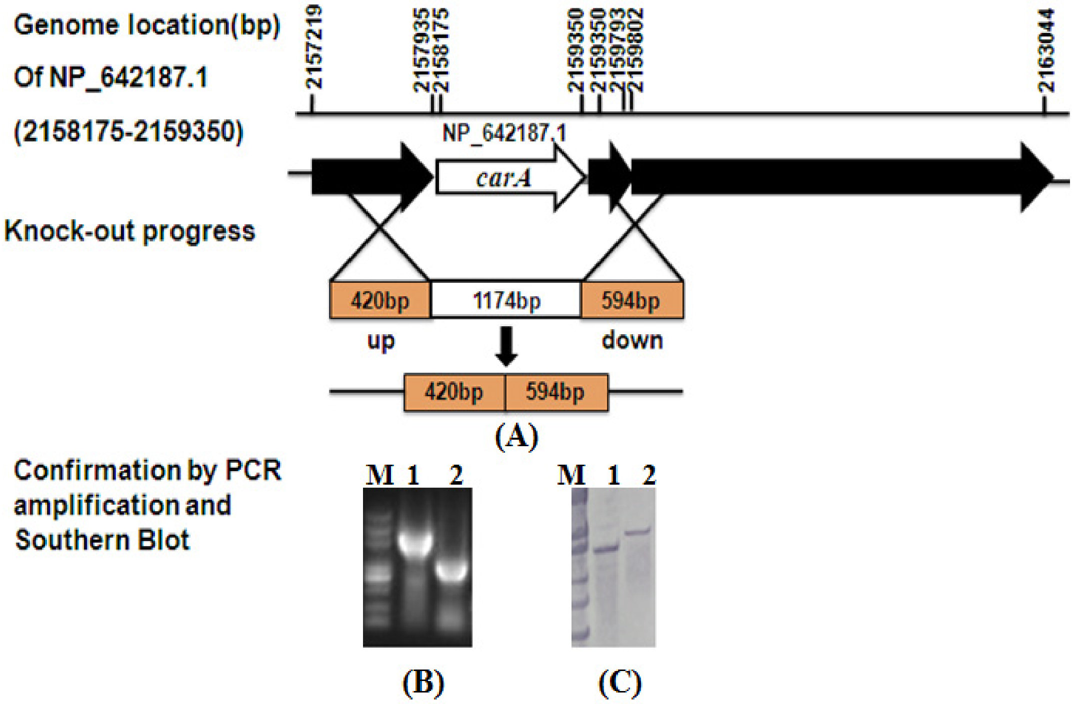
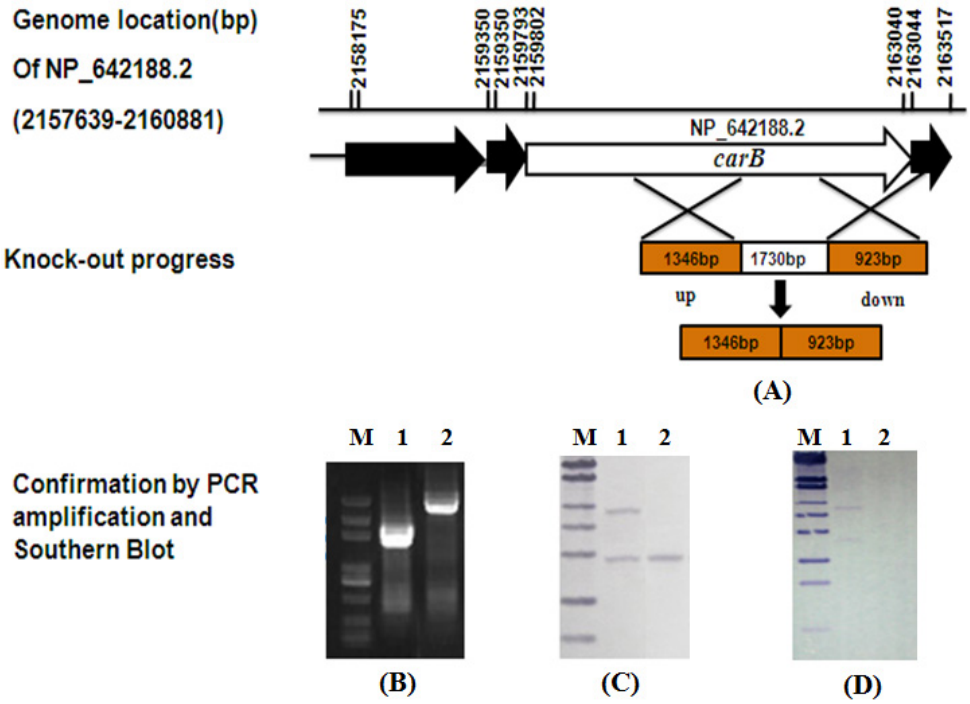


Appendix A Schematic map and molecular analysis of *carA* mutant of *Xanthomonas citri* subsp. *citri.* (A) Schematic process for construction of *carA* knock out mutant from *Xac* 29-1. The 420 bp left flanking fragment and 594 bp right flanking fragment were cloned into pK18mobSacB vector. The *carA* gene was knocked out through two-steps of homology recombination. (B) PCR analysis of *carA* mutant. Lane M, DL5000 marker; Lane 1, Wild type *Xac* 29-1; Lane 2, the *carA* mutant *ΔcarA*. (C) Southern blot for *carA* mutant. The Southern blot was carried out by using the 420 bp upside fragment after the genomic DNA was digested by *Pst* I. Lane M, λ-EcoT14 I marker; Lane 1, Wild type *Xac* 29-1; Lane 2, the *carA* mutant *ΔcarA*.



Appendix B Schematic map and molecular analysis of *carA* and *carAB* mutant of *Xanthomonas citri* subsp. *citri.* (A) Schematic process for construction of *carB* knock out mutant from *Xac* 29-1. The 1346 bp left flanking fragment and 923 bp right flanking fragment were cloned into pK18mobSacB vector. The *carB* gene was knocked out through two-steps of homology recombination. (B) PCR analysis of *carB* mutant. Lane M, DL5000 marker; Lane 1, the *carB* mutant *ΔcarB*; Lane 2, Wild type *Xac* 29-1. (C) Southern blot for *carB* mutant. The Southern blot was carried out by using left flanking fragment as probe after the genomic DNA was digested by *Pst* I. Lane M, λ-EcoT14 I marker; Lane 1, Wild type *Xac* 29-1; Lane 2, the *carB* mutant *ΔcarB*. (D) Southern blot for *carA* and *carB* double mutant. The recombinant construct for *carA* mutagenesis was introduced into *ΔcarB* genetic background to produce a double mutant. The Southern blot was carried out by using the 723 bp DNA fragment of *carA* gene as probe after the genomic DNA was digested by *Pst* I. Lane M, λ-EcoT14 I marker; Lane 1, Wild type *Xac* 29-1; Lane 2, the double mutant *ΔcarAB*.

Appendix C Primers used for molecular cloning in this study

Primer	Sequence (5’-3’)	Description
carA1.F	GCCTCTAGATCGAATCGCATCACGTGCACAA	A 420 bp fragment left to *carA*
carA1.R	GGTTCGGGCAAGCGAGAATTGTAAA	
carA2.F	TTTACAATTCTCGCTTGCCCGAACCTCGCTGTTCGATGGCACCAA	A 594 bp fragment right to *carA*
carA2.R	AATCTGCAGGTCCTCAGTAAAGTCGGTCC	
carB1.F	GGCTCTAGATCAACTGGCAGACGGTCGAAAAG	A 1346 bp fragment left to *carB*
carB1.R	CAGCGTGCGTACCGATTCTT	
carB2.F	AAGAATCGGTACGCACGCTGGAAGAGCTGGAACACCTGAAGTC	A 923 bp fragment right to *carB*
carB2.R	AAAACTGCAGGGTGCTCGAACAAGTCGTCGCCAAT	
ScarA.F	CCATGACCGGCTATCAGGAAGT	723 bp from *carA* as a probe for Southern blot
ScarA.R	CTTCTGCGCGATCAGTTCCTTG	
carA.F	TATAAGCTTACGTCGCGGCCTATTCATGCCTCAA	A 1409 bp *carA* gene
carA.R	TTTTCTAGACGGCAGCGAGGCCAGCCCTGTTTTC	
carB.F	TATTCTAGATGCCCGATCGCCCGACCAAATTACC	A 3385 bp *carB* gene
carB.R	TTTGAGCTCCGCTTGACCGACTTCAGGTGTTCCA	
wxaco.p.F	TTTCTCGAGGGTTCTACATGGCCGATACG	A 500 bp *wxaco* gene promoter
wxaco.p.R	CTCAAGCTTGCTGCCTGATTCATCGATGCC	

Appendix D Primers used for real time PCR analysis in this study

Genes	Sequence (5'-3')		Product sizes
	Forward primer	Reverse primer	
hrpG	ATGAACGACCACTCTCCCCCCAACG	GAGGCTGGCGTTGACCTGCGAGAC	87 bp
hrpX	GCGGATCGCCAATGCGCTGCGTCTG	GCGGCATCTTCCTGGCGCAGCGTGG	114 bp
hpa2	CCCCTACTGCAGCCCAGGTATTTCC	AGCTACGGAATCTCCAGGGACGCAT	115 bp
hpa1	CTTCTTTCAGGTTGACCCCAGCCAG	T GCTCGGCATTGTTGCTCTGCTGAA	138 bp
hrcC	ACCGAGCAACGGAATCTTCGACAGG	TGCAGGATACGCCTACGATGCCGAC	76 bp
hrcT	AATTGCGCGATGAAGACGCTGGT	CGAACCGTCGAATTTGAGTCAGCCA	87 bp
hrpB7	ATCGCGTCTTCTTCTTCCGCTGCC	GTGTATGCAGACAAAGCCGCCAGT	77 bp
hrcN	ACGAGCGATCGGAGGTTGCACA	AGTTCATCGAGCTCATTCTTGGCGC	75 bp
hrpB5	CAGGGTCGTGTCCGAGGATGATGTG	GATGAGTGGAACGAATCCGGCCTG	127 bp
hrpB4	TGATCGGCATCGCGCGGTAACA	TTGTATCGAGCGCGAGCGTCTGGA	122 bp
hrcJ	CGCGCGCTGAGATACCTGGTGG	CATGTCGTTCGCATCGTTTTCGGTG	102 bp
hrpB2	CGCACGCCATCGTTCTGCACATC	GCTTTCAAGCGCTGATGCAGTCCTC	109 bp
hrpB1	GCGAACAGGCAGCAGGCGTACAA	TGGACACGTTCGATGCATGGATTTC	133 bp
hrcU	CCGATGATCATTGGCCTTGCCTACC	AGCAGCACGCCCAATGCGAATA	95 bp
hrcV	TGGTCAACATCCTGGCCGGCAT	AGTGAGGCGATCTGCGACACCATG	123 bp
hpaP	GAGCTGGGAAGCCTGGCTGGATATC	GCGAACTGGTATTGAAGCGAAGCGA	107 bp
hrcQ	TGCTACTGAACGAGGACGACCACGC	CGAGGCGATCGGCCAGCAATAT	69 bp
hrcR	CGCACAACAGATCTGGCCCAAGGA	TCAATTCGCTGAGCGTGAAGGCC	92 bp
hrcS	GTTGCTGCTCTGCCTCAAGGTCTCC	CACCAGCTTGAGCGCGAACGAA	130 bp
hpaA	AACGAAGCCAAGCGCGAGTGCATA	CACTGCCGTGCTGATCGCCCT	100 bp
hrpD5	ACGCAGGTGCATCGTTATGATCCAG	TAACGGACGCTGAGCGCGGGAT	110 bp
hrpD6	GGATCCTTCTGGCGAGCGGCTGC	ACGGCATTGAAGTCGTTGCGTGAGG	120 bp
hrpE	GGTGTGTCCGGTGGAATCTCTGGTG	GTTGTTCATGGACTTCTGGGCCTCG	114 bp
hpaB	TCTATCTCCACGAGCCGACGCCA	GGCAGTCCGTAGGAGATGCGCAGAT	82 bp
hrpF	ACCGGATCTGAAGAAGGCATTGACG	CTTTGATCTTGCCGCCGCACTTG	101 bp
hpaF	CACGACTGCCCGCTCAATGCGATAT	TCGCGGATTTGCAGCAATTGGC	70 bp
gyrA	TGATGGCCTCAAGCCTGTGCACCGG	GCCGACGATACGCGCCGACTTGAAG	100 bp