**Supplementary Information**

# GDP-D-mannose epimerase regulates male gametophyte development, plant growth and leaf senescence in *Arabidopsis*

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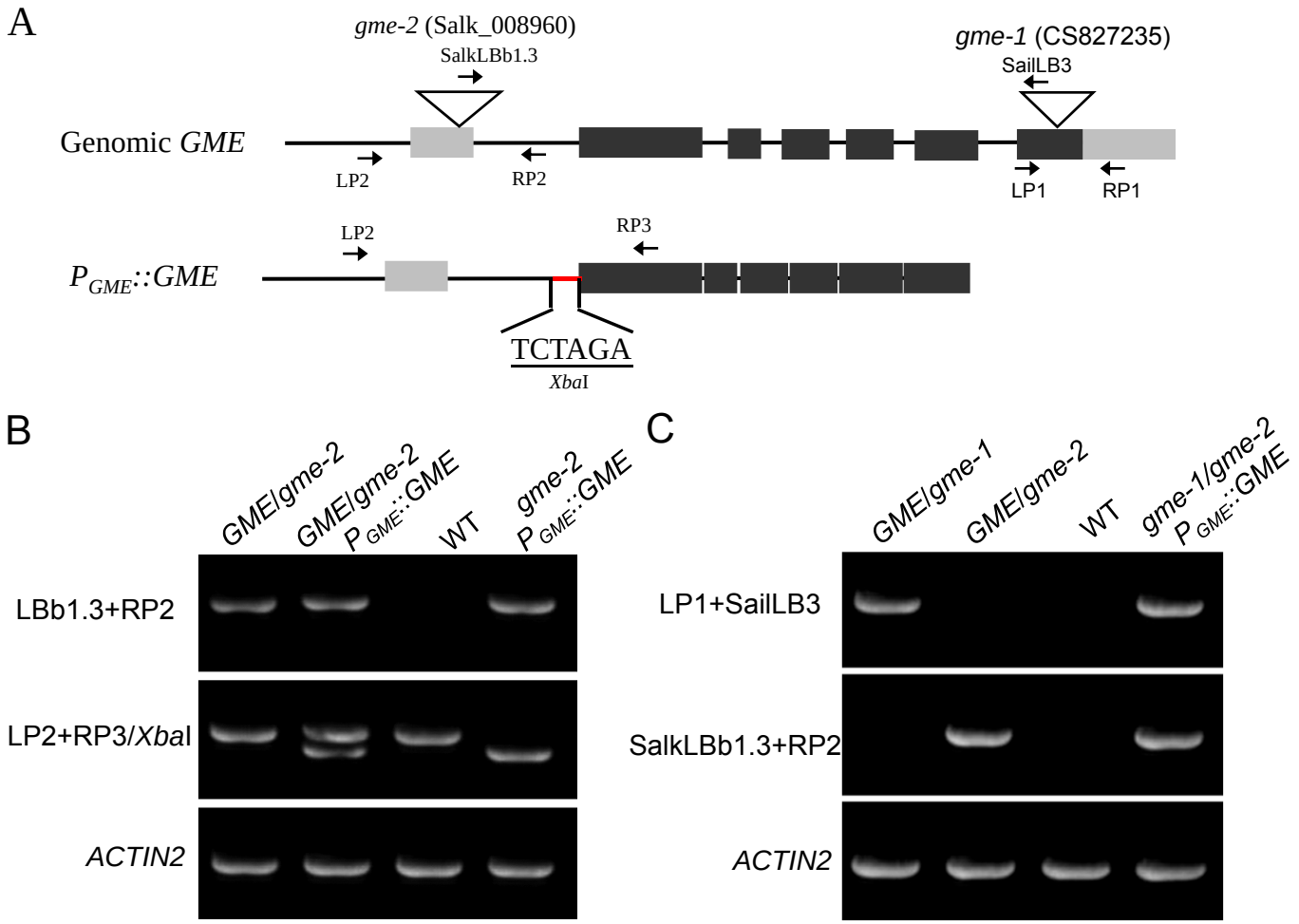



**Supplemental Figure 1. Genotyping of *gme* mutants and complementary transgenic lines.**

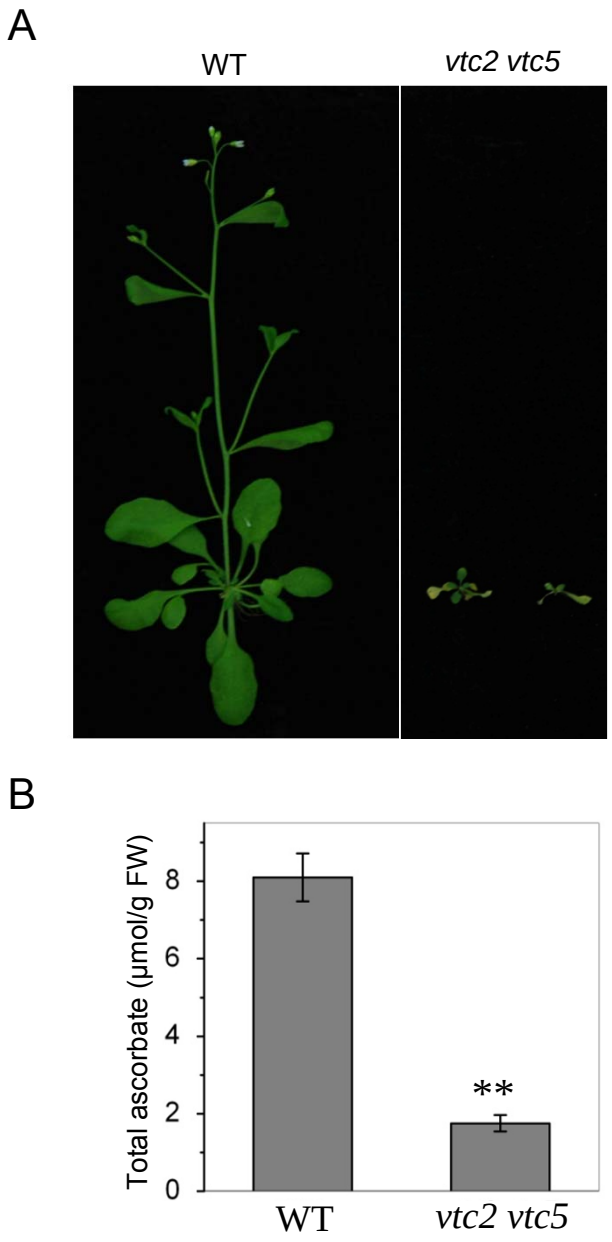
(A) Schematic diagrams showing the T-DNA insertion site in *gme-2*, and the $P_{GME}$::*GME* vector. The grey rectangle, black rectangle and triangle represent the UTR, exon, and T-DNA insertion site, respectively. The red line indicates the inserted artificial sequence in the $P_{GME}$::*GME* vector. The primers indicated by arrows were used to identify the mutant background in (B) and (C).

(B) PCR to identify the genetic background of the *GME*/*gme-2*, *GME*/*gme-2* $P_{GME}$::*GME*, WT and *gme-2*/*gme-2* $P_{GME}$::*GME* plants. The top panel shows the PCR products for the *gme-2* T-DNA insertion using primers RP2 and LBb1.3. The middle panel shows the results of the digestion of the PCR products amplified by primers LP2 and RP3 with *Xba*I. The bottom panel shows the PCR products for *ACTIN2* as a control.

(C) PCR to identify the genetic background of the *GME*/*gme-1*, *GME*/*gme-2*, WT and *gme-1*/*gme-2* $P_{GME}$::*GME* plants. The top and middle panels, respectively, show the PCR products for the *gme-1* T-DNA insertion (LP1 and LB3) and *gme-2* T-DNA insertion (LP2 and LBb1.3). The bottom panel shows the PCR products for *ACTIN2* as a control.


**Supplemental Figure 2. Phenotype of a *GME/gme-1* heterozygous plant.**

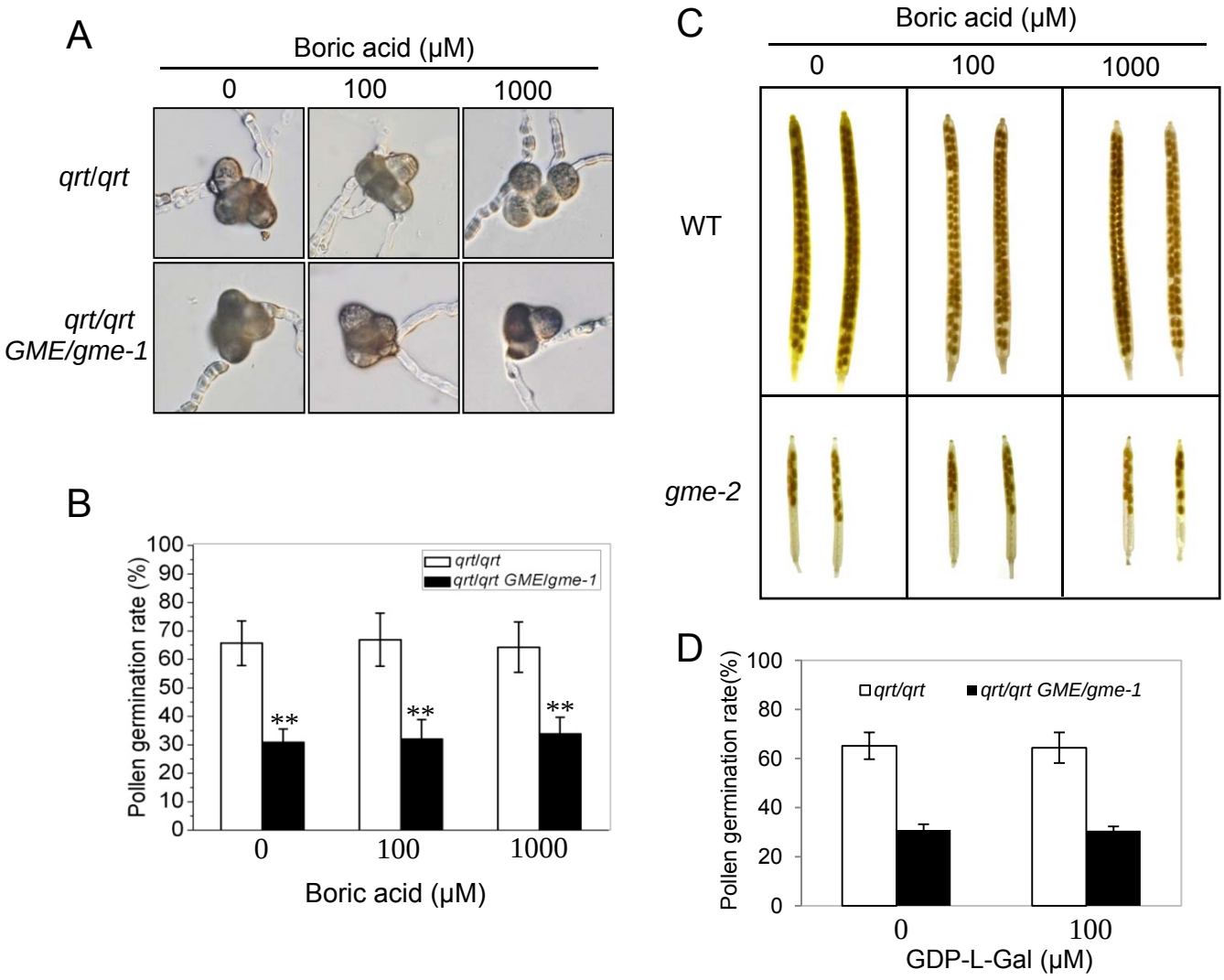
Six-week-old WT and *GME/gme-1* plants (top). The siliques were bleached with ethanol and imaged (bottom). As shown, the *GME/gme-1* plant grew normally and exhibited similar fertility to wild type.




**Supplemental Figure 3. Plant phenotype and total ascorbate content in the *vtc2 vtc5* double mutant.**

(A) Morphology of 5-week-old WT and *vtc2 vtc5* double mutant plants.

(B) Total ascorbate contents in the leaves of 4-week-old Col-0 WT and *vtc2 vtc5* plants. Error bars represent the SE (n=3). Asterisks represent Student's *t*-test significance compared with wild type (*P<0.05, **P<0.01).

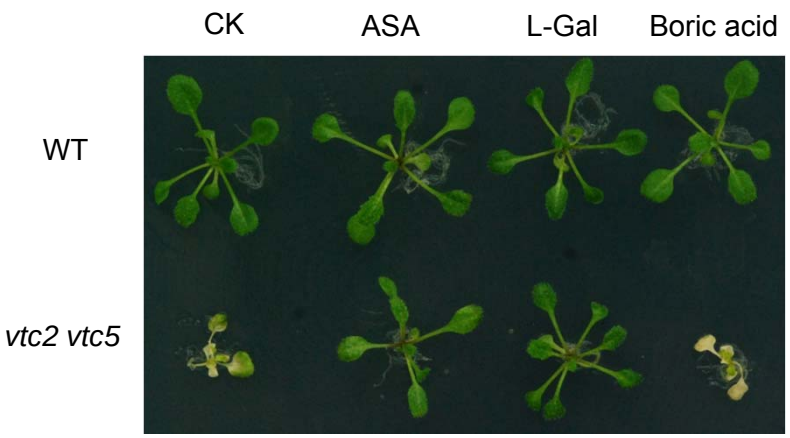



**Supplemental Figure 4. Treatment with boric acid or GDP-L-Gal could not rescue the fertility of the *gme* mutant.**

(A and B) *In vitro* pollen germination (A) and the pollen germination rates (B) of *qrt/qrt* and *qrt/qrt GME/gme-1* on pollen germination medium containing the indicated concentrations of boric acid. Error bars represent the SE (n=3).

(C) Inflorescences of 5-week-old WT and *gme-2* plants were treated with 0, 100 or 1000 μM boric acid for 10 days. The siliques were derived from flower buds of WT and *gme-2* plants treated with 0, 10 or 100 μM boric acid. Asterisks represent Student's *t*-test significance compared with *qrt*/*qrt* (**P<0.01).

(E) The pollen germination rates of *qrt/qrt* and *qrt/qrt GME/gme-1* on pollen germination medium containing the indicated concentration of GDP-L-gal sodium salt. Error bars represent the SE (n=3).




**Supplemental Figure 5. The growth of *vtc2 vtc5* could be rescued by treatment with ASA or L-Gal.**

Three-week-old seedlings of Col-0 WT and *vtc2 vtc5* double mutant plants grown on boric acid-free MS medium treated with mock, 100 μM ASA, 100 μM L-Gal or 100 μM boric acid.

Supplemental Table 1. Genetic transmission analysis of *vtc2* and *vtc5* alleles

| Genotype | T-DNA$^+$ | T-DNA$^-$ | TE(%) |
|---|---|---|---|
| ♀ WT × ♂ *VTC2/vtc2 vtc5/vtc5* | 134 | 141 | 48.7 |
| ♀ *VTC2/vtc2 vtc5/vtc5* × ♂WT | 107 | 101 | 51.4 |
| ♀ WT × ♂ *vtc2/vtc2 VTC5/vtc5* | 103 | 108 | 48.8 |
| ♀ *vtc2/vtc2 VTC5/vtc5* × ♂WT | 112 | 108 | 50.9 |

Progeny containing a T-DNA insertion (*vtc2* for the top two panels and *vtc5* for the bottom two panels) were identified by PCR. Transmission efficiency (TE)=Number of progeny with a T-DNA insertion/Number of progeny×100%. WT, Col-0 wild type.

**Supplemental Table 2. Primers used for identification of *gme* T-DNA mutants and generation of constructs.**

| | |
|---|---|
| *gme-1*(CS827235)-LP1 | GACAAAATCAGATTTCCGTG |
| *gme-1*(CS827235)-RP1 | GCTGAACTTAAAAGGCCATATTTG |
| *gme-1*(CS827235)-SAILB3 | TAGCATCTGAATTTCATAACCAATCTCGATACAC |
| *gme-2*(SALK_008960)-LP2 | TTCCTCTTCCTCAAATCTCTG |
| *gme-2*(SALK_008960)-RP2 | AGAGTTTTGACAGAGGTAAG |
| *gme-2*(SALK_008960)-SalkLBb1.3 | ATTTTGCCGATTTCGGAAC |
| *GME*-LP2 | TTCCTCTTCCTCAAATCTCTG |
| *GME*-RP3 | AATCACAGAGTGATTACTCTG |
| *GME* pro-HindIII-Forward | CCCAAGCTTGATCAAGATGACTAATTTAAC |
| *GME* pro-XbaI-Reverse | CTAGTCTAGATCTACATTAACAAAACAAATCTG |
| *GME*-XbaI-Forward | TGCTCTAGAATGGGAACTACCAATGGAACAG |
| *GME*-SacI-Reverse | ATCGAGCTCTCACTCTTTTCCATCAGCCGC |
| *35S::GME*-GFP-EcoRI-Forward | CCGGAATTCATGGGAACTACCAATGGAACAGACTATG |
| *35S::GME*-GFP-BamHI-Reverse | CGCGGATCCTCACTCTTTTCCATCAGCCGC |
| *35S::GME*-GFP-XhoI-Forward | ACCGCTCGAGATGGGAACTACCAATGGAAC |
| *35S::GME*-GFP- EcoRI-Reverse | GGGGAATTCGCTCTTTTCCATCAGCCGCGC |
| *GME*-Realtime-Forward | GGAGCTGGAGGTTTCATTGC |
| *GME*-Realtime-Reverse | CGTAATGACCTTCGTGCTTCAA |
| *GME*-RT-Forward | ATGCTTCGAGTGCTTGTATC |
| *GME*-RT-Reverse | GAAAGCAGCTGGAGCCTTCTC |
| *vtc2-2*(CS876707)-LP | CGGAGAGGTAAATCATAGAC |
| *vtc2-2*(CS876707)-RP | CCATACTCTATCGGACTAAC |
| *vtc2-2*(CS876707)-SAILB3 | TAGCATCTGAATTTCATAACCAATCTCGATACAC |
| *vtc5-2*(SALK_135468)-LP | GCTGAAGCCGATAATCCGTA |
| *vtc5-2*(SALK_135468)-RP | CCTCCATGCCTTCTCTTCTG |
| *vtc5-2*(SALK_135468)-SalkLBb1.3 | ATTTTGCCGATTTCGGAAC |
| *CAB1*-Realtime-Forward | GCAAGGAACCGTGAACTAGAA |

| | |
|---|---|
| *CAB1*-Realtime-Reverse | TCCGAACTTGACTCCGTTTC |
| *CAB2*-Realtime-Forward | TCAATCTTTTGAATTCGAGTGAGA |
| *CAB2*-Realtime-Reverse | TCCACCACAAACACAAACCTAC |
| *RBCS*-Realtime-Forward | CGCTCCTTTCAACGGACTTA |
| *RBCS*-Realtime-Reverse | AGTAATGTCGTTGTTAGCCTTGC |
| *SAG13*-Realtime-Forward | AGGAAAACTCAACATCCTCGTC |
| *SAG13*-Realtime-Reverse | GCTGACTCGAGATTTGTAGCC |
| *SAG21*-Realtime-Forward | CATTCCTCGGATATATCTCTCCTT |
| *SAG21*-Realtime-Reverse | TTCTTGAAAAGAGAGAAAACAGACTTT |
| *SEN4*-Realtime-Forward | AAGGTGACAAAGAGCAACAATTC |
| *SEN4*-Realtime-Reverse | CTCTCTAATGGGTGTGTCATCG |
| *ACTIN2*-RT-Forward | GCACCCTGTTCTTCTTACCG |
| *ACTIN2*-RT-Reverse | AACCCTCGTAGATTGGCACA |
| *ACTIN2*-Realtime-Forward | CCGCTCTTTCTTTCCAAGC |
| *ACTIN2*-Realtime-Reverse | CCGGTACCATTGTCACACAC |