Research Report

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Research Period	From: 2020/04/01 To: 2021/03/31
Research Field	Basic Medical Sceince

Research Theme at Tokai University

Title: Polymorphism and transcription analyses of Human Leukocyte Antigen (HLA) genes by next generation sequencing methods

Abstract:

The Human Leukocyte Antigen (HLA) is a highly polymorphic genomic region on chromosome 6 that encodes the transplantation and immune regulatory molecules. It receives special attention for genetic investigation because of its important role in the regulation of innate and adaptive immune responses and its strong association with numerous infectious and/or autoimmune diseases. In this study we aim to understand the functional changes that result from variations (polymorphisms) in the coding and non-coding regions of HLA genes. To achieve this goal, we are first proceeding to identify the association between HLA gene polymorphisms and transcription levels by using next-generation sequencing (NGS) both for genotyping full-length genes (non-coding regions and introns and coding exons) and for measuring the transcription levels. This study is expected to provide valuable HLA polymorphism and expression data for a better and more reliable interpretation of histocompatibility testing with important clinical implications.

Results / Achievements:

Please write a summary of your research results / achievements. Also, please share your research papers/articles, books, poster presentations if there is any.

We have developed a new Capture RNA-Seq method as part of our collaborative research that can simultaneously measure the transcription levels transcribed by 12 HLA loci and associate the relative transcription levels with HLA alleles. Last year, we found that 7 of the 74 HLA alleles were associated significantly with different transcription levels for 48 umbilical cord blood (UCB) samples and 161 peripheral blood mononuclear cell (PBMC) samples. This difference may reflect the regulation of transcriptional levels of specific HLA alleles due to differences in their cellular environment. In addition, we published a paper describing the capture RNA-Seq method and various analysis results based on the method (Yamamoto et al. Front Immunol. 11: 941, 2020). Our newly developed techniques and findings are expected to be helpful in the future for providing more beneficial information for hematopoietic stem cell transplantation and predicting the risk of rejection by HLA polymorphic expression levels.

URL (Research Gate, Research Map, etc.):
https://profiles.stanford.edu/fiona-fumiko-yamamoto, https://mpcore.sites.stanford.edu/people