Positive regulatory role of strigolactone in plant responses to drought and salt stress

Chien Van Ha[a,b], Marco Antonio Leyva-González[c,1], Yuriko Osakabe[d], Uyen Thi Tran[a], Rie Nishiyama[a], Yasuko Watanabe[a], Maho Tanaka[e], Motoaki Seki[e], Shinjiro Yamaguchi[f], Nguyen Van Dong[b], Kazuko Yamaguchi-Shinozaki[g], Kazuo Shinozaki[d], Luis Herrera-Estrella[c,2], and Lam-Son Phan Tran[a,2]

PNAS(2014), 111(2):851-856

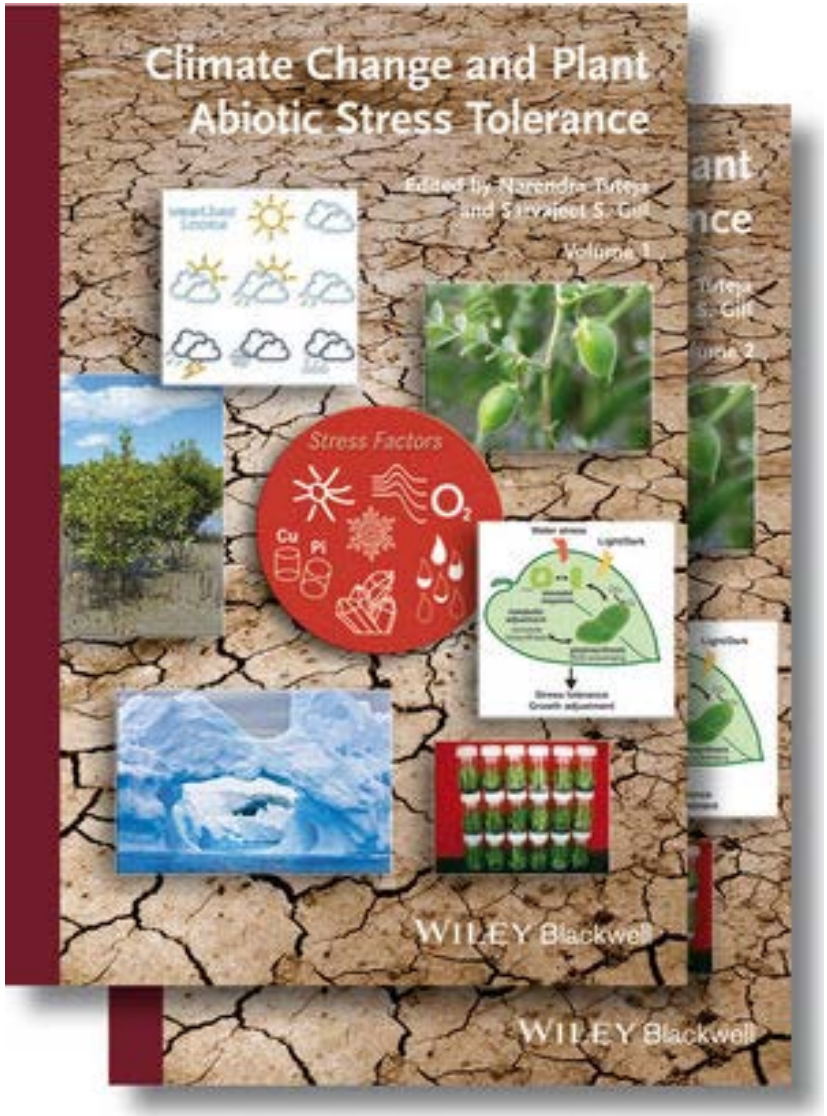
Abhijit Karve, Plant imaging group

Feb 3rd , 2014

Why it is interesting?

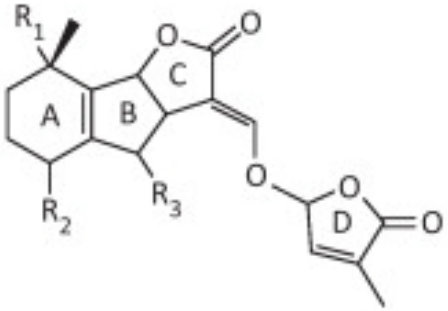
- General interest in plant adaptations to abiotic stress
- Little is know about the strigolactone biosynthesis and transport - It could be an interesting target for radiolabelling

Why this work is important

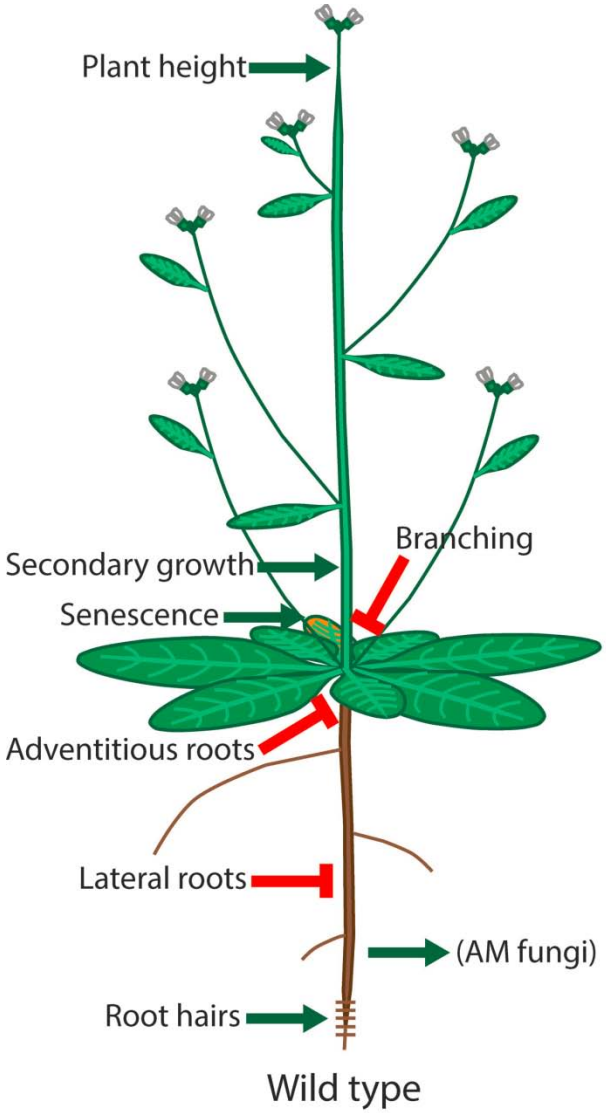


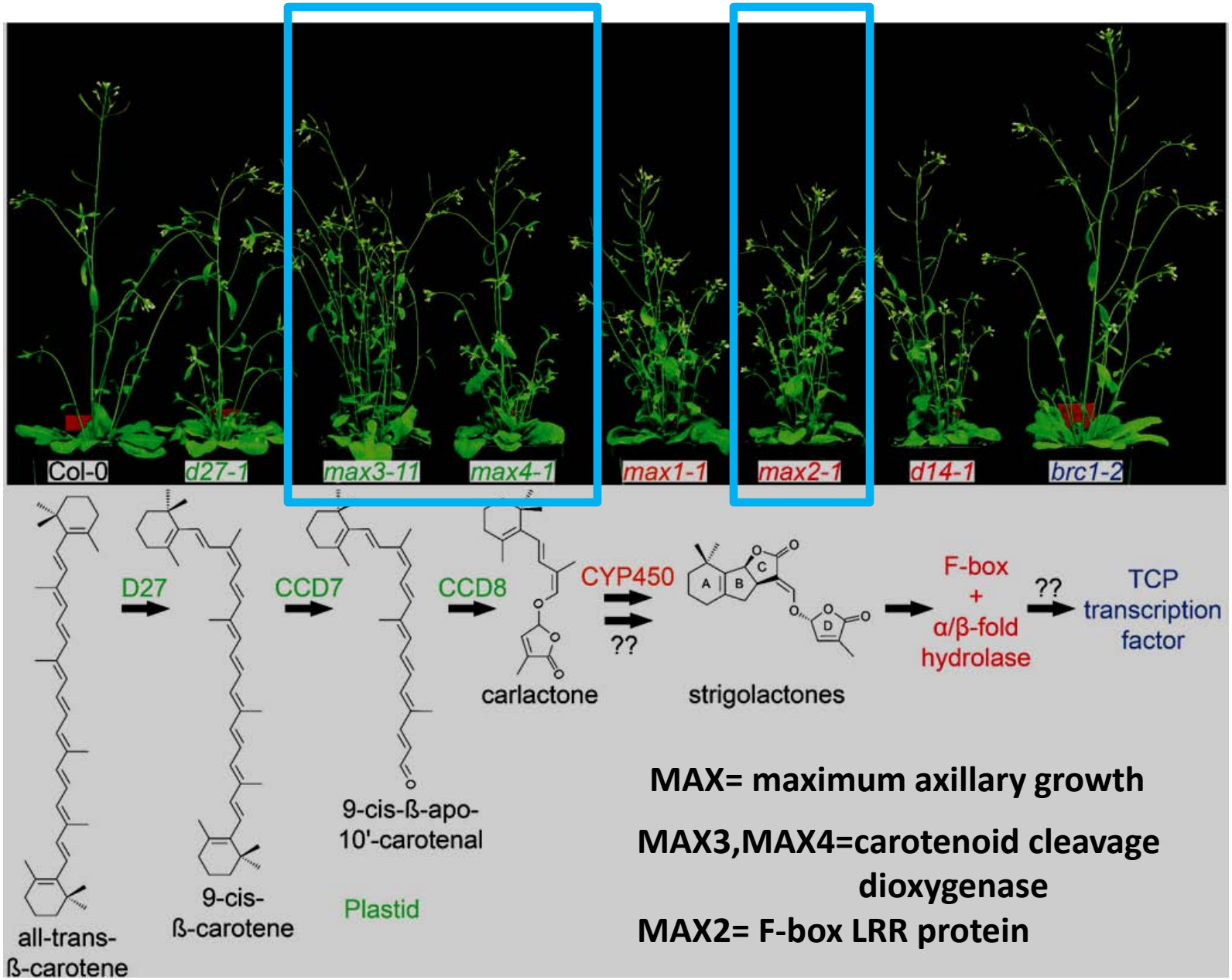
- Environmental stresses such as drought and salinity adversely affect plant growth and productivity
- Mechanisms of adaptation to these stresses are not clearly understood.
- This work describes the role of plant hormone “strigolactone” in mediating the responses to different abiotic stress stimuli in Arabidopsis

Strigolactone (SL): Striga+lactone

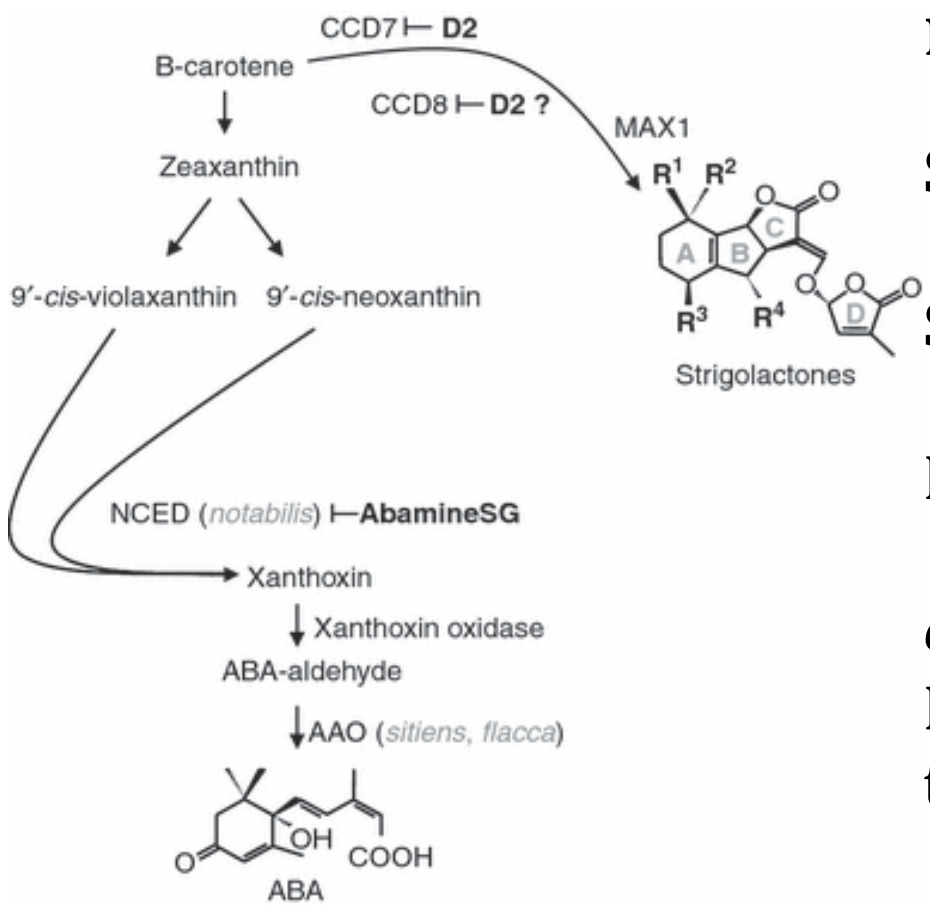


TRENDS in Plant Science




Col-0
d27-1
max3-11
max4-1
max1-1
max2-1
d14-1
brc1-2
D27
CCD7
CCD8
CYP450
??
F-box
+
α/β-fold
hydrolase
??
TCP
transcription
factor
carlactone
strigolactones
9-cis-ß-apo-
10'-carotenal
Plastid
all-trans-
ß-carotene
9-cis-
ß-carotene
MAX= maximum axillary growth
MAX3,MAX4=carotenoid cleavage
dioxygenase
MAX2= F-box LRR protein

Strigolactone- abiotic stress signaling



Lopez-Raez et al 2010

Role of SL in plant stress response is unknown

SL biosynthesis mutants

max3 and *max4*

SL signaling mutant

max2

Phenotypic analysis

Drought stress, salinity, osmotic stress , ABA treatment

High throughput transcriptomic analysis

Dehydrated leaves (WT Vs max2)

SL mutants are hypersensitive to drought and salt stress

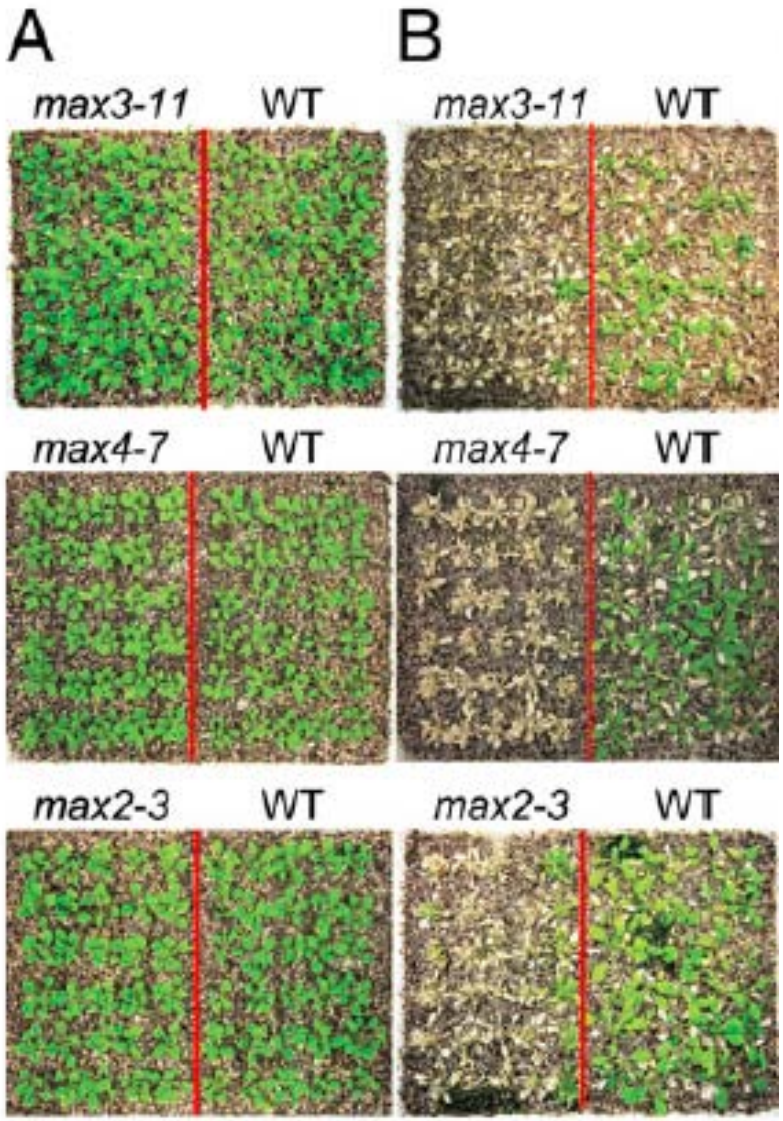


Fig 1

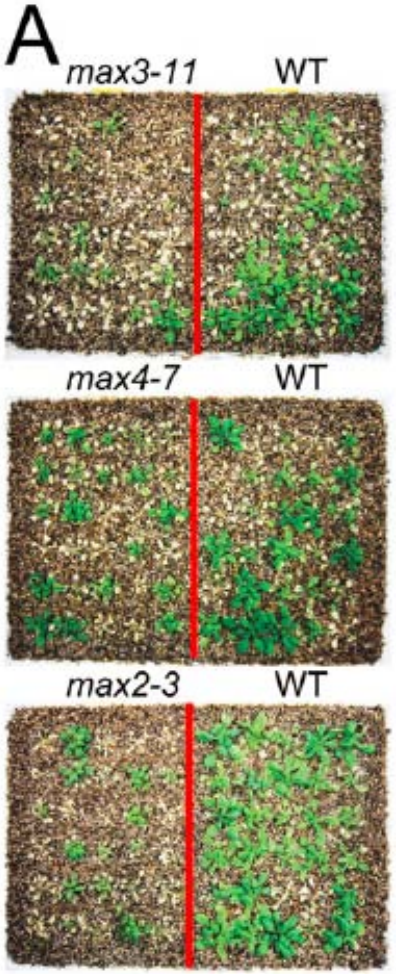
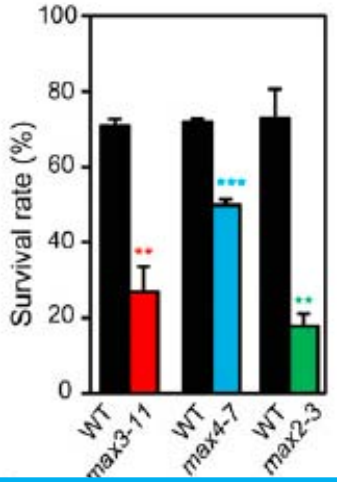
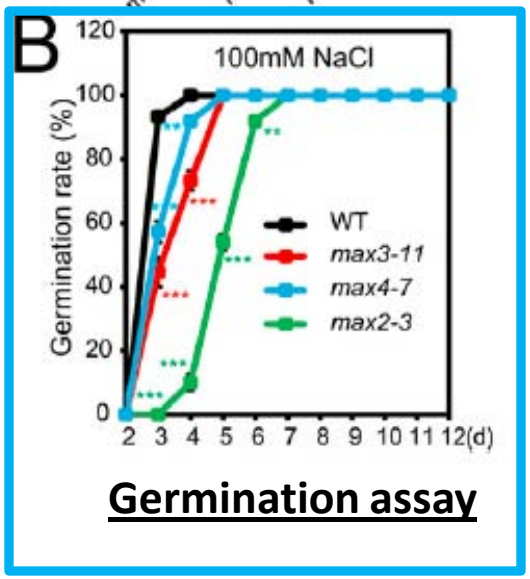


Fig S2





Germination assay

SL application affects drought sensitivity

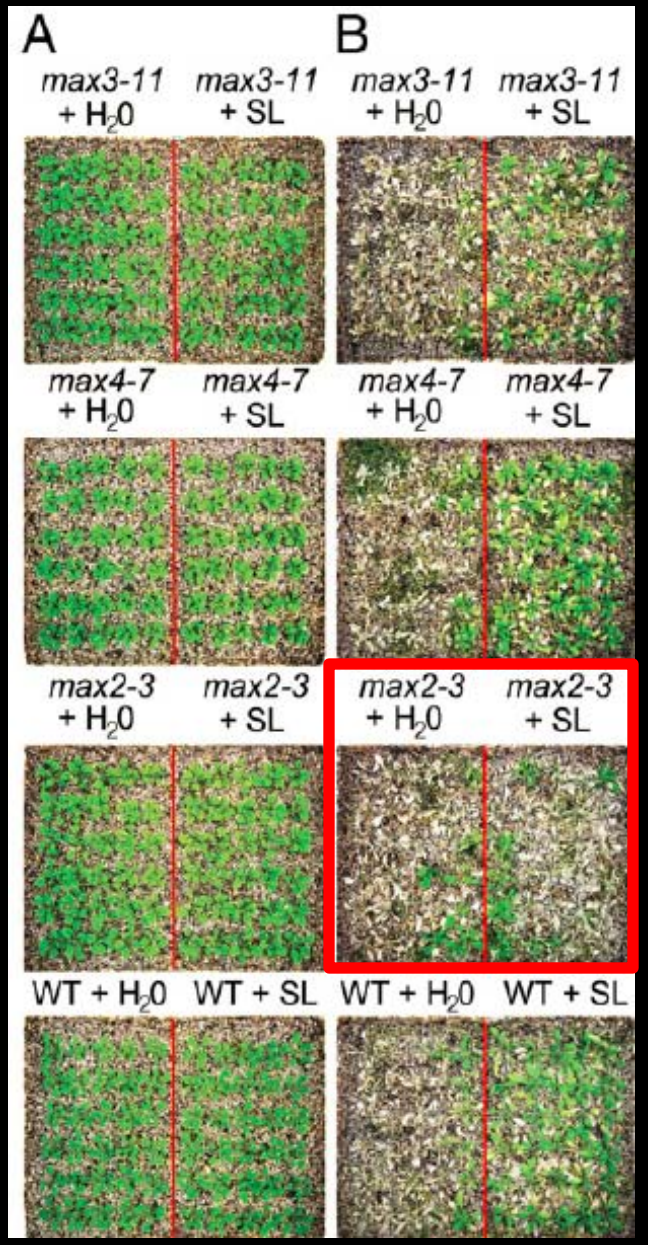


Fig 2

Exogenous application of SL

- Reduced the sensitivity of SL biosynthesis mutnats (*max3* and *max4*)
- No effect on the sensitivity SL signaling mutant, *max2*
- Improved drought tolerance of WT plants

SL mutants are less sensitive to exogenous ABA application

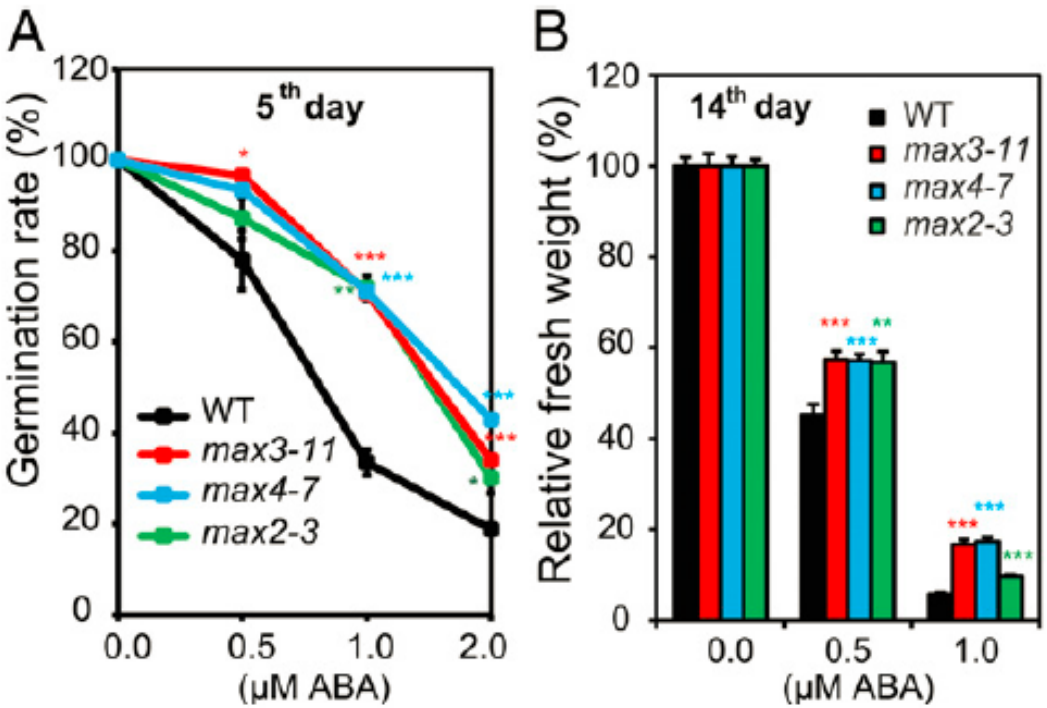


Fig 3

- ABA inhibits germination of WT seeds earlier than the mutant.
- ABA affects the post germination growth of SL mutants less severly than the WT

WT and SL mutants have similar root growth under salinity and osmotic stress

Salt stress

Osmotic stress

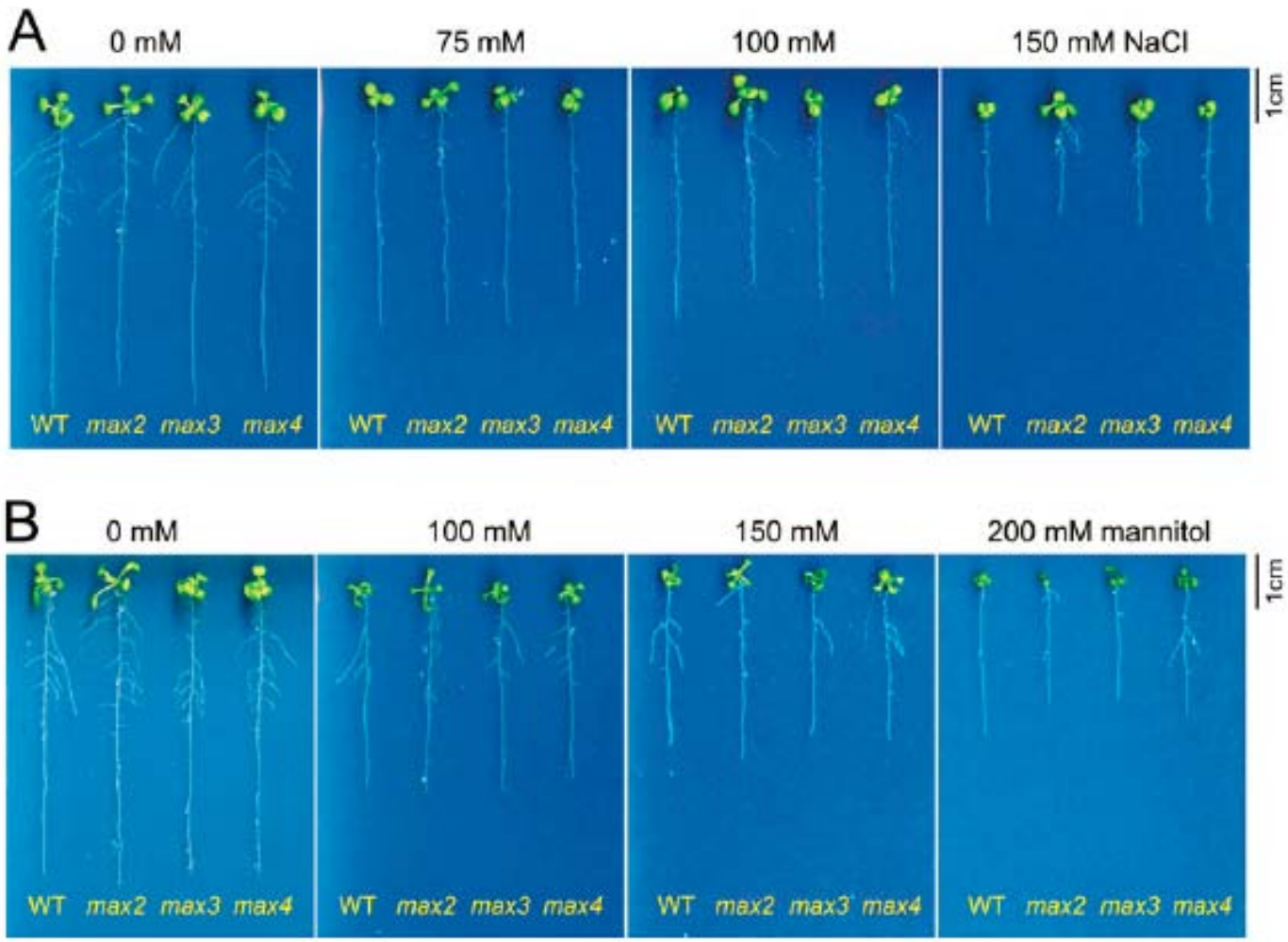


Fig S4

Could the SL mutants also have altered shoot ABA responses?

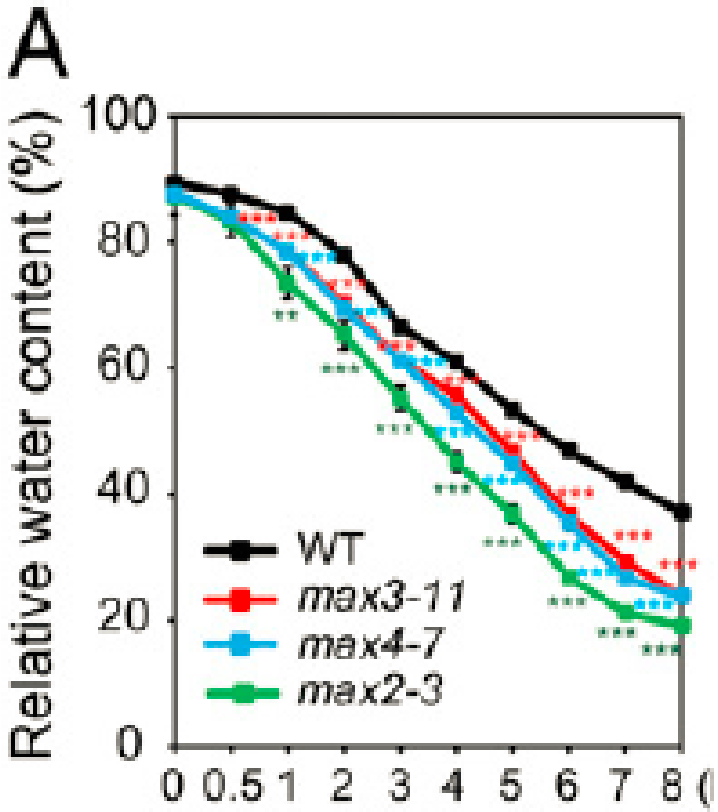


Fig 4A

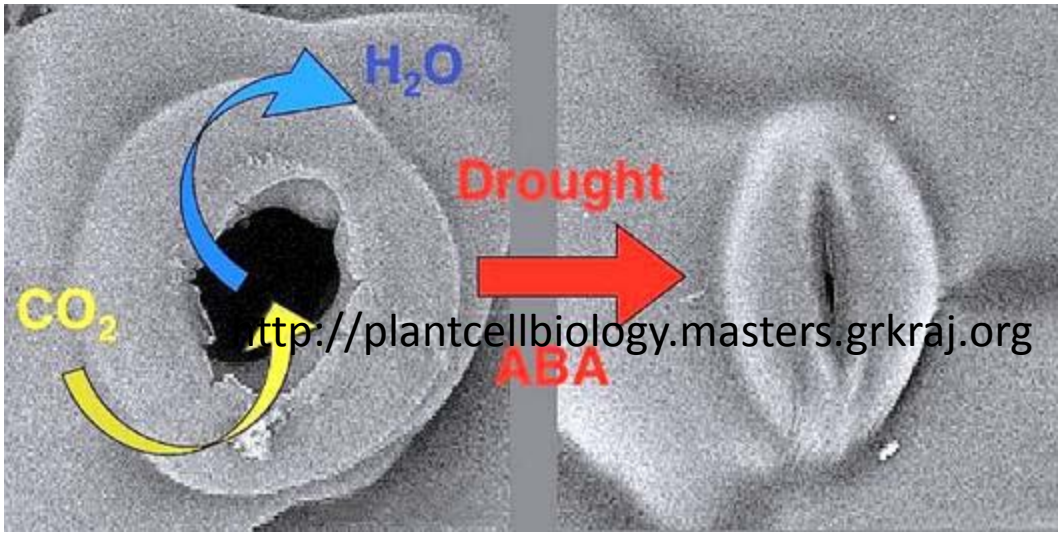
7 d old plant

↓

Remove from the growth medium

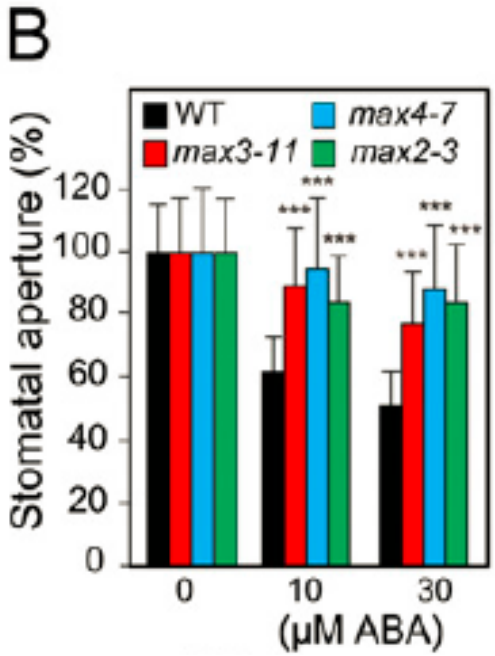
↓

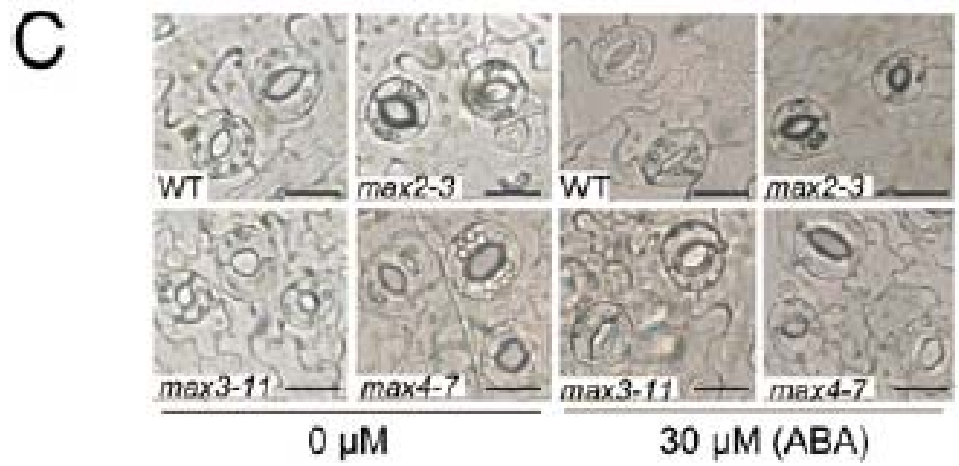
Weigh periodically unto 8h

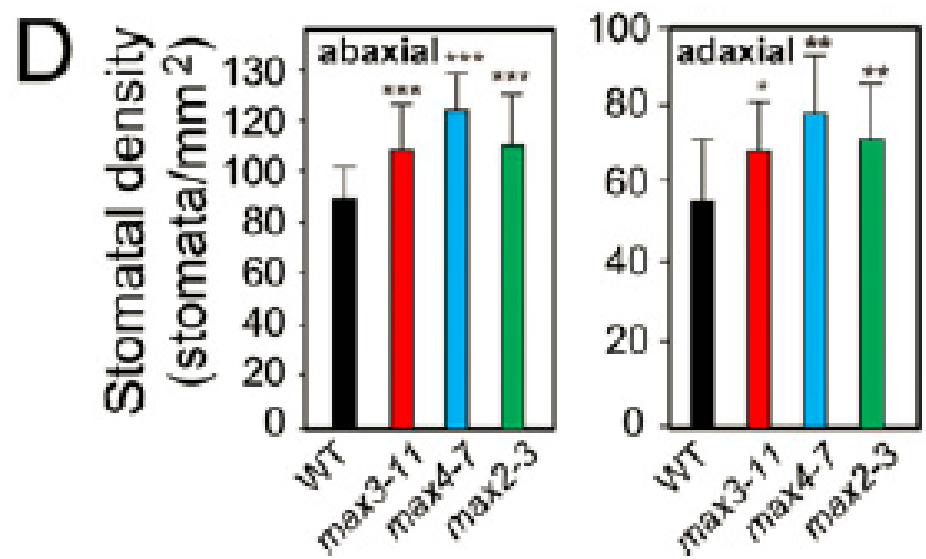


SL mutants loose water faster than the WT

Slower stomatal closure and higher density lead to higher water loss in SL mutants







SL mutants ,Delayed stomatal closure (B and C); Increased number of stomata (D).

Fig 4

Global transcriptomic analysis

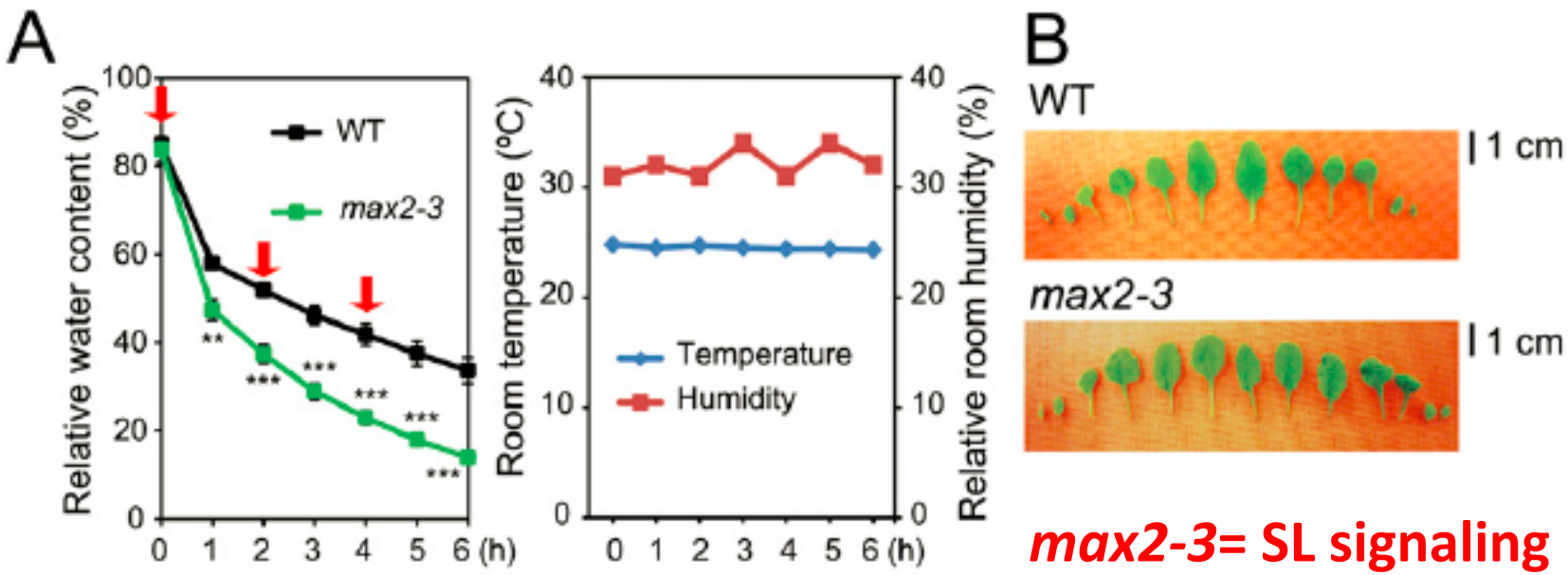


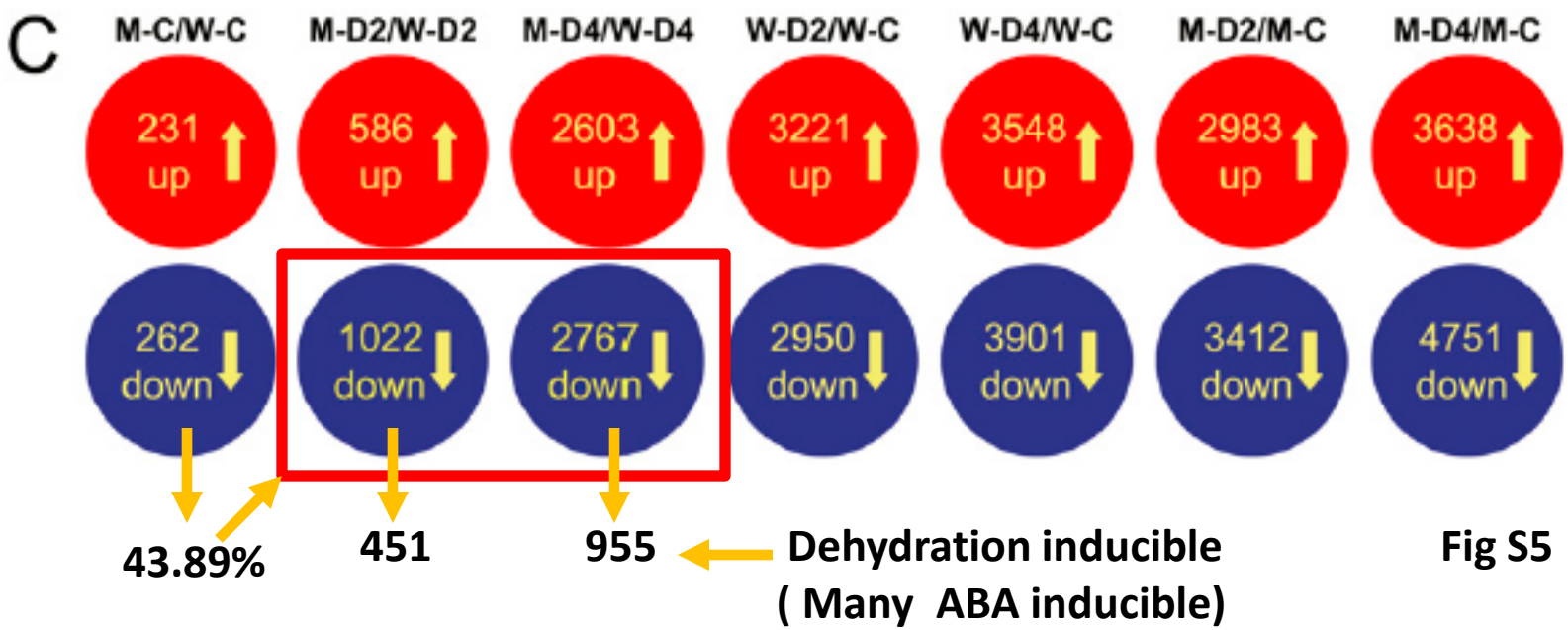
Fig 5 and S5

***max2-3*= SL signaling mutant**

To identify genes involved in downstream regulatory pathways affected by SL-mediated responses to abiotic stress

Hypothesis: A greater number of stress-inducible and/or ABA-inducible genes that are down-regulated in the *max2* when plants were exposed to water stress

Regulatory response to drought is severely affected in SL mutant



A greater number of stress-inducible and/or ABA-inducible genes that are constitutively down-regulated in the *max2* when plants.

Modulation of SL responses is essential for adaptation to abiotic stress

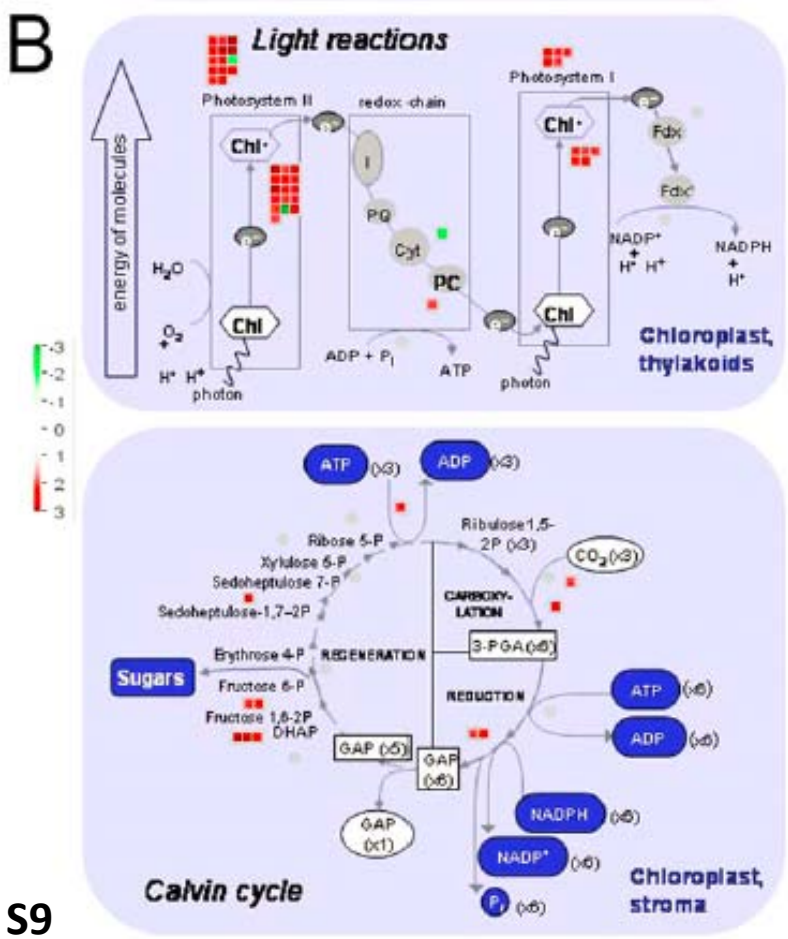


Fig S9

Misregualtion of genes associated with photosynthesis (ABA independent)

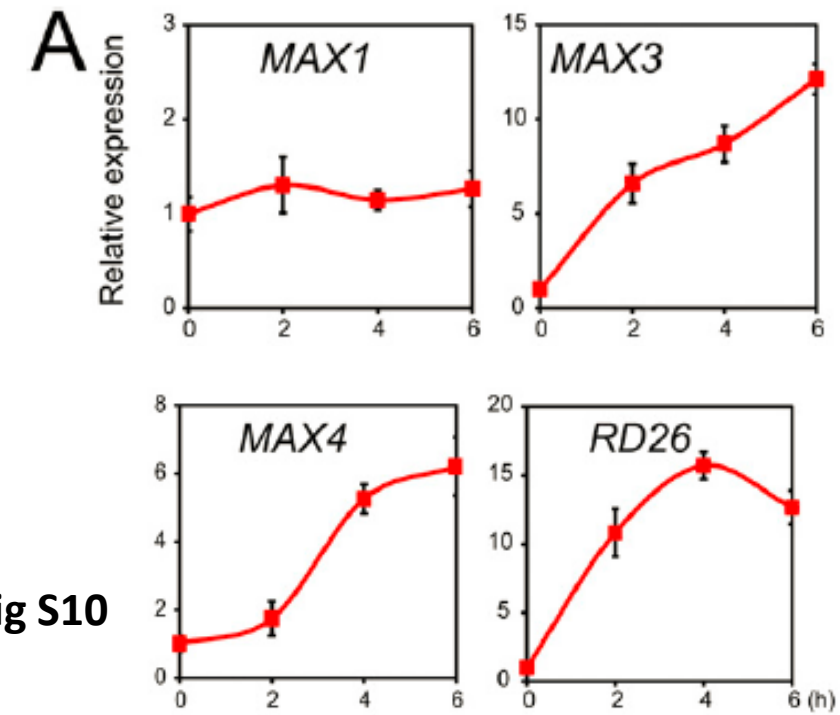


Fig S10

MAX3 and *MAX4* transcript is induced by drought (and salt and ABA) in WT leaves.

Conclusions

- Increased sensitivity of SL mutants to drought , salt and osmotic stress → SL is a positive regulator of abiotic stress
- Delayed stomatal closure and insensitivity to ABA of SL mutants→ SL positively regulates abiotic stress responses through ABA
- Induction of *MAX3* and *MAX4* by stress in the WT→ Stress triggers activation of SL biosynthesis, ultimately leading to an activation of SL signaling
- Overall SL positively modulates Stress responses in Arabidopsis through ABA dependent and independent pathways

AGI	Gene description	M-C/W-C		M-D2/W-D2		M-D4/W-D4		W-D2/W-C		W-D4/W-C	
		Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value	Fold change	q-value
AT5G13930	*CHS*	1.00	0.9992	-2.04	0.0502	-11.04	0.0044	3.67	0.0221	4.76	0.0154
AT3G51240	*F3H*	-1.24	0.4150	-1.91	0.0234	-7.33	0.0076	2.72	0.0100	4.25	0.0073
AT5G08640	*FLS1*	1.10	0.7997	-1.06	0.6422	-2.44	0.0413	3.69	0.0175	3.99	0.0303
AT1G56650	*MYB75*	2.51	0.0792	-2.49	0.0337	-3.07	0.0199	396.15	0.0001	340.25	0.0003
AT1G66390	*MYB90*	-1.06	0.2608	-20.35	0.0349	-25.12	0.0107	43.95	0.0001	33.59	0.0033
AT5G39610	*AtNAC2*	-2.86	0.0133	-2.02	0.0314	-2.08	0.0041	2.53	0.0007	3.06	0.0008
AT5G53290	*CRF3*	1.53	0.2257	-2.22	0.0287	-2.13	0.0186	32.09	0.0003	13.23	0.0010
AT3G18550	*BRC1*	-31.71	0.0117	-20.65	0.0244	-9.89	0.0073	-3.76	0.0093	-5.18	0.0005
AT1G54890	*LEA*	1.86	0.2879	-2.91	0.2257	-7.06	0.0044	12.19	0.0023	55.52	0.0003