CDB SEMINAR

Bungo Akiyoshi

Department of Biochemistry, University of Oxford, Oxford, UK

Tuesday, August 6, 2013

16:00~17:00 C1F Auditorium

Evolutionary cell biology of chromosome segregation

Summary

Faithful transmission of genetic material is essential for the survival of all organisms. Eukaryotic chromosome segregation is driven by the kinetochore, the macromolecular protein complex that assembles on centromeric DNA to capture spindle microtubules and move chromosomes. To date, kinetochores have primarily been studied in popular eukaryotes (e.g. yeasts, worms, flies, and human) that are closely related in an evolutionary timescale, and it is therefore not known whether all eukaryotes use the same segregation mechanisms. The evolutionary origin(s) of kinetochores also remains unknown. To gain insights into these questions, we work on *Trypanosoma brucei*, an experimentally-tractable kinetoplastid parasite that branched early in eukaryotic history. *T. brucei* has been shown to segregate a series of megabase, intermediate and minichromosomes. Although an intranuclear spindle is formed and kinetochore-like structures are seen via electron microscopy, not a single kinetochore component has been identified in kinetoplastids and the segregation mechanism remains unclear.

To reveal the mechanism of chromosome segregation in *T. brucei*, we performed a localization-based screening and proteomics approach, leading to the identification of 19 proteins that show dynamic localization patterns expected for kinetochore proteins. Consistent with this, RNAi-mediated knockdown results in severe chromosome mis-segregation. These proteins are well conserved among kinetoplastids (e.g. *T. cruzi, Leishmania,* and *Bodo saltans*). However, they bear no detectable homology to kinetochore proteins in other eukaryotes, raising a possibility that kinetoplastids use a chromosomal segregation mechanism involving novel components. We are currently studying the mechanism of how these unique proteins interact with DNA and spindle microtubules. By understanding the segregation mechanism in this evolutionarily distant eukaryote, we aim to reveal both fundamental and species-specific features of chromosome segregation in all living organisms.

Host:
Tomoya Kitajima
Chromosome Segregation, CDB
tkitajima@cdb.riken.jp
Tel:078-306-3346
(ext:4447)