

# The phytopathogen *Xanthomonas campestris* utilizes the divergently transcribed *pobA/pobR* locus for 4-hydroxybenzoic acid recognition and degradation to promote virulence

Bo Chen<sup>1</sup> Rui-Fang Li<sup>2</sup> Lian Zhou<sup>3</sup> Jia-Hui Qiu<sup>1</sup> Kai Song<sup>1</sup> Ji-Liang Tang<sup>4</sup>  
Ya-Wen He <sup>1</sup>

## Abstract

*Xanthomonas campestris* *campestris* *Xcc*  
*Xcc*  
 $\beta$   
*Xcc* *Xcc*  
*pobA pobR*

*pobA*  
*Xcc* *pobA*

Correspondence

*pobA* *pobR*

Funding information

*pobA* *pobR*  $\Delta$ *pobR* *Xcc*

## KEYWORDS

*pobA* *pobR* *Xanthomonas campestris*

## 1 INTRODUCTION

*Xanthomonas campestris* *campestris*

*Xcc* *et al*

*et al* *et al* *Xcc*

*Xcc*

*et al*

*et al*

Xcc

p

et al

p

et al

et al

Brassica

et al

Xcc

et al

et al

ortho

$\beta$

meta

et al

$\beta$

Azotobacter chroococcum Pseudomonas Rhizobium  
leguminosarum Acinetobacter calcoaceticus Cupriavidus necator  
et al et al

pobA

Xcc

$\beta$

et al

**FIGURE 2** *pobR/pobA*

*pobR pobA*

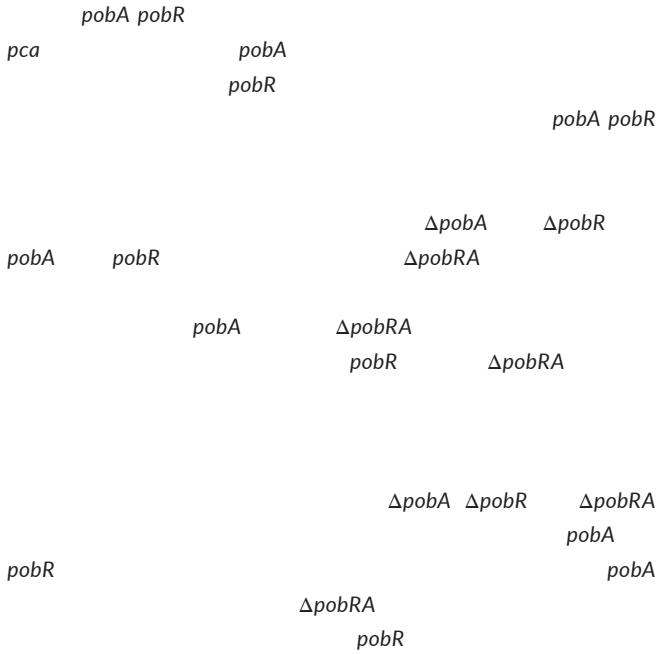
Xcc

*pobR*

*pobA*

## 2.2 The *pobA/pobR* locus is essential for 4-HBA degradation in XC1

*pobR*    *pobR*



## 2.3 Defining the overlapping promoters of *pobA* and *pobR*

*Xcc*

*pobA*    *pobR*

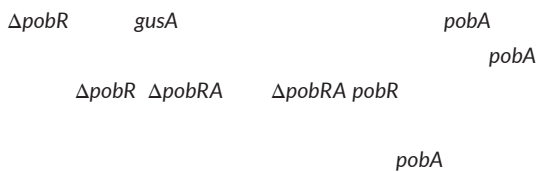
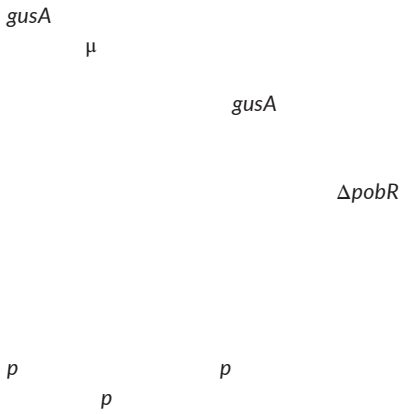
*pobA*

*E. coli*  $\sigma$

*et al*

*pobR*

FIGURE 3 *pobA*



**2.5 pobR is transcribed in the absence of 4-HBA, the presence of 4-HBA advances its expression**

*pobR* *gusA*

*gusA*

*gusA*

*gusA*

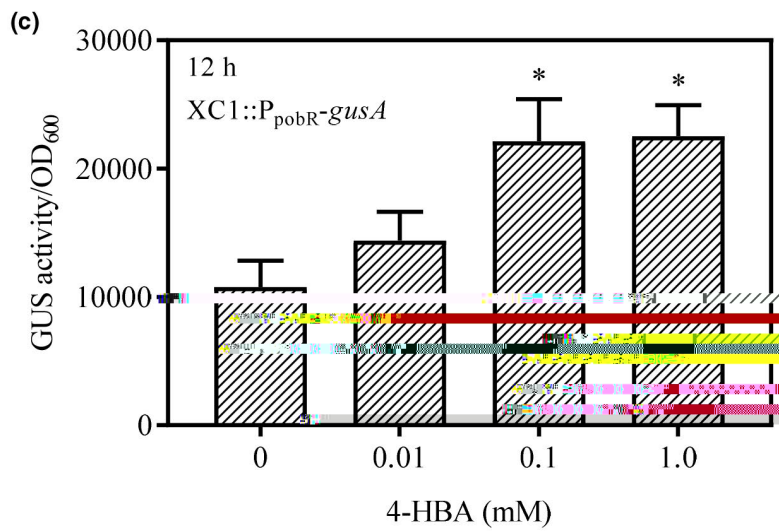
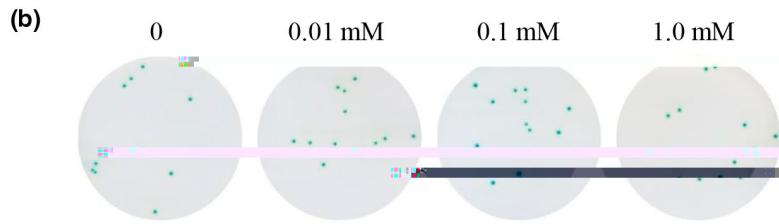
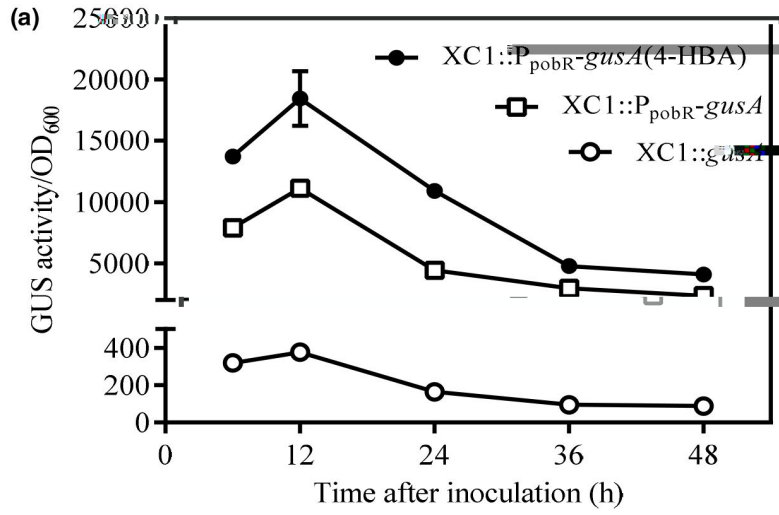


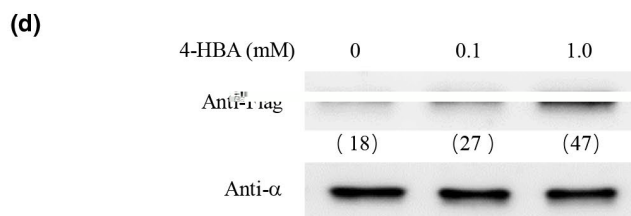
FIGURE 4 *pobR*

*gusA*

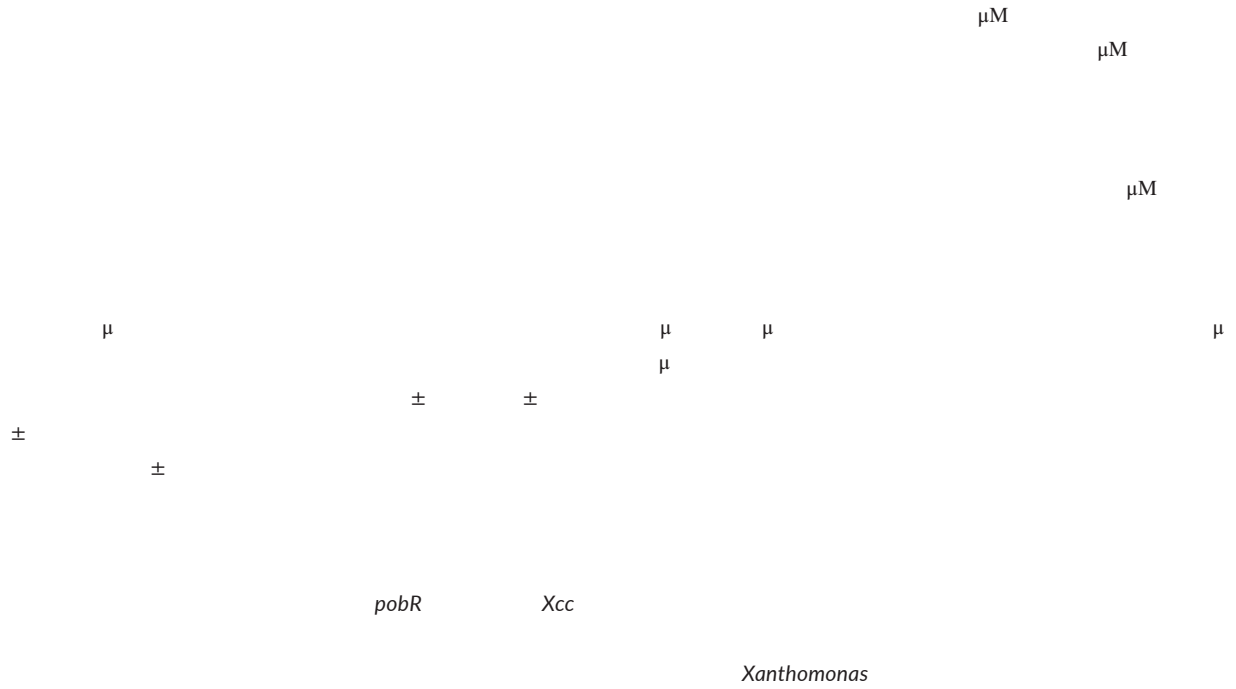
μ

α

*p*







**2.8 PobR specifically binds to a 25-bp site within the overlapping promoters**

*pobA*    *pobR*

Mutation	Dimerization	4-HBA binding (Kd) (μM)	4-HBA degradation ratio (%) at 18 hpi
	±	±	
	±		±
	±	±	
	±		±
	±	±	±
	±		
	±	±	±
			±

TABLE 1

Note: *p*



*Xcc*  
*Xcc*  
*pobA* *pobR*  
*gusA* *gusA*

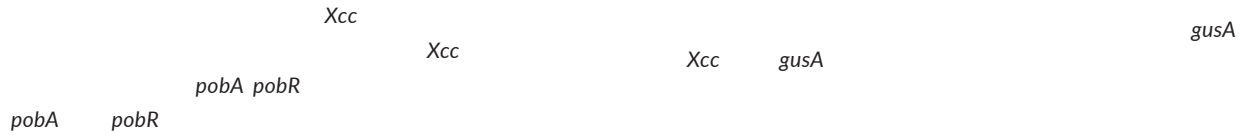
### 2.9 Both *pobR* and *pobA* are transcribed during *XC1* infection inside Chinese radish

*pobA* *Xcc* *pobR*  
*Xcc in planta*

## 2.10 pobR is required for full pathogenicity of XC1 in Chinese radish and cabbage

3 DISCUSSION

FIGURE 8 *pobR pobA*



3.1 Biochemical basis for 4-HBA recognition and PobR dimerization

*Streptomyces*  
*et al*

*Acinetobacter*

*et al*  
*S. coelicolor*

*et al*

*Xcc*

*et al*

*S. coelicolor*      *Acinetobacter*  
Xcc

*Acinetobacter*      *S. coelicolor*  
*pobA*

*S. coelicolor*      *et al*

*et al*

Xcc

Xcc

*Streptomyces*

*et al*

Xcc

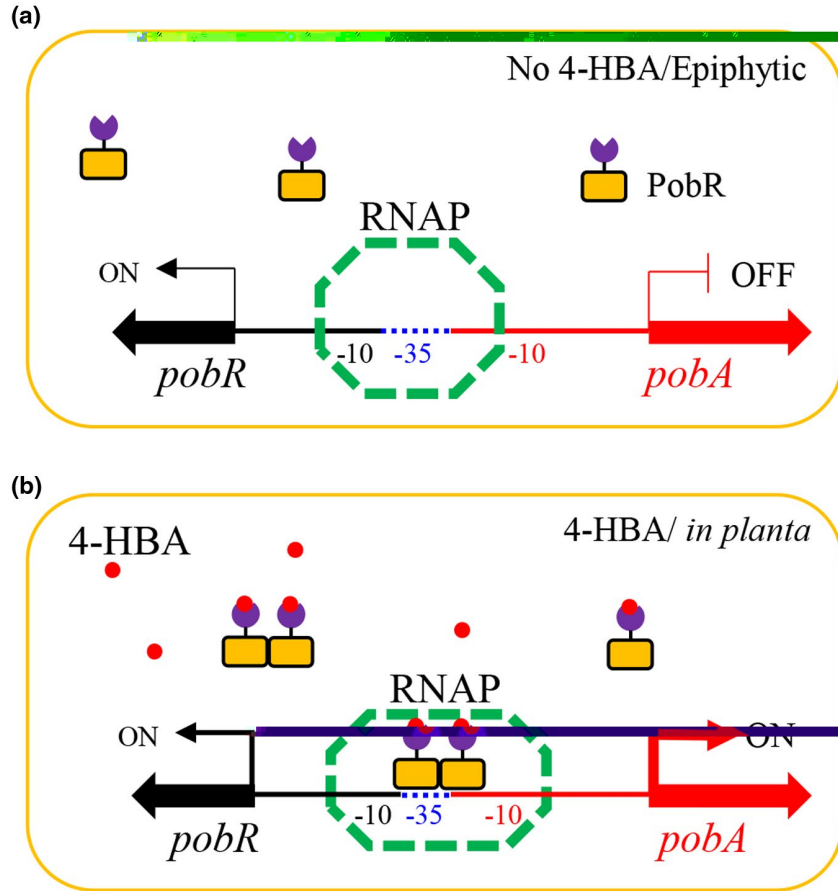
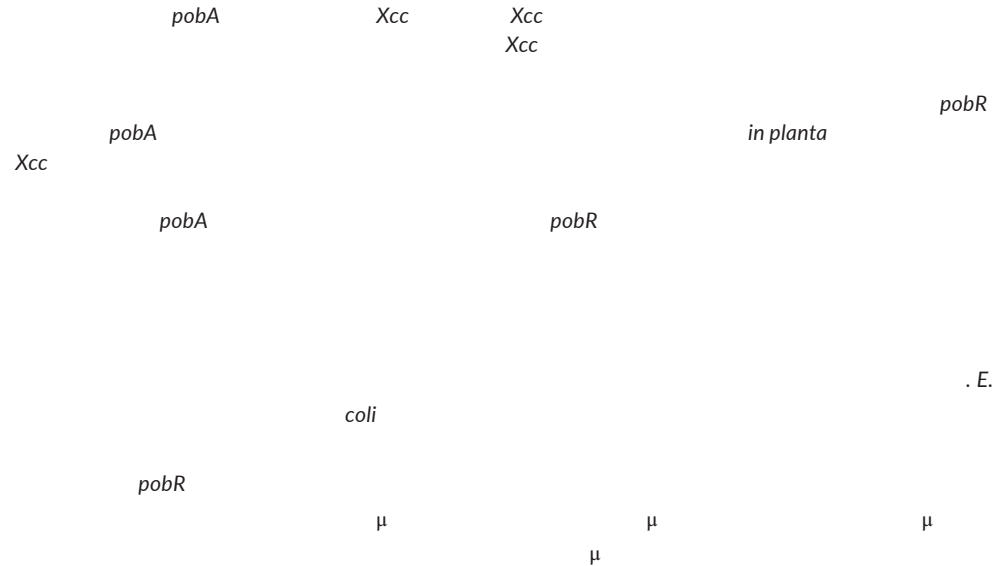


FIGURE 9



## 4 EXPERIMENTAL PROCEDURES

### 4.1 Bacterial strains and culture conditions

### 4.2 Gene deletion and functional complementation analysis

Xcc

Xcc

et al

### 4.3 Point mutagenesis of target gene in plasmid DNA and in Xcc chromosome

#### 4.9 Electrophoretic mobility shift assay (EMSA) and DNase I footprinting sequencing assay

*et al*

*pobA*

$\mu$

$\times$

$\times$

*et al*

#### 4.10 Isothermal titration calorimetry analysis

=

$\mu$

$\mu$

#### 4.11 We

#### 4.14 Virulence assay in Chinese radish and cabbage

Xcc

*Raphanus sativus*

×

#### 4.15 Statistical analysis

 $p =$  $p <$ 

#### ACKNOWLEDGMENT

#### CONFLICT OF INTEREST

#### AUTHOR CONTRIBUTIONS

#### ORCID

Ya-Wen He 

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Scientific Reports 6

*Xanthomonas campestris*      *campestris*

et al

Microbiology 104

*Pseudomonas aeruginosa*      Molecular

68s2.8.5 .7 a-9.1 e-20.8 d T J 1.156.2 01F-17.5 p a b 2.0 0.4 2.6 2.9 4.0 5.3 6.7 7.0 8.1 9.2 10.1 11.0 12.0 13.0 14.0 15.0 16.0 17.0 18.0 19.0 20.0 21.0 22.0 23.0 24.0 25.0 26.0 27.0 28.0 29.0 30.0 31.0 32.0 33.0 34.0 35.0 36.0 37.0 38.0 39.0 40.0 41.0 42.0 43.0 44.0 45.0 46.0 47.0 48.0 49.0 50.0 51.0 52.0 53.0 54.0 55.0 56.0 57.0 58.0 59.0 60.0 61.0 62.0 63.0 64.0 65.0 66.0 67.0 68.0 69.0 70.0 71.0 72.0 73.0 74.0 75.0 76.0 77.0 78.0 79.0 80.0 81.0 82.0 83.0 84.0 85.0 86.0 87.0 88.0 89.0 90.0 91.0 92.0 93.0 94.0 95.0 96.0 97.0 98.0 99.0