A New Method for Expression Profile Analysis Using Single-Strand Conformation Polymorphism Based on Capillary Electrophoresis

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Although DNA microarray allows high-throughput tool for analyzing expression profile of a large number ofgenes from small sample, relatively low accuracy is known to be major handicap due to the significant errors caused by inherent features of hybridization-driven technology. Single-strand conformation polymorphism (SSCP) is a novel approach to genetic screening and originally developed as a genotyping method to detect unknown mutations. And recently, adoption of capillary electrophoresis offers much higher throughput and sensitivity as well as greater reproducibility and full method automation. The nature of CE-based SSCP to separate a number of single-strand DNA molecules with highreproducibility and sensitivity makes this technique applicable to quantification of various mRNAs simultaneously.

In this work, we developed a new hybridization-free method for expression profile analysis using CE-based SSCP. Appropriate range of the mRNA concentrations and protein concentrations/activity to show linear correlation between the peak areas in target mRNA specific single strand DNA and protein concentration/activitywas determined and consequently it was shown that expression level could be quantified. The results illustrate that new method using CE-SSCP techniques can be more accurate and informative for analysis of expressionprofile in various biological regulatory systems.