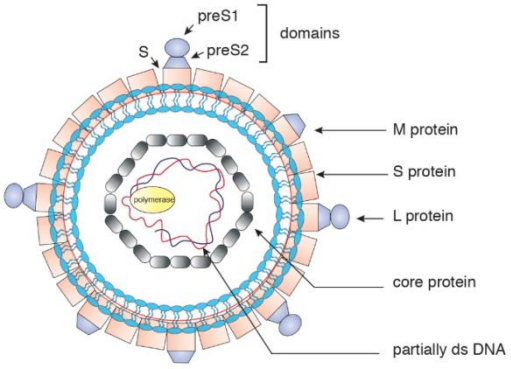
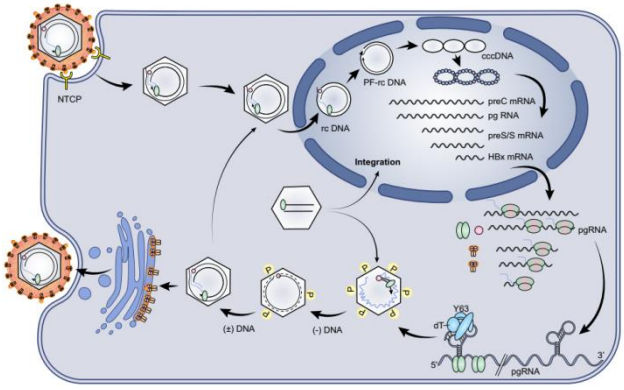
Master Thesis Project

Quantification of the interaction between Hepatitis B virus core and envelope proteins in a cellular context

Hepatitis B virus (HBV) infection is one of the major threats to public health with the chronic infection giving rise to different types of liver complications despite the availability of vaccines which gives scope to further development in therapeutic strategies. HBV is an enveloped double stranded DNA virus (3.2 kb) with the core protein (C) generating an icosahedral capsid. C has been reported to independently localize in the nucleus of the cell (Huh7) as well as in the cytoplasm. However, the C localization is greatly controlled by the presence of different forms of the HBV envelope proteins. The HBV envelope is made up of three closely related proteins namely small (S), middle (M) and large (L) carrying identical C terminal ends.





Self-assembly of these proteins form the virus like particles. Interaction between the C and envelope proteins have been reported in multiple studies but the role of different forms of the later has not been investigated deeply. Confocal imaging and biochemical studies show that the L interacts with C to modify its localization within the cytoplasm and this interaction is essential for the recruitment of S to the periphery of the nucleus. Physical quantification of such an interaction and its localization is not done yet and this is where we are focusing through this project. We will investigate the interplay of these proteins quantitatively in living cells, by applying state-of-the-art microscopy methods, such as Number & Brightness microscopy (N&B), Spatial Intensity Distribution Analysis (SpIDA) and super-resolution microscopy.

Techniques to be used:
Molecular cloning, mammalian cell culture, FCS, RICS, Number and brightness analysis.

For students with a background in biochemistry, biotechnology, biology or physics.

Languages: German or English.

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Physical Biochemistry - Cell Membrane Biophysics