=400
run3a_aggregData_slide_1000kb_aDEGc12-8 run3a_aggregData_slide_1000kb_aDEGc12-8 Chr12:16.86..18.29 Mbp (1.428 Mbp) score=400

Matches on Chr2

run3a_aggregData_1000kb_aDEGc2-1 run3a_aggregData_1000kb_aDEGc2-1 Chr2:2.036..3.031 Mbp (994.9 kbp) score=330
run3a_aggregData_1000kb_aDEGc2-2 run3a_aggregData_1000kb_aDEGc2-2 Chr2:6.057..7.046 Mbp (989 kbp) score=330

Matches on Chr4

run3a_aggregData_slide_1000kb_aDEGc4-1 run3a_aggregData_slide_1000kb_aDEGc4-1 Chr4:12..13.44 Mbp (1.442 Mbp) score=390
run3a_aggregData_slide_1000kb_aDEGc4-3 run3a_aggregData_slide_1000kb_aDEGc4-3 Chr4:17.13..18.52 Mbp (1.384 Mbp) score=390
run3a_aggregData_1000kb_aDEGc4-4 run3a_aggregData_1000kb_aDEGc4-4 Chr4:14.48..16.05 Mbp (1.569 Mbp) score=330

Matches on Chr5

run3a_aggregData_1000kb_aDEGc5-6 run3a_aggregData_1000kb_aDEGc5-6 Chr5:26.39..27.91 Mbp (1.517 Mbp) score=330
run3a_aggregData_1000kb_aDEGc5-7 run3a_aggregData_1000kb_aDEGc5-7 Chr5:28.4..29.39 Mbp (989.6 kbp) score=330

Matches on Chr9

run3a_aggregData_1000kb_aDEGc9-8 run3a_aggregData_1000kb_aDEGc9-8 Chr9:14.33..16.92 Mbp (2.599 Mbp) score=330

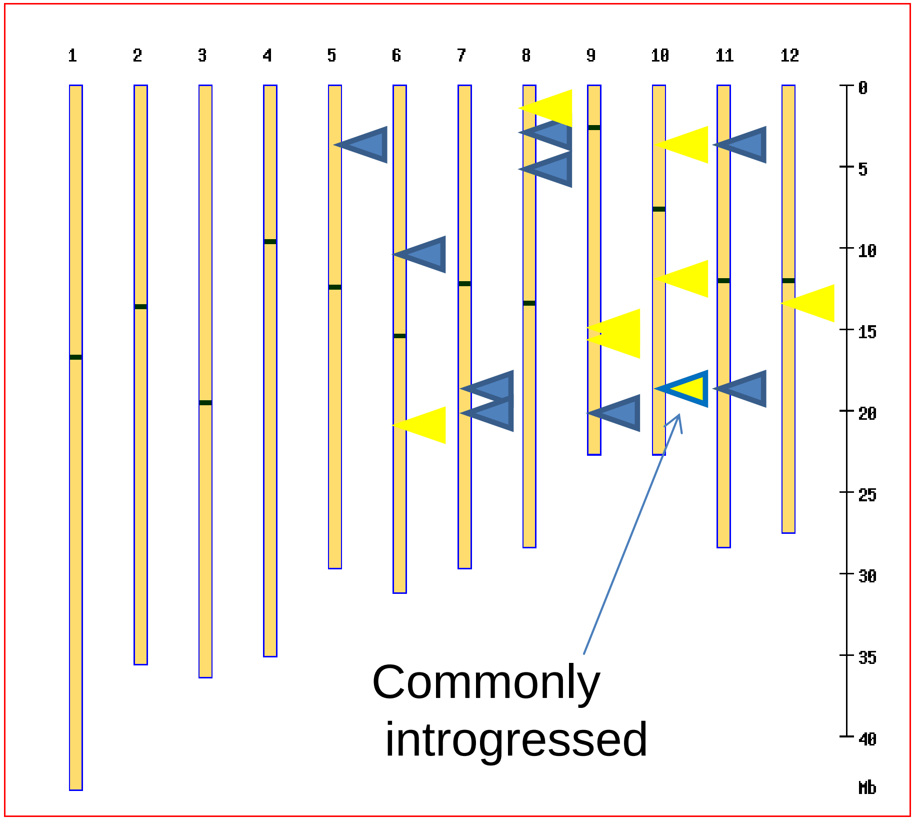
SNP analysis (Cornell Univ)

using the GoldenGate assay system

http://www.illumina.com/downloads/GOLDENGATEASSAY.pdf

sample id\snp id	chr	bp (IRGSP)	2_10R(AS)_vs_2_13	6_18R(AS)_vs_6_11
id5002528	5	4,800,200	0	1
id6006627	6	10,771,600	0	1
id6011853	6	23,928,100	1	0
id7003047	7	20,187,100	0	1
id7003748	7	22,937,300	0	1
id7003994	7	23,593,500	0	1
id8000975	8	3,085,300	1	0
id8001477	8	4,556,700	0	1
id8001641	8	5,315,900	0	1
id8001667	8	5,327,200	0	1
id8002194	8	6,239,600	0	1
id8002314	8	7,548,600	0	1
id9004072	9	15,342,300	1	0
id9004173	9	15,544,300	1	0
id9004233	9	15,650,900	1	0
id9004727	9	16,402,300	1	0
id9004741	9	16,419,100	1	0
id9007259	9	21,959,600	0	1
id10001318	10	4,161,700	1	0
id10003348	10	13,127,200	1	0
id10005853	10	19,482,800	0	0
id10005921	10	19,599,600	0	0
id10006100	10	19,833,400	0	1
id10006161	10	19,978,900	0	0
id10006328	10	20,426,100	0	1
id11001107	11	3,375,400	0	1
id11006022	11	19,036,700	0	1
id11006101	11	19,261,500	0	1
id11006588	11	20,322,400	0	1
id12004819	12	13,711,600	1	0

NOTE:
0 - SNP from Aday Sel (assoc with drt resistance) is introgressed
1 - SNP non introgressed



Commonly introgressed

◀ 10 vs 13

◀ 18 vs 11

10 regions

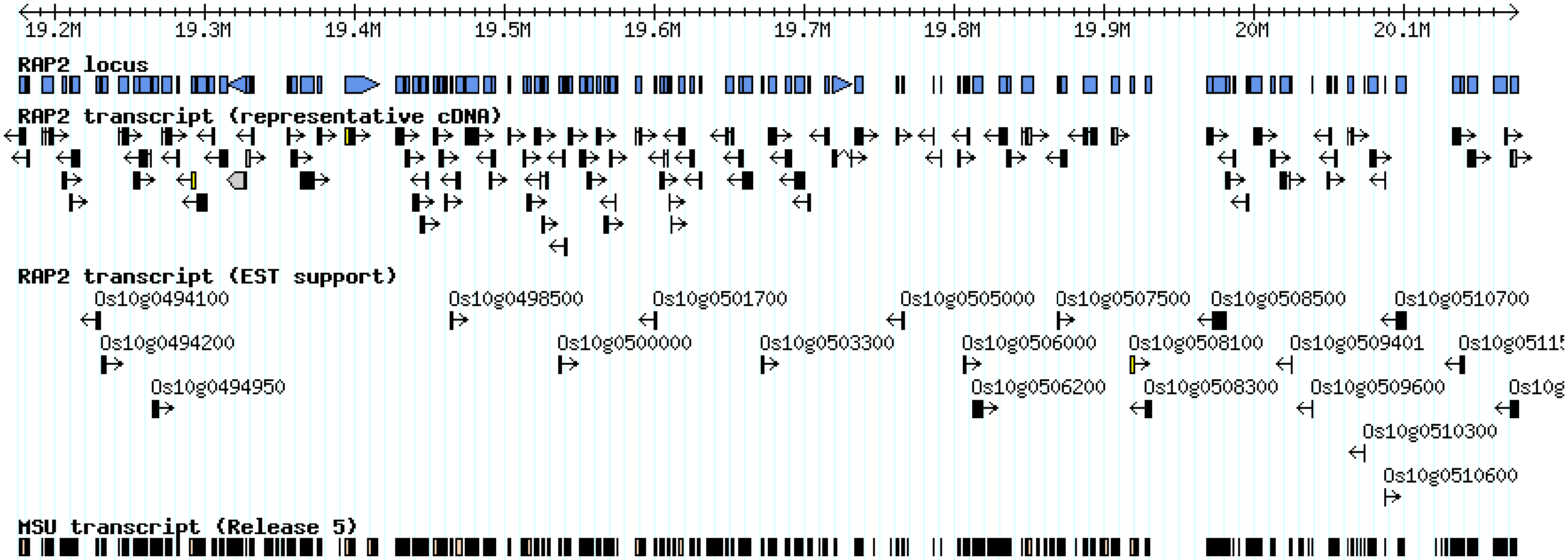
8 regions

Capture the genes in the introgressed regions

SNP analysis results

sample id\snp id	chromosome	bp	IR64_allele	1_2_10_allele	2_10_vs_IR64	1_2_13_allele	2_13_vs_IR64
id10005716	10	19249500	A	A	1	A	1
id10005853	10	19482800	G	A	0	G	1
id10005921	10	19599600	T	C	0	T	1
id10005962	10	19674400	G	G	1	G	1
id10006100	10	19833400	A	C	0	A	1
id10006161	10	19978900	G	T	0	G	1
id10006328	10	20426100	T	C	0	T	1
id10006353	10	20549300	G	G	1	G	1

Map of genes in the region



895 genes in the introgressed regions (13 vs 10)

510 genes in the introgressed regions (18 vs 11)

Gene expression analysis using 44k arrays (the Agilent Technologies)

Samples (three biological replications)
Lines:
IR64
NILs (parent: Aday selection x IR64)
IR77298-5-6-18, -5-6-11
IR77298-14-1-2-10, -1-2-13

Growth condition:
well watered (control)
mild drought (0.5FTSW)

Tissue:
Leaf
Panicle
Root

Hybridization:
In same tissue of same line
control x drought

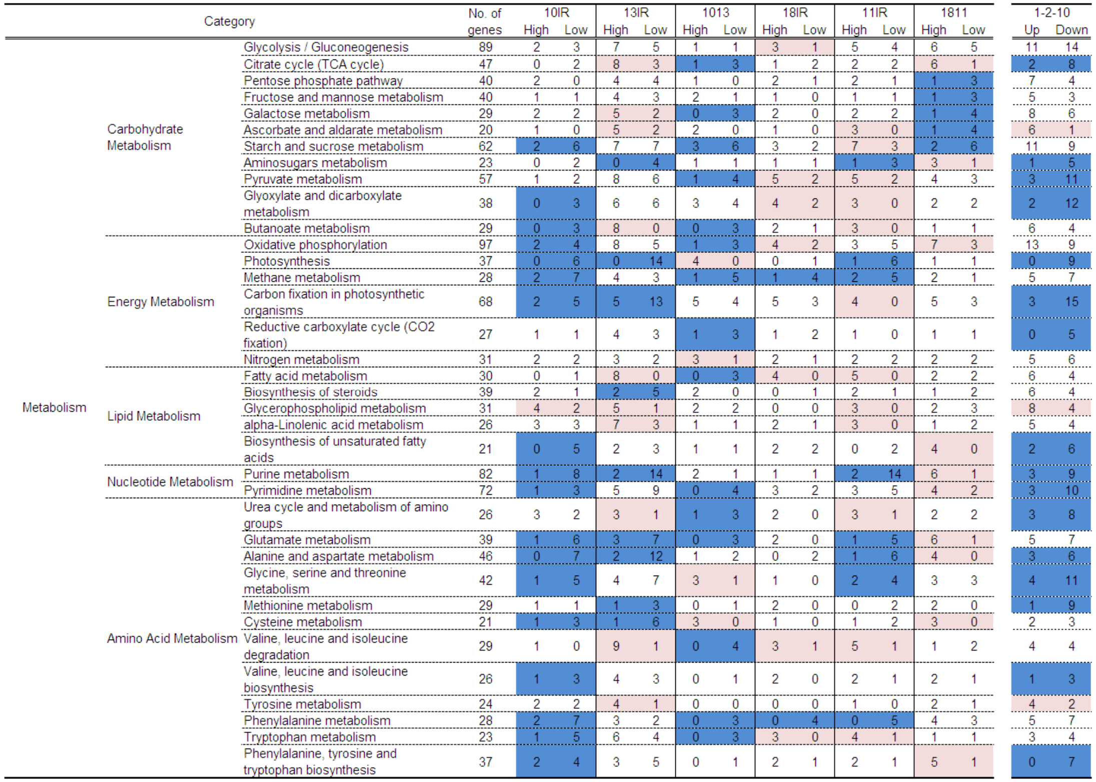
A. Global gene expression profiles of NILs

- Drought Responsive Genes
- Transporter genes

B. Differentially expressing genes in the introgressed regions

Global gene expression profiles in NILs

- “10” shows much drastic down-regulation of DRG than “13”.
- Many of down regulated DRG in “11” are in lower expression level even in the non-stressed condition in “18”.



Category			No. of genes	10IR		13IR		1013		18IR		11IR		1811		1-2-10	
				High	Low	High	Low	High	Low	High	Low	High	Low	High	Low	Up	Down
Metabolism	Carbohydrate Metabolism	Glycolysis / Gluconeogenesis	89	2	3	7	5	1	1	3	1	5	4	6	5	11	14
		Citrate cycle (TCA cycle)	47	0	2	8	3	1	3	1	2	2	2	6	1	2	8
		Pentose phosphate pathway	40	2	0	4	4	1	0	2	1	2	1	1	3	7	4
		Fructose and mannose metabolism	40	1	1	4	3	2	1	1	0	1	1	1	3	5	3
		Galactose metabolism	29	2	2	5	2	0	3	2	0	2	2	1	4	8	6
		Ascorbate and aldarate metabolism	20	1	0	5	2	2	0	1	0	3	0	1	4	6	1
		Starch and sucrose metabolism	62	2	6	7	7	3	6	3	2	7	3	2	6	11	9
		Aminosugars metabolism	23	0	2	0	4	1	1	1	1	1	3	3	1	1	5
		Pyruvate metabolism	57	1	2	8	6	1	4	5	2	5	2	4	3	3	11
		Glyoxylate and dicarboxylate metabolism	38	0	3	6	6	3	4	4	2	3	0	2	2	2	12
		Butanoate metabolism	29	0	3	8	0	0	3	2	1	3	0	1	1	6	4
	Energy Metabolism	Oxidative phosphorylation	97	2	4	8	5	1	3	4	2	3	5	7	3	13	9
		Photosynthesis	37	0	6	0	14	4	0	0	1	1	6	1	1	0	9
		Methane metabolism	28	2	7	4	3	1	5	1	4	2	5	2	1	5	7
		Carbon fixation in photosynthetic organisms	68	2	5	5	13	5	4	5	3	4	0	5	3	3	15
		Reductive carboxylate cycle (CO2 fixation)	27	1	1	4	3	1	3	1	2	1	0	1	1	0	5
		Nitrogen metabolism	31	2	2	3	2	3	1	2	1	2	2	2	2	5	6
	Lipid Metabolism	Fatty acid metabolism	30	0	1	8	0	0	3	4	0	5	0	2	2	6	4
		Biosynthesis of steroids	39	2	1	2	5	2	0	0	1	2	1	1	2	6	4
		Glycerophospholipid metabolism	31	4	2	5	1	2	2	0	0	3	0	2	3	8	4
		alpha-Linolenic acid metabolism	26	3	3	7	3	1	1	2	1	3	0	1	2	5	4
		Biosynthesis of unsaturated fatty acids	21	0	5	2	3	1	1	2	2	0	2	4	0	2	6
	Nucleotide Metabolism	Purine metabolism	82	1	8	2	14	2	1	1	1	2	14	6	1	3	9
		Pyrimidine metabolism	72	1	3	5	9	0	4	3	2	3	5	4	2	3	10
	Amino Acid Metabolism	Urea cycle and metabolism of amino groups	26	3	2	3	1	1	3	2	0	3	1	2	2	3	8
		Glutamate metabolism	39	1	6	3	7	0	3	2	0	1	5	6	1	5	7
		Alanine and aspartate metabolism	46	0	7	2	12	1	2	0	2	1	6	4	0	3	6
		Glycine, serine and threonine metabolism	42	1	5	4	7	3	1	1	0	2	4	3	3	4	11
		Methionine metabolism	29	1	1	1	3	0	1	2	0	0	2	2	0	1	9
		Cysteine metabolism	21	1	3	1	6	3	0	1	0	1	2	3	0	2	3
		Valine, leucine and isoleucine degradation	29	1	0	9	1	0	4	3	1	5	1	1	2	4	4
		Valine, leucine and isoleucine biosynthesis	26	1	3	4	3	0	1	2	0	2	1	2	1	1	3
		Tyrosine metabolism	24	2	2	4	1	0	0	0	0	1	0	2	1	4	2
		Phenylalanine metabolism	28	2	7	3	2	0	3	0	4	0	5	4	3	5	7
		Tryptophan metabolism	23	1	5	6	4	0	3	3	0	4	1	1	1	3	4
		Phenylalanine, tyrosine and tryptophan biosynthesis	37	2	4	3	5	0	1	2	1	2	1	5	1	0	7

Genes classified by the metabolic pathways

Transporter genes in root transcriptome

				up					down				
Class	Family	Materials	No of members	IR64	10	13	18	11	IR64	10	13	18	11
Ion Channel	MIP-PIP	H2O,CO2,NH3	10	0	0	0	0	0	3	6	2	4	6
Ion Channel	VIC-beta	Na+,K+,Ca2+	21	3	6	0	4	6	1	1	0	3	2
Pump	ABC-AOH(ABC1)	various	13	2	6	2	5	5	1	1	0	1	1
Pump	ABC-MDR	various	24	0	2	1	1	4	2	8	1	5	4
Pump	ABC-MRP	various	13	0	0	0	0	1	1	4	1	1	3
Pump	ABC-PDR	various	30	1	4	1	2	2	3	4	1	1	1
Pump	ABC-SMC	various	4	0	0	0	0	0	0	3	0	0	0
Pump	H+-PPase	H+	7	2	5	0	3	4	0	0	0	0	0
Pump	P-ATPase P2B	H+,Na+,Ca+	12	1	2	1	1	2	1	5	1	0	1
Pump	P-ATPase P4	H+,Na+,Ca+	13	0	2	1	0	1	1	4	2	0	1
Secondary transporter	AAAP-AUX	amino acid, auxin	16	0	3	2	2	2	3	6	2	5	4
Secondary transporter	AAAP-unknown	amino acid, auxin	45	5	10	3	6	7	6	17	11	11	16
Secondary transporter	AEC	auxin	7	0	0	0	0	1	0	4	0	2	1
Secondary transporter	CACA	Ca2+	23	2	8	4	7	7	2	4	0	3	3
Secondary transporter	DMT-P-DME	C3 carbohydrate, sugar nucleotide	30	3	2	2	2	2	4	11	3	11	7
Secondary transporter	MC	various	59	1	28	14	25	25	4	9	2	6	7
Secondary transporter	MFS-POT(Proton-dependent Oligopeptide Transporter)	oligoprptide	57	5	15	2	9	7	3	5	2	7	8
Secondary transporter	MFS-STP	C3 carbohydrate, sugar nucleotide	19	0	9	2	7	7	1	1	1	0	2
Secondary transporter	MFS-unknown	C3 carbohydrate, sugar nucleotide	93	12	33	18	27	30	11	15	4	10	17
Secondary transporter	MOP-MATE	polysaccharide,Drag	40	3	10	1	4	4	2	7	4	5	6
Secondary transporter	ZIP	Zn,Fe	16	0	5	1	5	4	0	4	3	4	2

- According to our previous paper (Nagata et al. 2008), the rice genes encoding transporter proteins are classified into 116 subfamilies. In this table 21 out of 116 are listed.
- Listed members are up-or down-regulated by the drought stress treatment specifically in “10” not in “13”.

10 vs 13

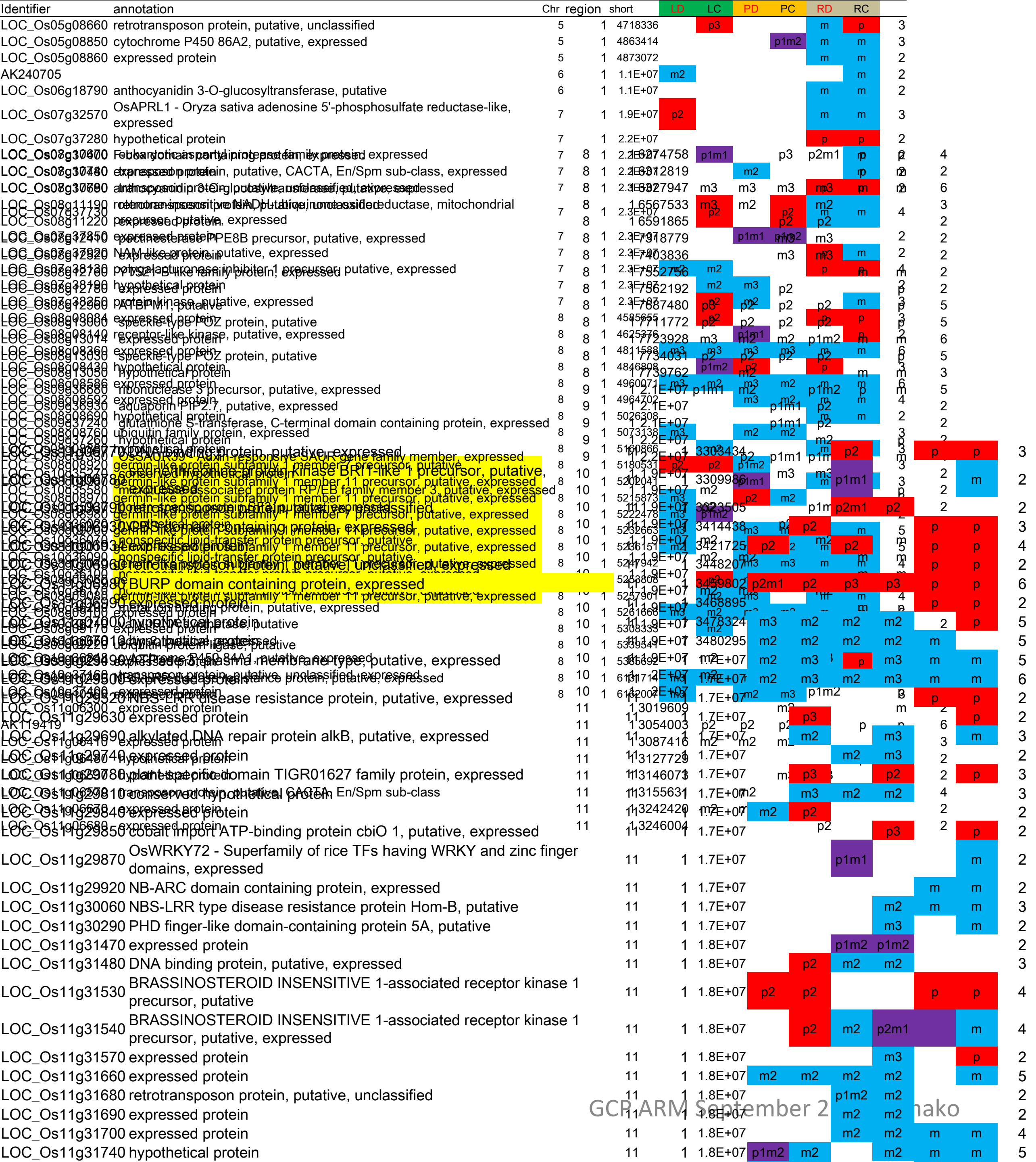
Total 116 genes were raised from the analysis

🟩 LD	🟩 LC	🟨 PD	🟨 PC	RD	RC

LD: leaf drought
LC: leaf control
PD: Panicle drought
PC: Panicle control
RD: Root drought
RC: Root control

🟥 p3 10 > 13 in three reps

🟦 m3 10 < 13 in three reps



Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC	
LOC_Os05g08660	retrotransposon protein, putative, unclassified	5	1	4718336		p3			m	p	3
LOC_Os05g08850	cytochrome P450 86A2, putative, expressed	5	1	4863414				p1m2	m	m	3
LOC_Os05g08860	expressed protein	5	1	4873072					m	m	2
AK240705		6	1	1.1E+07	m2					m	2
LOC_Os06g18790	anthocyanidin 3-O-glucosyltransferase, putative	6	1	1.1E+07					m	m	2
LOC_Os07g32570	OsAPRL1 - Oryza sativa adenosine 5'-phosphosulfate reductase-like, expressed	7	1	1.9E+07	p2				m	m	3
LOC_Os07g37280	hypothetical protein	7	1	2.2E+07					p	p	2
[illegible]	[illegible]										
LOC_Os11g29520	NBS-LRR disease resistance protein, putative, expressed	11	1	1.7E+07	[illegible]				p	p	2
LOC_Os11g29630	expressed protein	11	1	[illegible]	[illegible]					p	2
LOC_Os11g29690	alkylated DNA repair protein alkB, putative, expressed	11	1	[illegible]	[illegible]			m3		m	3
LOC_Os11g29740	expressed protein	11	1	1.7E+07			m2	m3			2
LOC_Os11g29780	plant-specific domain TIGR01627 family protein, expressed	11	1	1.7E+07		[illegible]		p2		p	3
LOC_Os11g29810	conserved hypothetical protein	11	1	1.7E+07	[illegible]	m3	m2	m2			3
LOC_Os11g29840	expressed protein	11	1	1.7E+07	m2	p2					2
LOC_Os11g29850	cobalt import ATP-binding protein cbiO 1, putative, expressed	11	1	1.7E+07				p3		p	2
LOC_Os11g29870	OsWRKY72 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	11	1	1.7E+07			p1m1			m	2
LOC_Os11g29920	NB-ARC domain containing protein, expressed	11	1	1.7E+07					m	m	2
LOC_Os11g30060	NBS-LRR type disease resistance protein Hom-B, putative	11	1	1.7E+07				m2	m	m	3
LOC_Os11g30290	PHD finger-like domain-containing protein 5A, putative	11	1	1.7E+07				m3		m	2
LOC_Os11g31470	expressed protein	11	1	1.8E+07			p1m2	p1m2			2
LOC_Os11g31480	DNA binding protein, putative, expressed	11	1	1.8E+07		p2	m2	m2			3
LOC_Os11g31530	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative	11	1	1.8E+07	p2	p2			p	p	4
LOC_Os11g31540	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	11	1	1.8E+07		p2	m2	p2m1		m	4
LOC_Os11g31570	expressed protein	11	1	1.8E+07				m3		p	2
LOC_Os11g31660	expressed protein	11	1	1.8E+07	m2	m2	m2	m2		m	5
LOC_Os11g31680	retrotransposon protein, putative, unclassified	11	1	1.8E+07			p1m2	m2			2
LOC_Os11g31690	expressed protein	11	1	1.8E+07			m2	m2			2
LOC_Os11g31700	expressed protein	11	1	1.8E+07			m2	m2	m	m	4
LOC_Os11g31740	hypothetical protein	11	1	1.8E+07	p1m2	m2		m2	m	m	5

Remarkable points 1 (almost always 10 < 13)

Cluster of Germin-like protein subfamily 1 member 7 or 11 on Chr 8

Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os08g08920	germin-like protein subfamily 1 member 7 precursor, putative	8	1	5180531	p2	p2	p1m2			
LOC_Os08g08960	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5202041			p1m1		m	m
LOC_Os08g08970	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5215873	m3		p2	m2		
LOC_Os08g08980	germin-like protein subfamily 1 member 7 precursor, putative, expressed	8	1	5222478	m3	p1m2				
LOC_Os08g09000	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5232663	m3		m3	m3	m	m
LOC_Os08g09010	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5236151	m2		m2	m2	m	m
LOC_Os08g09040	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5247942			m3	m3	m	m
LOC_Os08g09060	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5253808		p2	m2	m2	m	m
LOC_Os08g09080	germin-like protein subfamily 1 member 11 precursor, putative, expressed	8	1	5257901		m2	m3		m	m

Germin-like protein clusters are recently known to be related to the broad –spectrum disease resistance (Manosalva et al. 2009)

One NBS-LRR disease resistance protein (LOC_Os08g10440) on Chr 8

Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os08g10440	NBS-LRR disease resistance protein, putative, expressed	8	1	6131714	m3	m2	m3	m2	m	m

Cluster of nonspecific lipid-transfer protein precursor on Chr 10

Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os10g36070	nonspecific lipid-transfer protein precursor, putative	10	1	1.9E+07	m2			m2	m	m
LOC_Os10g36090	nonspecific lipid-transfer protein precursor, putative	10	1	1.9E+07	m2	m2			m	m
LOC_Os10g36100	nonspecific lipid-transfer protein precursor, putative, expressed	10	1	1.9E+07					m	m
LOC_Os10g36170	nonspecific lipid-transfer protein precursor, putative, expressed	10	1	1.9E+07	m2	m2		m2		

ATPase 3, plasma membrane-type on Chr 11

Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os11g29490	ATPase 3, plasma membrane-type, putative, expressed	11	1	1.7E+07	m2	m3		m3	m	m

Remarkable points 2

Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os08g12960	ATBPM1, putative	8	1	7687480	p3	p2	p2	p2		p
LOC_Os08g13000	speckle-type POZ protein, putative	8	1	7711772	p2	p2	p2	p2		p
LOC_Os08g13030	speckle-type POZ protein, putative	8	1	7734031	p2	p2	p2	p2		p
LOC_Os11g06980	BURP domain containing protein, expressed	11	1	3459802	p2m1	p2	p3	p3	p	p

ATBPM1

BURP domain containing protein (***OsBURP17***)

speckle-type POZ protein

(almost always 10 > 13)

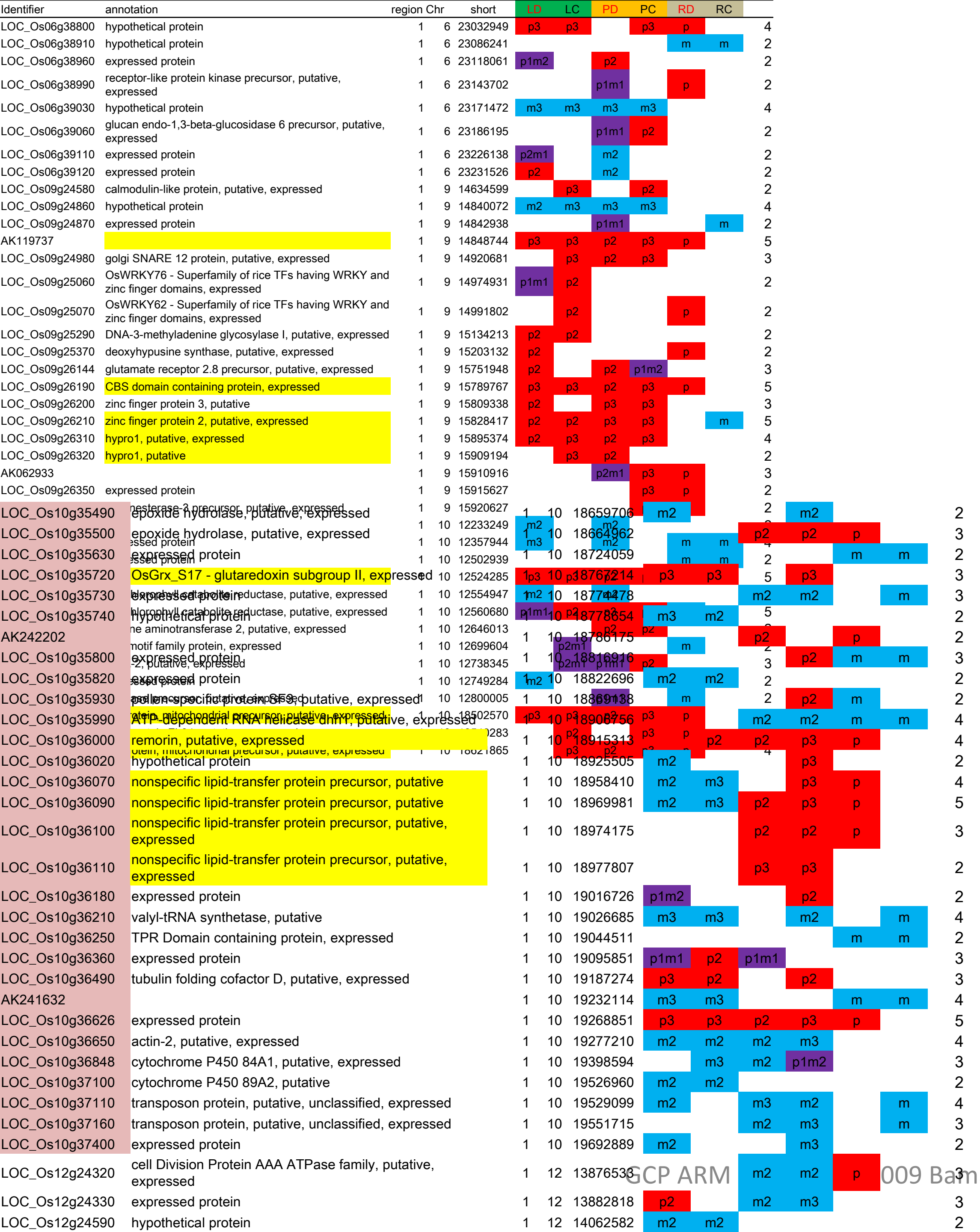
Genome-wide identification of BURP domain-containing genes in rice reveals a gene family with diverse structures and responses to abiotic stresses (Ding et al. 2009)

17 BURP genes in rice genome

7 subfamilies

except for two genes (OsBURP01 and OsBURP13), all other members were induced by at least one of the stresses including drought, salt, cold, and abscisic acid treatment.

OsBURP17 *: RD22-like subgroup*



Identifier	annotation	region	Chr	short	LD	LC	PD	PC	RD	RC	
LOC_Os06g38800	hypothetical protein	1	6	23032949	p3	p3		p3	p		4
LOC_Os06g38910	hypothetical protein	1	6	23086241					m	m	2
LOC_Os06g38960	expressed protein	1	6	23118061	p1m2		p2				2
LOC_Os06g38990	receptor-like protein kinase precursor, putative, expressed	1	6	23143702			p1m1		p		2
LOC_Os06g39030	hypothetical protein	1	6	23171472	m3	m3	m3	m3			4
LOC_Os06g39060	glucan endo-1,3-beta-glucosidase 6 precursor, putative, expressed	1	6	23186195			p1m1	p2			2
LOC_Os06g39110	expressed protein	1	6	23226138	p2m1		m2				2
LOC_Os06g39120	expressed protein	1	6	23231526	p2		m2				2
LOC_Os09g24580	calmodulin-like protein, putative, expressed	1	9	14634599		p3		p2			2
LOC_Os09g24860	hypothetical protein	1	9	14840072	m2	m3	m3	m3			4
LOC_Os09g24870	expressed protein	1	9	14842938			p1m1			m	2
AK119737		1	9	14848744	p3	p3	p2	p3	p		5
LOC_Os09g24980	golgi SNARE 12 protein, putative, expressed	1	9	14920681		p3	p2	p3			3
LOC_Os09g25060	OsWRKY76 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	1	9	14974931	p1m1	p2					2
LOC_Os09g25070	OsWRKY62 - Superfamily of rice TFs having WRKY and zinc finger domains, expressed	1	9	14991802		p2			p		2
LOC_Os09g25290	DNA-3-methyladenine glycosylase I, putative, expressed	1	9	15134213	p2	p2					2
LOC_Os09g25370	deoxyhypusine synthase, putative, expressed	1	9	15203132	p2				p		2
LOC_Os09g26144	glutamate receptor 2.8 precursor, putative, expressed	1	9	15751948	p2		p2	p1m2			3
LOC_Os09g26190	CBS domain containing protein, expressed	1	9	15789767	p3	p3	p2	p3	p		5
LOC_Os09g26200	zinc finger protein 3, putative	1	9	15809338	p2		p3	p3			3
LOC_Os09g26210	zinc finger protein 2, putative, expressed	1	9	15828417	p2	p2	p3	p3		m	5
LOC_Os09g26310	hypro1, putative, expressed	1	9	15895374	p2	p3	p2	p3			4
LOC_Os09g26320	hypro1, putative	1	9	15909194		p3	p2				2
AK062933		1	9	15910916			p2m1	p3	p		3
LOC_Os09g26350	expressed protein	1	9	15915627				p3	p		2
[illegible]	nesterase-3 precursor, putative, expressed	1	9	15920627				[illegible]	[illegible]		2
[illegible]	[illegible]	1	10	12233249	m2		m2				2
[illegible]	essed protein	1	10	12357944	m3		m2		m	m	4
[illegible]	essed protein	1	10	12502939					m	m	2
[illegible]	[illegible]	1	10	12524285	p3	p3	p2	[illegible]	[illegible]	[illegible]	5
[illegible]	hlorophyll catabolite reductase, putative, expressed	1	10	12554947	m2		m2	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	hlorophyll catabolite reductase, putative, expressed	1	10	12560680	p1m1	p2	p3	[illegible]	[illegible]	[illegible]	5
[illegible]	ne aminotransferase 2, putative, expressed	1	10	12646013			p2	p2			2
[illegible]	motif family protein, expressed	1	10	12699604		p2m1			m		2
[illegible]	-2, putative, expressed	1	10	12738345		p2m1	p1m1	p2			3
[illegible]	essed protein	1	10	12749284	m2			[illegible]	[illegible]	[illegible]	2
[illegible]	ase precursor, putative, expressed	1	10	12800005			[illegible]		m		2
[illegible]	otein, mitochondrial precursor, putative, expressed	1	10	18502570	p3	p3	p2	p3	p		[illegible]
[illegible]	[illegible]	1	10	[illegible]		p2		p3	p		[illegible]
[illegible]	otein, mitochondrial precursor, putative, expressed	1	10	18621865		p3	p2	[illegible]	[illegible]		4

Identifier	annotation	region	Chr	short	LD	LC	PD	PC	RD	RC	
LOC_Os10g35490	epoxide hydrolase, putative, expressed	1	10	18659706	m2			m2			2
LOC_Os10g35500	epoxide hydrolase, putative, expressed	1	10	18664962			p2	p2	p		3
LOC_Os10g35630	expressed protein	1	10	18724059					m	m	2
LOC_Os10g35720	OsGrx_S17 - glutaredoxin subgroup II, expressed	1	10	18767214	p3	p3		p3			3
LOC_Os10g35730	expressed protein	1	10	18774478			m2	m2		m	3
LOC_Os10g35740	hypothetical protein	1	10	18778654	m3	m2					2
AK242202		1	10	18786175			p2		p		2
LOC_Os10g35800	expressed protein	1	10	18816916				p2	m	m	3
LOC_Os10g35820	expressed protein	1	10	18822696	m2	m2					2
LOC_Os10g35930	pollen-specific protein SF3, putative, expressed	1	10	18869138				p2	m		2
LOC_Os10g35990	ATP-dependent RNA helicase dhh1, putative, expressed	1	10	18906756			m2	m2	m	m	4
LOC_Os10g36000	remorin, putative, expressed	1	10	18915313		p2	p2	p3	p		4
LOC_Os10g36020	hypothetical protein	1	10	18925505	m2			p3			2
LOC_Os10g36070	nonspecific lipid-transfer protein precursor, putative	1	10	18958410	m2	m3		p3	p		4
LOC_Os10g36090	nonspecific lipid-transfer protein precursor, putative	1	10	18969981	m2	m3	p2	p3	p		5
LOC_Os10g36100	nonspecific lipid-transfer protein precursor, putative, expressed	1	10	18974175			p2	p2	p		3
LOC_Os10g36110	nonspecific lipid-transfer protein precursor, putative, expressed	1	10	18977807			p3	p3			2
LOC_Os10g36180	expressed protein	1	10	19016726	p1m2			p2			2
LOC_Os10g36210	valyl-tRNA synthetase, putative	1	10	19026685	m3	m3		m2		m	4
LOC_Os10g36250	TPR Domain containing protein, expressed	1	10	19044511					m	m	2
LOC_Os10g36360	expressed protein	1	10	19095851	p1m1	p2	p1m1				3
LOC_Os10g36490	tubulin folding cofactor D, putative, expressed	1	10	19187274	p3	p2		p2			3
AK241632		1	10	19232114	m3	m3			m	m	4
LOC_Os10g36626	expressed protein	1	10	19268851	p3	p3	p2	p3	p		5
LOC_Os10g36650	actin-2, putative, expressed	1	10	19277210	m2	m2	m2	m3			4
LOC_Os10g36848	cytochrome P450 84A1, putative, expressed	1	10	19398594		m3	m2	p1m2			3
LOC_Os10g37100	cytochrome P450 89A2, putative	1	10	19526960	m2	m2					2
LOC_Os10g37110	transposon protein, putative, unclassified, expressed	1	10	19529099	m2		m3	m2		m	4
LOC_Os10g37160	transposon protein, putative, unclassified, expressed	1	10	19551715			m2	m3		m	3
LOC_Os10g37400	expressed protein	1	10	19692889	m2			m3			2
LOC_Os12g24320	cell Division Protein AAA ATPase family, putative, expressed	1	12	13876533			m2	m2	p		3
LOC_Os12g24330	expressed protein	1	12	13882818	p2		m2	m3			3
LOC_Os12g24590	hypothetical protein	1	12	14062582	m2	m2					2

18 vs 11

Total 73 genes were raised from the analysis

LD: leaf drought
LC: leaf control
PD: Panicle drought
PC: Panicle control
RD: Root drought
RC: Root control

p3	18 > 11 in three reps
m3	18 < 11 in three reps

Remarkable points 3

Identifier	annotation	region	Chr	short	LD	LC	PD	PC	RD	RC
LOC_Os09g26190	CBS domain containing protein, expressed	1	9	15789767	p3	p3	p2	p3	p	
LOC_Os09g26210	zinc finger protein 2, putative, expressed	1	9	15828417	p2	p2	p3	p3		m
LOC_Os10g35240	rf1 protein, mitochondrial precursor, putative, expressed	1	10	18502570	p3	p3	p2	p3	p	
LOC_Os10g35440	rf1 protein, mitochondrial precursor, putative, expressed	1	10	18621865		p3	p2	p3	p	
LOC_Os10g36000	remorin, putative, expressed	1	10	18915313		p2	p2	p3	p	

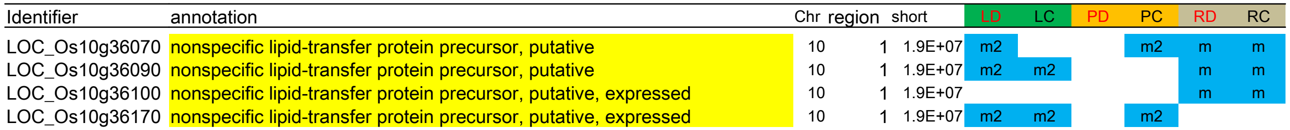
CBS domain containing protein on Chr 9
One zinc finger protein 2 (LOC_Os09g26210) on Chr 9
Tandemly repeated rf1 protein, mitochondrial precursor on Chr 10
remorin, putative on Chr 10

Are almost always 18 > 11

Genome wide expression analysis of CBS domain containing proteins in *Arabidopsis thaliana (L.) Heynh and Oryza sativa L.* reveals their developmental and stress regulation
Kushwaha et al. 2009
59 genes in rice.
the transcript levels of some members of this family are altered in response to various stresses such as salinity, drought, cold, high temperature, UV, wounding and genotoxic stress, in both root and shoot tissues.

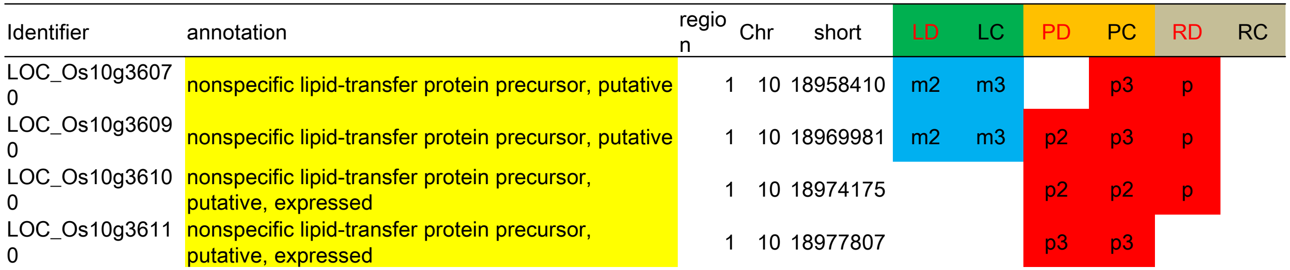
Remarkable points 4

Cluster of nonspecific lipid-transfer protein precursor on Chr 10



Identifier	annotation	Chr	region	short	LD	LC	PD	PC	RD	RC
LOC_Os10g36070	nonspecific lipid-transfer protein precursor, putative	10	1	1.9E+07	m2			m2	m	m
LOC_Os10g36090	nonspecific lipid-transfer protein precursor, putative	10	1	1.9E+07	m2	m2			m	m
LOC_Os10g36100	nonspecific lipid-transfer protein precursor, putative, expressed	10	1	1.9E+07					m	m
LOC_Os10g36170	nonspecific lipid-transfer protein precursor, putative, expressed	10	1	1.9E+07	m2	m2		m2		

10 vs 13



Identifier	annotation	region	Chr	short	LD	LC	PD	PC	RD	RC
LOC_Os10g36070	nonspecific lipid-transfer protein precursor, putative	1	10	18958410	m2	m3		p3	p	
LOC_Os10g36090	nonspecific lipid-transfer protein precursor, putative	1	10	18969981	m2	m3	p2	p3	p	
LOC_Os10g36100	nonspecific lipid-transfer protein precursor, putative, expressed	1	10	18974175			p2	p2	p	
LOC_Os10g36110	nonspecific lipid-transfer protein precursor, putative, expressed	1	10	18977807			p3	p3		

18 vs 11

These genes are located in the common introgressed region, but show the different expression profiles.

Conclusion

- Transcriptome analyses has represented the characteristic gene expression profiles of NILs under drought stressed condition.
- Collaborative analyses of NILs originated from Aday sel, such as physiological analysis, genotyping analysis and transcriptome analysis listed the genes located in the introgressed regions and show the differential expression.
- Some members of listed genes are interestingly related to the drought stress and other abiotic stresses.
- Germin-like protein clusters are known to be related to broad-spectrum disease resistance. Cross talk between disease resistance and drought tolerance?
- For the confirmation, sequence analysis of the promoter region of PDGE genes and transgenic works (ox or RNAi) are required.