Transcriptome analysis of *Acidovorax avenae* subsp. *avenae* cultivated *in vivo* and co-culture with *Burkholderia seminalis*

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Supplementary figure and table legends

Figure S1.

Dendrograms and Heatmap of the top 50 differentially expressed genes in *Acidovorax avenae* subsp. *avenae* strain RS-1 under *in vitro*, *in vivo* and co-culture conditions. The plot shows two well segregated groups that correspond to Claudin and Luminal subtypes. In the heatmap, green represents low levels of expression while red represents high levels.

Figure S2.

In silico prediction of genomic islands in strains RS-1 of *Acidovorax avenae* subsp. *avenae* by using IslandViewer software web server. Blue areas represent 7 putative genomic islands that contain 89 genes, while strain ATCC19860 was used as the guide reference.

Figure S3.

The correlation between RNA-Seq expression data (log_2) and qRT-PCR data (log_2). (a) *in vivo* ($P < 0.001$, $r^2 = 0.78$); (b) co-culture ($P < 0.001$, $r^2 = 0.69$).

Table S1.

List of specifically expressed genes under *in vivo* rice plant condition of *Acidovorax avenae* subsp. *avenae* strain RS-1 transcriptome.

Table S2.

Genome and transcriptome analyses of secretion systems in *Acidovorax avenae* subsp. *avenae* strain RS-1 by using strain ATCC19860 as the guide reference.

Table S3.

List of *in silico* predicted genomics islands and their individual genes based on genome and transcriptome data of *Acidovorax avenae* subsp. *avenae* strain ATCC19860 and RS-1.

Table S4.

List of genome-wide predicted ncRNAs verified by both RFAM database and RNA-Seq data of *Acidovorax avenae* subsp. *avenae* strain RS-1.

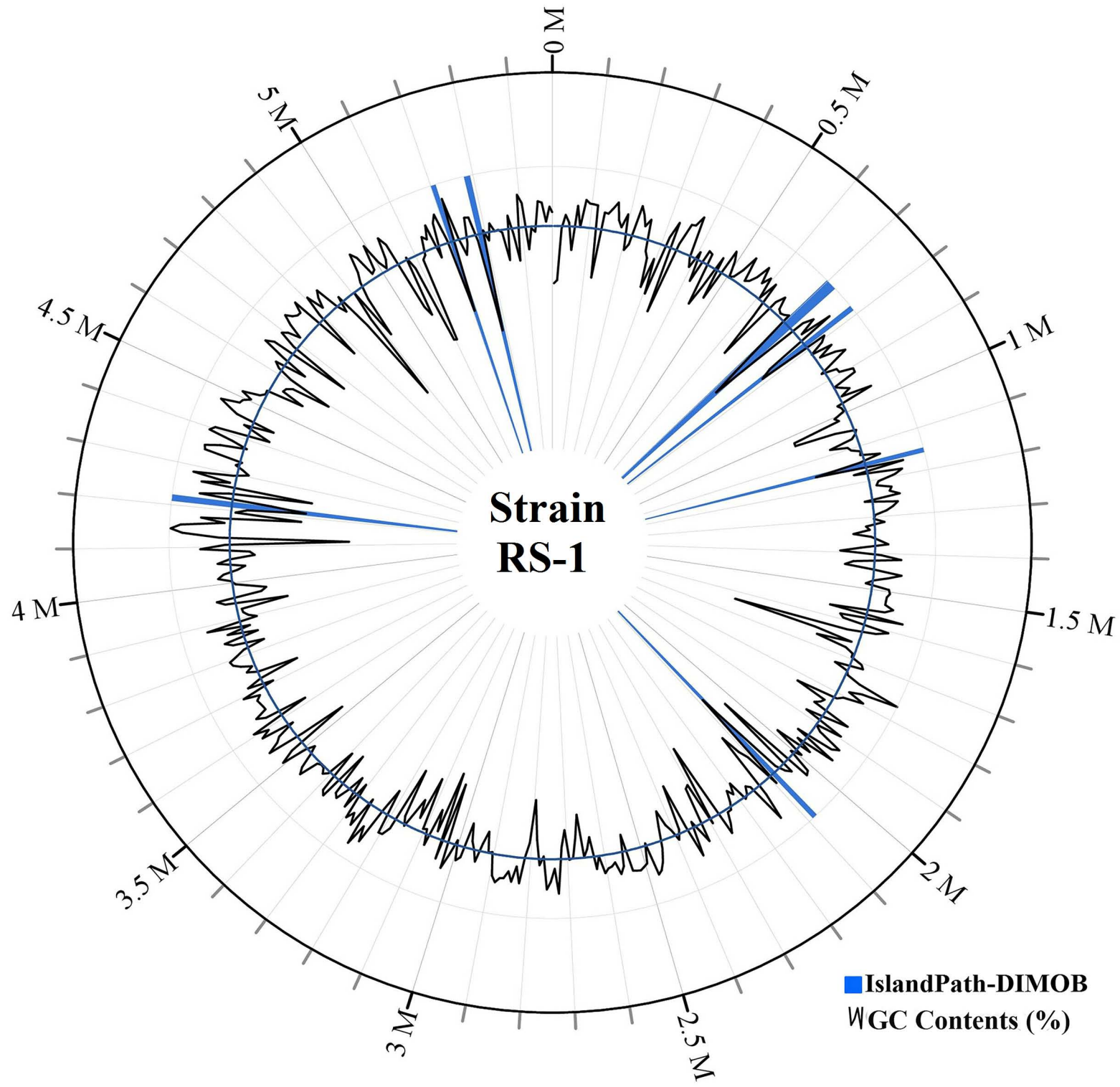
Table S5.

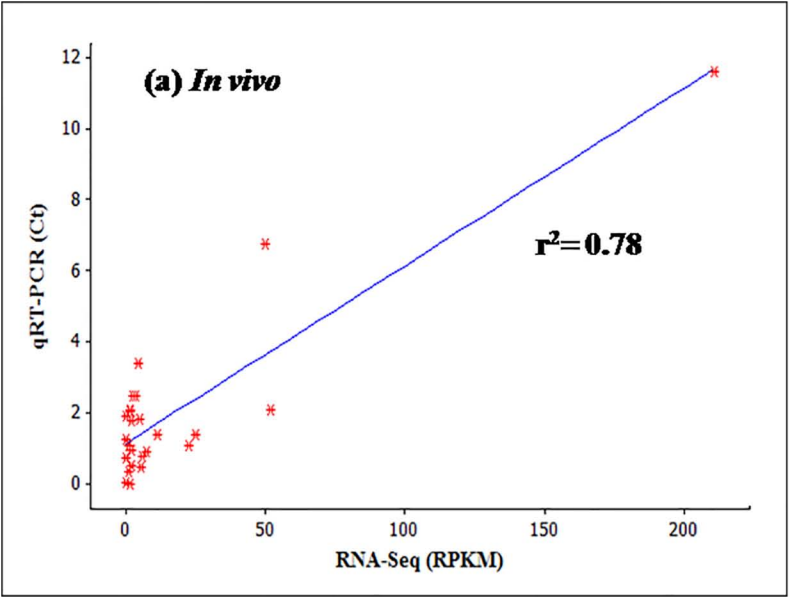
qRT-PCR analysis of T6SS genes expression in *Acidovorax avenae* subsp. *avenae* strain RS-1 under *in vivo* and co-culture conditions relative to the *in vitro* condition.

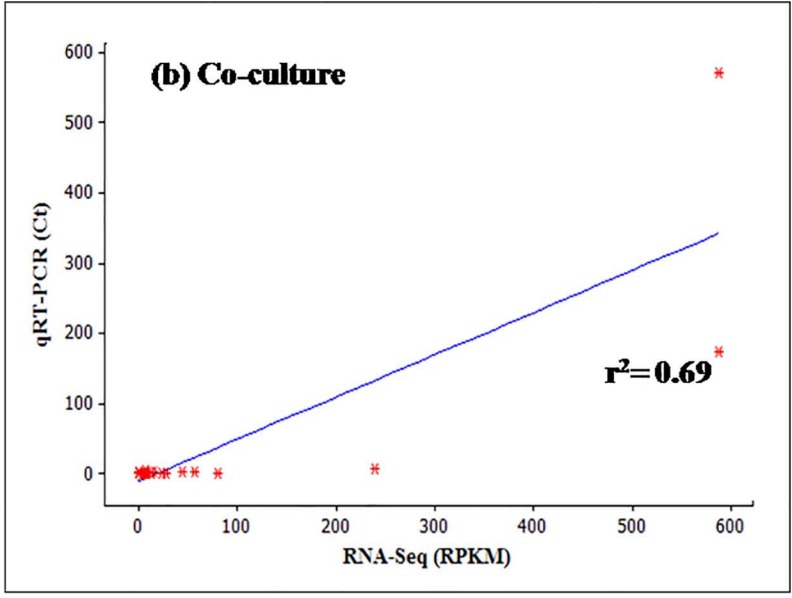
Table S6.

Primers of Type VI secretion system genes used for quantitative real-time PCR in *Acidovorax avenae* subsp. *avenae* strain RS-1.

−10
−5
0
5
Value
gi|326319364 Two-component response regulator
gi|326318004 Methyl-accepting chemotaxis protein
gi|326318868 Glucoamylase (EC 3.2.1.3)
gi|326315599 hypothetical protein
gi|326318937 Phosphoenolpyruvate-protein phosph
gi|326318021 Cell division inhibitor
gi|326318854 Ribose ABC transport system, perme
gi|326316660 FIG00349738: hypothetical protein
gi|326318579 Heme O synthase, protoheme IX farn
gi|326317418 TRAP-type transport system, periplas
gi|326318561 Osmotically inducible protein Y
gi|326319188 D-amino acid dehydrogenase small s
gi|326318211 SC5F2A.07, unknown, len: 109 aa
gi|326317113 FIG016425: Soluble lytic murein trans
gi|326315322 Ribulose-phosphate 3-epimerase (E
gi|326318570 FIG00348130: hypothetical protein
gi|326315045 NAD-specific glutamate dehydrogena
gi|326318679 Catalase (EC 1.11.1.6)
gi|326318560 Bacterioferritin
gi|326317557 Dihydrolipoamide acetyltransferase cc
gi|326316164 Outer membrane lipoprotein
gi|326316129 Methionine ABC transporter ATP-bind
gi|326317558 Pyruvate dehydrogenase E1 compone
gi|326314993 Phosphoenolpyruvate carboxykinase
gi|326317576 Iron-sulfur cluster assembly scaffold
gi|326316811 Dihydrolipoamide dehydrogenase of 2
gi|326316819 ATP-dependent Clp protease ATP-bi
gi|326318574 RNA polymerase sigma factor RpoH
gi|326316666 Translation initiation factor 2
gi|326316313 ATP-dependent protease La (EC 3.4.
gi|326318760 RNA binding methyltransferase FtsJ li
gi|326317742 Citrate synthase (si) (EC 2.3.3.1)
gi|326318773 Glutamate Aspartate periplasmic bind
gi|326315402 LSU ribosomal protein L5p (L11e)
gi|326318753 SSU ribosomal protein S9p (S16e)
gi|326316315 ATP-dependent Clp protease proteoly
gi|326316064 SSU ribosomal protein S18p @ SSU
gi|326316023 HtrA protease/chaperone protein
gi|326315227 LSU ribosomal protein L2p (L8e)
gi|326317577 Cysteine desulfurase (EC 2.8.1.7), Isc
gi|326315224 LSU ribosomal protein L3p (L3e)
gi|326318852 Ribose ABC transport system, peripla
gi|326318969 Chaperone protein HtpG
gi|326316059 Chaperone protein DnaJ
gi|326317447 Superoxide dismutase [Fe] (EC 1.15.1
gi|326315978 Aconitate hydratase (EC 4.2.1.3)
gi|326318556 DNA-binding response regulator, Lux
gi|326316321 Uncharacterized protein ImpD
gi|326316060 Chaperone protein DnaK
gi|326315731 Heat shock protein 60 family chaperor
gi|326317580 Biosynthetic Aromatic amino acid ami
gi|326316462 ThiJ/PfpI family protein
gi|326315608 Biotin carboxylase of acetyl-CoA carb
gi|326319522 Guanine-specific ribonuclease N1 an
gi|326315128 Alanine racemase, catabolic (EC 5.1.1
gi|326318867 Trehalose-6-phosphate phosphatase
gi|326316352 L-proline glycine betaine ABC transpo
gi|326319189 FIG00932717: hypothetical protein
gi|326316261 Quinate/shikimate dehydrogenase [Py
gi|326316128 Small heat shock protein
gi|326315287 Malate synthase G (EC 2.3.3.9)
gi|326314992 FIG00582290: hypothetical protein
gi|326316748 Putative TEGT family carrier/transport
gi|326318869 Alpha,alpha-trehalose-phosphate sy
gi|326317556 Dihydrolipoamide dehydrogenase of p
gi|326315559 ATP-dependent protease HslV (EC 3.
gi|326316640 TPR repeat containing exported prote
gi|326316809 2-oxoglutarate dehydrogenase E1 co
gi|326316084 ClpB protein
gi|326315560 ATP-dependent hsl protease ATP-bir
gi|326314997 Glucans biosynthesis protein D precu
gi|326314985 D-amino acid dehydrogenase small s
gi|326316350 L-proline glycine betaine binding ABC
gi|326318247 Methyl-accepting chemotaxis protein
gi|326318251 Methyl-accepting chemotaxis protein
gi|326318252 Methyl-accepting chemotaxis protein
gi|326318250 Signal transduction histidine kinase C
gi|326314871 Cobalt/zinc/cadmium efflux RND trans
gi|326317662 putative exported protein
gi|326317953 Flagellar transcriptional activator FI
gi|326319097 Flagellar hook protein FlgE
gi|326319077 Flagellar biosynthesis protein FliC
gi|326318580 Heme A synthase, cytochrome oxidas
gi|326316412 ABC transporter permease protein
gi|326319088 Flagellar biosynthesis protein FlhF
gi|326317954 Flagellar transcriptional activator FI
gi|326319103 Flagellar hook-associated protein Flg
gi|326319101 Flagellar P-ring protein FlgI
gi|326316829 Aldehyde dehydrogenase (EC 1.2.1.3
gi|326319078 Aminotransferase, DegT/DnrJ/EryC1/
gi|326319099 Flagellar basal-body rod protein FlgG
gi|326318181 Aerobic C4-dicarboxylate transporter
gi|326319104 Flagellar hook-associated protein Flg
gi|326315923 Acetylornithine deacetylase (EC 3.5.1
gi|326316973 Probable transmembrane protein
gi|326316177 Methyl-accepting chemotaxis protein
gi|326315448 Respiratory nitrate reductase alpha ch
gi|326319076 Flagellin protein FlaB
gi|326319416 Formiminoglutamic iminohydrolase (E
gi|326316530 FIG005548: transport protein
gi|326314870 Cobalt-zinc-cadmium resistance prot
In vivo vs. co-culture
In vitro vs. co-culture
In vitro vs. In vivo


0 M
0.5 M
1 M
1.5 M
2 M
2.5 M
3 M
3.5 M
4 M
4.5 M
5 M
Strain
RS-1
IslandPath-DIMOB
GC Contents (%)


(a) In vivo
qRT-PCR (Ct)
RNA-Seq (RPKM)
r²=0.78
0
2
4
6
8
10
12
0
50
100
150
200


(b) Co-culture
qRT-PCR (Ct)
RNA-Seq (RPKM)
r²=0.69
0
100
200
300
400
500
600
0
100
200
300
400
500
600