

Systematic evaluation of rice mutant collections for conditional phenotypes with emphasis on stress tolerance



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OBJECTIVES

- Compile a **stress associated gene (SAG) database** for comparative genomics.
- Identify **SAG knockout mutants** using international mutant collections: insertional mutants (Tos17/Ac-Ds transposon and T-DNA) and EMS/radiation mutant libraries using sequenced insertions (FSTs) or PCR based screens including TILLING.
- Generate **gain-of-function genotypes** for SAG candidates by transforming over-expression constructs or identifying activation tagged lines.
- **Forward drought stress screen** of sequence-indexed knockout mutant lines under controlled conditions.
- **Phenotype SAG mutant lines for drought stress and disease resistance.**
- Characterize **stress associated pathways** and mechanisms by expression analysis of mutants using microarrays to uncover downstream genes.



Stress Associated Genes (SAG)



- 400 abiotic stress associated genes identified from literature
- 480 disease stress associated genes obtained from literature and Microarray analysis
- 260 (>1.5 fold) and 104 (>2 fold) BTH induced disease stress associated genes
- 48 putative rice orthologs of Arabidopsis genes revealed in a drought stress regulon
- 16 putative rice orthologs of Arabidopsis stress related small-RNA mechanism genes

Oh et al 2005 Plant Physiol: Gene upregulated in CBF/ABF overexpressor



Gene Name	ID	DRE	ABRE	OryGenesDB	Chrom	FST name
Jacalin1	Os012955_01	1	2	J013068M17	12	CZ167940
Jacalin2	Os045285_01	2	0	J033079F10	12	AG023638 AG211669
Dip1	Os058175_02	2	0	J023042N13	2	2A-20284 2A-30030
Lip5	Os054629_01	2	1	001-023-B08	3	---
Lipoxygenase (LOX)	Os057173_02	3	0	J013079G10	12	---
Glutelin	Os051893_02	0	0	002-125-F02	2	---
Bowman Birk trypsin inhibitor1	Os012347_01	0	0	J013042O18	1	---
Bowman Birk trypsin inhibitor2	Os020201_01	2	3	001-125-D07	1	---
Receptor kinase containing LRR repeats	Os007983_02	2	0	001-201-B07	5	AG208230 AG208417
Unknown protein	Os043689_01	1	1	001-024-A10	11	---
Cytochrome P450	Os014905_01	0	0	J023014D12	3	AG022659
Seed imbibition protein(Sip1)	Os057469_02	1	1	J013001N01	3	2D-30415 AG209860
Microtubule-associated protein MAP65-1a	Os057277_02	1	1	001-024-B12	6	---
Unknown protein	Os056678_01	0	0	Os01g12460.1	1	---
Unknown protein	Os023328_01	0	1	002-131-D08	11	---
Unknown protein	Os058052_02	1	1	006-307-H03	1	---
Polygalacturonase (PG2)	Os024032_01	0	0	002-143-E12	5	---
FtsJ cell division protein	Os015414_01	1	2	J023044P22	3	---
mRNA cleavage factor I subunit	Os009708_01	1	5	006-212-B12	8	---
Beclin	Os007215_01	6	0	J023150N19	1	2B-20519 AB155525
Cyclophilin (CyP)	Os057250_02	0	0	001-021-E10	8	---
Phospho sulfolactate synthase (PSLS)	Os017443_01	0	2	J023149H22	6	---
Gag-pol polyprotein	Os043586_01	1	0	001-115-A11	3	---
Alpha-expansin OsEXPA5	Os057091_02	0	0	002-126-F08	2	CZ265791
Hsp70	Os057646_02	3	1	001-129-B01	3	2D-01725
Protein phosphatase 2Ca (PP2Ca)	Os045883_01	1	2	Os01g40090.1	1	1A-08436 1A-10945
Wsi18	Os011045_01	1	2	001-125-H02	1	---
RAB21	Os024549_01	1	3	Os11g26800.1	11	---

Oh et al 2005 Plant Physiol: Gene upregulated in CBF/ABF overexpressor



Gene Name	ID	DRE	ABRE	OryGenesDB	Chrom	FST name
Phosphate-induced protein 1(phi1)	Os007254_01	0	0	J023049J22	2	---
Antioxidant protein	Os012781_01	0	0	001-040-H08	11	---
LEA4	Os023575_01	0	1	002-135-A01	8	---
Protein phosphatase 2Cb (PP2Cb)	Os058121_02	1	5	J023012K18	3	---
PHD-type zinc finger protein	Os028034_01	0	0	001-025-G08	5	2C-40359 2D-21006
Unknown protein	Os010904_01	1	3	001-120-G06	11	2A-00340
Little protein (LP1)	Os010826_01	0	2	001-118-F12	1	---
Unknown protein	Os016779_01	0	0	J013102B21	1	CL517725 CL518598
Unknown protein	Os010861_01	1	1	001-119-E05	12	---
CCCH-type zinc finger protein	Os022309_01	0	5	002-102-F01	5	---
26S proteasome AAA-ATPase subunit	Os054623_01	0	0	001-013-G01	2	---
Unknown protein	Os000729_01	1	0	Os10g42070.1	10	---
Unknown protein	Os008761_01	3	1	Os08g08440.1	8	---
Unknown protein	Os053377_01	0	3	001-005-A09	2	3A-03053
Aquaporin (TIP4)	Os058010_02	1	2	J033067O03	4	1B-21618
Disease resistance protein (RPH8A)	Os054795_01	3	1	001-001-E07	5	---
Unknown protein	Os053992_01	1	0	001-200-C04	1	CL523476
1,4-beta-D xylan xylanohydrolase	Os033116_01	2	2	P0494A10.4	1	---
Spore coat protein	Os054016_01	0	0	002-152-H04	5	---
Cellulase	Os009632_01	0	0	Os03g50610.1	3	---
LTI6B-like	Os008566_01	1	1	001-024-G01	3	2B-50190
Fusarium resistance protein	Os058114_02	1	0	001-014-D10	1	---
ABC transporter	Os045894_01	0	0	001-201-E11	1	---
LEA	Os020130_01	2	4	J013111O15	1	---
LEA3	Os039406_01	2	5	J033081F22	5	06ET3_387_D_003_0
OsCBFs/DREBs and Rice ABF homologues						
OsDREB 1A	Os052625_01			001-200-A04	9	---
OsDREB 1B	Os013388_01			001-102-G08	9	---
OsDREB2A	Os021893_01			J013106O15	1	CL524672
Rice ABF homologue	Os012364_01			J013049N23	9	AB156477 AB156478
OsTRAB1	Os058288_02			001-101-F09	8	---

Arabidopsis small RNA Processor Genes and Orthologs in Rice



Genes in Arabidopsis	function	Arabidopsis Mutants with loss of function and morphological traits	Orthologs in Rice
DCL1: At1g01040	All necessary for miRNA accumulation	<i>dcl1</i> : Substantial reduction in miRNA accumulation <i>caf-1</i> : abnormal flower development, unfused carpel <i>dcl1 dcl3 (double mutants), sin-1</i> : more rosette leaves, late-flowering due to conversion of floral meristem to indeterminate inflorescence state. (Schauer et al. Trends Plant Sci (7) 487-791) <i>dcl1 dcl4</i> : increased anthocyanin accumulation, 90% died before flowering (Gascioli et al. Current Biology (15)1-7. 2005)	Os03g02970
HYL1: At1g09700		Reduced level of miRNAs	Os12g01920
HEN1: At4g20910		Reduced level of miRNAs	Os07g06970
AGO1: At01g48410		<i>ago1</i> : Reduced level of miRNAs. Major developmental defects: abnormal inflorescence (infertile flowers) leaf (small rosette with narrow leaves due to reduced auxiliary meristems development), and short stem. (Bohmert -et al. EMBO (17) 170-180.1998. <i>ago1-26</i> is hypersusceptible to CMV infection and eventually die while wild type can form seeds. (Morel et al. Plant Cell (14) 629-639.2002)	Os02g45070
RDR2: At04g11130	Synthesis and processing endogenous repeat and intergenic-region-derived siRNAs	<i>rdr2</i> : no obvious development effects	Os04g39160
DCL3: At03g43920		<i>dcl3</i> : no obvious developmental effects	Os01g68120
DCL2: At03g03300	Produce virus-derived siRNA	<i>dcl2</i> : no obvious developmental effects Increased susceptibility against turnip-crinkle-virus (Xie et al. PLoS biol.(2)642-652)	Os03g38740
RDR6: At03g49500	Produce <i>trans</i> -acting siRNAs (ta-siRNA). Gascioli et al. Current Biology (15)1-7. 2005 Transgene silencing and virus resistance	<i>rdr6</i> : leaf curling downward, variable seeds(stamen fail to touch stigma), temporal control of shoot development is disrupted. (Peragine et al. Genes & Development. (18)2368-2378)	Os01g34350
SGS3: At05g23570		<i>sgs3</i> : Similar to <i>ago1</i> . (Morel et al. Plant Cell Review (14) 629-639.2002), hypersusceptible to cucumber mosaic virus (CMV) (Mourraine et al. Cell (101)533-542.2000)	Os12g09580
DCL4: At05g20320		<i>dcl4</i> :reduction in ta-siRNA levels and 3 fold increase in ta-siRNA target mRNA accumulation. Curled leaves, downward margins	Os04g43050 Os10g34430

Arabidopsis Drought Transcriptome

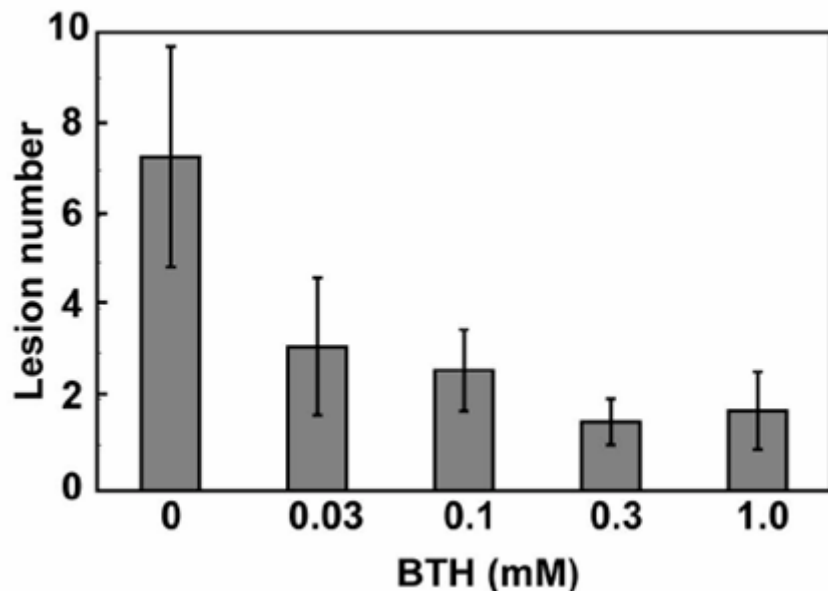
represented in

Drought tolerant
DREB1A regulon
rd29A:DREB1A

Putative
Rice
Orthologs

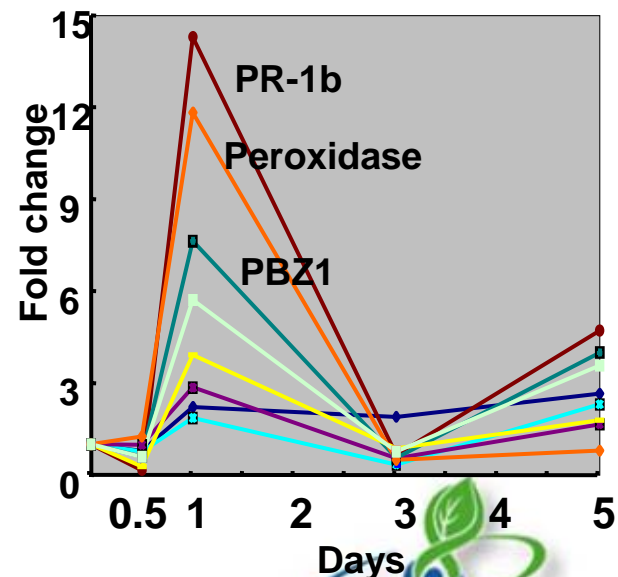
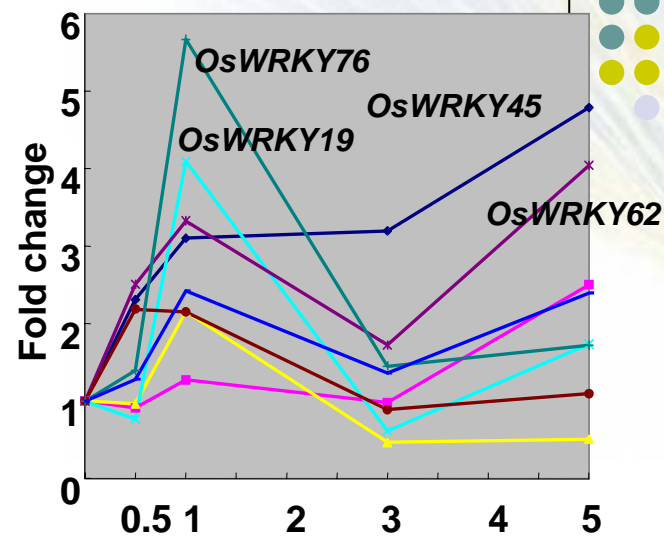
Gene	Gene Description	DROUGHT	DREB1A	CBF2	DREB1A	Rice	P
		26K	26K	24K	12K	orthologs	value
At5g52310	RD29A / COR78					Os04g52960	e-6
At1g20440	dehydrin COR47/RD17					Os02g44870	e-33
At1g20450	dehydrin ERD10 (LTI45)					Os02g44870	e-29
At2g23120	expressed protein (COR8.5)					Os09g30470	e-5
At5g04340	zinc finger (C2H2 type) family protein					Os12g39400	e-37
At1g01470	LEA14					Os01g12580	e-48
At4g24960	ABA-responsive protein (HVA22d)					Os11g30500	e-43
At2g42540	cold-regulated protein cor15a: Lea protein					Os03g07180	e-4
At5g50720	ABA-responsive protein (HVA22e)					Os11g30500	e-44
At1g78070	WD-40 repeat family protein					Os03g26870	e-47
At4g04020	plastid-lipid associated protein PAP					Os09g04790	e-91
At3g57020	strictosidine synthase family					Os03g53950	e-72
At4g27410	no apical meristem (NAM) (RD26)					Os01g66120	e-6
At2g15970	cold acclimation protein WCOR413-like					Os03g55850	e-67
At1g05170	galactosyltransferase family protein					Os03g38050	e-177
At1g58360	amino acid permease I (AAP1)					Os07g04180	e-173
At4g17550	glycerol 3-phosphate permease					Os08g06010	e-156
At3g12580	heat shock protein 70 / HSP70					Os03g60620	0
At3g28270	At14a related protein					Os03g10240	e-37
At1g02820	LEA3					Os01g21250	e-11
At4g27570	UDP-glycosyltransferase					Os11g27370	e-77
At4g36010	pathogenesis-related, PR5K					Os09g36560	e-97
At5g15970	KIN2 / COR6.6					Os01g13330	0.097
At5g17460	expressed protein					Os01g03500	e-104
At2g34720	CCAAT-binding transcription factor					Os12g41880	e-57
At3g15210	AtERF4					Os01g58420	e-34
At3g23000	CBL-interacting protein kinase 7 (CIPK7)					Os03g43440	e-106
At1g13930	drought-induced protein SDi-6					Os10g18340	e-19
At2g37760	aldo/keto reductase					Os05g38230	e-108
At2g39980	transferase family protein					Os01g63480	e-130
At3g61890	ATHB12, HD-ZIP transcription factor					Os09g35910	e-33
At2g46680	HD-ZIP protein ATHB-7					Os09g35910	e-34
At5g67300	myb family transcription factor					Os09g01960	e-66
At1g01720	ATAF1, no apical meristem (NAM)					Os01g66120	e-101
At2g21620	RD2/ universal stress protein (USP)					Os02g47650	e-74
At3g09390	MT2A, metallothionein protein					Os01g05650	e-25
At1g53580	hydroxyacylglutathione hydrolase					Os01g47690	e-114
At4g16760	ACX1, acyl-CoA oxidase					Os06g01390	0
At4g21580	zinc-binding dehydrogenase					Os02g56180	e-121
At1g17840	ABC transporter family protein					Os10g35180	0
At2g41190	amino acid/polyamine transporter					Os02g54730	e-175
At1g64780	ATAMT1:2, ammonium transporter 1					Os02g40710	0
At1g19570	dehydroascorbate reductase,					Os05g02530	e-77
At1g19550	dehydroascorbate reductase					Os06g12630	e-42
At4g27560	UDP-glucosyl transferase					Os11g27370	e-77
At4g39730	Polycystin-1, Lipoxigenase					Os02g51710	e-47
At1g54000	GDSL-like Lipase/Acylhydrolase					Os02g50690	e-31
At5g59320	LTP3, protease inhibitor					Os11g02400	e-25

BTH induction in rice reveals Disease Stress Associated Genes using microarray expression analysis



Rice blast resistance induced by BTH treatment. Rice plants sprayed with 0.03–1.0mM BTH at 3.5–4-leaf stage, followed by inoculation with *Magnaporthe grisea* (race 007) at 5-leaf stage 5 days after BTH application. Susceptible-type lesions were counted in the central 5-cm region of the fifth leaf 10 days after inoculation. BTH = benzothiadiazole

Temporal expression patterns of WRKY and PR protein genes.



NIAS

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- Generate **gain-of-function genotypes** for SAG candidates by transforming over-expression constructs or identifying activation tagged lines.
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International Rice Flanking Sequence Tag database for Identification of gene knockouts



Institution	Vector	No. of flanking sequences	No. of mapped sequences
CIRAD-INRA-IRD-CNRS, Genoplante (1)	T-DNA	7480	7170
CerealGene Tags, European Union (2)	Ac/Ds	1380	1380
National Institute of Agrobiological Sciences (3)	Tos17	18024	17937
University of California at Davis	Ac/Ds	2527	2464
PMBBRC (4)	Ac/Ds	1072	1044
Zhejiang University (5)	T-DNA	1017	917
National University of Singapore (6)	Ac/Ds	1469	1383
Postech (7)	T-DNA	23540	23540
CSIRO (8)	T-DNA	51	47
Total		56650	55882

OryGenes DB
<http://orygenesdb.cirad.fr>





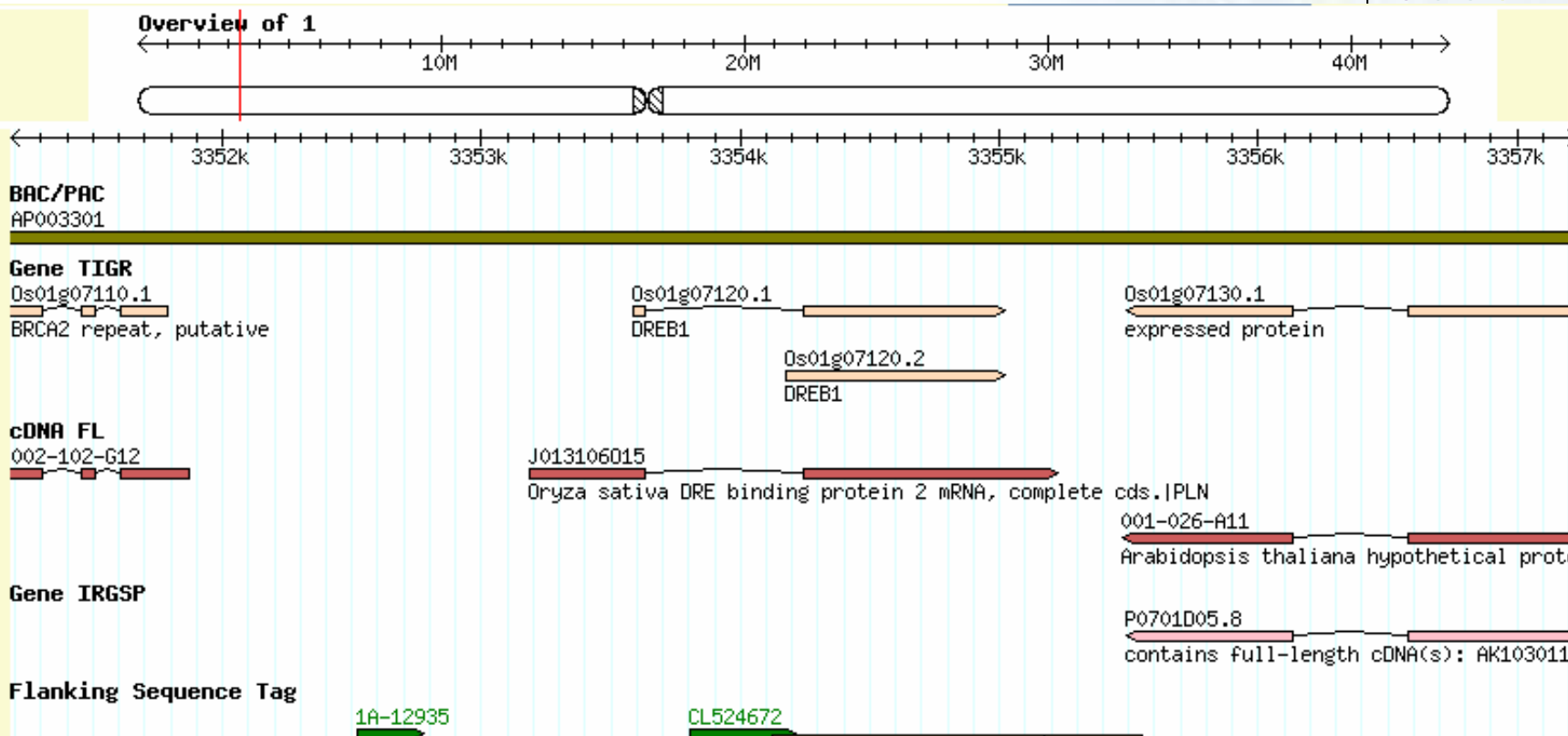
Distribution of different insertions on rice chromosomes

Chromosome	Length (Mb)	T-DNA	Tos17	Ac/Ds	Total
1	43.25	5181	2215	899	8295
2	35.88	3814	2063	957	6834
3	36.35	4346	1998	897	7241
4	35.00	2781	1529	541	4851
5	29.70	2318	1460	338	4116
6	31.20	2491	1616	420	4527
7	29.69	2184	1282	522	3988
8	28.31	2011	1293	431	3735
9	22.68	1674	1093	218	2985
10	22.70	1583	1037	407	3027
11	28.37	1660	1159	363	3182
12	27.49	1630	1192	278	3100
Total	370.63	31673	17937	6271	55982

OryGenes DB
<http://orygenesdb.cirad.fr>



OsDREB2A gene structure and insertion mutants



Data Source

Oryza sativa

Dumps, Searches and other

Annotate Restriction Sites

FSTs

Name : [CL524672](#)
Location : 1:3353808..3354211
Mutagen : T-DNA
Source : Genoplante
Method : Enhancer GUS

Tracks [Hide]

(External tracks italicized)

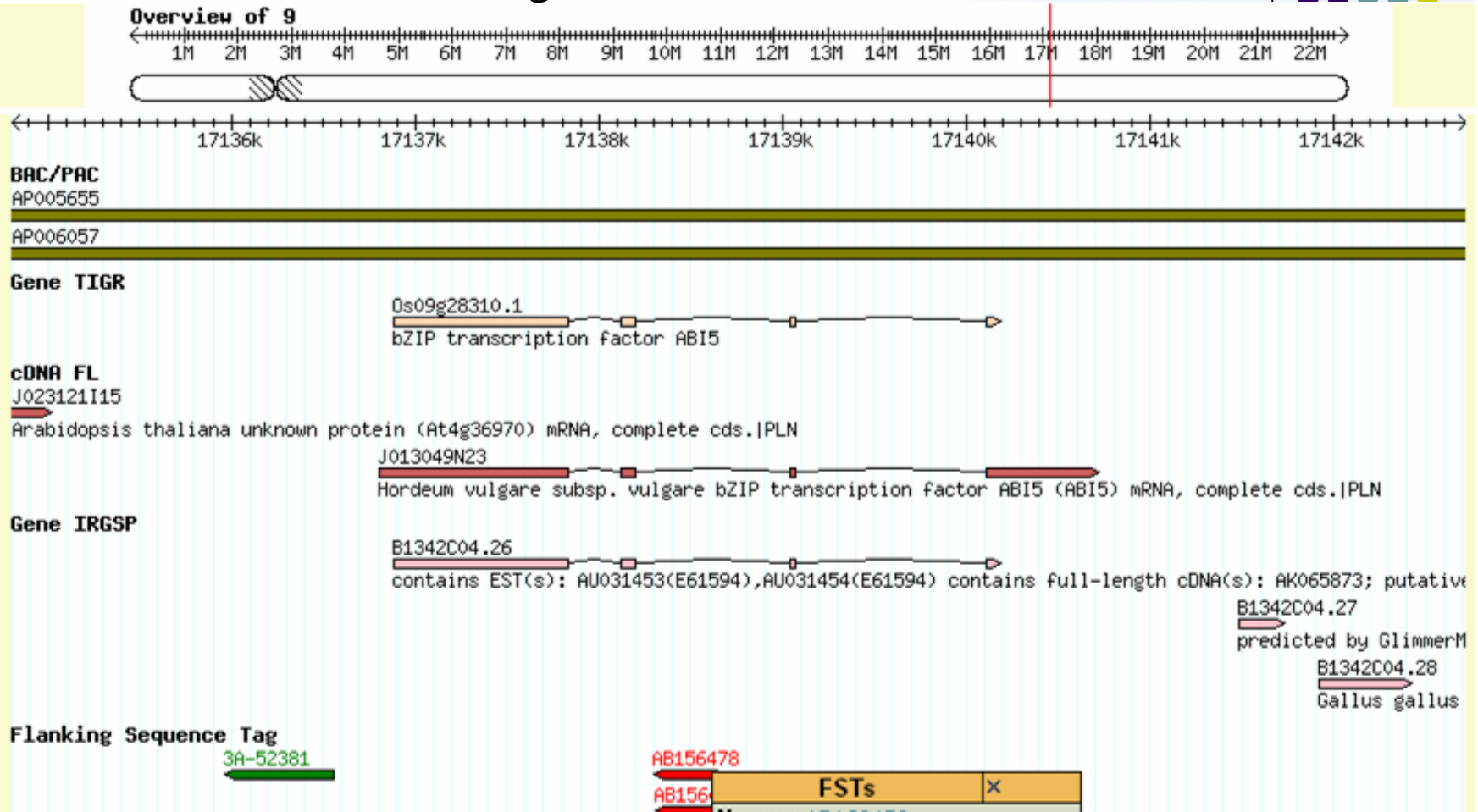
- Arabidopsis orthologs
- BAC/PAC
- Barley Gene Index
- cDNA FL

- Maiz
- Maiz
- Marker RFLP
- plugin:Restriction Sites

- Sorghum cluster Pratt
- Sorghum Gene Index
- Sorghum GSS
- Sorghum Markers



Os bZIP AtABI5-like gene structure and insertion mutants



Data Source

Oryza sativa

Dumps, Searches and other

Annotate Restriction Sites

Tracks [Hide]

- Arabidopsis orthologs
- BAC/PAC

- Maize
- Maize Markers

Name : [AB156478](#)
Location : 9:17138302..17138640
Mutagen : Tos17
Source : NIAS
Method : Retrotransposon

- Sorghum cluster Pratt
- Sorghum Gene Index



SCREENING 1400 LINES BY TILLING (Targeted Induced Local Lesions In Genomes) IRRI



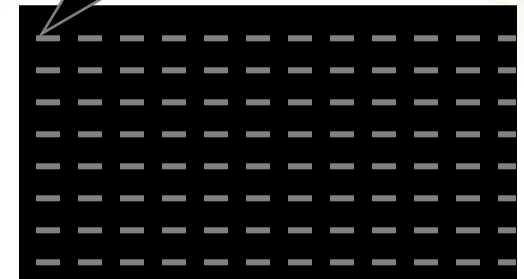
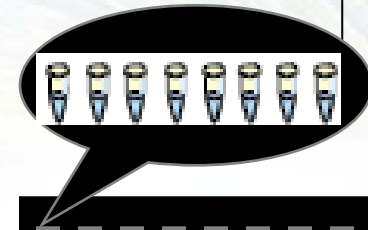
2%
EMS
treated
seeds



DNA
extraction
from M2
plant leaf



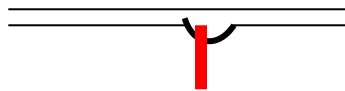
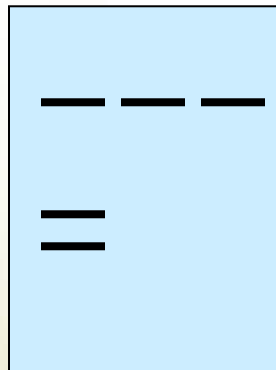
DNA Pool
(8x)



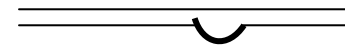
Gene-
specific
primers

PCR

Identify mutant
And study
phenotypes of
small RNA
accumulation



CEL1 digestion

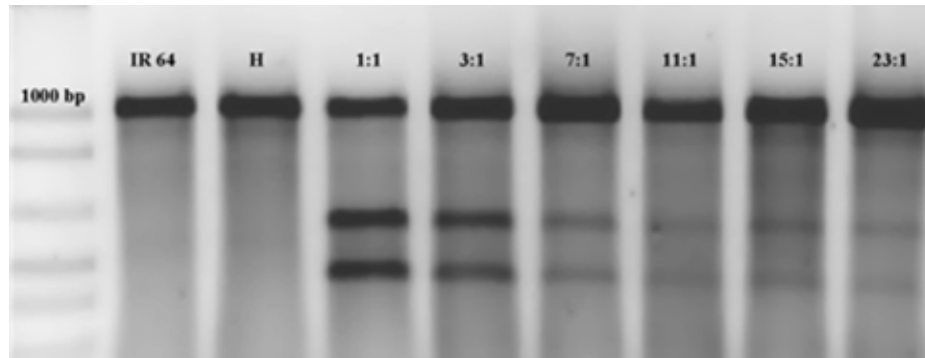


Hetero-duplex
formation

SNP (heteroduplex) detection by conventional agarose gel electrophoresis

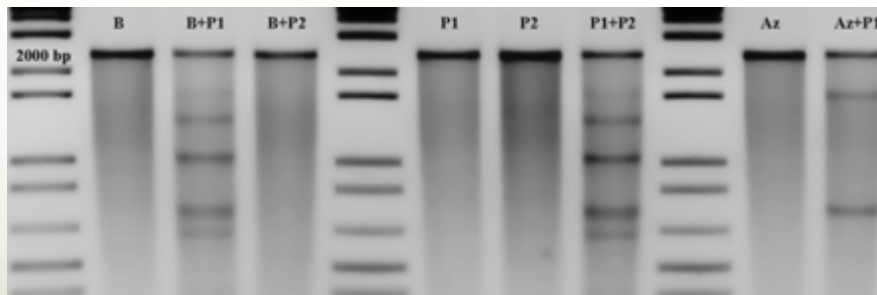


Increasing dilution of one template



Evaluation of pool capacity for detecting CEL I cleaved products. DNA from IR 64 and Huo-Shao-Tzu-Wu-Chan (H) were pooled at varying ratios prior to PCR amplification of the TPP gene. The PCR products were treated with CEL I.

BC line vs parents Parent1 vs parent2 *indica* vs *japonica*



SNP detection between rice varieties: Sanhuangzhan 2 (SHZ-2) (*indica*); Texianzhan-13 (TXZ-13) (*indica*), BC3F3 line BC10 and Azucena (Az) for the *MYB1* gene (LOC_Os12g41920).

IRRI



> 500 MUTANT LINES WITH MORPHOLOGICAL VARIATION



Choosing the lines with morphological trait for screening the candidate genes through **TILLING**:

- Extreme, semi dwarf
- rolled/ semi rolled leaf
- Dark green blade
- Tillering
- Narrow leaf
- Chlorina

‘Plants containing OsDCL1 RNAi construct showed various degree of developmental defects’ these trait includes “severe dwarfism, dark green color, rolled leaves and malformed shoots with tortuousness, reduced root elongation at vegetative stage.... These plants showed developmental arrest at young seedling stage and eventually died.’

Liu Bin et al. Plant Physiology Preview, Vol. 139, pp. 296-305. September 2005

<http://www.iris.irri.org/action/mutant?method=getMutants>

IRRI



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Functional Analysis of rice DREB/CBF genes



1
CBF3 RNAi
transgenic plants

2
Control plants
(transformed
with a vector)

3
CBF3 Over expression plants
showing resistant response to
drought stress.

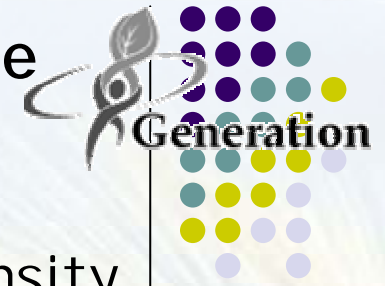
DREB/CBF genes identified
from rice genome and
full-length cDNA databases.

Full-length cDNAs amplified using RT-PCR
Constructs made for Over-expression & RNAi

Gene expression patterns of studied under
different drought stress conditions

↓
Drought stress phenotyping

Overexpression Drought Resistance Phenotype Conferred by *Arabidopsis SHN* gene in rice



SHN gene overexpression reduces stomatal density

14 day rice seedlings

9 days without water

1 week of recovery

after rehydration



WT

35S-SHN

WT

35S-SHN

OsSHN transformants are now tested
in Greenhouse screens in Bangalore, India

WUR-NL



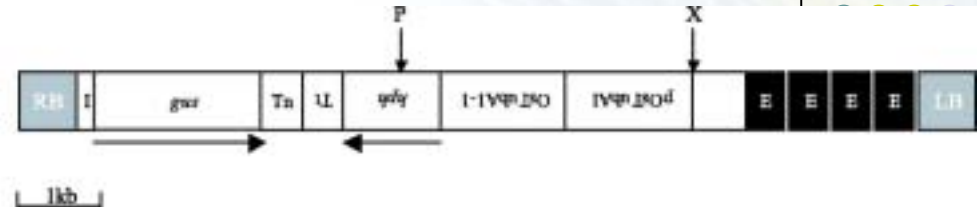
T-DNA Activation Tag lines



Activation Tagging T-DNA

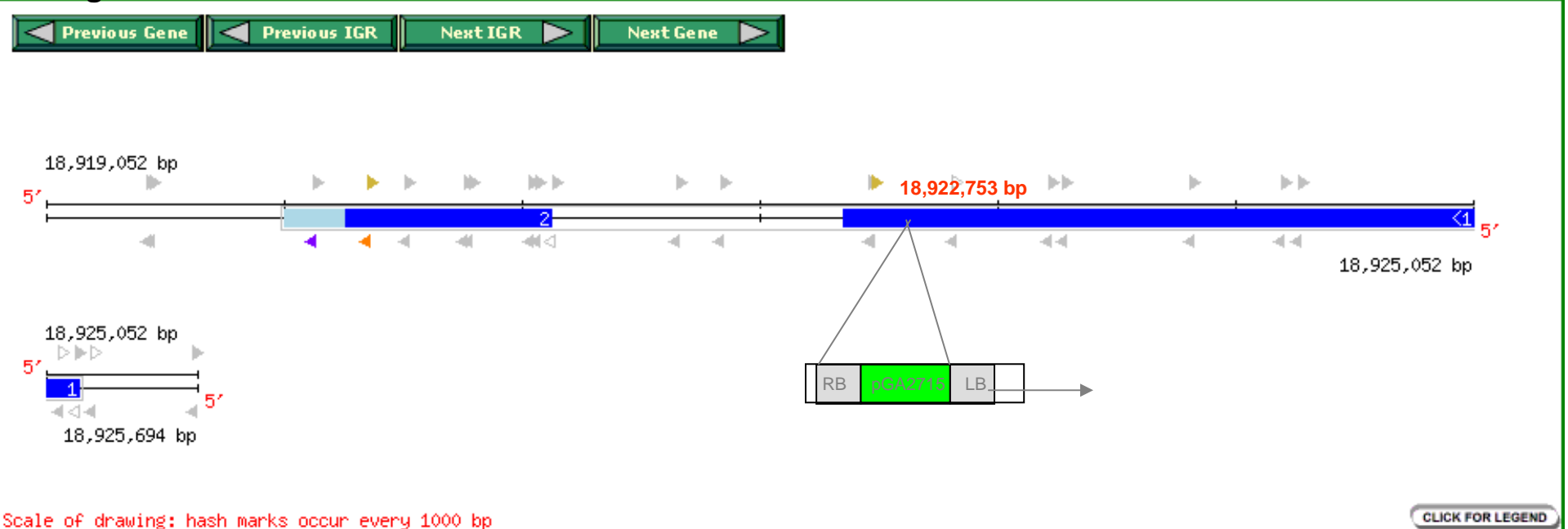
promoter-less gus reporter gene, pGA2715
4x 35S enhancer

Gyn An, Pohang Univ, Korea



1. Jeong et al. 2002. Plant Physiology. Vol. 130, pp. 1636-1644.
2. Ryu et al. 2004. Plant Molecular Biology. Vol. 54, pp. 489-502

Os01g34350



28 insertional mutants

10 candidate genes available

IRRI/Pohang

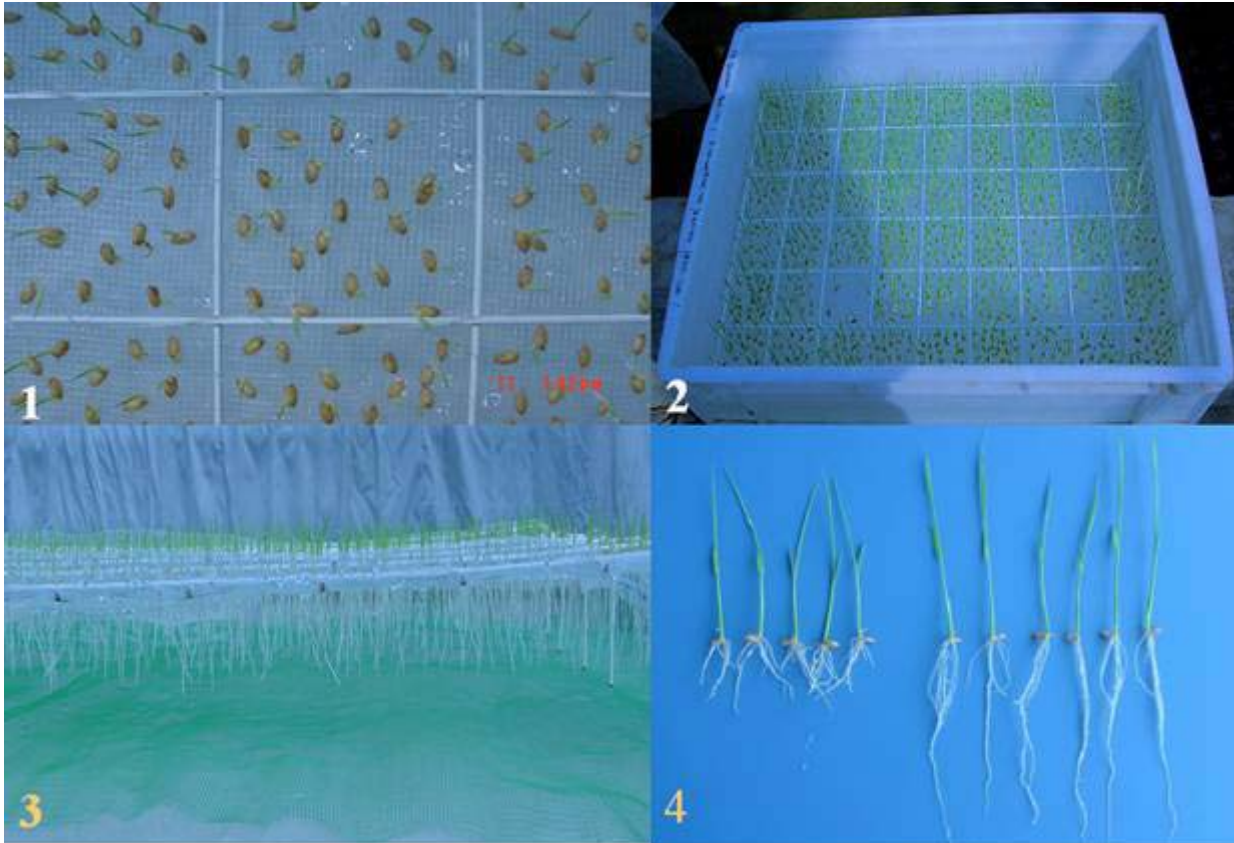


OBJECTIVES

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Forward mutant screens of FST indexed T-DNA insertion lines CAAS (China)



Screen for salt responsive mutants

- 2000 lines screened
- 2 salt sensitive mutants obtained
- 1, 2: seedlings of T-DNA tag lines
- 3: seedlings grown under salt stress (200 mM NaCl).
- 4: salt sensitive (left) and control (right) plants.

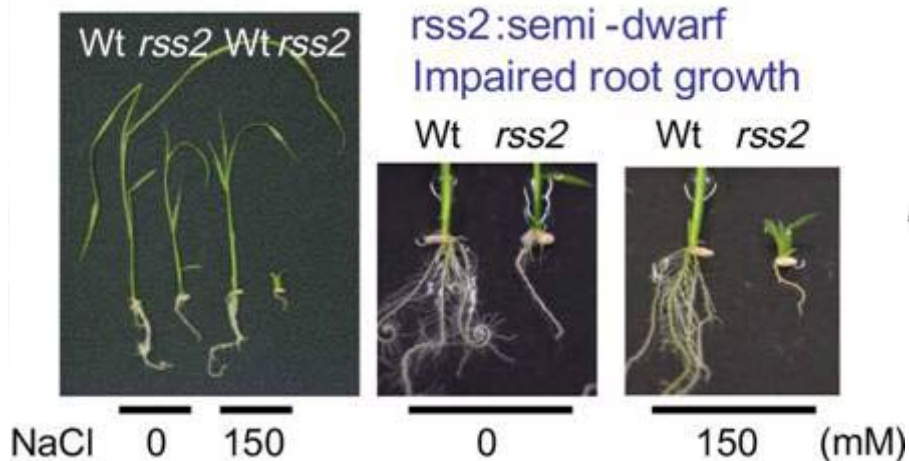
Screen for drought responsive mutants:

10-day-old plants with 15% PEG(6000).

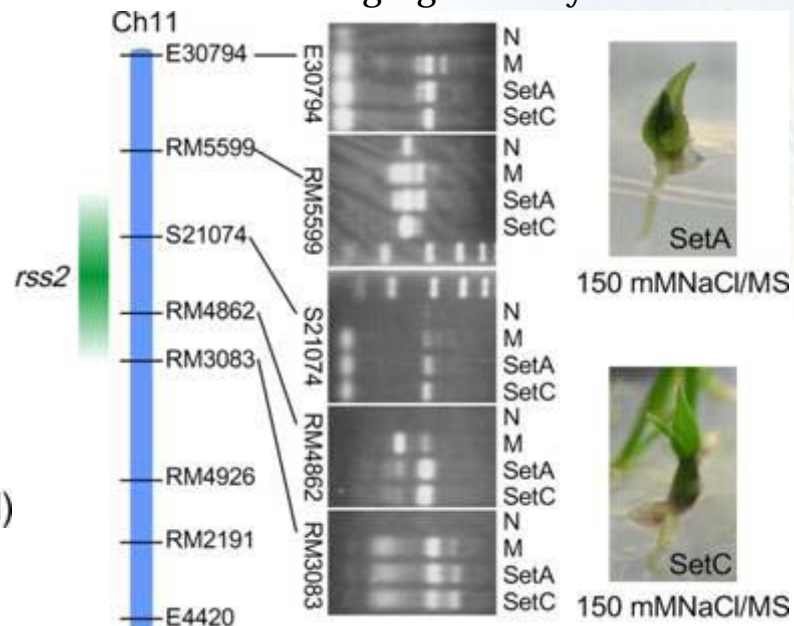
- 2000 lines screened
- 3 drought sensitive mutants obtained

Forward genetics: Map-based cloning of *RSS2*

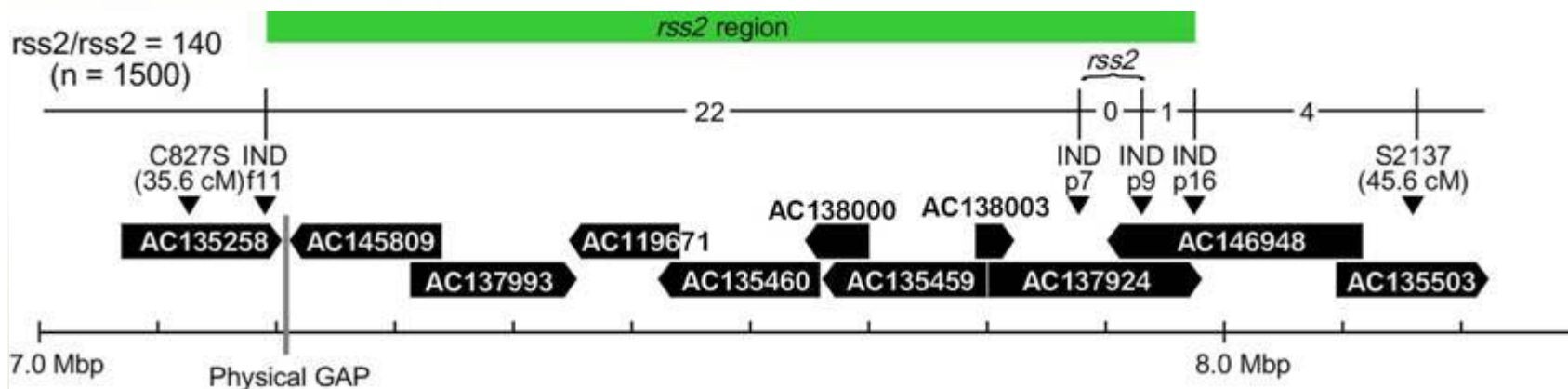
Phenotypes of *rss2* mutant



Bulked segregant analysis



Genetic analysis of *rss2* region



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Gene name	FST #	Chrom	Plant
AIR 1(Root) auxin -induced lateral root formation	236	4	ABVD01
OsDREB2A	279	1	ACCF03
OsUGE-1	832	5	AFCB07
AtLecRK2	2908	4	AMDD07
Arabidopsis thaliana NAC1 (NAC1)	2919	6	AMDF10
AtSRK2C	3025	7	AMHA06
Subtilisin-chymotrypsin inhibitor 2	3079	1	AMIH09
OsAR15	4458	4	AELE08
miR442	4927	7	AFEE02
SABRE	5271	3	AFUD07
miR436	5528	12	AGDF08
RGP1	6604	9	AIBH12
OsCDPK7	7215	4	AJLB01
Oryzains (EC3.4.22) Cysteine proteinases	7451	4	AKDF12
EIR1 (Roots)	7822	6	ANIE03
OsGSTU17	7908	9	APJE03
Ser/Thr specific protein kinase NPK15	4380	1	AEHE08
transketolase, putative	120	6	AAYC11
leucine-rich repeat receptor-like kinase	7994	1	AQFA05
protein kinase family protein	5951	7	AHAD12
zinc finger (C3HC4-type RING finger)	2009	1	AKJC06
phospholipid/glycerol acyltransferase family	2176	1	AKUF09
glycosyl hydrolase family 1 protein	6396	6	AHRB09
nodulin family protein	3753	12	ANNH06
VHS domain-containing protein	7142	8	AJGH07
ATP translocase 2	5372	5	AFXF01
cytochrome P450 family protein	1772	10	AKBC05
phosphoenolpyruvate carboxylase, putative	1589	1	AJWB05
COP1 regulatory protein	7219	2	AJLC05
oligopeptide transporter OPT family protein	2110	4	AKPH10
PP2A-2 catalytic subunit	119	3	AAYC07
PP2A-3 catalytic subunit	7106	2	AJEA02
third catalytic subunit OsPP2A-1	3394	6	AMUG05
homeotic BEL1-like protein	3370	1	AMTF09

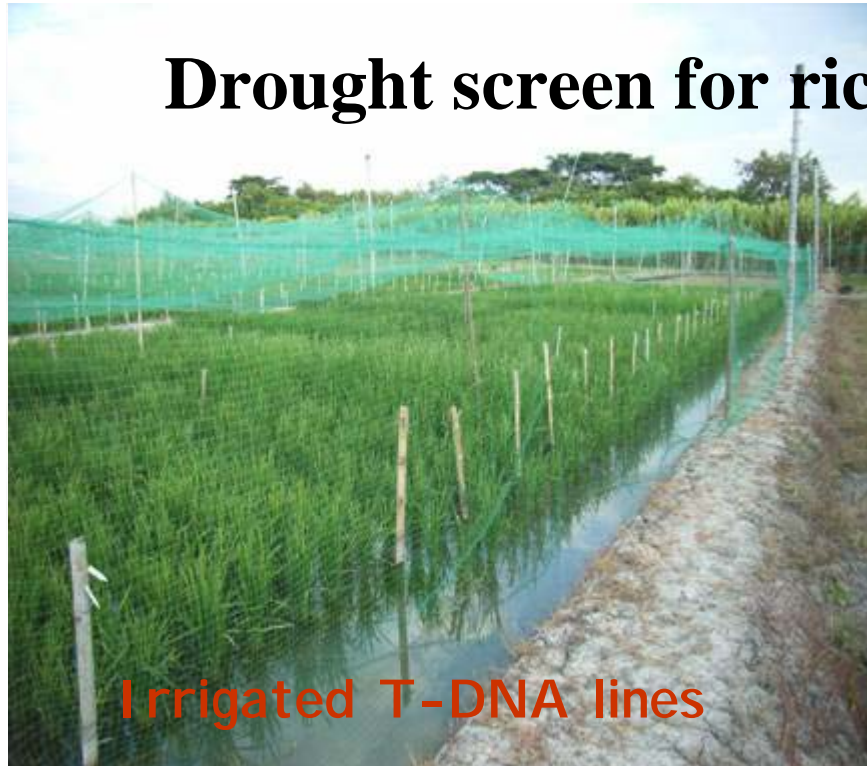
Short Compiled list
of 61 Rice SAGs with FSTs
being screened for
Drought Stress at CIAT

CIRAD-CIAT



Drought screen for rice T-DNA lines in the field

CIAT-Colombia



Irrigated T-DNA lines



T-DNA lines exposed to Drought

298 genes selected from literature searches



61 hits founded in 8,000 T-DNA FSTs



A total of 53 lines transplanted in the field
30 plants/line, 3 replications



Evaluation of drought tolerance started
one month after transplanting.

CIRAD-CIAT



Biotic Stress: Identify resistance gene pathways



Targeted Pathogens

Bacterial blight - *Xanthomonas oryzae*
Sheath blight - *Rhizoctonia solani*

Pathosystems studied

Transcriptome analyses
Other monocot/dicot candidate genes

Stress Candidate Gene List

T-DNA Mutant evaluation

Identify insertion lines

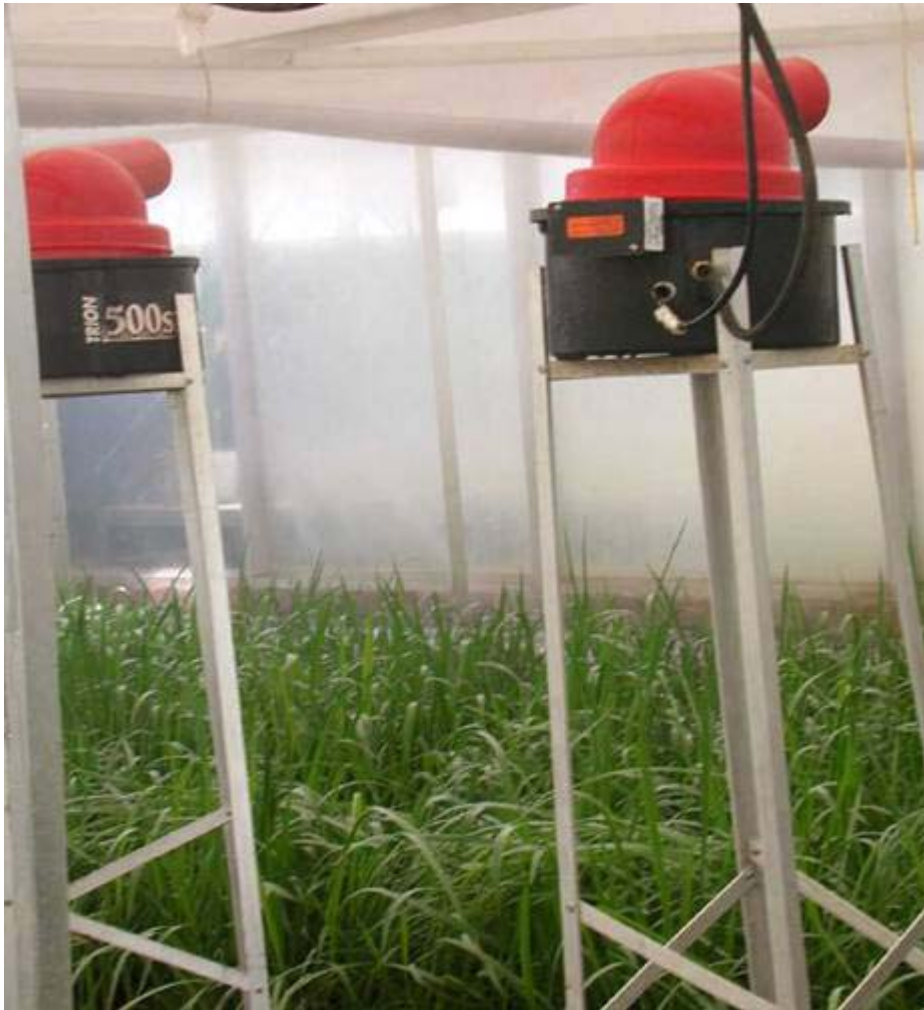
Functional validation

New strategies for breeding
MAS

CIRAD-IRD-CIAT



Sheath blight *Rhizoctonia solani* screen of rice T-DNA population @ CIAT



Pathogen inoculation using humidifiers



100 T-DNA lines selected based on a gene list



About only 60% lines germinated



Plants inoculated with *Rhizoctonia solani*
50 days after planting



Evaluation of resistance reaction

CIRAD-CIAT



Transcriptome analysis
BLB incompatible reaction
Gene list (479 candidates)



Nipponbare
PXO339



172 T-DNA lines identified with insertion in candidate genes
(OrygenesDB)

FST	Orientation	Region	Query	Gene	Expect	% Homology	Cnr	Function
3A-06443	T-DNA	Gene	c.nip.2.0.2.O2.f	Os02g39160.1	2.00E-50	99,04761905	2	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
3A-12256	T-DNA	Gene	c.nip.2.0.3.E6.r	Os02g40240.1	1.00E-152	100	2	Leucine Rich Repeat, putative
3A-14558	T-DNA	Promoter	c.nip.2.0.4.C24.r	Os02g40240.1	1,00E-171	100	2	Leucine Rich Repeat, putative
3A-12256	T-DNA	Gene	c.nip.2.0.4.C24.r	Os02g40240.1	1,00E-171	100	2	Leucine Rich Repeat, putative
3A-14558	T-DNA	Promoter	c.nip.2.0.4.C24.r	Os02g40240.1	1,00E-171	100	2	Leucine Rich Repeat, putative

90 lines screened for compromised resistance to *Xanthomonas oryzae*



IRD/CIRAD

Genotyping identified lines to confirm linkage
phenotype and T-DNA integration

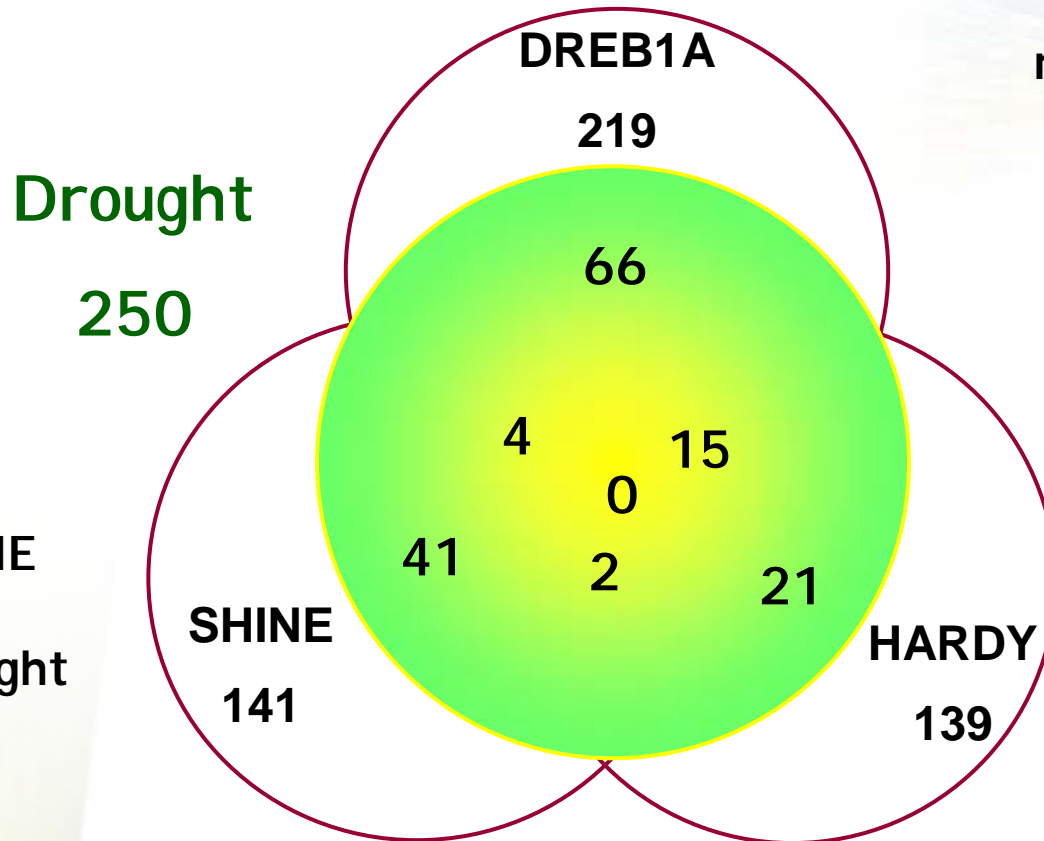


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Drought Transcriptome: 3 AP2/ERF Resistance Regulons



rd29A-DREB1A
vs
Wt no drought

35S-SHINE
vs
WT no drought

hrd-D mutant
vs
Wt no drought

All 3 genes transformed to rice
can now be used for
Comparative Transcriptome Analysis

WUR

