Cryo-ET Characterization of Novel Cellular Extrusions in *Escherichia coli* Induced by the Major Subunit Protein of Type IV Pili, PilA, from *Pseudomonas aeruginosa*

Juan Sanchez¹, Daniel Parrell², Alba Gonzalez-Rivera³, Nicoleta Ploscariu², Katrina Forest³, Elizabeth R. Wright^{2,4,5}

Extracellular membranous appendages are found in many prokaryotic species including archaea, Grampositive bacteria, and Gram-negative bacteria and have been termed nanotubes, nanopods, or nanowires [1-4]. During our studies of type IV pili, we discovered nanotube like structures correlated with heterologous expression of the *Pseudomonas aeruginosa* major type IV pilin, PilA, in some *Escherichia coli* strains. We have coined these membranous tubular structures P-pods for pilin-induced pods based partly on their appearance in negative stain transmission electron microscopy images. Biochemical analysis showed that the major protein inside of P-pods is the inner membrane protein PilA. Because some membranous appendages serve as transport tunnels, we tested horizontal gene transfer in the P-pods; these studies revealed that P-pods are unable to transfer plasmid DNA.

To further characterize the structure of P-pods we carried out both negative stain TEM imaging and cryoelectron tomography. The cells were incubated on LB agar with inducers for 16 hours. Cells were resuspended in LB liquid medium to an $OD_{600} = 0.01$ and spotted on to glow-discharged, Quantifoil R2/1 mesh, gold grids (Quantifoil, Germany) with 5 nm carbon coating, in a humified chamber for 3.5 hours. Three μ L of BSA-treated 10 nm colloidal gold (Electron Microscopy Sciences, USA) was applied onto the grids and then plunge-frozen in liquid ethane using a Leica EM GP (Leica Microsystems, Germany). Data collection was performed on a Titan Krios (Thermo Scientific, USA) FEG TEM operated at 300 kV and equipped with a Gatan K3 direct electron detector and a Gatan bioquantum energy filter, at the University of Wisconsin-Madison Cryo-EM Research Center. Images were acquired with a pixel size of 0.4603 nm on the specimen and a total electron does between 120 to 130 e⁻/Å². Data were collected at 2° increments from -60° to +60° (61 images) with a nominal defocus range of -4.0 to -6.0 μ m to enhance contrast of various cell components. Tilt series images were collected using SerialEM [5]. Tomographic reconstructions were generated using IMOD [6] following tilt-series image motion correction by motioncor2 [7] and data were binned two-fold during this process. Neural network based tomogram segmentation models of P-pods were produced with EMAN2 [8].

The resulting 3D reconstructions revealed that P-pods originate at the inner membrane and P-pod extrusion may occur in multiple ways (Figure 1). P-pods may exit the cells through breaks in the outer membrane or by blebbing of the outer membrane which eventually ruptures and releases P-pods (Figure 1). Also, our data indicates that P-pods are comprised of a single lipid-bilayer, do not transport other vesicles, and are typically observed as a string of segmented vesicles once outside of the cell (Figure 2).

¹Biophysics Program, University of Wisconsin – Madison, Madison, Wisconsin, United States,

²Department of Biochemistry, University of Wisconsin – Madison, Madison, Wisconsin, United States,

³Department of Bacteriology, University of Wisconsin – Madison, Madison, Wisconsin, United States,

⁴Cryo-Electron Microscopy Research Center, Midwest Center for Cryo-Electron Tomography, University of Wisconsin – Madison, Madison, Wisconsin, United States, ⁵Morgridge Institute for Research, University of Wisconsin – Madison, Madison, Wisconsin, United States,

Correlative light and electron microscopy (CLEM) could provide additional evidence for the localization of PilA within the cell and P-pods and may be the focus of follow up experiments. The biochemical and structural studies presented here reveal that, though similar to nanotubes, P-pods are novel membranous extracellular appendages that spontaneously assemble as the result of PilA over-expression in *E. coli* and may be a result of protein crowding that leads to positive membrane curvature of the inner membrane [9].

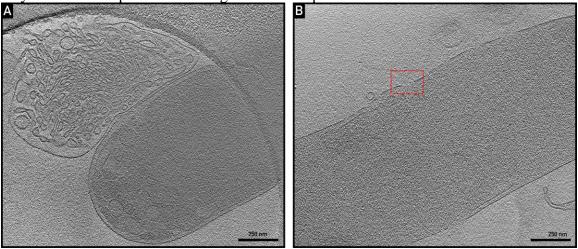


Figure 1. Characterization of P-pod extrusion via blebbing or membrane breach. A) Tomogram reconstruction of an *E. coli* cell expressing *P. aeruginosa* PilA protein resulting in blebbing of the outer membrane and localization of p-pods to the bleb. B) Tomogram reconstruction of the PilA expression system resulting in breaks along the outer membrane which allow for extrusion of p-pods. Figures represent a central slice with a thickness of 4.6 nm.

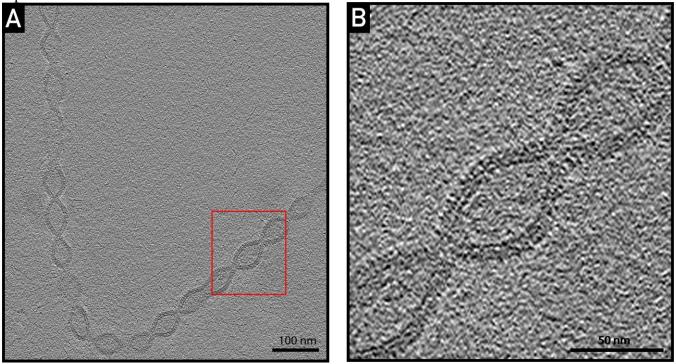


Figure 2. Extracellular P-pod structures. A) Tomogram reconstruction of extracellular p-pods as a string of segmented vesicles and B) a magnified view of a p-pod segment. Figures represent a central slice with a thickness of 4.6 nm.

References

- 1. Pal, R.R., et al., *Pathogenic E. coli Extracts Nutrients from Infected Host Cells Utilizing Injectisome Components*. Cell, 2019. **177**(3): p. 683-696.e18.
- 2. Weiner, J.H., et al., Overproduction of fumarate reductase in Escherichia coli induces a novel intracellular lipid-protein organelle. J Bacteriol, 1984. **158**(2): p. 590-6.
- 3. Shetty, A., et al., Nanopods: a new bacterial structure and mechanism for deployment of outer membrane vesicles. PloS one, 2011. **6**(6): p. e20725-e20725.
- 4. Wang, F., et al., Structure of Microbial Nanowires Reveals Stacked Hemes that Transport Electrons over Micrometers. Cell, 2019. **177**(2): p. 361-369.e10.
- 5. Mastronarde, D.N., *Automated electron microscope tomography using robust prediction of specimen movements*. Journal of Structural Biology, 2005. **152**(1): p. 36-51.
- 6. Kremer, J.R., D.N. Mastronarde, and J.R. McIntosh, *Computer Visualization of Three-Dimensional Image Data Using IMOD*. Journal of Structural Biology, 1996. **116**(1): p. 71-76.
- 7. Zheng, S.Q., et al., *MotionCor2: anisotropic correction of beam-induced motion for improved cryo-electron microscopy*. Nature methods, 2017. **14**(4): p. 331-332.
- 8. Chen, M., et al., Convolutional neural networks for automated annotation of cellular cryo-electron tomograms. Nature methods, 2017. **14**(10): p. 983-985.
- 9. This research was supported by funds from the University of Wisconsin-Madison, National Institutes of Health (R01GM104540 and R01GM104540-03S1) to E.R.W. J.C.S. was supported in part by the Biotechnology Training Program, T32GM135066. All EM data was collected at the University of Wisconsin-Madison, Department of Biochemistry Cryo-EM Research Center. The authors gratefully acknowledge use of facilities and instrumentation at the UW-Madison Wisconsin Centers for Nanoscale Technology (wcnt.wisc.edu) partially supported by the NSF through the University of Wisconsin Materials Research Science and Engineering Center (DMR-1720415).