医学セミナー・第 15 回分子遺伝疫学セミナー
"Seminars in Medical Sciences" Lecture

ゲノム医科学リサーチユニット　難治性免疫疾患・アレルギーリサーチユニット

Approaches to the identification and evaluation of functional disease-causal/susceptible variants in the human genome.

Speaker: Dr. Yuki Hitomi (Assistant Professor, Department of Human Genetics, The University of Tokyo)（人見祐基博士、東京大学大学院医学系研究科人類遺伝学分野助教）

Date:　December 18, 2017

Time:　17:00-18:15

Venue: Faculty of Medicine Building, Room 483（医学系学系棟 483）

This seminar is one of the seminars for the subject "Seminar in Medical Sciences" in Doctoral Programs in Biomedical Sciences and Clinical Sciences. The seminar will be given in English, but questions in Japanese are also welcome.

This seminar will NOT be recorded; therefore, be sure to attend if are interested.

Any of the genetic variations may cause differences in traits and disease risk. So far, genome-wide association study (GWAS) and next-generation sequencing (NGS) have become indispensable methods for comprehensive screening of disease-causal/susceptible variants in the human genome. However, due to linkage disequilibrium (LD), several single-nucleotide polymorphisms (SNPs) show similar levels of association with the most significantly associated GWAS tag-SNP, especially in the cases of common variants. Inaccuracy of variant calling by current NGS platforms also remains a problem.

For the identification of disease-causal/susceptible variants from numerous genetic variants in the human genome, evaluation by functional analyses should be performed. By systematic search for the disease causal/susceptible variants including functional analyses, we will come to understand the molecular mechanisms of diseases, establish novel drugs, and develop prediction kits for disease onset and adverse effects using genotyping of the variants.

In this seminar, I would like to introduce the approaches to the identification and evaluation of functional disease-causal/susceptible variants by comprehensive whole-genome analysis (GWAS and NGS), *in silico* functional analyses using several valuable computer tools, and *in vitro* functional analyses. We also discuss the clinical applications of the genetic variants to personalized medicine.

References

1. Hitomi Y and Tokunaga K. Significance of the functional disease-causal/susceptible variants identified by whole-genome analyses for the understanding of human diseases. **Proc Jpn Acad Ser B Phys Biol Sci** 93: 657-676, 2017.
2. Hitomi Y, et al. Identification of the functional variant driving ORMDL3 and GSDMB expression in human chromosome 17q12-21 in primary biliary cholangitis. **Sci Rep** 7: 2904, 2017.
3. Heinzen EL[#], Swoboda KJ[#], Hitomi Y[#], et al. ([#]equally contributed) De novo mutations in ATP1A3 cause alternating hemiplegia of childhood. **Nat Genet** 44: 1030-1034, 2012.

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