Zika Virus: Predicted Protein Interactions Involved In Human Brain Development

T KAZMIRCHUK[1], B BARNES[1], K DICK[1], D BURNSIDE[1], H MOTESHAREIE[1], M HAJIKARIMLOU[1], A SCHOENROCK[1], F DEHNE[1], J GREEN[1], A GOLSHANI[1]

[1]Carleton University

ABSTRACT

The Zika virus (ZIKV) is an arthropod-borne positive-sense RNA virus from the genus *Flavivirus*. Currently, the ZIKV is responsible for the pandemic plaguing South America, whereas of March 24th, 2016 the Pan American Health Organization (PAHO) reported on nearly 200,000 cases of suspected or confirmed infections. Recent studies have suggested a correlation between ZIKV infection and birth defects such as microcephaly and other neural defects, highlighting the importance of understanding the biology of ZIKV and its infection in a human host. Here, we report on the first prediction of global protein-protein interaction (PPI) map between ZIKV and human proteins. The interactions are reported on the basis of short re-occurring polypeptide regions that mediate PPIs. In this approach, sliding windows of 20 amino acids long (short motifs) in one protein is matched to all possible sliding windows of a second protein. The frequency of co-occurrence of a given pair of windows in the database of known *Flavivirus*-human and high confidence human-human PPIs in relations to their frequency over the entire genome forms the basis for the possibility of the two proteins to interact. In this way a set of more than 200 high confidence ZIKV-human PPIs were predicted. For example, we predicted an interaction between ZIKV protein NS5 and a neuroprotective protein ENO2, and another high confidence interaction between ZIKV protein PR and RNASET2, which when mutated leads to microcephaly. This PPI map provides scientists with a list of testable hypothesis to study ZIKV infection in humans. It also represents a list of priority candidates for further investigations