

EPOSTER PRESENTATION

Open Access

Polymorphisms in reverse transcriptase and protease genes of HIV-1 subtype C from Mumbai

Ritwik Dahake*, Shraddha Mehta, Sneha Yadav, Abhay Chowdhary, Ranjana A Deshmukh

From 2nd International Science Symposium on HIV and Infectious Diseases (HIV SCIENCE 2014) Chennai, India. 30 January - 1 February 2014

Background

Primary or transmitted HIV-1 drug resistance has caused an alarm in developed countries. While certain HIV-1 subtype C polymorphisms in relation to consensus subtype B sequences are known, there still exists a debate on the validity of these mutations being associated with/mistaken as, primary resistance. In this preliminary study, we have determined polymorphisms in reverse transcriptase (RT) and protease (PR) genes of HIV-1 subtype C from Mumbai, India.

Methods

The study was performed using plasma samples from 24 antiretroviral therapy-experienced and drug-naïve patients employing a 'home-brew' semi-nested reverse-transcriptase-PCR followed by sequencing and sequence analysis. Analysis and interpretation of polymorphisms and other drug-resistance mutations was carried out using the Stanford HIV drug-resistance database. We also analysed Surveillance Drug Resistance Mutations (SDRMs) for PR gene.

Results

We determined polymorphisms at a mutational frequency of 0.0670 ± 0.014 and 0.1337 ± 0.042 , while 12.5% and 16.6% samples harboured drug-resistance mutations in RT and PR genes respectively. Substitutions greater than 50% were at positions D121, K122, T165, K166, K173, D177, T200, Q207, R211 for RT and L19, V82, M36, R41, L63, H69, L89, I93 for PR gene. Additionally, PR gene SDRMs were observed in 15.0% samples.

Conclusion

Our study re-iterates that polymorphisms in HIV-1 subtype C from India may also include a number of major and minor/accessory mutations associated with resistance. We recommend that HIV subtype-specific drug-resistance databases be created to empower routine and unambiguous surveillance of drug resistance prior to initiating antiretroviral therapy, especially when including Protease Inhibitors.

Published: 27 May 2014

doi:10.1186/1471-2334-14-S3-E11

Cite this article as: Dahake et al.: Polymorphisms in reverse transcriptase and protease genes of HIV-1 subtype C from Mumbai. *BMC Infectious Diseases* 2014 **14**(Suppl 3):E11.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit



* Correspondence: ritwikdahake@gmail.com
Department of Virology, Haffkine Institute, Mumbai-400012, Maharashtra, India