OXFORD JOURNALS PRESS RELEASE

Computer models predict how patients will respond to HIV drugs without the need for resistance testing

Models could improve the treatment of HIV patients in countries with limited resources

Results of a study published online in the *Journal of Antimicrobial Chemotherapy* today (Thursday), demonstrate that computer models can predict how HIV patients whose drug therapy is failing will respond to a new treatment. Crucially for patients in poorer countries, the models do not require the results of expensive drug resistance tests to make their predictions. The study also showed that the models were able to identify alternative drug combinations that were predicted to work in cases where the treatment used in the clinic had failed, suggesting that their use could avoid treatment failure.

When a patient's HIV drugs begin to fail in well-resourced countries a genotypic resistance test is performed to identify mutations that cause the virus to become resistant to certain drugs. The results are used to predict whether the patient will respond to different drugs in a new treatment. These tests are generally not available in resource-limited settings. Today's study shows that computer models can predict how such a patent will respond, with comparable accuracy, without the need for such tests.

"This is the first time this approach has been tried with real cases of treatment failure from resource-limited settings", commented Julio Montaner, former President of the International AIDS Society, Director of the BC Centre for Excellence in HIV & AIDS, based in Vancouver, Canada and an author on the paper. "The results show that using sophisticated computer based algorithms we can effectively put the experience of treating thousands of patients into the hands of the under-resourced physician with potentially huge benefits."

The models were developed by The HIV Resistance Response Database Initiative (RDI), using information gathered from many thousands of patients in hundreds of clinics around the world. They make their predictions of the probability of the drugs reducing the level of virus below a low limit from the patient's treatment history, the CD4 count(i) and the viral load. The models were most accurate (over 70%) when they were used to make predictions for new cases from the clinics that provided the data used in their training. However they were 60-64% accurate when tested with cases from southern Africa, 57% for India and 67% for

Romania where resources are very limited. This compares favourably with accuracy of around 60-65% for genotyping, with interpretation using standard algorithms.

The models were also able to identify alternative, three-drug regimens, comprising locally available drugs that were predicted to produce a virological response for a substantial proportion of the treatment failures observed. This proportion ranged from 75% in Southern Africa, where the number of drugs available was highly restricted, to 93% in Romania and 99% in India. In all cases from the resource-limited countries, the models were able to identify regimens with a higher predicted probability of success than the regimen that failed.

"These results suggest that use of the system could help to avoid significant numbers of treatment failures", commented lead author Andrew Revell of the RDI. "The superiority of the models with cases from 'familiar' settings indicates that the full potential of this system to aid treatment decision-making could be realised by the collection of data from resource-limited settings and the use of these data to train the next generation of models."

The models are now available free of charge on the RDI web site at www.hivrdi.org.

It should be noted that, as the study was retrospective, no firm claims can be made for the clinical benefit that use of the system as a treatment support tool could provide. Nevertheless, the results were positive for clinics and cohorts in many different countries across five disparate regions of the world, which is very encouraging in terms of generalizability. The results also suggest that this approach has the potential to reduce virological failure and improve patient outcomes in less well-resourced countries.

[i] *CD4 (cluster of differentiation 4) is a glycoprotein found on the surface of immune cells such as T helper cells, monocytes, macrophages, and dendritic cells.*

** ENDS **

NOTES TO EDITORS:

'Computational models can predict response to HIV therapy without a genotype and may reduce treatment failure in different resource-limited settings' by Andrew D. Revell, Dechao Wang, Robin Wood, Carl Morrow, Hugo Tempelman, Raph Hamers, Gerardo Alcarez-Uria, Adrian Streinu-Cercel, Luminita Ene, Annemarie Wensing, Frank De Wolf, Mark Nelson, Julio Montaner, H. Lane, and Brendan Larder
Journal of Antimicrobial Chemotherapy, DOI: 10.1093/jac/dkt041

The *Journal of Antimicrobial Chemotherapy* is among the foremost international journals in antimicrobial research. The journal is published by Oxford University Press. The journal's homepage can be found at: http://jac.oxfordjournals.org/

For further information, contact:
Kirsty Doole, Publicity Manager, Oxford Journals
kirsty.doole@oup.com | +44 (0) 1865 355439 | +44 (0) 7557 163 098