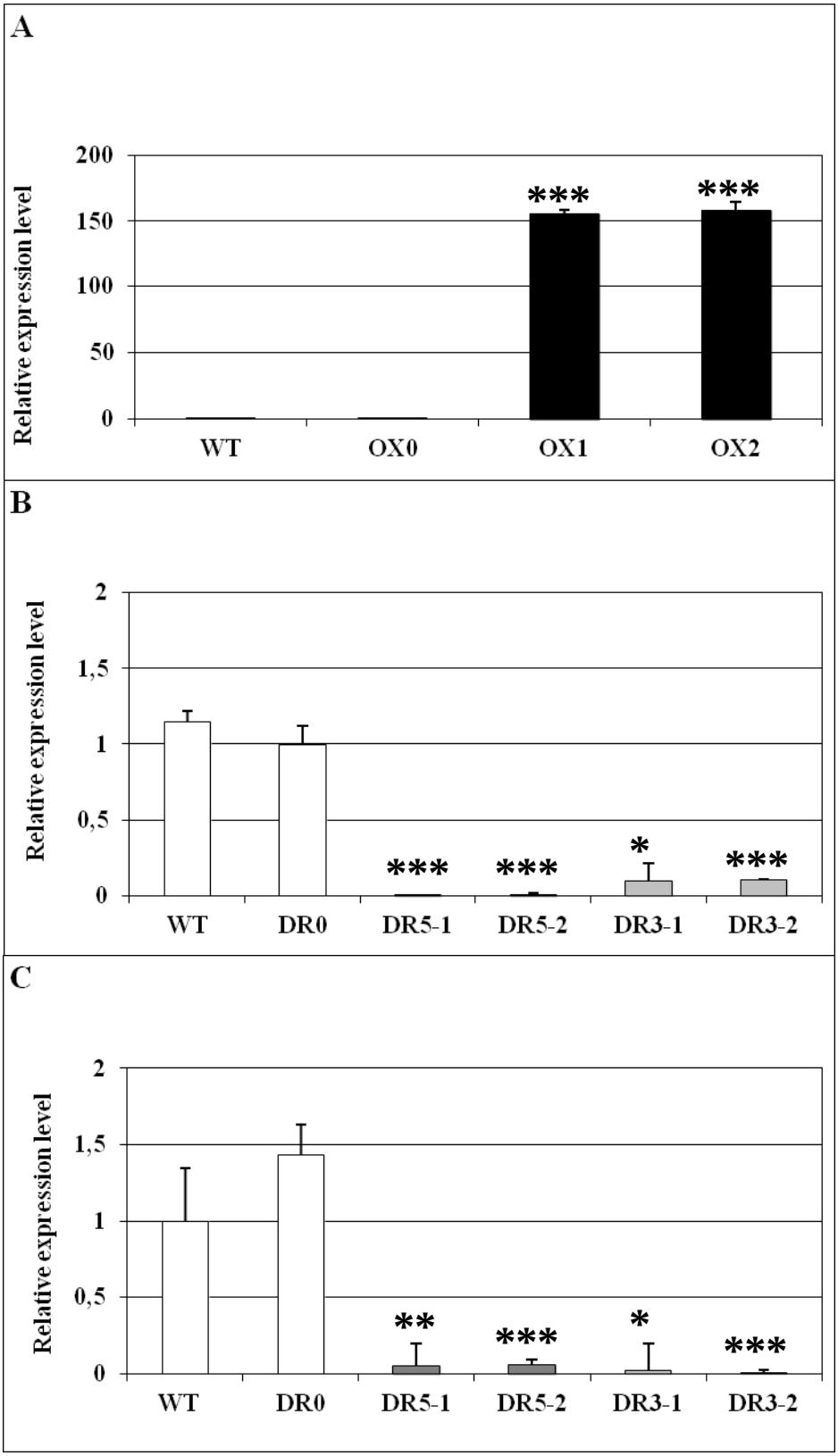

Figure S1: ***OsMADS26* over- or down-expression is stable across generations**

A, *OsMADS26* expression in overexpressing (OX1, OX2, dark bars) and corresponding control (OX0, WT, white bars) T4 plants. B, *OsMADS26* expression in interfered (DR5-1, DR5-2, DR3-1, DR3-2, grey bars) and corresponding control (PDP, WT, white bars) T4 plants. Mean value and standard error were obtained from two independent experiments. C, *OsMADS26* expression levels in RNA interfered (grey bars) and control (white bars) of 7-day-old T2 seedlings cultivated on MS/2 medium added with 125 mM of Mannitol. Mean and standard error were obtained from 14 individual plants of each line. A Student t-test was done to establish whether the RWC or the gene expression level in transgenic lines was different from corresponding control line; *: significant difference with $p<0.05$; ** : significant difference with $p<0.01$; *** : significant difference with $p<0.001$.

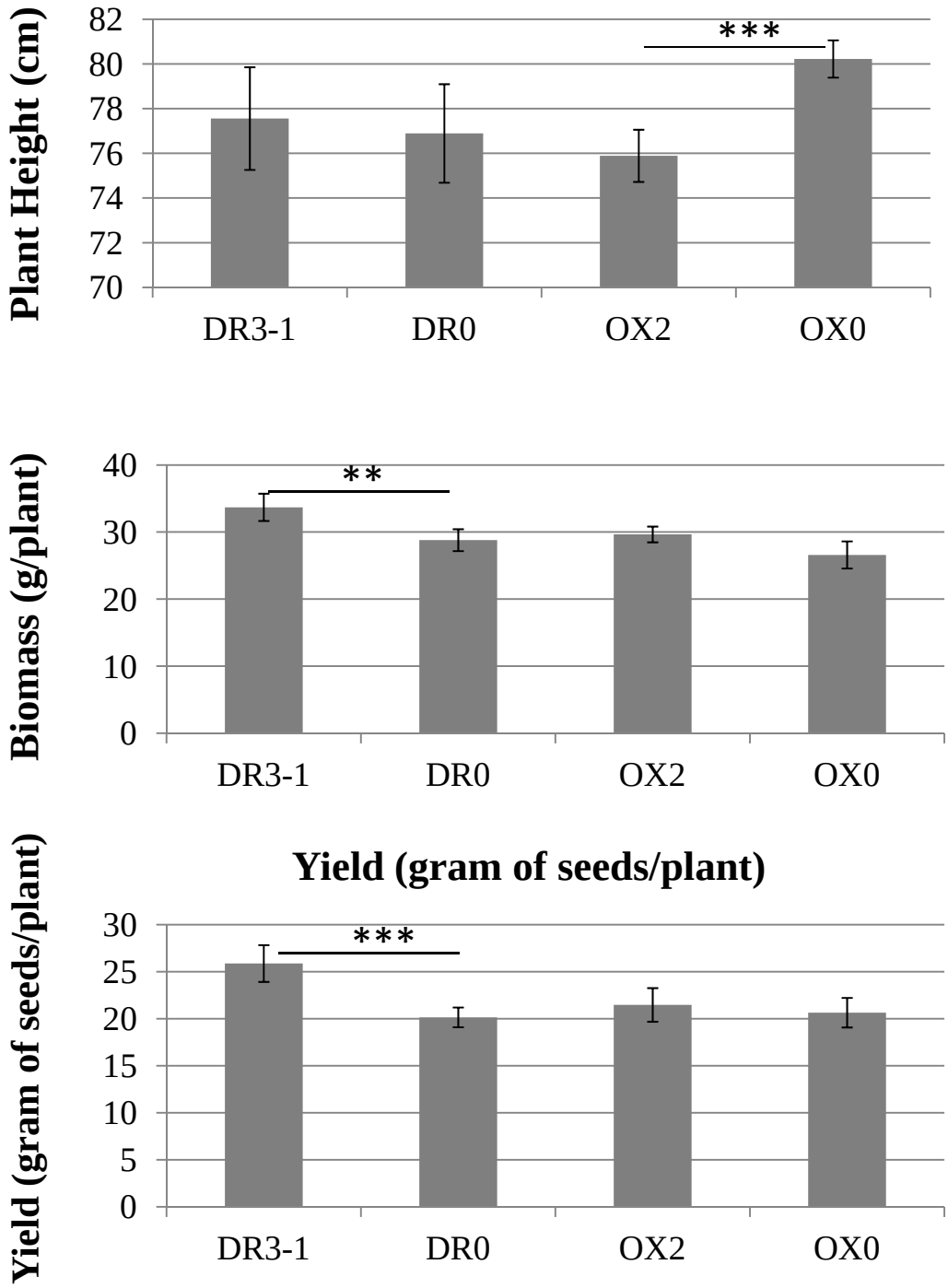

Figure S2: *OsMADS26* over-expressing and down-regulated lines growth under normal watering condition in the field.

Plants were grown under normal water condition in the field in CIAT (Colombia). The height, biomass and yield were measured at the end of the experiment. The mean and SD are shown and a T-test (n=9;**: P<0.01; ***: P<0.001) was used to evaluate statistical difference between the over-expressing OX2 and down-regulated DR3-1 transgenic lines with their respective controls OX0 and DR0.

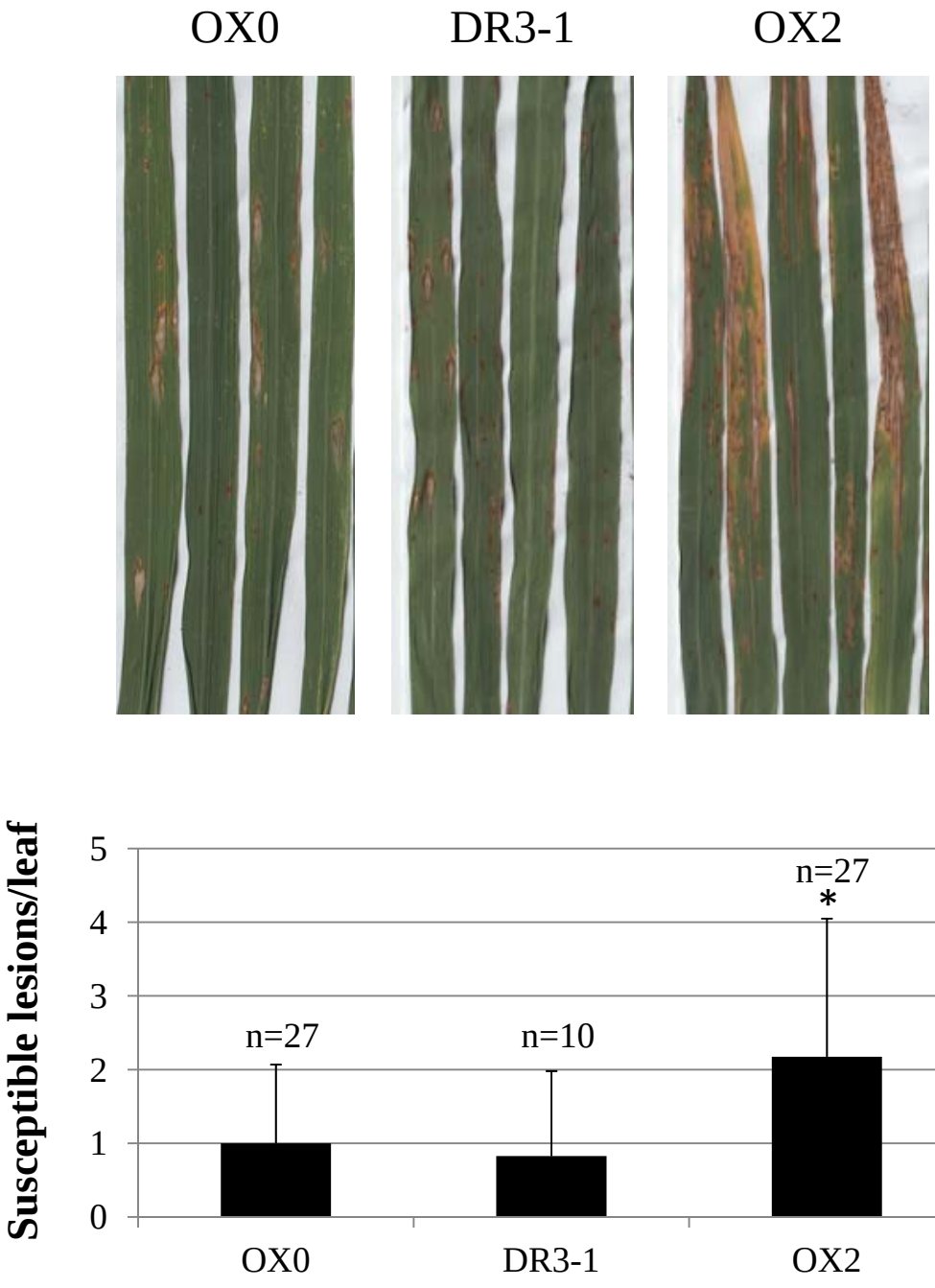

Figure S3: **Rice blast resistance evaluation of over-expressing or down-regulated *OsMADS26* lines under semi-controlled field conditions.**

Plants were grown in nethouses in LMI-RICE (Hanoi, Vietnam) and inoculated each week for four weeks with spores of the virulent *M. oryzae* isolate VT15. Symptoms were measured every week after epidemics started and one time point is provided. The greyish lesions were counted as a measure of susceptibility. The mean and SD are shown and a T-test (*: $P<0.05$) was used to evaluate statistical difference between the *OsMADS26* over-expressing OX2 and down-regulated DR3-1 transgenic lines with their respective controls OX0 and DR0.

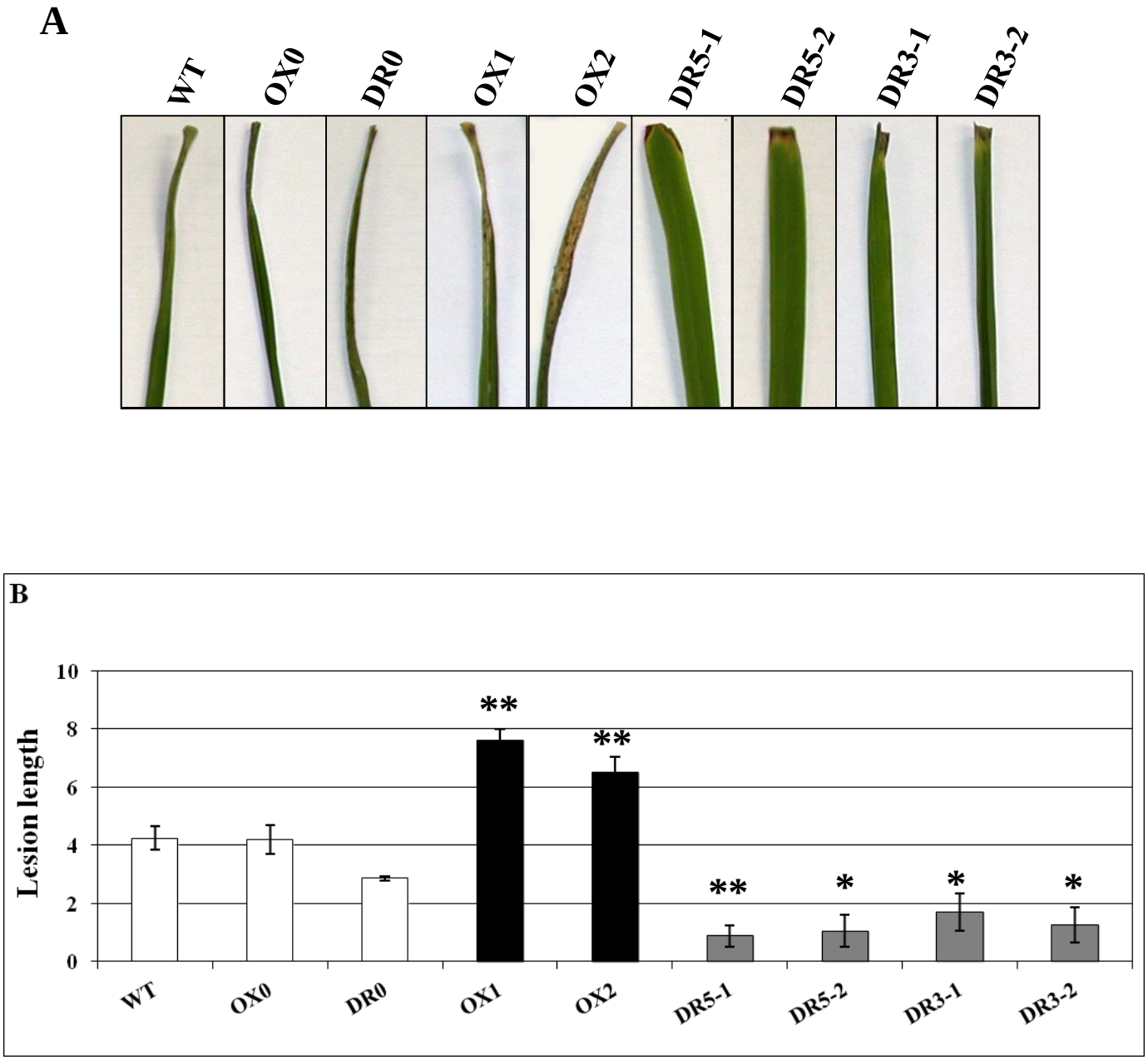

Figure S4: OsMADS26 negatively regulates resistance against *Xanthomonas oryzae* pv. *oryzae* (*Xoo*).

Plants over-expressing (OX1, OX2) (black bars) or down-regulated (DR5-1, DR5-2, DR3-1, DR3-2) (grey bars) *OsMADS26* and corresponding control lines transformed with empty vectors (OX0, DR0) or untransformed line (WT) (white bars) were tested. A: Symptom severity in leaves of transgenic and control plants inoculated with the PXO99A strain of *Xoo.* Photographs were taken at 14 days post inoculation (dpi). B: Length of lesion produced in *Xoo*-infected leaves at 14 dpi. Mean and standard error were obtained from nine inoculated plants for each line. Results shown are from one of two independent experiments that produced similar results.

A Student t-test was done to establish whether one given mutant line was different from its corresponding control line; *: significant difference with $p<0.05$; **: significant difference with $p<0.01$.

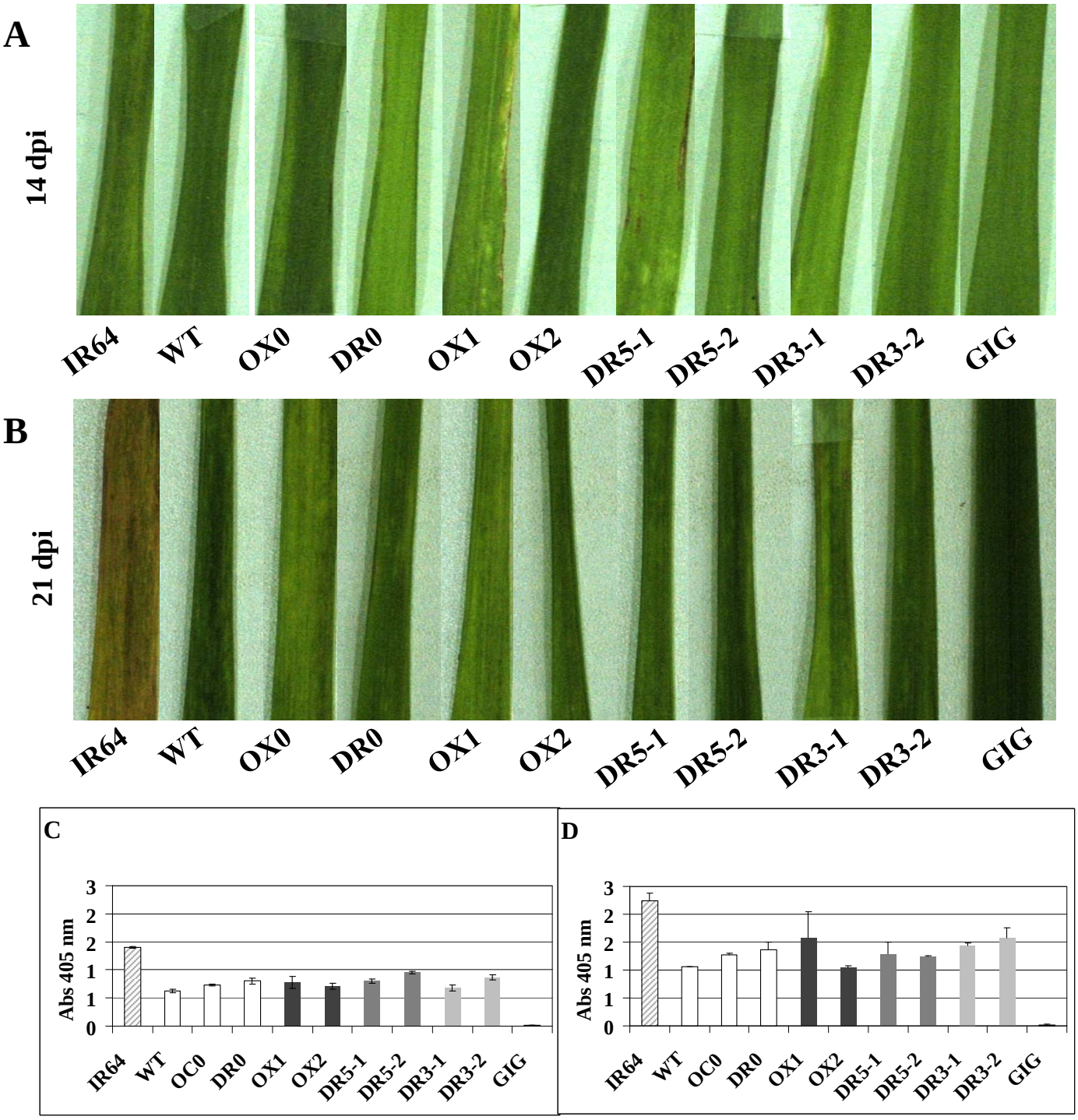

Figure S5: *OsMADS26* expression level does not affect resistance against Rice Yellow Mottle Virus (RYMV).

Nine independent lines of over-expressing (OX1, OX2, black bars), down-regulated (DR5-1, DR5-2, DR3-1, DR3-2, grey bars) *OsMADS26* lines and corresponding control lines transformed with empty vectors or untransformed line (OX0, DR0 WT, white bars), IR64 (susceptible control, dashed bar) and Gigante (resistant control) cultivars were tested. A,B, Symptom severity in leaves of transgenic and control plants inoculated with RYMV at 14, and 21 days postinoculation (dpi). C,D, ELISA virus accumulation quantification in leaves of transgenic and control plants inoculated with RYMV at 14 and 21 (dpi). WT and control transformed with empty vectors (white bars), over-expressing lines (black bars), down-regulated lines (grey bars) and reference cultivars (dashed bars) Gigante (GIG), and IR64. Leaves from ten plants for each line were pooled and the virus content determined by enzyme-linked immunosorbent assay using an antibody generated against the coat protein as described (N'Guessan et al. 2000). Mean and standard error were obtained from ten inoculated plants for each line. Results shown are representative of data obtained from two independent experiments.

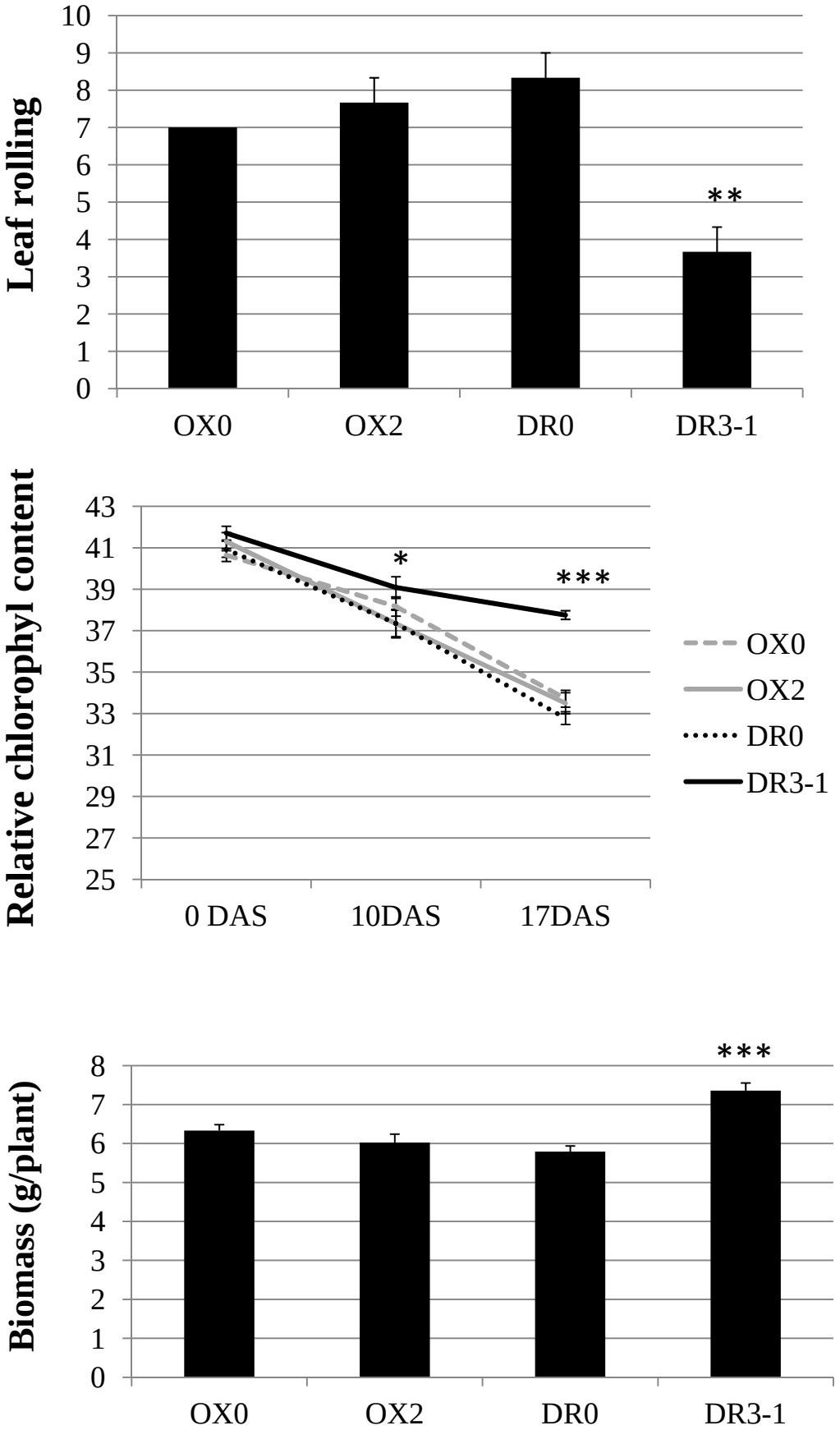

Figure S6: *OsMADS26* down regulation enhances water deficit tolerance in the field.
Plants were grown in the field in CIAT (Colombia) and a drought stress was applied (see Methods). The leaf rolling score (0-9 scale from the less to the more) of the plant 17 DAS (DAS= days after stress) is given (A) and SPAD value (B) was measured at the indicated times after stress in three independent blocks on three plants. The total biomass was measured at the end of the experiment (C). The mean and SD are shown and a T-test (n=9;*: P<0.05; **:P<0.01; ***: P<0.001) was used to evaluate statistical difference between the over-expressor OX2 and interfered DR3-1 transgenic lines with their respective controls OX0 and DR0.

GST1

gtaagcaagagatagggataaggg**GAAGAGGAGGAAGAAGGAGG**aggtgtagggaga
aaccggagcaacctcgaagctagtccaaactagtgggaggttgtctttccggcaagccggagcccggagc
tatcgatcatcaagctttctaccccgaccgacgaggaagaagacgactgatcaattgatcaaaccgatctct
ccatagctaggtag**acaggaggagaggaggaagaagaggg**ggagaggagacttatcttgatcg***ATG***gcg
cgaggcaaggtgcagctccgtcgcatcgagaacccggttcACCGTCAGGTCACCTTCTGCAA
gcgccgtgccggcctgctgaagaaggccagggagctctccatcctctgcgaggccgacatcggcatcatcat
cttctccgcccacggcaagctctacgacctcgccaccaccggaaccatggaggagctgatcgagaggtacaa
gagtgctagtggcgaacaggccaacgcctgcggcgaccagagaatggacccaaaacaggaggcaatggt
gctcaaacaagaaatcaatctactgcagaagggcctgaggtacatctatgggaacagggcaaatgaacaca
tgactgttgaagagctgaatgccctagagaggtacttagagatatggatgtacAACATTCGCTCCGC
AAAGATGCagataatgatccaagagatccaagcactaaagagcaaggaaggcatgttgaaagctgcta

GST2

*acgaaattctccaagaaaaga**tagtagaacagaatggtctg**atcgacgtagg**catgatggtagcagatcaac***
agaatgggcattttagtacagtcccactgttagaagagatcactaacccactgactatactgagtggctattcta
cttgtaggggctcggagatgggctattccttcTAA**cactaataatggcctgggggatacttgtgttcattacta**
gtgtgtaatatggttaataatgcttgtgttgctgtttgctttgctattctgatgtaccttatttagacaagttcccg
caggaagtgtcttttagtattgtatttgtcttgggctgtggtgctttgtttttccCTAAAGAACTCTT
GAGGAGCtctgttgttgaaccatttcaagtaattgagactattgtttcc

Primers used for *OsMADS26* cDNA amplification

Forward: 5'-gaagaggaggaagaaggagg -3'
Reverse: 5'-gctcctcaagagttctttag -3'

Primers used for GST1 amplification and cloning

I^st^ Amplification

Forward: 5'-aagcaagagatagggataag -3'
Reverse: 5'-cgatcaagataagtctcctc -3'

2^nd^ Amplification (with *att*B sequence)

Forward: 5'-**ggggacaagtttgtacaaaaaagcaggct**gaagaggaggaagaaggagg-3'
Reverse: 5'-**ggggaccactttgtacaagaaagctgggt**ccctcttcttcctcctcc -3'

Primers used for GST2 amplification and cloning

I^st^ Amplification

Forward: 5'-tagtagaacagaatggtctg -3'
Reverse: 5'-gttgaaccatttcaagtaat -3'

2^nd^ Amplification (with *att*B sequence)

Forward: 5'-**ggggacaagtttgtacaaaaaagcaggct**catgatggtagcagatcaac -3'
Reverse: 5'-**ggggaccactttgtacaagaaagctgggt**gctcctcaagagttctttag -3'

Figure S4: Sequence of *OsMADS26* cDNA, GST1 and GST2 position in 5' and 3'-UTR and primer sequences used for PCR amplification.

In bold: GST sequences cloned in pANDA vector and used for RNA interference induction; underlined: nested primers used for amplification of GST1 and GST2; Underlined capitals: primers used for the amplification of the cDNA sequence cloned in PC5300.OE vector for *OsMADS26* overexpression; Capitals: primers used for the analysis of *OsMADS26* expression by RT-qPRC in transgenic plants. In italic: Open reading frame (ORF), in italic, capital and bold: start and stop codons. In grey: BP recombination sequence (gateway cloning technology of INVITROGEN).