

# Supporting Information

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## SI Methods

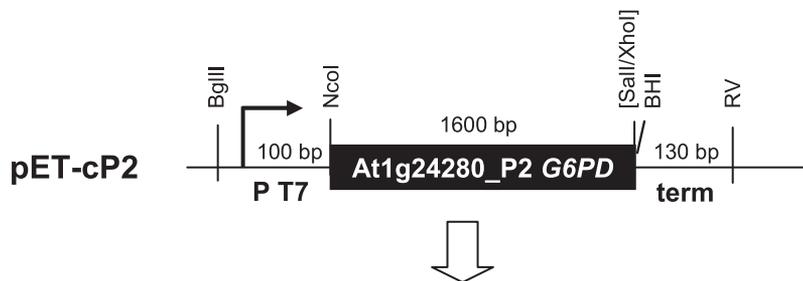
**Cloning of cP2-Expression Constructs.** To obtain cDNA fragments without transit sequence of *Arabidopsis* P2-type *G6PD* isoform (At1g24280), total RNA was isolated from *Arabidopsis* (Col) (grown on 2% sucrose-containing MS medium, pH 5.6, 16-h photoperiod with 24 °C day/18 °C night regime). Reverse transcription used a poly(A) primer mix (5'-A<sub>30</sub>C/G/T-3') and SuperScript II (Invitrogen), according to the protocol. Truncated cDNA fragments (lacking 5' 195 bp) were amplified with PfuI DNA polymerase (Stratagene) and ZM.S2 (5'-N<sub>6</sub>GGATCCAAGATGGTTGTCGTGCAAGATGGATCAGTAGCCACC-3') plus ZM.A3 (5'-N<sub>6</sub>GTCGACTCACTGATCAAGACTTAGGTCTCCCCATTG-3') primers, and directly cloned into BamHI- and SalI-opened pBluescript SK vector (Stratagene), yielding pZM3. Similarly, cP2 fragments were introduced into the multiple cloning site of pA35 (1) between cauliflower mosaic virus 35S promoter and OCS polyadenylation signal, yielding pZM4. The entire expression cassette was transferred by HindIII and partial PvuII digestion into HindIII/SnaBI-opened binary vector pGSC1704 [HygR] (Plant Genetic Systems), yielding final construct pZM5 suited for stable *Agrobacterium*-mediated plant transformation.

For *Escherichia coli* expression vector pET16b (Novagen), cP2 cDNA fragments were amplified from pZM4 with Phusion DNA polymerase (Finzymes) and primers pET-cP2 sense (without His

tag, NcoI underlined: 5'-NNNCCATGGTTGTCGTGCAAGATGGATCAGTAG-3') and ZM.A3 antisense (see above). NcoI/SalI-digested PCR products were first cloned in *E. coli* XL1 Blue (Stratagene) after ligation to NcoI/XhoI-opened pET16b (Novagen), yielding pET-cP2. G6PDH activity of the cP2 enzyme was determined in a G6PDH-deficient *E. coli* strain (2). Expression of cP2 was induced (1 mM IPTG) in logarithmically growing cultures, harvested by centrifugation after 2–3 h of growth at 37 °C, and adjusted to OD<sub>600</sub> of 10. Pelleted cells were extracted in 100 mM NaH<sub>2</sub>PO<sub>4</sub>, 10 mM Tris-NaOH (pH 8), 0.1 mM Pefabloc SC, and 0.02 mM NADP (to stabilize G6PDH activity) by sonication 3 times for 10 s at 50 W (Branson).

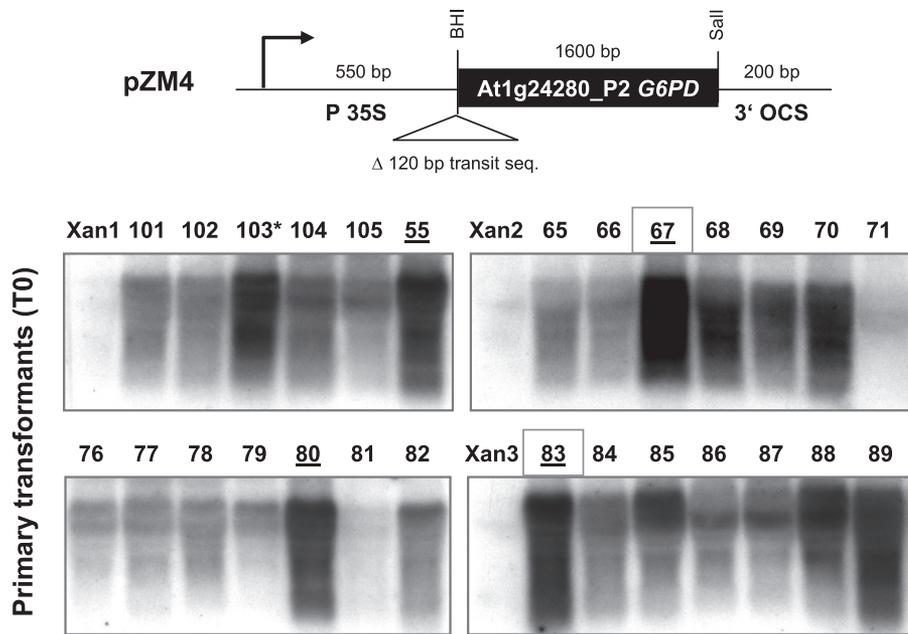
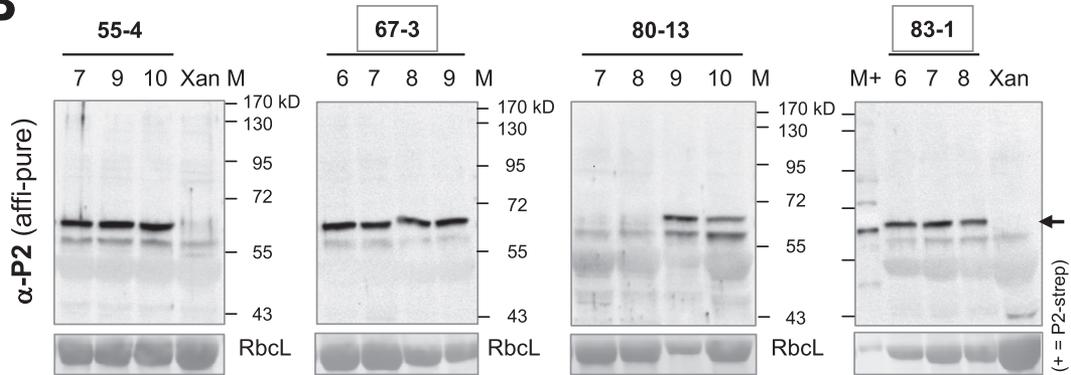
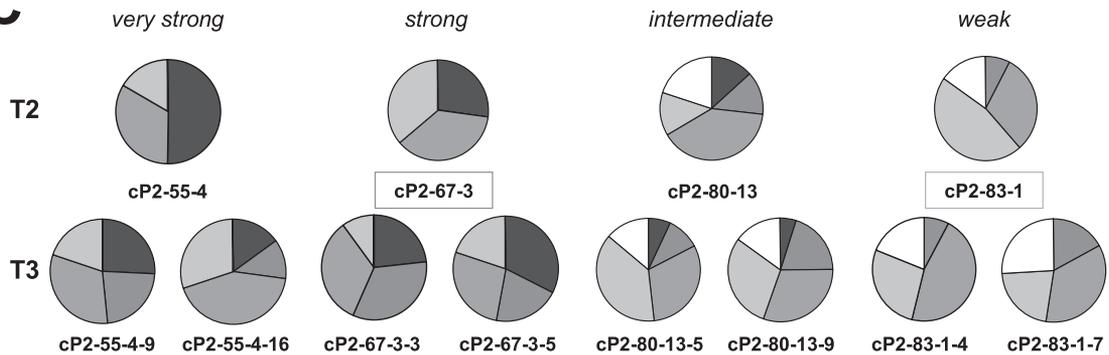
**Cloning of a Xanthi-Specific *cytG6PD*-RNAi Construct.** The RNAi construct was designed based on tobacco cytosolic *G6PD* isoforms (3). Approximately 400 bp of target sequence was amplified by RT-PCR from total RNA (described above) isolated from Xanthi source leaves with Phusion DNA polymerase using primers *cytG6PD*-sense (SalI underlined: 5'-CACCGTCCGACAATATGAAGGCTATAAGGATGACC-3') and *cytG6PD*-antisense (BamHI underlined: 5'-GGATCCTATATGACAGGTCTAATTCACCTTGAAC-3'). PCR fragments were inserted twice into vector pUC-RNAi. Then, the entire dsRNAi region was released by PstI and inserted into SdaI opened binary vector pBinAR[Kan] (4).

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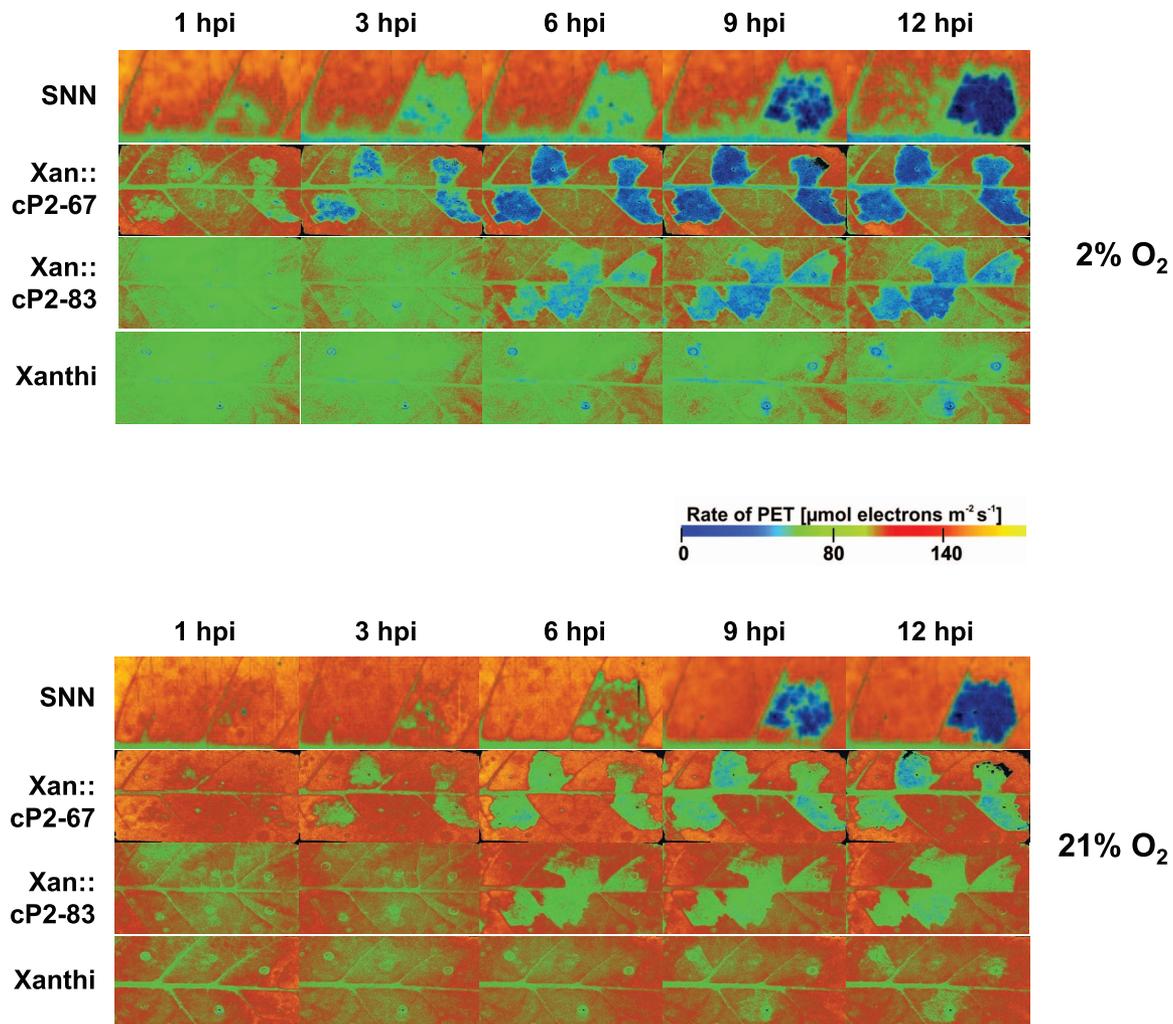


Xanthi (DTT <sub>red</sub> -resistant G6PDH activity of leaves)	cP2 ( <sup>66</sup> S→M, activity in <i>E. coli</i> G6PD <sup>minus</sup> extract)	SNN (DTT <sub>red</sub> -resistant G6PDH activity of leaves)
$K_M [G6P] = 0.25 \text{ mM}$	$K_M [G6P] = 0.57 \text{ mM}$	$K_M [G6P] = 0.24 \text{ mM}$
$K_i [NADPH] = 50 \text{ } \mu\text{M}$	$K_i [NADPH] = 60 \text{ } \mu\text{M}$	$K_i [NADPH] = 51 \text{ } \mu\text{M}$
$K_M [NADP] = 41 \text{ } \mu\text{M}$	$K_M [NADP] = 24 \text{ } \mu\text{M}$	$K_M [NADP] = 41 \text{ } \mu\text{M}$
$K_i [NADPH] \approx K_M [NADP]$	$K_i [NADPH] > K_M [NADP]$	$K_i [NADPH] \approx K_M [NADP]$

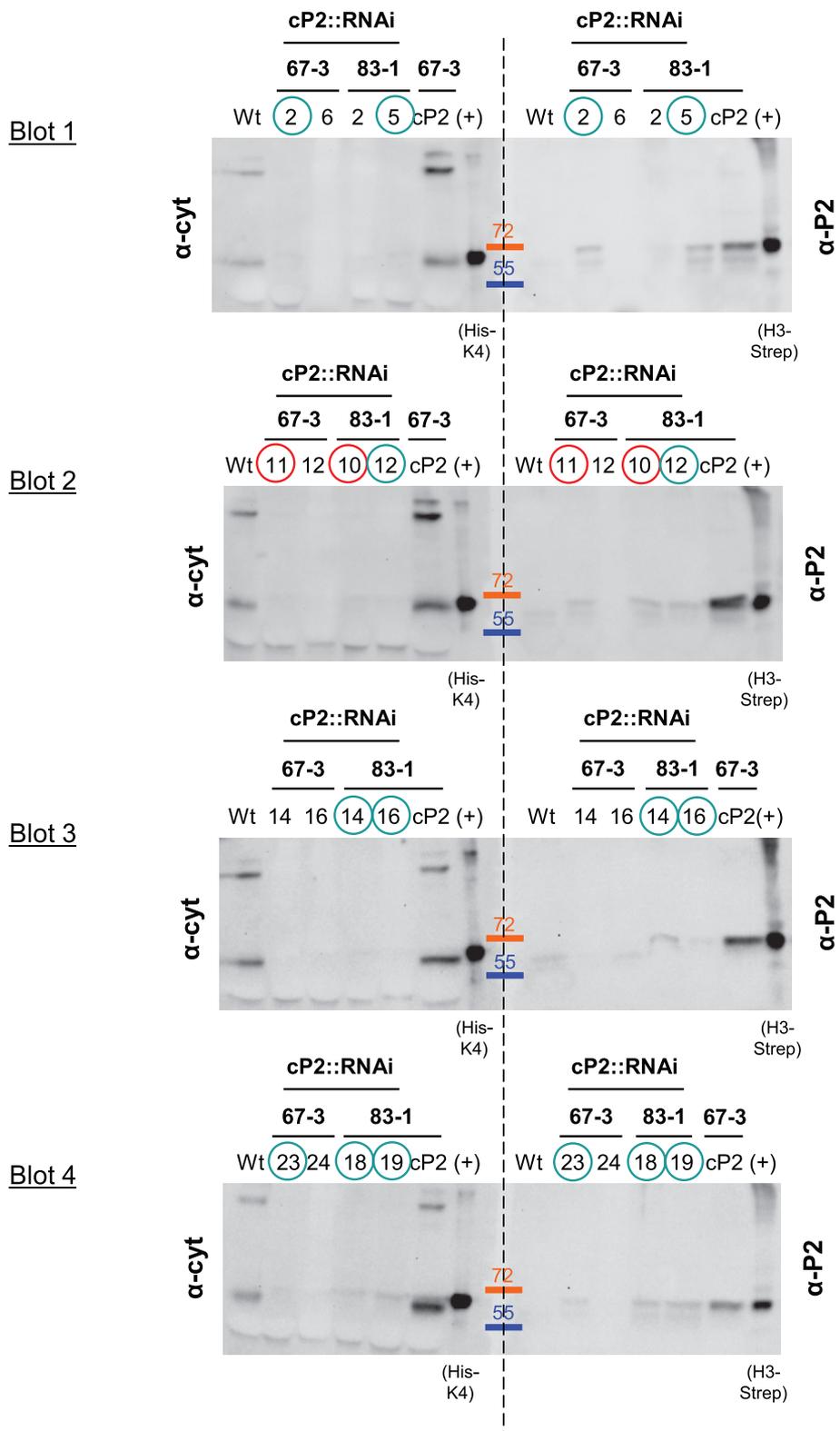
**Fig. S1.** Biochemical characteristics of cP2 versus tobacco cytosolic G6PDH. Kinetic parameters were determined for the recombinant cP2 enzyme after extraction from an *E. coli* G6PDH-minus strain (2) and compared with the DTT<sub>red</sub>-resistant (cytosolic) G6PDH activity extracted from source leaves of WT tobacco Xanthi and SNN cultivars ( $n \geq 3$ ). Leaf discs were frozen and crushed in liquid nitrogen and extracted in 100 mM Tris maleate buffer (pH 8), which inhibits 6PGDH, with 280 mM 2-mercaptoethanol. Extracts were centrifuged twice at high speed (4 °C) and supernatants were adjusted to 62.5 mM DTT<sub>red</sub> (in 100 mM Tris maleate, pH 8) followed by 30-min preincubation at room temperature (to inhibit plastidic isoenzymes), before measuring G6PDH activity by  $A_{340}$  in a double-wavelength spectrophotometer (Beckman DU 650, automatic subtraction of  $A_{405}$ ). Standard tests contained 0.2 mM NADP in 100 mM Tris maleate (pH 8). Minor rates recorded over 5 min before starting reactions with glucose 6-phosphate (G6P) were subtracted. Kinetic parameters were determined as described previously (5).  $K_i$  values for NADPH (at 0, 50, 70, or 100  $\mu\text{M}$ ) were assayed in the presence of NADP (at 0, 30, 60, 90, 120, or 150  $\mu\text{M}$ ) at saturating G6P (2 mM).

**A****B****C**

**Fig. S2.** Expression and immunoblot analysis of the Xanthi::cP2 lines plus stability of lesion formation. (A) Expression cassette of the binary vector construct used for the generation of Xanthi::cP2 lines, and Northern blot analysis of primary transformants (T<sub>0</sub>) using <sup>32</sup>P-labeled P2-cDNA fragments as described in ref. 6. (B) Immunoblot analyses of the T<sub>2</sub> progeny of very strong (55-4), strong (67-3), intermediate (80-13), and weak (83-1) cP2 lines. (C) Stability of lesion formation in the corresponding T<sub>3</sub> progeny. The cP2 lines marked by a frame were chosen for the RNAi approach.

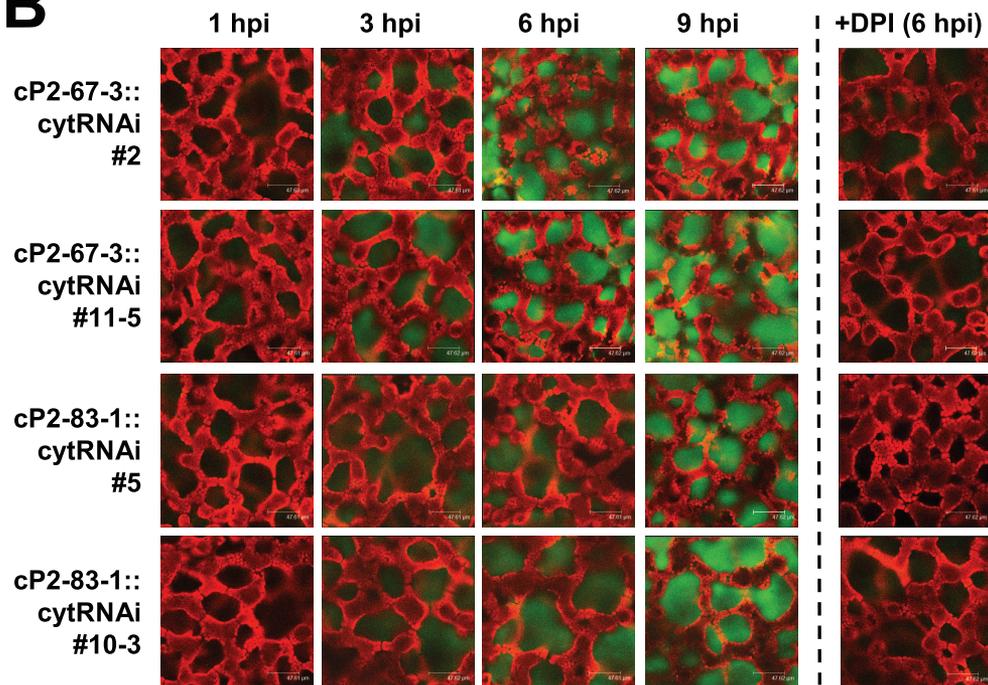


**Fig. S3.** Defense-induced inhibition of photosynthesis in the Xanthi::cP2 lines. The formation of hypersensitive lesions was preceded by defense-induced inhibition of photosynthesis, as visualized by chlorophyll-a fluorescence imaging (7). Transgenic Xanthi::cP2 lines behave more like the resistant cultivar SNN, whereas in susceptible Xanthi WT leaves no depression of photosynthesis is detected. Decline in photosynthesis is an integral part of the metabolic transitions that accompany plant defense and hypersensitive cell death, and it involves 2 steps. Early during infection, stomata at the infection sites close (compare Fig. 2C) and the rate of CO<sub>2</sub>-dependent photosynthetic electron transport (PET) decreases. This was analyzed by measuring PET in the presence of low oxygen (2% O<sub>2</sub>), enhanced CO<sub>2</sub> concentration (700 μL of CO<sub>2</sub> per L), and nearly saturating light (820 μmol of quanta m<sup>-2</sup> s<sup>-1</sup>). Under such conditions, photorespiration is largely suppressed (whereas mitochondrial respiration is not), and electrons are mostly consumed by CO<sub>2</sub> fixation (7). In the presence of ambient oxygen (21% O<sub>2</sub>), when electrons are consumed either by CO<sub>2</sub> fixation or by photorespiration, only weak inhibition was recorded during the first 6 hpi, but later photosynthetic flux equally decreased in the presence or absence of high oxygen. The O<sub>2</sub>-insensitive decline observed at later time points (>6 hpi) reflects a general decline of photosynthetic capacity in infected tissue, probably due to depression of the high-potential chain (7) or the Calvin cycle.

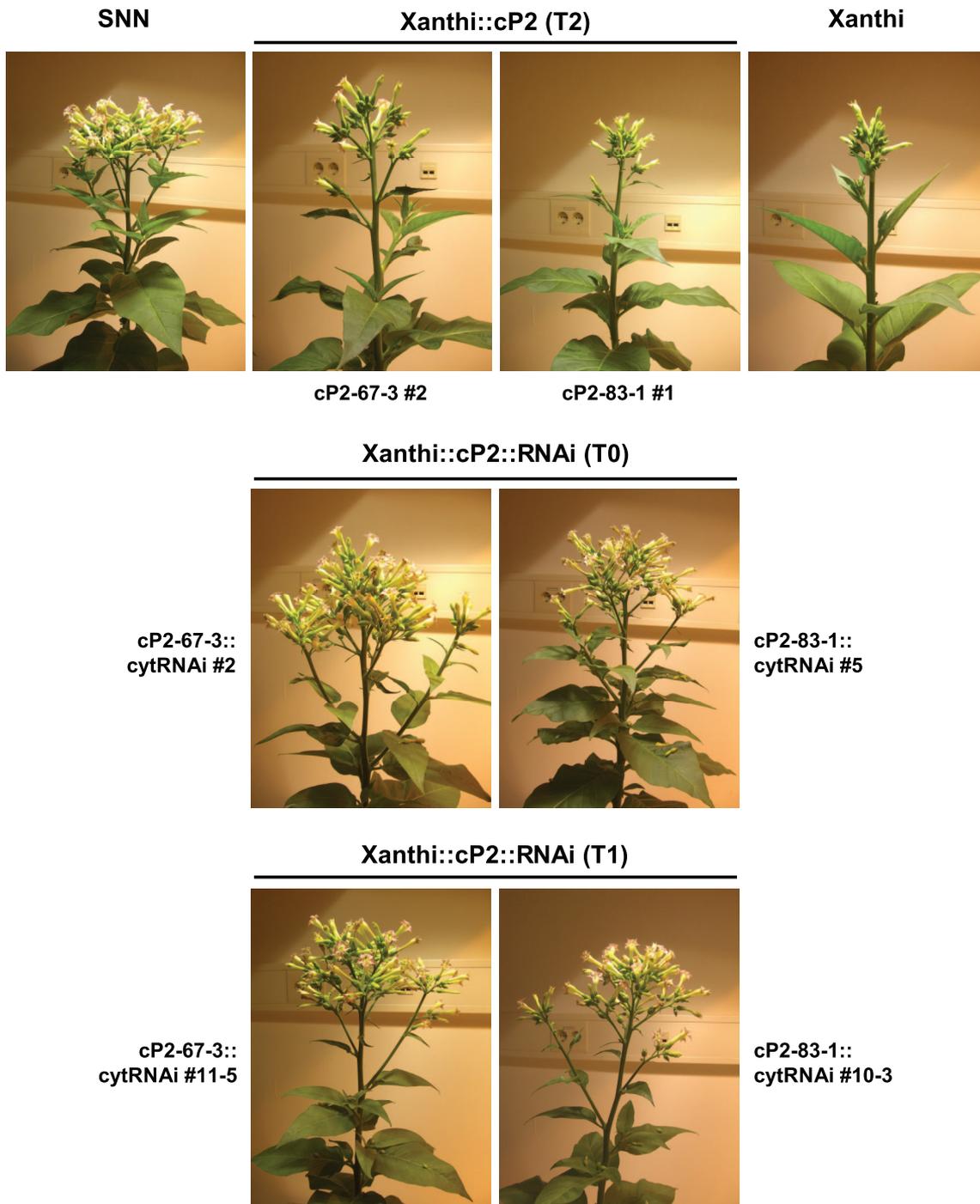


**Fig. S4.** Selection of isoenzyme-replaced Xanthi transformants. Immunoblot analyses of primary Xanthi::cP2::RNAi transformants (T<sub>0</sub>) with G6PDH isoform-specific antisera (6). Blots were cut along the dashed line before development. Positions of 2 molecular mass standards are shown (72 and 55 kDa). Supertransformed plants that lacked cytosolic G6PDH but retained cP2 signals were selected, and those circled were used for further analyses.



**A**cP2-67-3::  
cytRNAi  
#11-5cP2-67-3::  
cytRNAi  
#2cP2-83-1::  
cytRNAi  
#5cP2-83-1::  
cytRNAi  
#10-3**B**

**Fig. S6.** ROS analyses of selected isoenzyme-replaced Xanthi lines. Side-by-side photo of 5-week-old RNAi supertransformants ( $T_0$  versus  $T_1$ ) in the greenhouse, before their transfer to climate-controlled growth chambers for later measurement of pathogen-induced ROS release. Growth habit (A) as well as defense-induced ROS release (B) was much more homogenous in the isoenzyme-replaced Xanthi lines compared with the parental cP2 lines ( $T_2$  progeny of cP2-67-3 and cP2-83-1). For further explanation, see legend to Fig. 2.



Xanthi plants start to flower over a week later than SNN ( $n \geq 8$ )

**Fig. S7.** Flower development in cP2 overexpressors versus isoenzyme-replaced lines. Onset of flowering reflects the general tendency of the isoenzyme-replaced Xanthi lines to respond like the resistant tobacco cultivar SNN. Inflorescences of the parental cP2 lines are shown between SNN and Xanthi WT, with T<sub>0</sub> and T<sub>1</sub> individuals of the isoenzyme-replaced (cP2::RNAi) Xanthi lines underneath.