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Kinetochores and disease: keeping microtubule dynamics *in check!*

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Abstract

The essential role of microtubules in cell division has long been known. Yet the mechanism by which microtubule attachment to chromosomes at kinetochores is regulated has only been recently revealed. Here, we review the role of kinetochore-microtubule (kMT) attachment dynamics in the cell cycle as well as emerging evidence linking deregulation of kMT attachments to diseases where chromosome mis-segregation and aneuploidy play a central role. Evidence indicates that the dynamic behavior of kMTs must fall within narrow permissible boundaries, which simultaneously allow a level of stability sufficient to establish and maintain chromosome-microtubule attachments and instability, which permits error correction required for accurate chromosome segregation.

Introduction

Microtubules are a major component of the cytoskeleton [1,2]. Functions of microtubules range from intracellular transport, cellular motility, structural support, chromosome segregation and cell division [1]. Defects in microtubule function or structure leads to a range of cellular dysfunction and disease with the severity depending on the nature of the defect. For instance, in patients with Chédiak-Higashi, cellular microtubules have a subtle defect in microtubule polymerization [3]. This defect impairs phagocytosis in neutrophils leading to recurrent pyogenic infections, it also impairs melanosome transport in melanocytes, leading to partial albinism, and these patients also suffer from peripheral neuropathy as a result of axonal defects [4]. Understanding the dynamic nature of mitotic microtubules in cancer however has been underappreciated, despite the fact that microtubules constitute a longstanding, important, and effective drug target for cancer treatment [5]. Recent work is uncovering an important relationship between microtubule dynamics in mitosis and chromosomal instability (CIN) [6,7]. CIN, which constitutes increased rates of chromosome mis-segregation, is thought to play an important role in cancer progression, adaptation, and drug resistance [8-10].

Microtubule behavior in mitosis

Microtubules are not static polymers of tubulin subunits but they are in a state of constant polymerization and depolymerization through addition and loss of tubulin subunits from the polymer's ends. This growth and shrinkage behavior has been termed “dynamic instability”

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[11,12] and it confers to microtubules the ability to adapt to diverse functions, which require precise spatial and temporal coordination. Strikingly, the dynamic behavior of microtubules is vastly different based on the cell type and the phase of the cell cycle. For instance, in differentiated neurons, axonal microtubules turnover with a half-life of several days [13]. In contrast, microtubules in dividing cells polymerize and depolymerize so rapidly that their half-lives range from seconds to minutes [14]. Recent work suggests that the precise regulation of the dynamic behavior of microtubules is just as important to proper functioning as the structural integrity of microtubules themselves [15]. It was demonstrated that proper cell division and faithful chromosome segregation are meticulously sensitive to minor perturbation in microtubule stability [6,7]. This vulnerability appears to stem from the nature in which chromosomes attach to microtubules at kinetochores. In early mitosis, highly dynamic microtubules search and capture kinetochores and, in human cells, each kinetochore binds 20-25 microtubules [16]. Each kinetochore must bind microtubules emanating from a single spindle pole if the attached chromosome is to properly segregate during anaphase. Yet at kinetochores, microtubules constantly attach and detach. On average, individual microtubules are released from kinetochores every 10-20 seconds and new ones reattach [6]. Such dynamic behavior is error prone as occasionally microtubules emanating from one spindle pole could attach erroneously to a kinetochore that is mostly connected to microtubules from the opposite spindle pole [17-19]. These errors are called merotelic attachments and if left uncorrected prior to anaphase they will impair the proper movement of chromosome segregation and lead to increased probability of mis-segregation [17-19]. The consequence of merotely is lagging chromosomes in anaphase, which were shown to be the primary mechanism of chromosomal instability (CIN) in cancer cell lines [7,20]. Understanding the precise regulation of microtubule dynamics in mitosis has become an emerging focus in recent years due to its importance in the progression as well as fidelity of cell division.

Regulation of microtubule dynamics at kinetochores

Kinetochores are macromolecular organelles formed of ~100 proteins [21,22], many of which have been identified as important regulators of kinetochore-microtubules (kMT) dynamics [23]. Most notably, is the aurora kinase B (aurora B) and protein phosphatase 1 (PP1) [24-26]. Aurora B is localized to the centromeric region between sister kinetochores. From there, it can directly phosphorylate kinetochore components by forming an activity gradient that decays in the direction of kinetochores [27,28]. Inhibition of aurora B dramatically increases kMT stability. kMT half-lives in the presence of the aurora kinase inhibitor, hesperadin, increases from ~2-5 minutes to ~200-700 minutes [24]. Conversely, mislocalizing an active form of aurora B closer to kinetochores appears to perpetually destabilize microtubule attachments [28]. A major mechanism by which aurora B acts on kinetochore-microtubule attachments is through its phosphorylation of the outer kinetochore protein *hec1*, a component of the conserved Ndc80 complex [29]. In cells transfected with *hec1* phosphorylation-resistant mutants, kMT stability mimics these in cells where aurora B is pharmacologically inhibited. On the other hand, PP1 localizes to kinetochores where it potentially antagonizes the actions of aurora B [25,26]. Inhibition of PP1 was shown to increase aurora B activity [30]. This simple relationship however is far from sufficient to explain the precise spatial and temporal regulation of kMTs. Many of the approximately 100 kinetochore proteins play a role in regulating kMT attachments [16]. Furthermore, the attachment stability of microtubules at kinetochores is cell cycle dependent. In early mitosis, while kinetochores are not yet firmly attached to the mitotic spindle, kMT are relatively unstable with a half-life of ~2min [7,29]. As chromosomes align along the metaphase plate and the spindle matures, kMT stability increases 2-3 fold. These subtle changes in microtubule stability are unaccounted for by the all-or-none effects of the aurora B/PP1 axis

indicating that other kinetochore components participate in the subtle temporal control of kMT dynamics.

Many kinetochore proteins have been recently identified as important regulators microtubule attachment. An incomplete list includes Kif2b, MCAK, ska1, CLASP, astrin, nuf2, CenpE, CenpH, CenpF, CenpS, Cep57, HURP, SKAP, and Kif18a [7,15,31-43]. The magnitude of the effect of most of these proteins on kMT dynamics is much smaller than that of aurora B and hec1 and studies on various kinetochore components reveal that the function of kinetochores goes far beyond the simple act of their attachment to microtubules.

Work on kinetochore proteins, astrin, Kif2b and CLASPs recently provided important evidence supporting the precise regulation of kinetochores to their attached microtubules [15,38]. Most important was the temporal nature of this regulation whereby different proteins were recruited to kinetochores at different stages of mitosis to regulate microtubule dynamics. During prometaphase CLASP proteins recruit Kif2b – a kinesin-13 protein that depolymerizes microtubules – where it promotes the release of kMTs. On the other hand, as chromosomes align along the metaphase plate, Kif2b is replaced by astrin, which also binds CLASP proteins and in turn increases kMT stability. Interestingly, the presence of Kif2b and astrin on kinetochores was always mutually exclusive and their localization appears to be a response to aurora B activity and tension between sister-kinetochores. It was also shown that other kinetochore proteins, such as Kif18a, may act through the CLASP/astrin/Kif2b network suggesting the presence of a central, temporally regulated, molecular network at kinetochores that serves to integrate inputs from a plethora of kinetochore proteins to influence kMT dynamics [15,44-47].

Narrow permissible window of kMT dynamics

A striking feature of the CLASP/astrin/Kif2b network is the small magnitude by which it affects kMT stability. Whereas aurora B and Hec1 perturbation can influence stability by 100-200-fold [24,29], perturbation of either Kif2b or astrin only affects kMT turnover by 2-4 folds [6,7]. This relatively minor perturbation does not abrogate the physical attachment of kinetochores to microtubules however it has profound consequences on the progression and fidelity of cell division. Small reductions in kMT stability were sufficient to maintain spindle assembly checkpoint (SAC) signaling and delay or prevent the onset of anaphase. On the other hand, minor increases in kMT stability lead to the persistence of kMT microtubule attachment errors into anaphase, which in turn led to chromosome mis-segregation and chromosomal instability (CIN) [6,7].

The role of microtubule occupancy at kinetochores in silencing the SAC has long been appreciated [48-50]. Studies using quantitative fluorescence microscopy and electron microscopy show that kinetochores require a minimum number of attached microtubules to silence the SAC and allow anaphase onset. Decreasing kMT stability is synonymous to increasing kMT turnover or the rate of detachment of microtubules from kinetochores. At any specific time the number of microtubules attached to kinetochores is the product of the attachment and detachment rates, and subtle increases in the frequency of detachment can lead to a significant decrease in the number attached microtubules. Most perturbations that decrease the half-life of kMT by 2-fold during metaphase lead to anaphase delay [15]. Such a decrease means that individual microtubules are released from kinetochores every ~12 seconds instead of every 18 seconds [6]. It is striking that SAC signaling is maintained in conditions of unstable kMT attachments despite of chromosome alignment along the metaphase plate [15,28]. In experiments where astrin was depleted or a constitutively active aurora B was placed closer to kinetochores cells achieved full chromosome alignment but failed to progress through anaphase despite achieving typical inter-kinetochore tension

[15,28]. This demonstrates that kMT occupancy can serve as the primary regulator of the SAC signaling independent of the tension between sister-kinetochores brought about by alignment during metaphase [49], although this is a matter of continuous debate [49,51-56]. In addition, in experiments where kMT stability was prematurely increased either by inhibiting aurora B, modifying *hec1* or adding low doses of drugs that stabilize microtubules, cells prematurely underwent anaphase without achieving proper alignment of inter-kinetochore tension [57-60].

In the same way that subtle reductions in kMT stability influence cell cycle progression, minor increases in the stability of kMT attachments have a profound effect on chromosome segregation fidelity [7]. This effect is due to the stochastic nature of kinetochore microtubule interaction throughout mitosis, particularly in prometaphase [2]. As kinetochore pairs align along the mitotic spindle, they attach to microtubules emanating from opposite spindle poles. The constant and frequent attachment and release of microtubules together with the rigid centromere geometry that links sister kinetochores favor their biorientation, whereby each kinetochore of a pair is attached to only one spindle pole [6,61]. Increasing kMT stability however, means decreasing kMT release rates in such a way that if individual microtubules were improperly attached that they would remain until the onset of anaphase. Individual kinetochores that are merotelically attached are not detected by the SAC [17,18,62]. Consequently, the persistence of merotelic chromosomes into anaphase leads to a tug of war between opposing microtubules and frequently the lagging of these chromosomes in the middle of the anaphase spindles. These lagging chromosomes were shown to have a higher propensity to mis-segregate and are a common feature of cells with chromosomal instability (CIN) [20].

Examples where increasing kMT stability leads to CIN are plenty and a partial list includes depletion, inhibition, or perturbation of the following proteins: Kif2b, MCAK, *hec1*, aurora B, CLASP, APC [6,7,15,29,63]. The function of some of these proteins has been shown to be perturbed in tumors and the search is underway to find the mechanisms underlying the relationship between regulators of kMT dynamics and CIN. In human-derived cell lines, an increase of kMT by 2 to 4-fold is sufficient to induce chromosome mis-segregation. This change would increase the mean lifetime of a microtubule at kinetochores of a diploid chromosomally stable cell line (RPE1) from ~5 minutes to ~10-20 minutes or even higher [6]. This extension of attachment stability means that if a microtubule erroneously attaches to kinetochores it is likely to remain attached for that period of time before being released and this is likely not to take place prior to anaphase onset.

These findings uncover several important concepts about the process of chromosome segregation fidelity in human cells. First, at all times prior to anaphase, the rate of attachment and detachment of microtubules from kinetochores is balanced in such a way that attachment errors are corrected at sufficiently high probability before anaphase onset [6,24,64]. Second, the machinery involved in allowing for the correction of kMT attachment errors may not be sufficiently robust to withstand minor perturbations. These perturbations can either increase in attachment error rate or a decrease the correction rate [7,29,65,66]. The former was shown in cells containing multiple centrosomes where the transition from multipolar to bipolar spindles increases the formation of attachments errors and consequently lagging chromosomes [67,68]. Furthermore, transient treatment of cells with molecules that perturb spindle geometry such as monastrol or nocodazole leads to increased rates of lagging chromosomes without affecting kMT dynamics prior to anaphase. Concomitant increases in kMT stability dramatically compromises chromosome segregation fidelity whereas slightly promoting kMT turnover can increase the rate of microtubule release from kinetochores and lead to suppression of the drug treatment effects [7]. It was also shown that chromosomally unstable cancer cell lines have an inherent increase in kMT

attachment stability indicating their reduced efficiency to correct attachment errors whenever they arise [6]. Interestingly, promoting the turnover of kMT attachment in these cells was sufficient to significantly reduce the rates of lagging chromosomes and suppress CIN [7]. Thus it is evident that cancer cells exhibit defects in one or both processes of formation and correction of attachment errors [66].

Taken together, the evidence points to a narrow acceptable range for the attachment stability of kMTs (Figure 1). kMTs must be stable enough to reach full occupancy of kinetochores to satisfy the checkpoint, but sufficiently unstable to permit error correction. These narrow boundaries suggest the importance of the precise regulation of kMT attachment dynamics. In a peculiar manner, a kinetochore acts as a stabilostat for kMTs whereby stability must be appropriately maintained during all stages of mitosis (Figure 1). Phylogenetic analysis of kinesin-13 proteins from three species: humans (*Hs*), mice (*Mm*) and *Drosophila* *Melagnogaster* (*Dm*) shows that gene duplication occurred independently throughout evolution despite the fact that each has three copies of kinesin-13 gene that perform distinct function that is conserved among the three species [69] (Figure 2). This suggests that individual kinetochore proteins may not necessarily display high sequence conservation among various eukaryotes yet homologous genes have evolved to maintain the appropriate regulation of microtubules based on the requirement of the species and the number of microtubules that attach to its kinetochores.

Mosaic Variegated Aneuploidy (MVA) Syndrome

Given the tight requirements for the regulation of kMT dynamics it is expected that genetic mutations found in disease conditions may influence the kMT interface and perturb either the timely progression of the cell cycle or the fidelity of chromosome segregation process. Such an example is Mosaic Variegated Aneuploidy (MVA), which is a rare autosomal recessive syndrome associated with various trisomies and monosomies involving different chromosomes and tissues [70]. It causes severe intrauterine growth retardation, microcephaly, dysmorphism, and most importantly, increased risk of malignancy such as rhabdomyosarcoma, Wilms tumors, and leukemia [71-73]. MVA can be caused by mutations in BubR1 (encoded by Bub1B) as patients harbor two mutant alleles and are compound heterozygotes. BubR1 is a serine/threonine kinase that phosphorylates important SAC proteins and is thought to be necessary to maintain SAC signaling [74,75]. Thus, it is reasonable to suggest that MVA is caused by defects in the SAC [76,77]. It was postulated that sister chromatids lost cohesion prematurely, well before sister kinetochores were able to bi-orient and establish sufficiently stable attachments with microtubules. However, BubR1 is also known to be involved in regulating kMT dynamics and its depletion leads to unstable kMT attachments [78]. This finding together with the observation that in some patients with MVA many sister chromatids do not prematurely separate [71,74,79], suggest that kMT attachment dynamics may play an important role in the pathogenesis of MVA. This hypothesis is further supported by the finding that mutations in Cep57, a kinetochore and centrosomal protein involved in stabilizing kinetochore microtubules [40,41,80], is found in some patients with MVA [81]. It is thus reasonable to postulate that deregulated kMT attachments may have a role in MVA and there may be many molecular etiologies given the complexity of the kMT interface.

Kinetochore microtubule dynamics in cancer

In contrast to the inherited condition of MVA, most tumors arise due to the accumulation of somatic mutations. The effect of individual gene mutations on kMT dynamics is largely an unexplored field [82], however given the complexity of the kMT interface, it is possible that many of these mutations either directly or indirectly influence kMT stability. Many proteins

were shown to be overexpressed in cancer with the putative consequence of increasing kMT stability. Examples include CenpH, Cyclin E, Hec1/Ndc80 complex, and MCT-1 [83-88]. Conversely, other proteins were shown to be mutated, deleted, or underexpressed such as APC, beta catenin, pRB, and BRCA1 [6,89-93]. It is unclear however if these genes are initial triggers of chromosome mis-segregation and CIN or if they simply act by exacerbating mis-segregation rates after the onset of CIN. Furthermore, genetic analysis of CIN may be complicated by the fact that after the initial chromosome mis-segregation event, the levels of hundreds to thousands of proteins encoded by the mis-segregated chromosome would be disturbed [6,82,94]. This would lead to a significant imbalance in the ratio of proteins that either stabilize or destabilize kMT attachments. Such an imbalance may by itself lead to further mis-segregation events given the narrow permissible boundaries of kMT dynamics, in such a way that CIN may be a self-propagating event [6]. This hypothesis is testable and would lead to an important insight into the progression of CIN. Preliminary work on cancer cell lines with CIN demonstrates that each has a unique set of ratios of microtubule stabilizers and destabilizers suggesting that this imbalance could both be the consequence as well as the continuous driver for chromosome mis-segregation.

Concluding remarks

When put together, recent data in the field indicate that, during cell division, microtubule dynamics is a finely and temporally regulated process whereby the stability of kMT attachments must be constrained within a defined narrow window that is permissible for faithful mitotic progression. Decreasing kMT stability leads to cell cycle arrest whereas increasing their stability directly leads to chromosome segregation defects. Furthermore, cancer cells are either less efficient in correcting attachment errors or possess defects which lead to increased formation of these errors, necessitating a compensatory increase in the correction machinery. Thus, in theory, it is possible to exploit microtubule dynamics during mitosis to influence the progression of cell division. A targeted approach could either reduce the stability of the attachment for the purpose of halting cell division or reducing the rates of chromosome mis-segregation in an effort to reduce cancer's ability to adapt to the microenvironment or chemotherapeutic drugs. The advantage of such targeted therapy is the exquisite sensitivity of mitotic cells to minor perturbation of microtubules, which might spare novel drugs from the dose-limiting and neurotoxic side-effect exhibited by the widely used taxane class of anti-microtubule drugs.

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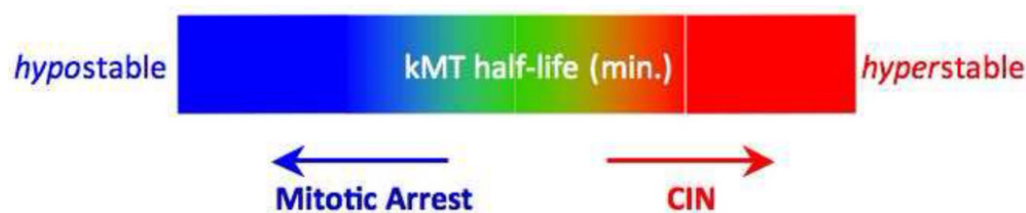


Figure 1.

Kinetochore-microtubule stabilostat model. Kinetochore-microtubules (kMT) attachment stability is regulated in a narrow range for high fidelity chromosome segregation. Hypostable kMT attachments fails to adequately satisfy the spindle assembly checkpoint leading to mitotic delay or arrest. Hyperstable kMT attachments lose efficient error correction with the consequence being the persistence of attachment errors in anaphase and an increase in chromosome mis-segregation leading to chromosomal instability (CIN).

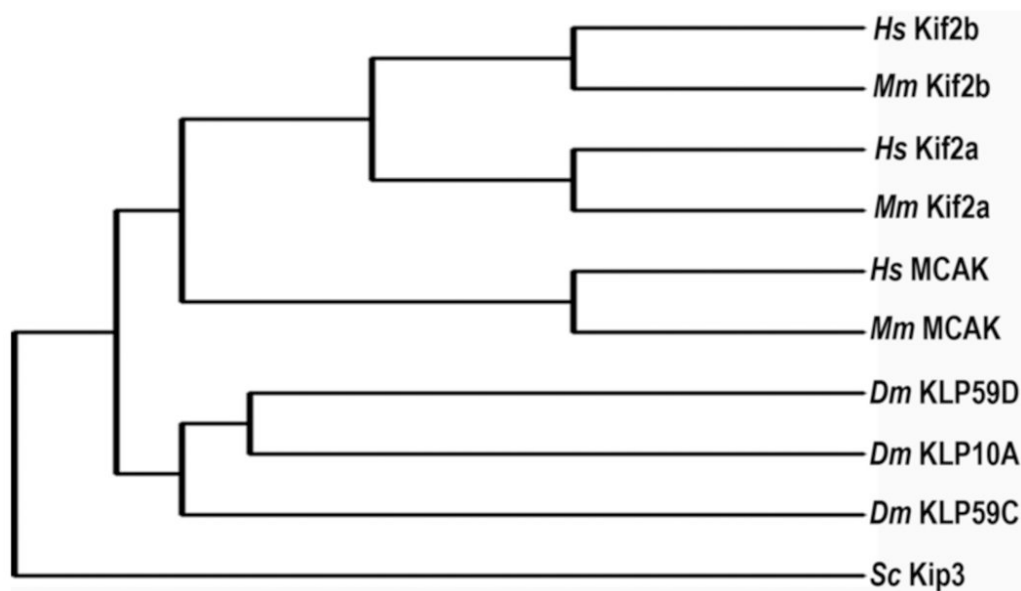


Figure 2. Phylogenetic comparison of kinesin-13 genes. Amino acid sequences from three kinesin-13 proteins encoded by fruit fly (Dm), mouse (Mm), and human (Hs) are compared using Clustal X. The sequence of yeast Kip3 is used as an outgroup to root the tree. Line lengths are not to scale. Reprinted from Manning et al. 2007 (<http://www.molbiolcell.org/content/18/8/2970>)