

Editor's Introduction to This Issue

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Growing evidence has shown that miRNAs are involved in diverse biological processes, including the control of cell proliferation and differentiation. Accordingly, a number of studies have reported that altered miRNA expression is related to tumor cell growth, invasion, and metastasis. Recent studies have revealed that tumor-associated miRNAs are present in human plasma and serum, suggesting that plasma miRNAs can be useful non-invasive biomarkers. In this issue, Dr. Yong Sung Kim's group (KRIBB) measured the plasma expression levels of three miRNAs to investigate the usefulness of miRNAs for gastric cancer detection. DNA microarray techniques have been widely used in biological research to understand the pathobiology of diseases. Microarray experiments also enable researchers to identify gene sets undergoing a response to a specific stimulus, as well as to analyze dynamic responses at the level of the gene regulatory network. Prof. Sangsoo Kim's group (Soongsil

University) has constructed an insulin-mediated regulatory network by using published gene expression microarray datasets of human skeletal muscle samples. In this issue, based on a motif discovery method, they developed a regulatory network for insulin-mediated genes by integrating methods based on TF binding motifs and gene expression variations. The development of transgenic biotechnologies has led to safety concerns regarding genetically modified organisms, particularly in food crops. Ik-young Choi's group (Seoul National University) demonstrated the success of NGS data in characterizing the genetically modified rice genome. There are three interesting and informative application notes in this issue: 'A Database of Gene Expression Profiles of Korean Cancer Genome,' 'VBioindex: A Visual Tool to Estimate Biodiversity,' and 'A Frequency Profile of the ChromHMM Promoter States.'

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