Supplemental Data

MscS-like Proteins Control Plastid Size and Shape in *Arabidopsis thaliana*

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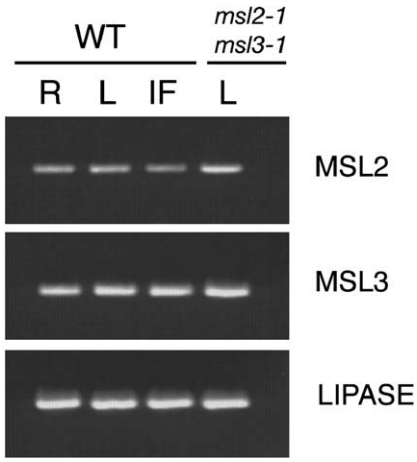

Figure S1. MSL2 and MSL3 Transcripts Are Widely Expressed and Are Present in the *msl2-1; msl3-1* Double Mutant

Reverse-transcriptase PCR analysis of *MSL2* (At5g10490) and *MSL3* (At1g58200) transcripts derived from root (R), leaf (L), and inflorescence (IF) tissue from wild-type and *msl2-1; msl3-1* double-mutant plants. *LIP* (At1g10740) was used as a loading control. First-strand cDNA generated from 2 μg of DNase-treated RNA was amplified for 20 cycles with HotStar Taq polymerase (Qiagen) and the following primer pairs: LIP.F/LIP.R for *LIPASE*, 10490.F1/MS.R for *MSL2*, and 58200.F1/58200.R3 for *MSL3*. The amplified portions of *MSL2* and *MSL3* are upstream of the mapped insertion sites in *msl2-1* and *msl3-1* lines, and both span multiple introns.

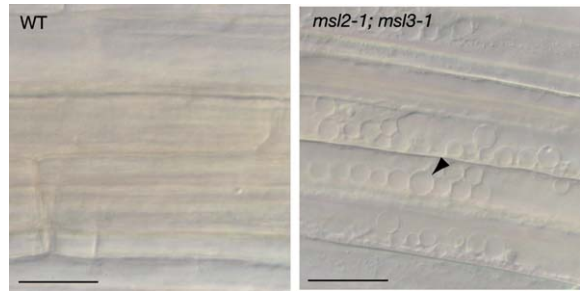

Figure S2. Amyloplasts Are Shaped Normally in the *msl2-1; msl3-1* Mutant

Confocal images of plastids from wild-type and *msl2-1; msl3-1* plants expressing the pRecARed plastid marker. Fluorescence images are overlaid with DIC images to show the outline of cells. Amyloplasts in the seedling root tip are marked with arrows. The size bars represent 25 μm.

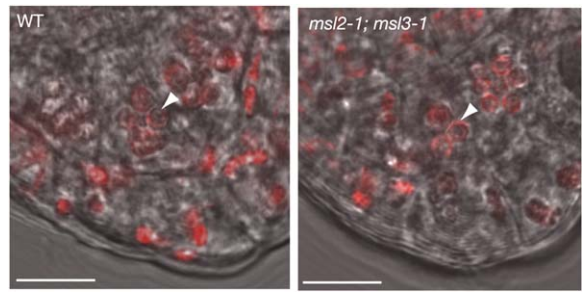

Figure S3. Spherical Plastids Are Present in *msl2-1; msl3-1* Mutants in the Absence of the pRecARed Plastid Marker

DIC light microscopy of root epidermis. Round plastids in the *msl2-1; msl3-1* mutant are indicated with an arrow and are not present in wild-type tissue. The size bars represent 10 μm.

Table S1. Name, Sequence, and Application for Oligos Referred to in Experimental Procedures

Name	Sequence	Use
JL-202	CATTTTATAATAACGCTGCGGACATCTAC	genotyping
MS2-WISB	TTACATCATGACTAGAGACAGGTAAGCTA	genotyping
MS3-WISB	TTTCTCCGTTTCTGTTTGTTACTTTCTAC	genotyping
10490.F5	TGAAGACGTCTCATCATCACGAAG	genotyping
58200.F5	TCCAGAGAACCAAGCCCTTA	genotyping
LIP.F	GTGTGAGAGGTCTCGTTGATTGCC	RT-PCR
LIP.R	TTCCTGCAACGTTGGAAGATGCTGTC	RT-PCR
10490.F1	ATGACTTCATATGTTCAACCTCTGTTAC	RT-PCR
MS.R	CACCTCTGATGATTGTAGGTGACCACCA	RT-PCR
58200.F1	ATGATGATGCGTACTGTTGCTTTAC	RT-PCR
58200.R3	CCCATGTAGCAAATGCAAGAATCC	RT-PCR
MscS.F	CCCAAGCTTGAAGATTTGAATGTTGTCGATAGC	bacterial expression
MscS.R2	ACGCGTCGACCGCAGCTTTCTCTTCTTTC	bacterial expression
MS3.Eco	GGAATTCCCGTACTGTTGCTTTACC	bacterial expression
MS3.Sal	CGCGTCGACTTCTGATCCAATACCAAG	bacterial expression
MS3tR.Eco	GGAATTCTGGGCTGGGTGACTTTTG	bacterial expression
MS2g.R	GGAAAGTGAATACGCGAGAACGAC	complementation
MS3g.R	GGTGTATTTTCATTGGTATTTCAACTATATTCCATG	complementation
10490.F1B	CACCATGACTTCATATGTTCAACCTCTGTTAC	GFP fusion
10490.R2	CGGCTCGGTTGAAGCACC	GFP fusion
58200.F1B	CACCATGATGATGCGTACTGTTGCTTTAC	GFP fusion
58200.R2	TTCTGATCCAATACCAAGTTCTTCTGAATC	GFP fusion
2.newATG.F	ATAAGAATGCTTCCGCATGGCCCTTTATGGTACA	GFP fusion
2.newATG.R	GGAATTCCATATGAAGTCATAACATGGTACGTACCAC	GFP fusion
10490p.F1	CACCCTGGAGGTTTCGTTCATGAC	GUS reporter
10490p.R2	ATTTTAATCAGATTCAATGACTTAGCCAGTAACGTT	GUS reporter
58200p.F1	CACCCACAACTTCTTCGATAGTGG	GUS reporter
58200p.R1	CCCAAATGTACAAAACAATGATCAAC	GUS reporter
RecA.F	CACCATGGATTCACAGCTAGTCTTG	RecARED plastid marker
RecA.R	GTCGCGATCGAATTCAGAACTGATTTTGTG	RecARED plastid marker
dsRed.F	CTGAAGTCGATCGCGACATGGCCTCCTCCGAG	RecARED plastid marker
dsRed.R	CTACAGGAACAGGTGGTGGC	RecARED plastid marker
MinE.F	ACGCGTCGACATGGCGATGTCTTCTGGAAC	CFP fusion
MinE.R	GGAATTCCTCTGGAACATAAAAATCGAACCTGA	CFP fusion
MSL2BF.Sal	ACGCGTCGACATGGCCCTTTATGGTACATTG	YFP fusion
MSL2R.Eco	GGAATTCCGGCTCGGTTGAAGC	YFP fusion
MSL3F.Sal	ACGCGTCGACATGATGATGCGTACTGTTGCTTTAC	YFP fusion
MSL3R.Eco	GCGGAATTCTTCTGATCCAATACCAAGTTCTTCTGA	YFP fusion