

Express and Purify the Capsid Protein (CP) of Human Astrovirus (HAstV) VP90^{71–782} to uncover the structure of CP

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Astroviruses (AstVs): Star-Like Viruses

Astroviruses (AstVs)

- Positive-sense, single stranded RNA, nonenveloped viruses
- Having a characteristic star-like appearance in the center
- Factor in diseases ranging from diarrhea to encephalitis

Human Astroviruses (HAstVs)

One of the main causes of gastroenteritis for infants and elderly people (Figure 2)

Capsid prote

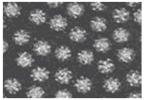


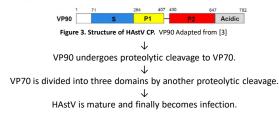
Image 1. Model of Astroviruses Adapted from [1]

Figure 2. Model of Human Astroviruses. Adapted from [2]

Role of Cleavage of Capsid Protein (CP) in Infectivity

- CP is a key to become infection
- CP interacts with the host cell during its entry and exit.

CP is synthesized as VP90.



Problem: CP Structure is unknown

- Structure of virus capsid is unknown.
- Revealing the structure of Capsid Protein will help making vaccines or medicines that can prevent the infections.

Project Objectives

Aim 1: Express and purify VP90^{71–782} capsid particles Aim 2: Make the crystals to characterize the structure by X-ray crystallization

Methods

Step1

- Culture bacteria which express the protein of VP90⁷¹⁻⁷⁸² •
- Purify the protein by Metal Affinity Chromatography
- Load SDS-PAGE to check the existence of the target protein Step2
- Separate the protein by Size exclusion chromatography
- Load SDS-PAGE to check the existence of the protein

Step3

Step1

Concentrate and screen the protein for crystal

Purification by FPLC

Contaminating protein

Target protein

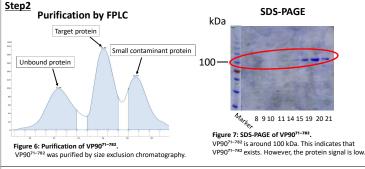
VP9071-782 was purified by metal affinity chromatography.

Figure 4: Purification of VP9071-782

Results



Figure 5: SDS-PAGE of VP9071-782 VP9071-782 is around 100 kDa. This indicates that VP9071-782 exists



Step3

Crystallization We are screening for crystal formation.



Image 8: Crystal Gryphon We used this for setting crystal plates.

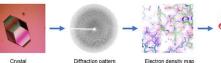
Conclusion

- Nickle affinity purification was successful.
- Size exclusion purification was low protein concentration.
- The factor for having low protein signal is due to the protein being diluted during the second FPLC
- Revised procedure to increase protein yield and currently are running it.

Future Work

When We Get a Good Crystal

- Send the crystal to X-ray source
- Get the atomic structure of the protein





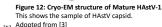
X-ray crystallography can be used to determine the atomic structure of proteins Adopted from [4]

When We Get a High Molecular Weight Protein

- Prepare the protein by negative staining
- Observe the sample by using electron microscopy (EM)
- If I could find a sample like Image 11,
- Observe the protein by cryo-EM (Figure 12)







Acknowledgments

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Citations

Medical Virology, White, DO, Fenner, FJ

1

Image 9: screening plate

We screen this plate

by optimal microscope

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- Creative Biostructure (n.d.) X-ray Crystallography Platform, Available at: https://www.creative-biostructure.com/2 ray-crystallography-platform 60.htm (Accessed: March 09 2019) Kelly A.Dryden, et al. (2012) Structure of Immature and Mature Human Astrovirus. 652.
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