



Title of Project : Transomic Analysis of Metabolic Adaptation

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【Purpose of the Research Project】

Living organisms dynamically adapt their metabolism in response to change in surrounding environment and maintain biological homeostasis. The result of the metabolic adaptation can be observed as characteristic metabolic phenotypes in the metabolic syndrome, diseases and pathological phenomena. For example, the blood glucose level in fasting human is maintained constant, but in diabetes, the homeostasis of blood glucose is lost and hyperglycemia appears. These metabolic adaptations are dynamic phenomena where metabolism adapts along with time from a normal base state to an adaptive state on metabolic network of over 1000 metabolites.

Metabolic adaptation is not controlled only by metabolite (metabolome) changes. Genome, epigenome, transcriptome, and proteome locates in upper layer of metabolome and they can also control metabolic adaptation. These omic layers shape transomic network and closely interact each other. Therefore, metabolic adaptation can be recognized as dynamical switching of the complex transomic network (Fig. 1). Due to the complexity, understanding metabolic adaptation needs simultaneous measurements of multiple omics data and needs technology development of transomic analysis that integrates multi-layer omics data across the hierarchy.

In this research area, we aim to achieve a unified understanding of individual phenomena as metabolic adaptation through transomic analysis.

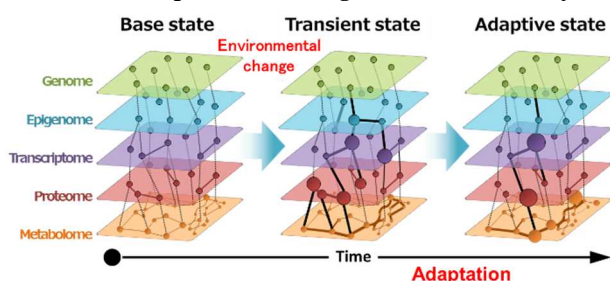


Fig. 1. Metabolic adaptation is realized by switching transomic network.

【Content of the Research Project】

We measure genome, epigenome, transcriptome, proteome and metabolome by preparing samples under the same condition for various phenomena such as type 2 diabetes, cancer, inflammatory disease, and drug resistance. We perform

transomic analysis to understand the mechanism of metabolic adaptation using both hypothesis-driven approach based on biological knowledge and data-driven approach based on statistics. We also improve throughput and sensitivities of omics measurements. Moreover, we develop advanced technologies of transomic analysis that integrate multiple layers based on various databases and statistical and information science for comprehensive understanding of the transomic network.

【Expected Research Achievements and Scientific Significance】

Conventionally, metabolic adaptation has been studied as individual life phenomena in different fields. In contrast this research area enables to understand these phenomena in a unified way as metabolic adaptation from the viewpoint of switching of transomics network. Furthermore, as a common strategy beyond individual phenomena, master switches to switch transomic network, biomarkers, and multidrug target molecules will be identified. We also clarify robust network structures which are commonly observed in many transomic networks of different molecules.

In more future, as life innovation, we expect identification of environmental factors of disease as well as genetic factors through Trans-OWAS (Trans-Ome-Wide Association Study). As green innovation, novel strategies for useful compound production using microbes and for breeding plants resistant to climate change are expected.

【Key Words】

Transomics analysis: an analysis to integrate multi-layer omic data (e.g. genome, epigenome, transcriptome, proteome, and metabolome) across hierarchies.

【Term of Project】 FY2017-2021

【Budget Allocation】 1,224,700 Thousand Yen

【Homepage Address and Other Contact Information】

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