1	Supplementary Material for Sulkowski et al
2	A multi-protein complex anchors adhesive holdfast at the outer membrane of Caulobacter
3	crescentus.
4	
5	Authors
6	Nina I. Sulkowski, ^{a,b,*} Gail G. Hardy, ^{c,*,#} Yves V. Brun, ^{c,d} Tanmay A.M. Bharat ^{a,b,#}
7	
8	Affiliations
9	^a Sir William Dunn School of Pathology, University of Oxford, Oxford OX1 3RE, UK
10	^b Central Oxford Structural and Molecular Imaging Centre, Oxford OX1 3RE, UK
11	^c Department of Biology, Indiana University, Bloomington, Indiana 47405, USA.
12	^d Département de microbiologie, infectiologie et immunologie, Université de Montréal, C.P.
13	6128, succ. Centre-ville, Montréal (Québec) H3C 3J7, Canada
14	
15	
16	Running Title
17	Caulobacter crescentus outer membrane holdfast anchor
18	
19	Correspondence
20	# Address correspondence to Gail Hardy, gahardy@indiana.edu or
21	Tanmay A.M. Bharat, <u>tanmay.bharat@path.ox.ac.uk</u>
22	
23	* N.I.S. and G.G.H. contributed equally to this work.
24	

25 SUPPLEMENTARY FIGURES



29 Figure S1. Cryo-ET gallery of *C. crescentus* stalk tips.

- 30 Collection of holdfast anchor mutants imaged in this study. (A-B) ΔhfaA (C-D) ΔhfaD (E-F)
- $\Delta h fa AD$ (G-H) $\Delta h fa B$.



32

33 Figure S2. Sub-tomogram averaging of the holdfast secretion complex mutant ($\Delta hfsDAB$). (A) $\Delta hfaB$ strain displays uniform curvature along the stalk tip. Panels A is same 34 as Figure 4A, shown here for comparison with B-D panels. (B-D) $\Delta h fs DAB$ mutant displays 35 36 aberrations in stalk morphology, with visible narrowing at various regions near the tip. (E) Subtomogram averaging analysis of $\Delta hfaB$ stalk tips. Panel E is same as in Figure 4C. The density 37 layers corresponding to the outer S-layer (OS), inner S-layer (IS), outer membrane (OM) and 38 39 the peptidoglycan (P) have been marked. (F) Sub-tomogram averaging analysis of $\Delta h fs DAB$ 40 stalks reveals increased OM curvature in the final average.

42 SUPPLEMENTARY TABLES

Strain or plasmid	Description or construction	Source or reference
Strains	•	
E. coli		
S17-1	<i>E. coli</i> 294::RP4-2(Tc::Mu)(KM::Tn7)	(1)
Alpha-select [™]	deoR endA1 recA1 relA1 gyrA96 hsdR17(r _k -	Bioline
-	m_k^+) supE44 thi-1 Δ (lacZYA-argFV169)	
	$\Phi 80\delta lacZ\Delta M15 F^{-1}$	
C. crescentus		
CB15	Wild-type	(2)
YB1109	CB15 NY111d1 is a clone that has the Abs	(3)
	phenotype (stalk abcission Abs2)	
YB2811	CB15 Abs2 <i>pstS</i> ::miniTn5	(4)
YB767	CB15N <i>pstS</i> ::miniTn5	(5)
YB7793	CB15 Abs2 <i>pstS</i> ::miniTn5, $\Delta hfsG$	This study
YB7795	CB15 Abs2 <i>pstS</i> ::miniTn5, ΔhfsDAB	This study
YB7797	CB15 Abs2 pstS::miniTn5, ΔhfaB	This study
YB8679	CB15 Abs2 pstS::miniTn5, ΔhfaA	This study
YB8680	CB15 Abs2 <i>pstS</i> ::miniTn5, ΔhfaD	This study
YB8681	CB15 Abs2 pstS::miniTn5, ΔhfaA, ΔhfaD	This study
Plasmids		
pNPTS138/9	pLitmus 39 derivative; with <i>nptI</i> , <i>sacB</i> and	M.R.K. Alley,
1	RK2 <i>oriT</i> sequences, and deleted <i>bla</i> gene; Km ^R	unpublished
pNPTS138∆hfaA	pNPTS138 parent vector containing 500 bp fragments upstream and downstream of <i>hfaA</i>	(6)
pNPTS138∆ <i>hfaB</i>	pNPTS138 parent vector containing 500 bp fragments upstream and downstream of <i>hfaB</i>	(6)
pNPTS138∆hfaD	pNPTS138 parent vector containing 500 bp fragments upstream and downstream of <i>hfaD</i>	(6)
pNPTS138∆ <i>hfsDAB</i>	pNPTS138 parent vector containing 500 bp fragments downstream of <i>hfsD</i> and downstream of <i>hfsB</i>	(6)
pNPTS138∆ <i>hfsG</i>	pNPTS138 parent vector containing 500 bp fragments upstream and downstream of <i>hfsG</i>	(7)

43 TABLE S1. Bacterial strains and plasmids used in this study.

44

45 Table S1. Bacterial strains and plasmids used in this study.

46 Description of bacterial strains and plasmids used in this study is provided in this table.

47

49 TABLE S2. Oligonucleotides used in this study

Oligo Name	Sequence (5' - 3')	Application
FhfaupA	GCGATCACGAAGCTTACGAGGTAG	hfaA in-frame deletion
RmhfadownA	GGCGTCAATGAATTCCGAGCGGAT	<i>hfaA</i> in-frame deletion
FhfaupD	GGCATCACCAAGCTTAACTACAAC	<i>hfaD</i> in-frame deletion
RmHfadownD	GCGGCCTGGGAATTCTAGTCCTGA	<i>hfaD</i> in-frame deletion
FupSphhfsG	CTGCCCGCATGCGTCGGCCTC	<i>hfsG</i> in-frame deletion
RdwnBamHihfsG	GTTGAGATCGGATCCGTAGGTGAT	<i>hfsG</i> in-frame deletion
hfsDHindend	GATCAGCTTAAGCTTCTCCTCAGG	hfsDAB in-frame deletion
hfsBHindend	TCCATAGCCAAGCTTAGGCGCCGG	<i>hfsDAB</i> in-frame deletion
FhfaBup	GCCTTCACGCCGGGATCCAACAATCTGGGA	<i>hfaB</i> in-frame deletion
RmHfadownB	CACGTTGGCGAATTCCGACTGGCT	<i>hfaB</i> in-frame deletion

52 Table S2. Oligonucleotides used in this study

53 Oligonucleotide sequences used in this study are listed in this table.

56 SUPPLEMENTARY MOVIE LEGENDS

57

58 Movie S1. Tomogram of CB15 cell stalks.

A movie containing sequential z-slices of a reconstructed tomogram of *C. crescentus* CB15
cell stalk tips is presented. This tomogram shows the presence of the holdfast anchor complex
at the stalk tip.

62

63 Movie S2. Tomogram of a cell stalk tip from the *hfsG* deletion strain.

64 A movie containing sequential z-slices of a reconstructed tomogram of *C. crescentus* $\Delta hfsG$ 65 cell stalk tips is presented. This tomogram also shows the presence of the holdfast anchor 66 complex at the stalk tip.

67

68 Movie S3. Tomogram of a cell stalk tip from the *hfaB* deletion strain

69 A movie containing sequential z-slices of a reconstructed tomogram of C. crescentus $\Delta h faB$

cell stalk tips is presented. This tomogram shows the absence of the holdfast anchor complexat the stalk tip.

73 74

SUPPLEMENTARY REFERENCES

R. Simon, U. Priefer and A. Puhler. 1983. A Broad Host Range Mobilization System
 for Invivo Genetic-Engineering - Transposon Mutagenesis in Gram-Negative Bacteria. Bio Technology 1:784-791.

- 78 2. J. S. Poindexter. 1964. Biological Properties and Classification of the Caulobacter
 79 Group. Bacteriol Rev 28:231-95.
- 3. J. S. Poindexter. 1978. Selection for nonbuoyant morphological mutants of Caulobacter
 crescentus. J Bacteriol 135:1141-5.

M. M. Ireland, J. A. Karty, E. M. Quardokus, J. P. Reilly and Y. V. Brun. 2002.
Proteomic analysis of the Caulobacter crescentus stalk indicates competence for nutrient
uptake. Mol Microbiol 45:1029-41.

85 5. M. Gonin, E. M. Quardokus, D. O'Donnol, J. Maddock and Y. V. Brun. 2000.
86 Regulation of stalk elongation by phosphate in Caulobacter crescentus. J Bacteriol 182:33787 47.

6. G. G. Hardy, R. C. Allen, E. Toh, M. Long, P. J. Brown, J. L. Cole-Tobian and Y. V.
Brun. 2010. A localized multimeric anchor attaches the Caulobacter holdfast to the cell pole.
Mol Microbiol 76:409-27.

91 7. E. Toh, H. D. Kurtz and Y. V. Brun. 2008. Characterization of the Caulobacter
92 crescentus Holdfast Polysaccharide Biosynthesis Pathway Reveals Significant Redundancy in
93 the Initiating Glycosyltransferase and Polymerase Steps. J Bacteriol 190:7219-7231.