

SUPPORTING INFORMATION

pH Gradient Mitigation in the Leaf Cell Secretory Pathway Attenuates the Defense Response of *Nicotiana benthamiana* to Agroinfiltration

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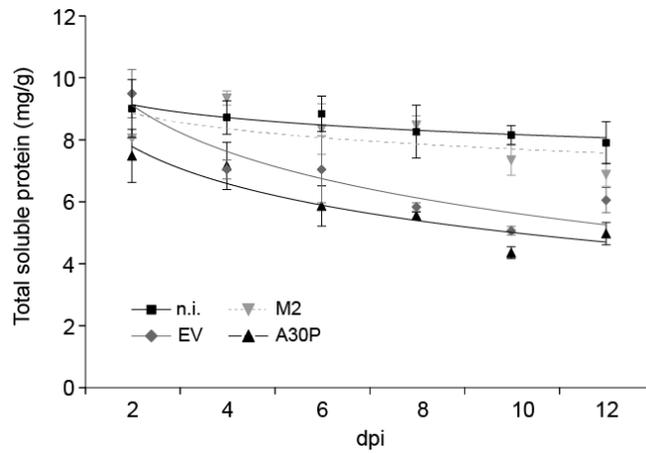
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SUPPLEMENTAL FIGURES 1–5 (this file)

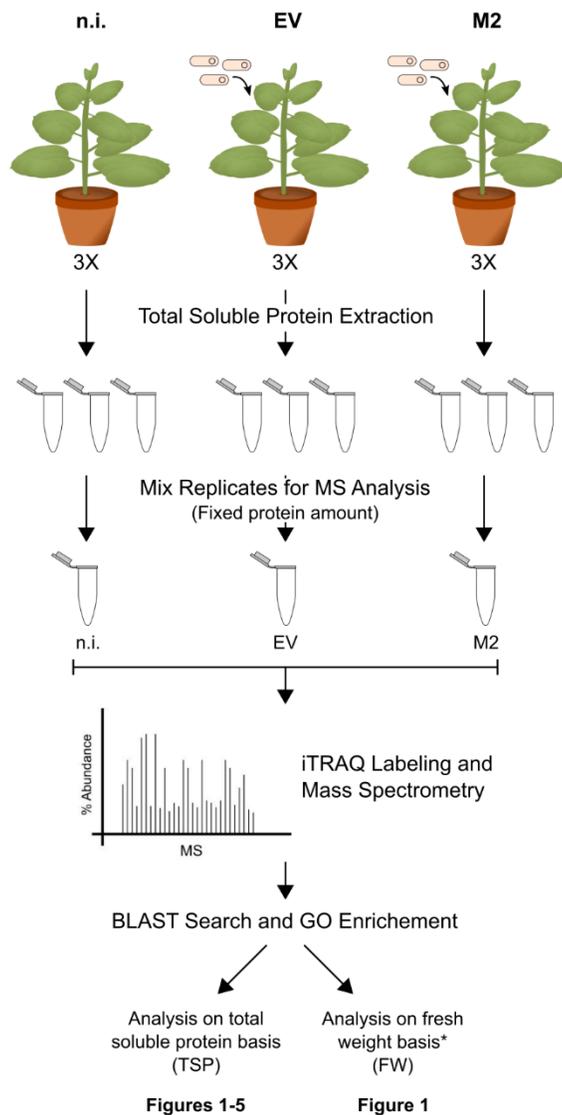
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Supplemental Table S2.	The 100 most abundant proteins in non-infiltrated leaves
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Supplemental Table S5.	The 60 most upregulated proteins in EV-infiltrated leaves compared to non-infiltrated control leaves
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Supplemental Table S7.	The 60 most upregulated proteins in M2 vector-infiltrated leaves compared to EV-infiltrated leaves
Supplemental Table S8.	The 60 most downregulated proteins in M2 vector-infiltrated leaves compared to EV-infiltrated leaves
Supplemental Table S9.	DNA primers for RT-qPCR amplifications

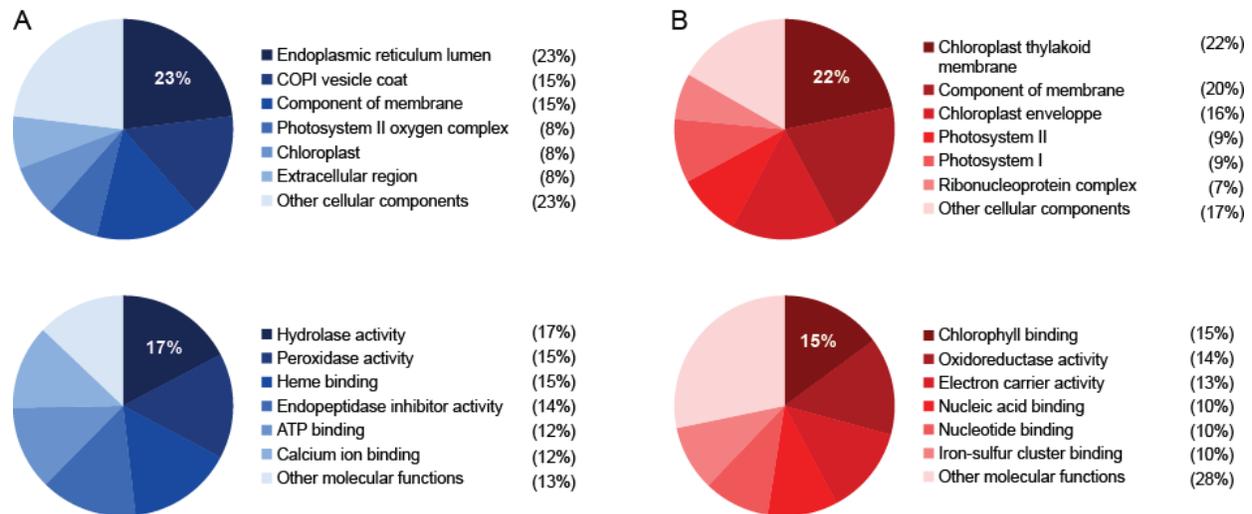


Supplemental Figure S1. Complement to Figure 1A,B—Soluble protein content over 12 d in non-infiltrated (n.i.) leaves or agroinfiltrated leaves expressing (or not) the M2 proton channel. The leaves were infiltrated with agrobacteria harboring an empty vector (EV), an M2-encoding vector or a vector encoding ^{A30P}M2 (A30P), a stable but inactive variant of M2 unable to drive proton transport (Holsinger et al., 1994). Data are expressed on a leaf fresh weight basis. Each data point is the mean of three biological (plant) replicate values ± SE.

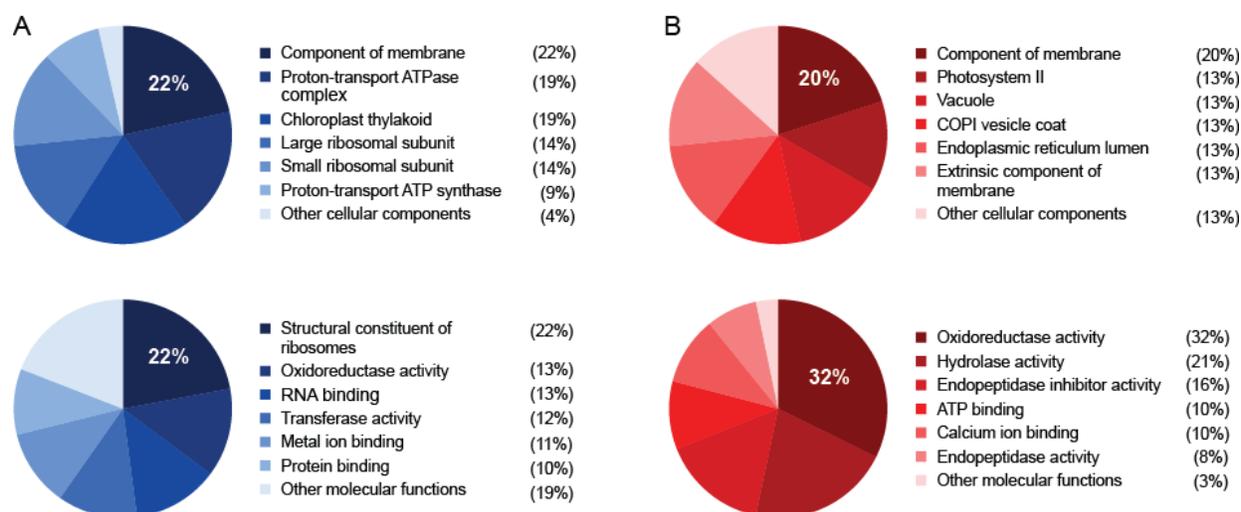


* Results are adjusted based on the initial protein concentration of plant extracts

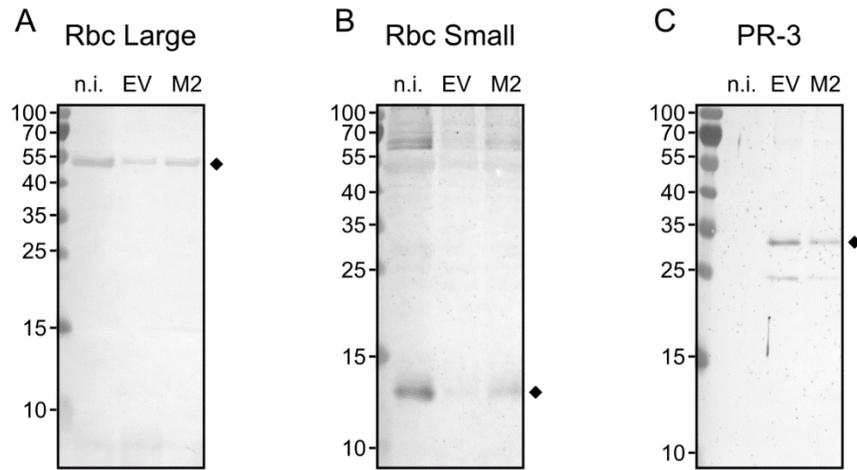
Supplemental Figure S2. Complement to Figure 1C,D—Experimental scheme for the iTRAQ proteomics analysis. The host plant leaves were infiltrated *A. tumefaciens* cells carrying (M2) or not (EV, for ‘empty’ vector) a DNA vector with the M2 proton channel-encoding gene. Non-infiltrated (n.i.) plants were grown in parallel and used as negative controls for the experiments.



Supplemental Figure S3. Complement to Figure 3—GO enrichment analysis of iTRAQ-quantified proteins up- (A, in blue) or down- (B, in red) regulated by at least twofold in EV-infiltrated leaves compared to non-infiltrated (n.i.) leaves. Pie charts identify the six most affected cellular components [or cellular environments] (upper charts) or the six most affected biochemical functions (lower charts), in leaf tissue as inferred from biological roles assigned to the 60 most upregulated, and 60 most downregulated, proteins in EV-infiltrated leaves. The 60 most upregulated, and 60 most downregulated, proteins in EV-infiltrated leaves compared to n.i. leaves are listed in **Supplemental Tables S5** and **S6**, respectively.



Supplemental Figure S4. Complement to Figure 4—GO enrichment analysis of iTRAQ-quantified proteins up- (A, in blue) or down- (B, in red) regulated by at least twofold in M2-expressing leaves compared to EV-infiltrated leaves. Pie charts identify the six most affected cellular components [or cellular environments] (upper charts), or the six most affected biochemical functions (lower charts), in leaf tissue as inferred from biological roles assigned to the 60 most upregulated, and 60 most downregulated, proteins in M2-expressing leaves compared to EV-infiltrated leaves. The 60 most upregulated, and 60 most downregulated, proteins in M2-expressing leaves compared to EV-infiltrated leaves are listed in **Supplemental Tables S7** and **S8**, respectively.



Supplemental Figure S5. Complement to Figure 6—Images for the entire membranes of immunoblot sections shown in Figure 6.