

## Évolution des centromères et séparation des chromosomes

Année de publication : 2020

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Senaratne AP, Muller H, Fryer KA, Kawamoto M, Katsuma S and Drinnenberg IA (2020 Jul 10)

### **Formation of the CenH3-deficient holocentromere in Lepidoptera avoids active chromatin**

*Current Biology, in press and bioRxiv* : [DOI : 10.1101/2020.07.09.193375](https://doi.org/10.1101/2020.07.09.193375)

#### Résumé

Cortes-Silva N, Ulmer J, Kiuchi T, Hsieh E, Cornilleau G, Ladid I, Dingli F, Loew D, Katsuma S and Drinnenberg IA (2020 Feb 24)

### **CenH3-independent kinetochore assembly in Lepidoptera requires CENP-T**

*Current Biology* : 30(4):561-572 : [DOI : 10.1016/j.cub.2019.12.014](https://doi.org/10.1016/j.cub.2019.12.014)

#### Résumé

Dispatch: Navarro AP and Cheeseman IM (2020 Feb 24)

### **Chromosome Segregation: Evolving a Plastic Chromosome-Microtubule Interface**

*Current Biology* : 30(4):R174-R177 : [DOI : 10.1016/j.cub.2019.12.058](https://doi.org/10.1016/j.cub.2019.12.058)

#### Résumé

Année de publication : 2019

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Drinnenberg IA, Berger F, Elsässer SJ, Andersen PR, Ausió J, Bickmore WA, Blackwell AR, Erwin DH, Gahan JM, Gaut BS, Harvey ZH, Henikoff S, Kao JY, Kurdistani SK, Lemos B, Levine MT, Luger K, Malik HS, Martín-Durán JM, Peichel CL, Renfree MB, Rutowicz K, Sarkies P, Schmitz RJ, Technau U, Thornton JW, Warnecke T, Wolfe KH (2019 Sep 26)

### **EvoChromo: towards a synthesis of chromatin biology and evolution**

*Development* : vol. 146 no. 19 : [DOI : 10.1242/dev.178962](https://doi.org/10.1242/dev.178962)

#### Résumé

Héloïse Muller, José Gil, Jr, Ines A Drinnenberg (2019 Jun 11)

### **The Impact of Centromeres on Spatial Genome Architecture**

*Trends in Genetics* : 35 : 565-578 : [DOI : 10.1016/j.tig.2019.05.003](https://doi.org/10.1016/j.tig.2019.05.003)

#### Résumé

The development of new technologies and experimental techniques is enabling researchers

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to see what was once unable to be seen. For example, the centromere was first seen as the mediator between spindle fiber and chromosome during mitosis and meiosis. Although this continues to be its most prominent role, we now know that the centromere functions beyond cellular division with important roles in genome organization and chromatin regulation. Here we aim to share the structures and functions of centromeres in various organisms beginning with the diversity of their DNA sequence anatomies. We zoom out to describe their position in the nucleus and ultimately detail the different ways they contribute to genome organization and regulation at the spatial level.

**Année de publication : 2018**

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Antoine Molaro, Ines A Drinnenberg (2018 Aug 3)

### **Studying the Evolution of Histone Variants Using Phylogeny**

*Histone Variants* : 273-291 : [DOI : 10.1007/978-1-4939-8663-7\\_15](https://doi.org/10.1007/978-1-4939-8663-7_15)

#### **Résumé**

Histones wrap DNA to form nucleosomes that package eukaryotic genomes. Histone variants have evolved for diverse functions including gene expression, DNA repair, epigenetic silencing, and chromosome segregation. With the rapid increase of newly sequenced genomes the repertoire of histone variants expands, demonstrating a great diversification of these proteins across eukaryotes. In this chapter, we are providing guidelines for the computational characterization and annotation of histone variants. We describe methods to predict the characteristic histone fold domain and list features specific to known histone variants that can be used to categorize newly identified histone fold proteins. We continue describing procedures to retrieve additional related histone variants for comparative sequence analyses and phylogenetic reconstructions to refine the annotation and to determine the evolutionary trajectories of the variant in question.

**Année de publication : 2017**

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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](https://doi.org/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

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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](https://doi.org/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**

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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](https://doi.org/10.1016/j.tcb.2016.02.001)

#### **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**

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

### **Recurrent loss of CenH3 is associated with independent transitions to**

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### holocentricity in insects.

eLife : [DOI : 10.7554/eLife.03676](https://doi.org/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

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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](https://doi.org/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

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Douglas A Bernstein, Valmik K Vyas, David E Weinberg, Ines A Drinnenberg, David P Bartel,

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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](https://doi.org/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](https://doi.org/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.