Supplementary Material

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

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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.