

Supplementary Material

Novel insights into the *Citrus sinensis* nonhost response suggest photosynthesis decline, abiotic stress networks and secondary metabolism modifications

Lucas D. Daurelio^{A,F}, *M. Laura Tondo*^A, *M. Soledad Romero*^B, *Paz Merelo*^C, *Adriana A. Cortadi*^D,
Manuel Talón^E, *Francisco R. Tadeo*^E and *Elena G. Orellano*^{A,F}

^AInstituto de Biología Molecular y Celular de Rosario – Consejo Nacional de Investigaciones Científicas y Técnicas), Facultad de Ciencias Bioquímicas y Farmacéuticas (FBIOYF) – Universidad Nacional de Rosario (UNR), Suipacha 531 (S2002 LRK), Rosario, Santa Fe, Argentina.

^BInstituto de Agrobiotecnología de Rosario (INDEAR), Ocampo 210 bis, Predio CCT Rosario, (2000), Rosario, Santa Fe, Argentina.

^CEuropean Molecular Biology Laboratory, Heidelberg, Meyerhofstraße 1, 69117 Heidelberg, Germany.

^DÁrea de Biología Vegetal, FBIOYF – UNR, Suipacha 531 (S2002 LRK), Rosario, Santa Fe, Argentina.

^ECentre de Genòmica, Institut Valencià d'Investigacions Agràries, Apt. Oficial, 46113 Montcada, València, Spain.

^FCorresponding authors. Emails: daurelio@ibr-conicet.gov.ar; orellano@ibr-conicet.gov.ar

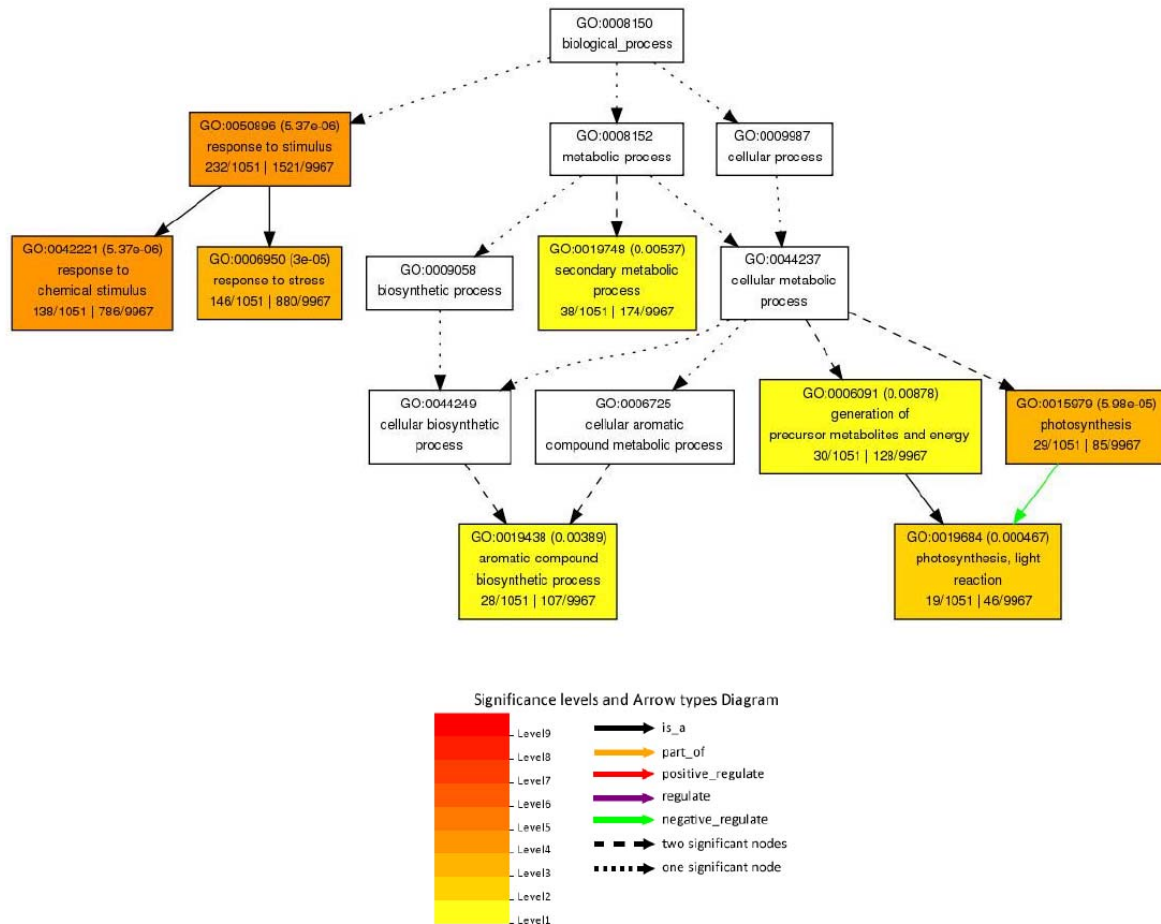


Fig. S1. Over-representation analysis of differentially expressed genes families during the orange non-host response to Xcv. The Gene Ontology category (GO term), *P*-value with false discovery rate correction (FDR), the number of genes with modified expression during the response over the number of genes in the input list and the number of genes represented in the microarray over the total number of genes in the reference list are indicated. The colours of squares indicate significance levels and the arrows indicate the relationship between categories, as observed at the bottom of the figure.

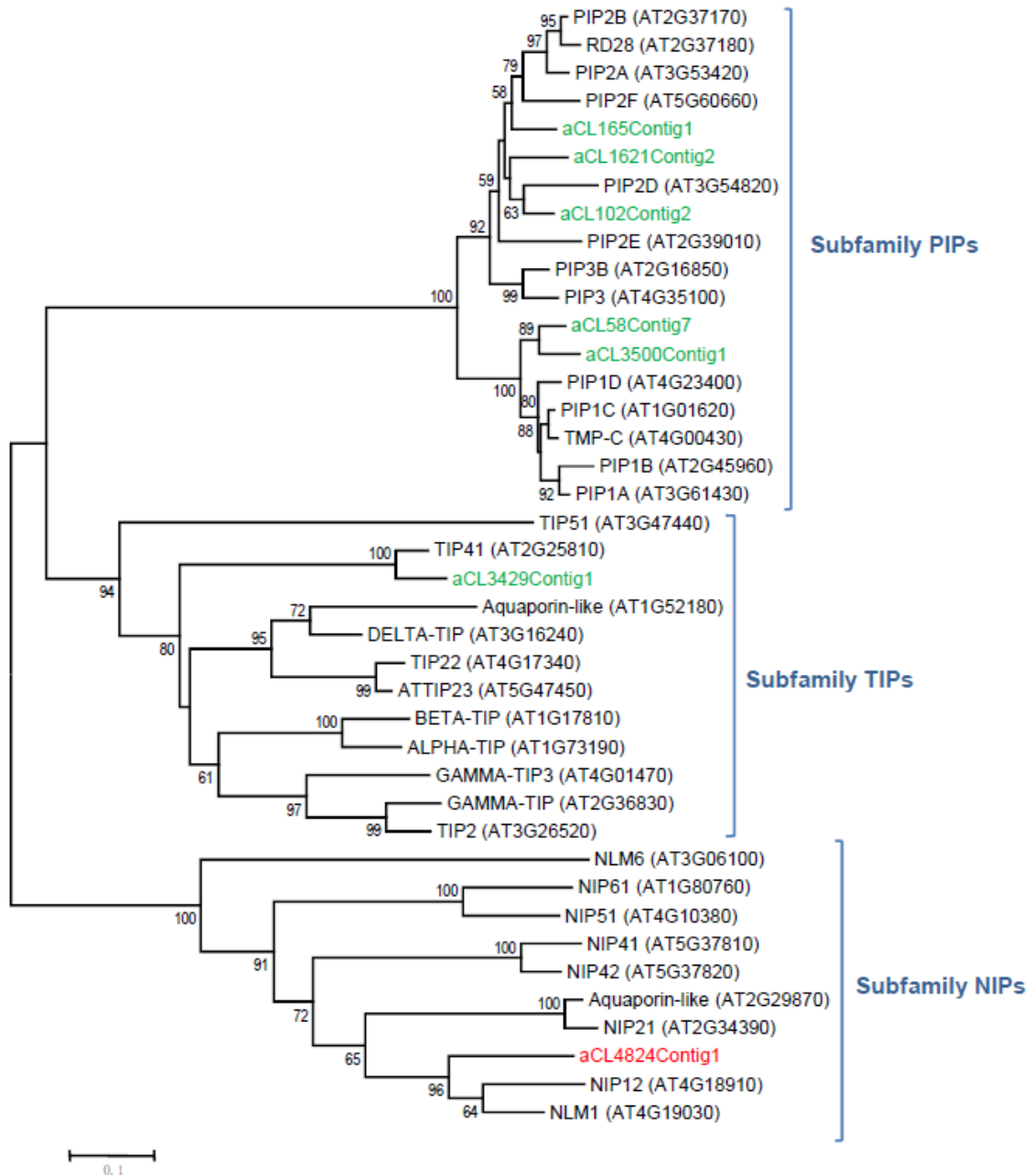


Fig. S2. Phylogenetic tree of orange and *Arabidopsis* aquaporins representative domains. Only citrus aquaporins differentially regulated by the Xcv treatment were included (red: induced, green: repressed). *Arabidopsis* subfamilies were named in the right brackets. Branches are drawn in proportion to genetic distance.

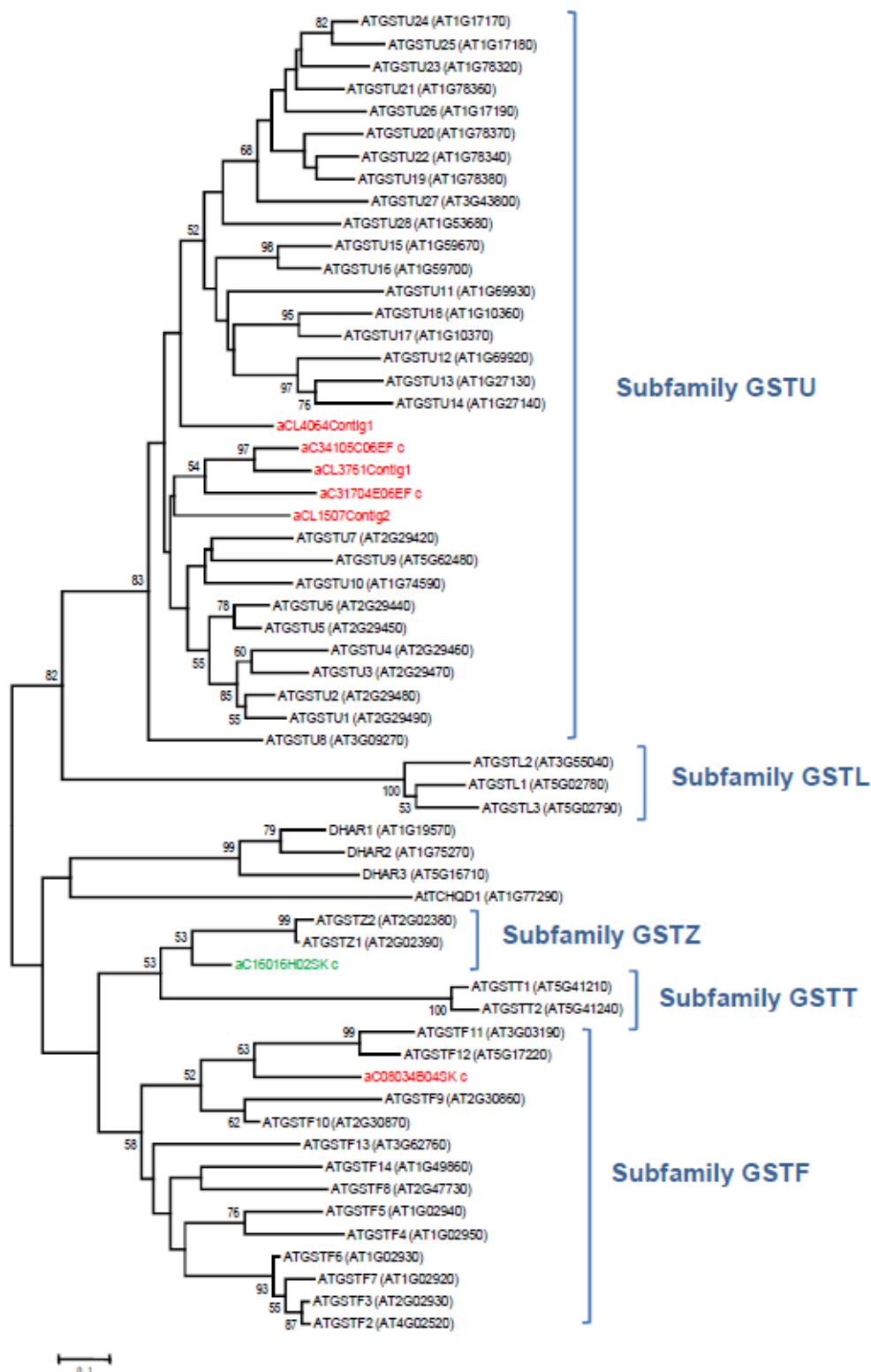


Fig. S3. Phylogenetic tree of orange and *Arabidopsis* GSTs representative domains. Only citrus GSTs differentially regulated by the Xcv treatment were included (red: induced, green: repressed). *Arabidopsis* subfamilies were named in the right brackets. Branches are drawn in proportion to genetic distance.

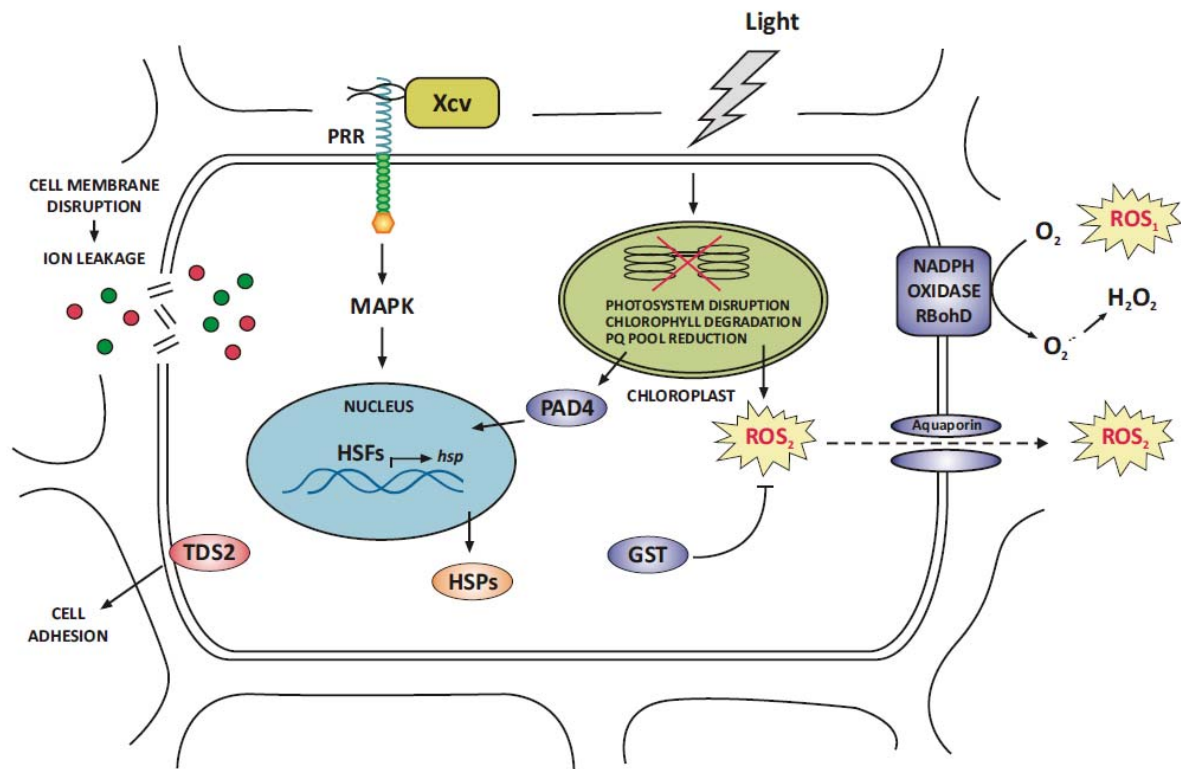


Fig. S4. *Citrus sinensis* non-host response to *Xcv*. Results obtained in this and the previous work (Daurelio *et al.* 2013) are included, showing the proteins and cellular components that participate in the resistance process to the phytopathogenic bacteria. Up-regulated genes are shown in blue and down-regulated genes in red. ROS produced by two different sources are indicated as ROS₁ and ROS₂. PQ: plastoquinone; PRR: pattern recognition receptor.