DENV host interaction and altered antiviral pathway during DENV infection

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ABSTRACT

Dengue is a mosquito borne viral disease. There are 4 distinct, but closely related serotypes of the virus (DENV-1, DENV-2, DENV-3 and DENV-4). There is a complex interplay going on between the human host and the virus and deciphering the crosstalk will lead us to better understand the virus life cycle and to develop strategies to combat the infection and design antivirals. Standing in this scientific scenario, we asked the very basic question: what are the human host factors that help or inhibit viral propagation and establishment inside the human host. We performed global Yeast two hybrid system screening for human host factors. Several newly identified host factors have been identified whose role in viral life cycle has not yet been deciphered. We prepared the viral interactome network and one host factor named BANP (BTG3 Nuclear Associated Protein) which interacts with DENV NS2A, caught our attention as its role in other viruses have already been reported. In our hypothesis we presumed that BANP might play a crucial role in Dengue viral infection establishment and it is worth deciphering the intricate mechanism. We performed in vitro interaction assay by co-immunostaining to confirm the interaction. Further confirmation is proposed by ITC. When a virus infects a human cell it tries to hijack antiviral pathways to escape the immune pressure. We performed CRISPR/Cas9 experiment to knockout the factor and propose to study the antiviral pathways which get perturbed or differentially regulated in presence and absence of the host factor. This information will be exploited to target the pathways which are getting differentially regulated and help to develop antivirals.

Keywords: BANP, NS2A, CRISPR/Cas9

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