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DNA methylation profiling can classify HIV-associated lymphomas

HIV-positive patients have 60 to 1000 fold higher risk of malignancies including non-Hodgkin lymphomas. Most HIV-associated lymphomas are high-grade B-cell lymphomas and frequently represent with poor prognostic features. General pathological features do not clearly differentiate HIV-associated lymphomas from non-HIV lymphomas. To understand the nature of HIV-associated lymphomas, we performed the genome-wide analysis of methylation profiling of HIV-associated lymphomas and non-HIV lymphomas. Analysis of gene and intergenic regions by Illumina Infinium Human Methylation 450 microarray identified unique methylation profiles in HIV-associated lymphoma examined at gene promoter regions (including CpG islands). Compared with non-HIV lymphoma DNA, HIV-associated lymphoma DNA tended to be hypomethylated. Data suggest that HIV-associated lymphomas were differentially categorized from non-HIV lymphomas. We next investigated the cancer-related gene methylation profiling of HIV-associated lymphomas using Illumina Golden Gate Methylation Cancer Panel I microarray. We identified the specific DNA methylation pattern in the recurrent cases of HIV-associated lymphomas. These findings support understanding the modes of HIV-associated lymphomas and identifying new prognostic biomarkers. Taken together with our results showing that peripheral blood cells of HIV-1 positive patients are susceptible to genomic instability, we discuss the possible mode of HIV associated lymphomas.

Biography

Yukihito Ishizaka graduated from Tohoku University, School of Medicine in Japan, and has obtained the Doctor of Medical Science from Jichi Medical School. He is the Director of Department of Intractable Diseases and the Vice Director General of Research Institute of NCGM. His scientific interest is genomic instability during carcinogenesis, and initiated the current project just when he started HIV-1 research.

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