【Grant - in - Aid for Scientific Research on Innovative Areas(Research in a proposed research area)】

Biological Science

Title of Project : Integral understanding of the mechanism of transcription cycle through quantitative, high-resolution approaches

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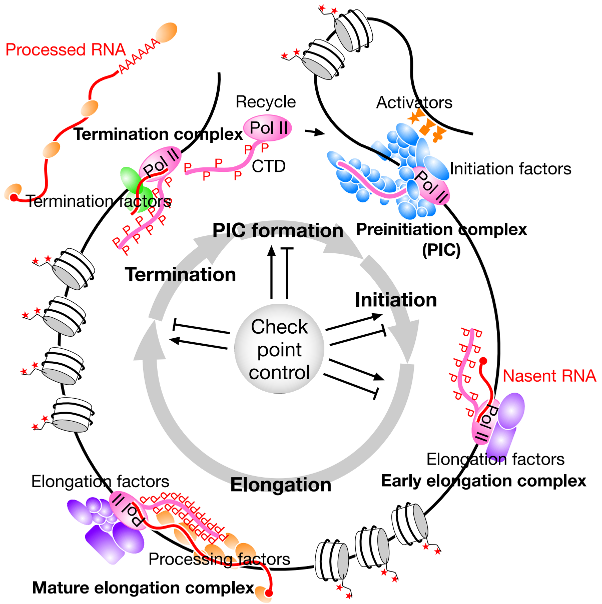
【Purpose of the Research Project】

The objective of this area is to elucidate the regulatory mechanism of “transcription cycle,” and to thereby contribute to the understanding of complex physiological functions. The difficulty lies in a highly hierarchical structure of the processenvolved; due to technical limitations, each layer of research has been carried out individually, and the integration of resulting data has not been possible. In this area, we aim to gain an integrative perspective on multiple steps and layers of transcription using “high-resolution approaches,” in which leading edge technology and computational science are combined with conventional methodology. A shift from qualitative to quantitative understanding and a shift from static to dynamic understanding would make it possible to understand the entire process of transcriptional regulation and to thereby contribute to the understanding of complex physiological functions.



【Content of the Research Project】

In this area, we will elucidate the remodeling cycle of transcription complexes, checkpoint control of transcription, and transcriptional regulation through gene looping; and thereby formulate the concept of “transcription cycle.” Moreover, a deeper understanding of complex physiological functions will be gained through the integration of the transcription cycle of individual genes with those of each cell and organism using “high-resolution approaches.” Specifically, leading-edge technology, including genome-wide analyses and new techniques for enabling kinetic and quantitative studies, will be developed and utilized. In addition, computer science will be fully utilized to process large datasets and to support kinetic studies. To promote the study on “transcription cycle,” a research initiative will be established to perform single-molecule analysis in live cells, dynamic structural analysis, and genome-wide analyses using next-generation sequencers.

【Expected Research Achievements and Scientific Significance】

Our goal is not to draw nonquantitative models for transcriptional regulation, but to provide a precise, detailed view of it through quantitative, comprehensive analyses. This study is indispensible for the simulation and prediction of changes in gene expression through a systems biology approach in future and will contribute to genomic and epigenomic drug discovery.

【Key Words】

Transcription cycle: This is the term named after the similarity between transcription and cell cycle, and represents the entire process of transcription. Like cell cycle, transcription cycle is spatiotemporally controlled by external stimuli, and there are a number of checkpoints whose defects often result in developmental disorders or cancers. Moreover, some regulators indeed control both of these processes. Thus, cell cycle and transcription cycle are likely to support the basis for living organisms in a coordinated manner.

【Term of Project】 FY2012-2016

【Budget Allocation】 1,198,300 Thousand Yen

【Homepage Address and Other Contact Information】

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