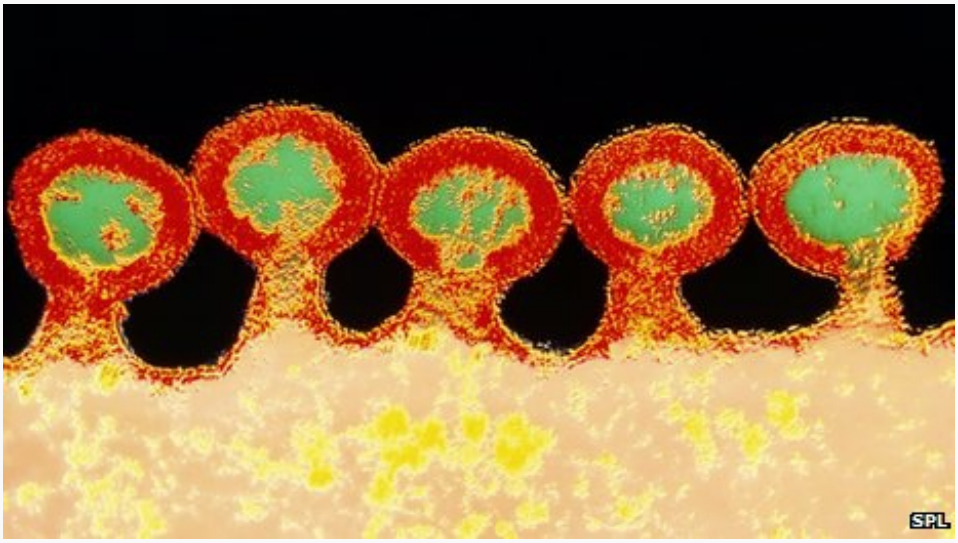
HIV inner shell structure revealed

30 May 2013 Last updated at 02:56 ET



HIV escaping from a white blood cell

Researchers have for the first time unravelled the complex structure of the inner protein shell of HIV.

The US team, reporting in Nature, also worked out exactly how all the components of the shell or 'capsid' fit together at the atomic level.

Until now the exact structure had proved elusive because of the capsid's large size and irregular shape.

The finding opens the way for new types of drugs, the researchers from the University of Pittsburgh said.

It was already known that the capsid, which sits inside the outer membrane of the virus, was a cone-shaped shell made up of protein sub-units in a lattice formation.

But because it is huge, asymmetrical and non-uniform, standard techniques for working out the structure had proved ineffective.

The team used advanced imaging techniques and a supercomputer to calculate how the 1,300 proteins which make up the cone-shaped capsid fit together.

Critical interactions

The process revealed critical interactions between molecules in areas that are necessary for the shell's assembly and stability.

These potential vulnerabilities in the protective coat of the viral genome could be exploited by scientists designing new drugs to tackle the problem of HIV resistance, the researchers explained.

Study leader Dr Peijun Zhang, associate professor in structural biology at the University of Pittsburgh School of Medicine said: "The capsid is critically important for HIV replication, so knowing its structure in detail could lead us to new drugs that can treat or prevent the infection.

"The capsid has to remain intact to protect the HIV genome and get it into the human cell, but once inside, it has to come apart to release its content so that the virus can replicate.

"Developing drugs that cause capsid dysfunction by preventing its assembly or disassembly might stop the virus from reproducing."

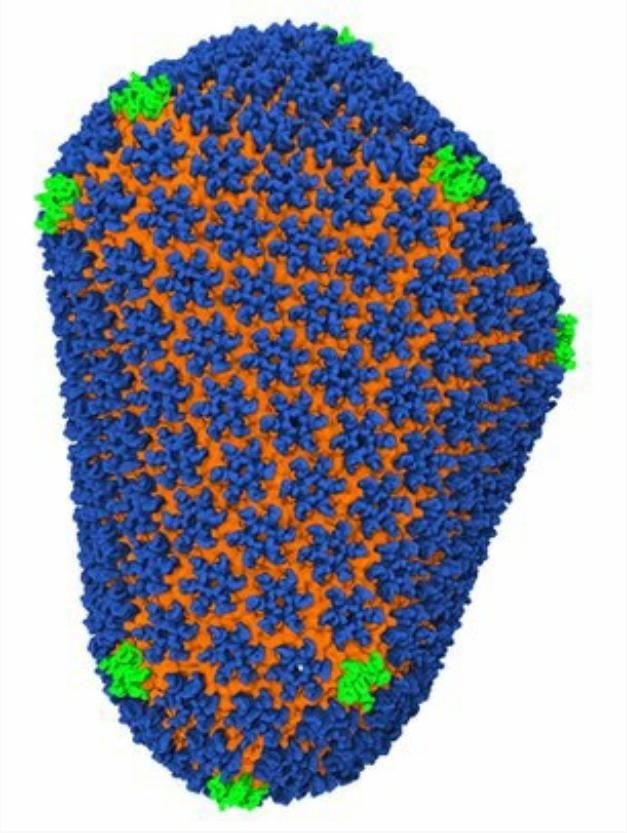
She added that the fast mutation rate of HIV made drug resistance a big problem.

"This approach has the potential to be a powerful alternative to our current HIV therapies, which work by targeting certain enzymes."

Prof Simon Lovell, a structural biologist at the University of Manchester, said not only had the researchers managed to achieve something that was very difficult, they had also found some really interesting results.

"The big problem with HIV is that it evolves so quickly that any drug you use you get drug resistance which is why we use a multi-drug cocktail.

"This is another target, another thing we can go after to develop a new class of drugs to work alongside the existing class."



Computer model of HIV capsid structure