

Table 1 Suppl. Primers used in the study (FP - forward primer, RP - reverse primer, T_m - melting temperature, WSI18 - *LEA3* gene, OsUbi1 - rice *polyubiquitin1* gene, COC - primer for PCR screening of *OnWsi18*-TR transgenics; restriction sites are marked in *bold*.

Primers	5' to 3' sequence	T _m [°C]	Purpose in brief
WSI18G FP	TAA AGGATCC ATGGCTTCTCAGCAGGAACG	68.1	PCR of <i>Wsi18</i> CDS (<i>Bam</i> HI site mentioned as bold)
WSI18G RP	TGC AGGTACCTT ACTGGTAGTCACTCCCAG	69.5	PCR of <i>Wsi18</i> CDS (<i>Kpn</i> I site mentioned as bold)
OsUbi1 FP	TTCTCCATCAATCGAATCC	55.3	RT-qPCR of <i>OsUbi1</i>
OsUbi1 RP	GGTGAGGGTCTTCACAAAGA	57.3	RT-qPCR of <i>OsUbi1</i>
WSI18 FP	ATGGCTTCTCAGCAGGAACG	64.1	RT-qPCR of <i>OsWsi18</i>
WSI18 RP	CGTACGCCTTCTCCTTGGTC	63.5	RT-qPCR of <i>OsWsi18</i>
COC FP	CAGTACGCCAAGGAAACCGCGA	63.0	PCR screening of <i>OnWsi18</i> -TR transgenics
COC RP	CTGCGCCCAAGCTGCATCATTG	63.4	PCR screening of <i>OnWsi18</i> -TR transgenics

Table 2 Suppl. Segregation analysis of hygromycin resistance gene (*hptII*) amongst T₁ progeny plantlets carrying *OnWsi18*-TR cassette.

Plants	Number of seedlings tested	Number of seedlings survived:died	Segregation ratio (survived:died)	χ^2 value	<i>P</i> -value
T ₁ -1.1	75	55:20	3:1	1.50	0.2
T ₁ -1.3	75	53:22	3:1	0.54	0.3
T ₁ -2.1	75	54:21	3:1	0.96	0.3
T ₁ -2.2	74	54:20	3:1	1.34	0.2
T ₁ -4.2	77	50:27	3:1	0.10	0.7
T ₁ -4.3	75	54:21	3:1	0.96	0.3
T ₁ -6.4	72	47:25	3:1	0.06	0.8
T ₁ -6.5	75	51:24	3:1	0.06	0.8
T ₁ -7.3	75	48:27	3:1	0.24	0.5
T ₁ -7.4	75	55:20	3:1	1.50	0.2
T ₁ -8.2	75	49:26	3:1	0.06	0.8
T ₁ -8.4	74	52:22	3:1	0.45	0.5
T ₁ -10.1	75	53:22	3:1	0.54	0.3
T ₁ -10.2	78	50:28	3:1	0.22	0.5

Table 3 Suppl. Physiological and biochemical analysis of transgenic plants at different conditions (AS - after stress, BS - before stress, SWS - soil water stress for 8 d and then rewatering, WW - well watered). Means $\pm$ SDs, for triplicate assays (RWC - relative water content, SWC - soil water content).

Plant line	<i>IR20</i> control	T ₁ -2.1	T ₁ -2.2	T ₁ -8.2	T ₁ -8.4
Fold expression of <i>Wsi18</i> (AS)	1.0	8.6 $\pm$ 0.3	9.1 $\pm$ 0.3	7.6 $\pm$ 0.4	8.1 $\pm$ 0.3
Survival rate [%] (AS)	18.5 $\pm$ 8.5	83.3 $\pm$ 11.7	87.0 $\pm$ 13	88.9 $\pm$ 11	85.2 $\pm$ 4
RWC [%]	35.0 $\pm$ 3.1	70.6 $\pm$ 4.0	72.1 $\pm$ 2.5	71.7 $\pm$ 4.7	68.0 $\pm$ 3.4
SWC [%] (WW)	67.7 $\pm$ 4.0	67.1 $\pm$ 4.2	65.6 $\pm$ 3.1	61.1 $\pm$ 4.7	69.2 $\pm$ 3.8
SWC [%] (AS)	8.1 $\pm$ 2.5	9.1 $\pm$ 2.1	9.8 $\pm$ 2.7	10.7 $\pm$ 1.8	8.7 $\pm$ 2.5
Mean filled grain [%] (WW)	82.8 $\pm$ 5.3	81.9 $\pm$ 4.8	82.9 $\pm$ 5.9	83.8 $\pm$ 4.2	85.4 $\pm$ 6.4
Mean filled grain [%] (SWS)	28.6 $\pm$ 4.2	65.6 $\pm$ 6.1	72.9 $\pm$ 3.4	63.6 $\pm$ 3.0	70.6 $\pm$ 4.6
Grain mass [(mg grain ⁻¹) (WW)	27.9 $\pm$ 3.2	27.1 $\pm$ 2.1	28.2 $\pm$ 2.0	28.4 $\pm$ 2.4	27.5 $\pm$ 2.2
Grain mass [(mg grain ⁻¹) (SWS)	13.2 $\pm$ 1.7	20.9 $\pm$ 1.7	22.1 $\pm$ 1.4	20.8 $\pm$ 1.8	19.9 $\pm$ 1.8
Proline content [μ mol g ⁻¹ (f.m.)] (BS)	0.8 $\pm$ 0.2	0.9 $\pm$ 0.1	0.9 $\pm$ 0.3	0.8 $\pm$ 0.2	0.9 $\pm$ 0.3
Proline content [μ mol g ⁻¹ (f.m.)] (AS)	2.2 $\pm$ 0.3	8.5 $\pm$ 0.4	9.1 $\pm$ 0.3	8.2 $\pm$ 0.4	7.8 $\pm$ 0.4
Soluble sugar content [mg g ⁻¹ (f.m.)] (BS)	0.9 $\pm$ 0.2	1.1 $\pm$ 0.3	1.2 $\pm$ 0.1	0.9 $\pm$ 0.2	1.0 $\pm$ 0.3
Soluble sugar content [mg g ⁻¹ (f.m.)] (AS)	2.2 $\pm$ 0.2	5.5 $\pm$ 0.3	6.5 $\pm$ 0.5	4.9 $\pm$ 0.4	4.5 $\pm$ 0.3
Relative electrolyte leakage [%] (BS)	4.1 $\pm$ 0.9	3.5 $\pm$ 0.8	2.9 $\pm$ 0.7	2.5 $\pm$ 0.9	4.0 $\pm$ 0.4
Relative electrolyte leakage [%] (AS)	29.1 $\pm$ 1.0	11.8 $\pm$ 0.8	10.3 $\pm$ 0.9	14.1 $\pm$ 1.1	15.4 $\pm$ 0.8

D26536	ATGGCTTCTCAGCAGGAACGGGCTAGCTACCACGCCGCGAGACCAAGGCCCCGCGCCGAG	60
<i>O. nivara</i>	ATGGCTTCTCAGCAGGAACGGGCTAGCTACCACGCCGCGAGACCAAGGCCCCGCGCCGAG	
D26536	GAGAAGACGGGGCGCATGATGGGCACGGCGCAGGAGAAGGCGCGGGAGGCCAAGGACACG	120
<i>O. nivara</i>	GAGAAGACGGGGCGCATGATGGGCACGGCGCAGGAGAAGGCGCGGGAGGCCAAGGACACG	
D26536	GCGTCCGACGCCGCGGGGCGCGCATGGGCAGGGGACACGGCGCCAAGGAGGCGACCAAG	180
<i>O. nivara</i>	GCGTCCGACGCCGCGGGGCGCGCATGGGCAGGGGACACGGCGCCAAGGAGGCGACCAAG	
D26536	GAGAAGGCGTACGAGACCAAGGACGCGACCAAGGAGAAGGCGTACGAGGCAAAGGACGCG	240
<i>O. nivara</i>	GAGAAGGCGTACGAGACCAAGGACGCGACCAAGGAGAAGGCGTACGAGGCAAAGGACGCG	
D26536	GCCTCCGACGCCACCGGCCGCGCCATGGACAAGGGCCGCG --- CCGCGGGCGCCACGAGG	300
<i>O. nivara</i>	GCCTCCGACGCCACCGGCCGCGCCATGGACAAGGGCCGCG GCGCCGCGGGCGCCACGAGG	
D26536	GACAAGGCGTACGATGCCAAGGACAGGGCGGCTGACACGGCGCAGTCCGCCGCCGACCGC	360
<i>O. nivara</i>	GACAAGGCGTACGATGCCAAGGACAGGGCGGCTGACACGGCGCAGTCCGCCGCCGACCGC	
D26536	GCCCGCGACGGCGCCGGGCGAGCCGGGAGCTACATTGGACAGACCGCCGAGGCCGCCAAG	420
<i>O. nivara</i>	GCCCGCGACGGCGCCGGGCGAGCCGGGAGCTACATTGGACAGACCGCCGAGGCCGCCAAG	
D26536	CAGAAAGCGGCCGGCGCCGCGCAGTACGCCAAGGAGACCGCGATCGCCGGCAAGGACAAG	480
<i>O. nivara</i>	CAGAAAGCGGCCGGCGCCGCGCAGTACGCCAAGGAAACCGCGATCGCCGGCAAGGACAAG	
D26536	ACCGGCGCCGTGCTCCAGCAGGCAGGGGAGCACGTGAAGAGCGTGCGGTGGGGGCGAAG	540
<i>O. nivara</i>	ACCGGCGCCGTGCTCCAGCAGGCAGGGGAGCAGGTGAAGAGCGTGCGGTGGGGGCGAAG	
D26536	GACGCGGTGATGTACACGCTCGGGATGTCAGGCGATAACAAGAACAACGCCGCTGCCGGC	600
<i>O. nivara</i>	GACGCGGTGATGTACACGCTCGGGATGTCAGGCGATAACAAGAACAACGCCGCTGCCGGC	
D26536	AAGGACACCAGCACCTACAAGCCTGGAAGTGGGAGTGACTACCAAGTAA	648
<i>O. nivara</i>	AAGGACACCAGCACCTACAAGCCTGAAAGTGGGAGTGACTACCAAGTAA	

Fig. 1 Suppl. Alignment of the *OnWsi18* nucleotide sequence (*GenBank* accession No. KX219624) with the *Wsi18* gene sequence from *O. sativa* spp. *japonica* (*GenBank* accession No. D26536). Region in box shows the addition of a 3 bp region in *OnWsi18* thereby making it as 648 bp. *O. nivara* should be in italics

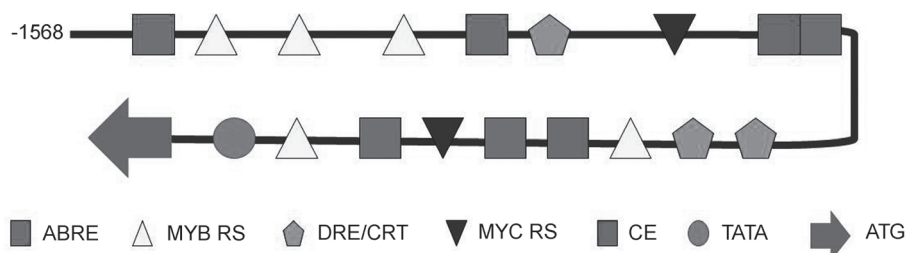


Fig. 2 Suppl. Summary of the common *cis*-regulatory elements found in the *OnWsi18* promoter (Kaur *et al.* 2017).

CLUSTAL O (1.2.1) multiple sequence alignment

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OnWsi18  MASQQRASYHAGETKARAEKGTGRMMGTAQEKAREAKDTASDAAGRAMGRGHGAKEATK
OsLEA3    MASHQDQASYRAGETKAHTEEKAGQVMGASKDKASEAKDRASEAAGHAAGKGQDTKEATK
          ***. *..***.*****..***.*. .**.. .*** ***** **.***. * *.*. .*****
          .  ..      .      .      .      .      .      .      .      .      .

OnWsi18  EKAYETKDATKEKAYEAKDAASDATGRAMDKGRGAAGATRDKAYDAKDRAADTAQSAADR
OsLEA3    EKAQAAKERASETAQAAKD-----KTSSTSQAARDK
          ***  .* . . * * ***                .. .*.*. * *.
          .  .  ..  .

OnWsi18  ARDGAGQTGSYIGQTAE-----AAKQKAAGAAQYAKETAIAGKDKTGAVLQQAG
OsLEA3    AESKDQTGGFLGEKTEQAKQKAAETAGAAKQKTAETAQYTKDSAIAGKDKTGSLVQQAS
          * .   *** .. *. . *                *****.* .***.*..*****.*****
          ..      ...  ...      .      .      .      .      .      .

OnWsi18  EQVKSVAVGAKDAVMYTLGMSGDNKNNAAG-KDTSTYKPETGSDYQ--
OsLEA3    EQVKSTVVGAKDAVMSTLGMTEDEAGTDDGANKDTSATAAATETTARDH
          ***** ***** *****.*.      *****.* *. .
          ..      .      .      .      .      .      .      .

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Percent Identity Matrix - created by Clustal2.1

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1: OnWsi18  100.00  55.91
2: OsLEA3   55.91  100.00

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Fig. 3 Suppl. Alignment of the *OnWsi18* protein sequence (*GenBank* accession No.KX219624) with *OsLEA3* (*GenBank* accession No.AAV67829) showing 55 % identity ((*asterisks* indicate positions which have a single, fully conserved residue; *colons* indicate conservation between groups of strongly similar properties; *dots* indicate indicates conservation between groups of weakly similar properties).