

Abstract

An effective and safe vaccine against Hepatitis B virus already exists, yet morbidity and mortality of this illness are still high. The key to developing a reliable treatment is a deep knowledge of the virus' life cycle and functions of all its components. In the presented work we explored an interactome of the Core protein of the Hepatitis B virus. Using proximity-dependent biotin identification technique (BioID) coupled to mass spectrometry we have identified a list of potential candidates that are either significantly enriched (in total 105 proteins) or less abundant in the presence of the HBV Core protein in the cell (40 proteins). The list also includes known HBV Core interacting proteins SRPK1 and SRPK2, and p53 protein whose expression is known to be repressed due to the HBV Core interaction with the E2F1 transcription factor. Many of the newly identified possible HBV Core interacting proteins are involved in biological processes already known or are suspected to be influenced by the HBV such as translational and transporting processes or gene expression and macromolecule production. Overall, this work comprehensively characterizes the interaction landscape of the HBV Core protein in the live cells and might thus serve as a reliable start for in depth HBV-host interaction analysis.

Key words: HBV, HBc, Core protein, proximity biotinylation