A Viral-Human Interactome Based on Structural Motif- Domain Interactions Captures the Human Infectome

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Abstract

Protein interactions between a pathogen and its host are fundamental in the establishment of the pathogen and underline the infection mechanism. In the present work, we developed a single predictive model for building a host-viral interactome based on the identification of structural descriptors from motif-domain interactions of protein complexes deposited in the Protein Data Bank (PDB). The structural descriptors were used for searching, in a database of protein sequences of human and five clinically important viruses; therefore, viral and human proteins sharing a descriptor were predicted as interacting proteins. The analysis of the host-viral interactome allowed to identify a set of new interactions that further explain molecular mechanism associated with viral infections and showed that it was able to capture human proteins already associated to viral infections (human infectome) and non-infectious diseases (human diseasome). The analysis of human proteins targeted by viral proteins in the context of a human interactome showed that their neighbors are enriched in proteins reported with differential expression under infection and disease conditions. It is expected that the findings of this work will contribute to the development of systems biology for infectious diseases, and help guide the rational identification and prioritization of novel drug targets.