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Gene expression and beyond: From Single-cell Biology to Human Cell Atlas

Varodom Charoensawan[1,2,3,*], Ponpan Matangkasombut[3,4]

[1] Department of Biochemistry, Faculty of Science, Mahidol University, Bangkok, Thailand
[2] Integrative Computational BioScience (ICBS) center, Mahidol University, Nakhon Pathom, Thailand
[3] Systems Biology of Diseases Research Unit, Faculty of Science, Mahidol University, Bangkok, Thailand
[4] Department of Microbiology, Faculty of Science, Mahidol University, Bangkok, Thailand
* Correspondence: varodom.cha@mahidol.ac.th

Abstract: Gene expression is highly dynamic and dependent upon external stimuli such as environmental stresses, as well as developmental signals. Mis-regulation of gene expression leads to several genetic diseases including developmental disorders and cancers; not to mention the gene regulatory network of immune systems that are substantially altered by viral and bacterial infections. Thanks to several "omic" techniques such as RNA-seq, now we can investigate the transcriptional changes at the genome scale within a short period of a few days. However, traditional "bulk" RNA-seq and other common high-throughput methods do not have sufficient resolution to dissect transcriptional variations in heterogeneous populations of cells. In this talk, we will first give an overview of the current applications of single-cell transcriptomics in biomolecular research around the world, using the international consortium Human Cell Atlas (HCA) initiative and recent studies that have implemented this technology in the context of COVID-19. I will also describe our latest progress, in collaborations with several research groups in Thailand, on establishing a single-cell omics facility and contributing to the country's core capacity and competency in using the technique to map out the cellular diversities and dynamics of human immune cells in response to external stimuli such as viral infections, as well as in cancer models. I will also give an overview of our latest contribution to HCA via the Asian Immune Diversity Atlas (AIDA) consortium. The project will uncover the landscape of the complex immune variations of diverse Asian populations, which have been influenced by different environments and endemic infectious diseases over several centuries.

Keywords: Systems Biology; Single-cell Biology; Gene Expression Regulation, Human Cell Atlas, Immune Diversity

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