1 125 259 575 59	625 759 812	1 125 259 375 549 625	754 875 1444 1476
RF +1		RF +1	
Specific hits PEI		Superfamilies ImpA_N superfamily	
TIZOC SUPERTAILING		Description	Max Total Query E Ident Accession
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serinethreonine-protein phosphatase (Acidovoras avenae)	535 535 99% 0.0 99% <u>WP_019703458.1</u>	top Visecreton system protein ISSA Academican manael      top Visecreton system protein ISSA Academican	602 602 9975 0.0 10076 WP 02545449/1
serine/breonine-scotein shoss/halase (Acidovorax onstae)	534 534 99% 0.0 99% <u>WP 025432125.1</u>	the Visection system protein ISSA Academic average     the Visection extent extent State Bridgeneral	537 537 3676 0.0 3976 WP 013701340.1
serinethreonine-protein phosphatase [Acidovoras avenae]	531 531 99% 0.0 99% <u>WP 013596962.1</u>	the insection system protein isso inclusion areas     the Mississian system rester.	580 580 9898 0.0 5238 mr 000998001
astinethreonine-protein phosphalase (Acidovorax obuili)	530 530 99% 0.0 98% <u>WP-011797882.1</u>		John John John C.C. Jillin III Viscoberger
1 540 1440 1540	2000 2500 2512	1	ops +5+ 525 522
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Description	Max Total Query E Ident Accession	Description	Max Total Query E Ident Accession
	SCORE SCORE COVER Value	ULTISPECIES: top VI secretion system contractile sheath small subunit Acidovorad	370 370 99% 6e-130 100% WP 019701341.1
HULISPECIES APP-element chapterions Cable Accounting     ATP-dependent chapterions Cable Accounting	1625 1625 3956 0.0 100% WP 012/02/40/1 1623 1623 99% 0.0 99% WP 011794382.1	tore Vi secretion system contractile sheath small subunit (Kidoorcar avenae)	369 369 99% 3e-129 99% <u>WP 013593959.1</u>
ATP-dependent chaperone CipB (Addonorax avenae)	1622 1622 99% 0.0 99% WP 013593720.1	tope VI secretion system contractile sheath small subunit likidoosras obuilit	366 366 99% 5e-128 98% <u>WP_011794617.1</u>
AIP-dependent chaperone CipB (Addonras califerae)	1618 1618 99% 0.0 99% <u>WP 092831795.1</u>	tppe VI secretion sustem contractile sheath small subunit likidovoras catilerael	364 364 99% 3e-127 98% <u>WP 092838496.1</u>
F 41	• • • • • • • • • • • • • • • • • • • •	259 546 759	1000 1250 1500
Specific hits		Superfamilies VipB superf	amily
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High Tamir hop VI secreton system effector (Addoorse)	201 201 337% 28-37 100% WP 013033948.1 272 272 98% 96-92 95% WP 092954457.1	type VI secretion system contractile sheath large subunit (Acidovorax avenae)	982 982 99% 0.0 99% <u>WP 013593960.1</u>
Hop 1 family type VI secretion system effector (Acidovorus otrufii)	271 271 98% 2e-91 96% WP 011794606.1	tipe. VI secretion system contractile sheath large subunit (Adidovorax citruli)	981 981 99% 0.0 99% <u>WP.011794618.1</u>
Hop1family tope VI secretion system effector (Acidovoras catilevae)	271 271 98% 4e-91 95% <u>WP 092838467.1</u>	tope VI secretion system contractile sheath large subunit (Acidovorax koniaci)	961 961 99% 0.0 98% <u>WP 092954430.1</u>
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type VI secretion system-associated FHA domain protein TagH (Acidovnrax ontae)	1033 1033 97% 0.0 98% <u>WP 025434459.1</u>	U WLITISPECIES virulence protein Sole tope (Acidovorau)	486 486 99% 5e-173 100% <u>WP 019701343.1</u>
tope VI secretion system-associated FHA domain protein TapH (Acidovorax avenae)	970 970 97% 0.0 88% <u>WP 053844517.1</u>	U vinience protein Solit the Rodovorar avenael	484 484 99% 5e-172 99% WP 013939511
tope VI secretion sustem-associated FHA domain protein TapH (Acidovorax avenae)	965 965 97% 0.0 85% <u>WP_013593951.1</u>	instance protein sole for Account and	403 403 57% 00-112 50% WF 303044021.1
type VI secretion system-associated FHA domain protein TagH (Acidovorax citrulit)	922 922 97% 0.0 80% <u>WP_011794609.1</u>	C WARTER DAME, SOE DRI HODWAR DRIF MANY II	410 410 33/8 20103 30/8 <u>CONSCRET</u>
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Superfamilies T6SS-SciN superfamily		Supertantites Grw_gp25 Supertantity	
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Description  RATIFECCES have it is another is safe in the series in has it indexes and to be it is another is another is ball indexes and it is an it is another is another is another it is another is another it i	NOTE SCORE         Code Work         Accession           349         359         74-753         NOVE         SCORE         357           357         357         95%         24-124         95%         107         201200251           343         348         95%         16-202         95%         107         202204621           344         346         95%         66-202         95%         107         202204621           344         346         95%         66-202         95%         107         202204621           344         346         95%         66-202         95%         107         107204111           345         346         95%         66-202         95%         107         107204111	HATEPECET to a l'accelte solen basedie solen TolE Noteend     tout la conten basedie solen TolE Noteend     tout la conten basedie solen TolE Noteend contend     tout la conten solen basedie solen TolE Noteen contend     tout la conten solen basedie solen TolE Noteen contend      For -1	327         327         59%         5+10         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%         10%
Decoption     MLTDPICEL see It some safe in balance safe     text it some the interaction. That it detormed in that it de	NOM         NOM         CARGED           309         309         74         700         800         CARGED           309         307         74         74         700         800         RECENDENT           307         307         976         24         976         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800         800 </td <td>HATEFACET too it toording and in based in solute That Robows and the Advanced in the Adva</td> <td>227         227         59%         5e+10         100%         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100&lt;</td>	HATEFACET too it toording and in based in solute That Robows and the Advanced in the Adva	227         227         59%         5e+10         100%         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100<
Decorption     MLTSPECIER See 11 secretion tasking interpretent in all Acchanges and the secretion tasking interpretent in all Acchanges and the secretion tasking interpretent interp	NOW SCOM         Come with Mont         Accession           359         359         596         596         596         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597         597	BLATERCEE to a literative antime based in advert fuel Roborned     too literative modern based in advert fuel Roborne annuel     too literative modern based in advert fuel Roborne annuel     too literative modern based in advert fuel Roborne annuel     too literative modern based in advert fuel Roborne annuel     too literative modern based in advert fuel Roborne annuel     for -1         Security fuel Roborne annuel         Security fuel Roborne	327         327         595         59-10         100%         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100<
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Decorption     WATEFECRET.Next X seconds and/or Tax220000000     WATEFECRET.Next X seconds and/or Tax2200000000000000000000000000000000000	Norm Scott         Constraint         Constraint           309         309         307         725         507         807         201720251           309         309         309         307         307         95%         201720251         308         308         95%         100         201720251         308         308         95%         100         201720251         308         308         95%         100         201720251         308         308         95%         100         201720251         308         308         95%         100         201720251         308         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100	HALTEPECEE to a li scotte subin hanni hanni na den li në Kotonund     tor li scotte subin hanni ti në Kotonu senid     tor li scotte subin hanni ti në Kotonu senid     tor li scotte subin hanni ti në Kotonu senid      Fr -1     Seperi fan li se     TeSS, Tesë     TeSS, Tesë     Seperi fan li se     Descoten subin hanni ti në Kotonu senid      Ku Altereto subin hanni ti në Kotonu dinë     Seperi se ti scotte subin hanni ti në Kotonu dinë     Descoten subin hanni ti në Kotonu dinë     Seperi se ti scotte subin hanni ti në Kotonu dinë     Descoten     Descoten     Seperi se ti scotte subin hanni ti në Kotonu dinë	327         327         59%         5+10         50%         100%         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100         100 </td
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**Figure S1.** BLASTX images, generated in NCBI databases, showing the presence of T6SS putative proteins in *Acidovorax avenae* subsp. *avenae* strain RS-2, which were homologs in closely related bacteria such as *A. avenae* subsp. *avenae* ATCC 19860 and *Acidovorax citrulli* AAC00-1. Note: Similar results were found for vgrG 1~8 due to high sequence similarity. Here only show one verG result as an example.



Figure S2. Phylogenetic tree, generated by the neighbour-joining method using T6SS gene sequences of bacteria from Acidovorax avenae subsp. avenae strain RS-1, RS-2, and ATCC 19860; Acidovorax citrulli AAC00-1, showing the homologs of T6SS among the members of the genus Acidovorax. The two-parameter Kimura correction of evolutionary distances was used. Bootstrap analysis (1000 replicates) for node values greater than 50% are given. Bar 0.1 substitutions per nucleotide position.

T6SS genes	Locus Tag	Putative Functions		
pppA	Acav_4620	protein serine/threonine phosphatase		
clpB	Acav_1267	ATP-dependent chaperone		
hcp	Acav_1504	hypothetical protein		
fHA	Acav_1507	FHA domain-containing protein		
lip	Acav_1509	type VI secretion lipoprotein		
impJ	Acav_1510	type VI secretion protein		
dotU	Acav_1511	type VI secretion protein		
icmF	Acav_1512	type VI secretion protein		
impM	Acav_1513	type VI secretion system-associated protein		
impA	Acav_1514	type VI secretion-associated protein		
impB	Acav_1515	type VI secretion protein		
impC	Acav_1516	type VI secretion protein		
impE	Acav_1517	type VI secretion protein		
impF	Acav_1518	Lysozyme-like protein		
dUF879	Acav_1519	type VI secretion protein		
impH	Acav_1520	type VI secretion protein		
clpV	Acav_1521	ATPase		
vgrG-1	Acav_0298	type VI secretion-associated protein		
vgrG-2	Acav_0662	type VI secretion-associated protein		
vgrG-3	Acav_2399	type VI secretion-associated protein		
vgrG-4	Acav_3111	type VI secretion-associated protein		
vgrG-5	Acav_3369	type VI secretion-associated protein		
vgrG-6	Acav_3676	type VI secretion-associated protein		
vgrG-7	Acav_3724	type VI secretion-associated protein		
vgrG-8	Acav_1905	type VI secretion-associated protein		

**Table S1** *In silico* predictions of type VI secretion system genes in *Acidovorax avenae* subsp. *avenae* strain RS-2 genome and their sequence homologies with that of strain RS-1, and ATCC 19860 of Aaa, as well as strain AAC00-1 of *Acidovorax citrulli*.

Table S2 Strains and plasmids used in this study.					
Strain or plasmid	Relevant characteristics <sup>a</sup>	Sources or references			
Acidovorax avenae subsp. avenae strains					
	Rif <sup>R</sup> ; The pathogen of bacterial brown stripe of rice,				
RS-2	isolated from the diseased rice from Zhejiang	Lab collection			
	province in China				
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
∆pppA	defective in <i>pppA</i>	This study			
	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta pppA$ complemented with				
<i>∆pppA</i> -comp	pRADK-pppA	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
∆clpB	defective in <i>clpB</i>	This study			
	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta clpB$ complemented with				
<i>∆clpB</i> -comp	pRADK-clpB	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
⊿hcp	defective in <i>hcp</i>	This study			
	Rif <sup><math>\mathbf{R}</math></sup> , Amp <sup><math>\mathbf{R}</math></sup> , Kan <sup><math>\mathbf{R}</math></sup> ; $\Delta hcp$ complemented with with				
<i>∆hcp</i> -comp	pRADK-hcp	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
ΔfHA	defective in <i>fHA</i>	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
$\Delta lip$	defective in <i>lip</i>	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
⊿ımpJ	defective in <i>impJ</i>	This study			
4.° T	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta impJ$ complemented with				
<i>∆ımpJ</i> -comp	pRADK-impJ	This study			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
⊿aotU	defective in <i>dotU</i>	This study			
4 1 <i>1</i> 1 T	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta dot U$ complemented with				
⊿ <i>aotU</i> -comp	pRADK- dotU	This study			
<b>4</b> · <b>F</b>	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This states			
$\Delta i C M F$	defective in <i>icmF</i>	This study			
<b>4</b> : <b>F</b>	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta icmF$ complemented with	This states			
⊿ <i>icmF</i> -comp	pRADK-icmF	This study			
4	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This states			
$\Delta impM$	defective in <i>impM</i>	This study			
	Rif <sup>R</sup> , Amp <sup>R</sup> , Kan <sup>R</sup> ; $\Delta impM$ complemented with	This stades			
⊿ <i>impl</i> vi-comp	pRADK- <i>impM</i>	This study			
A A	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation				
⊿ımpA	defective in <i>impA</i>	This study			
4. 5	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	TTL: 1			
⊿ıтрВ	defective in <i>impB</i>	This study			
∆impC	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study			

	defective in <i>impC</i>			
	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	<b>T1</b> • • 1		
⊿impE	defective in <i>impE</i>	This study		
Λ <i>ί</i> Γ	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	<b>T1</b> • • 1		
⊿impF	defective in <i>impF</i>	This study		
4.11.17.07.0	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	TT1 · / 1		
Zaur879	defective in <i>dUF879</i>	This study		
A	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation			
⊿ттрн	defective in <i>impH</i>	This study		
4 1 17	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	<b>TTI • • 1</b>		
ZCIPV	defective in <i>clpV</i>	This study		
Amore 1	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
ZUgrG-1	defective in <i>∆vgrG-1</i>	This study		
Amore 2	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
2087G-2	defective in <i>∆vgrG</i> -2	This study		
Amore 3	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
20810-5	defective in <i>∆vgrG-3</i>	THIS Study		
AziarC-4	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
203/01	defective in <i>△vgrG-4</i>	This study		
AwarG-5	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
_08,00	defective in $\triangle vgrG-5$	inis stady		
AwarG-6	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
-03100	defective in $\triangle vgrG-6$	This study		
∆norG-7	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
08,01	defective in $\triangle vgrG-7$	This study		
∆vorG-8	Rif <sup>R</sup> , Kan <sup>R</sup> ; RS-2 in-frame deletion mutation	This study		
	defective in <i>△vgrG-8</i>	1110 50000		
	Escherichia coli strains			
$DH5\alpha$	F- $\Phi$ 80d lacZ $\Delta$ M15 $\Delta$ (lacZYA-argF) U169 recA1endA1,	Invitrogen		
211000	hsdR17(rk⁻, mk+) phoAsupE44 λ⁻ thi-1 gyrA96relA1	invitiogen		
	$\lambda$ Lysogenic S17-1 derivative producing $\pi$ protein			
S17-1 $\lambda$ pir	for replication of plasmids carrying <i>oriR6K</i> ;	Simon et al., 1983		
	<i>recAprohsdR</i> RP4-2-Tc::Mu-Km::Tn7 λ-pir			
Plasmids				
pIP5603	Kan <sup>R</sup> ;R6K-based suicide vector; requires the	Penfold and		
r)- 0000	<i>pir</i> -encoded $\pi$ protein for replication	Pemberton, 1992		
pGEM-T	Amp <sup>R</sup> ; cloning vector	Promega		
pRADK	Amp <sup>R</sup> , Chl <sup>R</sup> , Km <sup>R</sup> ; broad host expression vector	Gao et al., 2005		
A D T D D		·		

<sup>a</sup>Amp<sup>R</sup>, Kan<sup>R</sup>, Rif<sup>R</sup>, Chl<sup>R</sup> indicate resistant to Ampicillin-, Kanamycin-, Rifampicin-, Chloramphenicol -, respectively.

Table S3 List of primers used in this study.				
Primers	Nucleotide sequences (5'-3')	Characterization		
pppA-F	CGCGGATCCAAGCCTGCGTGGACT (B)	324 bp internal upstream		
pppA-R	<u>GGAATTC</u> GCACCTGGAACTCATTG (E)	to create $\Delta pppA$ ; used		
clpB-F	CGGGATCCGGACGAGGGACAGAC(B)	339 bp internal upstream		
clpB-R	CGGAATTCATGTAGCGGTGGGAC(E)	create $\Delta clpB$ ; used to		
hcp-F	CGGGATCCGACCGACATCCGTTCC(B)	235 bp internal upstream		
hcp-R	<u>GGAATTC</u> GGTGAGGGTGATCTTGC(E)	fragment of <i>hcp</i> ; used to create $\Delta hcp$		
fHA-F	CGGGATCCTCAGCCCTGTTTCCA(B)	237 bp internal upstream		
fHA-R	CGGAATTCTTTCCTCGCTCTTGC(E)	tragment of <i>fHA</i> ; used to create $\Delta fHA$		
lip-F	CGGGATCCCAGCAACCTGAACCG(B)	192 bp internal upstream		
lip-R	CGGAATTCGCCTCGTCCTTGTCC(E)	fragment of <i>lip</i> ; used to create $\Delta lip$		
impJ-F	CGGGATCCAACAGGACCGCTACACC(B)	432 bp internal upstream		
impJ-R	CCGGAATTCGGCTCACCCACCCAT(E)	fragment of <i>impJ</i> ; used to create $\Delta impJ$		
dotU-F	CGGGATCCGGCATTCCAGCATTAC(B)	303 bp internal upstream		
dotU-R	CGGAATTCAAACCGAGCGTCAGG(E)	fragment of $dotU$ ; used to create $\Delta dotU$		
icmF-F	CGGGATCCCGGCAACAACCAGAA(B)	766 bp internal upstream		
icmF-R	<u>GGAATTC</u> CTCATGCGAGAAAACG(E)	create $\Delta icmF$ ; used to		
impM-F	CGGGATCCCGCTGCTATCCGCTCAC(B)	278 bp internal upstream		
impM-R	<u>CCGGAATTC</u> AACATCGCCTCGCCAC(E)	to create $\Delta impM$ ; used		
impA-F	<u>CGGGATCC</u> AGGACGGCGACTACTT(B)	355 bp internal upstream		
impA-R	CCGGAATTCTCGTTCAGCACCACC(E)	to create $\Delta impA$ ; used		
impB-F	CGGGATCCTGATGGCGGACCTCT(B)	147 bp internal upstream		
impB-R	CGGAATTCCCGTCAGCGTGTTGG(E)	to create $\Delta impB$ ; used		
impC-F	CGGGATCCGGACCAGAGCCCTAT(B)	468 bp internal upstream		
impC-R	CGGAATTCAACGAGCGGTTGATG(E)	to create $\Delta impC$ ; used		
impE-F	CGGGATCCCTCGGATGGATGGTG(B)	292 bp internal upstream		
impE-R	CGGAATTCCGTTCTGGAGCGTGA(E)	to create $\Delta impE$ ; used		
impF-F	CGCGGATCCGCCGAAGCGGTCTAT(B)	307 bp internal upstream		

impF-R	CGGAATTCGCAGGGTGTTGTGGTG(E)
dUF879-F	CGCGGATCCTTTCGTGCCGTTCTT(B)
dUF879-R	GGAATTCGCGAGGTAGTTGAGGG(E)
impH-F	CGCGGATCCATCCGCATCCGTTCG(B)
impH-R	<u>GGAATTC</u> CCGTTGGGACCATAGAG(E)
clpV-F	CGGGATCCGCTATGTGGGCTACG(B)
clpV-R	CGGAATTCCATCGACCGAACTCT(E)
vgrG-1-F	CGGGATCCCCGACCGTGAGAATA(B)
vgrG-1-R	CGGAATTCGGGGGTTTTGGAGTTT(E)
vgrG-2-F	CGCGGATCCTCGTGGAAGAGGTTT(B)
vgrG-2-R	CGGAATTCGCTTGGCACTGTTGAA(E)
vgrG-3-F	CGGGATCCACCAGAAGGGGATAGAG(B)
vgrG-3-R	CGGAATTCTTGGGACTGATGAGGCT(E)
vgrG-4-F	CGGGATCCTCGTGGAAGAGGTTTTGA(B)
vgrG-4-R	CGGAATTCGATGAGGTACTGCTGGTT(E)
vgrG-5-F	CGGGATCCCATCGCCTCTACTCCTAC(B)
vgrG-5-R	CGGAATTCCTGCTCTTCGTTGTGCTT(E)
vgrG-6-F	CGCGGATCCCGCCTGGGATTACTG(B)
vgrG-6-R	CGGAATTCGCTGTTGAACGAGGAA(E)
vgrG-7-F	CGGGATCCCGCCGAACTGAACAA(B)
vgrG-7-R	CGGAATTCGCAGCCCAGGATGAT(E)
vgrG-8-F	CGGGATCCCAACGACGACTACGAC(B)
vgrG-8-R	CCGGAATTCAGAGCCCTCTTCCTG(E)
Aaa-F	GACCAGCCACACTGG GAC
Aaa-R	CTGCCGTACTCCAGCGAT
pJP5603-F	CTGATGCCGCCGTGTTC
pJP5603-R	CCAATAGCAGCCAGTCCCT
16s rDNA-F	AGAGTT TGATCCTGGCTCAG
16s rDNA-R	GGTTACCTTGTTACGACT T

fragment of *impF*; used to create *∆impF* 396 bp internal upstream fragment of dUF879; used to create ⊿*dUF879* 226 bp internal upstream fragment of *impH*; used to create  $\triangle impH$ 526 bp internal upstream fragment of *clpV*; used to create  $\triangle clpV$ 564 bp internal upstream fragment of *vgrG-1*; used to create *∆vgrG-1* 367 bp internal upstream fragment of *vgrG-2*; used to create *∆vgrG*-2 424 bp internal upstream fragment of *vgrG-3*; used to create *∆vgrG-3* 574 bp internal upstream fragment of *vgrG-4*; used to create  $\Delta vgrG-4$ 637 bp internal upstream fragment of *vgrG-5*; used to create *∆vgrG-5* 593 bp internal upstream fragment of *vgrG-6*; used to create  $\Delta vgrG-6$ 737 bp internal upstream fragment of *vgrG-7*; used to create *∆vgrG*-7 367 bp internal upstream fragment of *vgrG-8*; used to create *∆vgrG-8* 370 bp A. oryzae RS-2 special primers used to screen A. oryzae 112 bp specific primers of pJP5603 for confirming the mutant 1000 bp specific primers of bacterial for checking

the strain sequence

	TGCCATGGTACCCGGGAGCTCGGATGGCG	10101 (	
pppA-comp-F	GCATTGAGCG (S)	1310 bp fragment using	
pppA-comp-R	CGCGTCTGCATGTGGAAGCTTTCAATCGG	nm4 mutant	
	TACGTAGCAACAATCG(H)	<i>ppp</i> <sup>21</sup> mutant	
clpB-comp-F	TGCCATGGTACCCGGGAGCTCCCGTAACA	2110 hp fragmont using	
	GAACCCGACAGC(S)	for complementation of	
clpB-comp-R	CGCGTCTGCATGTGGAAGCTTTTACCCCA	<i>clnB</i> mutant	
	CAGCCGCCGC(H)	<i>cipb</i> indiant	
hen-comp-F	TGCCATGGTACCCGGGAGCTCCCCTTGGA	082 hp fragmont using	
nep-comp-r	ACCCAGGTAGGG(S)	for complementation of	
hen-comp_R	CGCGTCTGCATGTGGAAGCTTTTACATTTC	hen mutant	
пер-сотр-к	CTTGTTGCCCTTGA(H)	nep matant	
dotU-comp-F	TGCCATGGTACCCGGGAGCTCCGGCCCGC	1853 hp fragmont using	
doto-comp-i	GGCCATGCCG(S)	for complementation of	
dotU-comp-R	CGCGTCTGCATGTGGAAGCTTTTAGTTCTT	dot11 mutant	
dote comp it	CGGTGTGCCGG(H)	word matality	
impl-comp-F	TGCCATGGTACCCGGGAGCTCGTGCCGCC	1835 hp fragmont using	
imp) comp i	GGCCGTCTTC(S)	for complementation of	
impl-comp-R	CGCGTCTGCATGTGGAAGCTTTCAGCGCC	<i>implementation of implementation</i>	
intpj-comp-r	GTATGGCCCA(H)	imp) indiant	
icmF-comp-F	TGCCATGGTACCCGGGAGCTCGCCAGTTC	1133 bp fragmont using	
ienn -comp-i	CTGGAGCCCG(S)	for complementation of	
icmE-comp-R	CGCGTCTGCATGTGGAAGCTTTCAGAGAT	<i>icmF</i> mutant	
ienn -comp-ic	TGCCAGGACACGC(H)	in mature	
impM-comp-F	TGCCATGGTACCCGGGAGCTCCGCTTCCG	1106 hp fragmont using	
Implui-comp-i	CCAGGGTGTC(S)	for complementation of	
impM_comp_R	<u>CGCGTCTGCATGTGGAAGCTT</u> CTATGCATT	<i>imnM</i> mutant	
ImpM-comp-R	CGGGCCTCCG(H)	impivi indiani	

<sup>a</sup> Underlined nucleotides in some of the PCR primers represent restriction sites of enzymes indicated in parentheses (B = *Bam*HI; E = *Eco*RI; S = *Sac*I; H: *Hind*III).

Strains	Plant height (cm)	Decrease (%)	Strains	Plant height (cm	) Decrease (%)
ddH2O	$5.78 \pm 0.10^{**}$		∆vgrG-7	$3.25 \pm 0.21^*$	43.77
∆pppA	$4.01 \pm 0.16^{**}$	30.62	∆vgrG-8	$3.57 \pm 0.05^{*}$	38.24
∆clpB	$4.41 \pm 0.17^{**}$	23.70	∆fHA	$2.95\pm0.07$	48.96
∆hcp	$5.41 \pm 0.16^{**}$	6.40	⊿dUF879	$2.93 \pm 0.32$	49.31
⊿impJ	$4.46 \pm 0.08^{**}$	22.84	∆impC	$3.07\pm0.79$	46.89
⊿dotU	$4.09 \pm 1.06^{**}$	29.24	∆impA	$2.58\pm0.27$	55.36
⊿icmF	$4.83 \pm 0.20^{**}$	16.44	⊿clpV	$2.95 \pm 0.22$	48.96
∆impM	$4.76 \pm 0.22^{**}$	17.65	∆impF	$2.67\pm0.23$	53.81
∆vgrG-1	$3.49\pm0.26^*$	39.62	∆impB	$2.92\pm0.08$	49.48
⊿vgrG-2	$3.44 \pm 0.14^{*}$	40.48	⊿impE	$2.41\pm0.12$	58.30
∆vgrG-3	$3.57 \pm 0.15^{*}$	38.24	∆lip	$2.86\pm0.10$	50.52
∆vgrG-4	$3.16 \pm 0.05^*$	45.33	∆impH	$3.04 \pm 0.12$	47.40
∆vgrG-5	$3.57 \pm 0.05^{*}$	38.24	wild-type	$2.15 \pm 0.08$	62.80
∆vgrG-6	$3.53 \pm 0.15^{*}$	38.93			

**Table S4** Effect of type VI secretion system on the plant height of *Acidovorax avenae* subsp. *avenae* strain RS-2 to rice seedling.

"\*" 0.01 , significant difference; "\*\*" <math>p < 0.01, very significant difference; not marked with 0.05 < p, no significant difference. The wild-type and ddH<sub>2</sub>O were used as the positive and negative control, respectively.