

## Supplementary Material

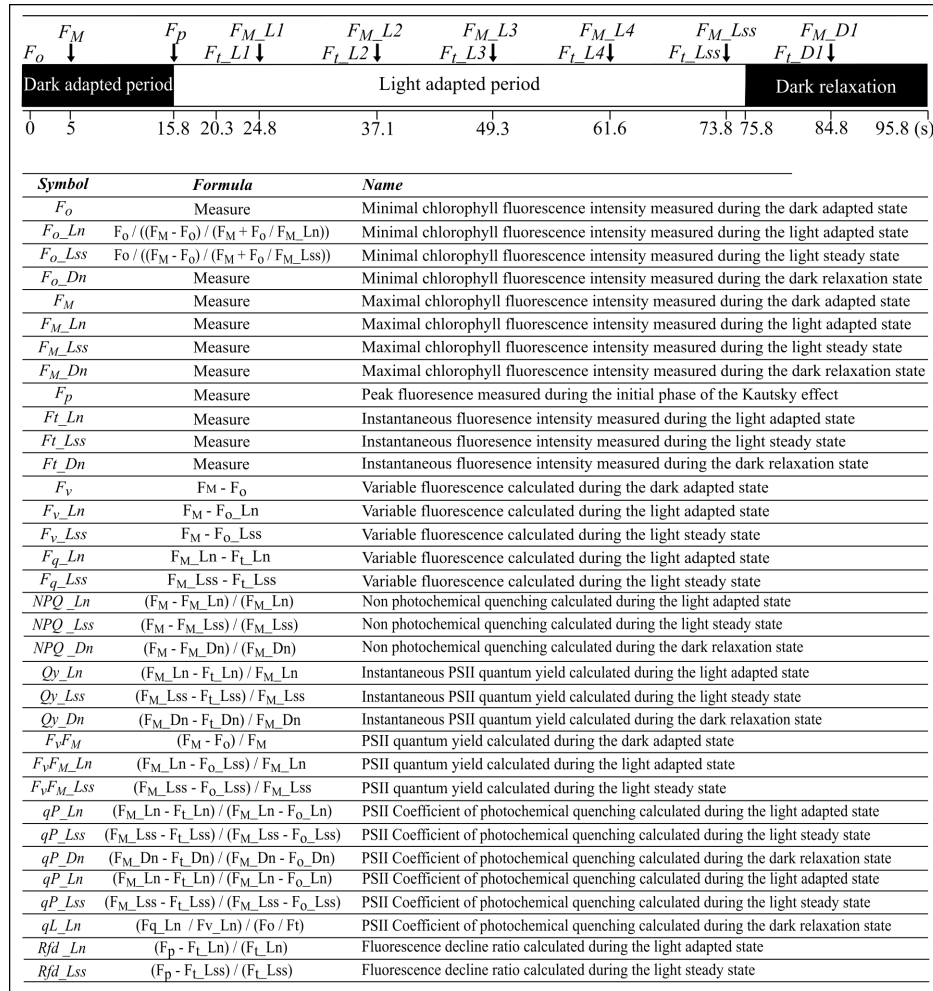
TABLE 1: Bacterial strains used in this study.

name in the text	full designation	accession	genotype or relevant phenotype	reference
7698R	7698R	CFBP 13420	spontaneous <i>Rif<sup>r</sup></i> derivative of strain CFBP 7698	Meline 2019
7698R pIJ3225	7698R pIJ3225	CFBP 13431	13431 pIJ3225	Meline 2019
C3	7698R pIJ3225 C3	CFBP 13465	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
F2	7698R pIJ3225 F2	CFBP 13468	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
F15	7698R pIJ3225 F15	CFBP 13467	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
G1	7698R pIJ3225 G1	CFBP 13470	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
G2	7698R pIJ3225 G2	CFBP 13472	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
G9	7698R pIJ3225 G9	CFBP 13474	<i>Rif<sup>r</sup>,Tetr,Kan<sup>r</sup></i>	Meline 2019
EHA105	<i>Agrobacterium</i> EHA105 no protein express	/	<i>genta</i>	this study
GUS	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>gus</i>	/	<i>genta,spec</i>	this study
AF	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopAF</i>	/	<i>genta,spec</i>	this study
L	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopL</i>	/	<i>genta,spec</i>	this study
G	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopG</i>	/	<i>genta,spec</i>	this study
V	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopV</i>	/	<i>genta,spec</i>	this study
T	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopT</i>	/	<i>genta,spec</i>	this study
AK	<i>Agrobacterium</i> EHA105 pB7FWG2- <i>xopAK</i>	/	<i>genta,spec</i>	this study

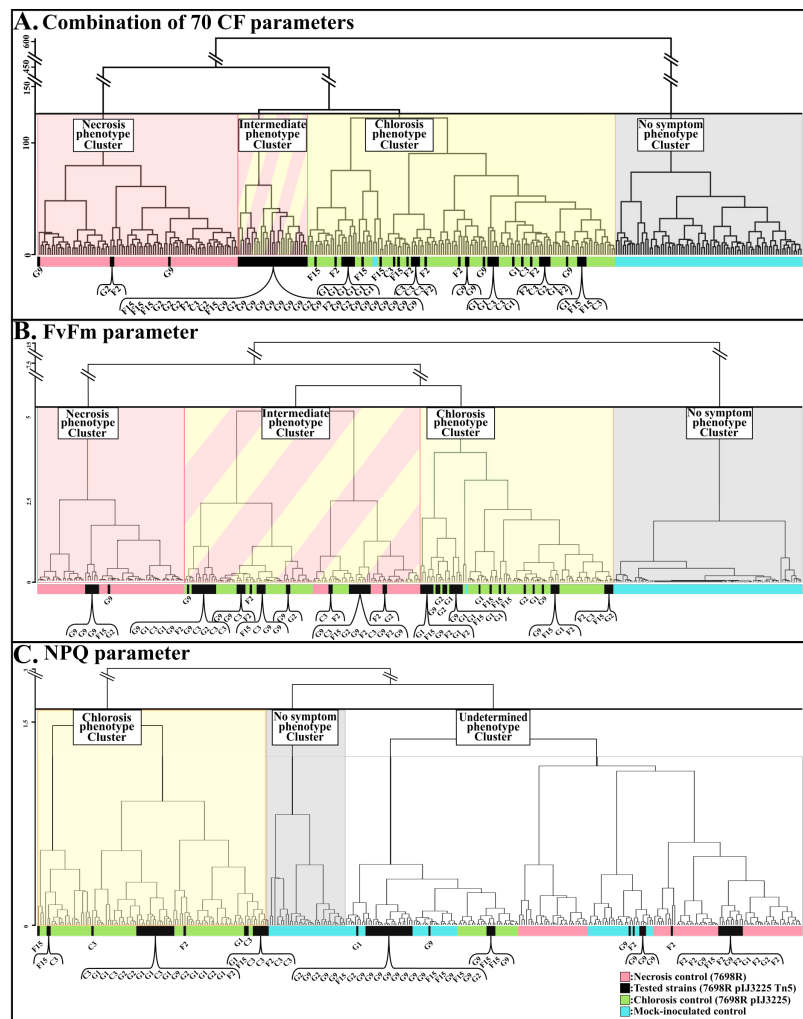
For more information on the localisation of the various Tn5 insertions in the *hrp* cluster, please see reference Meline et al. 2019, Molecular Plant Pathology.

TABLE 2: PCR primers used in this study. These PCR primers were designed on *X. fuscans* pv. *citri* 4834, dedicated to this study.

targeted gene	forward primers	reverse primers	amplicon (bp)
<i>xopAF</i>	CACCATGGGCCTATGCATTAC	GGCGGCAACCAAATGCTT	843
<i>xopG</i>	CACCATGCCAATCAGTCAAACAAAC	CATGCCGTGAGGCTTATATTTTTTGCG	642
<i>xopL</i>	CACCATGAACGAGGCGGCTGG	CTGCTGGCCTGAAGCTTCCGG	1716
<i>xopT</i>	CACCATGCGCCCTCTTTCGCCC	CGCTCCAGGGTGGTTCAACC	948
<i>xopAK</i>	CACCATGGGTGGGACTGTTGACC	CCACGACTTGTAGTAGAAGATGC	878
<i>xopV</i>	CACCATGAAATCTCCGGCTCGG	TTCGCCGTTCCGGATCAGAATG	996



**Figure S1.** A description of the CF quenching protocol providing the measured and calculated images of CF parameters used in this study. To measure  $F_0$ , a modulated light of  $0.1 \mu\text{mol.m}^{-2}.\text{s}^{-1}$  is used. Then 618 nm orange actinic light with intensities of 20% of the  $400 \mu\text{mol.m}^{-2}.\text{s}^{-1}$  is used during the light-adapted period of 60 sec. The protocol also provides 6 pulses of 0.8 sec duration of 455nm blue saturating light with an intensity of 50% of the  $3000 \mu\text{mol.m}^{-2}.\text{s}^{-1}$ : 5 pulses during the light-adapted period and 1 pulse during the dark-relaxation period. The whole duration of the illumination protocol is of 95.8 sec. Twelve parameters are used in the analysis:  $F_0$ ,  $F_m$ ,  $F_p$ ,  $F_t$ ,  $F_v$ ,  $F_q$ , NPQ, Qy, qp, qL, Rfd and  $F_v/F_m$ . Among these 12 parameters,  $F_0$ ,  $F_m$ ,  $F_p$ ,  $F_t$ ,  $F_v$  are measured to generate images. For each measured parameters, several measures/images are performed during the illumination process, as depicted in the upper part of the figure S1. For example, for parameter  $F_m$ , the initial measurement  $F_m$  is measured after 5 seconds during the dark-adapted period. Then, 5 measurements are realised during the light-adapted period ( $F_{m\_L1}$  to  $F_{m\_L4} + F_{m\_Lss}$ ). One last measurement is done during dark relaxation ( $F_{m\_D1}$ ). The precise timing of the measurement is mentioned in the X-axis of the chart. The other parameters are calculated according to the formulas. In total, the measures performed lead to the generation of 70 images, corresponding to the various parameters used in the analysis.



**Figure S2.** Dendrograms obtained from the computation method according to the use of a combination of the 70 images of CF parameters (A.), sole  $F_v/F_m$  parameter (B.) and sole NPQ parameter (C.) respectively. Dendrograms are based on three-dimensional Euclidean distances evaluation and Ward agglomeration method.