Année de publication : 2017

Ines A Drinnenberg, Bungo Akiyoshi (2017 Aug 26)

Evolutionary Lessons from Species with Unique Kinetochores.

Progress in molecular and subcellular biology : 111-138 : DOI : 10.1007/978-3-319-58592-5_5

Résumé

The kinetochore is the multi-protein complex that drives chromosome segregation in eukaryotes. It assembles onto centromeric DNA and mediates attachment to spindle microtubules. Kinetochore research over the last several decades has been focused on a few animal and fungal model organisms, which revealed a detailed understanding of the composition and organization of their kinetochores. Yet, these traditional model organisms represent only a small fraction of all eukaryotes. To gain insights into the actual degree of kinetochore diversity, it is critical to extend these studies to nontraditional model organisms from evolutionarily distant lineages. In this chapter, we review the current knowledge of kinetochores across diverse eukaryotes with an emphasis on variations that arose in nontraditional model organisms. In addition, we also review the literature on species, in which the subcellular localization of kinetochores has changed from the nucleoplasm to the nuclear membrane. Finally, we speculate on the organization of the chromosome segregation machinery in an early eukaryotic ancestor to gain insights into fundamental principles of the chromosome segregation machinery, which are common to all eukaryotes.

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.

Année de publication : 2011

Douglas A Bernstein, Valmik K Vyas, David E Weinberg, Ines A Drinnenberg, David P Bartel, Gerald R Fink (2011 Dec 17)

Candida albicans Dicer (CaDcr1) is required for efficient ribosomal and spliceosomal RNA maturation.

Proceedings of the National Academy of Sciences of the United States of America : 523-8 : DOI : 10.1073/pnas.1118859109

Résumé

The generation of mature functional RNAs from nascent transcripts requires the precise and coordinated action of numerous RNAs and proteins. One such protein family, the ribonuclease III (RNase III) endonucleases, includes Rnt1, which functions in fungal ribosome and spliceosome biogenesis, and Dicer, which generates the siRNAs of the RNAi pathway. The recent discovery of small RNAs in Candida albicans led us to investigate the function of C. albicans Dicer (CaDcr1). CaDcr1 is capable of generating siRNAs in vitro and is required for siRNA generation in vivo. In addition, CaDCR1 complements a Dicer knockout in Saccharomyces castellii, restoring RNAi-mediated gene repression. Unexpectedly, deletion of the C. albicans CaDCR1 results in a severe slow-growth phenotype, whereas deletion of another core component of the RNAi pathway (CaAGO1) has little effect on growth, suggesting that CaDCR1 may have an essential function in addition to producing siRNAs. Indeed CaDcr1, the sole functional RNase III enzyme in C. albicans, has additional functions: it is required for cleavage of the 3′ external transcribed spacer from unprocessed pre-rRNA and for processing the 3′ tail of snRNA U4. Our results suggest two models whereby the RNase III enzymes of a fungal ancestor, containing both a canonical Dicer and Rnt1, evolved through a series of gene-duplication and gene-loss events to generate the variety of RNase III enzymes found in modern-day budding yeasts.

Ines A Drinnenberg, Gerald R Fink, David P Bartel (2011 Sep 17)

Compatibility with killer explains the rise of RNAi-deficient fungi.

Science (New York, N.Y.) : 1592 : DOI : 10.1126/science.1209575

Résumé

The RNA interference (RNAi) pathway is found in most eukaryotic lineages but curiously is absent in others, including that of Saccharomyces cerevisiae. We show that reconstituting RNAi in S. cerevisiae causes loss of a beneficial double-stranded RNA virus known as killer virus. Incompatibility between RNAi and killer viruses extends to other fungal species in that RNAi is absent in all species known to possess double-stranded RNA killer viruses, whereas killer viruses are absent in closely related species that retained RNAi. Thus, the advantage imparted by acquiring and retaining killer viruses explains the persistence of RNAi-deficient species during fungal evolution.