Virol Mycol 2016, 5:3(Suppl)
http://dx.doi.org/10.4172/2161-0517.C1.015

A hypothetical mechanism of structural shifts in the hemagglutinin co-receptor binding site during epidemics revealed using multivalent (landscape) phage probes

Valery A Petrenko and Deepa Bedi
Auburn University, USA

During natural evolution, viruses have evolved into molecular structures with optimized relationships with a host. In particular, viruses acquired surface peptides that allow them to attach to a host cells and invade into the cells through interaction with cellular receptors and co-receptors. Identification of these cell recognition peptides would offer a strong basis for development of antiviral drugs, vaccines and diagnostics, prediction of viral drifts from one host to another and prediction and control of emergent infections. We demonstrated that bacteriophage fd-tet that has no natural tropism to mammalian cells can adapt the ability to specifically recognize cellular receptors and penetrate into the cellular compartments during their artificial molecular evolution *in vitro*, underlying the phage display technology, in exactly the same way as other viruses do that during their natural multimillion evolution *in vivo*. Thus, selection of the cell associated phage variants from their multibillion clone libraries and analysis of their cell binding peptides in comparison with proteins of natural viruses would allow disclosing the receptor and co-receptor binding sites on these viruses. To check this hypothesis, we analyzed similarity profiles of variety of human cell binding phages isolated from the phage display libraries to representative viral proteins hemagglutinins HA 1 from flu viruses isolated during the last century epidemics. We discovered that some families of selected peptides demonstrated very high level of structural similarity to particular cites of viral protein. In control experiments, peptides randomly picked from the phage display libraries showed much lower, background similarity to these proteins. Revealed potential receptor and co-receptor binding sites (RBS and CoRBS) on viral surface proteins lie in a close vicinity to previously mapped RBS, the finding that can justify our hypothesis on similar mechanisms of natural and artificial molecular adaptation of viruses to the cellular receptors. After their immunological attestation, the revealed phage borne peptides can be considered as leads for construction of molecular and phage based vaccines to the corresponding viruses.

petreva@auburn.edu