Towards determining a high-resolution structure of the coat proteins on PR772

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The bacterium specific virus, bacteriophage PR772 is interesting to study, because it has an inner lipid membrane and it has unique vertices, which can form a stalk during infection. It infects the male gram-negative *E. Coli.* The F^+-strain makes it possible to transfer genetic material between different bacteria. The PR772 has an icosahedral shape, with no stalk. During infection, it uses the internal membrane to create a stalk-like structure that helps injecting the DNA into the host. It is crucial to obtain a higher resolution of the bacteriophage structure, so that it is possible to get a deeper understanding of the mechanism of the infection. The first step to understanding the virus structure is to determine the structure of the coat proteins. In this project the coat proteins of interest are P30 and P6. P30 works as a cementing molecule and P6 helps out with DNA packaging in the virus. PRD1 is another widely studied member of the Tectiviridae family, which include PR772 There have been structural studies of PRD1, but very little is know about the infection mechanism. PR772 and PRD1 are both closely related with the amino acid identity as high as 97.2 %. This will make the results from earlier studies on PRD1 useful for determining the coat proteins structures.

The aim of the project is to determine the structure of coat proteins, P6 and P30 of the bacteriophage PR772. Cloning the coat protein genes and express the protein in a larger quantity is the necessary first step. It may then be possible to crystalize the proteins for X-ray crystallography. By X-ray crystallography we can determine the structure of the proteins to a high resolution.

So far, the proteins expression systems have been setup. These systems include proteins, P6 and p30 that are tagged with Strep on both the 5’ and 3’ end. In future work the Strep tags will be used for purification once the protein is expressed in high enough quantities. Further, we would like to setup crystal screens to crystallize the proteins for structure determination by X-ray crystallography. From X-ray crystallography, we determine the electron cloud for the atoms making up the protein. Then amino acids will then be fit into the electron cloud to get the final structure of the protein.

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