**Improved Allergy Diagnosis and Treatment Using Novel Technological Platforms**

Ting Fan LEUNG
Department of Paediatrics, The Chinese University of Hong Kong, Prince of Wales Hospital, Shatin, Hong Kong

The pathogenesis of allergic diseases involves complex interplay between genetic predisposition and a wide array of environmental factors such as microbial encounter, dietary intakes, tobacco smoke and pollutant exposure and psychosocial factors. Traditional labour-intensive but low throughput methods have limited capacity to generate the vast amount of laboratory data that are required to decipher such gene-environmental interactions. For example, culture-based studies failed to identify up to 80% of bacterial flora when compared with molecular approaches. The advent of powerful next generation sequencing (NGS) greatly facilitates the omics approach by identifying genomic, metagenomic, epigenomic and transcriptomic signatures of various allergic diseases. Our studies reported substantial differences in the epidemiology of asthma genes and loci between Chinese and Caucasians. Microbial characterisation at different body sites also enhanced our understanding of immunomodulatory roles of microbiota. Supported by improvements in sequencing technology and analytical support, recent NGS studies revealed the microbiota at body sites such as skin, airway and gut. The detection of cutaneous microbes in an ongoing birth cohort provided evidence that microbial compositions soon after birth modulated the risk for eczema development. This approach also confirmed the findings between atopic eczema and *Staphylococcus aureus* colonisation as well as between eczema flare and reduced skin microbiota diversity from cross-sectional studies. For children with asthma or recurrent wheeze, metagenomics analyses of their nasopharyngeal secretions revealed lower microbiota diversity and some suggestive microbial signatures. Very recently, dual RNA sequencing approach yielded exciting data on both transcriptomic (host) and metatranscriptomic (microbiota) sequences from the airway epithelium. Such sequencing data helped to unravel the human genes differentially expressed in asthmatics that regulated immune and inflammatory responses, the spectrum and functions of microbial genes that were related to asthma, and the interactions between microbiome and host upstream regulators that could explain patients' clinical manifestations. In conclusion, the development of novel technological platforms such as NGS opens a new horizon for deciphering the complex pathogenetic processes of allergic diseases. Such information will ultimately improve the precision of our diagnosis and treatment for these allergy sufferers.