

The Tetratricopeptide Repeat-Containing Protein Slow Green1 Is Required for Chloroplast Development in *Arabidopsis*

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Supplementary Information

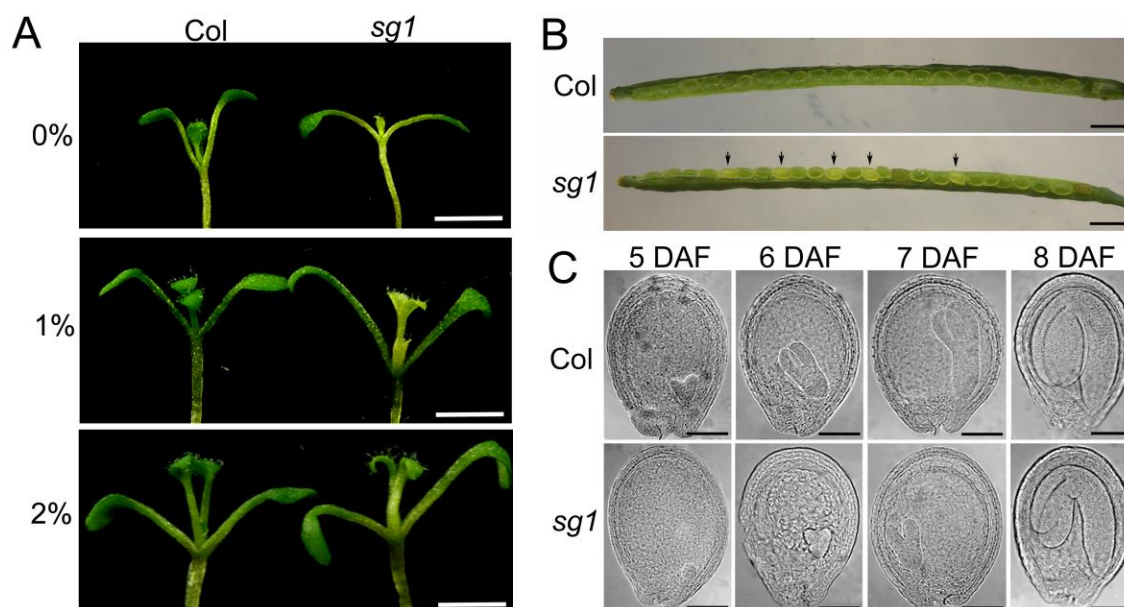
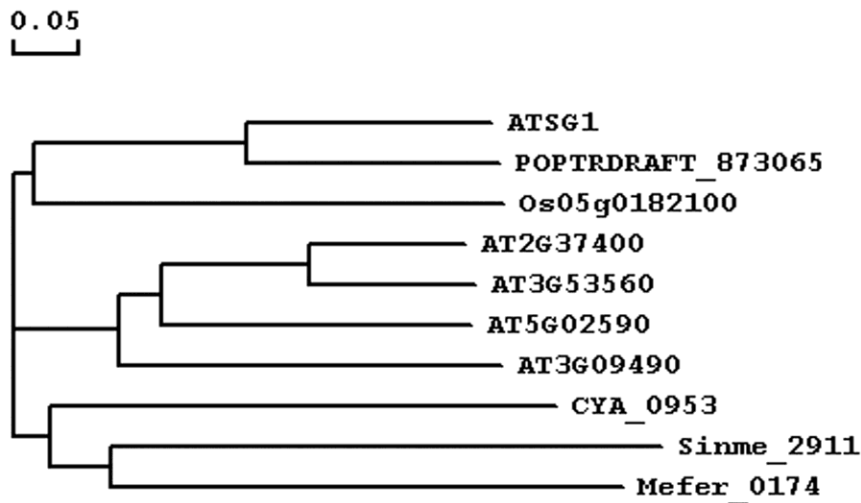


Figure S1. Early growth of *sg1* favored by sucrose, and delayed embryogenesis during *sg1* seed development. (A) 10 days old seedlings grew on Murashige–Skoog medium supplemented with 1% and 2% sucrose. (B) 10 DAF siliques from wild and *sg1*^{+/-} heterozygous. (C) Embryo development in wild-type (upper panels) and *sg1* plants (lower panels). Arrowheads showed the seeds of delayed embryogenesis. Abbreviations: DAF, day after fertilization. Bars = 0.5 cm in (A); 0.5 mm in (B); and 100 μ m in (C).

A



B

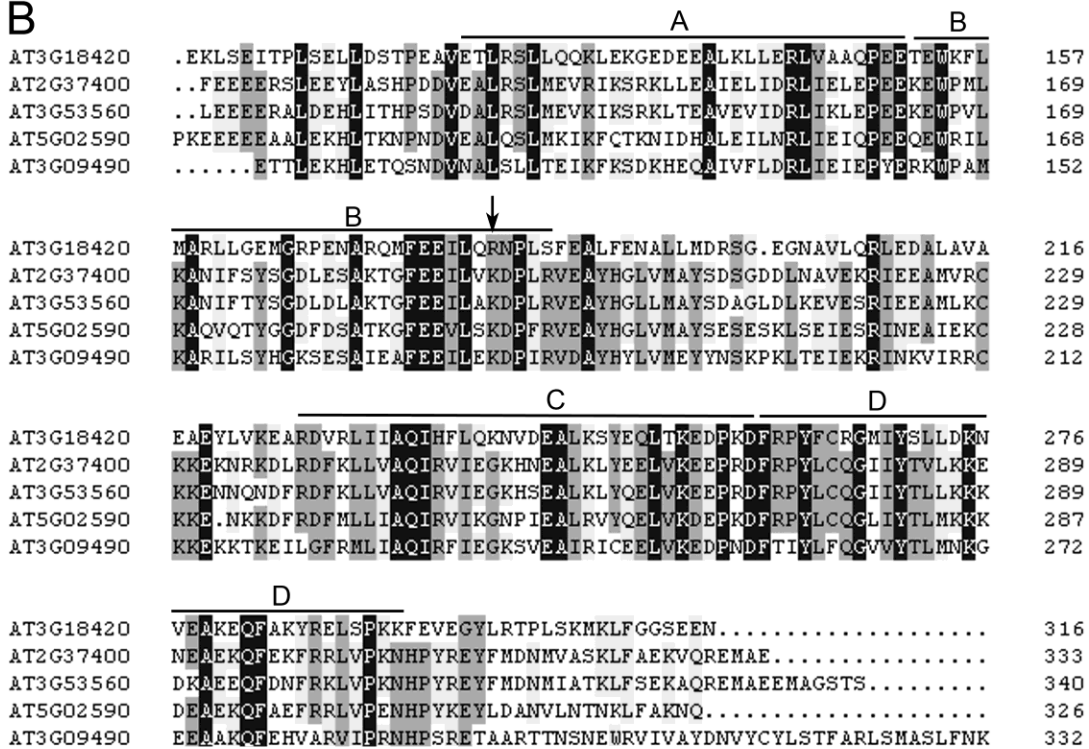


Figure S2. Phylogenetic analysis and amino acid sequence alignment of SG1 TPR domains. (A) Unrooted phylogenetic tree of SG1 and homologous proteins in *Arabidopsis thaliana*, *Populus trichocarpa*, *Oryza sativa*, *Synechococcus*, *Sinorhizobium* and *Methanocaldococcus*. (B) Comparison of the amino acid sequence of SG1 with *Arabidopsis thaliana* proteins AT3G09490, AT2G37400, AT3G53560, and AT5G02590. Black boxes indicate strictly conserved amino acids among these proteins. The arrow head indicates the mutation site of *sg1*; bars above the sequences labelled A to D indicate the four TPR domains of SG1.

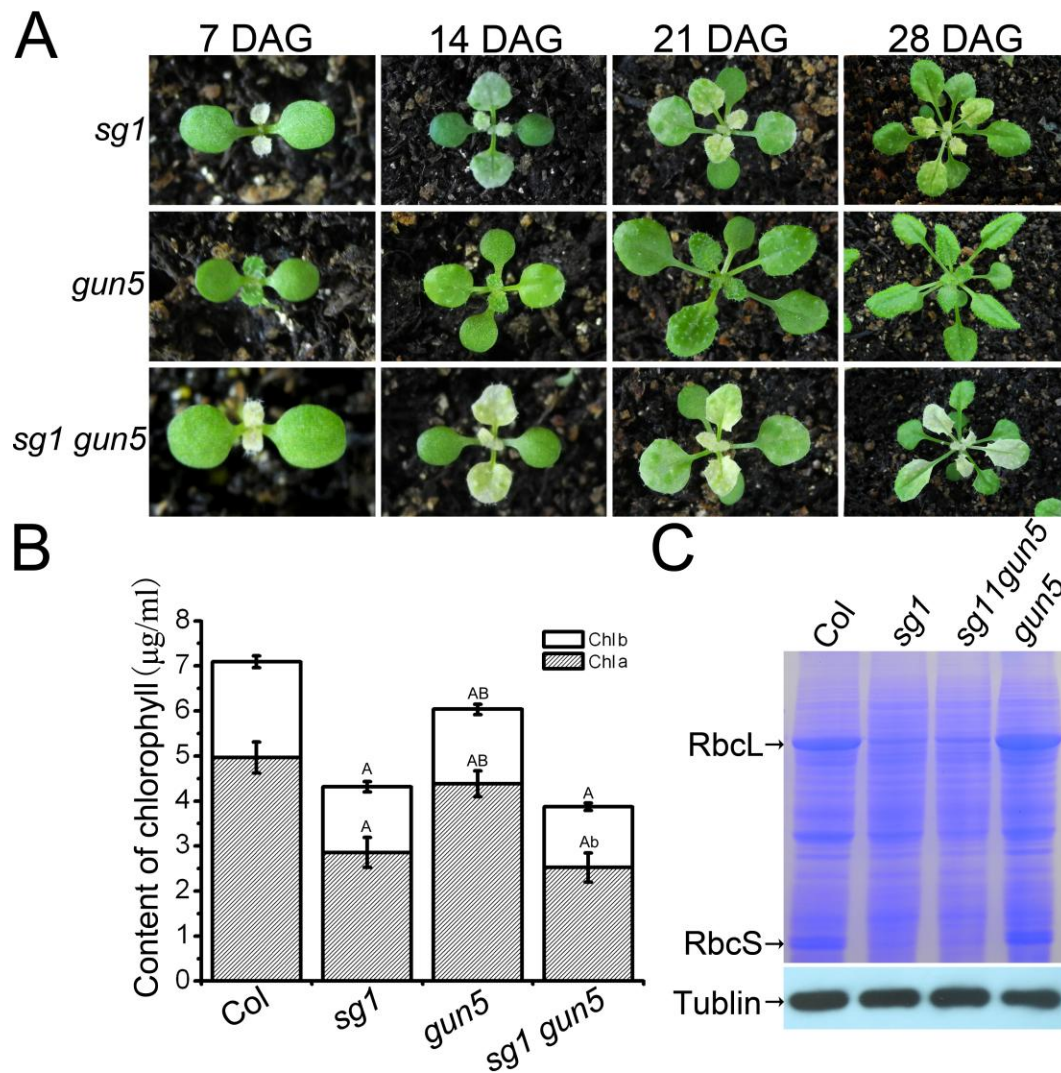


Figure S3. The phenotypes of *sg1 gun5* double mutant. (A) The seedlings of *sg1*, *gun5* and *sg1 gun5* grown for 1 to 4 weeks in soil. (B) Chlorophyll contents in 2-week-old Col, *sg1*, *gun5*, and *sg1 gun5* plants. (C) Total protein resolved by SDS-PAGE from Col, *sg1*, *sg1 gun5* and *gun5*, the arrows indicate the major bands of the large subunit (RbcL) and small subunit (RbcS) of RuBisCO. ^a Significantly different from Col, $P < 0.05$; ^A Significantly different from Col, $P < 0.01$; ^b Significantly different from *sg1*, $P < 0.05$; ^B Significantly different from *sg1*, $P < 0.01$.

Tables

Supplementary Table S1. Chlorophyll contents of leaves from different genotypes at different growth stages. Total chlorophylls were obtained from the sixth basal rosette leaves of 3-week-old, 4-week-old, and 5-week-old plants. Values represent mean \pm SD of three independent experiments.

^a Significantly different from Col, $P < 0.05$, ^A Significantly different from Col, $P < 0.01$, ^b Significantly different from *sgl*, $P < 0.05$, ^B Significantly different from *sgl*, $P < 0.01$.

		3 weeks	4 weeks	5 weeks			3 weeks	4 weeks	5 weeks
Chl <i>a</i>	Col	3.08 \pm 0.135	3.19 \pm 0.076	3.27 \pm 0.085	Chl <i>b</i>	Col	1.33 \pm 0.046	1.34 \pm 0.084	1.39 \pm 0.075
	<i>sgl</i>	0.87 \pm 0.037 ^A	1.70 \pm 0.084 ^A	2.66 \pm 0.066 ^A		<i>sgl</i>	0.434 \pm 0.049 ^A	0.82 \pm 0.059 ^A	1.18 \pm 0.085 ^A
	<i>gun1</i>	2.97 \pm 0.015 ^{aB}	3.06 \pm 0.047 ^B	3.17 \pm 0.043 ^B		<i>gun1</i>	1.20 \pm 0.032 ^{aB}	1.23 \pm 0.043 ^B	1.32 \pm 0.054 ^B
	<i>sgl gun1</i>	2.24 \pm 0.053 ^{AB}	2.90 \pm 0.042 ^{aB}	3.10 \pm 0.015 ^{aB}		<i>sgl gun1</i>	1.09 \pm 0.016 ^{AB}	1.25 \pm 0.024 ^{aB}	1.41 \pm 0.038 ^{aB}
	<i>gun4</i>	1.52 \pm 0.126 ^{AB}	1.76 \pm 0.11 ^{AB}	2.22 \pm 0.078 ^{AB}		<i>gun4</i>	0.55 \pm 0.07 ^{AB}	0.67 \pm 0.067 ^{AB}	0.81 \pm 0.081 ^{AB}
	<i>sgl gun4</i>	1.77 \pm 0.083 ^{AB}	2.15 \pm 0.091 ^{AB}	2.59 \pm 0.112 ^{AB}		<i>sgl gun4</i>	0.96 \pm 0.072 ^{AB}	1.07 \pm 0.044 ^{AB}	1.14 \pm 0.065 ^{AB}

Supplementary Table S2. The number of different phenotypic seedlings segregated in the F1 offspring of a reciprocal cross between Col and *sgl*. Seedlings of 10-day-old were examined to gather statistics. χ^2 was calculated based on an expected ratio of 3:1.

Cross	Number of seedlings		Approximate ratio of wild/mutant	χ^2
	Wild-type	Mutant		
<i>sgl</i> (σ) \times Col (♀)	249	79	3:1	0.14 ($P > 0.5$)
Col (σ) \times <i>sgl</i> (♀)	171	58	3:1	0.01 ($P > 0.5$)

Supplementary Table S3. Primers of markers for first mapping.

Chromosome	Markers	Forward (5'→3')	Reverse (5'→3')	
1	EAT	GCCACTGCGTGAATGATATG	CGAACAGCCAACATTAATTCCC	
	JV18I19	AATTCAGTATCGAGATACCC CTCT	TGTCGTATATCAATCGAAAAAG AGAT	
	NGA392	TTGAATAATTTGTAGCCATG	GGTGTAAATGCGGTGTTC	
	NGA280	CTGATCTCACGGACAATAGT GC	GGCTCCATAAAAAGTGCACC	
	NGA114	CCTTCACATCCAAAACCCAC	GCACATACCCACAACCAGAA	
2	5			
	6	CGCTACGCTTTTCGGTAAAG	GCACAGTCCAAGTCACAACC	
3	NGA168	TCGTCTACTGCACTGCCG	GAGGACATGTATAGGAGCCTCG	
	AthBIO2	TGACCTCCTCTTCCATGGAG	TTAACAGAAACCCAAAGCTTTC	
	b			
4	NGA172	AGCTGCTTCCTTATAGCGTC C	CATCCGAATGCCATTGTTC	
	NGA162	CATGCAATTTGCATCTGAGG	CTCTGTCACTCTTTTCCTCTGG	
	GAPAb	CACCATGGCTTCGGTACTT	TCCTGAGAATTCAGTGAACCC	
	NGA6	TGGATTTCTTCTCTCTTCA	ATGGAGAAGCTTACACTGATC	
5	NGA8	GAGGGCAAATCTTTATTTCTG G	TGGCTTTCGTTTATAAACATCC	
	NGA113	TAGCCGGATGAGTTGGTACC	TTTTTCCTTGTGTTGCATTCC	
	9			
	7	NGA110	GCGAAAAAACAAAAAATC CA	CGACGAATCGACAGAATTAGG
	NGA225	GAAATCCAAATCCCAGAGAG GG	TCTCCCCACTAGTTTTGTGTCC	
5	NGA106	GTTATGGAGTTTCTAGGGCA CG	TGCCCCATTTTGTCTTCTC	
	NGA76	GGAGAAAATGTCACTCTCCA CC	AGGCATGGGAGACATTTACG	
	NGA129	TCAGGAGGA ACTAAAGTGA GGG	CACACTGAAGATGGTCTTGAGG	

Supplementary Table S4. Primers of markers for fine mapping

Chromosome	Markers	Forward (5'→3')	Reverse (5'→3')
	T11118	GAAGGATATTTCCCAATTC G	GACCCCTACCCGCTCCTTGA C
	MSJ11	TAAGTGCATATATCCAGTAC	CATTCTTCAGTTCTTGTATG
3	MDC8	TCCAATCATGAATCGTATTG	ACTATGACTATCCATCCATG
	MKP6	ATCTTGTAATCTGGTGCGTG	GCAATAGCCCATGTGAATTC
	MYF24.3	GAAATGTCGTCATCTTGTTTC	TGTATAACTTCCTCCACAAG
	MYF24	ACGATAATGTATGTGTGTAC	TCAGTCTTCCTTACAATATG
	MIE15	TCTCTGTAATTTCTCCAGC	GTTGAGAAGCATACTAGAG A

Supplementary Table S5. Primers of qRT-PCR

Name	Forward (5'→3')	Reverse (5'→3')
β -tubulin	GATTTCAAAGATTAGGGAAGAGTA	GTTCTGAAGCAAATGTCATAGAG
<i>SG1</i>	GCTGAGGCTGAGTATTTGGTGA	GCTCTTCAATGCTTCATCCAC
<i>psaB</i>	GGACCCCACTACTCGTCGTA	ATTGCTAATTGCCCGAAATG
<i>psbA</i>	GAGCAGCAATGAATGCGATA	CCTATGGGGTCGCTTCTGTA
<i>psbB</i>	CGTGCGACTTTGAAATCTGA	TAGCACCATGCCAAATGTGT
<i>RbcL</i>	GTGTTGGGTTCAAAGCTGGT	CATCGGTCCACACAGTTGTC
<i>accD</i>	TGTGGATTCAATGCGACAAT	TTTTGCGCAGAGTCAATACG
<i>ycf2.2</i>	GGGTTCAACAAGCAATCGAT	CCGATGTATCATTTCTGGGT
<i>rpoA</i>	CAAGCCGACACAATAGGCAT	AGCGCGTTGCGCGTTCCAT
<i>PsbO</i>	CTCGAAACTTCCTCGGCTC	AATCCGGCGATTTTGACAG
<i>PORB</i>	GCAATGCTGCGGTTTATTTTC	GAGAAGAAAATGTCCCAAATGG
<i>rpoB</i>	GCGAAAGAATCCTCCTATGC	CCACCTCACATCAATAACTC
<i>CAB2</i>	TCGCAAGGAACCGTGAGCTA	AGCCTTGAACCAAACCTGCCT
<i>RbcS</i>	CCTAGACCCTCCGATCACTC	GGTTTGGTCTAGTGCTTTGG

METHODS USED IN SUPPLEMENTARY MATERIALS

Observation of embryo development

To examine the development of the embryos, ovules from the self-fertilising heterozygous siliques at different developmental stages were treated with a clearing solution of chloral hydrate, water, and glycerol (8:3:1, w/v/v) for 12 h. The developing embryos were then analysed under an optical microscope (Motic).