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EDITORIAL

Editor's Introduction to This Issue

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Recently, next-generation sequencing (NGS) technologies have become the most important part of genetic testing to understand life phenomena and disease mechanisms. As one of the important moves towards personalized medicine, NGS technology is being rapidly introduced to the clinical field. However, considering the cost and time for the analysis after sequencing per se, whole-genome or whole-exome sequencing might not be the most efficient genetic testing methods yet. Regarding this issue, Dr. Byung Chul Kim's group, Theragen Bio Institute, reports a fast and cost-effective NGS method to identify somatic mutations in lung cancer. They chose 30 genes potentially associated with lung cancer development, performed target gene capture, and analyzed the findings by NGS. This approach could be useful for detecting well-known key mutations as well as novel variants in lung cancer. Dr. Hyung Doo Shin's group, Sogang University, hypothesized that polymorphisms in the tyrosine-protein kinase Tec, which is involved in various immune responses, might be involved in aspirin-exacerbated respiratory disease pathogenesis. Although they did not observe a positive association, this study can help us understand the genetic component of this condition. Dr. Dorairaj Sudarsanam's group, Loyola College, India, reported the results of their exploration of the Gm18 and m1G37 modification positions in tRNA sequences. Dr. Satish Kumar's group, Mahatma Gandhi Institute of Medical Sciences, India, suggested the molecular interaction of natural inhibitors with the human papillomavirus-16 E6 oncoprotein. In the application note section, Dr. Dong Su Yu's group, KOBIC, reports a simple and fast protein function annotation system, named SFannotation.

Genomics & Informatics is already available in PubMed Central and PubMed. Taking these efforts together, we expect broader international visibility of *Genomics & Informatics*.

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