

Supplementary Table 1. Bacterial strains and plasmids used in this study

Bacterial strains and plasmids	Characteristics	Source or reference
<i>Escherichia coli</i>		
DH5 α	Strain used for cloning	Promega
EC100D	Strain used for generating Tn5 inserted plasmids	Epicentre
<i>Acidovorax citrulli</i>		
KACC17005	Wild-type, Rif ^r	Park et al. (2017)
<i>Ac</i> (EV)	Wild-type carrying the pBBR1-MCS5, Rif ^r , Gm ^r	This study
Δ GlpdAc	Tn5 insertional knock out mutant in glycerol-3-phosphate dehydrogenase (GlpdAc), Rif ^r , Km ^r	This study
Δ GlpdAc (EV)	Glycerol-3-phosphate dehydrogenase (GlpdAc) knock out mutant carrying pBBR1-MCS5, Rif ^r , Km ^r , Gm ^r	This study
Δ GlpdAc (GlpdAc)	The complemented strain, Δ G3PdH carrying pBBR1-G3PdH, Rif ^r , Km ^r , Gm ^r	This study
Plasmid		
pGem-T easy	TA cloning vector, Am ^r	Promega
pGem-GlpdAc	pGem-T easy inserted by 1058-bp glycerol-3-phosphate dehydrogenase (GlpdAc) fragment by TA ligation, Am ^r	This study
pBBR1-MCS5	Broad-host-range vector for generation of complemented strain, Gm ^r	Kovach et al. (1995)
PBBR1-GlpdAc	pBBR1-MCS5 inserted glycerol-3-phosphate dehydrogenase (GlpdAc) fragment from pGem-G3PdH, Gm ^r	This study

Rif^r, Gm^r, Km^r, and Am^r represent resistance to rifampicin, gentamycin, kanamycin, and ampicillin.

References

- Kovach, M. E., Elzer, P. H., Hill, D. S., Robertson, G. T., Farris, M. A., Roop, R. M. 2nd. and Peterson, K. M. 1995. Four new derivatives of the broad-host-range cloning vector pBBR1MCS, carrying different antibiotic-resistance cassettes. *Gene* 166:175-176.
- Park, H.-J., Seong, H. J., Sul, W. J., Oh, C.-S. and Han, S.-W. 2017. Complete genome sequence of *Acidovorax citrulli* strain KACC17005, a causal agent for bacterial fruit blotch on watermelon. *Korean J. Microbiol.* 53:340-341.

Supplementary Table 2. Proteins and PSMs from LC-MS/MS analysis

Strain	1st		2nd		3rd		Shared protein in 3 biological proteins
	Protein	PSM	Protein	PSM	Protein	PSM	
<i>Ac</i>	751	59,405	757	58,831	752	59,569	696
<i>Ac</i> Δ GlpdAc	726	59,367	695	58,960	722	59,261	658

PSM, peptide spectral match; LC-MS/MS, liquid chromatography-tandem mass spectrometry.

Supplementary Table 3. Classification of more abundant (>2 fold) proteins in *Ac* strain by clusters of orthologous group analysis

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group
C (energy production and conversion)	ATG94554	Aldo/keto reductase	*	-	-
	ATG95415	Ubiquinone biosynthesis protein UbiH	*	-	H
E (amino acid metabolism and transport)	ATG92932	Sulfate ABC transporter ATP-binding protein	*	-	-
	ATG93408	Cysteine synthase CysM	*	-	-
	ATG94174	Chorismate synthase	*	-	-
	ATG94599	Peptidase M14	*	-	-
	ATG95284	Imidazoleglycerol-phosphate dehydratase	*	-	-
F (nucleotide metabolism and transport)	ATG93697	HIT domain-containing protein	*	-	G
	ATG95028	dUTP diphosphatase	*	-	-
	ATG96186	Adenine phosphoribosyltransferase	*	-	-
G (carbohydrate metabolism and transport)	ATG94560	Fructose 1/6-bisphosphatase	*	-	-
	ATG94961	C4-dicarboxylate ABC transporter substrate-binding protein	*	-	-
H (coenzyme metabolism)	ATG96454	Uroporphyrinogen decarboxylase	2.70	0.005	-
	ATG93857	8-Amino-7-oxononanoate synthase	*	-	-
	ATG93863	Quinolinate synthase NadA	*	-	-
	ATG96237	Riboflavin synthase	*	-	-
J (translation)	ATG93509	50S ribosomal protein L33	*	-	-
	ATG95424	tRNA (N6-isopentenyl adenosine(37)-C2)-methyltransferase MiaB	*	-	-
	ATG96211	Ribosomal RNA small subunit methyltransferase A	*	-	-
	ATG96264	Methionyl-tRNA formyltransferase	*	-	-
	ATG96377	L-threonylcarbamoyladenylate synthase	*	-	-
	ATG93643	Bifunctional (p)ppGpp synthetase/guanosine-3'/5'-bis(diphosphate) 3'-pyrophosphohydrolase	*	-	T
K (transcription)	ATG95456	IcIR family transcriptional regulator	*	-	-
	ATG94954	Peptidase	*	-	-
	ATG95298	ABC transporter	*	-	-
	ATG95317	Penicillin-binding protein 1A	*	-	-
	ATG96717	dTDP-4-dehydrorhamnose 3/5-epimerase	*	-	-
N (cell motility)	ATG95628	Twitching motility protein PilT	*	-	U
	ATG95814	Methyl-accepting chemotaxis protein	*	-	-
O (post-translational modification, protein turnover, chaperone functions)	ATG93406	Hypothetical protein CQB05_04600	*	-	-
	ATG93868	Glutaredoxin 3	*	-	-
	ATG94255	Collagenase-like protease	*	-	-
P (inorganic ion transport and metabolism)	ATG92949	Multidrug efflux RND transporter permease subunit	*	-	-
	ATG93390	Sulfurtransferase	*	-	-
	ATG94583	Heavy metal translocating P-type ATPase	*	-	-
	ATG94851	ABC transporter substrate-binding protein	*	-	-
	ATG96541	Carbonate dehydratase	*	-	-
	ATG96708	Sulfurtransferase	*	-	-

S (function unknown)	ATG92898	Tripartite tricarboxylate transporter substrate binding protein	*	-	-
	ATG93031	Methyl-accepting chemotaxis protein	*	-	-
	ATG93690	FmdB family transcriptional regulator	*	-	-
	ATG94166	NAD(P)-dependent oxidoreductase	*	-	-
	ATG94412	Hypothetical protein CQB05_10510	*	-	-
	ATG94903	Virulence protein SciE type	*	-	-
	ATG94931	Hypothetical protein CQB05_13580	*	-	-
	ATG95978	Cluster of type VI secretion system tip protein VgrG	*	-	-
	ATG96183	tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmeE	*	-	-
	ATG96448	Universal stress protein	*	-	-
T (signal transduction)	ATG94151	Polyvinylalcohol dehydrogenase	*	-	-
	ATG96412	Two-component system response regulator	*	-	-
	ATG96581	DNA-binding response regulator	*	-	-

Asterisk indicate the protein is unique to *Ac*.

Ac, *Acidovorax citrulli*; COG, clusters of orthologous group.

Supplementary Table 4. Classification of more abundant (>2 fold) proteins in *AcΔglpD* strain by clusters of orthologous group analysis

COG function	Accession no.	Gene function	Fold change	P-value	Included in other group
C (energy production and conversion)	ATG93740	Ubiquinol-cytochrome c reductase iron-sulfur subunit	*	-	-
E (amino acid metabolism and transport)	ATG96202	Peptidase M20	4.20	0.04	-
	ATG96066	D-amino acid dehydrogenase	*	-	-
H (coenzyme metabolism)	ATG94848	cob(I)yrinic acid a/c-diamide adenosyltransferase	*	-	-
	ATG96398	Glutathione synthase	*	-	-
I (lipid metabolism)	ATG93257	Acyl-CoA dehydrogenase	*	-	-
	ATG96543	Acetyl-CoA C-acyltransferase	*	-	-
	ATG96632	3-Hydroxybutyryl-CoA dehydrogenase	*	-	-
J (translation)	ATG94046	TlyA family RNA methyltransferase	*	-	-
K (transcription)	ATG93025	Fe-S cluster assembly transcriptional regulator IscR	*	-	-
	ATG93642	DNA-directed RNA polymerase subunit omega	*	-	-
L (replication and repair)	ATG96328	DNA helicase II	*	-	-
M (cell wall/membrane/envelop biogenesis)	ATG94570	UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase	*	-	-
	ATG95133	Glycosyltransferase family 1 protein	*	-	-
	ATG95273	UDP-glucose 4-epimerase GalE	*	-	-
O (post-translational modification, protein turnover, chaperone functions)	ATG93858	7-Carboxy-7-deazaguanine synthase	*	-	-
P (inorganic ion transport and metabolism)	ATG94295	Catalase peroxidase	*	-	-
Q (secondary structure)	ATG94143	Imidazolonepropionase	*	-	-
S (function unknown)	ATG93438	Chemotaxis protein	*	-	-
	ATG93441	Twin-arginine translocation pathway signal	*	-	-
	ATG93629	Hypothetical protein CQB05_05935	*	-	-
	ATG94461	Serine protease	*	-	-
	ATG95025	Cupin domain-containing protein	*	-	-
	ATG96283	Hypothetical protein CQB05_21490	*	-	-
T (signal transduction)	ATG95368	Methyl-accepting chemotaxis protein	*	-	-
	ATG96144	DNA-binding response regulator	*	-	-
	ATG97068	Hypothetical protein CQB05_19715	*	-	-

Asterisk indicate the protein is unique to *AcΔglpD*.

Ac, *Acidovorax citrulli*; COG, clusters of orthologous group.