

Table 1 Suppl. Oligonucleotides for five WRKY transcription factors genes and *EF1-α* as a normalization gene, evaluated in this study by real-time qPCR analysis.

CGSNL RAP-BD	ID Japonica	ID Indica	Forward (5'-3')	Reverse (5'-3')
<i>OsWRKY11</i>	LOC_Os01g43650.1	BGIOSGA004027	AGGACACGGTGGTCAAGCAG	TGTCGTGGCTCGTCACATCC
<i>OsWRKY17</i>	LOC_Os01g74140.1	BGIOSGA005267	CCGACGGTCACAATTTTCGCT	GCGAGAAAACCACTGGGCTAC
<i>OsWRKY56</i>	LOC_Os01g62514.1	BGIOSGA000506	GTGGAGGAAGTACGGGCAGA	CACCTGGGATGTGGGTTGTT
<i>OsWRKY62</i>	LOC_Os09g25070.1	BGIOSGA029757	CGGCGCCACTATAAGAAACG	GGAGGAAGTACGGCGTGACA
<i>OsWRKY73</i>	LOC_Os06g05380.1	BGIOSGA022298	ATGACGTTGAGCCCTGAAGG	TGCGGTGTCATCCCTAGCAT
<i>OsEF1-α</i>	LOC_Os03g08020.1	BGIOSGA011972	TGGTATGGTGGTGACCTTTG	GTACCCACGCTTCAGATCCT

Table 2 Suppl. Analysis of variance for shoot length (SL), root length (RL), root number (RN), leaf number (LN), coleoptile length (CL), shoot fresh mass (SFM), shoot dry mass (SDM), root fresh mass (RFM), and root dry mass (RDM) of rice seedlings under submergence. * - Significant by the *F*-test ($P \leq 0.05$), DF - degrees of freedom, CV - coefficient of variation.

VF	DF	Mean square		RN	LN	CL	SFM	SDM	RFM	RDM
		SL	RL							
Genotype	2	13.447	3.724	33.190	0.367	0.078	0.108	0.002	0.5294*	0.019*
Treatment	4	21.075	0.418	5.853	0.596	0.088	0.185	0.001	0.0589*	0.003*
Interact. G×T	8	3.887	0.398	2.396	0.268	0.029	0.019	0.000	0.0402*	0.001*
Residue	30	5.991	0.784	1.406	0.283	0.034	0.012	0.000	0.011	0.000
Mean		10.310	4.304	6.074	3.198	0.628	0.592	0.086	0.550	0.089
CV		23	20	19	16	29	18	22	18	21

Table 3 Suppl. *Cis*-regulatory elements (CREs) in 1.5 kb upstream of transcription start site of WRKYs transcription factors. 1 indicates presence of CRE; 0 absence of CRE.

CRE Name	CRE Function	WRKY1	WRKY7	WRKY56	WRKY62	WRKY73
CREs involved in transcription						
5UTR Py-rich stretch	conferring high transcription levels	1	0	0	1	0
AT-rich sequence	element for maximal elicitor-mediated activation (2copies)	0	0	1	0	0
CAAT-box	common CRE in promoter and enhancer regions	1	1	1	1	1
TATA-box	core promoter element around -30 of transcription start	1	1	1	1	1
CREs involved in plant development						
AC-1	negative regulation of phloem and xylem expression	0	0	1	1	1
as-2-box	involved in shoot-specific expression; light responsiveness	0	0	0	1	1
circadian	involved in circadian control	0	1	0	0	0
GCN4_motif	involved in endosperm expression	0	0	0	1	1
O2-site	involved in zein metabolism regulation	1	1	1	1	1
RY-element	involved in seed-specific regulation	0	1	0	0	1
Skn-1_motif	required for endosperm expression	1	1	1	1	1
TATCCAT/C-motif	involved in sugar repression responsiveness	1	1	0	0	1
WUN-motif	wound-responsive element	0	0	0	0	1
CRE involved in biotic stress						
Box W1	fungal elicitor responsive element	1	0	0	1	0
CRE involved in abiotic stress						
HSE	involved in heat stress responsiveness	1	0	1	1	0
ARE	essential for the anaerobic induction	0	0	0	1	0
C-repeat/DRE	involved in cold- and dehydration-responsiveness	0	0	0	0	1
GC-motif	involved in anoxic specific inducibility	0	0	0	1	0
TC-rich repeats	involved in defense and stress responsiveness	0	0	1	0	0
CRE involved in light responses						
MNF1	light responsive element	0	0	1	0	0
3-AF1 binding site	light responsive element	0	0	0	1	0
4c1-CMA2b	light responsive element	0	0	0	0	1
ACA-motif	involved in light responsiveness	0	0	1	0	0
ACE	involved in light responsiveness	1	0	1	0	0
AE-box	part of a module for light response	0	0	1	0	0
ATGC-motif	involved in light responsiveness	0	0	0	0	0
ATCT-motif	involved in light responsiveness	0	1	0	0	0
Box 4	involved in light responsiveness	1	1	1	1	0
Box I	light responsive element	0	0	1	0	1
CATT-motif	part of a light responsive element	0	0	0	1	0
GAG-motif	part of a light responsive element	0	1	1	1	0
GA-motif	part of a light responsive element	0	1	0	1	1
GATA-motif	part of a light responsive element	0	1	0	1	0
G-box	involved in light responsiveness	1	1	1	1	1
G-Box	involved in light responsiveness	1	1	1	1	1
GT1-motif	light responsive element	1	1	1	1	1
I-box	part of a light responsive element	1	0	1	1	1
LAMP-element	part of a light responsive element	0	0	1	0	1
L-box	part of a light responsive element	1	0	0	0	1
Sp1	light responsive element	1	0	1	1	0
TCCC-motif	part of a light responsive element	0	0	1	0	0
TCT-motif	part of a light responsive element	1	0	0	1	1
CRE involved in hormonal responses						
ABRE	involved in the abscisic acid responsiveness	1	1	1	1	0
CGTCA-motif	involved in the MeJA-responsiveness	1	0	0	1	0
ERE	ethylene-responsive element	0	0	0	0	1
GARE-motif	gibberellin-responsive element	1	1	1	1	0
P-box	gibberellin-responsive element	1	0	1	0	1
TCA-element	salicylic acid responsiveness	1	1	0	1	1

TGA-element	auxin responsive element	0	0	0	1	0
TGACG-motif	involved in the MeJA-responsiveness	1	0	0	1	0
Transcription factors binding sites						
W-box	WRKY binding site	1	0	1	1	0
CCAAT-box	MYBHv1 binding site	0	0	1	0	0
MBS	MYB binding site	0	1	0	1	1
MRE	MYB binding site	0	0	0	1	0
CREs with unknown function						
AAGAA-motif	unknown	1	1	0	0	0
TCCACCT-motif	unknown	0	0	1	0	0
Unnamed_1	unknown	1	0	1	0	0
Unnamed_10	unknown	1	0	0	1	0
Unnamed_11	unknown	0	0	0	0	1
Unnamed_12	unknown	1	0	0	1	0
Unnamed_13	unknown	1	0	0	0	0
Unnamed_14	unknown	1	0	0	1	0
Unnamed_15	unknown	0	0	0	0	1
Unnamed_16	unknown	0	0	0	0	1
Unnamed_3	unknown	1	0	1	0	0
Unnamed_4	unknown	1	1	1	1	1
Unnamed_6	unknown	1	0	1	0	0
Unnamed_8	unknown	1	0	0	1	0
Unnamed_9	unknown	1	0	0	1	0

Table 4 Suppl. W-box presence in 1.5 kb upstream of transcription start site of genes involved in submergence stress and aerenchyma development.

Locus_ID	Gene symbol	Gene name	W-box	Score	References
				matrix	
LOC_Os09g35010	<i>OsDREB1B</i>	dehydration-responsive element-binding protein 1B	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os09g35030	<i>OsDREB1A</i>	dehydration-responsive element-binding protein 1A	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os03g01320	<i>qLTG3_1</i>	QTL of low-temperature germinability in chromosome3 -1	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os03g57220	<i>OsGLO1</i>	glycolate oxidase 1	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os05g06660	<i>OsGS5</i>	grain size 5/serine carboxypeptidase	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os06g49840	<i>OsSPW1</i>	SuperWoman 1	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os01g68870	<i>OsIMSP1</i>	multiple Sporocyte 1	2 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os05g39560	<i>OsZIP5</i>	metal cation transporter	1 W-box	6	Yoo <i>et al.</i> 2015
LOC_Os05g02070	<i>OsMT2b</i>	metallothionein-2b	1 W-box	6	Yamauchi <i>et al.</i> 2013
LOC_Os01g54940	<i>OsADH1</i>	alcohol dehydrogenase 1	1 W-box	6	Magneschi and Perata 2009
LOC_Os05g10780	<i>OsACS3</i>	1-aminocyclopropane-1-carboxilase synthase 3	1 W-box	6	Evans 2004
LOC_Os09g27820	<i>OsACO1</i>	1-aminocyclopropane-1-carboxilase oxydase 1	1 W-box	6	Evans 2004
LOC_Os01g06660	<i>OsPDC2</i>	pyruvate decarboxylase isozyme 2	2 W-box	6	Magneschi and Perata, 2009
LOC_Os02g45450	<i>OsDREB1G</i>	dehydration-responsive element-binding protein 1G	without	—	Yoo <i>et al.</i> 2015
LOC_Os03g08310	<i>OsTIFY11a</i>	OsTIFY11a/ZIM domain containing protein	without	—	Yoo <i>et al.</i> 2015
LOC_Os01g54620	<i>OsBC7</i>	brittle culm 7(t)	without	—	Yoo <i>et al.</i> 2015
LOC_Os09g25490	<i>OsBC6</i>	brittle culm 6	without	—	Yoo <i>et al.</i> 2015
LOC_Os03g30250	<i>OsBC1/CWA1</i>	brittle culm 1/cell wall architecture 1	without	—	Yoo <i>et al.</i> 2015
LOC_Os10g32980	<i>OsCESA7</i>	cellulose synthase catalytic subunit A7	without	—	Yoo <i>et al.</i> 2015
LOC_Os01g63510	<i>OsQHB</i>	quiescent center specific homeobox	without	—	Yoo <i>et al.</i> 2015
LOC_Os09g23300	<i>OsVIT2</i>	vacuolar iron transporter 2	without	—	Yoo <i>et al.</i> 2015
LOC_Os02g47020	<i>OsSBPase</i>	sedoheptulose-1,7-bisphosphatase	without	—	Yoo <i>et al.</i> 2015
LOC_Os04g57610	<i>OsARF12</i>	auxin response factor 12	without	—	Yoo <i>et al.</i> 2015
LOC_Os07g47100	<i>OsNHX1</i>	Na ⁺ /H ⁺ antiporter gene1	without	—	Yoo <i>et al.</i> 2015
LOC_Os01g66100	<i>OsSD1</i>	semi-dwarf 1	without	—	Yoo <i>et al.</i> 2015
LOC_Os06g12310	<i>OsLSI6</i>	low silicon rice 6	without	—	Yoo <i>et al.</i> 2015
LOC_Os01g53294	<i>OsRBOHA</i>	respiratory burst oxidase A	without	—	Yamauchi <i>et al.</i> 2013
LOC_Os03g51740	<i>OsACS1</i>	1-aminocyclopropane-1-carboxilase synthase 1	without	—	Evans 2004
LOC_Os04g48850	<i>OsACS2</i>	1-aminocyclopropane-1-carboxilase synthase 2	without	—	Evans 2004
LOC_Os09g27750	<i>OsACO2</i>	1-aminocyclopropane-1-carboxilase oxydase 2	without	—	Evans 2004
LOC_Os03g18220	<i>OsPDC3</i>	pyruvate decarboxylase isozyme 3	without	—	Magneschi and Perata 2009
LOC_Os11g33270	<i>OsXET2</i>	xyloglucan endotransglycosylase XET2	without	—	Yamauchi <i>et al.</i> 2013
LOC_Os05g20020	<i>OsPG</i>	Polygalacturonase (pectinase)	without	—	Yamauchi <i>et al.</i> 2013

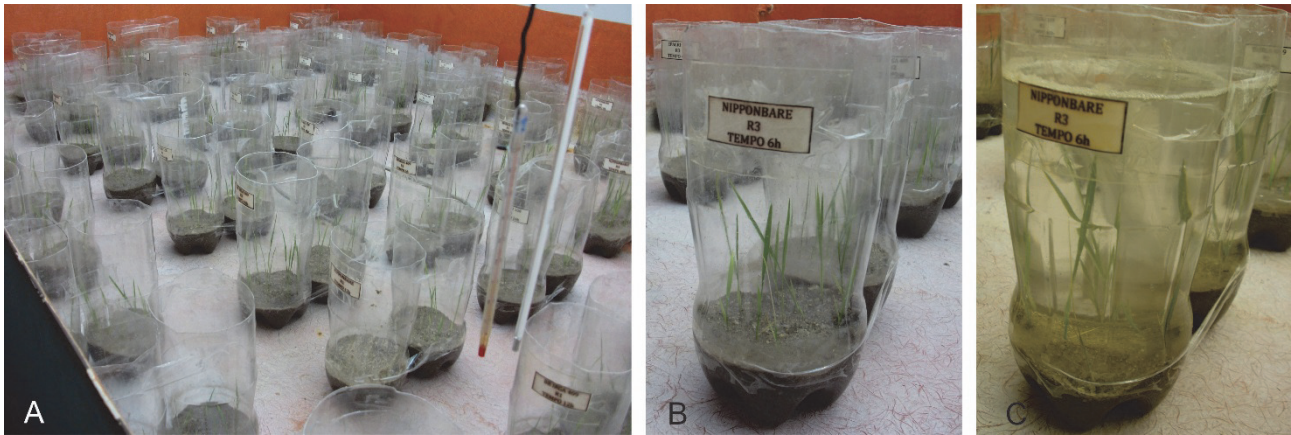


Fig. 1 Suppl. Experiment design of induced submergence stress (A), rice plants before total submergence (B), and submerged rice plants (C).

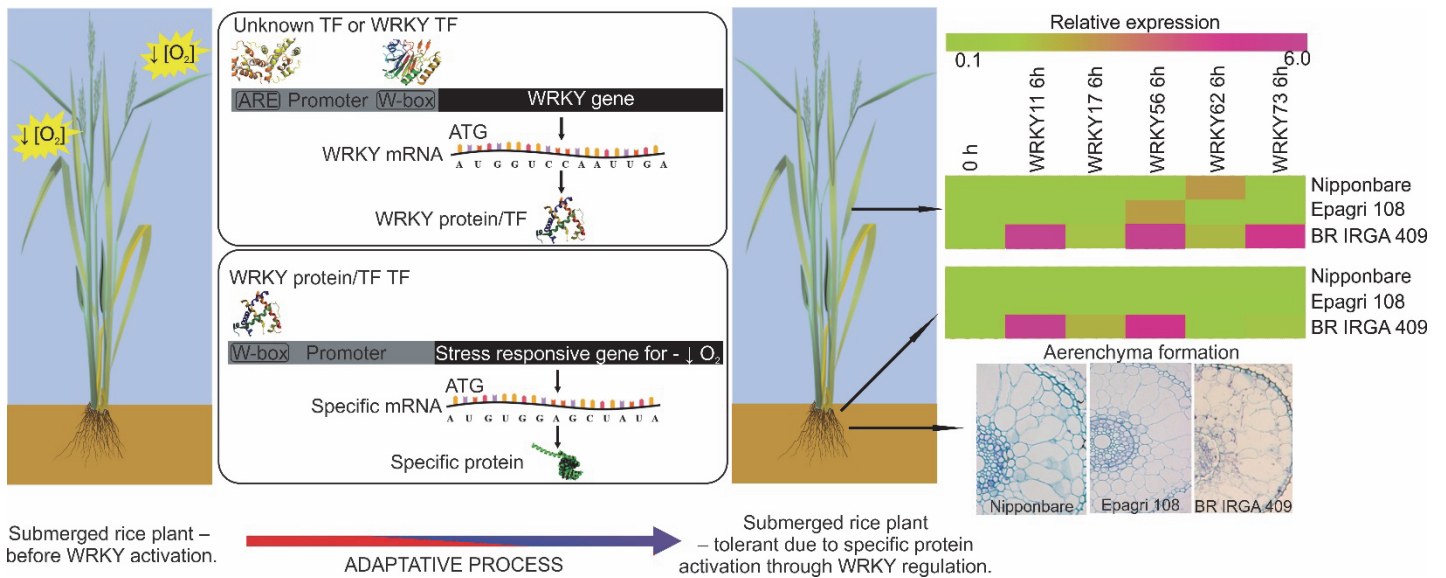


Fig. 2 Suppl. Model of the WRKYs mediated-response to submergence in rice plants. When submerged, rice plants experience oxygen depletion. WRKY transcription factors genes are up-regulated to produce their proteins, it can occur by an unknown transcription factor binding in their promoter region or, if a W-box sequence is present, by a WRKY transcription factor. WRKY proteins regulate specific tolerance genes, which are involved in adaptive processes under submergence. The up-regulation of WRKY transcription factors, which coordinate a molecular cascade in order to ensure plant survive under submergence events and morphological adaptations such as aerenchyma development in root tissue, arise as an adaptive mechanism.