



## PRESS RELEASE

### **New computer models predict how a patient will respond to HIV drug therapy without the need for HIV genotype**

*New models outperform genotyping and work well for cases in Africa*

**London, UK; Monday 25th November 2013.** New computer models described today in the *Journal of Antimicrobial Chemotherapy* predict how patients whose HIV therapy is failing will respond to any new combination of drugs, without the need for an HIV genotype: a test used in wealthy countries to read the genetic code of the virus and help select drugs to which the virus is sensitive.<sup>1</sup> In fact, the models were significantly more accurate predictors of treatment response than the genotype.

The HIV Resistance Response Database Initiative (RDI) developed these latest models specifically for use in the many settings where genotyping is unaffordable. They estimate the probability that any combination of HIV drugs will reduce the amount of virus to undetectable levels in patients whose current therapy is failing. They were trained with data from tens of thousands of patients in clinics all over the world, including for the first time, patients from Southern Africa. They were around 80% accurate, which is significantly better than the 57% accuracy achieved by genotyping.

“This study and these models are proof of principle that this could be a very helpful approach for selecting effective therapy in highly resource-constrained settings, such as Southern Africa,” commented Professor Robin Wood, Head of the Desmond Tutu HIV Centre, University of Cape Town, South Africa and a co-author on the paper. “As more of our patients fail first and even second line therapy, it is critical to optimise the selection from our limited range of drugs to achieve maximum suppression of the virus and this system could be very useful”.

The new models are now available to be used by healthcare professionals as part of the RDI’s HIV Treatment Response Prediction System (HIV-TRePS), which is freely available online at [www.hivr.org/treps](http://www.hivr.org/treps). The system also enables users to enter the costs of the drugs in their clinic and so model both the cost and the effectiveness of various treatment options. A previous pilot study



using data from an HIV clinic in India indicated that the system could identify more effective and less costly combinations of drugs than those actually used in the clinic.<sup>2</sup>

“Currently, most HIV patients in resource-limited settings are treated according to WHO public health guidelines that offer very limited treatment options”, explained Dr Hugo Tempelman, Clinical Director of the Ndlovu Care Group, Elandsdoorn, South Africa and co-author on the paper. “The HIV-TRePS system, incorporating these models, enables doctors to tailor the HIV treatment based on the cost and predicted effectiveness of the treatment. What is wonderful is that HIV-TRePS provides us with high predictive value at no cost.”

The data required by the system for its predictions includes a measure of the amount of virus in the patient’s bloodstream (the viral load), a test that is not widely used in resource-limited settings. However, the potential cost savings offered by the system are likely to cover the costs of viral load testing, many times over. Moreover, viral load monitoring of HIV therapy is now recommended by the World Health Organisation in all settings and initiatives are underway to fund it, including the formation of the Load Zero Foundation, formed specifically with this goal.<sup>3</sup>

“We are very encouraged by the results with these models.” Commented Dr Andrew Revell, Executive Director of the RDI. “They show that not having access to genotyping in resource-limited settings need not be a barrier to providing individualised, optimised HIV drug therapy”.

The RDI is an independent, not-for-profit international research collaboration set-up in 2002 with the mission to improve the clinical management of HIV infection through the application of bioinformatics to HIV drug resistance and treatment outcome data. Over the 10 years since its inception, the RDI has worked with many of the leading clinicians and scientists in the world to develop the world’s largest database of HIV drug resistance and treatment outcome data, containing information from approximately 100,000 patients in more than 30 countries.

HIV-TRePS is an experimental system intended for research use only. The predictions of the system are not intended to replace professional medical care and attention by a qualified medical practitioner and consequently the RDI does not accept any responsibility for the selection of drugs, the patient’s response to treatment or differences between the predictions and patients’ responses.

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**References:**

1. Revell AD, Wang D, Wood R *et al.* An update to the HIV-TRePS system: The development of new computational models that do not require a genotype to predict HIV treatment outcomes. *J Antimicrob Chemother* 2013; doi:10.1093/jac/dkt041.
  2. Revell AD, Alvarez-Uria G, Wang D, Pozniak A, Montaner JSG, Lane HC, Larder BA. Potential Impact of a Free Online HIV Treatment Response Prediction System for Reducing Virological Failures and Drug Costs after Antiretroviral Therapy Failure in a Resource-Limited Setting. *BioMed Res Int* 2013; doi 10.1155/2013/579741.
  3. World Health Organisation. *Consolidated guidelines on the use of antiretroviral drugs for treating and preventing HIV infection: Recommendations for a public health approach.* WHO; Geneva: 2013.
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**The paper**

Revell AD, Wang D, Wood R *et al.* An update to the HIV-TRePS system: The development of new computational models that do not require a genotype to predict HIV treatment outcomes. *J Antimicrob Chemother* 2013; doi: 10.1093/jac/dkt447

**Available at:**

<http://jac.oxfordjournals.org/cgi/content/abstract/dkt447?@ijkey=TttezQcQmob954k&keytype=ref>

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