Precise multiplex expression analysis using multiplex ligation-dependent probe amplification based on conformation-sensitive capillary electrophoresis

신기원, 황희성, 정보람, 나정경, 정규열*
포항공과대학교
(gyjung@postech.ac.kr*)

Quantification of mRNA provides information crucial for various biological studies. Real-time PCR is known to be the most accurate method for quantifying mRNA, and thus represents the state-of-the-art for gene expression analysis. However, the use of real-time PCR for mRNA quantification is limited to a single target per analytical run because of reductions in quantification power and limitations of fluorescence dyes associated with multiplex applications.

Multiplex ligation-dependent probe amplification (MLPA) is an alternative multiplex analysis method. However, MLPA has not been widely used for expression analysis because it uses DNA-size-dependent electrophoretic separation, which complicates probe design process and compromises accuracy of the analysis. In this study, we developed a new version of MLPA, which uses a conformation-sensitive electrophoretic separation. We have demonstrated that our method could be used to monitor expression of genes in *Escherichia coli*, *Caenorhabditis elegans* and *Arabidopsis thaliana*.