

***Bacillus velezensis* wall teichoic acids is required for biofilm formation
and root colonization**

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Running title: Wall teichoic acids involved in root colonization

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The authors declare no conflict of interest.

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Table S1: List of up-regulated proteins of SQR9 and the mutant *sfp* (SQR9: *sfp* > 4). Gene name in the blue color was selected for mutation experiment.

Protein Name	Accession number	Unused	Total	%Cov	%Cov(50)	%Cov(95)	Peptides (95%)	AVG. (SQR9: Δsfp)	Description
I. Cellular processes and signaling									
I.1 Cell wall/membrane/envelope biogenesis									
DacA	GI:631799371	46.03	48.69	67.95	59.37	51.02	37	5.56	serine-type D-ala-D-ala carboxypeptidase DacA
GgaA	GI:631802915	41.83	42.14	67.19	54.69	43.36	35	4.41	minor teichoic acid biosynthesis protein GgaA
GlmU	GI:631799412	35.84	36.60	62.06	55.48	54.61	53	8.88	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase
CwlC	GI:631801046	24.66	24.71	59.52	55.95	54.37	37	4.61	sporulation-specific N-acetylmuramoyl-L-alanine amidase CwlC
LytC	GI:631802906	24.45	28.79	45.77	34.68	31.45	15	4.28	N-acetylmuramoyl-L-alanine amidase (major autolysin)
I.2 Defense mechanisms									
YocD	GI:631801281	12.28	12.55	31.08	27.69	23.08	9	6.16	putative protein YocD
I.3 Posttranslational modification, protein turnover, chaperones									
AhpC	GI:631803324	17.60	24.35	83.42	73.80	70.05	29	4.80	alkyl hydroperoxide reductase subunit C (small subunit) AhpC
OhrB	GI:631800606	13.79	14.78	75.74	64.71	61.76	13	11.59	organic hydroperoxide resistance protein
II. Information storage and processing									
II.1 Signal transduction mechanisms									
LuxS	GI:631802410	6.13	6.17	63.06	49.04	27.39	4	8.28	catalyzes the hydrolysis of S-ribosylhomocysteine to homocysteine and autoinducer-2
II.2 Replication, recombination and repair									
HupA	GI:631801724	10.80	10.90	93.48	79.35	79.35	24	23.69	DNA-binding protein II HupA
II.3 Transcription									
RpoC	GI:631799472	108.35	107.81	72.81	60.13	55.63	85	4.68	DNA-directed RNA polymerase subunit beta'
RpoB	GI:631799471	88.92	88.69	66.79	59.30	52.91	91	5.42	DNA-directed RNA polymerase subunit beta
RpoA	GI:631799507	22.67	22.76	45.22	39.81	37.58	15	4.08	DNA-directed RNA polymerase subunit alpha
II.4 Translation, ribosomal structure and biogenesis									
GltX	GI:631799455	17.77	19.07	46.38	31.26	24.84	11	9.33	Charges one glutamine molecule and pairs it to its corresponding RNA trinucleotide
RpH	GI:631802191	15.31	17.78	56.33	49.80	47.35	10	10.10	tRNA nucleotidyltransferase
RplJ	GI:631799468	13.33	13.39	52.41	40.96	36.14	7	5.52	50S ribosomal protein L10
MtnA	GI:631800646	11.28	11.46	49.29	36.83	22.38	11	5.38	involved in methionine salvage pathway
RplA	GI:631799467	10.07	12.16	43.53	29.74	27.59	6	4.39	the binding site in the mRNA mimics the binding site in the 23S rRNA
RplF	GI:631799495	8.00	10.00	27.37	21.79	21.79	5	6.04	50S ribosomal subunit protein L6
TsF	GI:631800952	4.19	4.25	32.76	10.58	7.17	2	8.87	EF-Ts; functions during elongation stage of protein translation

RplQ	GI:631799508	3.34	5.46	25.00	11.67	11.67	3	22.28	50S ribosomal protein L17
RplR	GI:631799496	1.64	1.85	28.33	16.67	5.83	1	7.27	50S ribosomal protein L18
III. Metabolism									
III.1 Amino acid transport and metabolism									
MetE	GI:631800614	77.00	77.07	71.92	64.57	56.04	70	4.65	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase
DppE	GI:631800590	54.24	54.17	78.48	66.79	63.45	68	6.80	dipeptide-binding protein DppE precursor
Mpr	GI:631800169	41.33	41.46	73.93	71.62	67.99	264	11.64	extracellular metalloprotease precursorMpr
GlnH	GI:631802099	35.29	38.32	78.91	71.27	66.91	49	4.09	glutamine ABC transporter (glutamine-binding protein) GlnH
AsD	GI:631800977	32.14	32.18	81.21	69.36	64.16	28	8.17	catalyzes the formation of 4-aspartyl phosphate from aspartate 4-semialdehyde
IlvC	GI:631802184	29.62	29.90	72.22	65.50	58.77	32	9.21	ketol-acid reductoisomerase
SpeE	GI:631803094	23.62	23.64	54.71	51.45	47.10	17	8.43	catalyzes the formation of spermidine from putrescine and S-adenosylmethioninamine
IlvD	GI:631801567	22.10	22.13	32.80	26.88	25.81	13	4.82	dihydroxy-acid dehydratase
YyaH	GI:631803417	19.94	22.04	90.48	88.89	80.16	27	11.59	putative protein YyaH
AroE3	GI:631801705	18.74	18.83	54.91	44.63	42.06	15	11.24	3-phosphoshikimate 1-carboxyvinyltransferase
YjcI	GI:631800500	18.53	19.26	48.26	43.97	35.92	15	4.65	cystathionine gamma-synthase
GcvPA	GI:631801924	15.81	15.94	33.93	27.90	22.99	10	6.22	glycine dehydrogenase subunit 1
GabT	GI:631799737	12.23	12.37	32.87	23.45	22.53	10	6.54	4-aminobutyrate aminotransferase
MtnE	GI:631800649	12.05	12.15	26.13	16.08	14.57	6	11.70	pyridoxal phosphate-dependent aminotransferase
III.2 Carbohydrate transport and metabolism									
TpiA	GI:631802750	26.12	26.29	93.28	84.19	81.42	20	9.77	triosephosphate isomerase
NagB	GI:631802850	21.72	21.74	51.45	47.72	47.72	11	5.07	N-acetylglucosamine-6-phosphate isomerase NagB
YxiA	GI:631803273	18.28	18.34	43.80	33.12	32.26	15	4.41	putative protein YxiA
PtsH	GI:631800685	9.68	9.78	85.23	79.55	79.55	10	6.13	phosphocarrier protein HPr component PtsH
FbaA	GI:631803058	8.83	8.93	44.21	22.46	17.89	6	4.44	fructose-bisphosphate aldolase
YpqE	GI:631801666	7.16	7.21	53.57	45.24	40.48	5	4.05	PTS system IIA component YpqE
III.3 Coenzyme transport and metabolism									
NadA	GI:631802138	34.01	34.09	67.57	62.40	61.31	31	6.99	quinolinate synthetase
SerC	GI:631800328	33.56	34.14	78.55	72.42	64.07	80	5.02	phosphoserine aminotransferase
HemL	GI:631802167	19.16	19.24	49.88	41.72	36.36	21	4.22	glutamate-1-semialdehyde aminotransferase
LipA	GI:631802566	17.39	17.68	62.75	45.64	35.57	11	5.62	lipoyl synthase
BioB	GI:631801156	2.00	2.01	15.93	2.95	1.77	1	85.11	catalyzes the formation of biotin from dethiobiotin and sulfur 2 S-adenosyl-L-methionine
III.4 Energy production and conversion									
CitB	GI:631801110	64.23	68.24	58.59	47.36	46.37	51	4.97	Catalyzes the conversion of citrate to isocitrate

YugJ	GI:631802464	42.57	45.17	66.93	60.21	59.17	33	6.16	NADH-dependent butanol dehydrogenase YugJ
IcD	GI:631802266	22.77	25.06	50.35	34.52	29.55	13	8.35	Converts isocitrate to alpha ketoglutarate
YfhC	GI:631800161	22.04	22.12	88.66	78.87	77.84	24	4.16	putative protein YfhC
CccB	GI:631802871	12.10	12.36	53.98	46.90	39.82	11	7.69	cytochrome c551 (CccB)
Fer	GI:631801750	7.33	7.39	56.10	56.10	56.10	9	5.55	ferredoxin Fer
BkdB	GI:631801865	6.09	6.11	25.24	12.86	10.95	3	4.37	branched-chain alpha-keto acid dehydrogenase subunit E2
YdgI	GI:631803395	6.09	6.09	29.25	18.87	18.87	4	4.17	NADH dehydrogenase YdgI
III.5 Inorganic ion transport and metabolism									
YvgR	GI:631802684	39.18	39.26	57.48	48.01	42.03	60	6.46	sulfite reductase (NADPH2) flavoprotein YvgR
YclQ	GI:631799730	28.83	28.97	63.69	53.82	49.36	26	8.51	ferrichrome ABC transporter (periplasmic binding protein)
III.6 Lipid transport and metabolism									
YvaB	GI:631802695	27.89	27.96	82.94	82.94	82.94	45	8.42	FMN-dependent NADH-azoreductase
III.7 Nucleotide transport and metabolism									
YhcR	GI:631800241	57.46	57.84	59.21	55.70	54.09	70	5.37	5'-nucleotidase YhcR
DeoD	GI:631801336	23.83	23.93	78.45	75.43	75.43	29	7.67	purine nucleoside phosphorylase
III.8 Secondary metabolites biosynthesis, transport and catabolism									
BmyB	GI:631801148	53.94	66.94	20.18	9.01	6.19	39	8.61	bacillomycin D synthetase B
FenB	GI:631801176	32.79	35.31	24.37	10.57	8.46	29	4.13	fengycin synthetase B
DltA	GI:631803204	26.03	26.68	54.08	44.33	41.75	20	6.07	D-alanine--poly(phosphoribitol) ligase subunit 1
FenA	GI:631801177	21.20	25.50	19.47	8.82	5.92	23	5.74	fengycin synthetase A
DfnJ	GI:631801829	2.01	8.15	13.23	4.88	1.93	5	8.67	modular polyketide synthase of type I
IV. Poorly characterized									
IV.1 Function unknown									
YngK	GI:631801171	59.47	59.57	75.20	68.36	63.87	115	13.85	putative protein YngK
BacB	GI:631803125	21.49	21.52	73.31	65.25	64.83	35	4.95	bacilysin synthetase B
YbbR	GI:631799545	16.36	16.44	39.04	29.44	26.51	10	5.85	putative protein YbbR
YuaD	GI:631802430	7.42	7.49	32.64	32.12	32.12	5	7.36	putative protein YuaD
YloC	GI:631800867	6.04	6.11	29.55	20.96	11.68	3	4.17	putative protein YloC
YkoV	GI:631800630	2.01	4.41	21.50	11.26	9.90	3	4.24	putative protein YkoV
FhO	GI:631800176	2.01	2.04	13.59	3.83	2.56	3	4.23	putative protein FhO
NucB	GI:631801025	16.4	16.91	71.53	71.53	65.97	77	5.03	function unknown
9906	GI:631799906	24.62	24.69	69.15	65.96	56.38	34	21.06	function unknown
2739	GI:631802739	33.82	34.12	74.51	67.65	56.54	94	10.14	function unknown

3020	GI:631803020	31.77	32.75	84.65	70.61	60.53	94	17.60	function unknown
IV.2 General function prediction only									
YmfA	GI:631800980	32.83	33.05	49.55	36.04	32.61	21	5.88	putative protein YmfA
YvgN	GI:631802680	28.63	28.65	79.71	71.74	69.57	36	4.25	dehydrogenase YvgN
YvaA	GI:631802694	21.77	21.83	49.42	38.73	38.73	18	5.26	oxidoreductase YvaA
YkqC	GI:631800745	19.57	25.13	46.67	31.17	25.59	16	4.07	putative protein YkqC
AdhA	GI:631799867	17.73	17.81	54.15	44.13	40.40	17	6.28	NADP-dependent alcohol dehydrogenase AdhA
YhdP	GI:631800274	2.00	4.01	18.24	6.53	5.63	4	4.05	putative protein YhdP

Table S2: List of down-regulated proteins of SQR9 and the mutant *sfp* (SQR9: *sfp* < 0.25)

Protein Name	Accession number	Unused	Total	%Cov	%Cov(50)	%Cov(95)	Peptides (95%)	AVG. (SQR9: Δsfp)	Description
I. Cellular processes and signaling									
I.1 Cell motility									
Hag	GI:631802880	38.91	39.62	100.00	97.83	93.48	184	0.02	involved in elicitation of plant basal defence
I.2 Cell wall/membrane/envelope biogenesis									
YobO	GI:631801087	34.51	36.73	45.47	39.50	33.91	33	0.16	putative protein YobO
YnfF	GI:631801144	26.29	26.69	60.43	54.74	46.45	29	0.11	putative protein YnfF
Alr	GI:631799821	3.74	7.97	15.94	8.48	7.46	5	0.19	D-alanine racemase Alr
XlyA	GI:631800572	19.05	19.24	55.14	48.63	47.26	25	0.22	N-acetylmuramoyl-L-alanine amidase XlyA precursor (cell wall hydrolase) (Autolysin)
XlyB	GI:631800552	12.50	12.85	42.27	30.60	23.66	9	0.10	N-acetylmuramoyl-L-alanine amidase XlyB
YbfG	GI:631799586	3.60	5.75	13.90	6.40	3.41	3	0.19	putative protein YbfG
I.3 Defense mechanisms									
PenP	GI:631800511	32.65	34.82	81.25	60.53	51.97	26	0.11	beta-lactamase precursor PenP
I.4 Posttranslational modification, protein turnover, chaperones									
Vpr	GI:631803165	62.70	68.83	70.24	58.41	52.30	99	0.06	minor extracellular protease Vpr
Pcp	GI:631799620	23.88	27.10	94.42	87.44	84.65	27	0.12	pyrrolidone-carboxylate peptidase
AprX	GI:631801029	20.26	22.51	57.24	47.29	45.48	24	0.23	intracellular alkaline serine proteinase AprX
GroES	GI:631799931	14.82	14.93	87.23	82.98	67.02	9	0.06	co-chaperonin GroES
I.5 Signal transduction mechanisms									
YceC	GI:631799639	27.27	27.97	82.83	80.30	69.70	73	0.06	tellurium resistance protein YceC
YceD	GI:631799640	26.63	29.03	95.34	95.34	94.82	171	0.10	tellurium resistance protein YceD
YceE	GI:631799641	10.62	12.85	67.71	67.71	55.73	59	0.14	tellurium resistance protein YceE
YdcE	GI:631799823	6.00	6.02	51.72	44.83	44.83	3	0.03	putative protein YdcE
YtvA	GI:631802374	3.62	3.69	20.31	12.26	5.75	2	0.23	putative protein YtvA
RsbS	GI:631799825	2.00	3.62	16.53	16.53	12.40	3	0.22	negative regulator of sigma-B activity (antagonist of RsbT) RsbS
YqhA	GI:631801944	2.00	2.00	22.46	10.14	3.26	1	0.17	putative protein YqhA
II. Information storage and processing									
II.1 Replication, recombination and repair									
Bsn	GI:631802582	52.60	52.63	80.62	76.82	68.17	230	0.02	extracellular ribonuclease precursor Bsn

SSB	GI:631803423	18.26	18.43	75.58	54.07	51.74	40	0.16	single-strand DNA-binding protein (Helix-destabilizing protein) Ssb
YabD	GI:631799401	16.77	16.90	69.53	58.98	53.91	17	0.06	deoxyribonuclease YabD
II.2 Transcription									
YuaC	GI:631802433	8.98	9.02	41.30	35.87	33.70	6	0.11	putative protein YuaC
Hpr	GI:631800324	6.02	8.02	32.51	22.66	22.66	5	0.12	HTH-type transcriptional regulator Hpr
YwhA	GI:631803100	5.00	5.05	50.36	33.81	33.81	5	0.18	transcription regulator YwhA
III. Metabolism									
III.1 Amino acid transport and metabolism									
Ggt	GI:631801244	106.04	107.50	87.59	79.93	74.66	229	0.03	gamma-glutamyltranspeptidase; upregulated by plant exudate
OppA	GI:631800452	90.56	89.84	88.79	85.48	79.78	187	0.15	oligopeptide ABC transporter (binding protein) OppA
PabC	GI:631799439	24.75	25.25	65.31	61.56	54.08	20	0.04	4-amino-4-deoxychorismate lyase
PucG	GI:631802580	23.92	26.10	61.63	53.72	48.20	15	0.14	purine catabolism protein PucG
YhdR	GI:631800276	23.28	23.36	56.35	45.94	39.34	16	0.09	pyridoxal phosphate-dependent aminotransferase
YetH	GI:631800038	13.18	13.25	75.21	74.38	74.38	11	0.03	putative protein YetH
YwbC	GI:631803195	11.97	12.12	83.46	83.46	82.68	29	0.16	putative protein YwbC
AspB	GI:631801680	11.95	12.11	34.35	21.12	19.08	8	0.07	pyridoxal phosphate-dependent aminotransferase
AroH	GI:631801714	11.53	11.71	88.19	85.04	85.04	49	0.07	chorismate mutase (isozymes 1 and 2) AroH
YwkD	GI:631803048	5.47	5.52	26.77	22.83	22.83	4	0.05	putative protein YwkD
III.2 Carbohydrate transport and metabolism									
AmyE	GI:631799652	54.17	54.21	65.10	61.15	59.18	74	0.07	alpha-amylase AmyE
Tal	GI:631803057	23.80	23.88	84.43	75.00	71.70	23	0.04	transaldolase
IolH	GI:631803299	23.48	25.55	64.01	62.63	54.33	19	0.16	inositol utilization protein H (IolH)
XynD	GI:631801145	20.89	21.00	52.45	49.90	46.77	53	0.05	endo-1,4-beta-xylanase D precursor
BglS	GI:631803256	15.85	15.91	54.73	53.09	46.09	37	0.04	pfam00722; glyco_hydro_16; endo-beta-1,3-1,4 glucanase
GanA	GI:631800515	15.53	16.83	37.30	30.81	25.68	12	0.06	predicted arabinogalactan endo-1,4-beta-galactosidase
UxaC	GI:631800543	10.63	10.80	25.38	20.43	12.90	6	0.18	glucuronate isomerase
FriC	GI:631799663	6.01	8.02	29.01	16.41	12.60	4	0.09	sugar phosphate isomerase/epimerase
III.3 Coenzyme transport and metabolism									
RibH	GI:631801770	44.89	45.40	97.40	94.81	94.81	132	0.04	6,7-dimethyl-8-ribityllumazine synthase
HemE	GI:631800337	20.74	20.94	73.11	61.06	56.30	21	0.03	catalyzes the formation of coproporphyrinogen from uroporphyrinogen III
YkvK	GI:631800666	12.13	12.84	85.62	81.51	69.86	8	0.05	6-pyruvoyl tetrahydrobiopterin synthase homolog YkvK
FolA	GI:631799441	10.01	10.02	82.50	78.33	66.67	14	0.16	dihydroneopterin aldolase FolA
Moab	GI:631802290	8.05	8.77	72.35	45.29	38.82	8	0.03	molybdopterin precursor biosynthesis protein B (Moab)

III.4 Energy production and conversion

LpdV	GI:631801868	51.52	54.59	74.42	69.34	61.95	79	0.24	dihydrolipoyl dehydrogenase
GlpD	GI:631800252	30.18	30.59	59.46	45.23	35.14	22	0.07	glycerol-3-phosphate dehydrogenase GlpD
YfkO	GI:631800100	26.67	26.76	80.54	67.42	64.25	40	0.05	NAD(P)H nitroreductase YfkO
CitZ	GI:631802267	11.03	11.25	38.98	27.15	21.77	20	0.21	catalyzes the formation of citrate from acetyl-CoA and oxaloacetate
YfmT	GI:631800056	10.23	12.54	19.38	12.99	11.75	7	0.14	benzaldehyde dehydrogenase YfmT

III.5 Inorganic ion transport and metabolism

FeuA	GI:631799533	61.55	64.66	85.53	81.45	78.62	133	0.05	iron-binding protein FeuA
SsuA	GI:631800206	51.95	59.83	86.32	80.24	76.90	164	0.13	aliphatic sulfonates binding protein precursor SsuA
KatE	GI:631803254	39.95	40.33	38.21	32.06	31.33	25	0.14	catalase KatE
Dps	GI:631802407	24.13	24.17	92.41	89.66	89.66	54	0.15	DNA-protecting protein Dps
MrgA	GI:631802630	6.02	9.38	73.38	48.05	44.16	10	0.17	metalloregulation DNA-binding stress protein MrgA
YcjH	GI:631800499	4.00	4.00	19.17	7.92	7.92	2	0.02	putative protein YcjH

III.6 Lipid transport and metabolism

AcpD	GI:631803411	17.71	17.95	69.01	59.62	51.17	16	0.03	FMN-dependent NADH-azoreductase
FabZ	GI:631802984	12.38	13.11	63.83	56.74	51.77	12	0.15	beta-hydroxyacyl-ACP dehydratase
YngJ	GI:631801170	8.60	8.69	30.53	22.63	17.11	6	0.08	Acyl-CoA dehydrogenase YngJ
DfnL	GI:631801827	4.05	6.08	17.11	11.08	8.68	4	0.23	hydroxymethylglutaryl-CoA synthase

III.7 Nucleotide transport and metabolism

YfkN	GI:631800103	218.21	218.21	84.90	80.42	76.22	472	0.02	multifunctional 2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase/5'-nucleotidase
GuaB	GI:631799370	42.07	44.15	58.61	53.48	49.80	46	0.11	IMP dehydrogenase
DeoC	GI:631803282	20.19	22.78	73.42	65.77	61.71	17	0.16	deoxyribose-phosphate aldolase DeoC
NrdF	GI:631801044	6.93	9.08	27.05	22.80	17.93	5	0.24	class 1b ribonucleoside-diphosphate reductase subunit beta
PyrD	GI:631800853	4.00	6.00	22.19	10.29	10.29	3	0.22	dihydroorotate dehydrogenase

III.8 Secondary metabolites biosynthesis, transport and catabolism

DhbB	GI:631802523	12.02	12.05	42.86	31.49	27.92	6	0.10	isochorismatase
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IV. Poorly characterized**IV.1 Function unknown**

Ywfl	GI:631803119	31.06	31.11	84.25	70.47	68.11	56	0.06	putative protein Ywfl
YxaL	GI:631803318	24.42	24.47	70.60	60.24	56.87	67	0.01	putative protein YxaL
YukJ	GI:631802520	20.65	20.81	73.33	69.78	65.78	65	0.24	putative protein YukJ
YpuA	GI:631801778	15.37	15.53	53.85	44.15	39.13	20	0.09	putative protein YpuA

YueB	GI:631802513	6.08	8.20	20.46	6.08	3.18	5	0.17	bacteriophage SPP1 adsorption protein YueB
IV.2 General function prediction only									
YmaB	GI:631801045	21.55	21.61	81.07	66.99	53.40	20	0.08	putative protein YmaB
YraA	GI:631802315	20.51	21.41	91.12	87.57	81.07	32	0.15	putative protein YraA
YdaG	GI:631799768	20.34	20.48	92.14	92.14	86.43	23	0.10	general stress protein YdaG
YtcJ	GI:631802299	12.23	17.55	32.77	24.48	19.59	12	0.11	putative protein YtcJ
YkcA	GI:631800580	10.60	12.93	41.46	24.37	23.10	8	0.17	putative protein YkcA
YhcB	GI:631800226	10.56	10.61	49.72	37.85	37.85	10	0.17	putative protein YhcB
Hfq	GI:631801039	10.23	10.26	98.63	93.15	91.78	11	0.18	Stimulates the elongation of poly(A) tails
YrkL	GI:631799839	8.12	8.14	62.07	47.70	40.80	17	0.05	putative protein YrkL

Figure S1 Quantitative analysis of biofilms with crystal violet staining. OD₆₀₀ values of solubilized crystal violet were from pellicle cells at 24h. Error bars indicate the standard deviations based on three different replicated experimental values. Different letters above the bars indicate significant differences ($p < 0.05$).

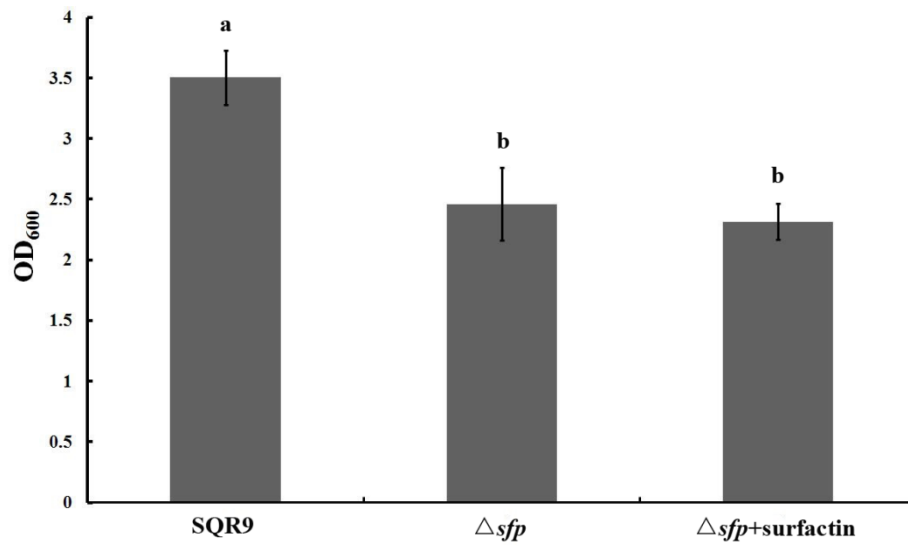


Figure S2 Comparison of biofilm formation after complementary of *ggaA* and *gtaB* gene by qualitative analysis.

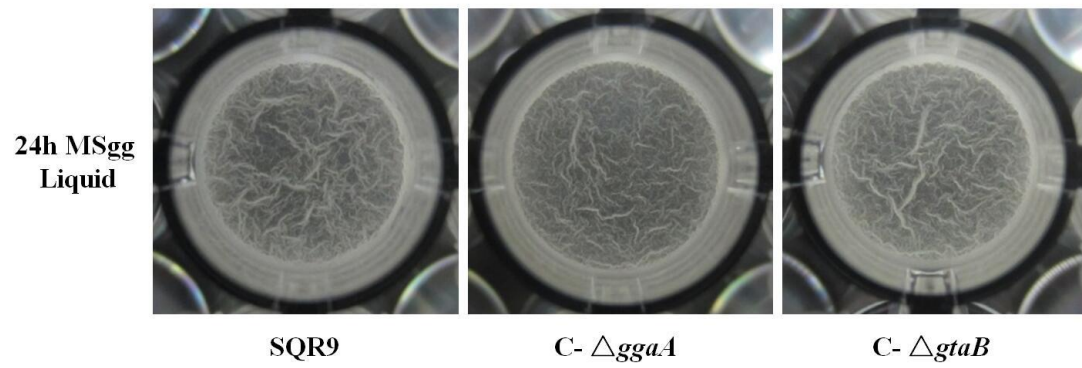


Figure S3 Growth curves of *ggaA*, *gtaB* mutant and wild-type strain of *B. velezensis* SQR9 in liquid MSgg medium.

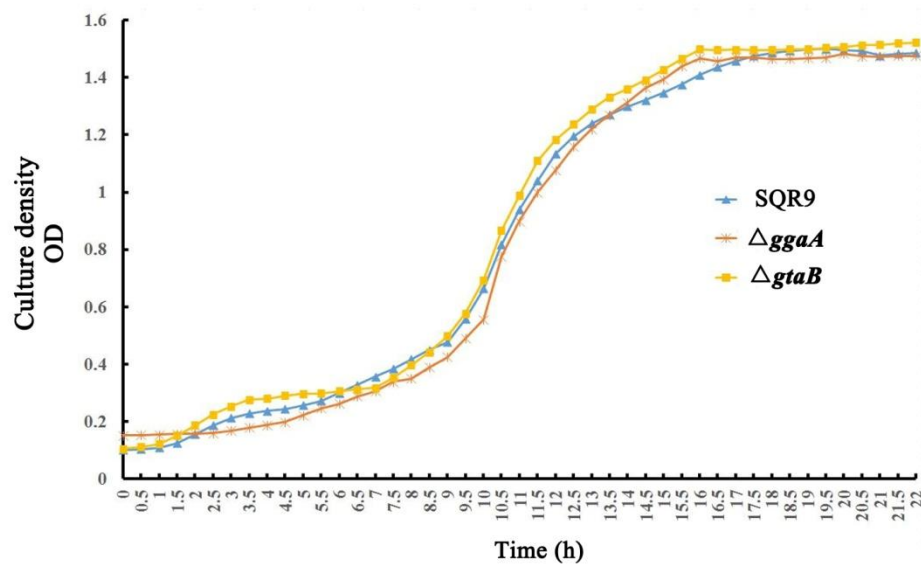


Figure S4 Transcriptional levels of *ggaA* and *gtaB* gene in wild-type strain SQR9. The experiments were carried out with pellicle obtained from microtiter plates when cells were grown in the presence of indicated plant polysaccharides for 24 h. The *B. velezensis* SQR9 *recA* gene was used as an internal reference gene. Bars represent standard deviations of data from three biological replicates.

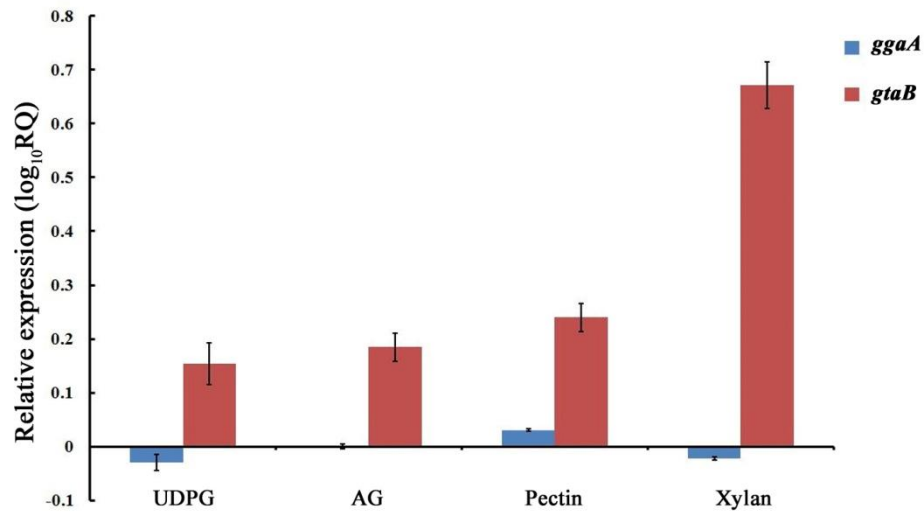


Figure S5 Quantification of EPS production of *ggaA*, *gtaB* mutant and wild-type strain by congo red binding assay. Error bars indicate the standard deviations based on three different replicated experimental values. Different letters above the bars indicate significant differences ($p < 0.05$).

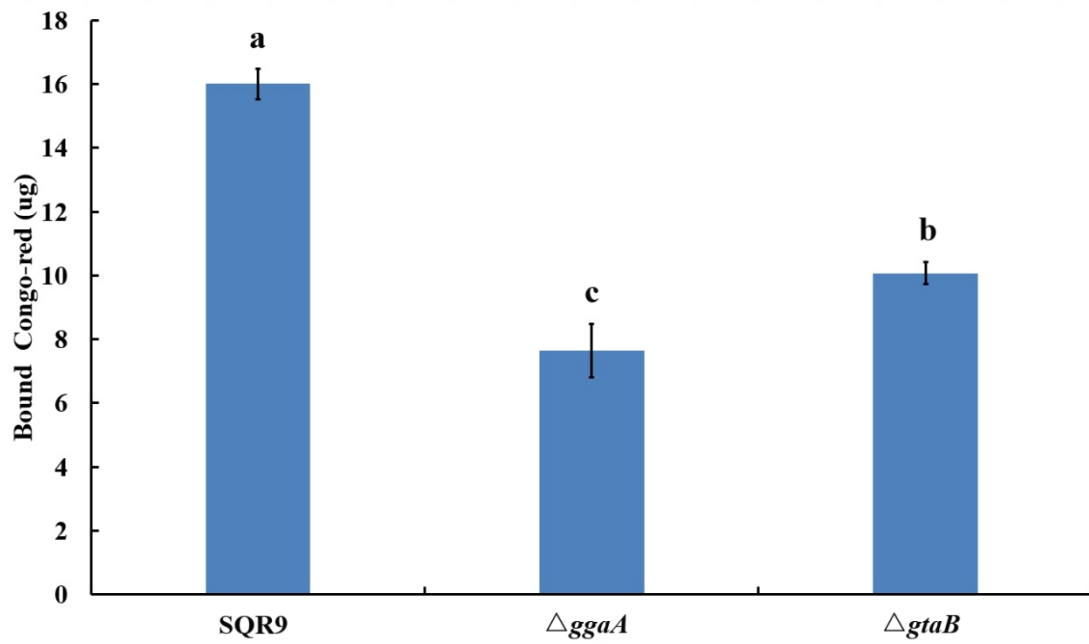


Figure S6 Quantifying attachment of individual strains (*ggaA*, *gtaB* mutant and wild-type strain) to cucumber root surface. Error bars indicate the standard deviations based on three different replicated experimental values. Different letters above the bars indicate significant differences ($p < 0.05$).

