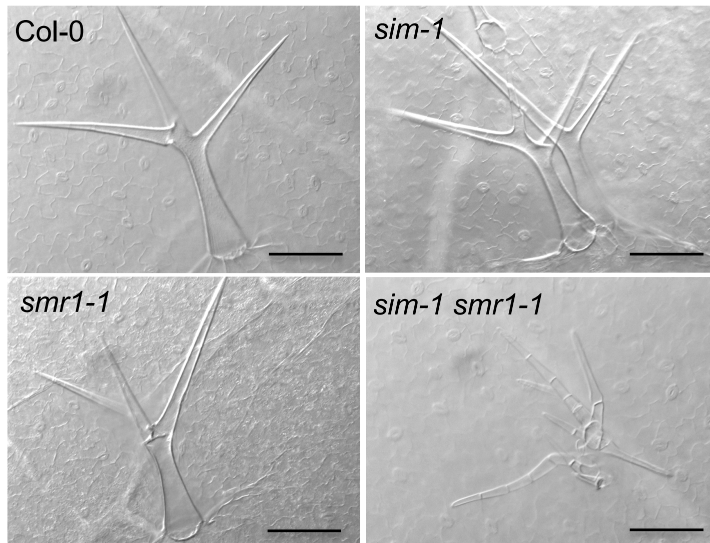


Figure S1. Trichome morphology. The fourth to sixth leaves of 25-day old plants were cleared overnight with ethanol and photographed using a dissecting microscope connected to a CCD camera. Scale bars are 100 μm. These experiments were repeated twice with similar results.

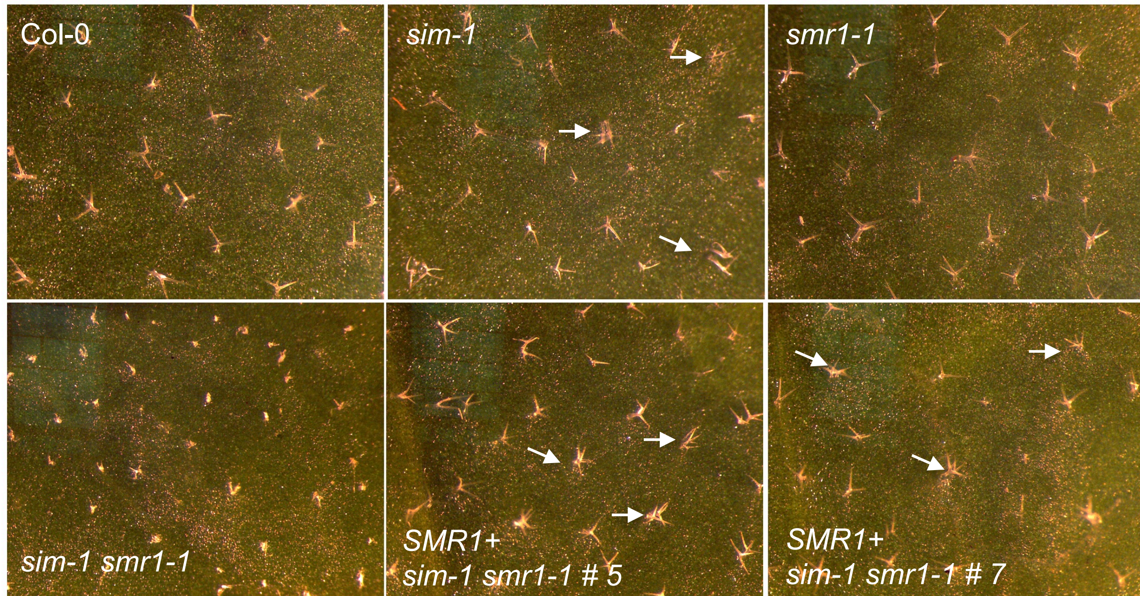


Figure S2. Rescue trichome phenotype of *sim-1 smr1-1* to that of *sim-1* by a *SMR1* genomic fragment. Leaves of 25-day old plants were photographed with a camera connected to a dissection microscope to show trichomes. Arrows indicate twin trichomes in *sim-1* and two transgenic *sim-1 smr1-1* plants complemented by a *SMR1* genomic fragment. These experiments were repeated twice with similar results.

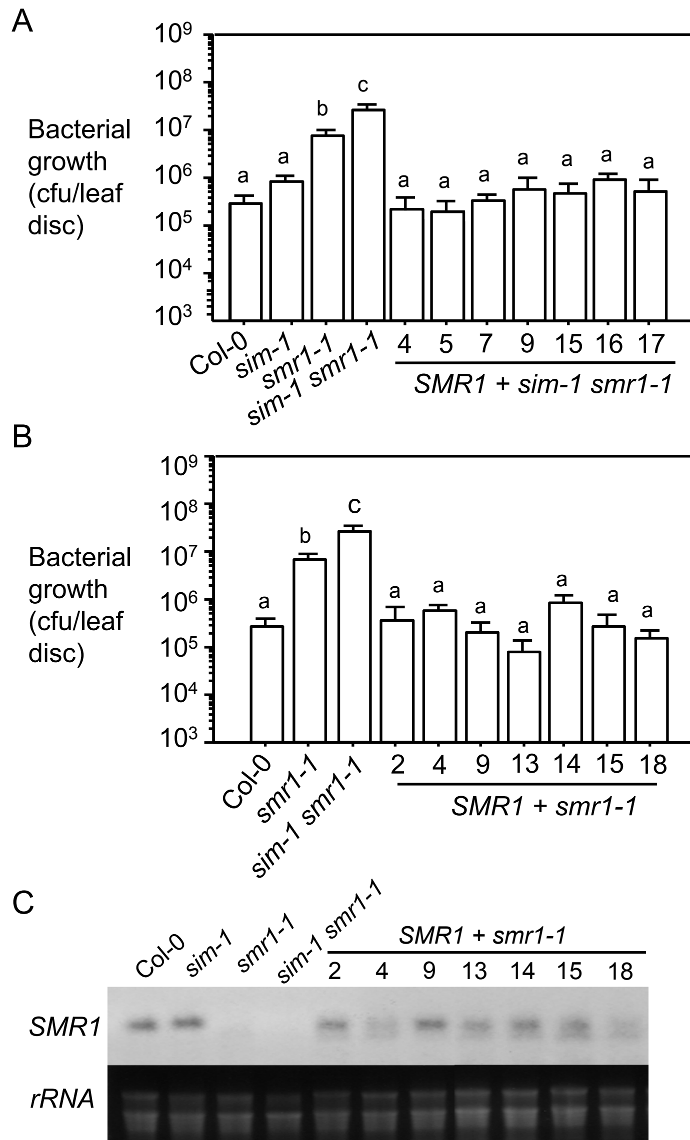
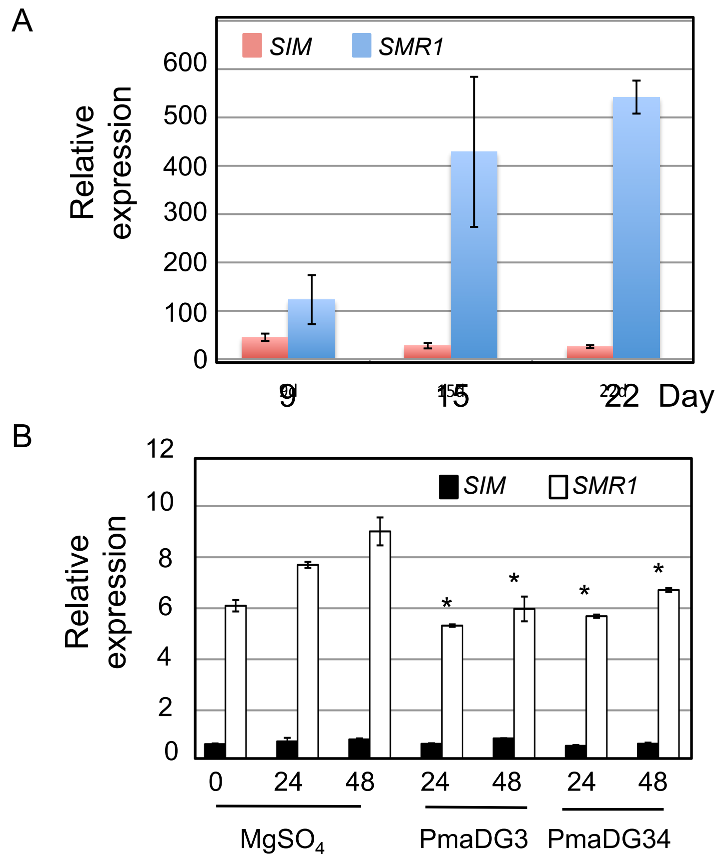


Figure S3. Complementation of enhanced disease susceptibility of *sim-1 smr1-1* and *smr1-1* by a *SMR1* genomic fragment. A. Bacterial growth assay with transgenic *sim-1 smr1-1* plants. B. Bacterial growth assay with transgenic *smr1-1* plants. The fourth to sixth leaves of 25-day old plants were infiltrated with *PmaDG3* (OD_{600}=0.0001). Leaf discs were taken 3 dpi for the measurement of bacterial growth. Statistical analysis was performed with Student's t-test (StatView 5.0.1). Letters indicate significant difference among the samples (n=6; $P<0.05$). C. Expression of *SMR1* in transgenic *smr1-1* plants. Total RNA was extracted and analyzed by northern blotting. These experiments were repeated twice with similar results.



SIM

SMR1

Figure S4. Expression analysis of *SIM* and *SMR1*. A. Microarray analysis. The relative expression values were average of three samples ± standard deviation. The original values were listed in Table S2 in the paper by Beemster et al (Beemster, 2005). Error bar strands for standard deviation. B. qRT-PCR analysis. Total RNA was extracted from 25-day old plants infected with *P. syringae* strains at the indicated time points. Asterisks indicate that expression of *SMR1* in PmaDG3 and PmaDG34 infected samples at 24 hr and 48hr were significantly different from those in mock-treated samples at 24 hr and 48hr, respectively ($P<0.05$). These experiments were repeated twice with similar results.

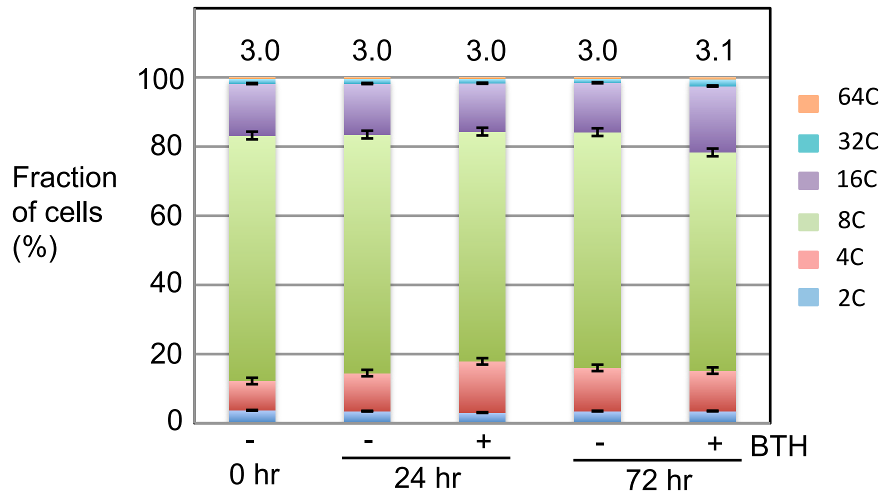
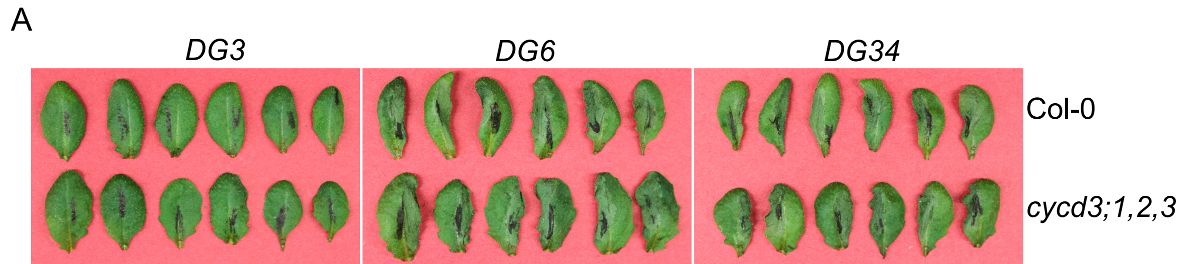


Figure S5. BTH treatment does not affect cell ploidy in Arabidopsis. Twenty-five-day old Col-0 plants were treated with 300 μM BTH or water for 24 hr or 72 hr and the fourth to fifth leaves of plants were collected for nuclei isolation followed by flow cytometry analysis. Data represent the averages of two experiments ± SEM. Ploidy indice were shown above the bars. Statistical analysis was performed with with one-way ANOVA Fisher's PLSD tests (StatView 5.0.1).

A



B

	HR leaves/Total infected leaves		
	DG3	*DG6*	*DG34*
Col-0	3/18	21/21	18/19
cycd3;1,2,3	4/18	20/20	27/27

Figure S6. The *cycd3;1,2,3* mutant is not compromised to the hypersensitive response induced by *PmaDG6* or *PmaDG34*. The fourth to sixth leaves of 25-day old plants were infiltrated with *PmaDG3*, *PmaDG6* or *PmaDG34* (OD_{600}=0.1) and examined for leaf collapse 18 hpi. A. Picture of infected leaves. *PmaDG3* was used as a negative control. Note leaf collapse was seen in leaves infected with *PmaDG6* or *PmaDG34* but not with *PmaDG3,* which was used as an HR negative control. B. Summary of the HR result shown in (A).