Special Seminar

共催： 第70回 免疫学セミナー

A Systems Level Understanding of the Hematopoietic System with Gene Expression Commons

Tue. November 14

17:00-18:30

8F Auditorium, Medical Health Sciences Innovation Building

健康医科学イノベーション棟8階講堂

Guest Speaker

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Abstract

Hematopoiesis is one of the most dynamic multi-lineage systems in our body. Throughout one's life, short-lived diverse types of functional blood lineages are continuously supplied from a single cell type, hematopoietic stem cells, through a hierarchical multi-layer of intermediate progenitor cells. Even minor disruptions in this carefully regulated system can lead to disease. To better understanding how this complicated system is regulated, we need to establish a robust systems approach.

One of major aspects is gene expression, however, gene expression profiling has been limited to relative difference in pair-wise comparisons, and many genes are scored as "not significant" regardless of their actual expression. More importantly, each gene has different dynamic-range of its expression. Biological significance of 2-fold change in gene X is not equivalent to 2-fold change in gene Y.

To address those limitations, we hypothesized that by examining expression of a given gene across thousands of samples, we could have one common reference for any samples. Computer simulations demonstrated if we accumulate over 5000 microarray data, meta-analysis could be applicable to compute statistical attributes for each gene, such as the dynamic-range of each probeset/gene expression or the threshold between active and inactive gene expression. Then by mapping new sample data against the result of the meta-analysis, a much more objective genome-wide gene expression profiling could be achieved for each sample independently. Thus, we collected entire microarray data available at NIH GEO public repository for meta-analysis, then developed a web-based platform named the "Gene Expression Commons (https://gexc.riken.edu) with an intuitive interface. To demonstrate the potential of the Gene Expression Commons, we generated gene expression microarray datasets of 39 hematopoietic populations covering almost the entire quantal stages of mouse adult hematopoiesis. As the Gene Expression Commons is designed as an open platform, any scientists can explore gene expression of any gene of interest, search for new genes by their expression pattern, and submit and analyze their own data by designing their own working model. After public launch on July 2012, the Gene Expression Commons has been used by over 4000 scientists around the world. Over 3500 new cell types have been submitted, about 2000 hypothesis were tested, and over 100 papers were published.

HBP

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This seminar is hosted by:

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