OMICS Group Conferences
Accelerating Scientific Discovery
3rd World Congress on Virology
November 20-22, 2013 DoubleTree by Hilton Baltimore-BWI Airport, USA

Partial analysis of a CRF11_cpx/HIV-1 subtype C-like recombinant from South Africa

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Abstract

The G*ag* and *Pol* gene regions of an HIV-1 subtype J-like virus (08MB26ZA), based on an initial phylogenetic analysis of the partial *Pol* gene sequence, were analyzed by phlyogenetic analysis and the REGA HIV subtyping tool. Additionally, the *Nef* and *Env* (C2-V5) regions were analyzed phylogenetically. The *Pol* and *Env* V-3 loop sequences were examined for genetic drug resistance mutations and predicted co-receptor usage respectively. There was concordance in the assignment of the *Gag* sequence to HIV-1 subtype C by phylogenetic analysis and REGA, while the *Pol* sequence was assigned to CRF11_cpx by phylogenetic analysis and to a CRF11_cpx/C recombinant by REGA. It was observed that the integrase gene (a portion of *Pol*) harbored the 'C' sequence. The GPGQ motif in the *Env* V-3 loop was indicative of a CCR5 utilizing virus. There was no important drug resistance related mutations in the protease, reverse transcriptase and integrase genes. This is apparently the first report from South Africa of a putative recombinant involving CRF11_cpx and HIV-1 subtype C genomes, and further suggests that complex viruses are being introduced into South Africa.

Biography:

Pascal O. Bessong is a professor and Head of the HIV/AIDS & Global Health Research Programme at the University of Venda, South Africa. He did his postdoctoral studies at the Myles H. Thaler Center for AIDS and Human Retrovirus Research, University of Virginia, USA. His research interests include HIV genetic diversity and drug resistance; and co-infections in HIV/AIDS.