Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Sequencing the whole genome of infected human cells obtained from diseased patients — a proposed strategy for understanding and overcoming AIDS or other deadest virus-infected diseases

Da-Yong Lu [a,*], Jian Ding [b]

[a] *School of Life Sciences, Shanghai University, Shanghai 200444, PR China*
[b] *Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai, PR China*

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Summary As the worry and pandemic about deadest virus such as AIDS and bird flu are intensified, eradical treatments for these virus-infected diseases are in high demand. However we currently know little about the virus involvement in human cells, which results poor therapeutic outcome. We propose that these viruses may penetrate into human genome in diseased cells that may finally result resistance to present applicable therapeutic options. Here proposes a strategy — sequence the whole genome (chromosomal as well as other genetic systems) of infected human cells obtained from diseased patients. This might help us to know greatly more about the consequences of virus infection and achieve biotherapy of specifically targeted in future.

Deadest virus, like AIDS, SARS (severe acute respiratory syndrome) and bird flu, in most circumstances are the causation of deadly symptoms and consequences in patients infected them and responsible for most of patients' death. They all arose large-scale pandemic in certain geographic areas. The treatments of these diseases are probably the least satisfactory ones. Nowadays, no final solution can be completely reliable to cut down these infections in patients and make the suffers free of the diseases in the rest of their lives. In our opinions, present therapeutic unsatisfactory for virus-infected diseases are resulted from producing endless vaccines [1] and putting into drug sensivity tests against infected cells without thoroughly understanding the mechanisms and the ranges of virus-infections occurred in humans. Therefore, we are horror and pandemic, when some new virus is about to occurs [2] and feel helpless. Since these viruses are so illusive and mobile in the infected cells, we have still not pinpointed their devastative ranges in etiological ways. We are constantly pessimism and worried about our future, but treatment options are still few and commonly unsatisfactory [2–4].

* Corresponding author. Tel.: +86 21 66163545; fax: +86 21 66132177.
E-mail address: ludayong@sh163.net (D.-Y. Lu).

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Problems arises and possible solution

To the etiology of virus-infected diseases, the farthest and worst outcomes will be in the changes of cellular genome. If these deadest virus or their influences really enter or devour into human genomes of infected cells in nature, we will not surprise why routine vaccines and exogenous chemical drugs could not eradicate the diseases after so many laboratory endeavors and high expenses of money. Therefore, we propose that final solution and eradication of these deadest diseases will only be based on thorough understanding the courses and ranges of virus infections. Since human genome project (HGP) has been just finished and has great potential in medicine [5], is it better to sequence the whole genome of infected human cells obtained from diseased patients? This strategy, though cumbersome and lack of experimental data to support, but it can be really reliable at present situations. It is a bold hypothesis and risky attempt, for we may find nothing but cost high. But the advantages for the project are also obvious because the project will pinpoint and identify the etiology and pathology of these diseases in detail and to the fullest, which can find useful and realizable biotherapies much easier and in faster speed. According to present technology, these combined DNA infection could only be rectified or silenced by biotherapy. This is one of the significances of the project. If it works, it must be an excellent model for finding ways and solution for most of virus-infected diseases. Our hypothesis is more imaginative and innovative than current attempted mainstream treatment option (vaccine and cocktail therapy). We believe people can really benefit from the project. Can we present our proposal open for discussion here? What is the most possible virus to undergo such change? Can we try to find one to initiate?

Conclusion and future direction

The technical innovations are rapid, thus the cost for whole genome sequencing in the future will continue to reduce. Therefore, the project we proposed will be more and more realizable. The risk and benefits of this attempt are all possible. It is the time to decide our future.

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