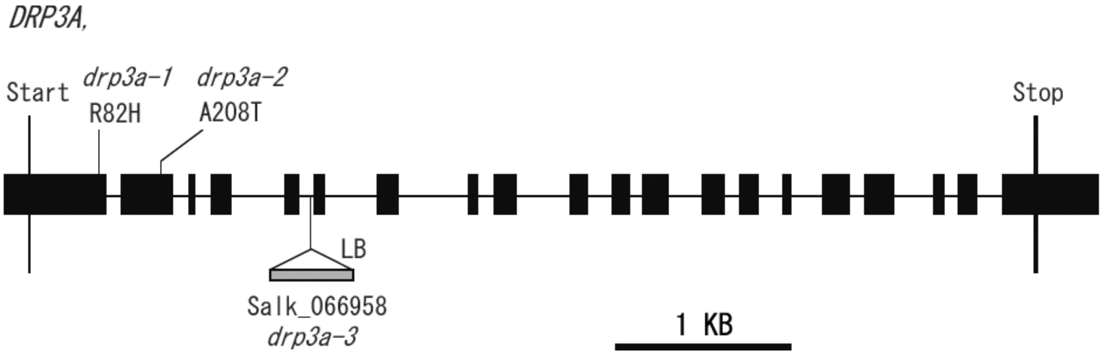
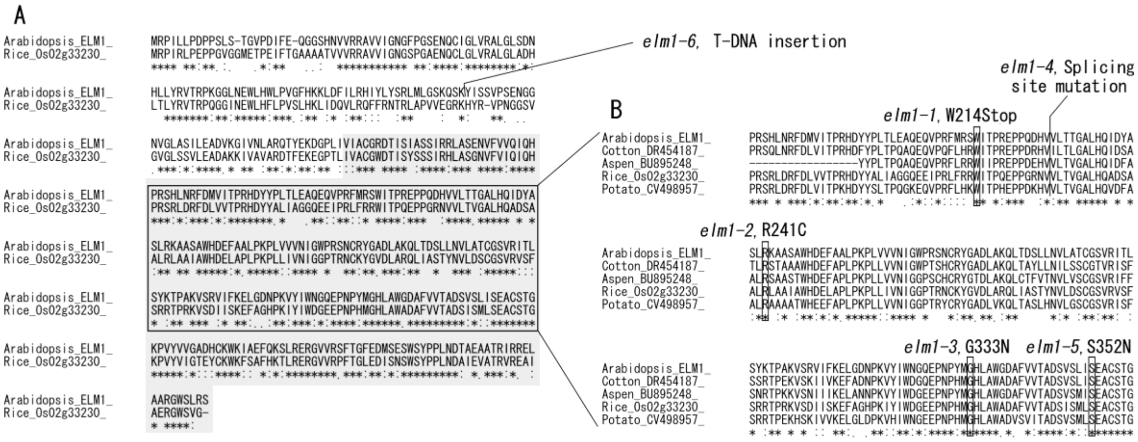
Supplemental Data. Arimura et al. (2008). *Arabidopsis* ELONGATED MITOCHONDRIA 1 is required for localization of DYNAMIN-RELATED PROTEIN 3A to mitochondrial fission sites.



Supplemental Figure 1. Two mutants with elongated mitochondria have nucleotide substitutions in the *DRP3A* gene.

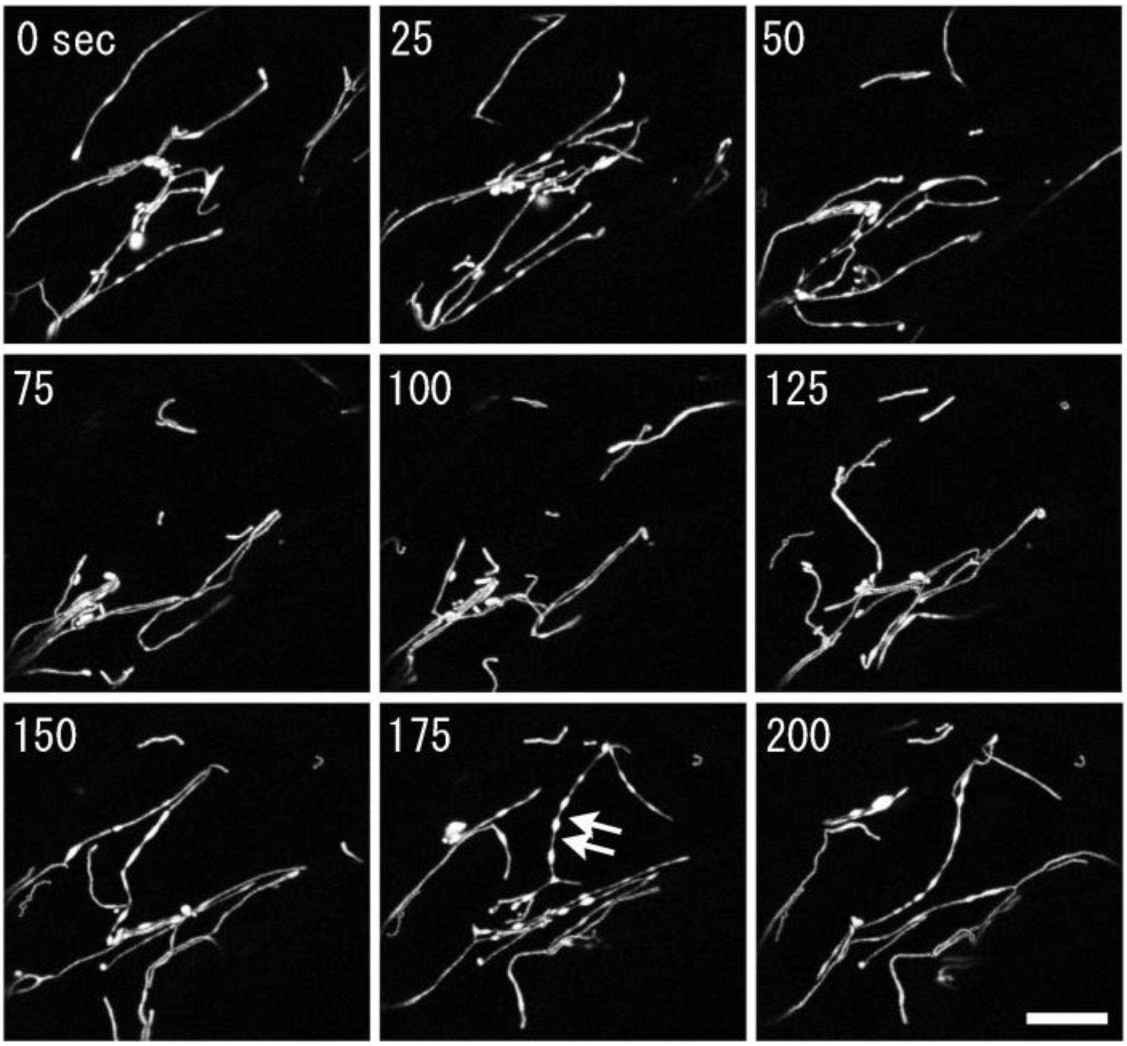
The point mutation sites and corresponding amino acid substitutions resulting in *drp3a-1* and *drp3a-2* are shown in a scheme of the *DRP3A* gene. R in position 82 of the wild type is replaced with H in *drp3a-1* and A in position 208 of the wild type is replaced with T in *drp3a-2*.

Boxes indicate exons, and solid lines indicate introns. A T-DNA-tagging allele (*drp3a-3*) is also shown.



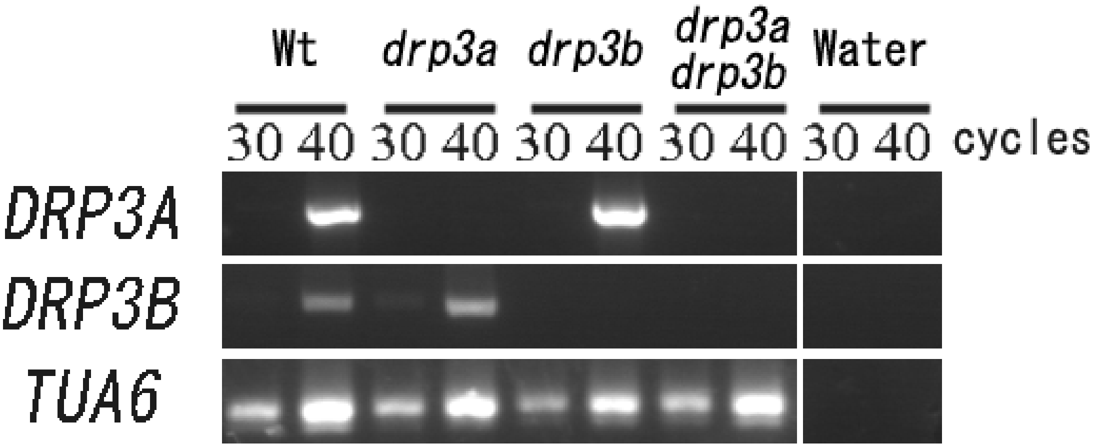
Supplemental Figure 2. Amino acid sequence alignments of ELM1 and its homologues in other plants.

A. An alignment between deduced amino acid sequences of *Arabidopsis* ELM1 and Rice Os02g33230 (identity 62.8% and similarity 86.7%). Shaded area shows the region similar to the bacterial sequences. B. A partial alignment between deduced amino acid sequences of *Arabidopsis* ELM1, Rice Os02g33230, cotton EST (*Gossypium hirsutum*, accession no. DR454187), aspen EST (*Populus tremula* x *Populus tremuloides*, BU895248) and potato EST (*Solanum tuberosum*, CV498957). An NCBI tblastn search for sequences similar to ELM1 found many ESTs from spermatophytes (seed plants) including eudicots, monocots and conifers, all with e values <1e-75. The aligned region in B matches to the region boxed in A. The mutated amino acids (and deduced splice defected region) in 5 *elm1* alleles are shown. Identical amino acids are marked with '*', and similar amino acids are indicated with ':' and '.' at their bottoms. ":" means that conserved substitutions have been observed. "." means that semi-conserved substitutions are observed.



Supplemental Figure 3. Mitochondria in *elm1-1* move and change their morphology.

Time course serial images of mitochondria (labeled with Mt-GFP) in *elm1-1* were taken by confocal laser scanning microscopy. Numbers in each figure show seconds after the start of the observation. Scale bar shows 10 µm. All 60 images taken at 5-second intervals are shown in Supplemental movie 1 online. Arrows in the 175-second frame indicate constriction sites in mitochondria with a beads-on-a-string shape.



Supplemental Figure 4. Full-length ORF transcripts of *DRP3A* and *DRP3B* were not detected in T-DNA insertion mutants.

RT-PCR of *DRP3A*, *DRP3B* and *TUA6* (α Tubulin 6, an internal control) in wild-type (Wt) and mutant (*drp3a*, *drp3b* and *drp3a drp3b*) plants. *drp3a* refers to *drp3a-3*. Primer sets used here are shown in Supplemental Table 1 online. This is a representative data set of 3 biological and 2 technical repeats. DNA in gels was stained by Sybr Gold (Invitrogen).

Supplemental Table 1. Oligonucleotide primer sequences.

Primer name	Gene	Sequence (5'-3')	Purpose
NP350TOPOF0	*ELM1*	CACCTTAACGATTCTTGTCTCC	Genomic ELM1 and ELM1pro:ELM1:GFP
NP350TOPOR0	*ELM1*	GGTCACGTGCGTGAAACATTG	Genomic ELM1
NP350G TOPOr-2	*ELM1*	AGACCGTAAACTCCATCCAC	ELM1pro:ELM1:GFP
350 TOPO Fw	*ELM1*	CACCATGAGGCCAATCCTATTGCC	ORF cloning, Yeast 2 Hybrid
350 RvT	*ELM1*	TCAAGACCGTAAACTCCATCC	ORF cloning, Yeast 2 Hybrid
FIS1aTOPOfw	*BIGYIN*	CACCATGGATGCTAAGATCGGAC	ORF cloning, Yeast 2 Hybrid
FIS1aTr1rv	*BIGYIN*	TCACTTTGTGATTTTGTCTTCGA	ORF cloning, Yeast 2 Hybrid
TUA6fw	*α Tubulin 6*	ATGAGAGAGTGCATTTCGATC	RT-PCR
TUA6rv	*α Tubulin 6*	TAGTATTCCTCTCCTTCATC	RT-PCR
ADL2b B1 Fw	*DRP3B*	AAAAAGCAGGCTCAATGTCCGTCGACGATCTCCC	ORF cloning, Yeast 2 Hybrid
ADL2b B2 RevT	*DRP3B*	AGAAAGCTGGGTTTTACATATGAAGCCGTCCGT	ORF cloning, Yeast 2 Hybrid
ADL2a B1 FW	*DRP3A*	AAAAAGCAGGCTCGATGACTATTGAAGAAGTTTC	ORF cloning, Yeast 2 Hybrid
ADL2a B2 RevT	*DRP3A*	AGAAAGCTGGGTTTAGAATCCGTATCCATTTTG	ORF cloning, Yeast 2 Hybrid
Salk T-DNA LBb1	*T-DNA*	GCGTGGACCGCTTGCTGCAACT	T-DNA
ADL2a Ex7 Fw	*DRP3A*	GGTGAATTAACAGAATCAAGG	RT-PCR
ADL2a Ex8 Rev	*DRP3A*	CTTCACAGTATTTGGAGAG	RT-PCR
ADL2abF4	*DRP3B*	TACTATGACATTGTAAGGAAGAAT	RT-PCR
ADL2bR1	*DRP3B*	TTAGAATCCGTATCCATTTTG	RT-PCR
DRP3A pro B1fw2	*DRP3A*	AAAAAGCAGGCTGTTGGGTATGACAAGTGAGTC	DRP3Apro:DRP3A:GFP
nP DRP3A rv	*DRP3A*	TCTTCAATAGTCATCGTTGGATCGGATTTTGAATG	DRP3Apro:DRP3A:GFP
nP DRP3A fw	*DRP3A*	AATCCGATCCAACGATGACTATTGAAGAAGTTTCC	DRP3Apro:DRP3A:GFP
DRP3A B2 RevG	*DRP3A*	AGAAAGCTGGGTAGAATCCGTATCCATTTTGG	DRP3Apro:DRP3A:GFP