A Novel Genomic Approach for the Understanding of the Structure and Function of Chromosomes

Katsuhiko Shirahige

(Tokyo Institute of Technology, Center for Biological Resources and Informatics, ssociate Professor)

Coutline of survey

The goal of this proposal is to build up an analytical system to understand the structure and function of the chromosome (i.e. replication, recombination, repair, and partition) through a genomic approach. Our genomic approach (ChIP-chip technology; Chromatin Immuno-precipitation combined with DNA chip technology) has made us to know how protein-DNA interactions are actually integrated into the chromosome functions, and how each function is connected to make a huge network for the faithful maintenance of genome. We will explore dynamic aspects of chromosomal behavior in two yeast species (Saccahromyces cerevisiae and Schizosaccharomyces pombe) at the whole genome level by the ChIP-chip technique, and newly develop an algorithm to investigate the correlation among protein binding profile maps. The system we develop will tell us not only the molecular basis of functional elements on eukaryotic chromosomes (replication origins, cohesin sites, centromeres and so on.), but also how these functional elements are organized to construct the flexible and dynamic chromosome structure. Moreover, comparison of the two yeast genomes differing in chromosome size in more than 10 folds should tell us how molecular requirements for the maintenance of chromosome will be variable depending on size and complexity of the chromosome.

Expected results

An entirely new picture for the molecular basis of chromosome structure and dynamics (will be revealed). (The analytical system constructed in this study will be easily expanded to the analysis of the molecular behavior of chromosomes of higher eukaryotes including human.

[References by the principal researcher **]**

• Y.Katou,K.Kaneshiro,H.Aburatani,and K. Shirahige.Genomic Approach for the Understanding of Dynamic Aspect of Chromosome Behavior. METHODS IN ENZYMOLOGY, Vol.409, Chapter 23, pp389-410, (2006)

• Y. Katou, Y. Kanoh, M. Bando, H. Noguchi, H. Tanaka, T. Ashikari, K. Sugimoto, and K. Shirahige: S-phase checkpoint proteins Tof1 and Mrc1 form a stable replication pausing complex. Nature, 424, 1078-1083, (2003)

• A. Lengronne, Y. Katou, S. Mori, S. Yokobayashi, G. Kelly, T. Itoh, Y. Watanabe, **K. Shirahige***, and F. Uhlmann* (*equally contributed author): Cohesin relocation from sites of chromosomal loading to places of convergent transcriptions. **Nature**, 430, 573-578 (2004)

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[Homepage address] <u>http://shirahigelab.bio.titech.ac.jp/</u>	