

Supplementary data

**Molecular and biochemical characterization of superoxide dismutase (SOD) in upland rice under drought**

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**Supplementary Table 1.** Quantification of results using a NanoVue Plus™ spectrophotometer (GE Healthcare). The purity of the samples was verified by determining the relationship between the absorbance of nucleic acids, 260 nm, and proteins, 280 nm. The RNA integrity (RIN) was obtained using a 2100 Bioanalyzer (Agilent).

Genotype	Developmental Stage	Tissue	Water regime	RNA concentration (ng/μL)	ABS (260/280)	RIN
Douradão	Vegetative	Leaf	100%	1832	2,025	6.40
Douradão	Vegetative	Leaf	50%	1922	2,033	6.30
Douradão	Vegetative	Root	100%	244,40	2,030	7.90
Douradão	Vegetative	Root	50%	88,4	2,028	7.70
Douradão	Reproductive	Leaf	100%	2386	1,953	7.30
Douradão	Reproductive	Leaf	50%	601,6	1,946	6.90
Douradão	Reproductive	Root	100%	173,2	1,800	8.40
Douradão	Reproductive	Root	50%	421,6	1,989	7.70
Primavera	Vegetative	Leaf	100%	1108,0	1,928	6.20
Primavera	Vegetative	Leaf	50%	1746,0	1,985	6.00
Primavera	Vegetative	Root	100%	140,8	1,978	8.00
Primavera	Vegetative	Root	50%	230,8	2,039	8.10
Primavera	Reproductive	Leaf	100%	934,8	2,140	8.10
Primavera	Reproductive	Leaf	50%	1207,0	2,028	7.00
Primavera	Reproductive	Root	100%	795,2	2,229	9.70
Primavera	Reproductive	Root	50%	122,0	2,075	6.80

**Supplementary Table 2.** SOD activity in the drought-tolerant (Douradão) and drought-susceptible (Primavera) cultivars in different developmental stages (vegetative and reproductive) and tissue samples (leaf and root) under different water regimes (50% and 100%). The results and standard deviation represented by different lowercase letters for the same developmental stage and tissue samples indicate statistically significant differences between the two genotypes and water regimes ( $p \leq 0.05$ ).

Developmental stages	Tissues	Genotypes	Water regime	SOD UN mg-1 PROTEIN
Vegetative	Leaf	Douradão	100%	91.06 ± 13.44 <sup>b</sup>
		Douradão	50%	125.43 ± 11.69 <sup>b</sup>
		Primavera	100%	164.70 ± 4.74 <sup>a</sup>
		Primavera	50%	116.82 ± 22.88 <sup>b</sup>
Reproductive	Leaf	Douradão	100%	131.68 ± 1.81 <sup>a</sup>
		Douradão	50%	104.95 ± 14.54 <sup>b</sup>
		Primavera	100%	52.64 ± 3.79 <sup>c</sup>
		Primavera	50%	112.17 ± 7.39 <sup>a,b</sup>
Vegetative	Root	Douradão	100%	139.87 ± 3.72 <sup>a</sup>
		Douradão	50%	76.53 ± 0.03 <sup>b</sup>
		Primavera	100%	170.65 ± 0.05 <sup>a</sup>
		Primavera	50%	112.15 ± 44.64 <sup>a,b</sup>
Reproductive	Root	Douradão	100%	85.84 ± 6.55 <sup>c</sup>
		Douradão	50%	268.00 ± 16.59 <sup>a</sup>
		Primavera	100%	93.84 ± 12.44 <sup>c</sup>
		Primavera	50%	172.56 ± 16.89 <sup>b</sup>

**Supplementary Table 3.** Primer sequences for the eight SOD isoforms. Three pairs of primers were design for each gene, referred to as A, B, and C. The GC base content, annealing temperature, primer extension in base pair (bp), and amplicon size were also provided.

ID	F/R sequences (5' → 3')	%GC content	Tm °C	bp	Amplicon (bp)
LOC_Os03g11960_A	F AGAGAATGGCAGGGAAAGC R GGGTCCTGGAAGAAGTGGGA	52.63 57.90	59.38 60.03	19	103
LOC_Os03g11960_B	F AGAGAATGGCAGGGAAAGC R CTCGGTATACCCGGTGGAG	52.63 63.16	59.38 60.34	19	122
LOC_Os03g11960_C*	F ACCGGGTATACCGAGGTGA R GTAGAGTTGCAGCCGTTGGT	57.90 55.00	60.20 60.32	19	104
LOC_Os03g22810_A	F TTACGGGTAGGGCACTGAAC R GCCCAAGGTCACGGACTG	55.00 66.67	59.99 62.74	20	125
LOC_Os03g22810_B	F GGGTCGCCTGAGATCACATTA R CATCTCCCTCTTGGACAAAAGT	52.38 47.62	62.32 58.24	21	100
LOC_Os03g22810_C*	F TCAACTGGGCCACACTACAA R CTTCTCCAGCGGTGACATTT	50.00 50.00	60.15 60.26	20	100
LOC_Os04g48410_A	F AGTGGAATTCCTGCACAC R GGAGGAAGAGGAGGAGTTGG	50.00 60.00	59.97 60.19	20	170
LOC_Os04g48410_B	F CAAGTTCCAAACTCTGAAGGAA R TGCAGAGTATCCAGCATTGTG	39.13 47.62	59.79 59.88	23	108
LOC_Os04g48410_C*	F AAGGGAACCCAAATGATTTTT R GCTTCAACTATAGCCAATTCCA	33.33 40.91	58.72 58.41	21	115
LOC_Os05g25850_A	F ACCTCCCCTACGACTACGG R TCGAGGGCCTTGTGTAGTT	63.16 50.00	59.03 59.73	19	112
LOC_Os05g25850_B*	F ACGTCGCCAACTACAACAAG R GTTGAACCTGATGGCGCTCT	50.00 50.00	58.85 60.41	20	101
LOC_Os05g25850_C	F CACCTACGTCGCCAACTACA R TCGCTGATAGGCTTGAGGTT	55.00 50.00	59.78 59.98	20	162
LOC_Os06g02500_A	F CTGCAGGGGAGAGAGTACGA R ATCCATTTACAGCATCGGAAG	60.00 45.00	60.55 60.04	20	124
LOC_Os06g02500_B	F CAGATGCCCTAGAGCCATACA R CACTACTGCCACCAATCAT	52.38 50.00	60.24 59.55	21	109
LOC_Os06g02500_C*	F GGATGGGTTTGGCTTGTTA R AAGAGGATTGATGGCATTTCG	45.00 45.00	59.80 60.04	20	123
LOC_Os06g05110_A	F TGATGCTTCAGGATGACAGG R AGGTTCACAAAAGCCTCAGC	50.00 50.00	59.79 59.48	20	109
LOC_Os06g05110_B	F GAGGCTTTTGTGAACCTTGG R CTCATGCATGCGAATCTCAG	50.00 50.00	59.71 60.53	20	159
LOC_Os06g05110_C*	F GCGATATTTTCGCATCCATT R TCCAAAGGCCATTACATTCAT	40.00 38.10	59.90 59.29	20	100
LOC_Os07g46990_A	F TCCCAAGAGGGAGATGGTC R CAGTTGACATGCAGCCATTAG	57.90 47.62	59.99 59.36	19	118
LOC_Os07g46990_B*	F CACTTCAATCCTACTGGGAAGG R TAGCAACACCATCTGCTCCA	50.00 50.00	59.99 60.41	22	100
LOC_Os07g46990_C	F CCGAGTTGCTTGCAGGAAT R TTTTTATTTCAACATCCATACGAG	55.56 29.17	62.29 57.39	18	101
LOC_Os08g44770_A	F CCGTGTGACGGGACTTACTC	60.00	60.57	20	100

LOC_ Os08g44770 _B	R	TGGGTAAAAATGTGGTCCTGT	40.91	60.49	22	
	F	AGGACCACATTTTAACCCAAA	38.10	58.34	21	119
	R	CAATGGTTGCCTCAGCTACA	50.00	59.86	20	
LOC_ Os08g44770 _C*	F	ACTTGCATGCGGTGTGT	47.37	60.18	19	107
	R	TCAGGCTCGAAGATGACAAA	45.00	59.52	20	

\*Selected primers for qPCR.

**Supplementary Table 4.** The relative quantification values (RQ) of the SOD genes, statistical significance of differences and standard deviations between the tolerant (Douradão, D) and susceptible (Primavera, P) cultivars in different developmental stages (vegetative and reproductive), tissues samples (leaf and root), and water regimes (50% and 100%). Different lowercase letters for the same gene at the same developmental stage and tissue sample between the two genotypes and water regimes indicate statistically significant differences ( $p \leq 0.05$ ).

Tissue	Developmental Stage	Genotype/ Water regime	RQ*							
			<i>CuZnSOD1</i>	<i>CuZnSOD2</i>	<i>CuZnSOD3</i>	<i>CuZnSOD4</i>	<i>CuZnSOD5</i>	<i>MnSOD</i>	<i>FeSOD1</i>	<i>FeSOD2</i>
Leaf	Vegetative	D 100%	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b,c</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>c</sup>
		D 50%	1,43 ± 0,24 <sup>a</sup>	1,36 ± 0,04 <sup>a</sup>	2,62 ± 0,23 <sup>a</sup>	2,02 ± 0,11 <sup>a</sup>	2,05 ± 0,18 <sup>a</sup>	2,00 ± 0,12 <sup>a</sup>	1,90 ± 0,19 <sup>a</sup>	1,23 ± 0,16 <sup>b</sup>
		P 100%	1,13 ± 0,09 <sup>ab</sup>	1,07 ± 0,04 <sup>b</sup>	1,20 ± 0,08 <sup>b</sup>	0,46 ± 0,02 <sup>c</sup>	0,92 ± 0,05 <sup>c</sup>	0,84 ± 0,12 <sup>b</sup>	0,27 ± 0,02 <sup>c</sup>	0,95 ± 0,04 <sup>c</sup>
		P 50%	1,47 ± 0,17 <sup>a</sup>	0,84 ± 0,07 <sup>c</sup>	2,48 ± 0,43 <sup>a</sup>	0,94 ± 0,15 <sup>b</sup>	1,22 ± 0,08 <sup>b</sup>	1,03 ± 0,05 <sup>b</sup>	0,35 ± 0,02 <sup>c</sup>	1,57 ± 0,05 <sup>a</sup>
Leaf	Reproductive	D 100%	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>b</sup>
		D 50%	0,45 ± 0,04 <sup>b</sup>	0,99 ± 0,05 <sup>a</sup>	1,94 ± 0,22 <sup>a</sup>	1,45 ± 0,07 <sup>a</sup>	0,76 ± 0,08 <sup>b</sup>	1,59 ± 0,08 <sup>a</sup>	0,38 ± 0,02 <sup>c</sup>	1,62 ± 0,27 <sup>a</sup>
		P 100%	0,09 ± 0,00 <sup>c</sup>	0,89 ± 0,03 <sup>b</sup>	1,23 ± 0,27 <sup>b</sup>	1,04 ± 0,07 <sup>b</sup>	0,31 ± 0,02 <sup>c</sup>	0,44 ± 0,02 <sup>c</sup>	0,003 ± 0,00 <sup>d</sup>	0,18 ± 0,01 <sup>c</sup>
		P 50%	0,48 ± 0,04 <sup>b</sup>	1,03 ± 0,02 <sup>a</sup>	1,12 ± 0,20 <sup>b</sup>	0,47 ± 0,04 <sup>c</sup>	1,02 ± 0,10 <sup>a</sup>	0,95 ± 0,15 <sup>b</sup>	0,54 ± 0,07 <sup>b</sup>	0,93 ± 0,05 <sup>b</sup>
Root	Vegetative	D 100%	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>a</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>b</sup>
		D 50%	5,51 ± 0,16 <sup>a</sup>	0,69 ± 0,03 <sup>b</sup>	0,39 ± 0,07 <sup>b</sup>	0,86 ± 0,03 <sup>b</sup>	0,95 ± 0,10 <sup>a</sup>	1,54 ± 0,19 <sup>a</sup>	2,38 ± 0,20 <sup>a</sup>	2,78 ± 0,24 <sup>a</sup>
		P 100%	0,83 ± 0,19 <sup>b,c</sup>	0,71 ± 0,03 <sup>b</sup>	0,24 ± 0,06 <sup>c</sup>	0,37 ± 0,02 <sup>c</sup>	0,43 ± 0,05 <sup>b</sup>	0,63 ± 0,09 <sup>c</sup>	0,65 ± 0,06 <sup>c</sup>	0,50 ± 0,10 <sup>c</sup>
		P 50%	0,64 ± 0,06 <sup>c</sup>	0,70 ± 0,07 <sup>b</sup>	0,10 ± 0,02 <sup>d</sup>	0,29 ± 0,00 <sup>d</sup>	0,45 ± 0,00 <sup>b</sup>	0,66 ± 0,04 <sup>c</sup>	0,30 ± 0,01 <sup>d</sup>	0,39 ± 0,04 <sup>c</sup>
Root	Reproductive	D 100%	1,00 ± 0,00 <sup>c</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>c</sup>	1,00 ± 0,00 <sup>b</sup>	1,00 ± 0,00 <sup>c</sup>	1,00 ± 0,00 <sup>c</sup>	1,00 ± 0,00 <sup>c</sup>	1,00 ± 0,00 <sup>b</sup>
		D 50%	9,43 ± 0,65 <sup>a</sup>	0,52 ± 0,03 <sup>c</sup>	0,45 ± 0,06 <sup>c</sup>	0,67 ± 0,00 <sup>c</sup>	1,09 ± 0,04 <sup>c</sup>	8,33 ± 0,30 <sup>a</sup>	2,25 ± 0,10 <sup>b</sup>	6,17 ± 1,02 <sup>a</sup>
		P 100%	0,75 ± 0,13 <sup>c</sup>	1,19 ± 0,07 <sup>a</sup>	2,25 ± 0,36 <sup>b</sup>	1,04 ± 0,01 <sup>a</sup>	1,49 ± 0,10 <sup>b</sup>	0,99 ± 0,08 <sup>c</sup>	0,15 ± 0,03 <sup>c</sup>	0,30 ± 0,01 <sup>b</sup>
		P 50%	3,97 ± 0,46 <sup>b</sup>	1,31 ± 0,04 <sup>a</sup>	3,14 ± 0,30 <sup>a</sup>	0,41 ± 0,02 <sup>d</sup>	3,99 ± 0,06 <sup>a</sup>	1,89 ± 0,12 <sup>b</sup>	18,04 ± 1,01 <sup>a</sup>	0,70 ± 0,08 <sup>b</sup>

\* Average RQ values.