

Supplementary Materials:

## **AhaP, a quorum quenching acylase from *Psychrobacter* sp. M9-54-1 that attenuates *Pseudomonas aeruginosa* and *Vibrio coralliilyticus* virulence**

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**Supplementary Table S1.** Quorum quenching enzymes used in this study as queries in the BLASTp search for the identification of the QQ enzyme in *Psychrobacter* sp. M9-54-1.

Enzyme	Accession number	Species	Enzyme type	Reference
<b>AiiA</b>	AAM61772.1	<i>Bacillus</i> spp.	Lactonase (Metallo-beta-lactamases superfamily)	[1]
<b>AaC <i>Shewanella</i> sp.</b>	BAF94155.1	<i>Shewanella</i> sp. MIB015	Acylase (Ntn-hydrolase)	[2]
<b>AaC <i>Ralstonia</i> sp.</b>	AAO41113.1	<i>Ralstonia solanacearum</i> GMI1000	Acylase (Ntn-hydrolase)	[3]
<b>AhID</b>	AAP57766.1	<i>Arhtobacter</i> sp. IBN110	Lactonase (Metallo-beta-lactamases superfamily)	[4]
<b>AhIK</b>	AAO47340.1	<i>Klebsiella pneumoniae</i> KCTC2241	Lactonase (Metallo-beta-lactamases superfamily)	[4]
<b>AhIM</b>	AAT68473.1	<i>Streptomyces</i> sp. M664	Acylase (Ntn-hydrolase)	[5]
<b>AhIS</b>	BAK54003.1	<i>Solibacillus silvestris</i> StLB046	Lactonase (Metallo-beta-lactamases superfamily)	[6]
<b>AidC</b>	BAP32158.1	<i>Chryseobacterium</i> sp. StRB126	Lactonase (Metallo-beta-lactamases superfamily)	[7]
<b>AiiM</b>	BAJ75775.1	<i>Microbacterium testaceum</i> StLB037	Lactonase (Metallo-beta-lactamases superfamily)	[7]
<b>AiiO</b>	ADI80348.1	<i>Ochrobactrum</i> sp. A44	Acylase (alfa/beta hydrolase)	[8]
<b>AttM</b>	AAD43990.1	<i>Agrobacterium tumefaciens</i> C58, M103	Lactonase (Metallo-beta-lactamases superfamily)	[9]
<b>Bpib01</b>	ABU51804.1	Metagenome	Hypothetical	[10]
<b>Bpib04</b>	ABU51107.1	Metagenome	Lactonase (Glycosyl hydrolase)	[10]
<b>Bpib05</b>	ABU51109.1	Metagenome	Hypothetical	[11]
<b>Bpib07</b>	ABU51111.1	Metagenome	Lactonase (Dienolactone hydrolase)	[10]
<b>HacA</b>	YP_235052.1	<i>Pseudomonas syringae</i> B728a	Acylase (Ntn-hydrolase)	[12]
<b>HacB</b>	YP237923.1	<i>Pseudomonas syringae</i> B728a	Acylase (Ntn-hydrolase)	[12]
<b>MCP</b>	AAS06218.1	<i>M. avium</i> subsp. <i>paratuberculosis</i> K-10	Phosphotriesterase-like lactonase (PLL)	[13]
<b>PON</b>	EAP_90803.1	<i>Oceanicaulis alexandrii</i> HTCC2633	Lactonase (Paraoxonase)	[14]
<b>PpH</b>	NP_214744.1	<i>Mycobacterium tuberculosis</i>	Phosphotriesterase-like lactonase (PLL)	[15]
<b>PvdQ</b>	NP_251075.1	<i>Pseudomonas aeruginosa</i> PAO1	Acylase (Ntn-hydrolase)	[16]
<b>QlcA</b>	ABV58973.1	Sin identificar ( <i>metagenoma</i> )	Lactonase (Metallo-beta-lactamases superfamily)	[17]
<b>QsdA</b>	AAT06802.1	<i>Rhodococcus erythropolis</i> W2	Phosphotriesterase-like lactonase (PLL)	[15]
<b>QsdB</b>	AFX82613.1	Sin identificar ( <i>metagenoma</i> )	Acilase (Amidase signature family)	[18]
<b>QsdH</b>	AFV15299.1	<i>Pseudoalteromonas byunsanensis</i>	Lactonase (GDSL-hidrolases family)	[19]
<b>QuiP</b>	AAG04421.1	<i>Pseudomonas aeruginosa</i> PAO1	Acylase (Ntn-hydrolase)	[20]
<b>Sislac</b>	Pdb 4G2D A	<i>Sulfolobus islandicus</i>	No identified	[21]
<b>SsoPox</b>	Q97VT7.1	<i>Sulfolobus solfataricus</i> P2	No identified	[22]

**Figure S1.** Alignment of the protein sequences of AhaP from *Psychrobacter* sp. M9-54-1 and PvdQ (NP\_251075.1) from *Pseudomonas aeruginosa* PAO1.

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AhaP M9-54-1      1 MSINVLNRRVRLTLLTMAVSLGTFGCSNDNFNGNIDDTGTDSTYAAADIQRTEFGIPHI
PvdQ PAO1        1 MGM-----R-----TVLTGLAGMLLGS-MMPVQADMPPRTGLAADI RWTAYGVPHI

AhaP M9-54-1     61 TARNYKGLGYGVGYAFEDNICSLAREIIVAKGESMRVYLGAEENE-----NSDVFYTW
PvdQ PAO1        46 RAKDERGLGYGLGYAVARDNACLLEIEIVTARGERARYFGSEGKSSAELDNLPSDIFYAW

AhaP M9-54-1     114 YNSPERRSGFLGAODPEVIDAVKGYAAGVNRVYLDHDKGVKNIEDPACAGAEWVREINIDDM
PvdQ PAO1        106 LNQPEALQAEFWQAQTPAVRQLLEGYAAGFNRFLREADG---KTTSGLGQPWLRATATDDL

AhaP M9-54-1     174 LADYGKANLRGGLSNFVKQIAQVAPPASGIVMGSSRMS SPEPIAESDEKFDMTTINVLDG
PvdQ PAO1        163 LRTTRRLLVGGVGGVADALVAAAPPGAEKVALSGEQA----FQVAE---QRRQRFRLER

AhaP M9-54-1     234 GSNAYAFVSGSKVTGTDSCVMYGNPHEPWEVQRFYEFHTTIPGKLDVMGSAQQGQPFINIG
PvdQ PAO1        216 GSNAIIVVSGERSADGKMLLANPHFPWNGAMRFYQMHLLTIPGRLDVMGASLPLPVPVNI

AhaP M9-54-1     294 FNKDVAVSHVSTAKRFTLYQLSLVNGSPFKVNYVNSDGKVEQRDIETVPVIVK--MPNN
PvdQ PAO1        276 FSRHLAWHTVDTSSHTLYRLALDPKDPRLVLDGRSLPLEEKS---VAIEVVRGADGKL

AhaP M9-54-1     352 QTITRNIVVSHYGPILNAKLLDPRLPWAGDANVVVYTIIRDAASENPRALNQWRSMNMATS
PvdQ PAO1        333 SRVEHKVYQSIYGPLVV---WPGKLDWNR--SEAYALRDANLENTRVLQQWYSINQASD

AhaP M9-54-1     412 VGDIVDRMOKILGLGFVNTIATDRNCKALYADISTVFNVTREKLVACSDAGAAALPLLIA
PvdQ PAO1        387 VADLRRRVEALQGIPTWNTLAADEQGNALYMNQSVVYLPKPELIPAC-----AIPQLVA

AhaP M9-54-1     472 ADLPAINGSTAACEWDTADADSPAGIFGGSKLFFLIRDDYVVLNSNDSYWLSNAEQPLTGF
PvdQ PAO1        441 EGLPALQGDQSRCAWSDPAAAQAGITPAAQLPVLRLRDFVQNSNDSAWLTPASPLOGF

AhaP M9-54-1     532 SPLRRDLPLISEDAAPLSLRTRMFTQVLDLNLNKDGLGHNFDLQVYVYGNRSYA
PvdQ PAO1        501 SPLVVSQEK-----PIGPRARVALSR---LQ----GKQPLEAKTLEEMVTANHVFS

AhaP M9-54-1     592 AELVLDVLEADCNANPMLPLTGGATIEAKQACSILNNWDRRNIDSRGAHVFRFVWNAAG
PvdQ PAO1        544 ADQVLPDLRLCRDNQG-----EKSLARACAALAQWDRGANLDSGSGFVYFQRFMQ-R

AhaP M9-54-1     652 FSEYTNDSFKVVFNEADPINTPRELKI-----TAQTRQALGDATAYFQNKGTALDASLGE
PvdQ PAO1        596 F-AELDGAVKPEPFDAQRELDTPQGIALDRPQVATQVRQALADAAAEVEKSGIPD GARWGD

AhaP M9-54-1     707 LQYVLDAGKNNQHIPMHGGYSGEIGFNVARCAGVNEAGNYIINNCPYMQSVTFDSKGPV
PvdQ PAO1        655 LQVST---RQERIAIAPGGDGHFCVYNAIQS--VRKGDHLEVVGCTSYIQLVTFPEEGEK

AhaP M9-54-1     767 VEALLAYSQAGDTRRPFYHRDQTRRYSDDKKWIRLPFSKSETISKQAVGEVIKLR
PvdQ PAO1        710 ARGLLAFSSDPRSPHYRDQTELESRQQWQTLPFSDRQIDADPQLQRLSIRE

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