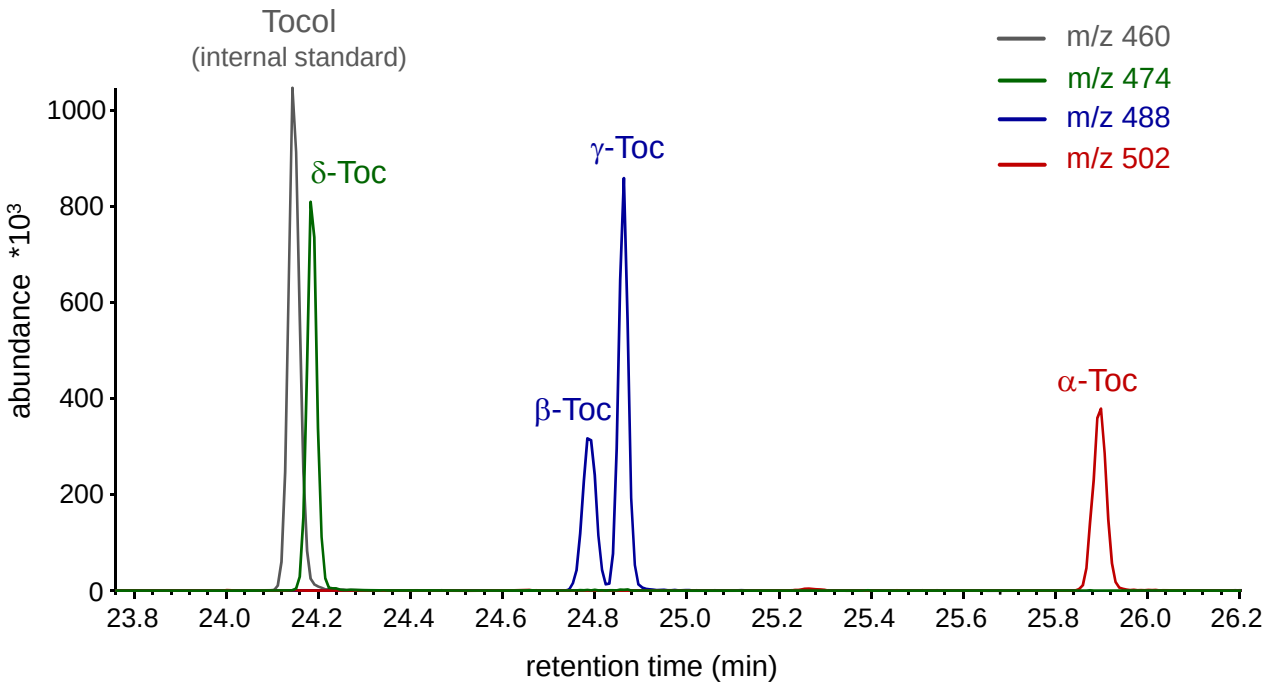
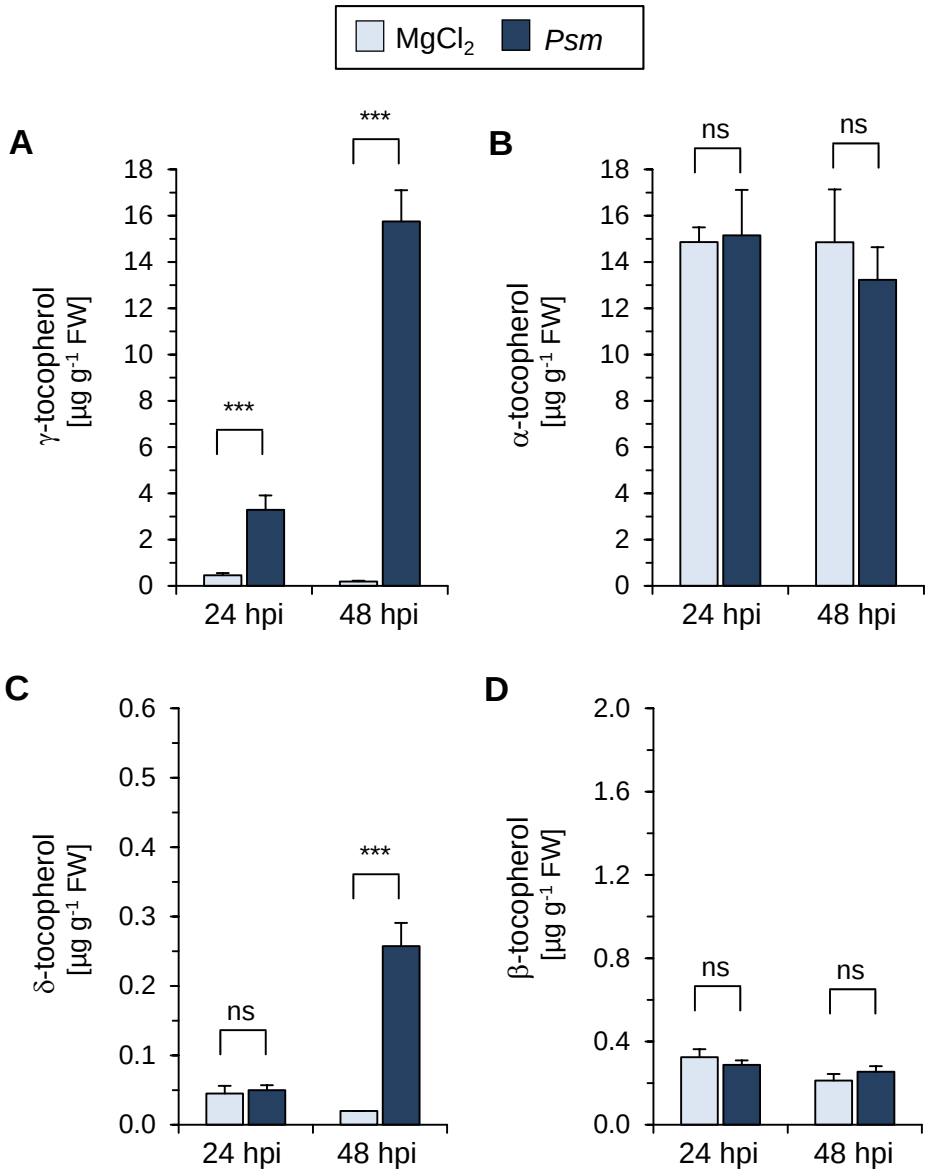


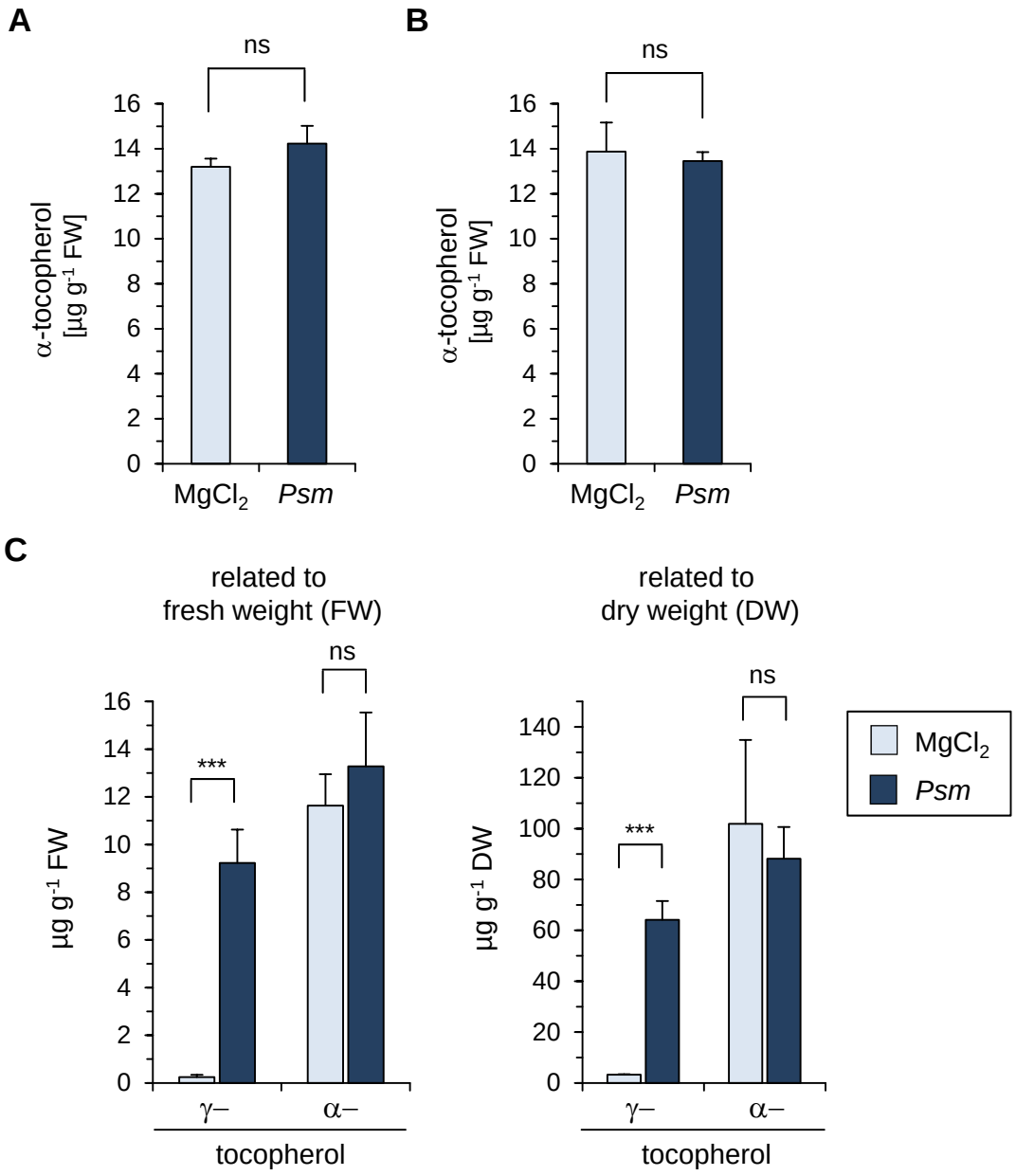
Supplemental Figure S1. Gas chromatography-mass spectrometry-based analysis of tocopherols.

A GC-MS-based procedure using sample derivatization with N-methyl-N-trimethylsilyl-trifluoroacetamide to produce mono-trimethylsilylated tocopherols was employed in this study for the analysis of tocopherols in leaf extracts. Overlaid ion chromatograms used for the quantitative determination of tocopherols are shown (m/z 502: α-tocopherol; m/z 488: β- and γ-tocopherol; m/z 474; δ-tocopherol). An equimolar mix of authentic tocopherols was analyzed here to illustrate the method. Tocol (m/z 460) served as an internal standard.



Supplemental Figure S2. Time-dependent accumulation of tocopherols upon *Psm*-inoculation.

Endogenous levels of γ-tocopherol (A), α-tocopherol (B), δ-tocopherol (C), and β-tocopherol in treated (local) leaves of Arabidopsis Col-0 plants at 24 and 48 h following mock-control treatment ($MgCl_2$) or *Psm*-inoculation. The figure is related to Fig. 3 and depicts the results of an independent experiment. Values represent the mean ± SD of four replicate leaf samples from different plants. Asterisks denote statistically significant differences between control and *Psm*-samples (***P < 0.001, ns: not significant; two tailed *t* test).



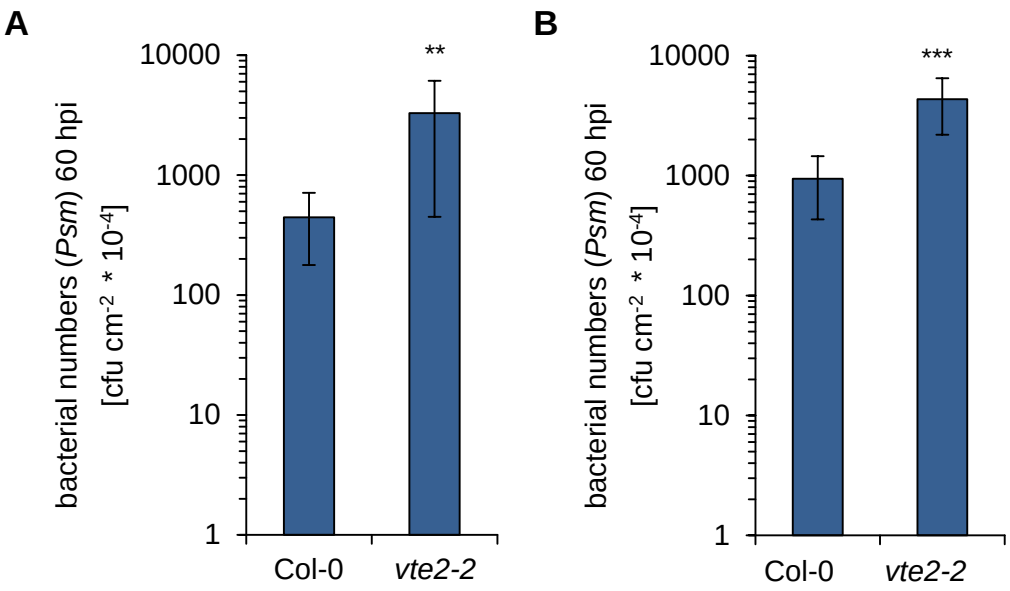
Supplemental Figure S3. Levels of α-tocopherol in *Psm*-inoculated leaves.

Endogenous levels of α-tocopherol in treated (local) leaves of Arabidopsis Col-0 plants at 48 h post mock-control treatment ($MgCl_2$) or *Psm*-inoculation. The figure is related to Fig. 3 and Supplemental Fig. S2. The figure depicts the results of three further experiments.

A and B, Leaf α-tocopherol levels from two different experiments. Levels are related to fresh weight (FW).

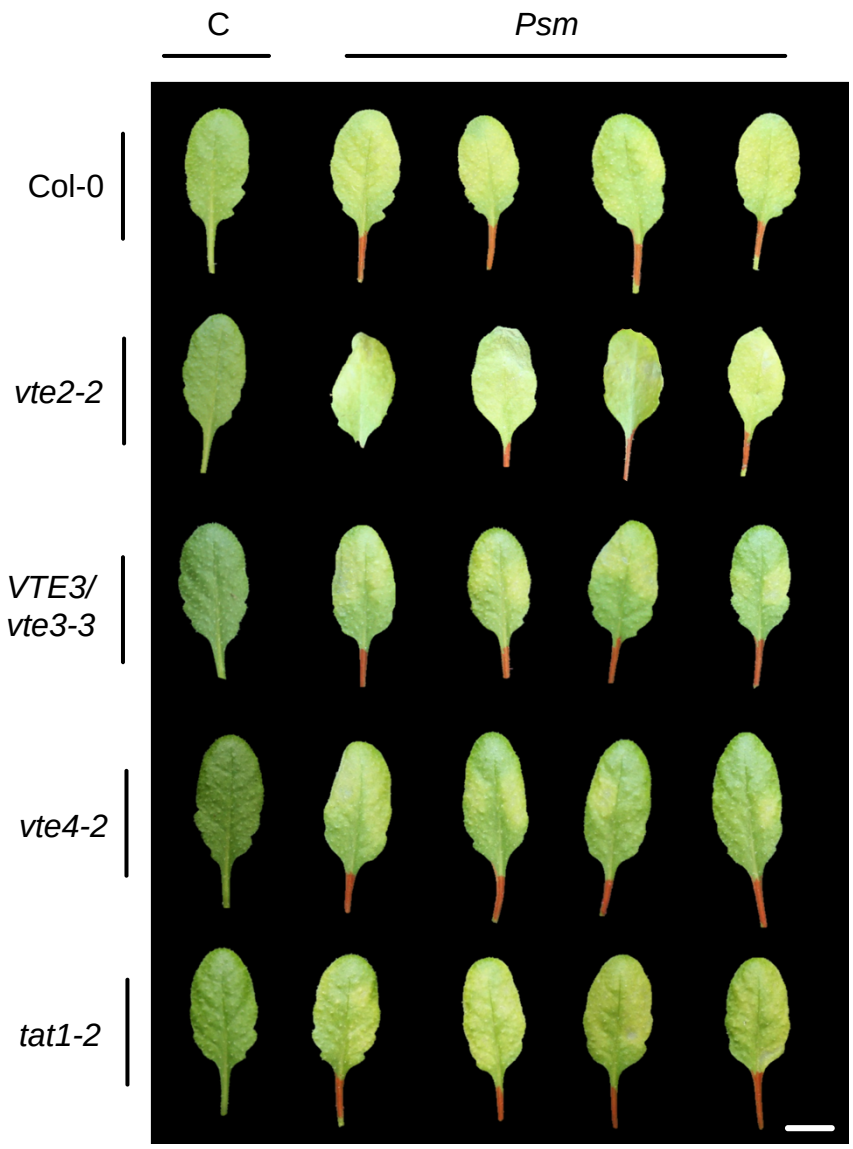
C, Leaf γ- and α-tocopherol levels from another experiment. Levels were related to both fresh weight (left) and dry weight (right).

Values represent the mean ± SD of three replicate leaf samples from different plants. Asterisks denote statistically significant differences between control and *Psm*-samples (***P < 0.001, ns: not significant; two tailed *t* test).



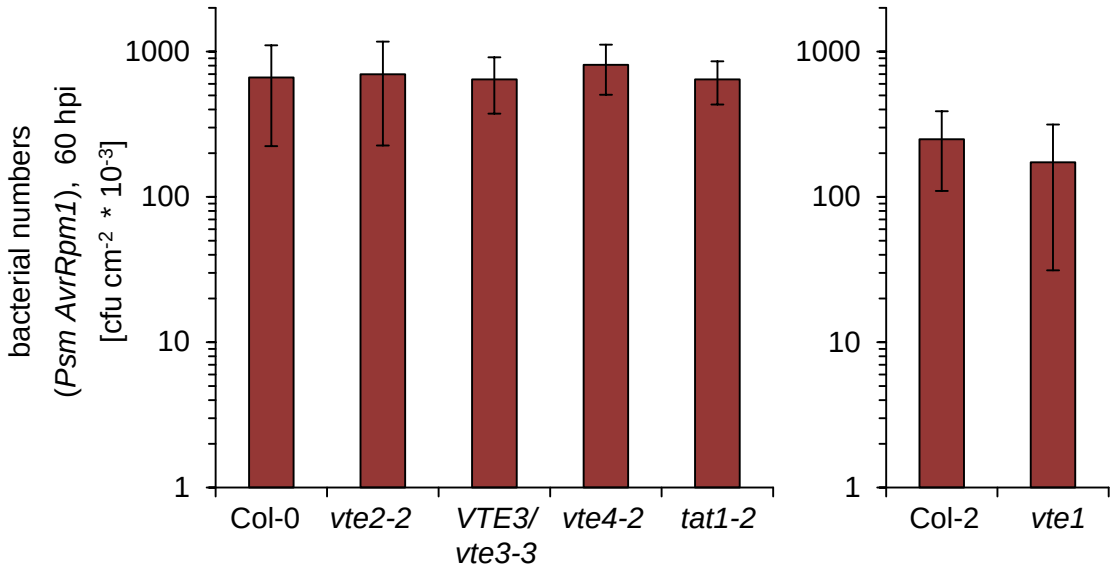
Supplemental Figure S4. *vte2* mutant plants are compromised in basal resistance to *P. syringae*.

Basal resistance to *Psm* infection of Arabidopsis *vte2-2* mutant and Col-0 wild-type plants. Results from two independent experiments (A and B) are shown. Three leaves of naïve plants were inoculated with bioluminescent *Psm lux* (OD_{600} = 0.001), and bacterial numbers in leaves were assessed 60 h later. Data represent the mean ± SD of growth values from at least 10 replicate plants. Asterisks denote statistically significant differences between growth values in Col-0 and *vte2-2* plants. (***P < 0.001 and **P < 0.01; two tailed *t* test). See also Fig. 6 (A-C).



Supplemental Figure S5. Disease symptoms of leaves of Col-0, *vte2-2*, *VTE3/vte3-3*, *vte4-2*, and *tat1-2* plants inoculated with compatible *Psm*.

Leaves were cut from plants at 60 h post inoculation with *Psm lux* (applied in titers of OD_{600} = 0.001), assembled, and jointly photographed. C (control): non-inoculated leaves. White scale bar = 1cm.

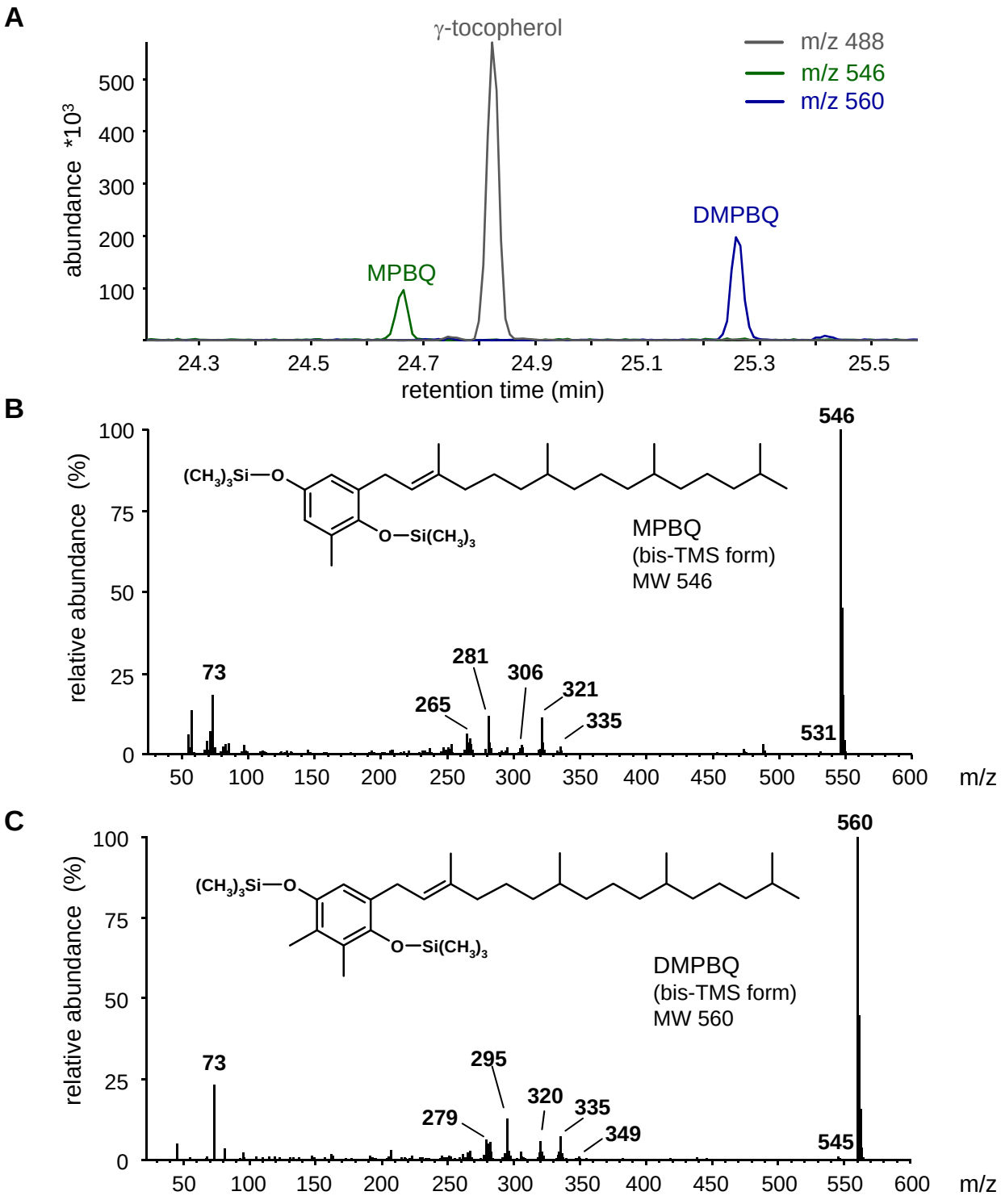


Supplemental Figure S6. Resistance against avirulent *Psm avrRpm1* of tocopherol biosynthetic mutants is similar to the wild type.

Bacterial growth quantification of *Psm* carrying the *avrRpm1* avirulence gene (*Psm avrRpm1*) in leaves of different Arabidopsis lines. Three leaves of each plant were inoculated with *Psm avrRpm1* (OD_{600} = 0.001), and bacterial numbers in leaves were assessed 60 h later by leaf homogenization and a plating assay. Data represent the mean ± SD of growth values from at least 8 replicate plants.

A, Col-0, *vte2-2*, *VTE3/vte3-3*, *vte4-2*, and *tat1-2* plants. No statistically significant differences between genotypes were detected ($P > 0.05$, ANOVA and post-hoc Tukey HSD test).

B, Col-2 and *vte1* plants. There are no statistically significant differences between genotypes.



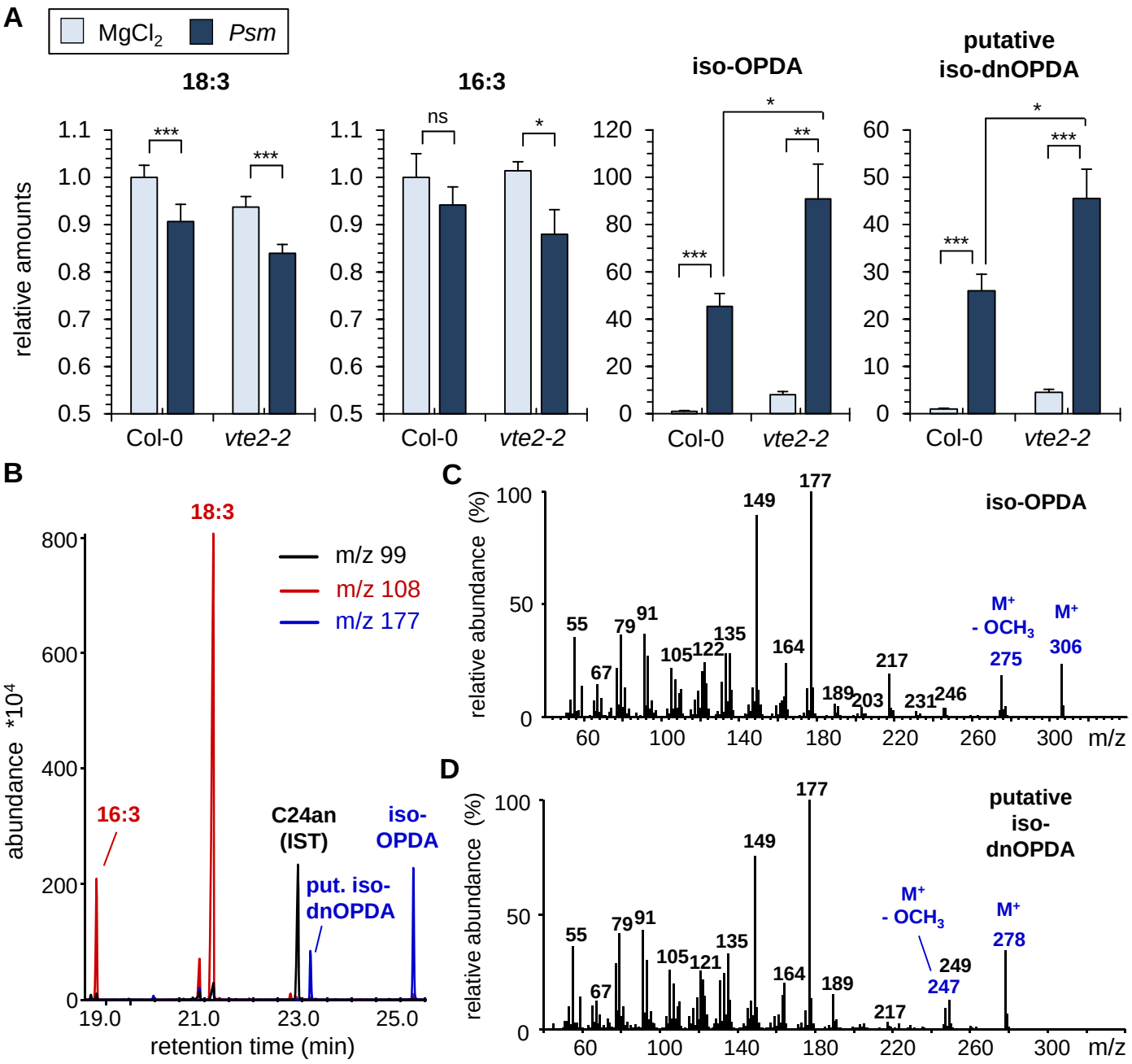
Supplemental Figure S7. GC-MS-based analysis of MPBQ and DMPBQ.

Detection of the tocopherol precursors MPBQ and DMPBQ in leaf extracts by GC-MS of trimethylsilylated extract samples.

A, Overlaid ion chromatograms m/z 546 [MPBQ, bis-trimethylsilyl (TMS)], m/z 560 (DMPBQ, bis-TMS), and m/z 488 (γ-tocopherol, mono-TMS) of an GC-MS-analyzed extract sample from *Psm*-inoculated Col-0 leaves.

B, Mass spectrum and structural formula of bis-trimethylsilylated MPBQ.

C, Mass spectrum and structural formula of bis-trimethylsilylated DMPBQ.



Supplemental Figure S8. Levels of lipid-esterified tri-unsaturated fatty acids and related oxylipins in the leaves of *Psm*-inoculated and control plants.

Leaf lipids were extracted from mock- ($MgCl_2$)-treated or *Psm*-inoculated leaves at 48 hpi, trans-esterified with BF_3/methanol, and fatty acid methyl esters identified and quantified by GC/MS.

A, Relative amounts of linolenic acid (18:3), hexadecatrienoic acid (16:3), iso-12-oxo-phytodienoic acid [iso-OPDA; as deduced from its mass spectrum (see C)], and a putative iso-dinor-OPDA homologue (mass spectrum in D). Bars represent the mean ± SD of three replicates. Values are expressed relative to the Col-0 $MgCl_2$-control samples. Asterisks above the bars denote statistically significant differences between indicated values. ***$P < 0.001$; *$P < 0.05$; ns: not significant (two-tailed *t* test).

B, GC-MS analyses of methyl esterified fatty acids. Overlaid ion chromatograms of m/z 108 (monitors 16:3 and 18:3), m/z 177 (monitors iso-OPDA and the put. iso-dnOPDA), and m/z 99 (monitors n-tetracosane (C24an), which was used for internal standardization).

C, Mass spectrum of iso-OPDA (a highly similar spectrum is reported in Dabrowska et al., 2011).

D, Mass spectrum of the putative iso-dnOPDA. The mass spectral pattern supports the interpretation of the substance being iso-dnOPDA, the ethylene homologue of iso-OPDA.

A

Gene Name	AGI Code		Mean Expression Value (± SD)		
			Mock	*Pst*	*Pst avrRpm1*
TAT1	At5g53970		106.9 ± 29.0	1893.0 ± 276.0	831.5 ± 94.4
HPPD	At1g06570		252.0 ± 46.7	1666.0 ± 146.4	736.4 ± 32.6
VTE2	At2g18950		291.8 ± 31.4	1037.2 ± 110.1	1153.9 ± 198.6
VTE3	At3g63410		2730.2 ± 197.8	442.9 ± 50.9	1029.4 ± 180.9
VTE1	At4g32770		300.2 ± 75.4	660.2 ± 61.0	419.9 ± 39.4
VTE4	At1g64970		468.6 ± 77.9	656.1 ± 59.2	500.7 ± 125.4

B

Gene Name	AGI Code		Mean Expression Value (± SD)	
			Mock	*Psm*
TAT1	At5g53970		600.8 ± 60.6	2097.5 ± 108.5
HPPD	At1g06570		580.5 ± 141.3	1833.8 ± 86.5
VTE2	At2g18950		40.9 ± 7.9	350.0 ± 79.9
VTE3	At3g63410		1186.8 ± 50.6	87.1 ± 11.7
VTE1	At4g32770		116.9 ± 25.8	78.6 ± 19.7
VTE4	At1g64970		166.6 ± 20.8	241.9 ± 20.3

Supplemental Table S1. Expression patterns of tocopherol biosynthetic genes in *Pseudomonas syringae*-inoculated *Arabidopsis thaliana* leaves according to publicly available microarray data sets.

Means of normalized expression values ± SD are given (n = 3).

A, Leaves of 5 week-old *Arabidopsis thaliana* Col-0 plants (rosette stage) were inoculated with *P. syringae* pv. *tomato DC3000* (*Pst*), *Pst avrRpm1* or infiltrated with mock-solution. Leaves were harvested at 24 hpi (TAIR-ME00331).

B, Leaves of 4-5 week-old *Arabidopsis thaliana* Col-0 plants (rosette stage) were inoculated with *P. syringae* pv. *maculicola* (*Psm*) or infiltrated with mock-solution. Leaves were harvested at 24 hpi (NASCARRAYS-414; Wang et al., 2008).

A

T-DNA line	**Primer sequence (5’ to 3’)**	
SALK_031151C *(VTE3/vte3-3)*	Left primer Right primer	CTCGGTGGCTACTAGATGCAG CAGAATTGAGTTTGGGAATCG
SALK_141402C (*tat1-2*)	Left primer Right primer	CTACCAAAAGCAAGATGACCG AGTTGCACCGAAACACTCAAC
Left border primer	**Primer sequence (5’ to 3’)**	
SALK	SALK_LBb1.3	ATTTTGCCGATTTCGGAAC

B

Gene	**Primer sequence (5’ to 3’)**	
TAT7	Forward primer Reverse primer	CTCGGAATGGGAGACCCAAC GGGAAGACCGACGGTAGTAG
HPPD	Forward primer Reverse primer	TTGCCAGGGTTCGAGCGTGT TCGGCGGTTCCAACGTCGTC
VTE1	Forward primer Reverse primer	TCCGGACTCCTCACAGTGGGTAA AAAGTAGTCGTCGAATGGTGAGCC
VTE2	Forward primer Reverse primer	AATGCCACTGCGGGTCAGCC GCACCTGCAAATCCAATCACAGAGC
VTE3	Forward primer Reverse primer	CCGGTGACTCTCCTCTCCAGGTC TCCCAGGAGGAAGCGTCCCAA
VTE4	Forward primer Reverse primer	GAAACGTGGCTGTGGCGGCT AGGAAGCTAACCAGTAACACCGGCA
PTB (reference gene)	Forward primer Reverse primer	GATCTGAATGTTAAGGCTTTTAGCG GGCTTAGATCAGGAAGTGTATAGTCTCTG

Supplemental Table S2. List of primers used in this study.

A, Primers used for genotyping of T-DNA insertion lines.

B, Primers used for qPCR analyses.