

Table S1: Summary of RNA-seq and mapping results.

Condition	Millions of reads	% reads aligned to genome
Biofilm 1	8.4	97.10
Biofilm 2	7.8	97.31
Biofilm 3	7.4	97.10
Planktonic 1	9.7	97.19
Planktonic 2	10.8	96.00
Planktonic 3	4.8	96.53

Table S2: Summary of statistical analysis with DESeq2.

	Nbr of features	UP	DOWN
Total in genome	5780	/	/
Total RNAseq detected	5480	/	/
Total DEG	3693	1846	1847
CDS, fCDS DEG	3615	1816	1832

DEG: Differentially expressed genes.

Table S3: *syp* genes cluster in *V. tapetis*.

Gene ID	Gene name	FC	Log2FC	function
<i>b1501</i>		0.3	-1.5	Sugar transferase SypR involved in lipopolysaccharide synthesis
<i>b1502</i>		0.2	-2.	Glycosyltransferase SypQ
<i>b1503</i>		0.2	-2.5	Glycosyltransferase SypP
<i>b1504</i>		0.06	-4	Hypothetical protein
<i>b1505</i>		0.2	-2.2	Polysaccharide biosynthesis chain length regulator SypO
<i>b1506</i>		0.3	-1.7	Glycosyltransferase SypN
<i>b1507</i>		0.1	-2.9	Acethyltransferase SypM
<i>b1508</i>		0.1	-3.1	Membrane protein SypL involved in exopolysaccharide production
<i>b1509</i>		0.1	-3.6	Membrane protein SypL involved in exopolysaccharide production
<i>b1510</i>		0.2	-2.3	Oligosaccharide translocase SypK
<i>b1511</i>		0.2	-2.3	Glycosyltransferase SypJ
<i>b1513</i>		0.26	-1.9	Glycosyltransferase SypI
<i>b1514</i>	<i>sypH</i>	0.7	-0.6	Glycosyltransferase SypH
<i>b1515</i>	<i>sypG</i>	1.5	0.6	Sigma-54 dependent transcriptional regulator SypG
<i>b1516</i>		0.4	-1.3	Signal transduction histidine kinase SypF
<i>b1517</i>		0.3	-1.8	Predicted protein SypD
<i>b1518</i>		0.2	-2.3	Periplasmic protein SypC involved in polysaccharide export
<i>b1519</i>		0.2	-2.1	Outer membrane protein SypB
<i>b1520</i>		0.1	-2.8	Anti-anti-sigma regulatory factor SypA

Table S4: List of T4SS genes down-regulated in biofilm condition.

Gene ID	Gene name	FC	Log ₂ FC	Product
<i>a3553</i>	<i>virB2</i>	0.3	-1.6	Putative type IV secretion system protein B2
<i>a3552</i>	<i>virB3</i>	0.3	-1.7	Putative type IV secretion system protein B3
<i>a3554</i>	<i>virB4</i>	0.1	-2.6	Putative type IV secretion system protein B4
<i>a3557</i>	<i>virB6</i>	0.2	-2.3	Putative type IV secretion system protein B6
<i>a3558</i>	<i>virB8</i>	0.2	-2.4	Putative type IV secretion system protein B8
<i>a3559</i>	<i>virB9</i>	0.2	-2.5	Putative type IV secretion system protein B9
<i>a3560</i>	<i>virB10</i>	0.14	-2.8	Putative type IV secretion system protein B10
<i>a3565</i>	<i>virB11</i>	0.2	-3.9	Putative type IV secretion system protein B11

Table S5: Genes identified in virulome of *V. tapetis* CECT4600 using all *Vibrio* genomes available in the MAGE platform.

Gene	Product	Organism	Function	<i>V. tapetis</i> CECT4600	
				Gene id	Log ₂ FC
<i>luxS</i>	S-ribosylhomocysteinase	<i>V. cholerae</i>	1	<i>a0117</i>	2.2
<i>a0599</i>	putative Paraquat-inducible protein B	<i>V. parahaemolyticus</i>	2	<i>a0599</i>	not DEG
<i>ompU</i>	Outer membrane protein U	<i>V. vulnificus</i>	2	<i>a1598</i>	6.6
<i>apxIB</i>	Toxin RTX-I translocation ATP-binding protein	<i>V. cholerae</i>	3	<i>b0152</i>	-1.3
<i>b1661</i>	Thermolabile hemolysin	<i>V. parahaemolyticus</i>	3	<i>b1661</i>	-1.3
<i>cqsA</i>	CAI-1 autoinducer synthase	<i>V. cholerae</i>	1	<i>b1774</i>	not DEG

Functions: 1. Regulation of virulence-associated genes, Regulation, Quorum sensing. 2. Offensive virulence factors, Adherence. 3. Secreted proteins. Not DEG: not differentially expressed gene ($p_{adj} > 0.05$).

Table S6: Genes involved in Type VI Secretion System.

Gene ID	Gene name	FC	Log₂FC	Product
<i>b0557</i>	<i>icmF</i>	2	1	T6SS component TssM (IcmF/VasK)
<i>b0558</i>		2.1	1	T6SS outer membrane component TssL (ImpK/VasF), DotU family
<i>b0559</i>		3	1.5	T6SS component TssK (ImpJ/VasE)
<i>b0560</i>		3	1.5	T6SS secretion lipoprotein TssJ (VasD)
<i>b0561</i>		3.6	1.8	T6SS FHA domain protein ImpI/VasC
<i>b0562</i>		2	1	Hypothetical protein
<i>b0563</i>		2.4	1.2	Hypothetical protein
<i>b0564</i>		1.9	1	Hypothetical protein
<i>b0565</i>		3.2	1.7	D-ala D-ala ligase and related ATP-grasp enzymes-like
<i>b0566</i>	<i>clpV</i>	3	1.6	T6SS chaperone ClpV (TssH)
<i>b0567</i>	<i>vasB</i>	3.7	1.9	T6SS component TssG (ImpH/VasB)
<i>b0568</i>	<i>vasA</i>	5.3	2.4	T6SS component TssF (ImpG/VasA)
<i>b0569</i>		4.3	2.1	T6SS lysozyme-like component TssE
<i>b0570</i>		5.1	2.3	Putative T6SS protein VasRB-1
<i>b0571</i>		62.6	6	T6SS component TssC (ImpC/VipB)
<i>b0572</i>		90	6.5	T6SS component TssB (ImpB/VipA)
<i>b0573</i>		138.9	7.1	T6SS component Hcp
<i>b0574</i>		20	4.3	T6SS component TssA (ImpA)
<i>b0575</i>		3	1.6	VgrG protein

Table S7: Primers used in qRT-PCR. Primer were designed with Primer Express software.

Primer	Sequence (5'→3')	Amplified gene (ID)
<i>luxOF</i>	GAG-CGT-GTT-CAT-TTG-CGG-A	<i>luxO</i> (a1225)
<i>luxOR</i>	TCC-GCG-CAG-ACT-TCT-TTA-CC	
<i>pilCF</i>	AAC-GCC-GCA-GTG-TTT-CTT-TT	<i>pilC</i> (a0251)
<i>pilCR</i>	TCG-CAC-TGA-CTT-TGT-TGG-AGA	
<i>16SF</i>	TTT-GCC-AGC-GAG-TAA-TGT-CG	<i>16srRNA 2</i>
<i>16SR</i>	GGT-TTA-TCA-CCG-GCA-GTC-TCC	
<i>cqsSF</i>	TGG-CGG-GTA-TGA-GAA-TCT-CG	<i>cqsS</i> (b1775)
<i>cqsSR</i>	ATC-AGA-AAG-GCA-CCG-CAG-G	
<i>hcp1F</i>	GGG-CAT-GGT-GGC-TTT-AAG-C	(b0573)
<i>hcp1R</i>	CGC-ACC-ATC-CAC-TTG-TTT-TG	
<i>luxSF</i>	CCT-GAT-CGG-AAC-CCC-TTC-A	<i>luxS</i> (a0117)
<i>luxSR</i>	GCC-GCT-AAC-CAA-GAA-TCA-GC	
<i>ompUF</i>	GCG-ACA-CCC-TAG-AGC-ATC-GT	<i>ompU</i> (a1598)
<i>ompUR</i>	CGA-AGT-TAC-CGC-CGA-TAC-CA	
<i>pilPF</i>	TGC-GAA-GTA-AGC-AGA-AAG-GGA	putative Pilus assembly protein PilP (a2966)
<i>pilPR</i>	CCA-ACA-GCC-ACA-CTC-CAA-CC	
<i>virB4F</i>	GTG-AGC-TGG-AGC-GGA-TAA-GC	putative Type IV secretion system protein B4 (a3554)
<i>virB4R</i>	GTA-TGA-CAG-CCA-CTC-CCC-GT	
<i>sypAF</i>	AAC-ATA-ACC-GCA-GCA-TGC-G	Anti-anti-sigma regulatory factor (b1520)
<i>sypAR</i>	TTT-CAA-GTG-GCT-GCC-CCT-T	