平成２８年度「共同利用・共同研究・熊本地震支援」成果報告書

Title: Transcriptomic analysis of activated T cells

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Aspect: A-1. Next-generation sequencing and microarray analyses (organized by Professor Toyomasa Katagiri)

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In the research, we aimed to reveal at single cell level the transcriptional mechanism of the T cell activation processes upon antigenic stimulation, and thereby to identify new non-stochastic mechanisms behind T cell activation, and to reveal the interaction of key transcirption factors and their relationships to key surface molecules.

We analysed a small number of T cells using a quasi-single cell RNA-seq approach, using primary murine CD4+ T cells will be isolated from immunised mice. RNA was extracted and amplified for RNA-seq. We are currently analyzing this dataset.

Through the data analysis, we are aiming to reveal the mechanism behind T cell activation and identify new mechanisms may lead to the development of a new class of immunotherapy. Thus, we will investigate the stochastic and non-stochastic events following antigen recognition, and thereby reveal how sequentially these transcriptional mechanisms occur in response to TCR signal, how these transcriptional mechanisms induce key surface proteins, and how these can be manipulated to enhance the negative regulatory mechanisms.

Outcomes: We are currently analyzing the data, which will be included in our publication, which we aim to submit in the next academic year (2017/18). In order to further facilitate the data analysis process and the collaboration between Imperial College London and Tokushima University, we have recently applied for a JSPS London funding for research visit, and will further seek for a support to realise these aims.