SR-CD Study on the Protein Assembling of Hepatitis C Virus Core Protein

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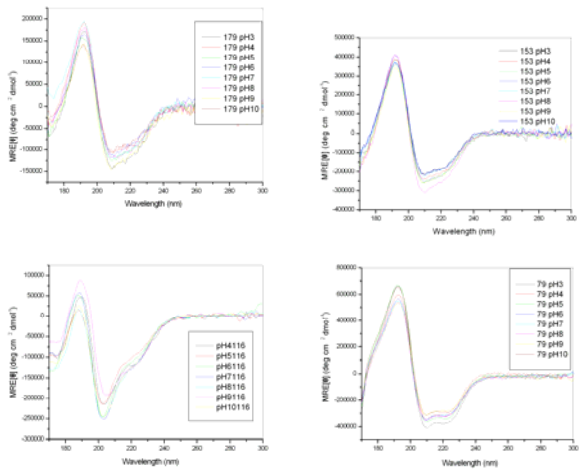
HCV core protein is one of the virus structural proteins and interacts directly to the viral genomic RNA to form high ordered virus nucleocapsid. However, core protein also shows multiple cellular functions including cellular proliferation, apoptosis and others. Therefore, in this project, SR-CD will be used as a tool to explore the assembly of hepatitis C virus core protein and the corelation of its secondary structural contents. The protein assembling under different conditions may play an important role to regulate the formation of mature HCV virus particle.

Fig. 1: The SRCD



spectra for HCV core protein (a) 1-179, (b) 1-153, (c) 1-116 and (d) 1-79

The average spectra in Fig. 1 were used to calculate secondary structural content using the website DICROWEB[1-3] with the CDSSTR program and reference set, SP175. The analyzed results are list in Table 1. The secondary structural content in HCV core 1-179, with 75 % helix and 8% strand in pH8, are similar with the other pH value. Same observation also been discovered in the other truncated HCV core protein. The N-terminal of HCV core protein is a well structural region and is resistant to pH caused protein denaturation. Previously, we demonstrated only the HCV core protein itself could form virus-like particle in regular particle diameter. Therefore, the highly stable N-terminus is the critical determinant for the assembly of HCV core protein.

Moreover, the helical content of the truncated C-terminal hydrophobic domain was significantly decreased t from 75 % in core 1-179 to 53 % in core 1-79 in pH8. The C-terminus of HCV core protein is an important region to anchor the core protein on lipid droplet and regulate replication of viral protein and genomic RNA[4-6]. When the C-terminal hydrophobic domain has been deleted, the truncated HCV core protein would translocate from the cytoplasm to cell nucleus[7]. The exactly position in C-terminus of the mature, infectious viron associated HCV core protein are not yet been verified, but it is very possible lies between 173-183[8, 9]. Base on the present study, result suggests that the helical structure in the C-terminal is the key structure to regulate the cellular localization of HCV core protein. These domains involved regulation of cellular localization are likely to regulate HCV capsid assembly or the other cellular functions.

Table I: The estimated secondary structure of HCV core proteins.

	Core 1-179		*Core 1-153*		*Core 1-116*		*Core 1-79*	
	Helix	**Strand**	**Helix**	**Strand**	**Helix**	**Strand**	**Helix**	**Strand**
pH3	***0.74***	**0.1**	**0.78**	**0.09**			**0.43**	**0.3**
pH4	***0.79***	**0.06**	**0.69**	**0.12**	**0.54**	**0.18**	**0.47**	**0.27**
pH5	***0.74***	**0.08**	**0.69**	**0.12**	**0.53**	**0.18**	**0.47**	**0.26**
pH6	***0.75***	**0.1**	**0.74**	**0.1**	**0.53**	**0.18**	**0.49**	**0.24**
pH7	***0.86***	**0.04**	**0.75**	**0.12**	**0.52**	**0.19**	**0.51**	**0.22**
pH8	***0.75***	**0.08**	**0.61**	**0.18**	**0.5**	**0.22**	**0.53**	**0.19**
pH9	***0.74***	**0.08**	**0.66**	**0.15**	**0.57**	**0.15**	**0.83**	**0.04**
pH10	***0.75***	**0.07**	**0.71**	**0.12**	**0.5**	**0.22**	**0.9**	**0.04**

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