2-SL05 Special Lecture5

Harnessing gut commensals to combat disease

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The mammalian alimentary tract harbors hundreds of species of commensal microbes that critically influence a multitude of host physiological functions. Unfavorable alterations of the gut microbiota composition often correlate with several negative health outcomes. Thus, the amelioration of microbiota dysfunction is a promising route for future therapeutics for several diseases. We have been aiming to understand the features and functions, particularly immunological attributes, of the microbiota, and trying to identify responsible bacterial species and factors for shaping the immune system. We have succeeded in isolation of human and mouse gut-associated commensal bacterial strains that specifically affect the development and function of Th17 cells, Treg cells, Th1 cells or CD8 T cells. In addition, we have identified trypsin-degrading bacterial species. Our findings would allow for designing bacterial consortia that activate or suppress specific adaptive immune programs, potentially resulting in development of better therapeutics for numerous diseases involving the immune system, including infectious disease, autoimmunity, allergy, and cancer.

ほ乳類の腸管には数百の腸内細菌（マイクロバイオータ）が存在し、宿主の生理機能に深く影響を及ぼしている。従ってマイクロバイオータに人為的に介入することが出来れば、複数の疾患に対する新たな治療戦略となり得る。我々は、消化管の恒常性維持機構を理解すると共に、個々の腸内細菌種が免疫システムにどのように影響を与えているかを還元化して把握して行く独自の研究手法を確立してきた。この方法によってこれまでに、制御性T細胞、Th17細胞、Th1細胞、CD8 T細胞を特異的に誘導する腸内細菌種の同定に成功した。これらの成果は、免疫系が関わる様々な疾患（感染症・アレルギー・自己免疫・がんなど）に対する新しい治療法開発に繋がる可能性がある。