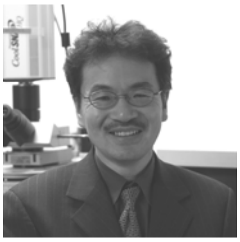

Title of Project : Systematical studies of chromosome adaptation

Term of Project : FY2010-2014

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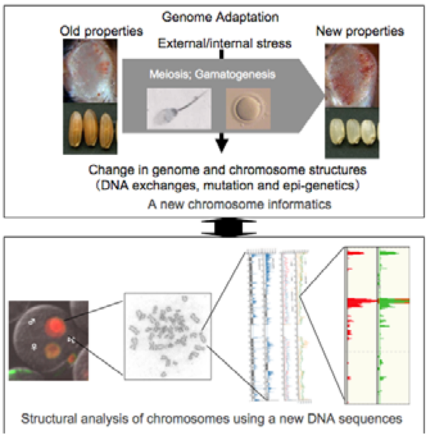
【Purpose of the Research Project】

"Genome adaptation" is defined as phenomenon which generates diversity in phenotypes or properties of a single organism with homogeneous genome. In order to understand the genome adaptation in a systematic way, this project aims to reveal (1) mechanism in which variation of genome generated by genome drift such as recombination and mutation is inherited into next generation (2) mechanism in which chromosomal alternation induced by external or internal stress is propagated and maintained in a organism in short or long terms. Furthermore, (3) we will develop systematical approaches to reveal fine time-scale chromosomal dynamics by modeling using raw data and systematic multi-task comparison



【Content of the Research Project】

We will set three research areaes to aim understanding of genome adaptation in a systematic way. In area (1), we will study molecular relationship of recombination and chromosome changes during meiosis with genome adaptation (Shinohara, Osaka U.), molecular mechanism of mating type switching in the fission yeast, which is connected with genomic imprinting and hetero-chromatin as a model of genome adaptation (Iwasaki, TITEC) as well as ability of cells to adapt drastic chromosomal change induced by rearrangement of chromosome such as deletion of kinetochores (K. Ishii, Osaka U.). In area (2), we will analyze molecular mechanism which generates genome adaptation by external stress such as heat (S. Ishii, RIKEN), domestification mechanism of rice (Izawa) and adaptation mechanisms in fertilized egg as well as male and female gamates (Okada Kyoto U.). In area (3), we will try to understand dynamics of chromosomes based on systematical approaches of binding profile/distributions of proteins involved in chromosomal functions and modifications of proteins such as histones. Furthermore, we will try to develop more precise methods to analyzed the distribution of proteins on genomes of complicated organisms such as human, mouse and fly (Itoh TITEC; Shirahige U. Tokyo).Data mining as well as modeling of alternation of genome will be complementary approach to understand the genome adaptation.

【Expected Research Achievements】

This research project will establish a novel concept of "genome adaptation". In this project, we will establish systematical method to reveal dynamics of proteins on chromosomes and may foster a new field in genome informatics. In addition, our area may help us understand diseases which generate various symptom even with a single genetic alternation. Furthermore, we can develop a systematic approach to generate new domestic animals and plants.

【Key Words】

Genome adaptation; phenomenon which generates diversity in phenotypes or properties of a single organism with homogeneous genome.

【Homepage Address】

http://genome-adaptation.bio.titech.ac.jp