【Grant-in-Aid for Transformative Research Areas（B）】

EvoCytology

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Project Information	Project Number : 26B301　Project Period (FY) : 2026-2028 Keywords : Chromosomes; Sex chromosomes; Genome evolution; Cytology; Meiosis

Purpose and Background of the Research

●Outline of the Research

Background: Life has persisted on Earth by transmitting genetic information to the next generation through germ cells (sperm and eggs), while accumulating changes that drive evolution. Evolution is driven by changes in DNA, the blueprint of living organisms, which generate new traits. Previous studies have mainly inferred evolutionary processes by comparing DNA sequences. However, recent evidence suggests that specific cellular events can directly initiate heritable changes.

For example, alterations in a single protein can cause chromosomes to become abnormally fused. Errors in chromosome segregation during meiosis can also result in the loss of sex chromosomes and loss of sexual dimorphism. These events may represent key triggers of evolutionary transitions.

Objective: This study aims to directly investigate cellular events that trigger evolution using advanced microscopy techniques and genetic manipulation. By experimentally examining these evolutionary events, this research seeks to reveal how evolutionary change arises at the cellular level.

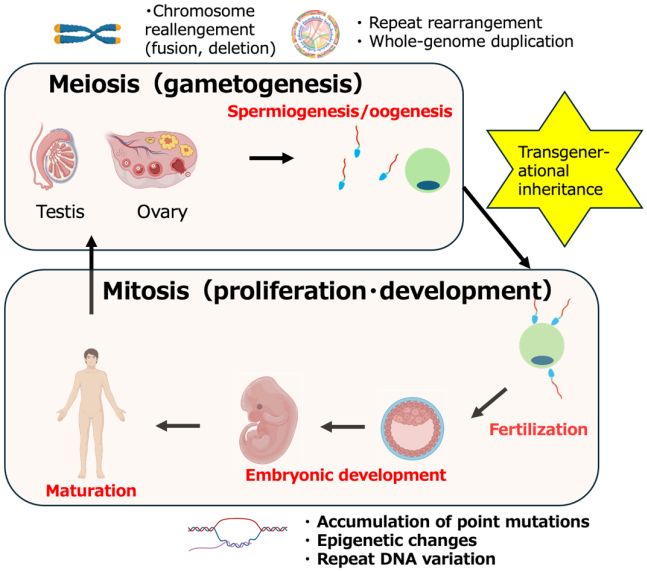

Figure. Evolutionary Cytology: Changes in DNA and epigenetic states across the life cycle are transmitted through germ cells to the next generation, driving evolution. This field seeks to understand evolutionary processes from a cell biological perspective.

Expected Research Achievements

●Project①【Regulation of Chromosome Ends during Meiosis】

①**Hiroki Shibuya**
RIKEN・BDR

Infertility affects approximately 15% of couples worldwide, and abnormalities in meiosis—the specialized cell division that produces sperm and eggs—are a major cause. The telomere-associated protein **TERB1** plays a critical role by linking telomeres to the nuclear membrane and promoting proper pairing and segregation of homologous chromosomes. However, the mechanism linking DNA to the nuclear membrane remains unclear, as do the long-term consequences of such abnormalities across generations. This study aims to elucidate this mechanism using advanced microscopy and genetic manipulation, providing new insights into the causes of infertility and chromosome evolution.

●Project②【Cytological validation of sex chromosome evolution】

②**Yukiko Yasui**
Tohoku Univ.

Sexual reproduction ensures genetic diversity and the modes of sex determination and their underlying molecular mechanisms are highly diverse. In this study, we focus on genomic events associated with transitions in sexual systems in liverworts, which determine sex in the haploid generation. Recent studies have revealed that, during multiple independent transitions from dioicy to monoicy in liverworts, the male sex chromosome is retained whereas the female one is lost. Based on the hypothesis that aberrant segregation of sex chromosomes during meiosis has driven these transitions, we aim to elucidate the mechanisms of sex chromosome segregation in liverworts and to experimentally recapitulate the transition from dioicy to monoicy.

● Project③　【Evolution driven by sequence changes at chromosome ends】

③**Junko Kanoh**
The Univ. of Tokyo

Adjacent to telomeres at chromosome ends lie regions known as subtelomeres. These regions contain many genes, some associated with human diseases, and are highly prone to variation. However, the mechanisms driving subtelomeric DNA changes during evolution remain largely unknown. In this study, we aim to address these questions by "reconstructing biological evolution in the laboratory." Specifically, we will investigate how subtelomeric DNA changes alter chromatin structure and, in turn, affect gene expression and organismal phenotypes. This work is expected to provide new insights into diseases associated with subtelomeric regions.

● Project ④【*In situ* visualization of higher-order architectures within nuclei】

④**Reiya Taniguchi**
RIKEN・IMS

In eukaryotic cells, DNA is stored inside the nucleus, where long DNA molecules are tightly and intricately folded into characteristic architectures. Such structures are essential for DNA function and play important roles in inheritance and evolution through germ cells.

In this project, we will use cryo-electron tomography to directly visualize these DNA structures inside nuclei at nanometer resolution. Based on the structural information of these higher-order architectures, we aim to understand how these structures are formed, which molecules are involved, and how their failure may contribute to evolutionary changes.

Website(s)	https://evocytology.jp/