

Corrections

PLANT BIOLOGY. For the article “*Arabidopsis* TAO1 is a TIR-NB-LRR protein that contributes to disease resistance induced by the *Pseudomonas syringae* effector AvrB,” by Timothy K. Eitas, Zachary L. Nimchuk, and Jeffery L. Dangl, which appeared in issue 17, April 29, 2008, of *Proc Natl Acad*

Sci USA (105:6475–6480; first published April 18, 2008; 10.1073/pnas.0802157105), the authors note that an incorrect protein blot was inadvertently used in Fig. 1*B*. This error does not affect the conclusions of the article. The corrected figure and legend appear below.

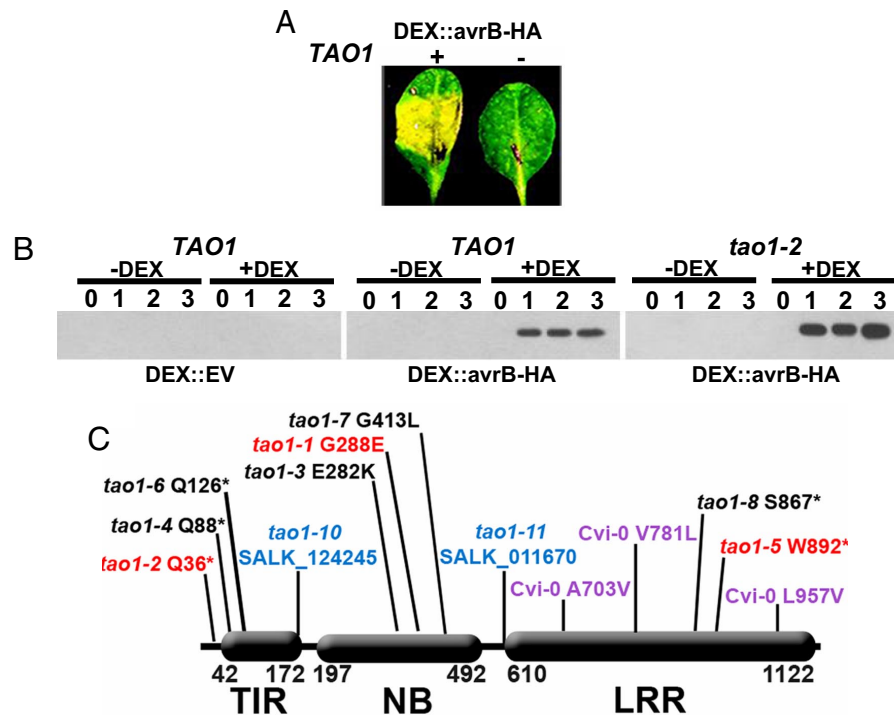


Fig. 1. TAO1 is a TIR-NB-LRR R protein required for AvrB-induced chlorosis in *rpm1* host plants. (A) Mt-0 leaves were inoculated with *Agrobacterium* containing T-DNA with a *DEX::avrB-HA* transgene (4). Leaves were treated with DEX 48 h after inoculation. The picture was taken 72 h after inoculation. (B) Plants of *TAO1* genotype shown above the blots, and carrying the transgenes shown below the blots, were sprayed with either DEX or carrier (see *Methods*), and tissue samples were harvested at 1, 2, and 3 days after treatment. Protein blots were probed with an anti-HA monoclonal antibody. (C) Deduced structure of *TAO1* alleles recovered in Mt-0 (red and black), Col-0 Salk T-DNA insertion lines (blue), and as polymorphisms in Cvi-0 (purple). For all missense mutations, the wild-type Mt-0 residue is listed first. TIR, amino acids 42–172; NB, amino acids 197–492; LRR, amino acids 610–1122. All *TAO1* alleles in Mt-0 were generated by EMS mutagenesis except *tao1-8*, which is a fast neutron deletion of 1 bp in codon 5667. Red *tao1* alleles represent alleles that were out-crossed away from the *DEX::avrB-HA* transgene and used for further analyses. The *tao1-10* (Salk_124245) insertion begins at amino acid 168. The *tao1-11* (Salk_011670) insertion begins at amino acid 597. The only amino acid difference between Mt-0 and Col-0 is V489M. Genomic *TAO1* sequences for Mt-0 (EU031442) and Cvi-0 (EU031443) have been deposited in GenBank.

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