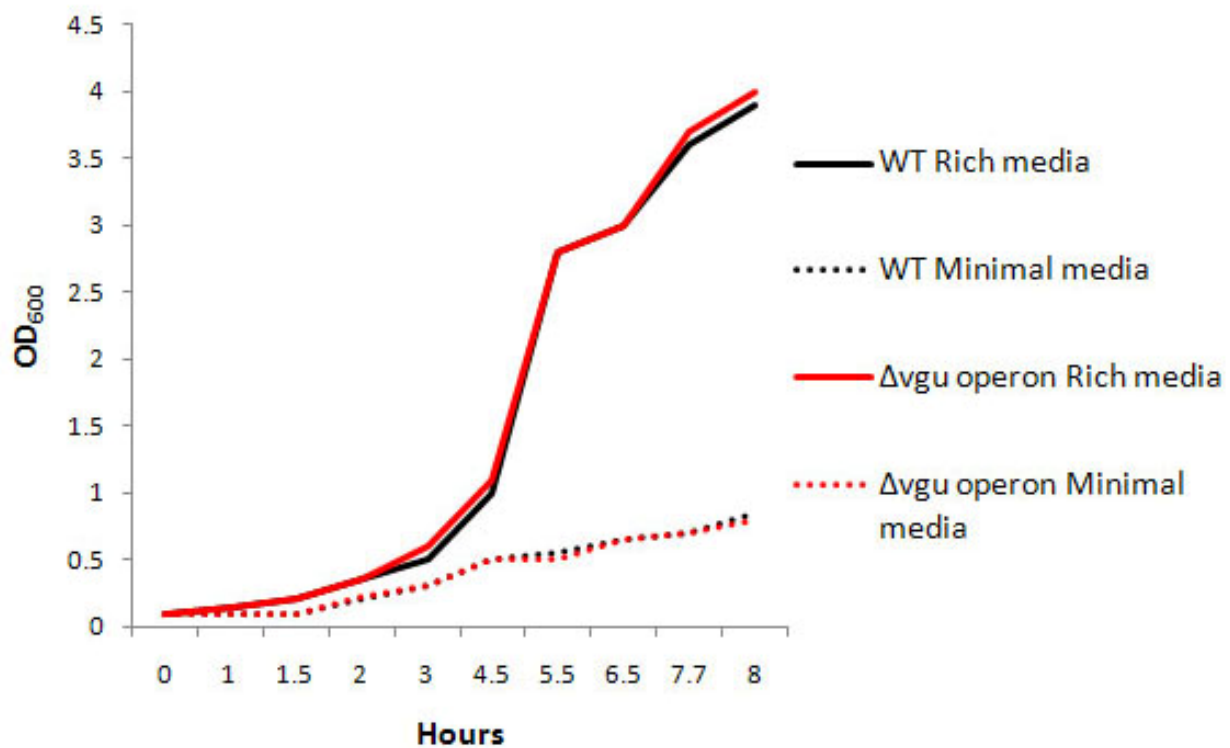
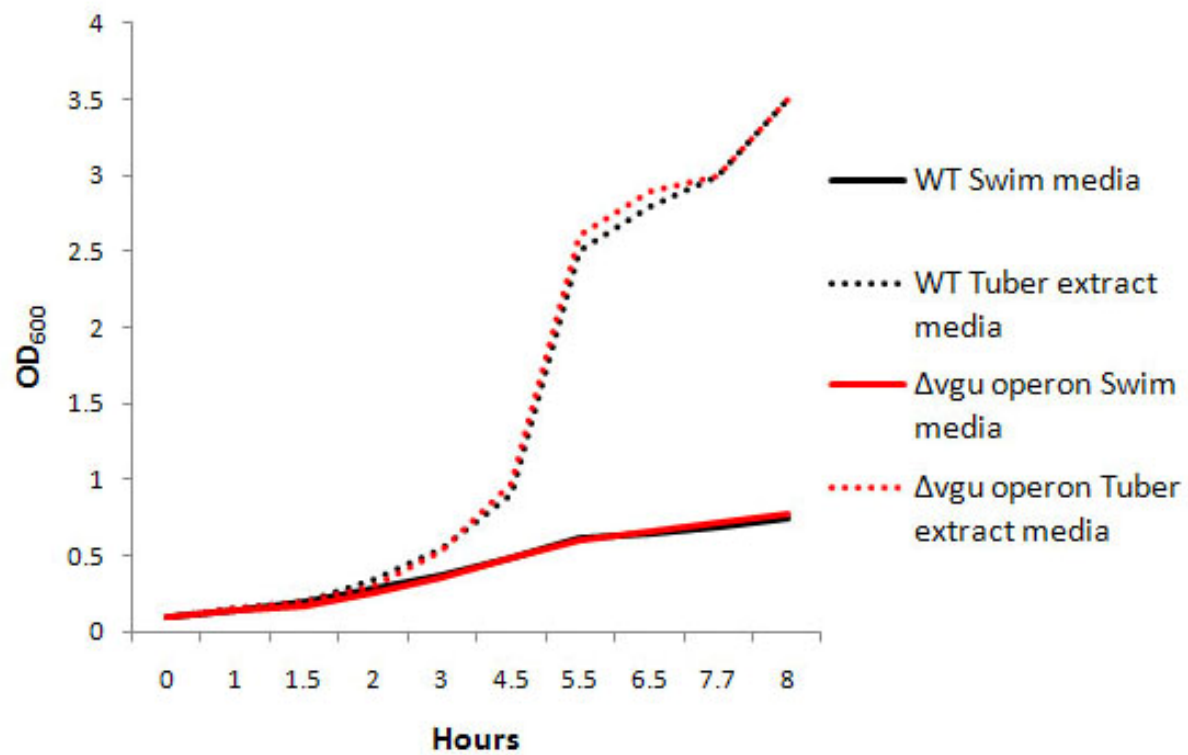


Supplemental Fig. S1. *vgu* operon organization is conserved in enterobacteria. Phylogenetic tree constructed using a Bayesian inference of phylogeny (MrBayes software, 2005) of *vguB* homologs from select species, which represent the range of *vgu* distribution. Coupled to the tree is a cartoon depiction of the chromosome region in which the *vgu* homolog lies. The structure of the *vguABCD* operon in *P. carotovorum* is generally conserved in species with the closest *vguB* homologs. The operon is often flanked by a DeoR-like transcription regulator on one side and a gluconate permease on the other. However, some species lack the complete operon, such as *Yersinia enterocolitica*, *Yersinia intermedia*, and *Yersinia mollaretti*, which appear to only carry the *vguB* homolog and the *vguC* putative aldolase in the region. Interestingly, *Burkholderia phymatum* contains two copies of the *vguA* oxidoreductase gene, but lacks the *vguC* and *vguD* genes two genes at the 3' side of the operon. Nearly all of the chromosome regions are flanked by other genes predicted to be involved in sugar metabolism, such as epimerases and decarboxylases.

The genes used for the analysis, with their GenBank accession numbers are:

>gi|227328790|ref|ZP_03832814.1| hypothetical protein PcarcW_16208 [Pectobacterium carotovorum subsp. carotovorum WPP14];
>gi|227113832|ref|ZP_03827488.1| hypothetical protein PcarbP_12749 [Pectobacterium carotovorum subsp. brasiliensis PBR1692];
>gi|50123248|ref|YP_052415.1| hypothetical protein ECA4328 [Pectobacterium atrosepticum SCRI1043];
>gi|157369734|ref|YP_001477723.1| type III effector Hrp-dependent outers [Serratia proteamaculans 568];
>gi|77979838|ref|ZP_00835254.1| COG3395: Uncharacterized protein conserved in bacteria [Yersinia intermedia ATCC 29909];
>gi|123442733|ref|YP_001006710.1| hypothetical protein YE2503 [Yersinia enterocolitica subsp. enterocolitica 8081];
>gi|188534494|ref|YP_001908291.1| hypothetical protein ETA_23670 [Erwinia tasmaniensis Et1/99];
>gi|193069621|ref|ZP_03050573.1| YgbK domain protein [Escherichia coli E110019];
>gi|77960714|ref|ZP_00824573.1| COG3395: Uncharacterized protein conserved in bacteria [Yersinia mollaretii ATCC 43969];
>gi|74313303|ref|YP_311722.1| hypothetical protein SSON_2885 [Shigella sonnei Ss046];
>gi|152970156|ref|YP_001335265.1| hypothetical protein KPN_01604 [Klebsiella pneumoniae subsp. pneumoniae MGH 78578];
>gi|57635340|emb|CAI44008.1| tRNA synthase-like protein [Salmonella enterica subsp. enterica serovar Typhimurium];
>gi|186471579|ref|YP_001862897.1| type III effector Hrp-dependent outers [Burkholderia phymatum STM815];
>gi|224826923|ref|ZP_03700022.1| type III effector Hrp-dependent outers protein [Lutiella nitroferum 2002];
>gi|66043732|ref|YP_233573.1| type III effector HopAN1 [Pseudomonas syringae pv. syringae B728a];
>gi|212707846|ref|ZP_03315974.1| hypothetical protein PROVRUST_02791 [Providencia rustigianii DSM 4541];
>gi|42631330|ref|ZP_00156868.1| COG3395: Uncharacterized protein conserved in bacteria [Haemophilus influenzae R2866];
>gi|62317098|ref|YP_222951.1| hypothetical protein BruAb2_0144 [Brucella abortus bv. 1 str. 9-941];
>gi|152996569|ref|YP_001341404.1| type III effector Hrp-dependent outers [Marinomonas sp. MWYL1];
>gi|153832595|ref|ZP_01985262.1| ygbK domain protein [Vibrio harveyi HY01];
>gi|145589814|ref|YP_001156411.1| type III effector Hrp-dependent outers [Polynucleobacter necessarius subsp. asymbioticus QLW-P1DMWA-1];
>gi|237781680|ref|YP_002848627.1| conserved hypothetical protein [Citrobacter sp. 30_2];
>gi|187930796|ref|YP_001901283.1| type III effector Hrp-dependent outers [Ralstonia pickettii 12J];
>gi|107025568|ref|YP_623079.1| type III effector Hrp-dependent outers [Burkholderia cenocepacia AU 1054]



Supplemental Figure S2. Growth of the *vgu* operon mutant was compared with wild type in all relevant media types, rich (2× YT), minimal, tuber extract, and swimming media.

Supplemental Table S1. List of primers used.

#	Designation	Sequence, 5'-3'
1	opkoupfwd	ACAAACAGACATAAACACCCCCC
2	opkuprev	GGGAACAGCAATATTTTTCCGCGATAACGTCGACCGTGGTTGCCTTGTTAAAATTAGTG
3	opkdownfw	CACTAATTTTAAACAAGGCAACCACGGTTCGACGTTATCGCGGAAAAATATTGCTGTTCCC
4	opkdownrev	CCGCTCCCCATTGTGAAATTTTACGCT
5	1180pro Fwd	CACCGCTCAGCAGCAGGCCGTCCTGCTCCAACCTTTTGCACATCGCGCCG
6	3244 Rev	TTATTTCTTTAGATAGGGTTTAGCCCATCCC
7	hrpL F RT	AGAGTCAGCAAATGGAAATGTCTAC
8	hrpL R RT	ATTTATCCTGATGTTTGAGCACTTC
9	ffh fwd	ATGGGCGATGTGCTTTCACT
10	ffh rev	TCAAACCCATCGCCTTTCTT
11	kdgR F1	AGCAAGGCTACGGAGAAGAC
12	kdgR R1	CGAATCGTTGGGAAAGAAAT
13	rsmB F1	ATGCATGCCGAAGTAAAACA
14	rsmB R1	ATCAGGATGACGACGAATCA
15	flhD F	TGAAAAAGCTTCTGCGATGT
16	flhD R	TCTGCCAGTTTCACCATCTG
17	hexA F	TTGCTGACCGAACATGGTAT
18	hexA R	GGATGGTGTCTGCAGTATCG
19	hrpN F	ATTGACTGACTCGGTTGCG
20	hrpN R	TGAGATGGAAATAAACCGCC
21	gntP F	CGAAGCGATGAAGGTGATTA
22	gntP R	CGGACACTTCGATCATTCTG

Supplemental Table S2. Growth of *Pectobacterium carotovorum* subsp. *carotovorum* WPP14 and the *vgu* operon mutant in simple sugars as a sole carbon source. -- indicates sugars tested in M9 salts with a single carbon source as described in Methods in the main text. D-Gluconate utilization was tested using both M9 salts and Biolog GN2 Plates.

Carbon Sources	WPP14	Δvgu operon	Complement
Acetic Acid	+	+	+
α -D-Glucose	+	+	+
α -D-Glucose-1-P	+	+	+
α -D-Lactose	+	+	+
α -Keto Butyric Acid	+	+	+
α -Keto Glutaric Acid	+	+	+
Bromosuccinic Acid	+	+	+
Cis-Acontic Acid	+	+	+
Citric Acid	+	+	+
D-cellulobiose	+	+	+
Dextrin	+	+	+
D-Fructose	+	+	+
D-Galactose	+	+	+
D-Galacturonic Acid	+	+	+
\rightarrow D-Gluconate	+	--	+
\rightarrow Ribulose	+	+	+
\rightarrow Xylulose	+	+	+
D-Glucose-6-P	+	+	+
D-Glucuronic Acid	+	+	+
D-L, alpha Glycerol phosphate	+	+	+
D-Mannitol	+	+	+
D-Mannose	+	+	+
D-Saccharic Acid	+	+	+
Formic Acid	+	+	+
Gentiobiose	+	+	+
Glucuronamide	+	+	+
Glycerol	+	+	+
Glycyl-L-Aspartic Acid	+	+	+
i-Erythritol	+	+	+
Inosine	+	+	+
Lactulose	+	+	+
L-Alaniamide	+	+	+
L-Arabinose	+	+	+
L-Asparagine	+	+	+
L-Aspartic Acid	+	+	+
L-Glutamic Acid	+	+	+
L-Serine	+	+	+
m-Inositol	+	+	+
N-Acetyl-D-Glucosamine	+	+	+
Succinamic Acid	+	+	+
Succinic Acid	+	+	+
Thymidine	+	+	+
Tween	+	+	+
Uridine	+	+	+