Electron microscopy is an important tool, which can provide essential low- and medium-resolution information on the size and quaternary structure of membrane proteins stabilized with detergent or in a lipid membrane. This abstract describes the results from the electron microscopy studies on APEC ClyA protein. Escherichia coli cytolysin A also known as hemolysin E (ClyA, also known as hemolysin E, HlyE) is a 34 kDa cytolytic α-helical pore-forming toxin. The crystal structure of soluble monomeric E. coli K-12 ClyA was previously solved at high resolution and this showed that ClyA had a novel structure that had not previously been seen in the data bank of proteins. Avian pathogenic E. coli (APEC), strain JM4660ClyA is 75% sequence identical to E. coli K-12 ClyA and has many significant similarities.

To investigate Avian pathogenic E. coli ClyA pore formation, purified Avian pathogenic E. coli ClyA was incubated with detergent 1% β-octylglucoside (β-OG). The result shows the majority of the pores were circular from the top view and bind together in complex but uniformly sized clusters. The pores can be seen as spikes from the side view. The clusters may well be spherical assemblies of pore, not unlike virus particles. Seen from above some appear to have a central pore surrounded by 6 others. This may be consistent with 12-fold symmetry seen for K12 ClyA pores in the crystal structure. Future work will focus on further experiments on electron microscopy of the pores forming toxins to enable greater understanding of mechanisms of pore formation.