

Table S1 Strains and plasmids used in this study

Strains/Plasmids	Characteristics	Source
<b><i>P. protegens</i></b>		
Pf-5	Wild type, Ap <sup>r</sup>	[19]
$\Delta ofaA$	Pf-5 deleted the <i>ofaA</i> gene, Ap <sup>r</sup>	This study
$\Delta pltB$	Pf-5 deleted the <i>pltB</i> gene, Ap <sup>r</sup>	This study
$\Delta phlA$	Pf-5 deleted the <i>phlA</i> gene, Ap <sup>r</sup>	This study
$\Delta prnA$	Pf-5 deleted the <i>prnA</i> gene, Ap <sup>r</sup>	This study
$\Delta rzxB$	Pf-5 deleted the <i>rzxB</i> gene, Ap <sup>r</sup>	This study
$\Delta hcnABC$	Pf-5 deleted the <i>hcnABC</i> gene, Ap <sup>r</sup>	This study
$\Delta pFL4656$	Pf-5 deleted the <i>pFL4656</i> gene, Ap <sup>r</sup>	This study
<b><i>P. ananatis</i></b>		
DZ-12	Wild-type	[2]
DZ-12( <i>gfp</i> )	Wild-type transformed with pBBR-GFP, Gen <sup>R</sup>	[2]
<b><i>E. coli</i></b>		
Top10	<i>mcrA</i> $\Delta$ ( <i>mrr-hsdRMS-mcrBC</i> ) $\phi$ 80 <i>lacZ</i> $\Delta$ M15 $\Delta$ <i>lacX74</i> <i>recA1</i> <i>araD139</i> $\Delta$ ( <i>ara-leu</i> )7697 <i>galU</i> <i>galK</i> <i>rpsL</i> (Str <sup>r</sup> ) <i>endA1</i> <i>nupG</i>	TaKaRa Company
<b>Plasmids</b>		
pK18mobsacB	Broad-host-range gene replacement vector; <i>sacB</i> , Km <sup>r</sup>	Laboratory stock
pRK-2013	Helper plasmid for triparental mating; Km <sup>r</sup>	Laboratory stock
pK18- <i>ofaA</i>	pK18mobsacB with <i>Sal</i> I- <i>Hind</i> III insert of 330 bp and 308 bp segments flanking <i>ofaA</i> , Km <sup>r</sup>	This study
pK18- <i>pltB</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 770 bp and 770 bp segments flanking <i>pltB</i> , Km <sup>r</sup>	This study
pK18- <i>phlA</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 542 bp and 512 bp segments flanking <i>phlA</i> , Km <sup>r</sup>	This study
pK18- <i>prnA</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 770 bp and 770 bp segments flanking <i>prnA</i> , Km <sup>r</sup>	This study
pK18- <i>rzxB</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 740 bp and 733 bp segments flanking <i>rzxB</i> , Km <sup>r</sup>	This study
pK18- <i>hcnABC</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 452 bp and 518 bp segments flanking <i>hcnABC</i> , Km <sup>r</sup>	This study
pK18- <i>pFL4656</i>	pK18mobsacB with <i>Xba</i> I- <i>Hind</i> III insert of 566 bp and 529 bp segments flanking <i>pFL4656</i> , Km <sup>r</sup>	This study

Table S2 DNA primers used in this study

Primer	Primer sequence (5'→3')
<b>For mutants construction</b>	
<i>ofa</i> - F1	ACGCGTCGACTGGGTCAAGCCCTTGCGA ( <i>Sal</i> I)
<i>ofaA</i> -R1	TGACATGGGAAGCCGGGAGGCGGAAAAATGCGTCAT
<i>ofaA</i> -F2	ATGACGCATTTTTCCGCCTCCCGGCTTCCCATGTCA
<i>ofaA</i> -R2	CCCAAGCTTAGCAGGTCCTCCTGTTCC ( <i>Hind</i> III)
<i>ofaA</i> -outF	AAATCGCTGATCGATGCGC
<i>ofaA</i> -outR	TCCGGGGTGATCCTGAAGG
<i>pltB</i> -F1	CTAGTCTAGATCGACTACATCTTCATTCACT ( <i>Xba</i> I)
<i>pltB</i> -R1	ATCAGCTCGGCCCCGTGACAATCCACTCCCGATGATTGCAA
<i>pltB</i> -F2	TTGCAATCATCGGGAGTGGATTGTCACGGGCCGAGCTGAT
<i>pltB</i> -R2	CCCAAGCTTGTGCAGGGCCACCAGGGAT ( <i>Hind</i> III)
<i>pltB</i> -outF	AAGGCCAAGATGGTGGTGG
<i>pltB</i> -outR	CGCTTGAGCGCAAGGATCA
<i>phlA</i> -F1	CTAGTCTAGAGGAAGTGAGAATGGCTTTA ( <i>Xba</i> I)
<i>phlA</i> -R1	CTTGCGTAGACAGGCGTAAGTTCATTTTCCTCTTGATTCC
<i>phlA</i> -F2	GGAATCAAGAGGAAAATGAACTTACGCCTGTCTACGCAAG
<i>phlA</i> -R2	CCCAAGCTTATAGCCGAACCTCTGGAAG ( <i>Hind</i> III)
<i>phlA</i> -outF	TAAACCTCGGCGATCAACG
<i>phlA</i> -outR	CGCTGTTCTTCAACACTTCC
<i>prnA</i> -F1	CTAGTCTAGACTGGCCCATGACGGCCCG ( <i>Xba</i> I)
<i>prnA</i> -R1	TTCCTGAGCCGCGAGCGTGCGGTGCCGCCGCCACG
<i>prnA</i> -F2	CGTGGGCGGCGGCACCGCACGCTCGCGGCTCAGGAA
<i>prnA</i> -R2	CCCAAGCTTTTCTCGATAAGCTGGGTCGTCC ( <i>Hind</i> III)
<i>prnA</i> -outF	GCTTCGTGGCCATGGAAAT
<i>prnA</i> -outR	CGCAGCAGGACCTTGAAGA
<i>rxzB</i> - F1	CTAGTCTAGACGTTGTCTTGCAGCAAGCG ( <i>Xba</i> I)
<i>rxzB</i> -R1	GCGCTGGTGAAGGACATCAGAGCTCGCGCAGGTAGTGG
<i>rxzB</i> -F2	CCACTACCTGCGCGAGCTCTGATGTCCTTACCAGCGC
<i>rxzB</i> -R2	CCCAAGCTTCGGACAAACCTTCATCCCACT ( <i>Hind</i> III)
<i>rxzB</i> -outF	TTGCCATTGGCAATTTTTCTG
<i>rxzB</i> -outR	CTCGATCAGCACCTGATTG
<i>hcnABC</i> -F1	CTAGTCTAGAGCCGTGGTCTGGCTTGAAA ( <i>Xba</i> I)

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<i>hcnABC</i> -R1	GCCAGCGCCTACAGAGCGGTGTGGGTTCATCCGTGAAAA
<i>hcnABC</i> -F2	TTTTCACGGATGAACCCACACCGCTCTGTAGGCGCTGGC
<i>hcnABC</i> -R2	CCCAAGCTTCATCGACTACCTGGAAACCC ( <i>Hind</i> III)
<i>hcnABC</i> -outF	TGGAAGAAGCCAAGCAGGC
<i>hcnABC</i> -outR	CTGCCCTTCGAGCATCACT
<i>pFL4656</i> -F1	CTAGTCTAGACCATTTTTTCAGCAACCCGCA ( <i>Xba</i> I)
<i>pFL4656</i> -R1	GGCGTTCATGGAGGTTTCTGATATCCCTGCCTTGTTGTT
<i>pFL4656</i> -F2	AACAACAAGGCAGGGATATCAGAAACCTCCATGAACGCC
<i>pFL4656</i> -R2	CCCAAGCTTAGGTCTTCTGGATGTGCTCC ( <i>Hind</i> III)
<i>pFL4656</i> -outF	CTGATCATCGAGCCGATCCA
<i>pFL4656</i> -outR	TACAGCAGGATGCCGAGAT

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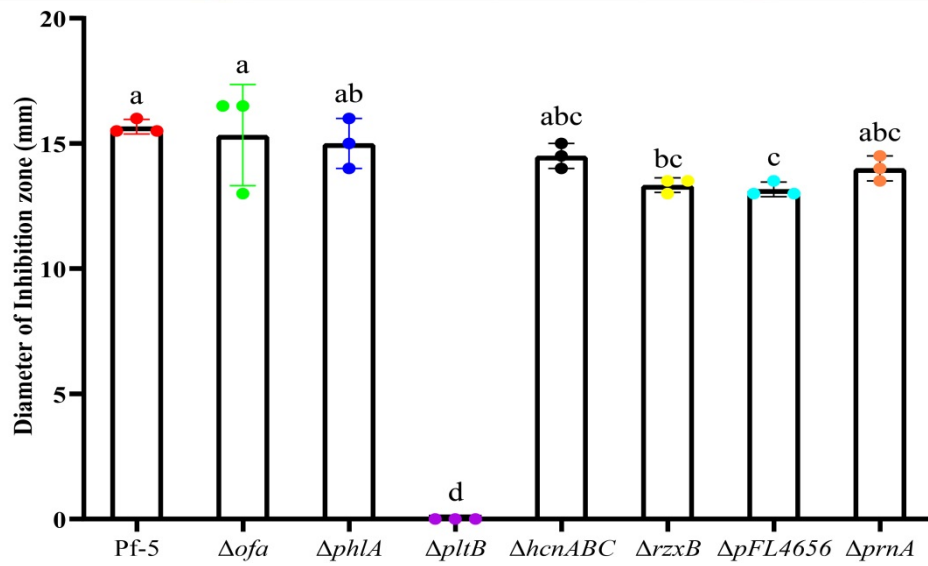
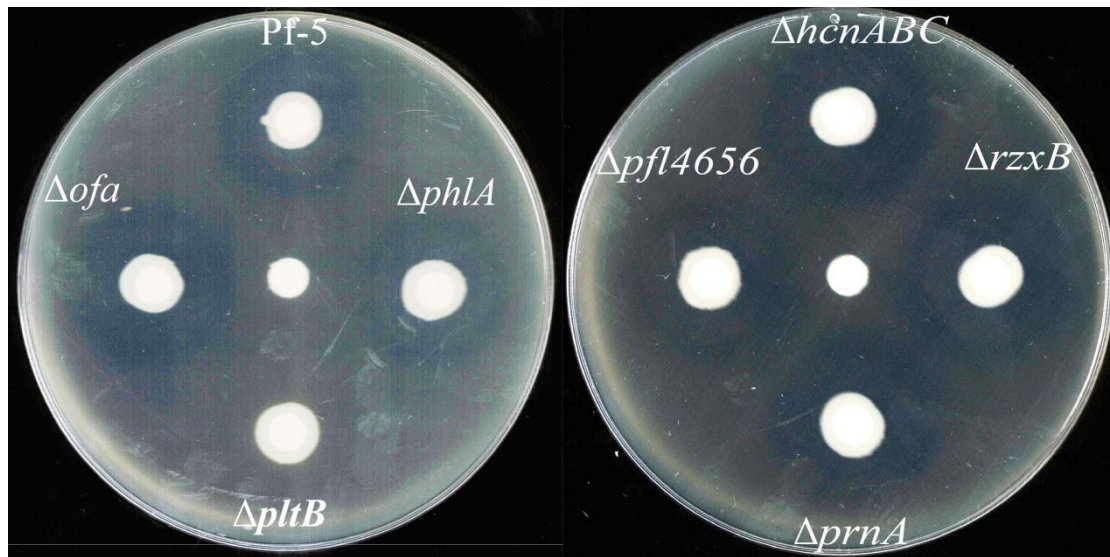


Figure S1 The antibacterial activity detection of Pf-5 and its mutants. The graph data show the average diameter (mm)  $\pm$  standard deviation (SD) of three replicates. Different letters represent statistically significant differences according to the one-way ANOVA test ( $P < 0.05$ ).