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Molecular epidemiology of HIV-1 in central region of Nepal

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Full length HIV-1 genome sequencing provides important data needed to address on research and development on diagnosis, treatment and prevention of HIV-1 infection. About 0.5% (64,000) of Nepal population was estimated to be HIV positive. Cross border trafficking of sex workers is a major problem contributing to increasing HIV rates in both India and Nepal. Here we examined the genetic diversity of HIV-1 isolated from central region of Nepal. 136 blood samples were collected from HIV-1 infected individuals attending VCT (voluntary counseling and testing) clinic between May-August 2011 at Bharatpur Hospital in Nepal. Based on complete clinical, epidemiological, and viral load data, 40 individual samples from total 136 representing all risk groups of HIV, were selected for further studies. Nucleotide sequence analysis was done following protocol of near full length genome (NFLG). There was intermixing of subtypes within transmission risk groups. However phylogenetic analysis then allowed assignment of most samples amplified belongs to HIV-1 subtype C (a distinct lineage from India). Around 10% of samples were identified as CRF01_AE and CRF08_BC. The identification of these subtypes and CRFs in the central region of Nepal is important in epidemiological tracking as well as will provide information of new antigenic regions of circulating strains, which may unfold the development of an effective vaccine in future.

Biography

Nirajan Bhusal has completed MBBS in 2006 from University of Science and Technology, Bangladesh and PhD in 2014 from Mahidol University, Thailand. Since then, he has been working as a Lecturer in Kathmandu University School of Medical Sciences. He has been contributing on routine clinical service of diagnostic microbiology laboratory as an expert virologist. Beside academic activities, he has been involved in various research activities too.

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