Quantitative and State-specific DNA methylation analysis using CE-SSCP

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DNA methylation is an epigenetic mechanism of regulation, which is responsible for transcriptional silencing of tumor suppressor genes. Without any change of DNA sequence, phenotype can be differentiated by epigentic changes, and the changes are heritable through cell cycles and generations. Particularly, determination of DNA methylation state of promoter region is not a problem of on-and-off, meaning that DNA methylation pattern is heterogeneous in a population. However, there is no technology which can detect those heterogeneous patterns quantitatively. Capillary electrophoresis-based single strand conformation polymorphism analysis has great potentials in quantitative DNA methylation analysis. High-resolving ability of CE-SSCP makes possible that differently methylated DNA fragments can be separated after sodium bisulfite conversion. The differentiated fragments are only different in their sequences, and the difference causes altered ssDNA conformation which can be resolved by CE-SSCP analysis. To analyze various methylation states in one reaction, differently methylated DNA fragments were prepared and CE-SSCP analysis on the fragments has been demonstrated.