

A tight adherence (*tad*) like gene cluster of *Pseudomonas chlororaphis* PCL1606 exhibits a crucial role in avocado roots colonization, fostering its biological control activity.

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Table S1 Primers sequences used for the construction of bacterial mutant in both *pilA* genes ($\Delta pilA$)

Primer name	Primer sequence (5' -3')	Amplicon (bp) ^a
<i>pilAR1Fw</i>	CAGTGTTCGCGATGTACCG	Upstream region (899 bp)
<i>pilAR1Rv</i>	CCCTATAGTGAGTCGGATCCTCGTCCTGTACGCTGTCTTG	
<i>pilAR2Fw</i>	GGATCCGACTCACTATAGGGTGGCATTTCGTCCTAGCTCT	Downstream region (958 bp)
<i>pilAR2Rv</i>	CTGGGTGAACTGGAACAGGT	
<i>pilAintFw</i>	CCACCAGCACATTGTTGAAG	Internal region (458 bp)
<i>pilAintRv</i>	GCGTTCCAAGGAGAAGTCTG	

Table S2 Primers used in this study for RT-PCR experiments

Primer name	Primer sequences (5'-3')	Amplicon size (bp)
1F	CCAGTGTTCTGCGATGTACC	467 bp
1R	ACCTGTTCCGCAAGCCCATC	
2F	CCAGCAGGCGTACGTGATAG	240 bp
2R	TCAAGCTGGCCCTGCAACAC	
3F	TCGTCCACAAGAAGAAGCTG	180 bp
3R	GCGATCTTCAACAATGTGCT	
4F	GTTGAAGATCGCCAGTACCC	149 bp
4R	TGGAGTATCTGTGGCTCAGG	
5F	GCCTGAGCCACAGATACTCC	153 bp
5R	GCGATCTTCAATAGCGTCCT	
6F	GGGAAGTCAGGACGCTATTG	192 bp
6R	GCGTTCCAAGGAGAAGTCTG	
7F	CAACAAAGTTCGGAGCAACA	256 bp
7R	GTTTCATGACGGCATTCTTT	
8F	GACCTGCACCTGGAGAACT	398 bp
8R	TCCTGCTTGAGCTTGTCATC	
9F	CAGCAACCTGTTCCAGTTCA	265 bp
9R	TTCTGGCTCATTGCGATAAC	
10F	AGTGAAGTGAGCGGACTGGT	422 bp
10R	ACAATGTGCTGGAAGTGCTG	
11F	GTACGCATGAATGCCAAGAA	347 bp
11R	GATGTACTCGGCCACCTTGT	
12F	TTTCCCCTATGAGATGGAG	423 bp
12R	CTTCCTGGACGAAGTCGAAG	
13F	CTGGACGTGGTGATTCAACT	329 bp
13R	GGTTGAGGATCCTTTCGGTA	
14F	CAAGACCGATACCGAAAGGA	436 bp
14R	GTTACGCCCAGACTGACAT	
15F	TGAAGGTCAACCATCGCTAC	470 bp
15R	AACTTGCTGTCACCGAGGAT	
16F	GATCCTCGGTGACAGCAAGT	416 bp
16R	GCAATTCATGGGTCAAGTCC	
17F	AGATGTCGGTGGTGATGATG	352 bp
17R	CAACTACCAGATCGCCTGTG	
18F	CGAGCTCGATAGGTTTCTGG	259 bp
18R	TGGACAGGGTGAAGTCTCAG	
19F	GCACCGGTAACCACTGTTTT	376 bp
19R	CTCTGGTTCCTGCTCATGTC	
20F	GACATGAGCAGGAACCAGAG	348 bp
20R	ATGGATGCTGCACTCCTCTT	
21F	GAGGAGTGCAGCATCCATAG	394 bp
21R	GTGTAAGTCAACACCGCATC	
22F	TGCTGATGATGCAGTCCTTC	237 bp
22R	TCAGCTTGTCGGTGGAGTAG	
23F	GATGCGGTGGTGACTTACAC	443 bp
23R	GCTGCCGCGCCAGTCCAGGT	
24F	GAACAGCAGCACCATAACCA	469 bp
24R	CCTCGACATACTGCTGGACA	
25F	TGATCAACCTGCTGGTCAAC	568 bp
25R	ATCAACCTGATCCAGCATCC	
26F	TGCGCACGTAGATGCGGTTG	481 bp
26R	CTGGTCGATACCGATATCAG	
27F	ACCACCACCGTGACAACAG	529 bp
27R	AGCAGGTCACCACCAACTAC	

Table S3 Functional annotation of the proteins of each gene belonged to the *tad* like gene cluster by eggNOG-mapper v2

Genes	Gene number	E value	COG_category	Description	PFAMs
ADCP	1	1.21e-299	S, Function unknown	Autotransporter beta-domain	Autotransporter
RR	2	2.1e-77	T, Signal transduction mechanisms	cheY-homologous receiver domain	Response_regulator
<i>pilA1</i>	3	6.73e-14	U, Intracellular trafficking, secretion, and vesicular transport	Flp/Fap pilin component	Flp_Fap
<i>pilA2</i>	4	4.96e-16	U, Intracellular trafficking, secretion, and vesicular transport	Flp/Fap pilin component	Flp_Fap
<i>cpaB</i>	5	4.76e-152	U, Intracellular trafficking, secretion, and vesicular transport	Flp pilus assembly protein RcpC/CpaB	RcpC,SAF
<i>cpaE</i>	6	5.43e-235	U, Intracellular trafficking, secretion, and vesicular transport	COG4963 Flp pilus assembly protein, ATPase CpaE	TadZ_N
<i>cpaF</i>	7	4.92e-286	U, Intracellular trafficking, secretion, and vesicular transport	Type II/IV secretion system protein	T2SSE
<i>tadB</i>	8	3.27e-159	U, Intracellular trafficking, secretion, and vesicular transport	Type II secretion system protein F	T2SSF
<i>tadC</i>	9	2.94e-146	UN, Intracellular trafficking, secretion, and vesicular transport and Cell motility respectively	Type II secretion system (T2SS), protein F	T2SSF
<i>luxR</i>	10	5.76e-159	T, Signal transduction mechanisms	helix_turn_helix, Lux Regulon	GerE,Response_reg
PEP	11	6.13e-62	OU, Post-translational modification, protein turnover, and chaperones and Intracellular trafficking, secretion, and vesicular transport respectively	Type IV leader peptidase family	Peptidase_A24
<i>tadE</i>	12	7.78e-70	U, Intracellular trafficking, secretion, and vesicular transport	Pilus assembly protein TadE	TadE
PAS HK	13	0.0	T, Signal transduction mechanisms	Histidine kinase	HATPase_c,HiskA,PAS_3,PAS_4
<i>tadG</i>	14	1.06e-192	S, Function unknown	Putative Tad-like Flp pilus-assembly	Tad,Tad_C
HP	15	1.59e-117	S, Function unknown	Lipoprotein/Hypothetical protein	DUF4136