

Predicting treatment response more accurately

2 September 2013

The HI virus is feared, not least, because of its great adaptability. If the virus mutates at precisely the point targeted by a drug, it is able to neutralise the attack and the treatment fails. To minimise these viral defence mechanisms, doctors treat patients with modern combination therapies involving the simultaneous administration of several drugs. This approach forces the virus to run through a series of mutations before it becomes immune to the drugs.

Sequential nature of mutations

"It is not easy to decide which of the over 30 combination therapies is best suited to a patient," says Huldrych Günthard from Zurich University Hospital, president of the Swiss HIV Cohort Study. The decision is based on the prospects of success and therefore on the genetic make-up of a particular [virus](#). The established [prediction models](#) already consider the genetics of the virus but they neglect that the virus continuously evolves through sequential [mutations](#).

Choosing the right therapy for each patient

In cooperation with the Swiss HIV Cohort Study, Niko Beerenwinkel and his team from ETH Zurich have now developed a more accurate prediction model based on a probabilistic method*. This model calculates the possible evolutionary paths of the virus and yields a new predictive measure for the development of resistances: the so-called individualised genetic barrier. When applied retrospectively to 2185 patients of the HIV Cohort, the new approach made it possible to predict [treatment success](#) more accurately compared to the existing models. "We are now introducing the individualised genetic barrier in a [pilot project](#) and hope that it will help us in the future to identify the best therapy for each patient," says Günthard.

The Swiss HIV Cohort Study

Established in 1988, the Cohort Study aims to generate knowledge about HIV infection and AIDS as well as to improve the care given to patients. All Swiss hospitals specialising in HIV (Basel, Berne, Geneva, Lausanne, Lugano, St. Gallen and Zurich) have collected and analysed data from over 18,000 HIV-positive persons. More than 8,800 persons are currently taking part in the Swiss HIV Cohort Study. Almost a third of them are women.

www.shcs.ch

More information: * Niko Beerenwinkel, Hesam Montazeri, Heike Schuhmacher, Patrick Knupfer, Viktor von Wyl, Hansjakob Furrer, Manuel Battegay, Bernard Hirschel, Matthias Cavassini, Pietro Vernazza, Enos Bernasconi, Sabine Yerly, Jürg Böni, Thomas Klimkait, Cristina Cellera, Huldrych F. Günthard, and the Swiss HIV Cohort Study (2013). The Individualized Genetic Barrier Predicts Treatment Response in a Large Cohort of HIV-1 Infected Patients. PLoS Computational Biology online. DOI: [10.1371/journal.pcbi.1003203](https://doi.org/10.1371/journal.pcbi.1003203)

Provided by Schweizerischer Nationalfonds zur Foerderung der wissenschaftlichen Forschung

APA citation: Predicting treatment response more accurately (2013, September 2) retrieved 15 June 2021 from <https://medicalxpress.com/news/2013-09-treatment-response-accurately.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.