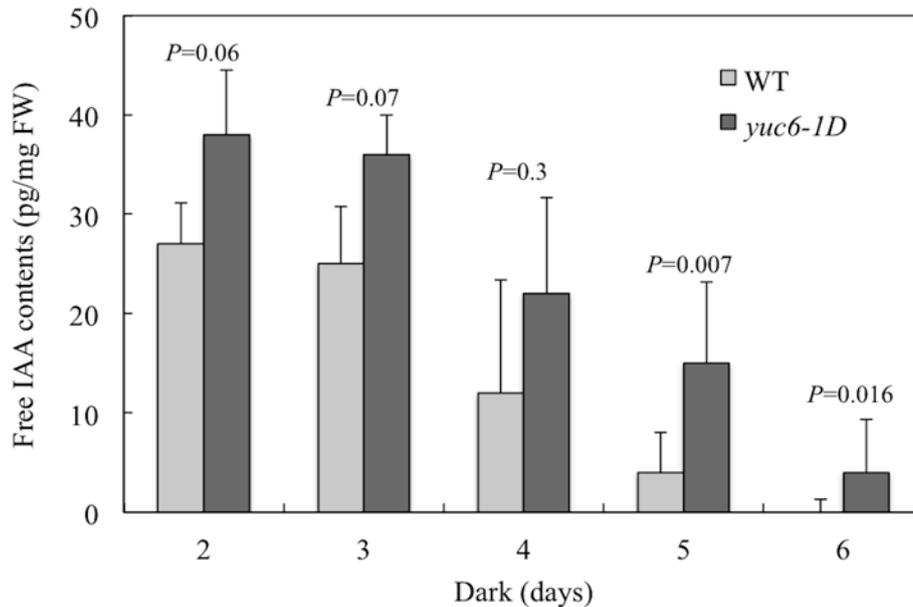


***YUCCA6* overexpression demonstrates auxin function in delaying of leaf senescence in *Arabidopsis thaliana*.** Jeong Im Kim, Angus S Murphy, Dongwon Baek, Shin Woo Lee, Dae-Jin Yun, Ray A Bressan, and Meena L Narsimhan

SUPPLEMENTARY MATERIAL



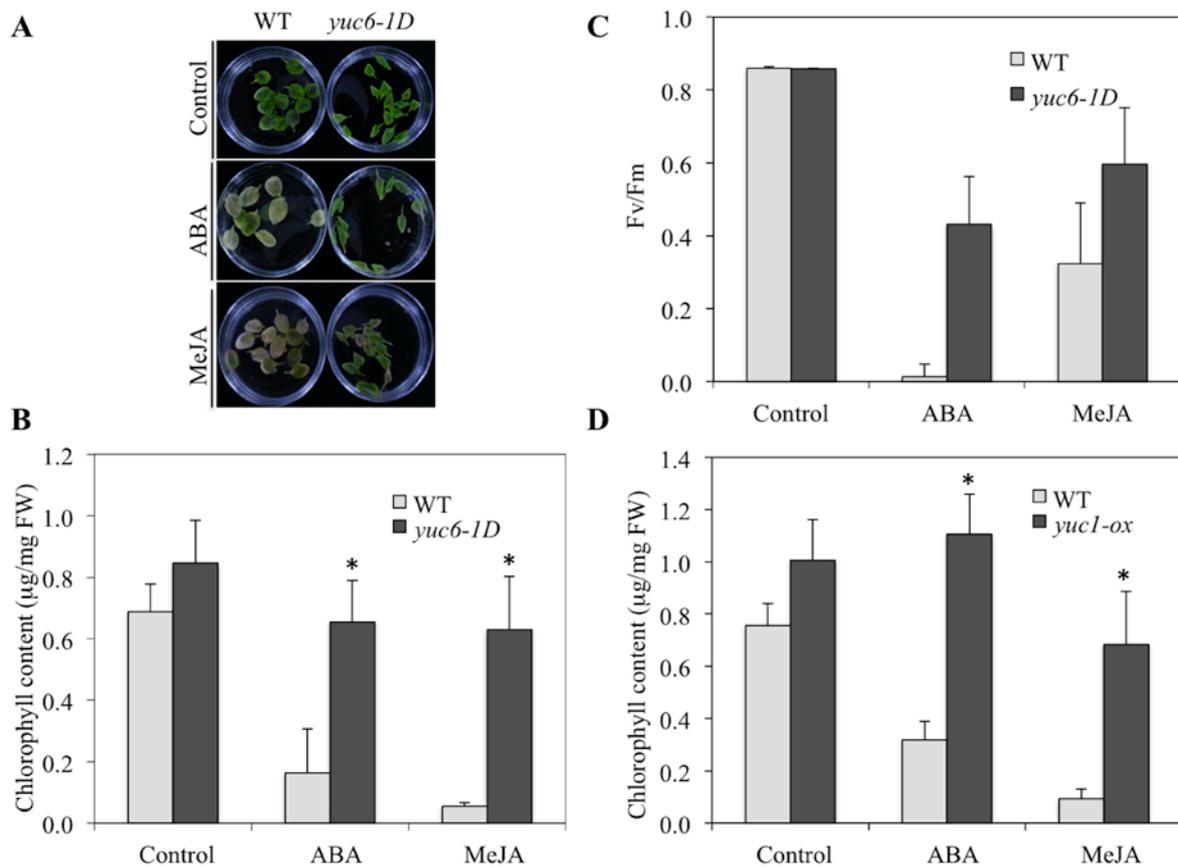
Supplementary Fig. S1. Free IAA levels decrease during dark-induced senescence of *yuc6-1D* leaves but remain high compared with wild type leaves.

Shown are free IAA levels in WT and *yuc6-1D* leaves over the dark treatment. Twenty leaves from each time point were pooled for IAA measurement. Data shown are the means \pm SD (n=3) from three biological and technical repeats.

Gene	Expression
<i>ARR4</i> (At1g10470)	0.37
<i>ARR6</i> (At5g62920)	0.18
<i>ARR15</i> (At1g74890)	0.55
<i>ARR16</i> (At2g40670)	0.38

Supplementary Fig. S2. Expression of Type-A *Arabidopsis response regulators* (*ARRs*) is down-regulated in *yuc6-ID* rosette leaves.

Relative expression levels of *ARRs* in wild type and *yuc6-ID* were calculated from microarray analysis data that was published in *Kim et al.*, (2007). Numbers indicate the ratio of expression in *yuc6-ID* to expression in wild type. RNA was extracted from 3 week-old soil grown plants that were before bolting and roots were not included. Three biological and technical repeats were performed.



Supplementary Fig. S3. ABA and methyl jasmonate induced senescence is delayed in *yuc6-1D* and *yuc1-ox* plants compared to wild type.

Third and fourth rosette leaves from wild type (WT), *yuc6-1D* and *yuc1-ox* were detached and incubated in the dark for five days in 3 mM MES (pH 5.7) without and with 100 μ M ABA and 50 μ M methyl jasmonate (MeJA). Shown are results of analyses at the end of dark incubation. (A) Photographs, (B) total chlorophyll contents, and (C) photosystem II efficiency (Fv/Fm) of WT and *yuc6-1D*. (D) Total chlorophyll contents of *yuc1-ox* compared to WT. '*' indicates p -value < 0.05 from student t -test. Data represent the mean \pm SD (n=10).

Supplemental Table S1. Quantitative RT-PCR Primer sequences

Name	Primers (5' -> 3')
<i>GH3.3</i> (At2g23170)	F: TCCACTAAGGACGTGAAGGCTCTAAG R: TGCTGGTAATCCACCGGGAGTCTTCG
<i>GH3.5</i> (At4g27260)	F: AGCCCTAACGAGACCATCCT R: AAGCCATGGATGGTATGAGC
<i>GH3.1</i> (At2g14960)	F: CTCGGTGCTGCTTGGAAATG R: TGGGCTGAAGTGTGTAGATA
<i>GH3.6</i> (At5g54510)	F: GGCGTATTTTCGAGTTCCTTGC R: GCGTTTTGAAGCTCAACCTC
<i>UBQ10</i> (At4g05320)	F: GGCCTTGTATAATCCCTGATGAATA R: AAAGAGATAACAGGAACGGAAAC
<i>IAA2</i> (At3g23030)	F: TCCTTACCTTCGCAAGATCG R: ATCACCAACCAACATCCAGTC
<i>SAG12</i> (At5g45890)	F: GTTAATGATGAGCAAGCACTG R: GGAAATCAAAACCACCTCC
<i>NAC6</i> (At5g39610)	F: TCGTCTCACGTGACCTGCTT R: GGACTCGTGGACAAGTCTTTTGT
<i>NAC1</i> (At1g56010)	F: TGGGAGGGAAGGATTGGTATT R: GCCCCGTCGCGTATTTT
<i>YUC6</i> (At5g25620)	F: GGGCTGTCCATGTTCTTACTGAA R: CGGGAAACAACCAAAAGGAA
<i>YUC1</i> (At1g21430)	F: TCGCTCCAAGGTTCAACAAGA R: TCCAGAAACCGGAGGAAGAA