

**SUPPLEMENTARY DATA**

**FIG. S1.** Multiple alignments of protein sequences of (A) PhaZ1 from *H. seropedicae* SmR1 (Hsero\_1622) against PhaZ1a1 from *R. eutropha* H16 (A1150) and (B) PhaZ2 from *H. seropedicae* SmR1 (Hsero\_0639) against PhaZ2a2 from *R. eutropha* (A2862) were carried out using Clustal Omega and the default parameters (1). The asterisks (\*) indicate fully conserved residues, while colons (:) indicate conservation in residues of strongly similar properties and points (.) indicate conservation in residues of weakly similar properties.

<b>A</b>			
PhaZ1	MLYQLHELNRAF LNPMMQWAETSAKLFSDPVSLAHTPFQSQRIAAGYELLYRLSKEYEKP	60	
PhaZ1a1	MLYQLHEFQRSILHPLTAWAQATAKTFNPLSPLSLVPGAPRLAAGYELLYRLGKEYEKP	60	
	*****:.*:.*:* **::** *:.*:***: .* : *.*****.*****		
PhaZ1	QFNIDAVPVDGKSVGIVEEVVEEKPFCLRHFRKDLRSARQAT--ALKQPTVLVWAPLSGH	118	
PhaZ1a1	AFDIKSVRSNGRDIPIVEQTVLEKPFCKLVRFKRYADDPETIKLLKDEPVVLAAPLSGH	120	
	*.*:* *:*:* **:* * **:*:*:*: . . : : .*.***.*****		
PhaZ1	HSTLLRETVRALLQEHDVYITDWDARMPVEEQGAFHLHDYVYVQDFIRTLGP-DVHVI	177	
PhaZ1a1	HATLLRDTVRTLLQDQHKVYVTDWIDARMPVEEGAFHLSDYIYYIQEFIRHIGAENLHVI	180	
	*.****.***.***.* *.*.*** *****.***** **.*.*.*.*** .* :.***		
PhaZ1	SVCQPTVPVLAAILMASANDPMLPKSMTMMGGPIDARKSPTAVNDLATEKPYSWFENTV	237	
PhaZ1a1	SVCQPTVPVLAAILMASAGE-KTPRTMTMMGGPIDARKSPTAVNSLATNKSFEWFENNV	239	
	*****.*****.: *.:*****.*****.***.* :.***.*		
PhaZ1	IYSVPANYPGFRKVPYVPGFLQHAGFVAMNPRRHAQSHWDFYMHLDGDDASAEHRKFYD	297	
PhaZ1a1	IYTPANYPGHRRVYPGFLQHAGFVAMNDRHLSHYDFYLSLVEGDADDAEHRVRYD	299	
	*.*.*****.*.:*****.***** ** .*.***: * :** .** * :***		
PhaZ1	EYNAVLDMPAEFYLETIKVVFQDFNLARGTWEIEGQVLRPQDIKSVALFTIEGELDDISG	357	
PhaZ1a1	EYNAVLDMAEYVLDTIREVFQEFRLANGTWAIDGNPVRPQDIKSTALMTVEGELDDISG	359	
	***** **.*.*.*: **.*.*.*** *.*: *****.*.*:*****		
PhaZ1	SGQTQAAQELCCSIPKARKQHTVPKAGHYGIFSGRRWREIVCPKIGEFIRANA-----	411	
PhaZ1a1	AGQTAAAHDLCAIGPKIRKQHLNAACHGHYGFSGRRWREEIYVQLRDFIRKYHQASATR	419	
	:** *.:*.*:*** **:*.*. :.***** : *.: :***		
<b>B</b>			
PhaZ2	MIPTYQLYQNYADATDPLRACARMAQALGATWPGIPVHPYWRKMASACEVFARTQLTHA	60	
PhaZ2a2	--MLYHAYQIYADMI LPACTLAE LAEAATLAA-NPRSGGFDAVPRLRAACELIALVRLTHH	57	
	*. ** *** * :.*: *.* * . :.:***:* :.***		
PhaZ2	RPPFGIATVEEGCTISVHEEEIHATPFCGLLHFRKDSATVQPKVLVWAPMSGHFATLLR	120	
PhaZ2a2	RPAFGIDHATVGGQVPVTEEVVARTPFCSLLHFRRHGIVGQPRVLLVAPMSGHFATLLR	117	
	** *** . * : * ** : **.*.***:.. . **.*:*****		
PhaZ2	GTVRTLLRDHDVYITDWRNARDVATAHGRFGLDEYVSHIIDFLGVLGPGAHLAVCQPTV	180	
PhaZ2a2	GTVQTMLADHDVYITDWHNPRDIPLLAGRFGDFVQHLIGFLQTLGGGTHLVAICQPAV	177	
	***.*.* *****.***.* ** : **.*.*.*.* ** *.*.*:***.*		
PhaZ2	AALTAAVMAADGHPAQPRSMTLMAGPIDTRVNPTAVNALAKSKPIAWFEKNMISTVPAR	240	
PhaZ2a2	AALAAALMAEDGPAQPPSLTLMAGPIDARVNPTKVNALAMSQPLEWFERTLIGMVPLR	237	
	***.***.* ** *.*.* *.:*****.***** ***** *.*: **:*.*. ** *		
PhaZ2	HAGAGRVPYVPGFVQLAAFMNMNLSRHVEAFGKLYHHLVDGEHARADQIKDFYEEYFAMAD	300	
PhaZ2a2	FAGAMRRVYPGHVQLAFMNMNPERHEQALRELYALRERGEHDKADAIRDFYIEYFATMD	297	
	.*** *****.* ** *.*.* **.*: :** **.* ** *.*.*** ** ** *		
PhaZ2	LPAEFYLETVRTVFQEHALPLGKLSYAGRPVEPRAIRRTALFTIEGKDDICAVGQTLAA	360	
PhaZ2a2	LTAEFYLETVSLVFQRFLLAQGLLDVSGRRVTRAIHRTALLTVEGERDDICAIQQTVA	357	
	* ***** **.*.* * *.*: ** * .***.***.*:***.***.***.***.*		
PhaZ2	QELCSGIRPYMRLHHVQTVAGHYGVFNRRWDNEIYPRDRDFINMHR	408	
PhaZ2a2	QDLCSSLRPYMRMHVQTVGHHYGVFNRRWETQVYPLVRNITYSS-	404	
	*.*.*.:*****.*****.*****.***:.*: *		

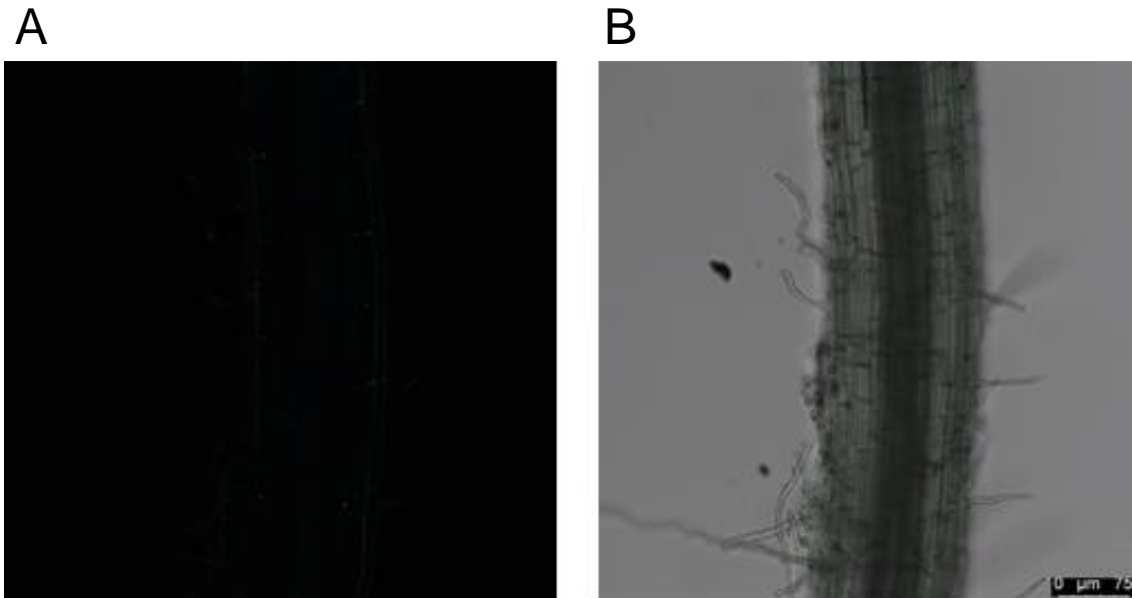
FIG. S2. Multiple alignment of protein sequences of FliA from *H. seropedicae* SmR1 (Hsero\_2029) against FliA from *E. coli* MG1655 (b1922) was carried out using Clustal Omega and the default parameters (1). The asterisks (\*) indicate fully conserved residues, while colons (:) indicate conservation in residues of strongly similar properties and points (.) indicate conservation in residues of weakly similar properties.

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FliA_Hs      ---MYNVKGGKGGKNDLLEQHAPLVKLAHQLKAKLPPSVEVDDLIQAGMMGLLDAVNRYE      57
FliA_Ec      MNSLYTAEGVMDKHSWQRYVPLVRHEALRLQVRLPASVELDDLQAGGIGLLNAVERYD      60
              :*.:.*  .*.:.*  :.:.*.*.: * :*.:.* **:*.*.*.* :*.:*.*.*:
FliA_Hs      ETHGAQFETYAVQRIRGAMLDELRSDDLPRVSRIRQNARKVEEAMQTLLQQLGRQPKEAEL      117
FliA_Ec      ALQGTAFTTYAVQRIRGAMLDELRSRDWVPRSVRRNAREVAQAIGQLEQELGRNATETEV      120
              :* : * ***** **:*.*:*.*.*.* :*: * *.*.*: .*.:*
FliA_Hs      AQHMQISLEDYQSLLSECGGHQLIYYEDFHDDGGHEHFLDRHQTSDSDPLQNLINGGF      177
FliA_Ec      AERLGIDIADYRQMLLDTNNSQLFSYDEWREEHGDSIELVTD--DHQRENPLQQLDSNL      178
              *.:.* *.: *.*.:.* : .. **:* :*.:*.:*.*. .: : :*.*.*.:*.:*
FliA_Hs      REAVVDSIKALPEREQILMALYYEQEMNLKEIGAVMGVSESRVCQLHSQAISRMRSYLRE      237
FliA_Ec      RQRVMEAIETLPEREKLVLTLYYQEELNLKEIGAVLEVGESRVSQQLHSQAIKRLRKLKLGK      238
              *:* :*.:*:*.*.*.*.:*.:*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
FliA_Hs      HSWGVA      244
FliA_Ec      L-----      239

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FIG. S3. Confocal microscopy analysis of uninoculated *Setaria viridis* roots showing a low intrinsic green fluorescence. (A) Confocal GFP fluorescence image and (B) merged images of confocal fluorescence and bright field images



## References

1. Sievers F, Wilm A, Dineen D, Gibson TJ, Karplus K, Li W, Lopez R, McWilliam H, Remmert M, Soding J, Thompson JD, Higgins DG. 2011. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol Syst Biol* 7:539.