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Supplementary Material

Proteomic analysis of young sugarcane plants with contrasting salt tolerance

Denise A. Chiconato^{A,C}, Marília G. de Santana Costa^B, Tiago S. Balbuena^B, Rana Munns^{C,D,E} and Durvalina M. M. dos Santos^A

^ADepartment of Biologia Aplicada à Agropecuária, Universidade Estadual Paulista ‘Julio de Mesquita Filho’, 14884-900 Jaboticabal, SP, Brasil.

^BDepartment of Tecnologia, Universidade Estadual Paulista ‘Julio de Mesquita Filho’, 14884-900 Jaboticabal, SP, Brasil.

^CCSIRO Agriculture and Food, GPO Box 1700, Canberra, ACT 2601, Australia.

^DSchool of Agriculture and Environment, and ARC Centre of Excellence in Plant Energy Biology, University of Western Australia, Crawley, WA 6009, Australia.

^ECorresponding author. Email: rana.munns@csiro.au

Table S1. Differentially regulated proteins in the more salt tolerant cultivar SP 81-3250 under salinity (160 mM NaCl for 15 days)

Listed are differentially regulated proteins with 5% probability and change above 1.5. Transcript names are of *Sorghum bicolor*, available in Phytozome

	Sobic number	Description	Fold change
1	008G007800.1.p	GDSL-motif Lipase/Acylhydrolase family protein,	2.96
2	008G007800.2.p	GDSL-motif Lipase/Acylhydrolase family protein,	2.30
3	010G189300.2.p	Type III chlorophyll a/b binding protein	1.80
4	003G305900.1.p	Lipoxygenase (9-LOX)	1.71
5	002G276000.1.p	Histone H2A	1.71
6	001G417200.1.p	H ⁺ -transporting ATP synthase chain 9-like protein	1.66
7	003G246400.1.p	50S ribosomal protein L12, chloroplast precursor	1.66
8	010G072900.1.p	Peroxiredoxin Q, chloroplast precursor	1.63
9	004G212400.2.p	GrpE protein homolog, mitochondrial	-1.53
10	009G132900.2.p	Pyruvate phosphate dikinase, chloroplast precursor	-1.63
11	009G132900.1.p	Pyruvate phosphate dikinase, chloroplast precursor	-1.68
12	003G172300.1.p	Photosystem II P680 chlorophyll A apoprotein	-1.68
13	02G0316700.1.p	ATP synthase subunit gamma, chloroplast precursor	-1.70
14	010G272800.2.p	Cell division protease ftsH homolog, chloroplast precursor	-1.71
15	003G431700.1.p	Ferredoxin	-1.76
16	004G055200.1.p	Phosphoglycerate kinase, cytosolic	-1.81
17	004G331700.1.p	Aspartate aminotransferase	-2.09
18	004G202200.1.p	Chloroplast translational elongation factor Tu	-2.75

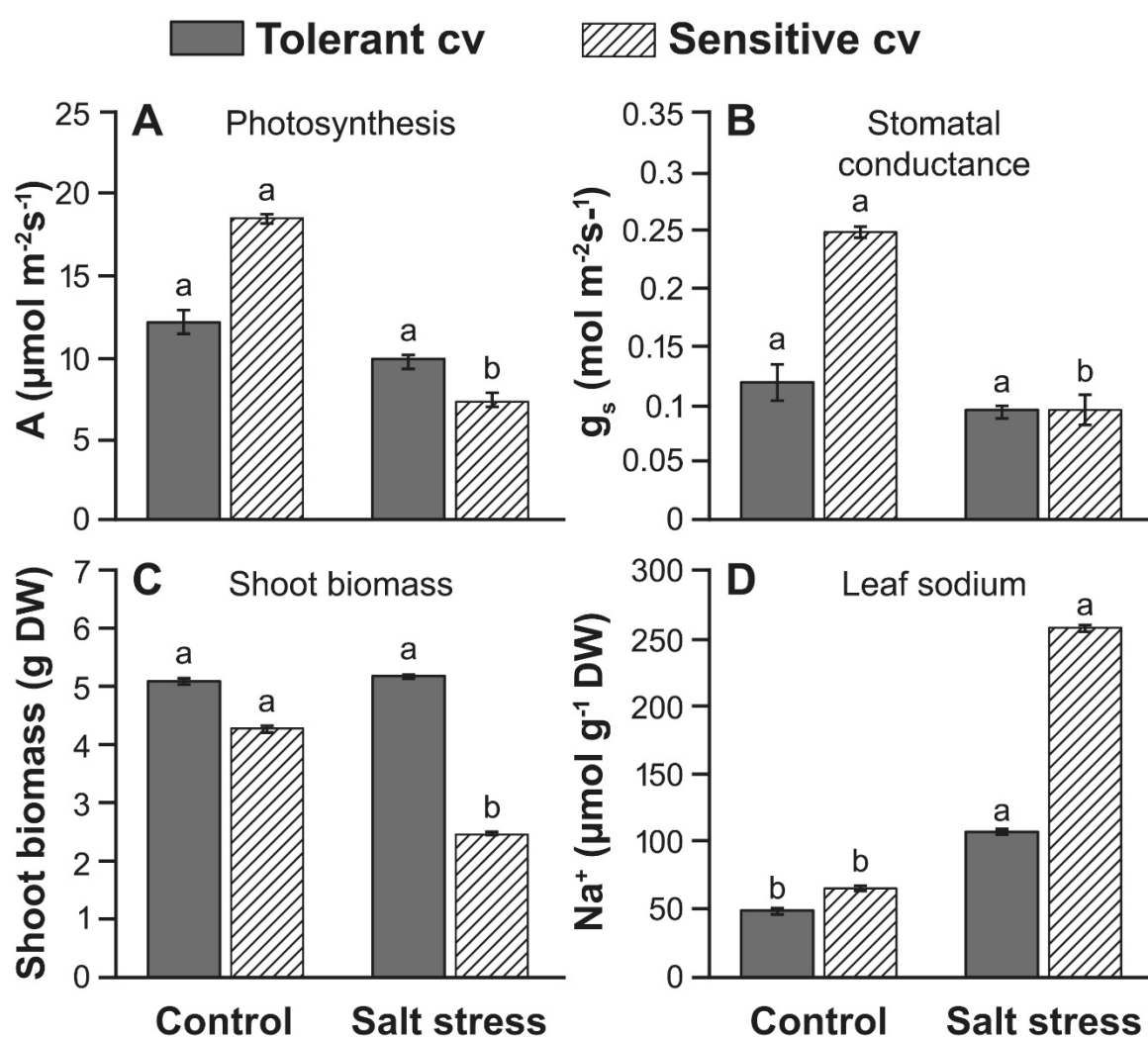
Table S2. Differentially regulated proteins in the more salt-sensitive cultivar IAC 87-3396 under salinity (160 mM NaCl for 15 days)

Listed are differentially regulated proteins with 5% probability and change above 1.5. Transcript names are of *Sorghum bicolor*, available in Phytozome

	Sobic number	Description	Fold change
1	002G277100.1.p	Triosephosphate isomerase	2.99
2	004G087000.1.p	ATP synthase subunit beta, chloroplastic	2.45
3	004G168500.1.p	2-Cys peroxiredoxin BAS1, chloroplast precursor	2.24
4	007G166200.3.p	Malate dehydrogenase [NADP], chloroplast precursor	2.15
5	007G166200.1.p	Malate dehydrogenase [NADP], chloroplast precursor	2.12
6	002G047400.1.p	Putative tyrosine phosphatase	2.02
7	004G235200.1.p	ATP synthase delta chain, chloroplast precursor	1.95
8	006G102000.1.p	Probable plastid-lipid-associated protein 2, chloroplast precursor	1.82
9	001G129000.1.p	Heat shock protein 70 kDa	1.71
10	010G073700.1.p	Putative uncharacterized protein	1.62
11	002G278700.1.p	RNAse S-like protein	1.57
12	006G203900.2.p	B0403H10-OSIGBa0105A11.13 protein	-1.56
13	010G189300.2.p	Type III chlorophyll a/b binding protein	-1.64
14	007G116950.1.p	Chromosome chr14scaffold_21 whole genome shotgun sequence	-1.66
15	004G055200.1.p	Phosphoglycerate kinase, cytosolic	-1.69
16	003G305700.1.p	Glutathione S-transferase 1	-1.73
17	007G068300.1.p	Polyphenol oxidase	-1.79
18	001G177000.1.p	Chlorophyll a/b binding protein 151, chloroplast precursor	-1.81
19	010G189300.1.p	Type III chlorophyll a/b binding protein	-1.96
20	005G087000.1.p	Chlorophyll a/b binding protein apoprotein CP26 precursor	-2.05
21	001G326900.1.p	Cytosolic pyruvate orthophosphate dikinase	-2.14
22	001G326900.2.p	Cytosolic pyruvate orthophosphate dikinase	-2.19
23	010G160700.1.p	Phosphoenolpyruvate carboxylase 1	-2.26
24	010G023700.2.p	Transketolase (Glycoaldehyde transferase)	-2.30
25	009G180800.1.p	Glutamate-1-semialdehyde- 2,1-aminomutase	-2.53

26	008G065000.1.p	Chromosome chr18scaffold_1, whole genome shotgun sequence	-2.55
27	010G108900.2.p	Putative uncharacterized protein	-2.64
28	004G329300.1.p	Leucine aminopeptidase 2, chloroplast precursor	-2.70
29	001G116500.1.p	Phosphoglucomutase, cytoplasmic 1	-3.71
30	010G108900.1.p	Putative uncharacterized protein	-4.45
31	006G220800.1.p	Aminomethyltransferase	-6.41
32	003G291500.1.p	Elongation factor 2	-6.72
33	001G021400.1.p	Translation factor	-6.72

Fig. S1. (A) Photosynthesis and (B) stomatal conductance of the youngest fully expanded leaf, (C) shoot biomass, and (D) leaf Na^+ concentration in the third youngest fully expanded leaf of young sugarcane plants in response to salinity (160 mM NaCl for 30 days). Dark columns show data for the tolerant cv. SP 81-3250 and columns with diagonal hatching for the sensitive cv. IAC 87-3396. Bars show standard error of the mean ($n = 4$). Letters above the columns show significance between control and NaCl treatments for each cv. by Tukey test at 5% of probability. (Adapted from Chiconato *et al.* 2019).



Reference

Chiconato DA, da Silveira Sousa G, Junior, dos Santos DMM, Munns R (2019) Adaptation of sugarcane plants to saline soil. *Environmental and Experimental Botany* **162**, 201–211. doi:10.1016/j.envexpbot.2019.02.021