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Analysis and evaluation of candidate genes in association with HIV-1 latency

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We found 70 candidate genes in association with the establishment and maintenance of HIV-1 latency through integrative analysis with DNA methylation, histone modification and expression profile in HIV-1 latently infected cell lines. To select more effective genes on HIV-1 latency among 70 genes, we performed the functional enrichment analysis using the Database for Annotation, Visualization and Integrated Discovery (DAVID). The p-value<0.1 was selected as cut off criterion. The significantly enriched Gene Ontology (GO) categories were identified as cell cycle, cell death and signal transduction. 24 genes from the significantly enriched categories included 13 up-regulated and 11 down-regulated genes. To identify the expression level of 24 genes between normal cells (A3.01, Jurkat) and HIV-1 latently infected cells (ACH2, NCHA1, NCHA2, NCHA3, J1.1); we analyzed microarray data and found that gene expression level of 24 genes was very different according to cell lines. Among them, 10 genes showed similar patterns in more than three HIV latently infected cells and were selected as candidate genes: *TNFSF13B, APBB2, ANK1, MSRA, AVEN, NQO1, FOXN4, RASAL1, JAG2* and *PLOD1*. To evaluate how the expression level of 10 genes in vivo, we measured the quantitative RNA expression in HIV-1 infected patients using real time-PCR. *TNFSF13B* and *APBB2* were highly expressed as shown in HIV-1 latently infected cell lines. Therefore, these results suggest that selected genes may be potential biomarkers and play a key role in HIV-1 latency.

Biography

Kyung-Chang Kim has completed his PhD from Korea University and Postdoctoral studies from Northwestern University. He is working as a Researcher in the Division of AIDS, Korea National Institute of Health. He has published several papers in peer reviewed journals and has been serving as a Board Member of the Korean Society for AIDS since 2016.

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