New instrument for analyzing viruses

March 8 2011

Scientists in Israel and California have developed an instrument for rapidly analyzing molecular interactions that take place viruses and the cells they infect. By helping to identify interactions between proteins made by viruses like HIV and hepatitis and proteins made by the human cells these viruses infect, the device may help scientists develop new ways of disrupting these interactions and find new drugs for treating those infections.

According to Doron Gerber, a professor at Bar Ilan University in Ramat Gan, the PING system (Protein Interaction Network Generator) can be used to examine thousands of potential interactions at a time, and it detects them at a sensitivity 100- to 1,000-time greater than current methods. Gerber developed PING with collaborators at Stanford University, and he will describe the technology today at the 55th Annual Biophysical Society Meeting in Baltimore.

When a virus infects a human cell, it hijacks the machinery of that cell, recruiting certain host proteins and subverting them to the task of manufacturing new viral particles. This feature of viral biology has made viral infections notoriously difficult to treat, as therapies must specifically target the virus without harming the cell.

One approach that has been successful is to identify key interactions between viral and host proteins, which can then serve as targets for new drugs. For example, the HIV drug Fuzeon works by blocking a viral protein from attaching to proteins on the surface of immune system cells, barring entry to the cell.

Like many antivirals, Fuzeon is used in combination with other drugs in a "cocktail." This is because, like most viruses, HIV mutates rapidly, acquiring resistance to individual drugs. Therefore, the need for new antiviral drugs is constant and ongoing.

Using PING, the Israeli and California scientists identified novel cellular partners for proteins from hepatitis C and hepatitis D. "And we can now use the same system to screen for inhibitors," says Gerber, who adds that new treatments are urgently needed for hepatitis C, for which only one treatment exists that works in only half the patient population.

Because PING employs microfluidics, very small samples can be used; gathering enough material has been a particular challenge with existing methods.

More information: The presentation, "Mapping Virus-Host Protein Interactions Using the PING Microfluidics Platform," is at 5:00 p.m. on Tuesday, March 8, 2011 in Room 307 of the Baltimore Convention Center. ABSTRACT: tinyurl.com/67lnomy

Provided by American Institute of Physics