

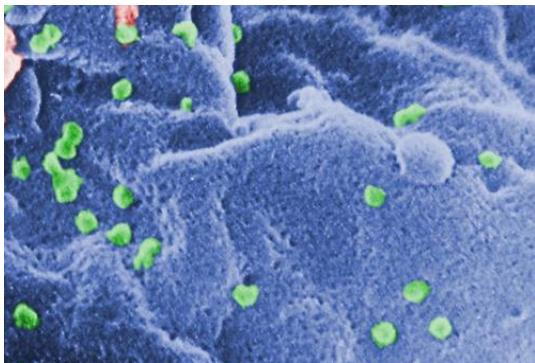
Bioinformatics experts from Pázmány help search for weak points of HIV

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Results achieved by Professor Sándor Pongor and co-worker Attila Kertész-Farkas can be used in developing strategies against AIDS. As members of an international research team scientists have come to the findings that give new insights into the incorporation of HIV into the genom.

Based on Hungarian Academy of Sciences sources

Results achieved by Professor Sándor Pongor of Pázmány Péter Catholic University and co-worker Attila Kertész-Farkas as members of an international research team could be utilized in developing new strategies against AIDS. Their publication that appeared in Nature recently gives a new explanation for the incorporation of HIV into the genom. AIDS research is pursued with intense attention all over the world nowadays, since eradication of the virus is not yet possible, although there are several ways of delaying its spreading. This fact gives rise to several theoretical problems. Not much is known about e.g. its hiding in the cell. We know already that it is incorporated into the human chromosome but it is still not clear, how it chooses the section of the DNA where it starts to attack. This problem has been investigated in the project started by Professors Mauro Giacca from Trieste and Marina Lusic from Heidelberg. It turned out that the virus chooses its incorporation sites not randomly but according to the three-dimensional structure of the nucleus, namely it is „looking for” chromosomal sections under transcription in the vicinity of the nuclear pore.



HIV particles are green in the electronmicroscopic photo of a cell's surface. Source: Wikimedia Commons

Coarse data mining

This behaviour of the virus has been demonstrated by new experimental data, but it was very important to track if it can be shown in data published formerly in connection with other investigations.

We should concentrate here of course not on ordered databases but on archived data deposited here and there as coarse sequences of ambiguous quality. The work hypothesis has been formulated using these coarse data and the answer has been backed up by the statistics of large data sets. Sándor Pongor, external member of the Hungarian Academy of Sciences and his co-worker, Attila Kertész-Farkas, presently at Washington State University in Seattle, have completed this task.

The theoretical point of the article published in the March 2 issue of Nature is that it connects two distinct phenomena, molecular mechanisms and the topography of the cell, synchronizing these with the dynamics of the cell cycle. Data obtained during sampling can be mingled and it is more difficult to separate them than to look for a needle in a haystack. Regarding the consequences of HIV infection, it is very important that we are again one step closer to getting to know its behaviour, so hopefully new therapeutic approaches can be formulated, like specific inhibition of the process of its entering into the nucleus.