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Comparative analysis of RCGY sites methylation in the genomes of Raji and U-937 malignant and normal lung fibroblast cell lines

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An aberrant methylation of the genomic regulatory regions may disrupt normal functioning of cells and often accompanies the human diseases including cancer. Thus, DNA methylation markers have significant diagnostic value and attract attention of many biomedical researchers. Unfortunately, the existing approaches for genome-wide methylation study are rather expensive and laborious. We have developed and successfully tested a novel method of the methylated sites mapping in the genomes. The method is based on a property of methyl-dependent site-specific DNA endonuclease GlaI to cleave DNA only at R(5mC)GY sites forming blunt-ended fragments. The following next generation sequencing of the fragments obtained after GlaI hydrolysis of DNA from Raji malignant cell line allows to reveal more than 2,617,000 positions of R(5mC)GY sites in genome. We have applied this approach to find differentially methylated RGCY sites in the genomes of malignant Raji and U-937, as well as non-malignant L-68 lung fibroblast cell lines. The positions of methylated RCGY sites in the genomes have been determined using pair-ended sequencing of GlaI fragments. A comparison of the obtained data has revealed significant differences in methylation of RGCY sites in CpG islands, putative regulatory regions and some repetitive DNA families between all three genomes. GO enrichment analysis of genes with highly methylated regulatory regions has shown the metabolic processes, which may be affected epigenetically in carcinogenesis. The new method allows determining positions of many modified cytosine bases in the genomes and may be a simple alternative to the existing methods of genome-wide methylation analysis.

Biography

Viktor N Tomilov has graduated from EPFL, Lausanne, Switzerland and obtained his MS degree from Novosibirsk University, Russia. He is the Head of Bionformatics Department, Department of Mathematical Biology in SibEnzyme Ltd. He has published more than 20 papers in the various scientific fields (chemistry, genetics, genomics, computer sciences, etc.).

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