EDITORIAL

Editor's Introduction to This Issue

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This is a special issue, consisting of three selected dissertations that were awarded the KOGO Young Scientist Best Paper Award, hosted by KOGO (Korea Genome Organization) in 2016. A dissertation (Seungkyu Choi *et al.*) on analyzing the mutational profiles of extranodal NK/T-cell lymphoma (NKTCL) using targeted sequencing with a comprehensive cancer panel revealed that *KMT2D* is a novel driver gene in NKTCL.

The second paper that was awarded (Ki-Sung Kwon *et al.*) describes the recapitulation of candidate systemic lupus erythematosus-associated variants in Koreans. In this study, the authors aimed to replicate SNPs that were recently discovered in a GWAS but have not been validated in Koreans or have only been replicated in Koreans with an insufficient sample size to conclude any association.

Nuclear mitochondrial DNA segment (Numt) insertion describes a well-known phenomenon of mitochondrial DNA transfer into a eukaryotic nuclear genome. However, it has not been well understood, especially in plants. Numt insertion patterns vary from species to species in different kingdoms. In the third paper that was awarded (Young-Joon Ko and Sangsoo Kim), the authors analyzed nuclear mitochondrial DNA segments of nine plant species.

Transposable elements are one of the major sources of genomic instability through various mechanisms, including de novo insertion, insertion-mediated genomic deletion, and recombination-associated genomic deletion. Among them, Alu is the most abundant element, constituting ~10% of the human genome. In this issue, Dr. Jungnam Lee's group (University of Florida, USA) comprehensively reviewed the mechanisms of Alu amplification and their roles in generating genomic rearrangements, as well as human genetic disorders.

The other four papers are about the virtual screening of natural inhibitors against influenza A (H1N1) neuraminidase protein and potential inhibitors of NS3 protein of Zika virus, in silico prediction of miRNA-based gene regulation in diverse cancers, and the identification of potential virulence factors of *Helicobacter pylori*.

For further details, please visit the G&I homepage (http://www.genominfo.org/).

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