

Identification of pathogenic code causing itch and development of therapeutic basis

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Atopic dermatitis is thought to affect more than one million people in Japan. In particular, 80% of patients are under the age of 44 in the active stage of the disease, and it is a serious problem that chronically impairs quality of life. In clinical practice, in addition to existing immunosuppressive agents including steroids and other drugs, anti-IL-4/IL-13 receptor antibodies are used as biological agents for treatment. However, a major problem with these current treatments is the long-term administration of expensive antibody preparations increases the burden on the medical economy itself. In addition, existing treatments only suppress symptoms and do not prevent or cure the disease.

On the other hand, recent advances in science and technology have made it possible to perform trans-omics analysis, in which RNA, proteins, and metabolites are comprehensively analyzed and their parameters are linked to each other. These tools can be very powerful to capture events occurring at the molecular level in disease lesions and identify new therapeutic targets. However, due to the complexity of the system and experimental limitations, trans-omics analysis using immune cells is still lagging behind, and there is a strong requirement for such efforts in terms of therapeutic applications. Against this background, the applicant was the first to construct a system that combines RNA-seq and proteome analysis using the same samples and combines each parameter. Furthermore, we have identified pathogenic Th2 cells (Tpath2) that cause allergic disease. In addition to these achievements, we have recently identified cutaneous T cells that specifically produce IL-3 and IL-31. Therefore, we have conceived this research proposal to identify pathogenic codes that cause atopic dermatitis and itch and to develop new therapeutic targets and platforms by utilizing the applicant's trans-omics analysis system and CRISPR tools that can be applied *in vivo* to cutaneous T cells.