

SAXS Study on the Protein Assembly of Hepatitis C Virus Core Protein

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Hepatitis C virus (HCV) core protein is one of the virus structural proteins and interacts directly to the viral genomic RNA to form highly ordered virus nucleocapsid. In the other hand, core protein also shows multiple cellular functions including cellular proliferation, apoptosis and others. More importantly, HCV core protein also found an key determinant in the replication of virus genome. Therefore, there should have a mechanism to modulate the transition between protein assembly into virus like particle and cellular signaling regulator in host cell.

In our previous studies, atomic force microscopy (AFM) and transmission electron microscopy (TEM) has been applied to investigate the morphology of the virus-like particle. We demonstrated the N-terminal of HCV core protein only is able to form virus like particle in regular diameter. Therefore, in this project, we tried to use SAXS to explore the possible mechanism that regulate the protein assembly of HCV core protein.

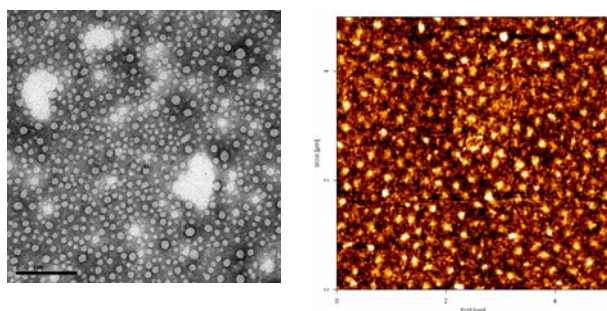
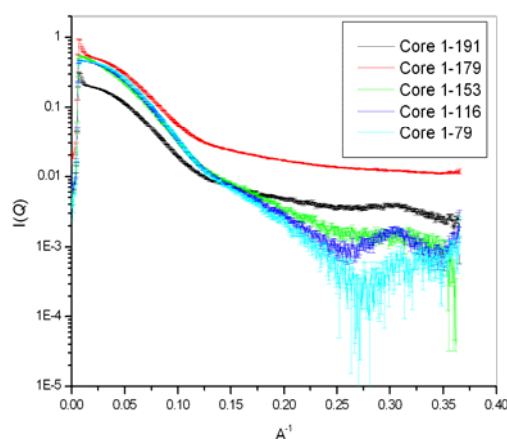


Fig. 1: shown the averaged data of different HCV core protein which are all C-terminal truncation. All of this



five fragments of HCV core protein are demonstrated by AFM and TEM in our previous research to assemble into virus like particle. However, due to the lack of structural

of mature, infectious virus particle, we concern that the ability to form virus like particle is only a protein aggregation. In some protein misfolding disease has been demonstrated to form large aggregation in regular size and shape. In Table 1 shown the radius of gyration of five different C- terminal truncation. In the ongoing data analysis, we are trying to build the possible 3D model by DAMMIN program. The electron density will shoe us much more detail structure. By comparison with the data collected in SR-SD (also in NSRRC), we could demonstrated the roughly structural distribution of each region.

	Core 1-191	Core 1-179	Core 1-153	Core 1-116	Core 1-79
RG (nm)	28.07	27.69	33.83	29.25	19.67
*the protein concentration are all 1 μ M.					
**the refinement is not completed yet.					

Table 1: Radius of Gyration for different fragments of HCV core proteins.

References

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