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Analyse et Modélisation de la Dynamique des Chromosomes durant la Mitose chez la Levure à Fission

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« The dream of every cell is to become two cells. »

François Jacob, 1974

Résumé

La mitose est une étape clé du cycle cellulaire, très préservée chez toutes les cellules eucaryotes, durant laquelle le matériel génétique de la cellule (les chromosomes) est séparé en deux puis réparti de manière égale dans les deux cellules filles. Cette équpartition du matériel génétique est cruciale pour le maintien de la stabilité génétique. Durant ce processus, la cellule forme une plaque métaphasique au centre du fuseau mitotique composé des chromatides sœurs. Chaque chromatide est attachée à son pôle respectif (on parle d'attachement bipolaire) vers lequel elle se dirigera durant l'anaphase.

Les chromatides sont l'unité indivisible du matériel génétique durant la mitose, à l'image des atomes dans une molécule. Initialement chacun de ces « objets » est libre (non attaché) et positionné de manière non ordonné dans le noyau. Toute la compléxité de la mitose est d'attacher chacune des chromatides au bon pôle afin d'exercer des forces sur ces derniers pour les positionner sur la plaque métaphasique au centre du fuseau avant leur séparation et migration vers les pôles durant l'anaphase.

Cette étape de la division cellulaire requiert donc non seulement un complexe réseau d'interaction et de signalisation métabolique comme dans beaucoup d'autre processus biologiques mais aussi un fin contrôle spatio-temporel du mouvement et du positionnement de ces objets de grande taille à l'échelle de la cellule: les chromatides.

Il semblerait que l'origine du mouvement des chromosomes provienne pour une grande part de la dynamique des microtubules. Ce qui est moins certain est la part relative accordée aux différents processus régulant cette dynamique; que ce soit la dynamique intrinsèque (appelé instabilité dynamique des microtubules) ou l'effet de différentes protéines sur les microtubules comme les MAPs et les kinésines. On notera par ailleurs que le mécanisme de transfert d'énergie entre la dynamique des

microtubules et le mouvement des chromosomes est encore très largement hypothétique.

La dynamique des chromosomes durant la mitose est par ailleurs largement contrôlée par un grand nombre d'acteurs autres que les microtubules. Certains d'entre eux étant responsables de l'attachement MTs-kinétochore comme les complexes NDC80 et DAM1, tandis que d'autres sont impliqués dans la régulation de la dynamique des microtubules comme la kinésine-8 et la kinésine-13.

Durant mon travail de thèse j'ai étudié la dynamique des chromosomes en mitose chez la levure à fission qui à l'avantage de conserver les mécanismes primordiaux de la mitose avec les eucaryotes supérieurs. Deux mécanismes que l'on retrouve chez de nombreuses cellules sont l'alignement des chromosomes durant la métaphase ainsi qu'un mouvement de va et vient plus ou moins régulier le long du fuseau aussi appelé oscillations des chromosomes. J'ai montré en analysant les trajectoires des chromosomes que ces deux processus sont pour une large part indépendants chez la levure à fission (article accepté). De plus le processus d'alignement des chromosomes, encore mal compris, est en parti contrôlé par la kinésine-8 via une activité dépendante de la longueur des microtubules. Il semblerait donc qu'une protéine, la kinésine-8, soit capable de fournir une information spatiale le long du fuseau mitotique afin de positionner correctement les chromosomes. Enfin j'ai utilisé un modèle mathématique du fuseau mitotique développé dans l'équipe afin de tester de manière quantitative les hypothèses de mécanisme du centrage des chromosomes par la kinésine-8.

L'ensemble de mon travail s'est donc intéressé au contrôle du mouvement, de l'attachement et du positionnement des chromosomes durant la mitose afin de mieux comprendre la biophysique du fuseau mitotique.

Summary

Mitosis is a highly preserved process in all eukaryotic cells during which genetic material (chromosomes) is divided in two parts and then spread in both daughter cells. This equipartition is crucial for maintaining genetic stability. During this process, cell forms a metaphasic plate at the center of the mitotic spindle composed of sisters chromatid. Each chromatid is attached to his respective pole (called bipolar attachment) toward which it will go during anaphase.

Chromatids are the indivisible units of genetic material during mitosis just like atoms in a molecule. Originally each of these « objects » is not attached and located without a specific order. All the complexity of mitosis is to attach each of the chromatids to the correct pole to be able to exert forces and then position them on the metaphasic plate at the center of the mitotic spindle just before their separation and migration toward the poles during anaphase.

This step of cell division not only requires complex interaction networks and metabolic signaling pathways just like many others biological processes but also a fine spatio-temporal control of the movement and positioning of these big objects relative to the cell size: the chromatids.

It would seem that the origin of chromosome movements comes largely from microtubule dynamics. What is less clear is the relative weight of the various processes regulating the movement: the intrinsic dynamic instability of microtubules or the effect of their associated proteins such as MAPs and kinesins. Note also that the energy transfer mechanism between microtubule dynamics and movement of chromosomes is still largely hypothetical.

Moreover chromosome dynamics during mitosis is largely regulated by a large number of actors other than microtubules. Some of them being responsible for the MT-kinetochore attachment such as NDC80 and DAM1 complex. While others are involved in the regulation of MT dynamic such as kinesin-8 and kinesin-13.

During my PhD work I studied chromosome dynamic during mitosis in fission yeast which has the advantage of sharing many fundamental mechanisms of symmetric division with higher eukaryotes. Two mechanisms that are found in many cells are chromosome alignment during metaphase and a back and forth movement more or less uniform along the spindle called chromosomes oscillation. By analyzing chromosomes trajectories I showed that both processes are in large part independent in fission yeast (article accepted for publication). Moreover the chromosome alignment process, still not well understood, is in part regulated by the kinesin-8 via a length dependent activity on the microtubules. This suggests that a protein, the kinesin-8, is capable of providing a spatial information along the mitotic spindle to properly position chromosomes. Finally, I used a mathematical model of the mitotic spindle, in order to test quantitatively different hypotheses about chromosome centering mechanism by the kinesin-8.

This work thus examines the control of the movement, the attachment and the positioning of chromosomes during mitosis and seeks to better understand the mitotic spindle biophysics.

Remerciements

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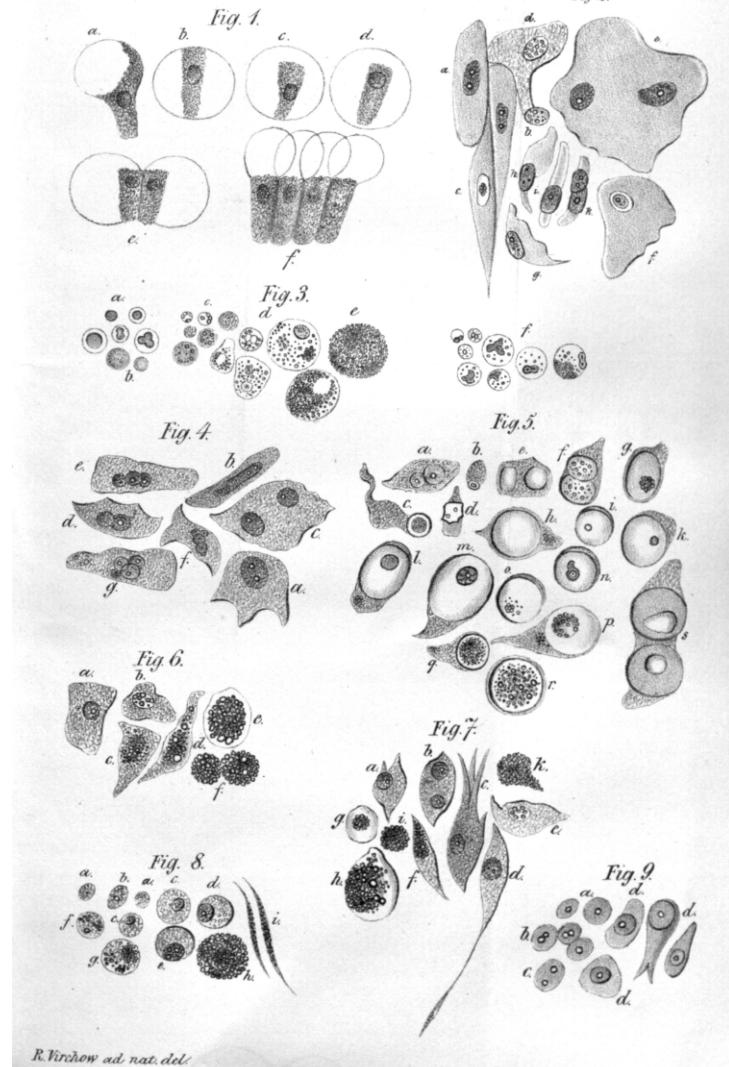
Introduction

La cellule est un objet complexe que l'Homme, depuis longtemps maintenant, essaie de comprendre. En effet c'est en 1665 que Robert Hooke, un savant anglais, observa pour la première fois au microscope des «petites unités structurelles» qu'il décrira plus tard dans un ouvrage intitulé « *Micrographia* » (Hooke, 2003). Sans vraiment réaliser la portée de son observation, il venait de découvrir la cellule.

Plus tard, au début du 19ème siècle, la théorie cellulaire apparaît; stipulant que tous les organismes sont formés de cellules. La cellule devient alors la plus petite unité indivisible qui compose le vivant.

Au milieu du 19ème siècle, un médecin allemand nommé Rudolf Virchow va alors révolutionner la théorie cellulaire (Figure 1.1) en démontrant qu'une cellule provient nécessairement d'une autre cellule (Virchow, 1860). Il écrivait alors « *Omnis cellula e cellula* » qui signifie « Toutes les cellules sont issues d'autres cellules. » Ses travaux seront ensuite confirmés par un scientifique français du nom de Louis Pasteur qui malgré de nombreuses controverses parvint à faire tomber le mythe de la génération spontanée qui stipulait que la vie pouvait naître de la matière inerte.

C'est véritablement au 20ème siècle que toute la complexité de la cellule se dévoile à nous grâce à l'apparition de nombreuses avancées technologiques tel que la découverte de l'ADN (Watson et al., 1953), l'apparition de la biologie moléculaire ainsi que la création de microscope toujours plus précis.



R. Virchow ad nat. del.

Figure 1.1: Illustration du livre « Cell theory » de Rudolf Virchow (Virchow, 1860)

Ce travail de thèse a pour objectif l'étude d'une phase tout à fait cruciale durant la vie d'une cellule: le moment où elle se divise. Cette étape, appelé la mitose, permet selon le second axiome de la théorie cellulaire, le maintien de l'intégrité cellulaire tout au long des générations.

La mitose est un domaine de recherche important pour deux raisons majeures. Mieux comprendre le fonctionnement du vivant par la compréhension de ce mécanisme primordial sans lequel la vie ne serait jamais apparue sur Terre. Ainsi que son rôle fondamentale dans la compréhension du cancer; qui n'est autre qu'un ensemble de maladie impliquant un dérèglement de la division cellulaire.

Mais avant de comprendre comment une cellule se divise, replaçons ce processus de division dans un contexte plus large qui consiste à comprendre de quoi est composée la vie d'une cellule.

1.1 La vie d'une cellule

Comme le disait François Jacob en 1974, « *The dream of every cell is to become two cells.* ». Et quand elle n'essaie pas de devenir deux cellules, elle prépare tout afin que la division se passe bien. L'ensemble de ces processus qui dictent la vie d'une cellule est un cycle qui se répète depuis longtemps maintenant : le cycle cellulaire.

Le cycle cellulaire est l'ensemble des étapes qui composent la vie d'une cellule. Cette série d'événement varie de manière considérable d'une cellule à une autre. Le cycle cellulaire dépend de l'identité de la cellule (principalement défini par son matériel génétique) ainsi que son contexte écologique; c'est à dire le milieu environnant dans lequel elle se trouve.

Malgré son incroyable diversité, on peut diviser le cycle cellulaire en deux grandes étapes communes à l'ensemble des organismes. Une étape de croissance appelé l'interphase ainsi qu'une étape de division appelé la mitose.

C'est durant l'interphase que la cellule va passer la plupart de son existence (Figure 1.2). Celle-ci est composé de plusieurs sous-étapes (Norbury and Nurse, 1992):

- une phase de croissance (**phase G1**) durant laquelle la cellule va augmenter sa taille ainsi que son volume cellulaire. C'est aussi durant cette période qu'elle va synthétiser l'ensemble des protéines spécifiques à son identité ainsi qu'en réponse au milieu dans lequel elle se trouve.

- une phase de synthèse (**phase S**) durant laquelle la cellule va répliquer son matériel génétique, l'ADN. La duplication des chromosomes est une étape crucial pour le maintien de la stabilité génétique. En effet chacun des nucléotides (allant de quelques milliers à plusieurs milliard selon le type de cellule) doit être dupliqués avec une grande précision afin que les deux cellules filles se voit transmettre la même information génétique.
- une phase de préparation de la division cellulaire (**phase G2**) durant laquelle la cellule relance la synthèse de protéine et croît rapidement afin de préparer sa division. Cette phase est importante car elle possède un système de blocage du cycle cellulaire (aussi appelé «checkpoint» ou «point de contrôle») qui permet de retarder l'entrée en mitose en cas de problème de réPLICATION de l'ADN apparu en phase S.
- la phase de division (**mitose ou phase M**) qui fait suite à l'interphase est l'étape durant laquelle la cellule se divise en deux cellules filles.



Figure 1.2: Les différentes étapes du cycle cellulaire

Il est important de souligner que dans la réalité, il existe autant de cycle cellulaire différent qu'il existe de type de cellule. Donc malgré la conservation de certains mé-

canismes primordiaux, chaque type de cellule possède son propre cycle cellulaire (Lodish et al., 2000; Norbury and Nurse, 1992).

D'une manière plus générale on peut aussi souligner que l'un des enjeux de la biologie cellulaire aujourd'hui est de comprendre quelle part des mécanismes étudiés est conservé entre différents type cellulaire et quelle part est spécifiques de l'organisme étudié.

La dernière phase du cycle cellulaire est donc la mitose, c'est à dire le moment où une cellule va devenir deux cellules.

1.2 La mitose : une étape du cycle cellulaire

La dernière étape du cycle cellulaire est la mitose. Durant cette étape la cellule mère va se diviser en deux cellules filles. Tous les mécanismes précédent et ceux composant la mitose ont pour objectif d'assurer une division intègre et égale entre les deux cellules filles.

L'entrée en mitose est un événement contrôlé en grande partie par la kinase Cdc2 aussi appelé Cdk1 (Nasmyth and Reed, 1980; Nurse and Thuriaux, 1980). Cette protéine, conservée de la levure à l'Homme, s'associe avec une protéine régulatrice, la Cycline B. Le complexe s'active alors de manière transitoire pour former le fuseau mitotique.

1.2.1 Les phases de la mitose

De manière étonnante, la mitose est un processus relativement bien conservé chez la majorité des cellules eucaryotes. Les grandes phases la composant peuvent donc être décrites de manière commune pour un grand nombre d'organismes, allant de la cellule humaine aux eucaryotes unicellulaires comme la levure.

Cette étape cruciale du cycle cellulaire est d'autant plus importante que des défauts durant le processus peuvent être à l'origine de cellule possédant un nombre défectueux de chromosomes (cellule aneuploïde). Par ailleurs on sait aussi que les cellules aneuploïdes peuvent contribuer à la formation de tumeur cancéreuse (Kops et al., 2005).

Les différentes phases de la mitose sont (Figure 1.3) :

- la **prophase** : les brins d'ADN (la chromatine) se condensent pour former des structures ordonnées et séparées les unes des autres; les chromosomes. Les deux pôles, appelé centrosome chez les eucaryotes supérieurs, se séparent et commencent à migrer vers leurs extrémités respectives afin de former le fuseau mitotique.

Note: certains fuseaux mitotiques peuvent se former sans pôles (« *acentrosomal spindle formation* » en anglais). Ce type de division très particulière n'est pas discuté dans ce travail.

- la **prométaphase** : la membrane nucléaire se désassemble dans le cas d'une mitose ouverte (Boettcher and Barral, 2013) tandis qu'elle reste intact dans les mitoses fermées (répandu chez les protistes et organismes unicellulaires). Les chromosomes s'attachent aux microtubules par l'intermédiaire d'une structure protéique qui s'assemble au même moment au niveau du centromère des chromosomes: le kinétochore.
- la **métaphase** : les chromosomes alors attachés aux pôles par l'intermédiaire des microtubules viennent alors se positionner à l'équateur de la cellule pour former la plaque métaphasique. Cette étape cruciale de la mitose possède des mécanismes de détections des chromosomes mal attachés afin de retarder le passage à l'étape suivante si besoin.

La transition métaphase/anaphase possède un point de contrôle appelé le SAC (Spindle Assembly Checkpoint) qui permet à la cellule d'arrêter la mitose en cas d'attachement incorrect (Musacchio and Salmon, 2007). L'anaphase commence au moment où le complexe Cdc2-Cyclin B s'inactive par l'activation de l'APC (Anaphase Promoting Complex). L'APC est une ubiquitin ligase capable de dégradé la Cyclin B (Sivakumar and Gorbsky, 2015).

- l'**anaphase** : durant l'anaphase A, le complexe cohésine reliant les chromatides soeurs est dabord dégradé (Oliveira et al., 2010). Ensuite chaque chromatide est «tiré» vers son pôle respectif par la dépolymérisation des microtubules qui les attachent tandis que durant l'anaphase B, le fuseau mitotique s'allonge, éloignant alors les pôles et les chromosomes loin du centre de la cellule. On notera que ces deux phases peuvent être distinctes ou pas selon le type de cellule étudié.

- la **télophase** : les microtubules attachant les kinétochores se désagrègent, les chromosomes se décondensent retournant à leurs états initiaux de brins d'ADN. L'enveloppe nucléaire se reforme dans le cas d'une mitose ouverte.
- la **cytokinèse** : à ce stade, la mitose est fini. Durant cette période, la cellule va alors se diviser grâce à la formation d'un sillon au niveau de la membrane cytoplasmique qui s'invagine jusqu'à «couper» la cellule mère en deux cellules filles.

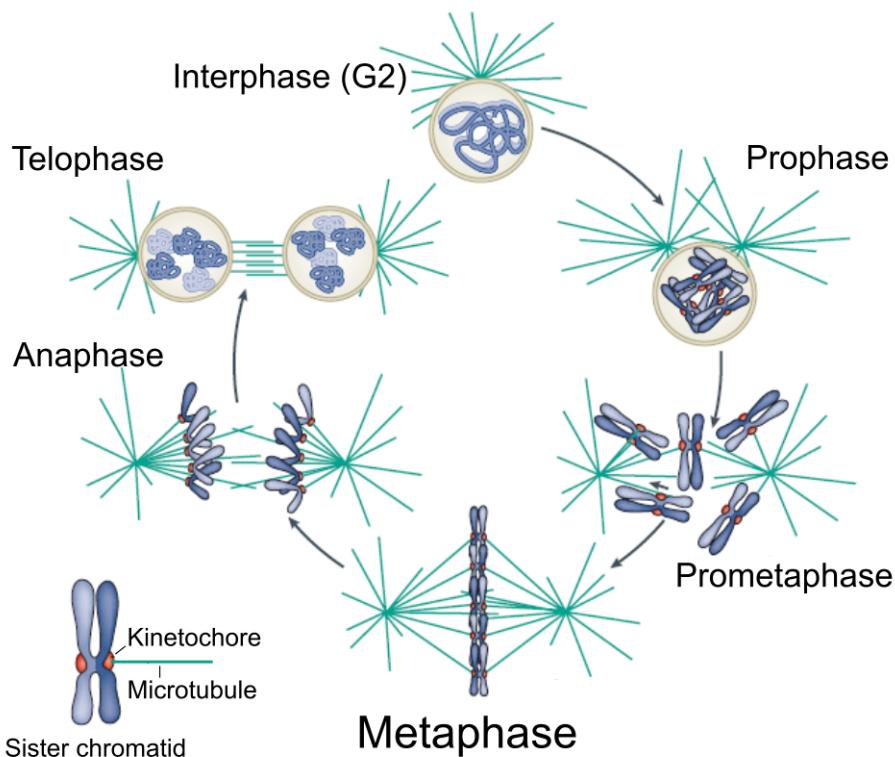


Figure 1.3: Les différentes étapes de la mitose (adapté de Cheeseman and Desai (2008))

On voit bien à travers la description des différentes étapes de la mitose que l'une des caractéristiques essentielles des chromosomes durant la mitose est leur capacité à se mouvoir dans la cellule de façon coordonnée à la fois dans le temps et dans l'espace.

Nous allons à présent voir qu'un grand nombre d'acteurs sont nécessaires afin de produire et réguler ce mouvement.

1.2.2 Le kinétochore

Le kinétochore est un assemblage de protéine de très grande taille, possédant plusieurs dizaine de type de protéines différents (jusqu'à 80 chez les cellules humaine). L'assemblage se situe sur la partie centromérique des chromatides au niveau des variants d'histone H3 (appelé CENP-A) qui aide le kinétochore à s'associer à l'ADN.

Il est composé de deux régions (Figure 1.4) :

- **la plaque interne** s'associe de manière très spécifique avec la chromatine centromérique par l'intermédiaire entre autre de l'histone CENP-A.
- **la plaque externe**, épaisse de 50 à 60nm, est responsable des interactions avec le fuseau mitotique, notamment les microtubules kinétochoriens. Cette région possède des sites d'ancrage pour les microtubules au kinétochore permettant le mouvement des chromosomes durant la mitose. Le nombre de site d'ancrage varie fortement d'une espèce à une autre allant d'une quarantaine chez l'humain à seulement un site d'attachement pour la levure (*S. cerevisiae*).



Figure 1.4: **A.** Vu d'un kinétochore humain de côté par microscopie électronique (McEwen et al. (2007)). **B.** Schéma des différentes plaques d'un kinétochore

Le kinétochore se forme durant la prométaphase et joue plusieurs rôle important. En plus d'être un acteur essentiel dans le bon déroulement du point de contrôle de la transition métaphase/anaphase (le SAC), il a aussi un rôle structurel dans l'attachement entre le chromosome et les microtubules.

TODO: EN DIRE PLUS ???

1.2.3 Les microtubules

Les microtubules sont un des constituants majeurs du cytosquelette. Ce sont des structures de forme tubulaire d'un diamètre de 20nm et d'une longueur très variable pouvant aller jusqu'à plusieurs micromètre. Ils sont formés de dimères de tubuline, eux même composé de deux sous unités, la tubuline α et la tubuline β .

La formation d'un microtubule requiert un complexe protéique qui jouera le rôle de patron de construction, constitué de la γ tubuline. Celui-ci forme un anneau permettant la disposition de chaque protofilament tel que présenté Figure 1.5A. L'extrémité + est coiffé de dimère GTP et c'est son hydrolyse en GDP qui permet l'assemblage des protofilaments.

Par ailleurs le microtubule est un polymère extrêmement dynamique dont les extrémités passent leur temps à basculer entre deux états : la polymérisation et la dépolymérisation (voir Figure 1.5B). Les deux extrémités étant chargé différemment en GTP et GDP, elle possède une dynamique plus ou moins importante. On parle d'extrémité + pour celle chargée en GTP et donc très dynamique (coiffée par la tubuline β) et d'extrémité - pour celle chargée en GDP donc moins dynamique (coiffée par la tubuline α).

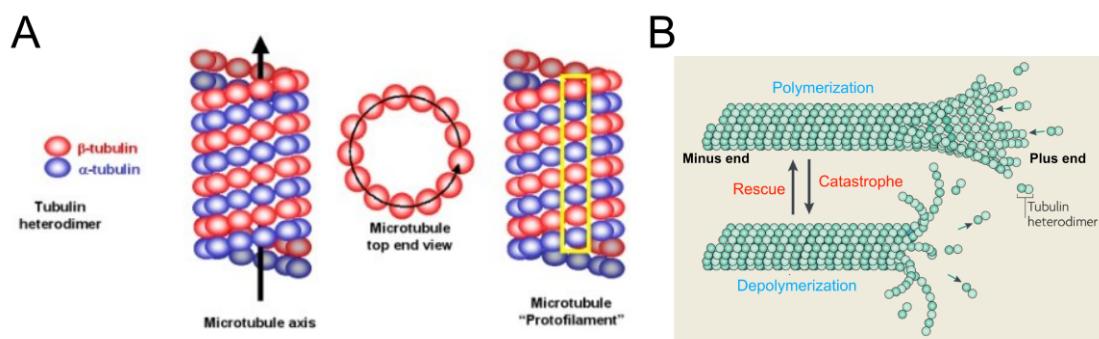


Figure 1.5: **A.** Organisation d'un microtubule (schéma de Dr. Michael Blaber). **B.** Les microtubules sont des structures hautement dynamique (Walczak et al., 2010).

Les microtubules, et d'une manière plus générale l'ensemble des protéins du cytosquelette, jouent un rôle essentiel dans la cellule en lui conférant une réalité physique. En effet ces protéines de structure permettent le maintien de la forme tridimensionnelle et participent aussi au processus de migration des cellules. C'est ainsi qu'il est possible d'apprécier la grande diversité de forme et d'élasticité des cellules composant l'ensemble des organismes connus.

Les microtubules sont aussi connus pour leur rôle dans le transport cytoplasmique de divers composants tel que des vésicules ou autre grande protéines. En effet leur polarité et leur grande rigidité permettent un déplacement sur de longue distance et de manière dirigée. Par exemple les neurones contiennent un grand nombre de microtubules nécessaires au déplacements de nombreuses protéines soit vers les prolongements cellulaires ou bien vers le corps cellulaire.

Le transport est rendu possible grâce à des protéines associées aux microtubules (appelé Microtubules-Associated Proteins ou MAP en anglais). Par exemple les moteurs moléculaires sont des MAP très connus et étudiés. Parmi eux les kinésines se déplacent vers l'extrémité + tandis que les dynéine se déplacent vers l'extrémité -.

Enfin le rôle des microtubules dans la mobilité cellulaire est aussi très étudié. Ce sont par exemple les composant majeurs de l'axonème qui forme les flagelles des cellules eucaryotes (spermatozoïde et certains protistes).

Pour finir on soulignera leur importance capitale durant la mitose car c'est eux qui forment l'essentiel du fuseau mitotique. En plus d'un rôle structurelle durant la division cellulaire, ils participent aussi de manière active en fournissant une partie de l'énergie nécessaire au déplacement des chromosomes.

Bien que les microtubules soit des structures très dynamique, un grand nombre de molécules et de protéines sont capable de modifier cette dynamicité. Notamment une famille de protéine est connu pour induire la dépolymérisation des microtubules pendant la mitose.

1.2.4 Les kinésines dépolymérisatrice de microtubule

Les premières études sur cette famille de kinésine ont commencé dans les années 1990 (voir cette excellente revue à propos de cette famille de kinésine par Claire E. Walczak (Walczak et al., 2013)). La kinésine 13 fut la première à être décrite comme une kinésine dépolymérisatrice de microtubule. Par exemple, la déplétion de la kinésine 13 dans des extraits d'oeufs de *Xenopus* (appelé XKCM1) a pour effet

d'agrandir la taille des microtubules qui présentent par ailleurs un taux de catastrophe plus élevé (Walczak et al., 1996). Par la suite la kinésine 13 a été retrouvé chez un grand nombre d'autre organismes pour lesquel il a été montré un rôle dans la destabilisation des microtubules (Ganem et al., 2005; Maney and Hunter, 1998).

Étonnement personne ne retrouva la kinésine 13 chez les champignons et c'est au début des années 2000 que la kinésine 8 commença à être décrite chez la levure. Chez la levure à fission (*Schizosaccharomyces pombe*), la déplétion de la kinésine 8 (Klp5 et Klp6) entraîne un allongement des microtubules cytoplasmiques ainsi qu'un défaut dans l'alignement des chromosomes en métaphase (Garcia et al., 2002; West et al., 2002). Tandis que chez la levure à bourgeon (*Saccharomyces cerevisiae*), les cellules mutantes pour la kinésine 8 (Kip3) présentent un défaut de positionnement du noyau (Cottingham and Hoyt, 1997). D'une manière plus générale de nombreuses études ont montré que la kinésine 8 est localisé à l'extrémité + des microtubules kinétochoriens et que sa délétion entraîne un allongement du fuseau mitotique, un décentrage des chromosomes ainsi qu'un délai du démarrage de l'anaphase dû à l'activation du point de contrôle de la transition métaphase/anaphase (le SAC) (Goshima et al., 2005; Jaqaman et al., 2010; Mayr et al., 2007; Stumpff et al., 2008; Wargacki et al., 2010).

Une étude phylogénique sur les kinésines (Wickstead and Gull, 2006) suggère que tout les eucaryotes possèdent au moins un gène codant pour une kinésine parmi la kinésine 8 et la kinésine 13. Il a même été montré qu'un parasite protozoaire (*Theileria annulata*) ne possède que deux kinésines: la kinésine 8 et la kinésine 13. Tout ceci révèle l'importance fondamentale des kinésines dépolymérisatrices dans l'activité des microtubules des cellules eucaryotes.

Par ailleurs l'analyse de la structure 3D de ces deux kinésines (Ogawa et al., 2004; Peters et al., 2010) montre une très forte similarité dans l'agencement spatial des brins et des hélices les composant (Figure 1.6), ce qui suggère des activités catalytiques similaires.

On notera aussi la grande conservation des domaines protéiques qui composent la kinésine 8 chez un grand nombre d'organismes modèle (cellule humaine, levure à bourgeon, levure à fission, cellule de drosophile) comme le montre la Figure 1.7.

Si les protéines dépolymérisatrices influent le comportement de l'attachement entre le microtubule et le kinétochore, elles ne sont pas responsable de l'attachement. Celui-ci dépend de protéines spécifiques au kinétochore qui permettent l'ancrage du microtubule et ainsi que le maintien de l'attachement.

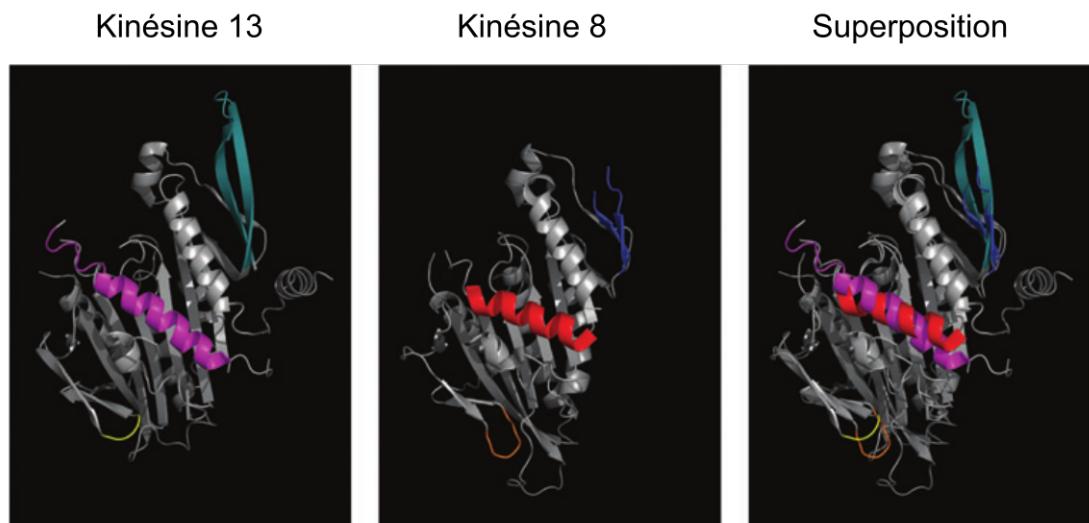


Figure 1.6: Vue 3D de la kinésine 13 (MCAK) et de la kinésine 8 (Kif18a) chez des cellules humaines. La troisième vue montre une superposition des deux protéines. (Walczak et al., 2013)

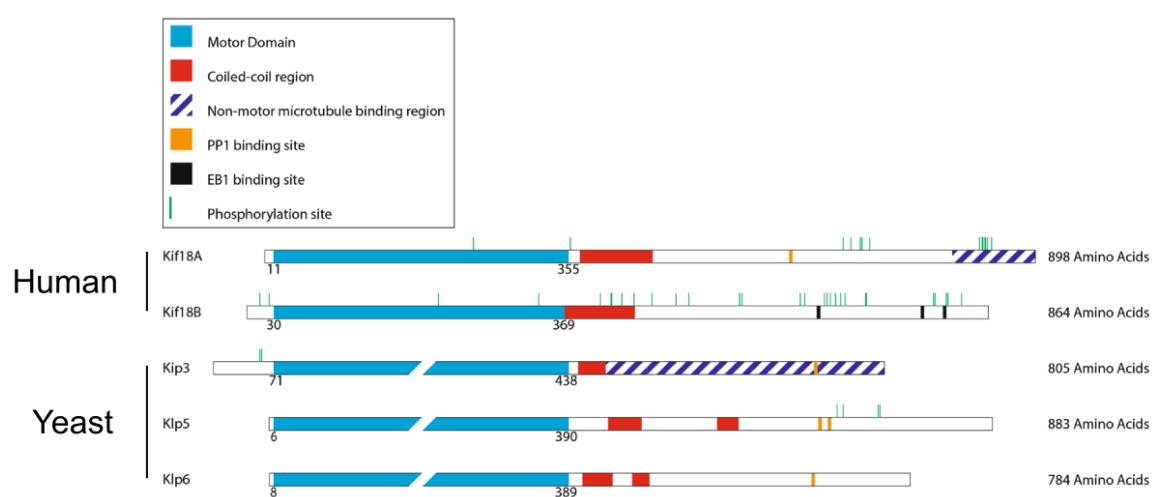


Figure 1.7: Vue schématique des domaines protéiques composant la kinésine 8 chez la cellule humaine, la levure à bourgeon et la levure à fission (Messin and Millar, 2014).

1.2.5 L'ancrage du microtubule au kinétochore

Durant la mitose, les microtubules attachent les chromosomes par l'intermédiaire d'une grande structure protéique appelé le kinétochore. L'attache se situe au niveau de la plaque externe du kinétochore et est principalement réalisé grâce au complexe NDC80 (DeLuca et al., 2002, 2006; McCleland et al., 2004; Wigge and Kilmartin, 2001).

Ce complexe est un hétérotetramère composé de quatre protéines (voir Figure 1.8A): Ndc80, (Hec1 chez les humains), Nuf2, Spc24 et Spc25 (Wei et al., 2005). La tête composé de Ndc80-Nuf2 accroche le microtubule tandis que la tête Spc25-Spc24 attache la plaque externe du kinétochore.

Chez la levure un autre complexe protéique, appelé Dam1 ou DASH, a été décrit comme participant à l'attachement KT-MT. Ce complexe forme un oligomère autour du MT en forme d'anneau partiel ou complet (Miranda et al., 2005; Westermann et al., 2006).



Figure 1.8: **A.** Vue schématique de la structure du complexe NDC80 ainsi que sa localisation dans le kinétochore. **B.** Interaction non contrainte entre des complexes NDC80 (en rouge) avec différents microtubules (en vert) (Zaytsev et al., 2014).

Plus récemment J.G DeLuca et al. et son équipe ont proposé un modèle continu de l'attachement des microtubules au kinétochore (Zaytsev et al., 2014). En effet les site d'attachement ne sont plus vus comme un espace bien défini qu'il est possible de compter mais comme une surface sur laquelle les attachements se font de manière

non exclusive (voir Figure 1.8B).

1.2.6 Les différents type d'attachements

L'association des kinétochores soeurs avec leurs pôles respectifs s'appelle un attachement amphitélisque, on parle aussi de chromosomes biorientés (voir Figure 1.9). Il a été montré que les erreurs d'attachement sont fréquentes en prométaphase et qu'elles sont pour la plupart corrigées avant le début de la séparation des chromosomes, l'anaphase.

On distingue trois types d'erreurs dans les attachements KT-MT (voir Figure 1.9):

- **monotélique** : seulement un des deux kinétochores est attaché à aux MTs provenant tous du même pôle.
- **syntélique** : les deux kinétochores sont associés à des MTs provenant du même pôle.
- **mérotélique** : un kinétochore est associé à des MTs provenant des deux pôles.



Figure 1.9: Les différents types d'attachements des kinétochores aux microtubules.

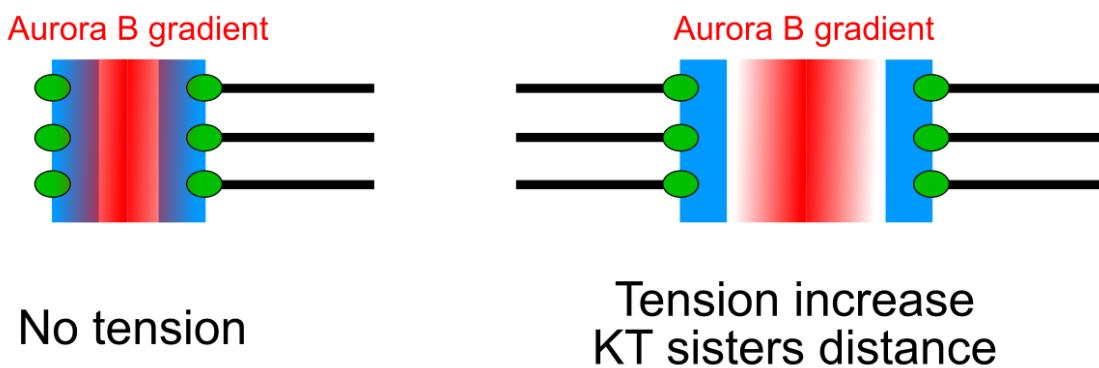
Un attachement incorrect des kinétochores durant l'anaphase peut entraîner une perte de chromosome et par la suite la mort cellulaire ou bien la dégénérescence d'un tissu. La cellule a donc développé des mécanismes robuste de correction.

D'abord de manière purement géométrique suite au processus de réPLICATION et de condensation, les deux kinétochores soeurs sont placés face à face dans des directions opposées. Il en résulte que si l'un des kinétochores est accroché à un pôle, l'autre kinétochore sera alors plus susceptible de s'associer avec le pôle opposé.

Dans les années 90, Nicklas et al. montra dans un expérience de micromanipulation des chromosomes de spermatocyte de sauterelle, que l'attachement KT-MT est par nature instable et qu'il se stabilise à mesure que la tension augmente (Nicklas et al., 1982).

Par ailleurs des expériences de laser ablation sur des chromosomes en métaphase (Skibbens et al., 1995) ont montré que les deux chromatides soeurs se déplacent vers leurs pôles respectif après avoir ablater leur région centrale, ce qui indique que l'attachement d'un microtubule à un kinétochore produit une force dans la direction du pôle qui attache le microtubule. Par conséquent un chromosome amphitélique, correctement attaché, est nécessairement sous tension tandis que les attachements monotéliques ou syntéliques doivent subir une tension plus faible. Ainsi les attachements incorrects devraient être éliminé avec le temps tandis que les attachements corrects auraient tendance à être maintenu jusqu'au début de l'anaphase (Kirschner and Mitchison, 1986).

Un des mécanismes proposés pour expliquer l'instabilité des attachements incorrects, sous une moindre tension, est basé sur la protéine kinase appelé Aurora B, localisé au centre du centromère. La phosphorylation de certaine protéines du kinétochore par Aurora B réduit l'affinité de l'attachement (DeLuca et al., 2006). Comme présenté sur la Figure ??, si la distance entre les deux kinétochores est grande, dû à une tension élevé, Aurora B n'a pas accès aux protéines du kinétochore et ne pourra donc pas destabiliser l'attachement (Tanaka et al., 2002).



spindle_assembly Ces mécanismes ne peuvent néanmoins pas corriger les attach-

ments mérotélique. En effet les deux kinétochores étant partiellement attachés aux deux pôles, le fuseau exerce quand même une tension à travers le centromère. Le déséquilibre de tension se situe alors au niveau du kinétochore. Bien que ces mécanismes de correction soit encore mal compris, l'un d'entre eux semble impliqué Aurora B (Cimini et al., 2006). Un autre mécanisme propose une correction structurelle en détectant le déséquilibre de force présent en anaphase sur le kinétochore mérotélique par l'intermédiaire d'une protéine appelé Ase1 (Courtheoux et al., 2009).

Les mécanismes en charge de l'intégrité et de la correction des attachements des chromosomes prennent du temps. La cellule a donc développé un point de contrôle afin de mettre la mitose « en pause » avant l'entrée en anaphase, afin que tous les attachements puissent être corrigés.

1.3 La métaphase : point d'orgue de la division cellulaire

La métaphase correspond au moment où l'ensemble des chromatides sont encore attachées entre elles et alignées au milieu du fuseau mitotique entre les deux pôles. Voir par exemple ces deux photos de microscopie à fluorescence de deux cellules différentes en métaphase (Figure 1.12).

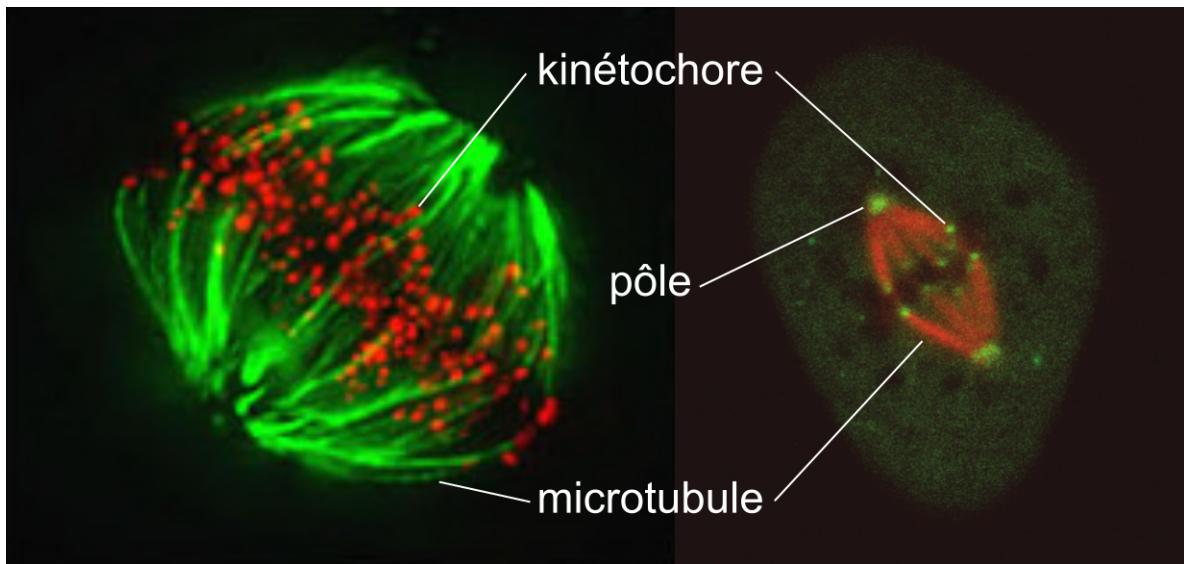


Figure 1.10: Deux cellules en métaphase (cellule HeLa à gauche et cellule Ptk1 à droite). Pour les deux cellules les kinétochores de l'ensemble des chromosomes sont marqués respectivement en rouge et vert tandis que les microtubules sont marqués respectivement en vert et rouge. (Huang et al., 2008; Wan et al., 2012)

1.3.1 La congression des chromosomes

L'étape d'alignement des chromosomes s'appelle la congression et a lieu durant l'étape précédant la métaphase, la prométaphase. Une cellule passe donc du temps et dépense de l'énergie à regrouper et aligner ces chromosomes au milieu du fuseau mitotique.

En début de prométaphase les chromosomes initialement non attachés commencent à se bi-orienter. C'est à ce moment qu'ils vont subir une série de mouvement de va et vient (aussi appelé oscillation) pour venir, petit à petit, s'aligner au niveau de la plaque équatoriale (au milieu du fuseau mitotique). On peut observer ce processus à l'oeuvre en microscopie à fluorescence en marquant les kinétochores et les microtubules d'une cellule humaine par exemple (Figure 1.11).

TODO: REVIEW DE L ALIGNEMENT et des différent mecanisme

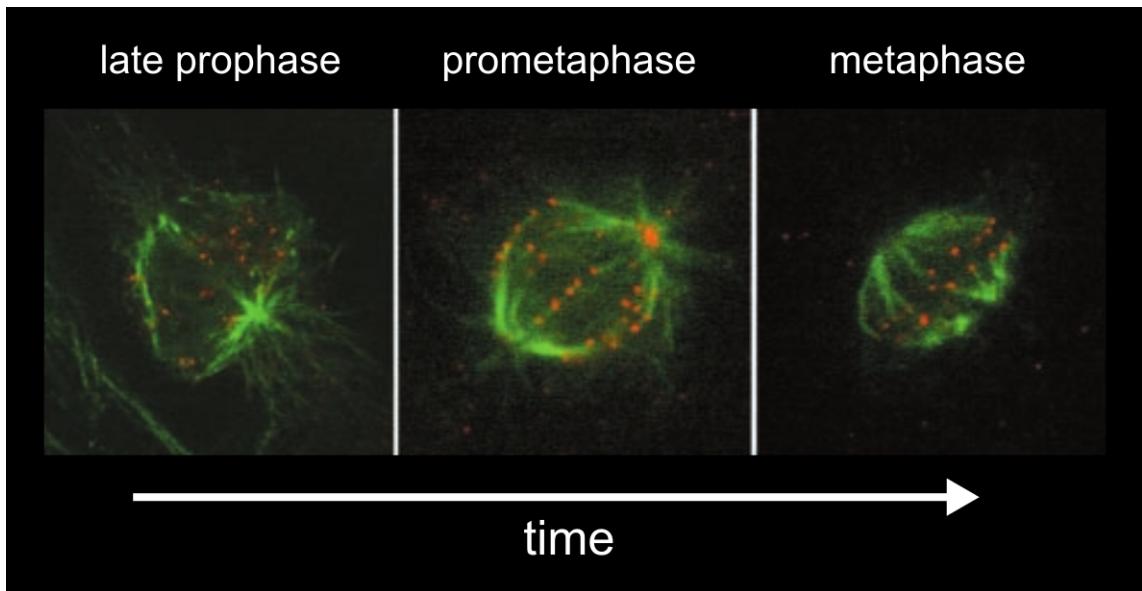


Figure 1.11: Cellule humaine (RPE1) en début de mitose. Les kinétochores (en rouge) sont alignés à la fin du processus durant la métaphase. On peut deviner les deux pôles du fuseau en suivant où les microtubules (en vert) convergent. (DeLuca et al., 2002)

1.3.2 Le fuseau mitotique : un objet sous contrainte

TODO: point orgue et propriété biophysique

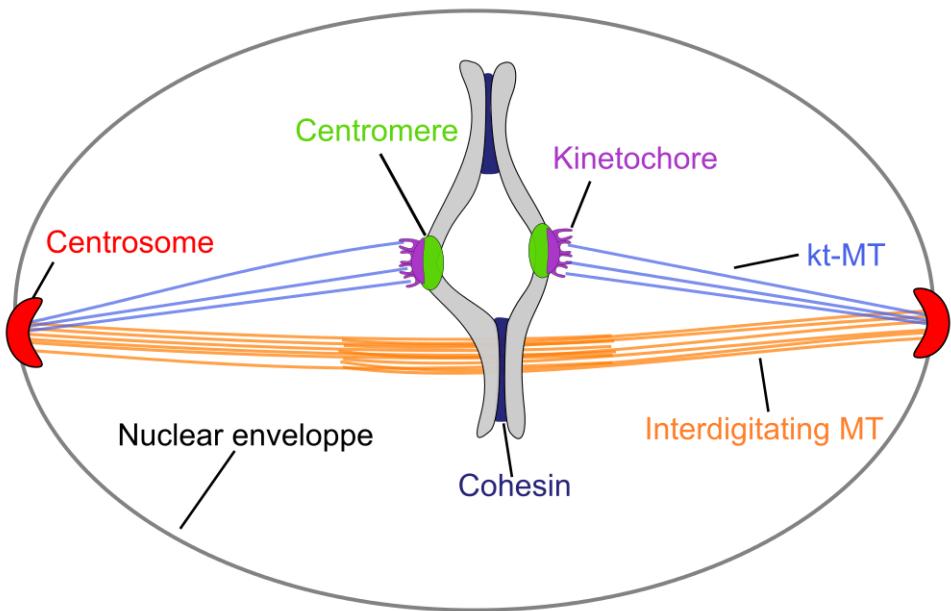


Figure 1.12: Schéma d'un fuseau mitotique (mitose fermé).

1.3.3 Le point de contrôle de la transition métaphase/anaphase

TODO: SAC review (Musacchio and Salmon, 2007)

1.4 Modélisation mathématique de la mitose

La mitose est un processus qui fascine depuis longtemps les biologistes mais aussi les scientifiques en dehors des sciences du vivant. Les physiciens s'intéressent aux propriétés mécaniques du fuseau mitotique ainsi qu'aux forces mis en jeu durant ce processus. Tandis que les mathématiciens sont plus concernés par le développement d'un modèle mathématique de la mitose.

1.4.1 La modélisation : quésako ?

La modélisation est un vaste champs de recherche et il existe une grande variété de classe de modèle. Les expériences de modélisation effectuée durant ce travail et d'une manière plus générale les modèles utilisés en biologie cellulaire pour décrire la mitose sont « des modèles de connaissance ». C'est à dire qu'ils sont tous construits à partir d'une analyse physique, biologique et chimique des connaissances existantes sur la mitose.

Un modèle de connaissance est bâti à la fois sur un ensemble de lois générales (mécanique, électromagnétisme, thermodynamique, etc) ainsi que sur un ensemble de lois empiriques qui gouvernent les différents phénomènes du processus étudié.

C'est la classe de modèle par excellence car les équations le composant décrivent directement les processus en jeux. Cependant certains phénomènes très complexe ne peuvent pas toujours être modélisés par cette approche. On utilise donc parfois d'autre classe de modèle (comme les modèles de « boites noires », non discutés ici). On notera qu'il est aussi possible appliquer une série d'approximation afin de réduire la compléxité du processus étudié et ainsi utiliser un modèle de connaissance, au prix d'une précision moins importante.

Avant de continuer, il est important de répondre à une question primordiale qui revient souvent chez les biologistes : pourquoi modélise-t-on ?

Un scientifique tire des conclusions en fonction des différents résultats produisent par ces expériences. Une déduction logique lui permet donc de bâtir un « modèle » qualitatif du processus qu'il étudie. Ce modèle est parfois représenté sous la forme d'un schéma à la fin d'un article ou d'une présentation.

Un modèle mathématique est la version quantitative de ce modèle-schéma décrivant un processus biologique (Figure 1.13).

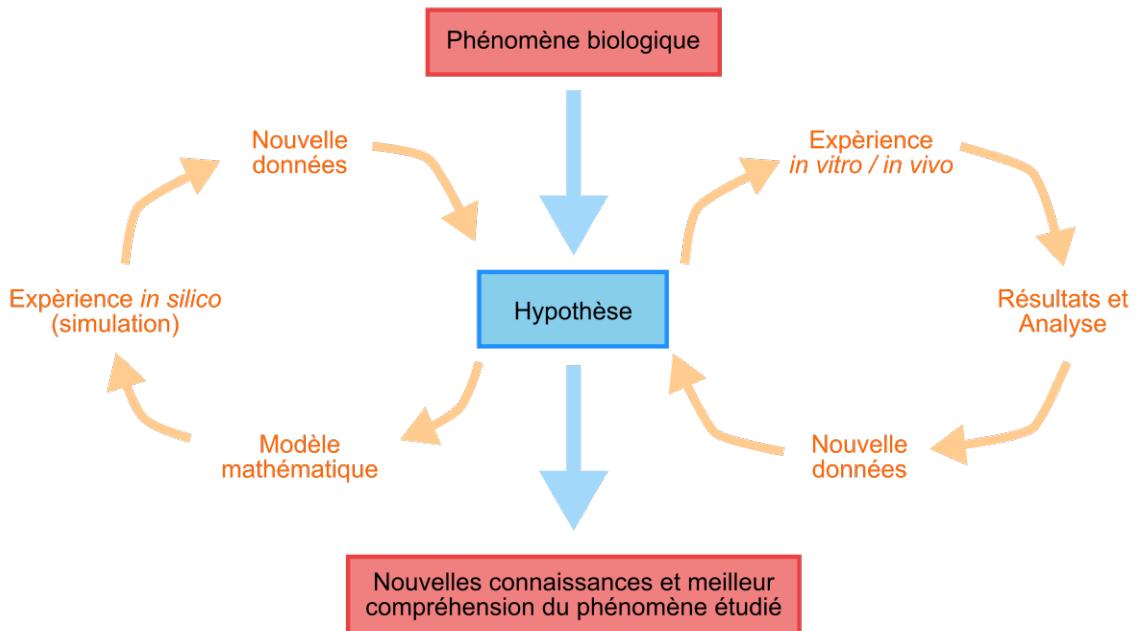


Figure 1.13: Schéma reproduisant un workflow expérimentale possible lors de l'étude d'un phénomène biologique par une approche de modélisation (adapté de Woelke et al. (2010)).

Il peut apporter une vision plus précise du processus étudié, notamment en chiffrant différents paramètres et propriétés du système qui peuvent par la suite être comparés à des mesurables décrivant le processus *in vivo*.

La modélisation mathématique a pris son essor avec la modernisation des ordinateurs et du calcul numérique durant ces 20 dernières années. Cet outil, parfois complexe à appréhender et à comprendre, est la continuité naturelle des modèles mentales que les scientifiques établissent par la déduction logique depuis toujours.

La mitose est un processus cellulaire d'une extrême compléxité en grande partie dû aux grand nombre de phénomènes mis en jeux dans un volume si petit. Il en résulte qu'il est à ce jour, en 2015, encore hors de notre portée de modéliser avec précision la mitose dans son intégralité. Chaque modèle s'applique donc à décrire un moment bien spécifique de la mitose avec un niveau de précision plus ou moins important. Ces deux variables expliquent la grande diversité des modèles existant.

Pour finir on soulignera l'existence de nombreux modèles décrivant des phénomènes biologiques très spécifiques tel que l'instabilité dynamique des microtubules (Bowne-Anderson et al., 2013; Nedelec and Foethke, 2007), la génération de force au niveau de l'attachement kinétochore-microtubule (Keener and Shtylla, 2014, Shtylla and Keener, 2011), l'effet de certaine kinésines sur la dynamique des microtubules (Hough et al., 2009; Reese et al., 2014). Ces modèles sortent du cadre d'une description générale du processus de la mitose et ne seront pas discutés ici.

1.4.2 L'assemblage du fuseau mitotique

Le modèle le plus répandu décrivant l'assemblage du fuseau mitotique est celui appelé « recherche et capture ». Durant la prométaphase, les microtubules s'assemblent des deux pôles du fuseau et vont « sonder » l'espace afin d'attacher chacun des kinétochores. Des simulations numériques ont montré que ce processus seul n'est pas assez efficace pour expliquer les temps de prométaphase rencontrés dans la plupart des organismes de l'ordre d'une dizaine de minute (Wollman et al., 2005). Il existe donc des biais durant ce processus permettant une capture plus rapide et fidèle des chromosomes.

Un modèle propose que l'un de ces biais pourrait être la présence d'un gradient de RanGTP autour des kinétochères. Une plus forte concentration de RanGTP stabilisera les microtubules et les ferait croître en direction des kinétochore (loin des

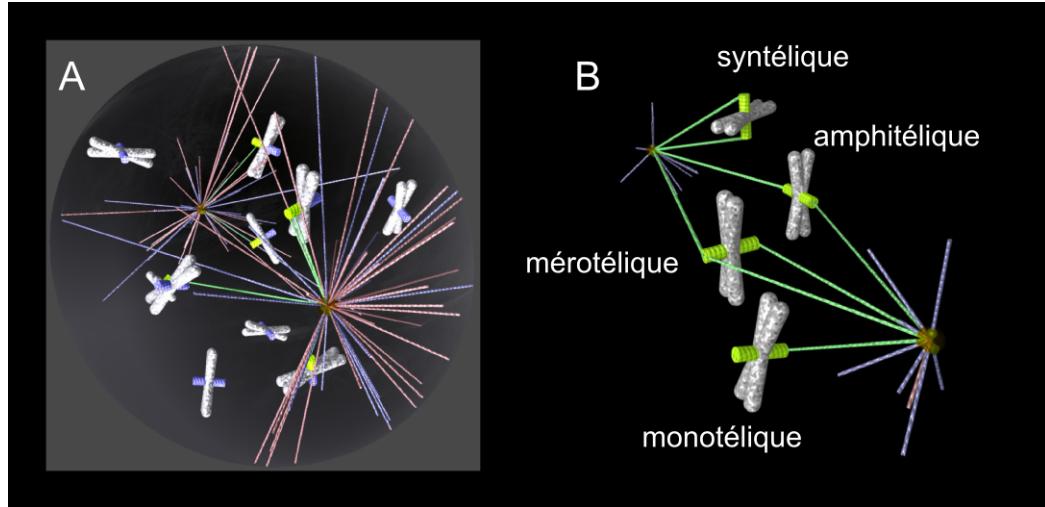


Figure 1.14: Modèle numérique de l’assemblage du fuseau (Paul et al., 2009). A. Des chromosomes durant la phase « recherche et capture ». Certains kinétochore sont attachés (en vert) et d’autre sont non attachés (en bleu). B. 4 type d’attachements possibles des chromosomes.

pôles). Des simulations numériques ont montré que ce biais spatial lors du processus de recherche augmenterait la vitesse de capture (Wollman et al., 2005).

Cependant ce modèle encore trop naïf n’explique pas la précision avec laquelle le fuseau attache les chromosomes, en évitant les attachements syntélique et mérotériques. En effet des simulations de « cherche et capture » aléatoire ont montré la présence de 65% d’attachement mérotériques et seulement 15% d’attachement amphitériques (Paul et al., 2009).

Deux mécanismes pourraient expliquer la précision des attachements *in vivo*. Le premier stipule que lors d’un attachement monotérique, le chromosome effectue une rotation de telle façon que le kinétochore attaché se positionne face à son pôle tandis que son kinétochore soeur ferait face au pôle opposé et aurait donc une plus forte probabilité de s’attacher à lui (Figure 1.15A). Ce mécanisme réduit de manière importante le pourcentage d’erreurs quand il est inclus dans des simulations numériques (Paul et al., 2009).

Le second mécanisme serait que l’attachement amphitérique apparaît de manière évolutive (un peu à la façon d’un processus Darwinien). C’est à dire que la capture serait un processus d’essaie et erreurs. Au début les attachements syntélique sont fréquents et disparaissent souvent (Lampson et al., 2004) jusqu’à que seulement les attachements amphitériques soit conservés. Ceci n’est possible que si les taux d’attachement et détachement dépendent de l’attachement du kinétochore comme illustré Figure 1.15B. Ici aussi des simulations numériques ont montré que ce mécanisme réduit de manière très importante le nombre d’erreur d’attachement (Paul

et al., 2009).

Le mécanisme modulant les probabilités d'attachement en fonction de l'état du kinétochore pourrait impliquer une protéine tel que Aurora B comme déjà discuté en 1.2.6.

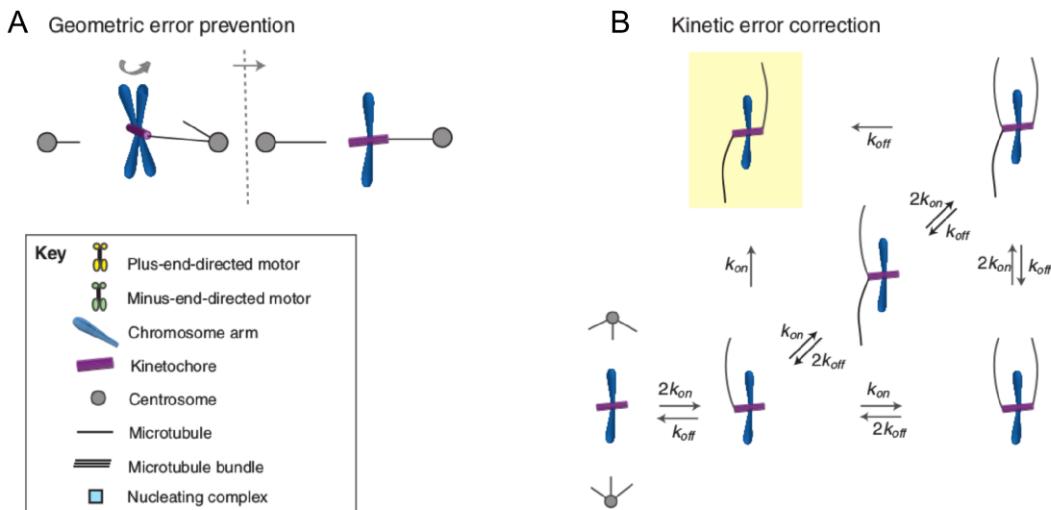


Figure 1.15: Deux mécanismes expliquant la fidélité des attachements durant le processus de « recherche et capture » (Mogilner and Craig, 2010).

1.4.3 La dynamique des chromosomes

1.5 La levure à fission : un organisme modèle pour l'étude du cycle cellulaire

- historique en tant qu'organisme modèle
- autre utilité

1.6 Problématique

Enfin l'approche biophysique dans l'étude de la mitose se justifie par le fait que ce processus implique le mouvement de grand objets à l'échelle de la cellule (les chromosomes) et donc l'existence de force. Toute la question est comment sont régulées ses forces dans le temps et l'espace et par quel type de réactions chimiques

2

Résultats

2.1 « Fission yeast Kinesin-8 controls chromosome congression independently of oscillations »

Chez les eucaryotes supérieurs, la congression des chromosomes dépend entre autre de l'activité des chromokinésines. Cette étude analyse de manière quantitative l'oscillations et le positionnement des chromosomes dans la levure à fission (*S. pombe*), un organisme modèle qui ne possède pas de chromokinésine.

Dans des cellules sauvages, les chromosomes s'alignent durant la prophase et tout en oscillant, maintiennent leur alignement jusqu'à la métaphase. L'oscillation des chromosomes n'est pas indispensables à l'alignement des chromosomes en métaphase.

Chez les eucaryotes supérieurs, la kinésine 8 contrôle la congression des chromosomes en régulant leur oscillations. De manière opposée, nous montrons que la kinésine 8 de la levure à fission contrôle la congression des chromosomes par un mécanisme alternatif. Nous proposons que la kinésine 8 aligne les chromosomes en contrôlant les forces de traction en fonction de la longueur des microtubules attachés aux chromosomes.

De plus un modèle mathématique de la ségrégation des chromosomes implé-

mentant ce mécanisme dépendant de la longueur est suffisant pour reproduire l’alignement des chromosomes et prévenir l’apparition de chromosomes retardataires en anaphase.

Dans l’ensemble, ces données illustrent comment l’action local d’une protéine moteur au kinétochore peut fournir une information spatial à l’ensemble de fuseau afin de permettre l’alignement des chromosomes.

Fission yeast Kinesin-8 controls chromosome congression independently of oscillations

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Running title: Kinesin-8 function in kinetochore alignment

Keywords: Fission yeast / mitosis / Kinesin-8 / kinetochore alignment

ABSTRACT

In higher eukaryotes, efficient chromosome congression relies, among other players, on the activity of chromokinesins. Here, we provide a quantitative analysis of kinetochore oscillations and positioning in *S. Pombe*, a model organism lacking chromokinesins. In wild type cells, chromosomes align during prophase and while oscillating, maintain this alignment throughout metaphase. Chromosome oscillations are dispensable both for kinetochore congression and stable kinetochore alignment during metaphase. In higher eukaryotes, Kinesin-8 controls chromosome congression by regulating their oscillations. Oppositely, we demonstrate that fission yeast Kinesin-8 controls chromosome congression by an alternative mechanism. We propose that Kinesin-8 aligns chromosomes by controlling pulling forces in a length dependent manner. A coarse grained model of chromosome segregation implemented with a length-dependent process that controls the force at kinetochores is necessary and sufficient to mimic kinetochore alignment and prevents the appearance of lagging chromosomes. Altogether, these data illustrate how the local action of a motor protein at kinetochores provides spatial cues within the spindle to align chromosomes and to prevent aneuploidy.

(180 words max)

INTRODUCTION

Chromosome congression is an evolutionary conserved feature of mitosis thought to promote faithful segregation of sister chromatids into daughter cells (Kops et al., 2010). In higher eukaryotes, efficient chromosome congression relies on multiple mechanisms and involves several microtubule-dependent motor proteins. On chromosome arms, the chromokinesins create the polar ejection forces (PEFs) that allow chromosome congression (Antonio et al., 2000; Funabiki and Murray, 2000; Rieder et al., 1986; Wandke et al., 2012). A second mechanism of congression involves CENP-E at kinetochores for the sliding of chromosomes along spindle microtubules (Cai et al., 2009; Kapoor et al., 2006). In addition to chromosome congression, bi-oriented sister kinetochores undergo oscillatory movements between the two spindle poles before chromosome segregation (Amaro et al., 2010; Pearson et al., 2001; Skibbens et al., 1993). Oscillations and congression of chromosomes are complex movements that require a spatio-temporal control of tensional forces and attachment at the level of kinetochores that is far from being understood (Dumont and Mitchison, 2009). Multiple actors are involved in these processes, such as kinetochore components, non-kinetochore forces such as PEFs, motor proteins and microtubule-associated proteins, which control MT dynamics (Civelekoglu-Scholey et al., 2013; Joglekar et al., 2010; McIntosh, 2012). However, chromosome oscillations are not absolutely required for the execution of mitosis since several cell types seem to successfully segregate chromosomes in the absence of oscillations (Desai et al., 1998; LaFountain et al., 2001).

Among the different players controlling kinetochore congression and oscillation, Kinesin-8 is emerging as one of the most important motor protein that participates in the correct distribution of forces within the spindle. Kinesin-8 is a highly processive motor known to regulate microtubule dynamics thanks to its plus end-directed motility and plus-end-specific destabilizing activity (Gupta et al., 2006; Mayr et al., 2007). A combination of these two activities led to a novel length-dependent mechanism that was proposed to maintain the cellular microtubule length homeostasis (Foethke et al., 2009; Tischer et al., 2009; Varga et al., 2006; Varga et al., 2009). Seminal works of West *et al.* and Garcia *et al.* attested that Klp5 and Klp6, the fission yeast homologs of Kinesin-8, are also required for normal chromosome movement and attachment (Garcia et al., 2002a; West et al., 2002). Interestingly, no chromokinesin homolog is present in fission yeast (Wood et al., 2002), so there are supposedly no anti-poleward ejection forces. There is also no poleward flux of tubulin within the spindle in this model system (Mallavarapu et al., 1999) as opposed to higher eukaryotes (Mitchison, 1989). Thus, *S. pombe* has several features that make it a simple and attractive model to study the respective role of kinetochore components or MT dynamics in chromosome congression and oscillation. Mitosis in *S. pombe* consists of three phases (Nabeshima et al., 1998; Tatebe et al.,

2001). During phase 1, a short ($< 2.0 \mu\text{m}$) spindle is formed (prophase). In phase 2 (pro-metaphase/metaphase/anaphase A), the spindle maintains roughly the same length and the kinetochores make frequent, rapid movements between the poles. At the end of phase 2, sister chromatids separate and move towards the SPBs during anaphase A (Tournier et al., 2004). In phase 3 (anaphase B), the spindle elongates along the longitudinal axis of the cell.

To obtain a quantitative understanding of chromosome segregation, mathematical models of metaphase chromosome dynamics have been developed over the past few years (Civelekoglu-Scholey and Cimini, 2014; Vladimirov et al., 2011). Most of these models analyze how various components of a force-balance system affect chromosome oscillation, congression or segregation (Brust-Mascher et al., 2004; Civelekoglu-Scholey et al., 2013; Civelekoglu-Scholey et al., 2006; Courtheoux et al., 2009; Gay et al., 2012; Joglekar and Hunt, 2002; Paul et al., 2009). However, to date, there are no specific and quantitative descriptions of the mechanisms controlling fission yeast chromosome alignment or oscillation in mitosis or their role in kinetochore attachment.

Here, we present a quantitative analysis describing chromosome positioning and oscillation in wild type fission yeast cells. Fission yeast chromosomes align during prophase and while oscillating, remain aligned throughout metaphase. We demonstrate that chromosome oscillation is dispensable for kinetochore congression. Importantly, the role of Kinesin-8 in chromosome congression is independent from its function in restricting chromosome oscillations to the spindle midzone. Finally, *in silico* and *in vivo* evidence suggest that a length-dependent process could participate in chromosome congression in fission yeast.

RESULTS

Kinesin-8 actively controls and maintains kinetochore alignment during mitosis

To explore the mechanisms controlling kinetochore alignment in *S. Pombe*, we performed 3D live-cell imaging in wild type and Kinesin-8 deleted cells. We simultaneously imaged the pericentromere region of chromosome 2, Cen2-gfp (Yamamoto and Hiraoka, 2003) and the spindle pole bodies (SPBs) (Cdc11-gfp) (Tournier et al., 2004) during mitosis. The observed trajectories confirmed that kinetochores of cells deleted for Klp6 were often found near the poles as opposed to kinetochores of wild type cells, which were confined in the vicinity of the spindle center (Fig. 1A and 1B and Supplemental Movie S1 and S2).

To characterize and quantitatively measure the chronology of kinetochore positioning from phase 2 (pro-metaphase/metaphase) to anaphase onset, we computed from multiple trajectories the average distance (d) between sister centromeres (red line) and the spindle center (purple line) as a function of time in parallel with spindle elongation (SPB position in black, Fig. 1C and D; see details in methods; note that the graph is not normalized to spindle size). This measure provides an estimate of the mean gap between kinetochores and the spindle center throughout metaphase, while its standard deviation (pink zone) reveals the spreading of this measure. In both cell lines, the average gap between Cen2 signals (red) and the spindle pole (black) was unchanged throughout the metaphase process (starting from 1.5 μm spindles) until anaphase onset. Chromosome position is maintained throughout phase 2 suggesting that a stationary process controls kinetochore alignment during metaphase progression. In the absence of Kinesin-8, kinetochores are constantly positioned further away from the spindle center and the large standard deviation suggests that they are widely spread over the entire spindle (Fig 1B and D). Statistical analysis performed immediately before anaphase confirmed that sister kinetochores are found at an average distance from the spindle center of 0.113 ± 0.01 for wild type cells ($n=52$) and 0.239 ± 0.01 for $klp6\Delta$ cells ($n=63$) (normalized distance relative to spindle size; Fig. 1E). Consistently with the heterodimeric association of Klp5 and Klp6, which is required for Kinesin-8 function (Unsworth et al., 2008), both $klp5\Delta$ and $klp5\Delta klp6\Delta$ double mutant showed the same deficiency in kinetochore centering (Fig. S1).

Since Kinesin-8 deleted cells exhibit larger spindles and a substantial metaphase delay as can be seen in Fig. 1B and F (Garcia et al., 2002b), we wondered whether these defects could indirectly be the cause of kinetochore mis-alignment. We tested the former hypothesis by increasing spindle size of both cell types using the temperature-sensitive cell cycle progression mutant *cdc25-22*. To increase spindle size, we arrested *cdc25-22* and *cdc25-22 klp6\Delta* cells at the restrictive temperature

for 3 hours (Fig. 1E and F; Fig.S1 D). Increasing spindle size in the *cdc25-22* background had no effect on kinetochore alignment (Fig. 1E and F). Thus, the increased outward pushing forces developed at the spindle midzone when Kinesin-8 is absent are not the cause of kinetochore misalignment.

Since wild type chromosomes were correctly aligned in metaphase, we hypothesized that kinetochore centering may occur earlier possibly during prophase. We thus followed the position of the 6 kinetochores (*ndc80-gfp*) according to the spindle poles (*cdc11-cfp*) from phase 1 to the onset of phase 2 by tracking the maximum intensity of Ndc80 signals over time (Fig 2A and 2B). The average position of kinetochores obtained from multiple Ndc80 trajectories was plotted according to time (Fig 2C). In wild type, at the onset of spindle pole separation (spindles under 0.5 μm), kinetochores progressively aligned to reach their relative metaphase position at a spindle size of 1.2 μm (time 4 min; Fig 2A and 2C). Oppositely, in Kinesin-8 deleted cells, kinetochores remained randomly distributed during phase 1, phase 2 and the onset of anaphase (Fig. 2B and 2C).

To conclude, our results suggest that kinetochore centering in fission yeast takes place very early in mitosis, prior to metaphase, is maintained until anaphase onset and requires the function of Kinesin-8.

Decreasing the amplitude of chromosome oscillation is not sufficient to correct Kinesin-8 centering defects

Previous results obtained in higher eukaryotes showed that the misalignment of kinetochores during metaphase correlates with larger and faster kinetochore movement in Kinesin-8 deleted cells (Jaqaman et al., 2010; Stumpff et al., 2008). In order to accurately quantify chromosome movement in *S. pombe*, we imaged the centromeres of chromosome 2 (Cen2) and the spindle poles (Cdc11) at high frame rate (i.e one image each 0.1s) on limited segments of metaphase in wild type and Kinesin-8 deleted cells. Fig. 3A and 3B illustrate the typical trajectories obtained (Movie S3 and S4 in supplementary material). To abolish kinetochore movement during metaphase, wild type and Kinesin-8 deleted cells were filmed in the presence of low doses of thiabendazole (TBZ; 10 $\mu\text{g}/\text{ml}$), a drug known to destabilize fission yeast interphase and spindle microtubules when used at high doses (Umesono et al., 1983). In the presence of TBZ, spindle size in phase 2 was similar to control conditions (Fig S1C), suggesting that the global structure of the spindle is not affected by this treatment. Yet, an analysis of interphase microtubule dynamics in cells expressing *atb2-gfp* (tubulin-gfp) showed that the addition of TBZ reduces MT shrinkage rate and rescue frequency by a factor 2 while the growth rate and catastrophe frequency were not significantly affected by this

treatment (Fig S2).

To accurately quantify the variations in kinetochore movements, we determined the amplitudes and half-periods of oscillations in both cell types using Fourier analysis (Fig. 4A; FigS3; see methods). The analysis revealed that the half-period ($T_{1/2}$) of these oscillations was not significantly different in the absence of Kinesin-8 (Fig. 4B), while its corresponding amplitude was increased by a factor ≈ 1.5 (Fig. 4C). These results were confirmed using a second independent method to characterize the half-periods and amplitudes of chromosome oscillations (see methods; Fig. S3). Both methods gave qualitatively similar results (Fig S3D and E). Thus, Kinesin-8 in fission yeast dampens chromosome motions by reducing their speed as observed in human Hela cells (Jaqaman et al., 2010; Stumpff et al., 2008). Importantly, amplitudes and periods of oscillations were not significantly affected by increasing spindle size (Fig. S3F,G).

To address whether chromosome congression defects observed in Kinesin-8 deleted cells result from an increase in the amplitude of oscillations, we analyzed chromosome movements in wild type and Kinesin-8 deleted cells in the presence of low doses of TBZ. The amplitude of chromosome movements was significantly reduced in both cell types as compared to control conditions (Fig.4C) while the period of oscillations was unchanged (Fig. 4B). Thus, fission yeast kinetochore oscillations are largely powered by MT depolymerisation. Interestingly, chromosome alignment in the presence of TBZ was slightly improved in both wild type and mutant cells. However, abrogating oscillations was not sufficient to fully rescue kinetochore alignment defects observed in Kinesin-8 deleted cells (Fig. 4D).

Together, these observations demonstrate that an increase in microtubule-driven chromosome oscillation is not sufficient to explain chromosome congression defects of cells deleted for Kinesin-8. Thus, an alternative mechanism controls chromosome congression in fission yeast independently of MT depolymerisation and chromosome oscillation.

The presence of unattached kinetochores is not sufficient to explain the centering defects of Kinesin-8 mutants

We hypothesized that imbalanced traction forces at kinetochores could lead to chromosome alignment defects by causing the appearance of drifts in kinetochore trajectories (Fig.4A). Indeed, the analysis revealed the presence of large drifts in cells deleted for Kinesin-8 as shown in Fig.5A and measured in 5B. Since previous studies reveal that Kinesin-8 is required for correct microtubule attachment (Garcia et al., 2002a), we reasoned that these large drifts in trajectories could be due to

attachment defects. To test this hypothesis, we simultaneously analyzed kinetochore dynamics and the localization of the checkpoint protein Mad2 in a *cen2-gfp mad2-mCherry* strain deleted for Klp6. As previously described, in wild-type cells Mad2 localizes diffusely around the nuclear envelope during G2. As cells enter mitosis, Mad2 relocates to a region underlying the unseparated spindle poles that co-localizes with unattached kinetochores, remaining in this area as the spindle forms (Ikui et al., 2002). Once the spindle reaches a length of between 1 and 2 μm , Mad2 no longer co-localizes with the bi-oriented kinetochores (Courtheoux et al., 2007). In the Klp6 mutant as opposed to wild type, we observed bursts of Mad2 appearing on the kinetochore pair just prior to these large drifts suggesting in this case a total loss of chromosome attachment (an example of this phenomenon is shown in Fig. 5C). In agreement with this hypothesis, kinetochore speed during such crossing was similar to kinetochore speed at anaphase indicating that chromosomes must be detaching from one of the poles (Fig. 5D). Soon after the drifts, chromosomes rapidly reattached as judged by the disappearance of Mad2 and the reappearance of kinetochore oscillations (Fig. 5C).

Thus, kinetochore detachment may explain the increased amplitude of oscillations observed in Kinesin-8 deleted cells. However, these drifts (as well as Mad2 bursts) were absent in the presence of low doses of TBZ (Fig 5B). Since the centering defects were still observed in the presence of TBZ in Kinesin-8 deleted cells, our results suggest that the role of kinesin-8 in kinetochore centering is independent of stable kinetochore attachment.

Kinesin-8 accumulates at the plus-end of intra-nuclear spindle MTs in a length-dependent manner

In order to clarify the Kinesin-8 dependent mechanism at the origin of kinetochore centering, we analyzed Klp5 movements on nuclear microtubule in mitosis. Although it is currently admitted that Klp5 translocates to the nucleus during mitosis (Unsworth et al., 2008) where it can be found at the kinetochores (Garcia et al., 2002b), the precise coordination between Klp5 movements and nuclear microtubule dynamics in mitosis has never been investigated. As it was not possible to visualize Klp5-gfp on individual microtubules within the spindle, we instead recorded the progression of Klp5 along intra-nuclear microtubules emanating from the spindle pole bodies in mitosis (Gachet et al., 2008) using a *klp5-gfp atb2-rfp* strain. During microtubule growth, Klp5-gfp patches rapidly moved on microtubules to accumulate at the +TIP of intra-nuclear microtubules. Then, the disappearance of Klp5-gfp patches correlated with the rapid depolymerization of microtubules (Fig. 6A; Movie S5 in supplementary material).

To quantify the accumulation of Klp5-gfp at the plus end of these microtubules we performed

high frame rate acquisitions (Fig. 6B and Movie S6 in supplementary material). We reported the intensity profile of Klp5-gfp along microtubules for different microtubule length (see Methods for the normalization process). An accumulation of Klp5 was detectable at the +TIP of microtubules in all cases, on either short (Fig. 6C, top panel) or long microtubules (Fig. 6C, bottom panel). Yet, the maximum intensity of fluorescence at the plus-end of intra-nuclear microtubules increased with microtubule length (Fig. 6D), suggesting that Kinesin-8 accumulates strongly on long microtubules but less on short ones during metaphase. Such behavior suggests that Kinesin-8 could control traction forces at the kinetochore in a length-dependent manner, meaning that the longer is the microtubule, the higher is its probability of catastrophe or its depolymerization rate. In agreement with this hypothesis, the length of intra-nuclear microtubules was increased in cells deleted for Kinesin-8 as opposed to wild type (data not shown).

Together, these observations suggest that Kinesin-8 controls the size of microtubules and thus forces, through microtubule depolymerisation, in a length dependent manner.

A length-dependent control of pulling force is sufficient for kinetochore centering and prevents the appearance of lagging chromosomes

Our work suggests that Kinesin-8 motors could act as regulators of force balance exerted on the bi-oriented chromosomes according to their position within the spindle. To test this hypothesis, we explored *in silico* the mechanisms of sister kinetochore centering during mitosis. We originally designed a force-balance model of mitosis that describes global spindle dynamics and predicts chromosome segregation defects (Gay et al., 2012). In this model summarized in Fig.7A and B, kinetochore pairs breathing and oscillatory movements are modeled by a series of stochastic events of attachment and detachment at each microtubule attachment site, the pulling force being “on” when a microtubule is attached and “off” when it detaches. The overall pulling forces exerted on the outer side of the kinetochores are then balanced at their inner side by the cohesin retraction force. At the poles, an additional pushing force exerted on the interdigitated microtubules tends to elongate the spindle and prevents it to collapse (Courtheoux et al., 2009; Gay et al., 2012). In order to mimic the effect of Klp5 on the dynamics of kinetochores, we compared kinetochore centering in the absence (Fig.7C) or presence (Fig.7D) of a length dependent pulling force by assuming the following hypothesis. If the catastrophe frequency or the depolymerization rate is higher for long kinetochore microtubules than for short ones, then the force exerted on kinetochores attached to long microtubules is on average higher than on short ones. Therefore, the modeled pulling forces on each attachment site were modulated by a spatial factor proportional to the distance between the

kinetochore position and the spindle pole (see Methods and Table S1 for a description of model parameters). The value of this factor was set to reflect the distribution of kinetochore positions at anaphase onset. Typical examples of simulated trajectories with the length-dependence pulling force turned on and off are shown in Fig. 7B and D. We observed that the length-dependent pulling force faithfully reproduced the positioning of kinetochores throughout metaphase, as observed *in vivo* (Fig. 7D). Quantitative analysis confirmed that the presence of this pulling force was sufficient to reproduce kinetochore alignment in metaphase and prior to anaphase while its removal mimics the effect of Kinesin-8 deletion (Fig. 7D and E). Previous work showed that the number of lagging chromosomes at anaphase increased in *klp5A* cells, while the number of mis-segregation remained low (Sanchez-Perez et al., 2005). We used our model to evaluate the role of the centering mechanism in preventing chromosome segregation defects. As expected, *in vivo*, we found that the delay between the arrivals of the two sister chromatids at their respective pole was on average increased in Kinesin-8 mutant compared to WT (Fig. 7F). The values obtained were comparable to *in silico* data when the length-dependence was turned on or off (Fig. 7F). However, our model predicts that the rate of chromosome mis-segregation (two cen2 signals at the same pole) is very low in both conditions consistently with what has been reported *in vivo* (Sanchez-Perez et al., 2005; data not shown). Importantly, we modified other model parameters (including kinetochore attachment/detachment parameters, force/velocity characteristics of pulling motors or cohesin stiffness) to evaluate their influence on chromosome alignment (Fig. 8A). Interestingly, only the addition of the length-dependent process substantially increased kinetochore centering during metaphase (Fig. 8A) without introducing aberrant mitotic phenotypes in simulations (Fig. 8B).

Together, our results suggest that a length dependent pulling force is necessary and sufficient to align chromosomes and to prevent the appearance of lagging kinetochores. Our observations also imply that lagging chromosomes in Kinesin-8 mutants are not caused by defective kinetochore attachment but rather due to kinetochore mis-alignment at anaphase onset.

DISCUSSION

Our study reveals the basic mechanisms required to align chromosomes in fission yeast. Chromosome alignment before anaphase onset relies on two discrete steps. Firstly, during phase 1 (prophase), kinetochores congress between the two spindle poles through an active mechanism. Secondly, during phase 2 (pro-metaphase, metaphase), kinetochores maintain this alignment at the spindle midzone while oscillating. Kinetochore oscillatory movements have been previously characterized in mammalian cells (Gardner et al., 2005; Jaqaman et al., 2010; Stumpff et al., 2008; Vladimirov et al., 2013) and in budding yeast (Pearson et al., 2001) but their role in chromosome alignment is unclear. Our work reveals that chromosome oscillations (ie. triggered by microtubule depolymerisation) is dispensable for chromosome centering since suppression of oscillations with low doses of TBZ had no impact on kinetochore alignment throughout metaphase. In fission yeast, it is likely that kinetochore oscillations are mainly triggered by microtubule depolymerisation. In agreement with this finding, the speed of kinetochores moving poleward (microtubule depolymerizing) is largely reduced in the presence of low doses of TBZ while the speed of kinetochores moving in an anti-poleward manner (polymerizing microtubules) is barely unchanged (data not shown).

Kinesin-8 is emerging as one of the most important motor protein that participates in the correct distribution of forces within the spindle. In fission yeast, Kinesin-8 is required not only in phase 1 for chromosome congression but also in phase 2 to maintain stable kinetochore positioning. We favor a model where Kinesin-8 controls the establishment of kinetochore centering (and thus controls the force balance at the kinetochore) to prevent kinetochore detachment at the spindle poles. In agreement with this hypothesis, we observed that kinetochore detachment generally occurs when chromosomes are located near the spindle poles (data not shown). The accumulation of Kinesin-8 at the plus-ends of microtubules and its function in controlling the size of intra-nuclear microtubules may be reminiscent of what has been reported *in vivo* in interphase fission yeast cells (Tischer et al., 2009) and *in vitro* for the budding yeast Kinesin-8 homolog, Kip3p or the human homolog Kif18A (Mayr et al., 2007). The role of length dependent forces in kinetochore centering may be analogous to length dependent pulling forces required for spindle centering in vertebrates (Mitchison et al., 2012; Wuhr et al., 2009), except that Kinesin-8 would play a role as a centering agent able to measure MT length in order to place the kinetochore at the spindle center.

Our study also reveals that an increase in microtubule-driven chromosome oscillation is not sufficient to explain the centering defects of Kinesin-8 mutants since abolishing chromosome oscillation does not restore alignment. It is thus tempting to speculate that the early stage of

congression in fission yeast is reminiscent of Kinesin-7's role (CENP-E) in the sliding of chromosomes along spindle microtubules (Cai et al., 2009; Kapoor et al., 2006). Accordingly, *in vitro* studies suggest that *S. pombe* Kinesin-8 may have plus-end directed motor activities and share some properties with Kinesin-7 family (Grissom et al., 2009).

The role of Kinesin-8 in kinetochore positioning can be mathematically reproduced by adapting the pulling force applied at kinetochores according to its position within the spindle. Indeed, a non-uniform pulling force is sufficient to align and maintain kinetochore alignment throughout metaphase. Similarly, modeling a non-uniform distribution of MT plus ends across the spindle is also sufficient to align chromosomes (data not shown) but further work would be necessary to discriminate between these two hypotheses. Oppositely, increasing or decreasing other model parameters such as kinetochore attachment/detachment rate (ie. frequency of kinetochore movements) is not sufficient for chromosome centering. Our model makes no hypothesis on the nature of the molecular motor involved in this centering mechanism or the origin of this length-dependence mechanism. Yet, *in vivo* accumulation of Kinesin-8 during mitosis according to microtubule length is consistent with a modulation of the frequency rate of catastrophe (Gardner et al., 2008; Tischer et al., 2009; Varga et al., 2009) and as observed by electron-microscopy, the size of microtubules in the spindle is not uniform (Ding et al., 1993). Our model is not considering that chromosome alignment may also be influenced by correlated movements of non sister kinetochores as recently described in human cells (Vladimirou et al., 2013). However, the spatial organization of chromosomes may be important for chromosome congression (Kitajima et al., 2011; Magidson et al., 2011), especially considering that physical links exists between telomeres of chromosomes in mitosis (Reyes et al., 2015).

Either way, our work demonstrates that a gradient of force is sufficient to align chromosomes, to maintain this alignment and to prevent the appearance of lagging chromosomes at anaphase onset. Since the biological function for chromosome movements in mitosis remains elusive, our study provides the basis to understand this important question.

MATERIALS AND METHODS

Cell culture

Media, growth, maintenance of strains, and genetic methods were performed as previously reported (Moreno et al., 1991). Cells were grown at 25°C in yeast extract before mounting on an imaging chamber. The strains used in this study are listed in Table S2.

Live-cell imaging

Live-cell microscopy was performed on an imaging chamber (CoverWell PCI-2.5; Grace Bio-Labs, Inc.) filled with 1 ml of 2% agarose in minimal medium and sealed with a 22 × 22 mm glass cover-slip. The temperature was maintained at 25°C during acquisitions. Images were acquired from an inverted wide-field microscope (Nikon Eclipse TI) equipped with a Neo sCMOS camera (Andor Technology Ltd), a LED light source (Lumencor Spectra) and a 100x objective (1.45 NA). Images were recorded using the free open-source Micro-Manager software (Edelstein et al., 2010).

For quantitative analysis of kinetochore alignment (using Cen2-gfp or Ndc80-gfp), images were acquired every 10 s with 10 Z of 300nm at each time step. It has been previously reported that the distance between Cen2-gfp and Ndc80-gfp spots was about 120 nm, less than the typical size of these spots (Gay et al., 2012). Thus, in this study the term kinetochores of chromosome 2 will be often used instead of pericentromeric region of chromosome 2.

For high frame rate acquisitions (analysis of chromosome oscillations), images were acquired with a single Z section and a time step of 100ms. The Z position was manually modified during acquisitions to maintain the focus on the spindle. In Thiabendazole (TBZ) assays, cells were imaged in minimal medium supplemented with 10 μ g.ml⁻¹ TBZ (from a stock solution of 10mg ml⁻¹ in DMSO). Cells were incubated for 30 min at 25°C before image acquisitions.

For *cen2-gfp cdc11-gfp mad2-rfp* acquisitions, images were acquired every 7 seconds with 3Z of 600nm. To image Klp5-gfp on intra-nuclear microtubules, images were acquired every 2 seconds with 3Z of 300nm; while Cdc11-cfp signal was acquired every 30 seconds.

To record the position of kinetochores at the very beginning of mitosis, cells with Ndc80-gfp and Cdc11-cfp markers were used (Tournier et al. 2004). Acquisitions were made every 5 seconds with 5Z of 400 nm each.

Image analysis

Image analysis was done using Fiji (Schindelin et al., 2012), Python programming language and scientific python ecosystem: Scipy library (Oliphant, 2007) and custom software developed in the lab. All source code used in this paper is open source and freely available at https://github.com/hadim/spindle_tracker.

Peak detection and tracking. Cdc11-gfp (SPB) and Cen2-gfp (centromeres of chromosome 2) spots were first detected after a maximum Z-projection of images using LoG detector from TrackMate (Fiji plugin). Then, tracking was performed with custom software developed in Python. To link these spots with time, we assumed that the most distant spots were the SPBs while the two remaining were the centromeres. Each trajectory is then projected on the spindle axis defined by the two SPBs.

Quantification of fluorescence signal. Intra-nuclear microtubules (iMt) were manually detected. For each iMt, a mean profile of Klp5-gfp intensity of 4-pixel width was computed. For normalization, intensities were divided by the median intensity of the profile. Then, for each range of length, the intensities of all iMts were averaged.

Quantification of microtubule dynamics. Microtubule dynamics quantification was performed with a custom ImageJ macro working as follows. The image stack was smoothed using the *Gaussian Blur* filter before applying a maximum Z-projection. The projected images were then filtered in the Fourier space to remove wavelengths larger than 12 pixels (0,8 μm) and smaller than 3 pixels (0,2 μm). ROIs were defined around individual interphasic microtubules and the *Triangle* auto-thresholding algorithm was applied in these regions. Binary images were then skeletonized to produce unidimensional shapes whose length L was extracted at each time-step. The curve L(t) is manually divided into growing and shrinking periods, fitted with a linear function to extract growing and shrinking rates.

Kymographs. Kymograph representations were performed with a custom Fiji macro available upon request (https://github.com/hadim/fiji_tools/blob/master/macros/AutoInstall/custom-macros.ijm#L45).

Characterization of amplitudes and periods of oscillations

Fast Fourier transform analysis

To characterize kinetochore oscillations, we performed Fast Fourier Transform (FFT) analysis

on each tracked trajectory of chromosome 2 (middle of the two Cen2-gfp spots; blue line in Fig. S3A). To convert the power spectrum into an amplitude of movement (in μm), we normalized it by the length of the signal and multiplied by 2 (half of spectrum is removed so energy must be preserved). Peaks were detected as local maxima of the FFT curve. Peaks with frequency lower than 5×10^{-3} Hz were excluded (high-pass filter). The peak of highest amplitude was used for the characterization of the oscillatory movement.

Detection of local maxima

To characterize kinetochore oscillations, we first smoothed kinetochore trajectories by fitting a spline function (red line in Fig. S3C). The middle time point between the two peaks of two consecutive local extrema defines the start of a semi-period and the following middle time point indicates the end of the semi-period (Fig. S3C).

Statistical analysis

Errors mentioned in text and figures indicate the standard error of the mean of the distribution (SEM) excepted when specified. The violin plots used in this paper combines a standard box plot with a density trace. Each circle represents a value in the dataset and the horizontal bar represents the mean of the distribution. Statistical tests were performed using the t-test (Python library Scipy, `scipy.stats.ttest_ind`). Statistical significance is defined as follows: p-value greater than 0.05 is labeled as NS, p-value lower than 0.05 as *, p-value lower than 0.01 as **, p-value lower than 0.001 as *** and p-value lower than 0.001 as ****.

Modeling

The source code of the mitotic model (Gay et al., 2012) is available under an open source license at https://github.com/bnol/kt_simul.

General assumption.

As previously described, Klp5 and Klp6 re-localize at the spindle midzone during anaphase (West et al., 2001). Thus, in the simulations the length-dependent mechanism described below was turned off during anaphase.

Length-dependent pulling force

In the initial model (Gay et al., 2012), the pulling force (F) applied on single attachment sites follows a linear force-velocity relationship:

$$(Eq. 1) F = \pi F_k \left(1 - \frac{v}{V_k} \right)$$

Where F_k and V_k are the stall force and the motor maximum velocity, v is the speed of the attachment site and π is the attachment state (equal to 1 when the site is attached to the correct pole, -1 when it is attached to the opposite pole and 0 when it is detached).

The length-dependent mechanism was implemented by adding a prefactor L_{dep} to this pulling force:

$$(Eq. 2) F = L_{dep} \pi F_k \left(1 - \frac{v}{V_k} \right)$$

L_{dep} is calculated according to the actual distance between the attachment site and its corresponding pole ($d_{site-pole}$) following a linear relationship:

$$(Eq. 3) L_{dep} = 1 + \alpha (d_{site-pole} + d_{mean})$$

Where α is a free parameter governing the strength of the relation between the distance $d_{site-pole}$ and force magnitude. d_{mean} is the average *in vivo* distance measured between the kinetochore attachment site and the pole during metaphase. Finally, $d_{site-pole}$ is the actual distance between the kinetochore attachment site and the pole. In this study we used $d_{mean} = 1 \mu\text{m}$ and $\alpha = 0.2$. The value of α is optimized to reproduce kinetochore centering as observed *in vivo*.

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FIGURE LEGENDS

Figure 1. The stability of sister kinetochore centering during metaphase depends on Kinesin-8 activity

(A-B) Typical time-lapse fluorescent images of wild type or *klp6Δ* cells expressing Cen2-gfp (centromeric region of chromosome 2) and Cdc11-gfp (spindle poles) during metaphase and anaphase. Frames were taken every 10 s. The lower panel is showing the corresponding trajectories of Cen2 (red) and SPBs (black) projected on a 1-D axis whose origin is the spindle center. **(C-D)** Mean positioning of centromere 2 as a function of time from metaphase to anaphase. For each time point, the absolute distance between Cen2 (red line) and the spindle center (purple line, 0 on the y axis) or between the poles (black line) and the spindle center was computed and averaged from multiple movies of mitotic cells. Pink and grey intervals indicate the standard deviations of the mean. **(E)** Global distribution of the normalized distances between Cen2 to the spindle center at anaphase onset in wild type (n=52), *klp6Δ* cells (n=63), *cdc25-22* (n=19) and *cdc25-22 klp6Δ* (n=26). Each distance *nd* between sister kinetochores to the spindle center is normalized according to spindle size so that sister kinetochore position varies between 0 (spindle center) to 0.5 (spindle poles). **(F)** Spindle size at anaphase onset in wild type (n= 52), *klp6Δ* cells (n=63), *cdc25-22* (n=19) and *cdc25-22 klp6Δ* (n=26).

Figure 2. Kinesin-8 dependent chromosome alignment is performed through an active process before metaphase

(A-B) Upper panel. Typical kymographs of wild type or *klp6Δ* cells expressing Ndc80-gfp (shown in red) and Cdc11-cfp (shown in green) from prophase to metaphase. Frames were taken every 5 s. The lower panel shows a computed kymograph where each time-point was normalized to the median intensity of the Ndc80 signal in the whole stack. **(C)** Upper panel; Average kinetochore distance to the spindle center normalized to spindle size. The position of the maximum peak of intensity in the normalized kymographs (example in lower panel A and B) is used to identify the average position of the three chromosomes (assuming that they are close to each other in prophase). Data obtained from multiple kymographs of cells (n=27 for wild type; n=34 for *klp6Δ*) were used to plot the average position of kinetochores according to time. The time zero represents phase 1 onset while error bars represents SEM. Note that the value of kinetochore positioning obtained at 4 min is very similar to Fig.1E. Lower panel; corresponding average spindle size.

Figure 3. Low doses of the microtubule-depolymerizing drug TBZ abolish chromosome oscillation but not centering

(A-B) Typical kymographs obtained at high frame rate (frames were taken every 0.1 s) and corresponding tracked trajectories of wild type or *klp6Δ* cells expressing Cen2-gfp (sister centromeres in red and their mid position in blue) and Cdc11-gfp (SPBs, black) during metaphase. **(C-D)** Typical kymographs obtained at high frame rate (frames were taken every 0.1 s) and corresponding tracked trajectories of wild type or *klp6Δ* cells expressing Cen2-gfp (sister centromeres in red and their mid position in blue) and Cdc11-gfp (SPBs, black) during metaphase, in the presence of 10 μ g/ml of TBZ.

Figure 4. Kinetochore oscillations are not required for the role of Kinesin-8 in chromosome congression

(A) Schematic representation of oscillation periods, amplitudes and drifts in kinetochore trajectories. **(B)** Periods of kinetochore oscillations obtained with the Fourier transform method during metaphase in wild type (control, n=24; TBZ, n=19) and *klp6Δ* (control, n=18; TBZ, n=14) cells in the presence or absence of 10 μ g/ml of TBZ. **(C)** Amplitude of kinetochore oscillations obtained with the Fourier transform method during metaphase in wild type (control, n=24; TBZ, n=18) and *klp6Δ* (control, n=19; TBZ, n=14) in the presence or absence of 10 μ g/ml of TBZ. **(D)** Global distribution of the normalized distances between Cen2 to the spindle center for each high frame rate time-point during metaphase in wild type (control, n=73460; TBZ, n=63390) and *klp6Δ* (control, n=89101; TBZ, n=59997). Each distance nd between sister kinetochores to the spindle center is normalized according to spindle size so that sister kinetochore position varies between 0 (spindle center) to 0.5 (spindle poles).

Figure 5. Kinesin-8 mutants display imbalanced traction forces at kinetochores leading to chromosome detachment and instability in kinetochore positioning

(A) Typical kymographs obtained at high frame rate (frames were taken every 0.1 s) of *klp6Δ* cells expressing Cen2-gfp (sister centromeres) and Cdc11-gfp (SPBs) during metaphase. Note the instability of kinetochore positioning in metaphase (also called drift; fig.4A). **(B)** Determination of drift amplitudes between each oscillation event during metaphase in wild type (control, n=171; TBZ, n=141) and *klp6Δ* (control, n=104; TBZ, n=114) cells in the presence or absence of 10 μ g/ml TBZ. **(C)** Typical kymograph obtained at high frame rate (frames were taken every 0.1 s) and

corresponding trajectories of *klp6Δ* cells expressing Cen2-gfp (sister centromeres, green), Cdc11-gfp (SPBs, green) and Mad2-mcherry (spindle checkpoint protein, red) during metaphase. The red circles on kinetochore trajectory and the red area illustrate the detection of Mad2-mcherry during the burst. **(D)** Determination of the maximum kinetochore speed at anaphase A in wild type and *klp6Δ* cells as compared to the maximum kinetochore speed during a detachment event (as judged by the Mad2 burst) in *klp6Δ* cells in metaphase.

Figure 6. Kinesin-8 accumulates at the tip of mitotic microtubules in a length-dependent manner

(A) Typical time-lapse fluorescent images of wild type cells expressing Atb2-gfp (tubulin) and Klp5-gfp (frames were taken every 5 s). Scale bar = 1 μ m. **(B)** Kymograph representation of Klp5-gfp localization on intra-nuclear microtubule (note the accumulation at the plus-end). Cells were blocked in G2 at the restrictive temperature, released into mitosis at 25°C and Klp5-gfp signal was captured at high frame rate (frames were taken every 2 s). **(C)** Klp5-gfp signal intensity is shown according to its position along mitotic microtubules for several sizes of microtubule. Multiple frames were used for each respective plot and originate from 37 individual cells (from top panel to bottom panel; 0.5 to 1 μ m, n=29; 1 to 2 μ m, n=240; 2 to 3 μ m, n=154; 3 to 4 μ m, n=81). Blue lines indicate mean values and cyan intervals represent standard deviations. **(D)** Normalized Klp5-gfp intensities at the plus end of microtubules as a function of intra-nuclear microtubule length (0.5 to 1.0 μ m, n=29; 1.0 to 1.5 μ m, n=94; 1.5 to 2.0 μ m, n=146; 2.0 to 2.5 μ m, n= 90; 2.5 to 3.0 μ m, n=64; 3.0 to 3.5 μ m, n=59). The blue bars indicate standard error of the mean (SEM).

Figure 7. A length-dependent pulling force centers kinetochores and prevents lagging chromosomes in a force-balance model.

(A) Schematic representation of the metaphase spindle. The two SPBs (black) are linked by overlapping interdigitated microtubules (orange). The chromosome (grey) is linked to the SPBs by its centromere regions (green). The three microtubule-binding sites located on each kinetochore (purple) are connected to the SPBs by ktMTs (blue lines). The two sister chromatids are held together by the cohesin complex (red). **(B)**. Biophysical representation of the metaphase spindle. The SPBs are linked by the interdigitated microtubule force generator (F_{mz} , orange). Each microtubule attachment site on the kinetochore (purple) is linked to the SPB through a ktMT (blue). The three microtubule-binding sites (purple) are associated to the chromosomes by the centromere (green) and represented by a spring and a dashpot (purple). Cohesin between the sister chromatids

(red) is modeled as a single spring linking both centromeres (K_c). A simple stochastic process of microtubule attachment and detachment reproduces the directional instability. At any time, MT attachment sites (purple) attach with the frequency k_a (force F_k is ON) or detach with the frequency k_d (force F_k is OFF). This attachment/detachment process leads to an imbalance of the forces applied on the chromosome and to chromosome dynamics within the spindle. The parameter d_α (Aurora B-like activity) modulates the probability of microtubule detachment as a function of the distance between the microtubule attachment site and the centre of the kinetochore pair. Thus, the parameter d_α is defined as the spatial range of Aurora B activity. The kinetochore orientation effect parameter (β) controls the probability for a new kinetochore-microtubule attachment to be correct or incorrect depending on the previous attachment state of the kinetochore to the poles. When β equals 1 and the kinetochore is attached to a single spindle pole, the next attachment cannot be erroneous. When β equals 0, correct or erroneous attachments are equiprobable (the model parameters are detailed in Gay et al. 2012). **(C-D)** Top panels. Diagrams depicting the presence (D) or absence (C) in the force balance model of a length dependent pulling force (Movie S7 for animated trajectories). Lower panel. Typical *in silico* trajectories of the 3 pairs of kinetochores (blue, red, green) and the two SPBs (black) obtained in the presence (D) or absence (C) of a length-dependence pulling force. **(E)** Distance (nd) between kinetochores to spindle center at anaphase onset normalized according to spindle length *in vivo* (wild type, n=52 and *klp6Δ*, n=63) or *in silico* (in the presence, n=600 or absence of length-dependence, n=600). **(F)** Kinetochore lagging time from anaphase A onset *in vivo* (wild type, n=37 and *klp6Δ* cells, n=34) or *in silico* (in the presence, n=503 or absence of length-dependence, n=451).

Figure 8. Influence of several model parameters on kinetochore alignment.

(A) Normalized distance between sister kinetochore position to the spindle center at anaphase onset. Several model parameters were either increased (High) or decreased (Low) as compared to the default value (table S1) to study their influence on kinetochore alignment. Simulations were obtained with the length-dependent pulling force turned off. These parameters correspond to several functions within the spindle (ie. Microtubule dynamics, correction of Kt-MT attachment, kinetochore, cohesion, spindle midzone motor). **(B)** Simulations showing the impact of parameters found to increase kinetochore alignment in the absence of a length-dependent mechanism. Left panel: Increasing the rate of attachment/detachment, K_α had a dramatic effect on mitotic progression such as failure to maintain spindle size in metaphase or presence of unattached kinetochores. Middle panel: The parameter d_α which represents the typical range of action of

Aurora B (red) favors kinetochore alignment when it is decreased. However, in this condition, kinetochore attachments are hyperstabilized, kinetochores exhibit almost no dynamicity and merotelic kinetochore attachment is frequent (see Gay et al. 2012). Right panel: Diminishing the parameter k_c (cohesin spring constant) also seems to favor kinetochore alignment. However, this phenotype is due to the unrealistic inter-kinetochore distance reaching the entire spindle length (about 2 μm) while the *in vivo* value only equals 0.5 μm . In this condition, each chromatid is pulled towards a pole and the position of the sister kinetochores corresponds to the spindle center.

SUPPLEMENTAL INFORMATION

The supplemental information contains 3 figures, 2 tables and 7 movies

Figure S1. *klp5Δ* or double mutant *klp5Δ klp6Δ* are deficient for chromosome centering.

(A-B) Typical time-lapse fluorescent images of *klp5Δ* or *klp5Δ klp6Δ* double mutant expressing Cen2-gfp (centromeric region of chromosome 2) and Cdc11-gfp (SPBs) during metaphase and anaphase. $\Delta t = 10$ s. The lower panel is showing the corresponding trajectories of Cen2 (red) and SPBs (black) projected on a 1-D axis whose origin is the spindle center. **(C)** Spindle size at anaphase onset for various cell type: wild type (n=52, with TBZ n=21), *klp6Δ* (n=63, with TBZ, n=36), *klp5Δ* (n=30), *klp5/6Δ* (n=21). **(D)** Global distribution of the relative distances between Cen2 to the spindle center at anaphase onset in wild type (n=52), *klp6Δ* cells (n=63), *klp5Δ* cells (n=30), *klp5/6Δ* cells (n=21), wild type cells with low dose of TBZ (n=21), *klp6Δ* cells with low dose of TBZ (n=36), *cdc25-22* cells (n=19) and *cdc25-22 klp6Δ* cells (n=26). Each distance d between sister kinetochores to the spindle center is normalized according to spindle size so that sister kinetochore position varies between 0 (spindle center) to 0.5 (poles).

Figure S2. Analysis of microtubule dynamics in the presence or absence of TBZ.

(A). Microtubule growth rate for wild type (n=22, with TBZ n=19) and *klp6Δ* (n=27) cells. **(B)**. Microtubule shrinkage rate for wild type (n=29, with TBZ n=33) and *klp6Δ* (n=37) cells. **(C)**. Microtubule catastrophe frequency for wild type (n=19, with TBZ n=15) and *klp6Δ* (n=17) cells. **(D)**. Microtubule rescue frequency for wild type (n=20, with TBZ n=26) and *klp6Δ* (n=21) cells.

Figure S3. Characterization of kinetochore oscillation periods and amplitudes.

(A). Kinetochore (Cen2) trajectories used to illustrate oscillation analysis (frames were taken every 0.1 s). The blue line represents the middle of the Cen2 spots (shown in red). **(B)** Fourier transform analysis of kinetochore trajectories. The peak of highest amplitude is identified in the Fourier spectrum of each kinetochore trajectories obtained from high frame rate experiments. The corresponding amplitudes are reported as a function of the half periods of oscillations. **(C)** Position of the middle of Cen2 spots according to time (blue). This trajectory is interpolated by a spline function (red). The local maxima of the interpolated curve are identified and used to determine half

periods ($T_{1/2}$, horizontal arrow) and amplitudes (A, vertical arrow) in kinetochore trajectories. **(D-E)**. Amplitude and period comparison between the two methods (see B and C) in various cell lines (wild type and *klp6Δ*) and different conditions (presence or absence of low doses of TBZ). Note that the two methods reproduce qualitatively but not quantitatively the differences between wild type or mutant cells. **(F-G)**. Amplitudes and periods in wild type and *klp6Δ* cells in control or *cdc25-22* background. Amplitudes and periods are not significantly different when cells are elongated in a *cdc25-22* background. Amplitude: wild type (n=24, *cdc25-22* n=13), *klp6Δ* (n=18, *cdc25-22* n=13). Period: wild type (n=24, *cdc25-22* n=13), *klp6Δ* (n=18, *cdc25-22* n=13).

Supplemental Table 1: List of parameters and default values used in the study

| Parameter | Description | value |
|------------|---|-------|
| L_{dep} | Factor controlling force load on kinetochore in a length dependent manner | 0.2 |
| K_α | Microtubule Attachment/detachment rate per min | 3.6 |
| d_α | Range of action of Aurora like activity (μm) | 0.05 |
| β | Kinetochore orientation parameter | 1 |
| V_k | Kinetochore maximum velocity ($\mu\text{m}/\text{min}$) | 2.4 |
| F_k | Kinetochore stall force (pN) | 10 |
| K_c | Cohesin spring constant (pN/ μm) | 67 |
| M_k | Number of microtubules per kinetochore | 3 |
| F_{mz} | Midzone force generator stall force (pN) | 58 |
| V_{mz} | Midzone force generator maximum velocity ($\mu\text{m}/\text{min}$) | 1.2 |

Supplemental Table 2: Strains used in this study

| Strain number | Genotype | Reference |
|---------------|---|------------|
| ST1237 | <i>cdc11-gfp::kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp</i> | This study |
| ST1266 | <i>cdc11-gfp::kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp klp5::ura4</i> | This study |
| ST1442 | <i>cdc11-gfp-kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp cdc25-22</i> | This study |
| ST1522 | <i>cdc11-gfp-kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp cdc25-22 klp6::his3</i> | This study |
| ST1375 | <i>h- klp5-GFP::kr leu1-32 ura4-D18 pPT77 nmt1-ura4-mRFP-atb2</i> | This study |
| ST945 | <i>klp5-GFP cdc25-22 ndc80-CFP-kr cdc11-CFP-kr</i> | This study |
| ST1513 | <i>cdc11-gfp-kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp klp6::his3 mad2mcherry:CLONAT</i> | This study |
| ST1513 | <i>ndc80-GFP:kr cdc11-CPF:kr</i> | This study |
| ST1539 | <i>ndc80-GFP:kr cdc11-CPF:kr klp6::his3</i> | This study |
| ST1516 | <i>cdc11-gfp-kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp klp5::ura4</i> | This study |
| ST1518 | <i>cdc11-gfp-kr cen2(D107)-kanR-ura4+-lacO his7+-lacI-gfp-gfp klp5::ura4 klp6::his3</i> | This study |

Supplemental Movies

Movie S1

Fluorescent time-lapse imaging of centromere 2 (Cen2-gfp) and spindle pole (Cdc11-gfp) dynamics in a wild type fission yeast cell. Frames were taken every 10 s.

Movie S2

Fluorescent time-lapse imaging of centromere 2 (Cen2-gfp) and spindle pole (Cdc11-gfp) dynamics in a *klp6Δ* cell. Frames were taken every 10 s.

Movie S3

High frame rate fluorescent time-lapse imaging of centromere 2 (Cen2-gfp) and spindle pole (Cdc11-gfp) dynamics in a wild type fission yeast cell. Frames were taken every 0.1 s.

Movie S4

High frame rate fluorescent time-lapse imaging of centromere 2 (Cen2-gfp) and spindle pole (Cdc11-gfp) dynamics in a *klp6Δ* cell. Frames were taken every 0.1 s.

Movie S5

Fluorescent time-lapse imaging of tubulin (Atb2-rfp) and Kinesin-8 (Klp5-gfp) during metaphase showing Klp5 accumulation at the tip of an intranuclear microtubule bundle. Frames were taken every 5 s.

Movie S6

High frame rate fluorescent time-lapse imaging of Klp5-gfp during metaphase. Frames were taken every 2 s.

Movie S7

Cartoon recapitulating a typical simulation calculated with the force balance model of the mitotic spindle. The position of spindle poles and kinetochores are shown, as well as the attachment state of each attachment site (green = correct attachment, red = incorrect attachment, blue = unattached).

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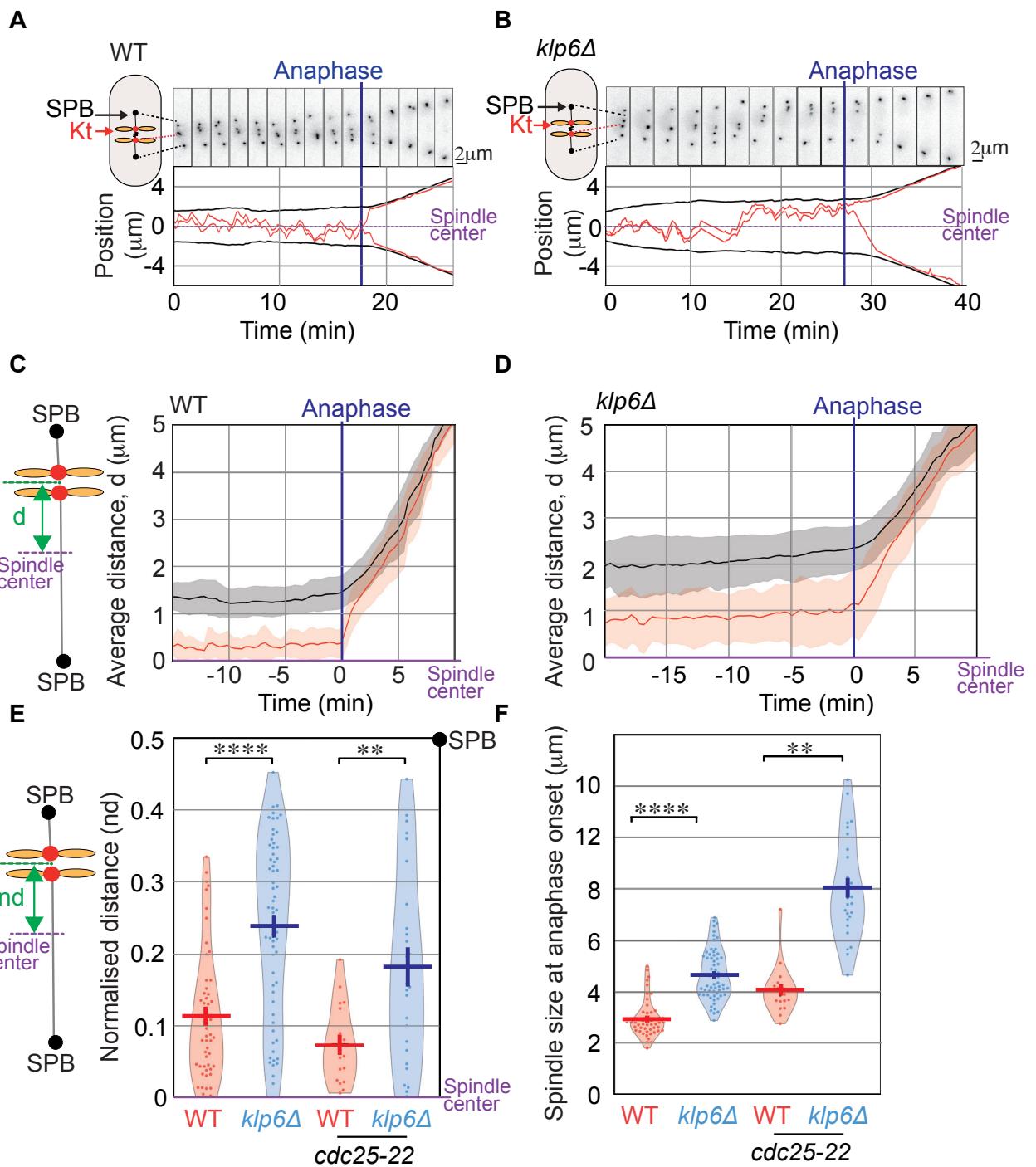
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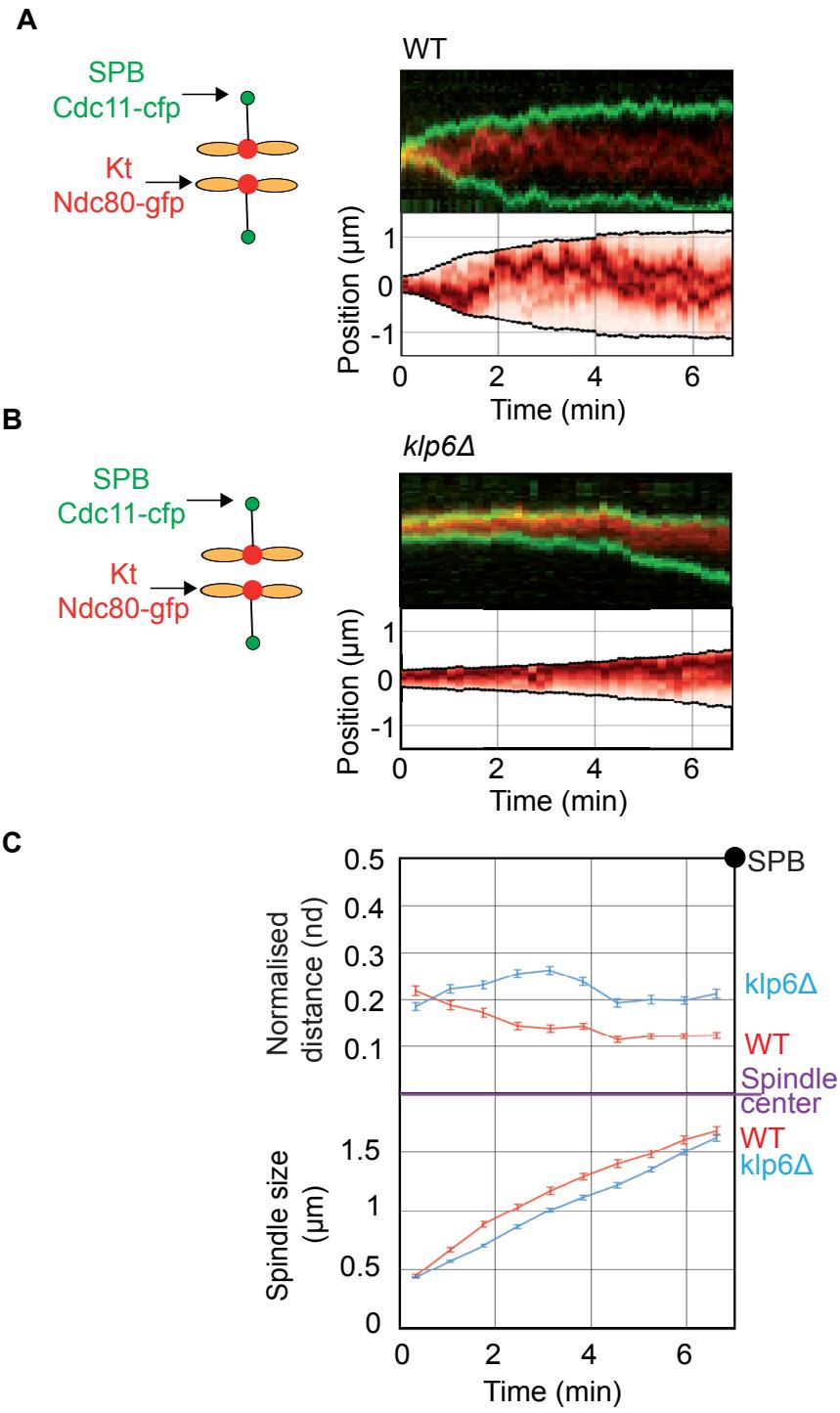
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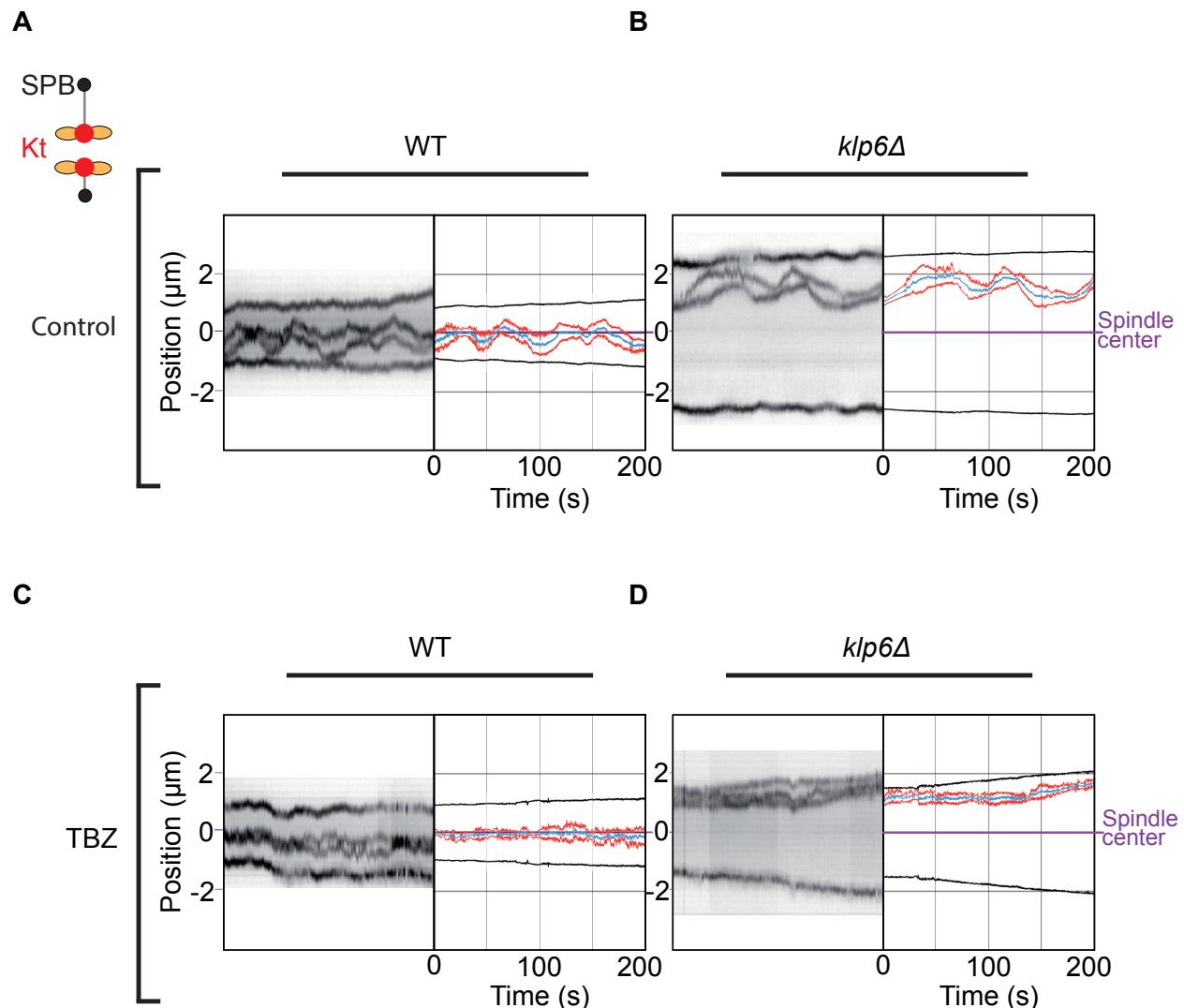
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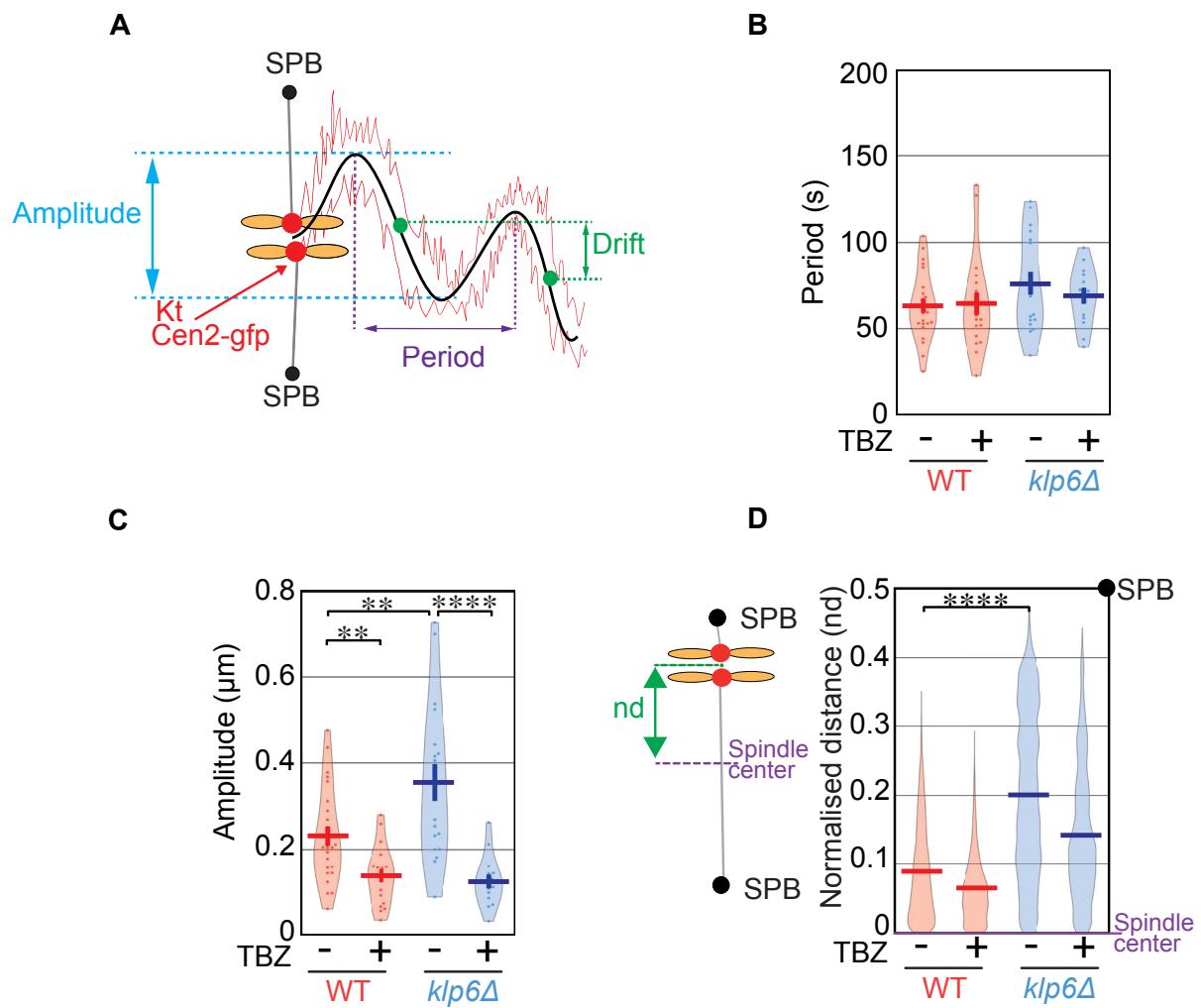


Mary et al. Figure 1

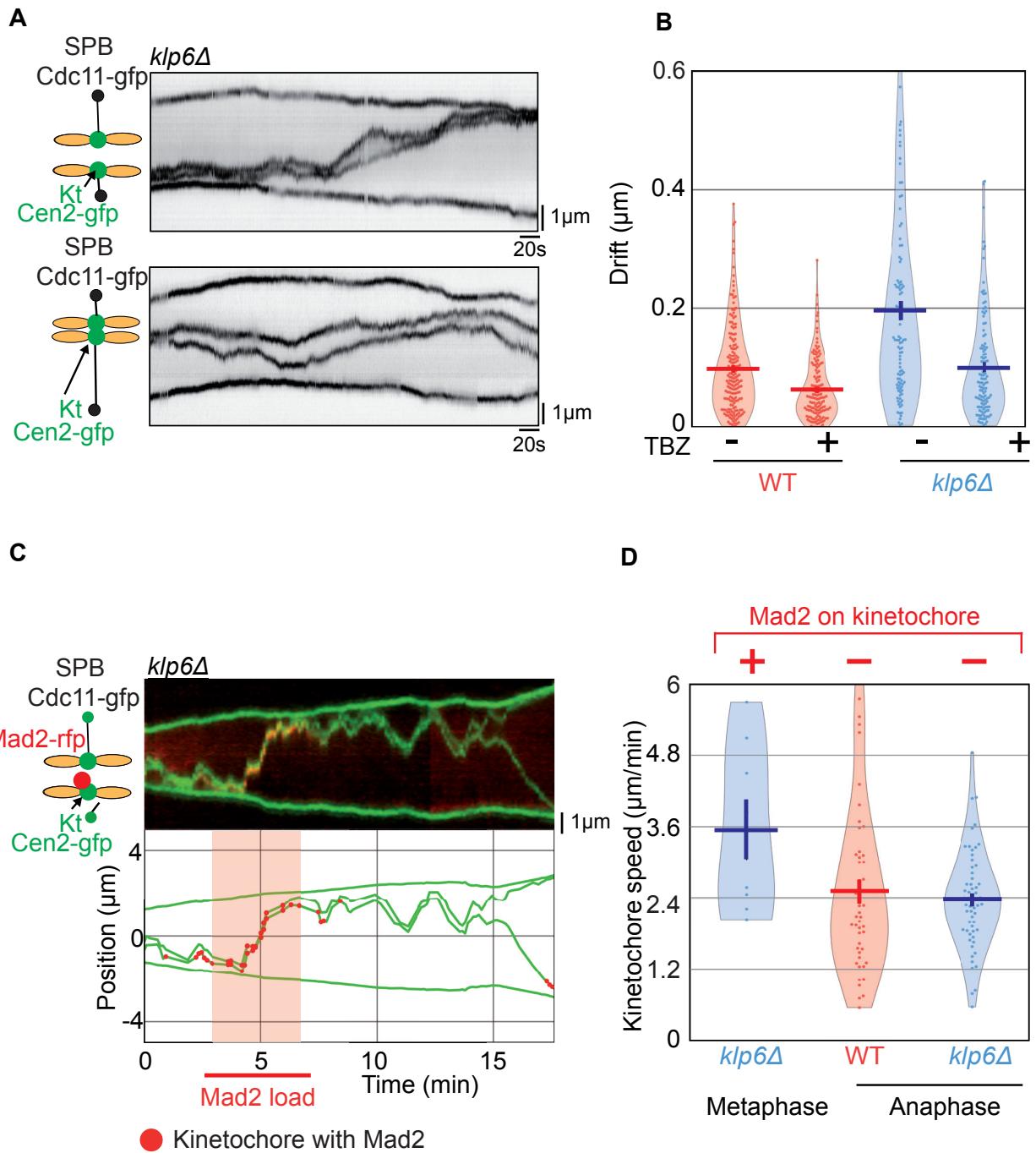


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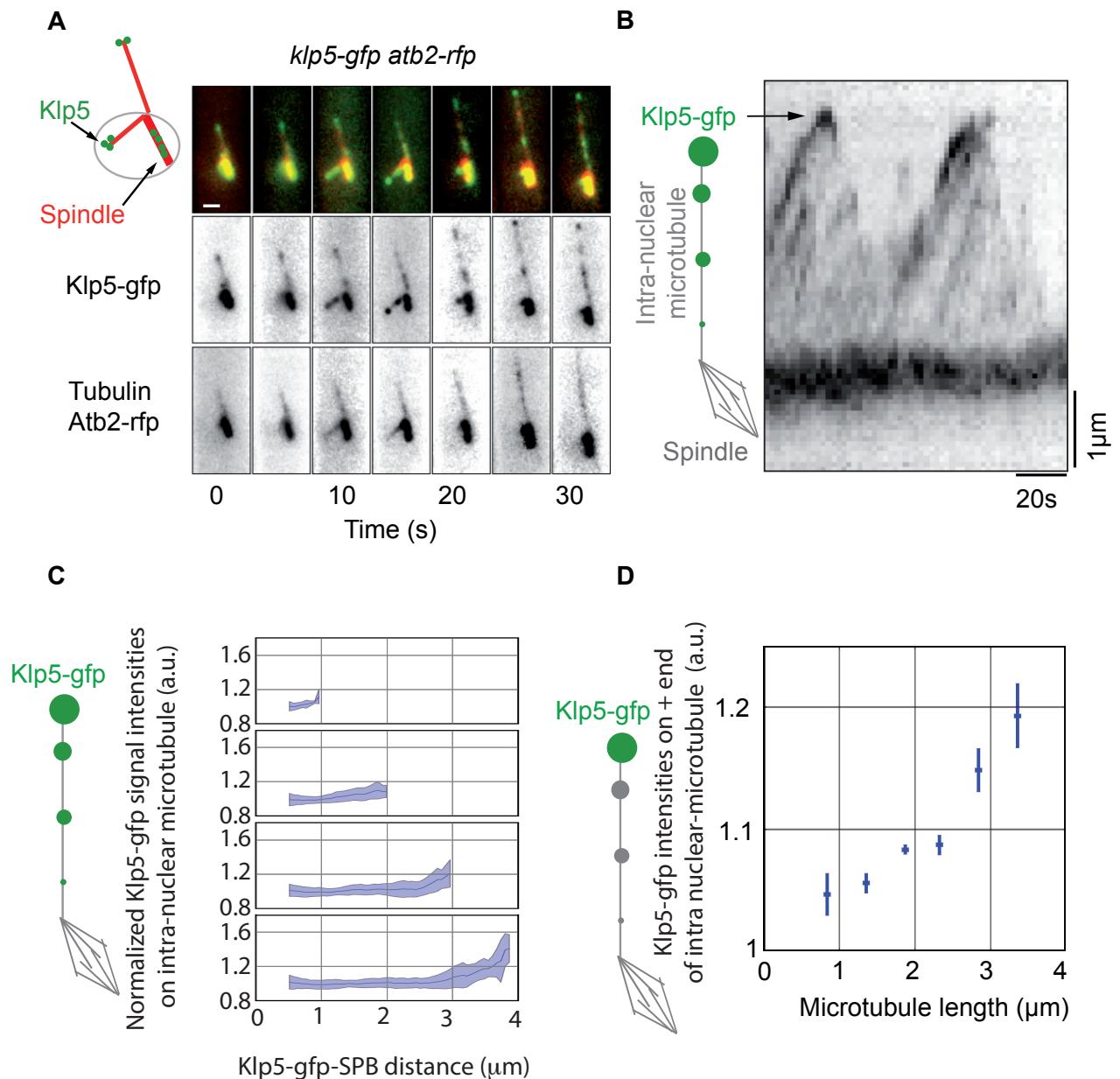




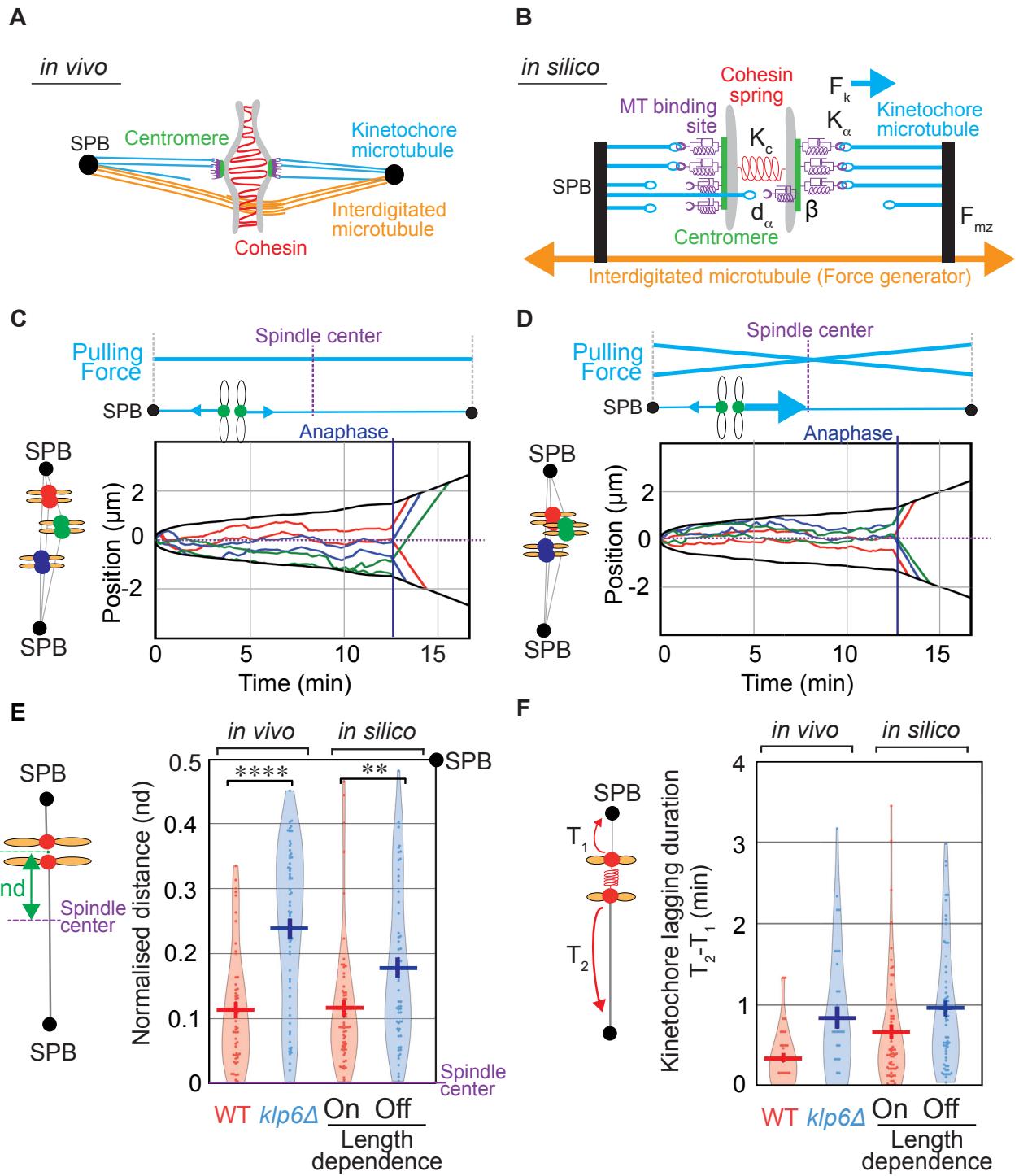
Mary et al. Figure 4



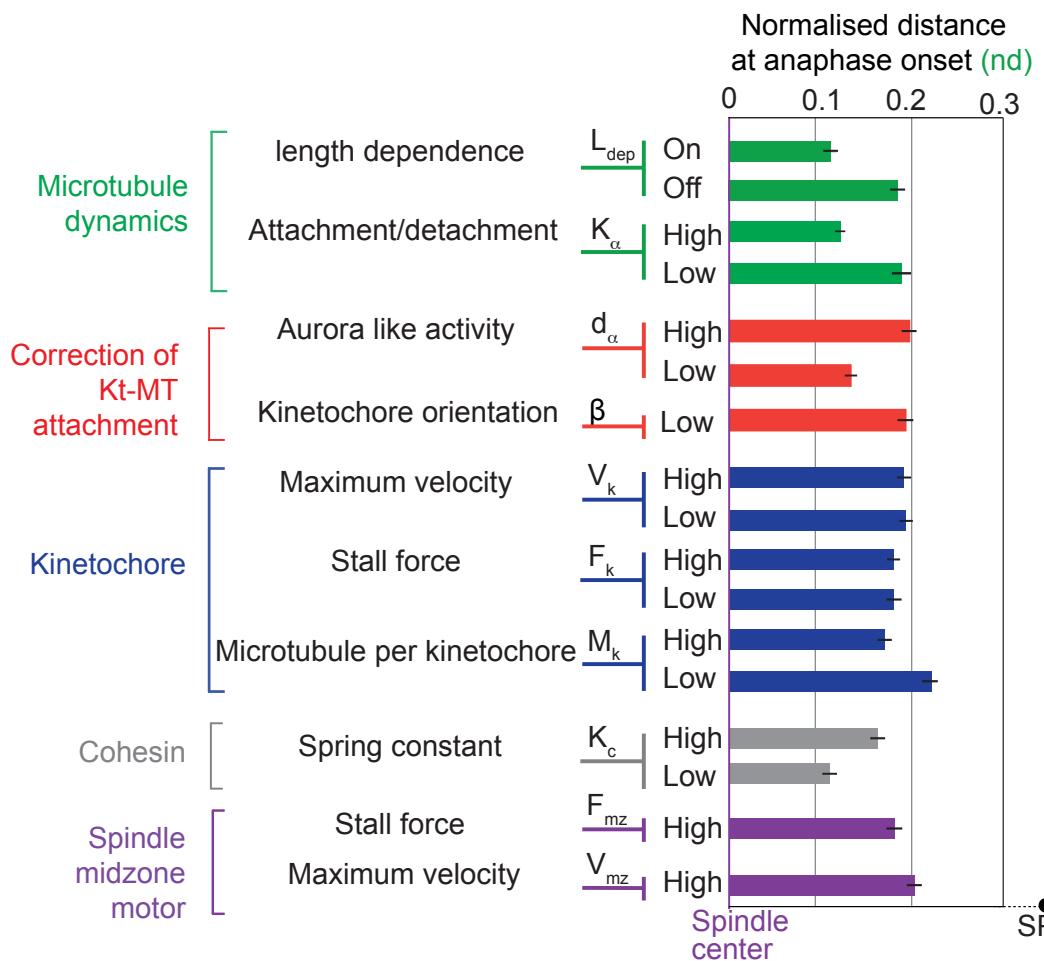
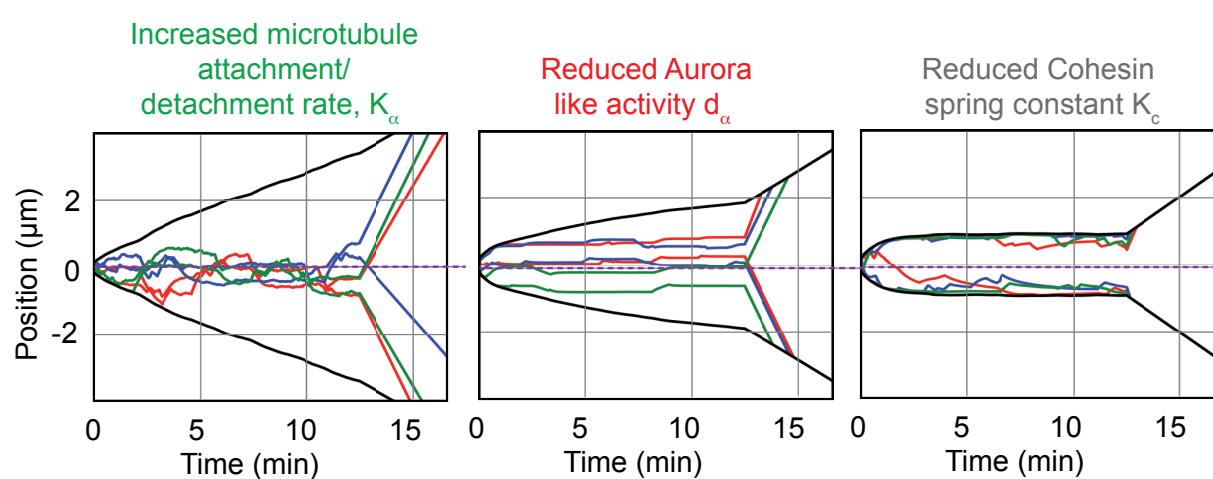
Mary et al. Figure 5



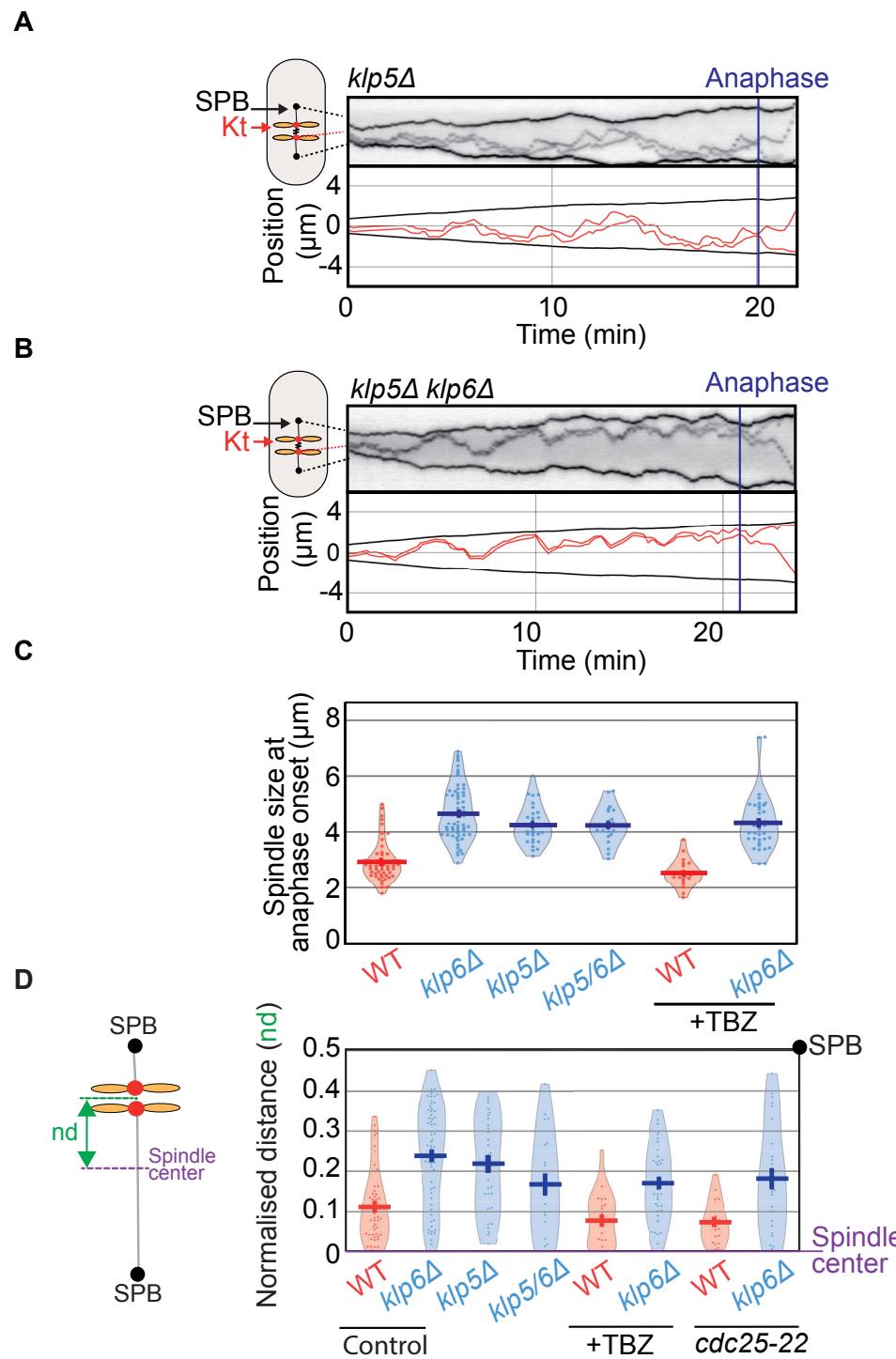
Mary et al. Figure 6



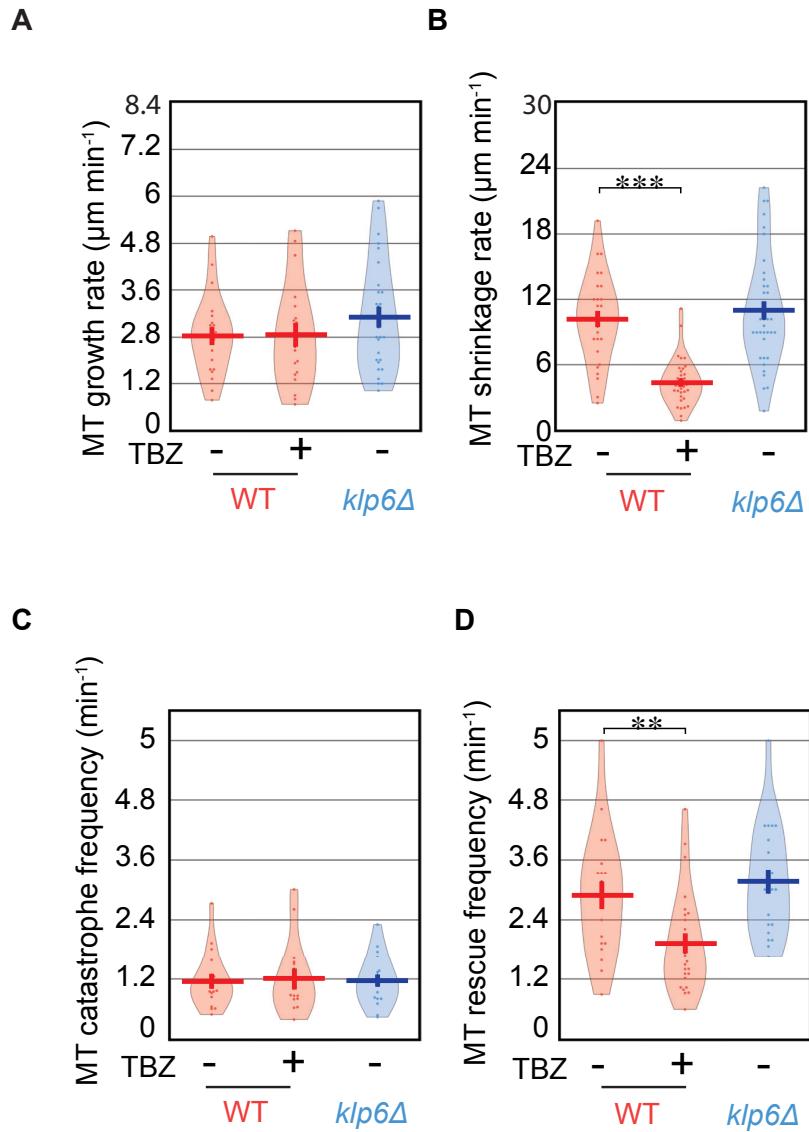
Mary et al. Figure 7

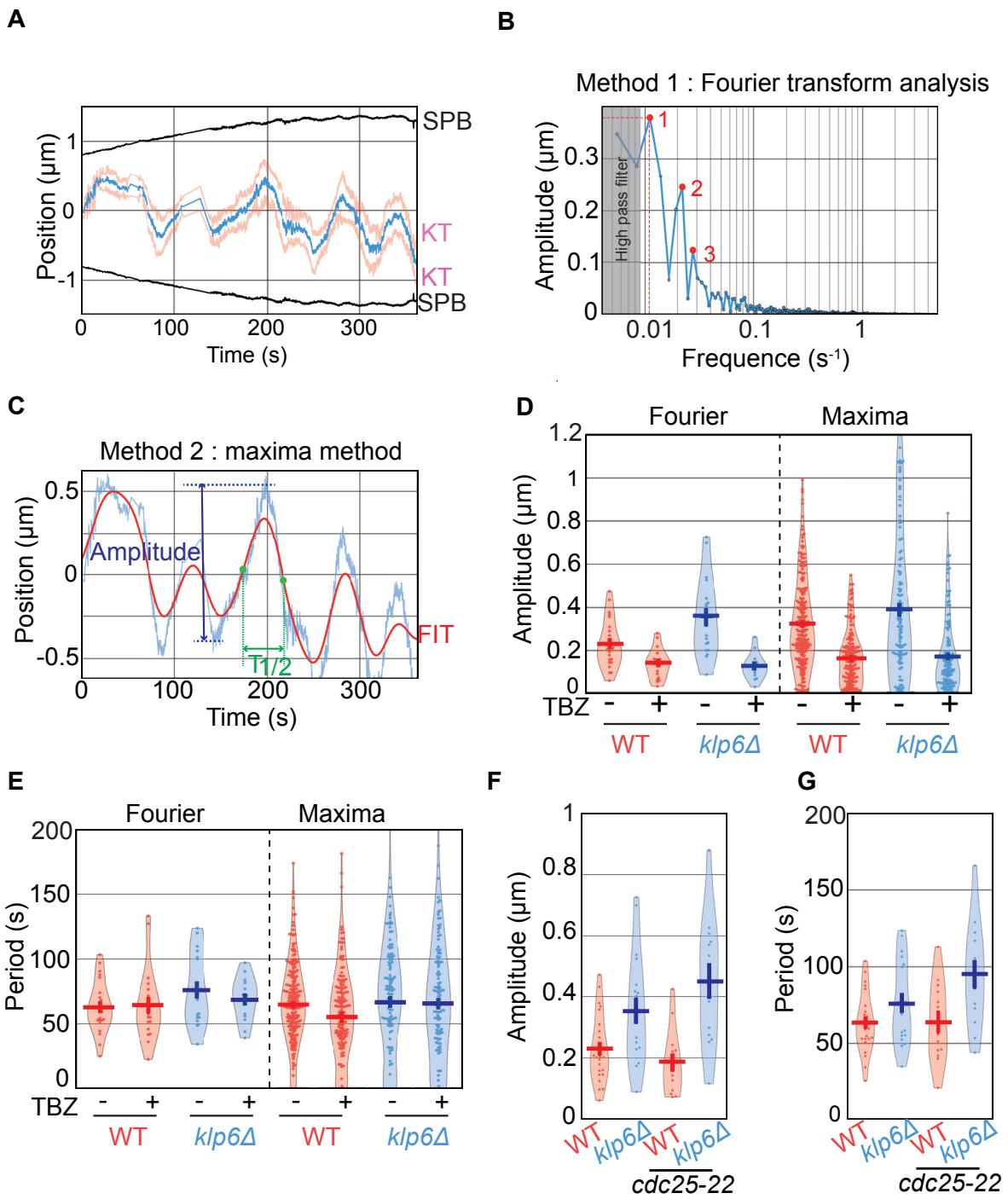
A**B**

Mary et al. Figure 8



Mary et al. Figure S1





Mary et al. Figure S3

2.2 Modélisation bio-mécanique du fuseau mitotique

- parler modèle d'attachement à deux états et des avantages d'un modèle à trois états

3

Discussion

- 3.1 Le mouvement de chromosomes durant la mitose**
- 3.2 Le mécanisme d'alignement des chromosomes: de l'*in silico* à l'*in vivo***

A

Annexes

A.1 Annexe 1 : bla bla bla bla

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