Évolution des centromères et séparation des chromosomes

Année de publication : 2017

Aruni P Senaratne, Ines A Drinnenberg (2017 Jan 22)

All that is old does not wither: Conservation of outer kinetochore proteins across all eukaryotes?

*The Journal of cell biology* : 291-293 : DOI : 10.1083/jcb.201701025

**Résumé**

The kinetochore drives faithful chromosome segregation in all eukaryotes, yet the underlying machinery is diverse across species. D’Archivio and Wickstead (2017. J. Cell Biol. https://doi.org/10.1083/jcb.201608043) apply sensitive homology predictions to identify proteins in kinetoplastids with similarity to canonical outer kinetochore proteins, suggesting some degree of universality in the eukaryotic kinetochore.

Année de publication : 2016

Ines A Drinnenberg, Steven Henikoff, Harmit S Malik (2016 Feb 16)

Evolutionary Turnover of Kinetochore Proteins: A Ship of Theseus?

*Trends in cell biology* : DOI : S0962-8924(16)00011-8

**Résumé**

The kinetochore is a multiprotein complex that mediates the attachment of a eukaryotic chromosome to the mitotic spindle. The protein composition of kinetochores is similar across species as divergent as yeast and human. However, recent findings have revealed an unexpected degree of compositional diversity in kinetochores. For example, kinetochore proteins that are essential in some species have been lost in others, whereas new kinetochore proteins have emerged in other lineages. Even in lineages with similar kinetochore composition, individual kinetochore proteins have functionally diverged to acquire either essential or redundant roles. Thus, despite functional conservation, the repertoire of kinetochore proteins has undergone recurrent evolutionary turnover.

Année de publication : 2014

Ines A Drinnenberg, Dakota deYoung, Steven Henikoff, Harmit Singh Malik (2014 Sep 24)

Recurrent loss of CenH3 is associated with independent transitions to holocentricity in insects.

*eLife* : DOI : 10.7554/eLife.03676

**Résumé**

Faithful chromosome segregation in all eukaryotes relies on centromeres, the chromosomal sites that recruit kinetochore proteins and mediate spindle attachment during cell division.
The centromeric histone H3 variant, CenH3, is the defining chromatin component of centromeres in most eukaryotes, including animals, fungi, plants, and protists. In this study, using detailed genomic and transcriptome analyses, we show that CenH3 was lost independently in at least four lineages of insects. Each of these lineages represents an independent transition from monocentricity (centromeric determinants localized to a single chromosomal region) to holocentricity (centromeric determinants extended over the entire chromosomal length) as ancient as 300 million years ago. Holocentric insects therefore contain a CenH3-independent centromere, different from almost all the other eukaryotes. We propose that ancient transitions to holocentricity in insects obviated the need to maintain CenH3, which is otherwise essential in most eukaryotes, including other holocentrics.

Année de publication : 2013

Phillip A Dumesic, Prashanthi Natarajan, Changbin Chen, Ines A Drinnenberg, Benjamin J Schiller, James Thompson, James J Moresco, John R Yates, David P Bartel, Hiten D Madhani (2013 Feb 19)

Stalled spliceosomes are a signal for RNAi-mediated genome defense.

Cell : 957-68 : DOI : 10.1016/j.cell.2013.01.046

Résumé

Using the yeast Cryptococcus neoformans, we describe a mechanism by which transposons are initially targeted for RNAi-mediated genome defense. We show that intron-containing mRNA precursors template siRNA synthesis. We identify a Spliceosome-Coupled And Nuclear RNAi (SCANR) complex required for siRNA synthesis and demonstrate that it physically associates with the spliceosome. We find that RNAi target transcripts are distinguished by suboptimal introns and abnormally high occupancy on spliceosomes. Functional investigations demonstrate that the stalling of mRNA precursors on spliceosomes is required for siRNA accumulation. Lariat debranching enzyme is also necessary for siRNA production, suggesting a requirement for processing of stalled splicing intermediates. We propose that recognition of mRNA precursors by the SCANR complex is in kinetic competition with splicing, thereby promoting siRNA production from transposon transcripts stalled on spliceosomes. Disparity in the strength of expression signals encoded by transposons versus host genes offers an avenue for the evolution of genome defense.