Determination of the Methods to Analyze DNA Methylation in the Liver of Low Dose-Rate-Irradiated Mice

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Abstract

We have previously observed extensive alterations in gene expression in the livers of mice exposed to low dose-rate radiation. The object of the present study is to identify epigenetic mechanisms (e.g., DNA methylation) responsible for the alterations in gene expression. This year, we validated three methods for analyzing DNA methylation in specific genes: 1) next generation sequencing in combination with bisulfite conversion; 2) microarray analysis following methylated DNA capture with MBD (methyl binding domain); and 3) PCR amplification following methylated DNA capture with MBD. Results showed that the three methods yielded similar results regarding DNA methylation profiles and they differentiated between DNA methylation in young and aged mice. Between the two methods of comprehensive analyses, next generation sequencing was superior to microarray analysis in both resolution and sensitivity. PCR amplification, a non-comprehensive analysis, may be applied to a limited number of genomic regions and was most economical to use when comparing large numbers of samples. For future experiments, we will therefore, be using next generation sequencing for genome-wide studies, and PCR amplification for comparing large numbers of samples.

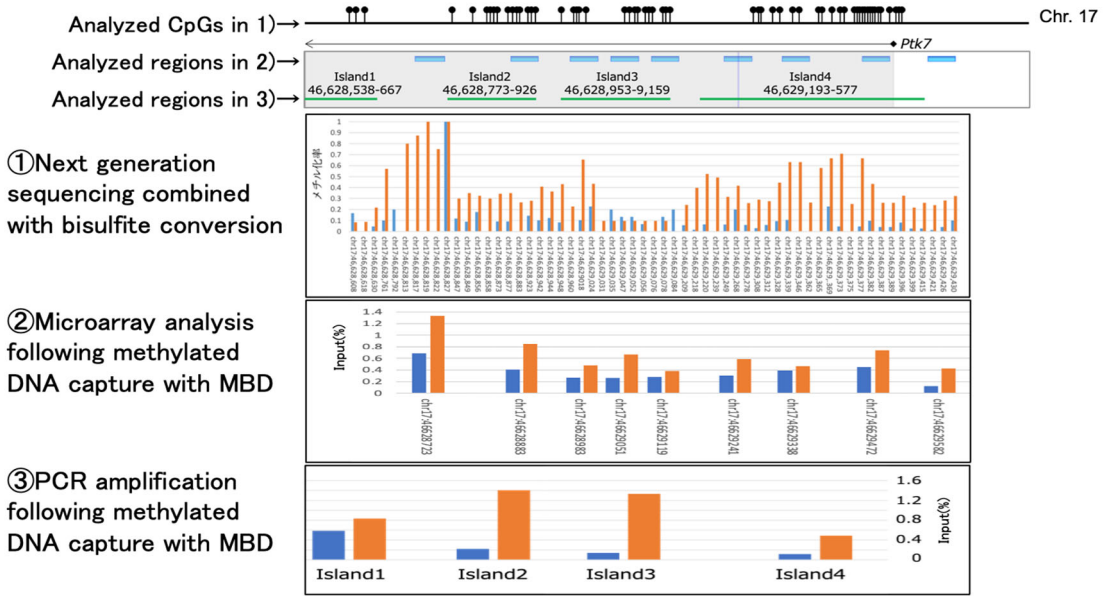

Fig. 1 Comparison of three methods for analyzing methylated DNA.