**Support Information** 

## The host-plant metabolite glucose is the precursor of diffusible signal factor (DSF) family signals in *Xanthomonas campestris*

Yinyue Deng<sup>1,2,3\*</sup>, Xiaoling Liu<sup>4</sup>, Ji'en Wu<sup>1</sup>, Jasmine Lee<sup>1</sup>, Shaohua Chen<sup>1,3</sup>, Yingying Cheng<sup>3</sup>, Chunyan Zhang<sup>2</sup>, and Lian-Hui Zhang<sup>1,3\*</sup>

<sup>1</sup>Institute of Molecular and Cell Biology, Proteos, 61 Biopolis Drive, Singapore 138673, Singapore

<sup>2</sup>Guangdong Innovative and Entepreneurial Research Team of Sociomicrobiology Basic Science and Frontier Technology, South China Agricultural University, Guangzhou 510642, China

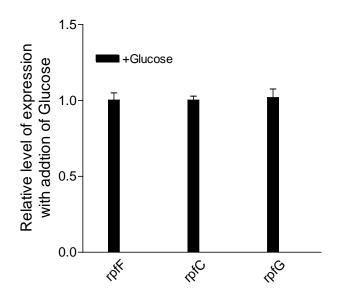
<sup>3</sup>Guangdong Province Key Laboratory of Microbial Signals and Disease Control, South China Agricultural University, Guangzhou 510642, China

<sup>4</sup>Chongqing Academy of Chinese Materia Medica, Chongqing 400065, China

## **Experimental methods:**

## **RNA extraction and qRT-PCR analysis**

Xc1 was grown in NYG medium in the absence and presence of 15mM glucose till OD<sub>600</sub> of 1.0. Total RNA was isolated using the RNeasy mini kit (Qiagen) according to the manufacturer's instructions. The concentration and purity of RNA were determined by agarose gel electrophoresis and spectrometry.qRT-PCR quantifications were performed with a LightCycler® (Roche<sup>TM</sup>) and QuantiFast SYBR Green (Qiagen<sup>TM</sup>) according to the manufacturers' instructions. The experiments were performed in triplicate, and the data were determined from two independent experiments. Expression levels were normalized to levels of the 16S RNA gene transcript in each experiment.



**Figure S1.** Real-time PCR analysis of glucose effect on transcriptional expression of selected genes in Xc1 compared to the control in the absence of glucose. Data shown are means of two replicates and error bars indicate the standard deviations.