

## Review

# Understanding microtubule dynamics for improved cancer therapy

S. Honore, E. Pasquier and D. Braguer\*

FRE-CNRS 2737, UFR Pharmacie, 27 bd Jean Moulin, 13005 Marseille (France), Fax: +33 4 91 83 56 35, e-mail: diane.braguer@pharmacie.univ-mrs.fr

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**Abstract.** Microtubules (MTs), key components of the cytoskeleton, are dynamic polymers of tubulin that form a well-organized network of polarized tube filaments. MT dynamics are highly regulated both spatially and temporally by several MT-related proteins, themselves regulated by several kinases and phosphatases via signaling cascades, and also by coordinated interactions with actin cytoskeleton and adhesion sites. Regulation of MT dynamics is crucial for mitosis, cell migration, cell sign-

aling and trafficking. MT-targeted drugs (MTDs), which constitute a major anticancer drug family with antimitotic and antiangiogenic properties, inhibit tumor progression mainly by altering MT dynamics in both cancer and endothelial cells. Identification of proteins regulating the MT network will lead to a better understanding of tumor progression regulators and will be helpful in improving cancer therapy.

**Key words:** Microtubule dynamics; tumor progression; microtubule-targeted drugs; mitosis; migration; cytoskeleton.

## Introduction

Microtubules (MTs) are dynamic polymers of  $\alpha/\beta$  tubulin heterodimers, arranged head to tail to form hollow tubes of 25 nm diameter, up to several micrometers long. The two MT poles differ in their dynamic properties, the plus end being more dynamic than the minus end. In eukaryotic cells, MTs form a well-organized network in which the minus ends are generally anchored at the centrosome or MT organizing center (MTOC) whereas the free plus ends probe the cytoplasm, in a search-and-capture-process, to reach specific targets. MT dynamics are tightly regulated both spatially and temporally. This

regulation involves nucleotides, MT-associated proteins (MAPs), kinases and phosphatases as well as coordinated interactions with other cytoskeletal components, such as actin filaments, and integrin-containing adhesion sites. This intrinsic dynamic behaviour and its regulation are crucial for MT-specific functions such as cell shape maintenance, cell division, cell signaling, intracellular vesicles and organelle transport, cell polarity and locomotion. Disturbance of MT dynamics regulation thus has critical consequences for cell fate and represents a potent therapeutic target, especially in oncology.

Here, we present a review of the most recent studies focusing on the regulation of MT dynamics, investigating their involvement in mitosis and migration, and the effects of MT-targeted anticancer drugs (MTDs) on these dynamic properties during tumor growth and neoangiogenesis.

\* Corresponding author.

## Microtubule dynamics

### Dynamic instability and treadmilling of microtubules

Polymerization of MTs occurs by a nucleation-elongation mechanism in which the formation of a short MT 'nucleus' is followed by elongation of the MT at its ends by reversible, non-covalent addition of  $\alpha/\beta$  tubulin dimers. In 1984, Mitchison and Kirschner [1, 2] proposed the dynamic instability model of MT assembly, in which individual MTs exist either in an elongation state or a rapidly shortening state, with abrupt and apparently random transitions between these two states. Several studies performed *in vitro*, using purified tubulin [3, 4], or in living cells [5] have confirmed this mechanism of MT assembly/disassembly. MTs are thus governed by an intrinsic property involving repetitive spurts of shortening from their plus ends, followed by periods of polymerization. This non-equilibrium behavior is based on the binding and hydrolysis of GTP at the nucleotide exchangeable site (E-site) in  $\beta$  tubulin. Only dimers that have GTP in their E-site can polymerize. This nucleotide is then hydrolyzed and becomes non-exchangeable. The GTP cap model proposes that the GDP-tubulin core of MT is stabilized at the plus end by a layer of GTP-tubulin subunits that may act to maintain association between protofilaments [6, 7]. When this cap is stochastically lost, the protofilaments peel outward and the MT rapidly depolymerizes. Although both MT ends can either grow or shorten, the changes in length at the plus end are much greater than at the minus end.

MTs exhibit another important dynamic behavior called treadmilling or flux. It corresponds to a polymer mass steady state resulting from the net growth at one MT end and the net shortening at the opposite end [8]. In other words, treadmilling is a process by which tubulin subunits continuously flux from one end of the polymer to the other, due to net differences in the critical subunit concentrations at the opposite MT ends.

Both dynamic instability and treadmilling can be produced as distinct phenomena *in vitro* using purified tubulin, and they have also been observed in living cells [8, 9]. These dynamic properties have been recently reviewed [10, 11].

### Microtubule dynamics analysis in living cells

Dynamic instability is characterized by four main parameters: the rates of MT growth and shortening, the frequency of transition from growth or pause to shortening (called catastrophe) and the frequency of transition from shortening to growth or pause (called rescue). Periods of pause are the condition in which changes in MT length are drastically attenuated or completely stopped. The parameter called 'dynamicity' is used to describe the overall rate of tubulin subunits exchange at MT ends [12]. Several techniques can be used to measure MT dynamics

in living cells. Individual fluorescent MTs can be readily visualized in thin peripheral regions of cells after microinjection of fluorescent tubulin (e.g. rhodamine-labeled tubulin) or by expression of GFP-labeled tubulin. MT growth and shortening dynamics are recorded by time-lapse video microscopy. To determine how MT length changes with time, individual MTs ends are traced by a cursor on succeeding time-lapse frames. Rate, length and duration of growth and shortening events are calculated from the recorded x-y positions of the MT ends.

While it was possible to measure dynamic instability of individual MTs at the cell periphery, direct measurements in the cell interior were nearly impossible because of the cell shape and the high number of MTs in this zone. The use of GFP-labeled proteins that specifically bind MT plus ends, such as EB1, made it possible to follow some parameters of MT dynamics (i.e. MT growing events) throughout the cell and was particularly useful for examining MT dynamics during mitosis [13, 14].

MT dynamic behavior can also be estimated by fluorescence recovery after photobleaching (FRAP) of YFP- or GFP-tubulin [15, 16]. This technique enables measurement of MT turnover, which reflects both dynamic instability and treadmilling. In addition, this technique appears to be very useful as MT dynamics seem to differ according to the proximity of MTs with the centrosome [17].

### Regulation of microtubule dynamics in cells

Using the photobleaching strategy, Komarova et al. were able to image MT dynamics deep in the cytoplasm of CHO and NRK cells [17]. The majority of nascent MTs begin to grow from the centrosome without experiencing a shortening phase until they reach the cell cortex. In other words, dynamic instability is highly suppressed in the cell interior. This protection against depolymerization in the cell interior may be mediated by a kinesin-dependent pathway [18]. Several lines of evidence also implicate the actin cytoskeleton in stabilizing and guiding the MTs on their trek from the centrosome to the cell periphery [19, 20]. Indeed, dual-wavelength fluorescent speckle microscopy (FSM) [21] reveals growth of MTs along F-actin bundles in epithelial cells [22]. In addition, myosins sliding along actin filaments help in guiding MTs toward the actin-rich cortex [23].

In living cells, MT dynamics are regulated both spatially and temporally. In fact, MTs interact with an impressive number of binding proteins, and cellular MT dynamics are thus the result of the combined effect of stabilizing and destabilizing factors. Regulation can occur at many levels, some proteins regulating tubulin folding, some stabilizing existing MTs such as structural MAPs, and some interacting with MT ends to influence their dynamics, location and lifespan. The main MT-related proteins that regulate MT dynamics are presented in Table 1 and figure 1.

Table 1. Major microtubule-related proteins and their effects on MT dynamics

	MT-related proteins and homologues	Effects on MT dynamics	References
<b>Structural MAPs</b>	MAP1A; MAP1B; MAP2; MAP4; Tau	MT stabilization MT cross-linking suppression of MT dynamics	[39; 41]
<b>Destabilizing +TIPs</b>	kinesin-13 family	MT depolymerization catastrophe factors anti-rescue factors	[48; 49; 54]
<b>Stabilizing +TIPs</b>	EB1, 2, 3	MT stabilization MT elongation	[55; 62]
	Dis1/TOG family	MT polymerization anti-catastrophe factors	[57; 64; 65]
	CLIP family CLIP 170 ; CLIP 115	MT stabilization and capture at the cell cortex rescue factor	[58; 68; 69; 70]
	CLASPs	MT stabilization and capture at the cell cortex rescue factor suppression of MT dynamics	[58; 76]
	LIS1	anti-catastrophe factor	[60]
	dynactin	MT nucleation	[55]
	APC	MT polymerization MT stabilisation	[63]
	ACF7	actin cross-linking MT stabilization and capture at the cell cortex suppression of MT dynamics	[59]
<b>Stathmin</b>	stathmin	MT depolymerization catastrophe factor tubulin sequestering activity	[79]

**Regulation by tubulin folding and isotype composition.** Tubulin undergoes a complex folding and association process of one  $\alpha$  and one  $\beta$  subunit. Monomer folding by the chaperonin CCT (chaperonin-containing TCP-1) and the formation of functional dimers by folding cofactors determine, together with transcriptional control, the amount of tubulin subunits available to polymerise which may influence MT dynamics [24].

In vertebrates, there are six  $\alpha$  and seven  $\beta$  tubulin genes identified so far, leading to isotypes which mainly differ by their C-terminal sequences [25]. Tubulin isotypes are differently expressed depending on the stage of development and tissue. *In vitro*,  $\beta$  tubulin isotype composition strongly influence MT dynamics [3, 26, 27]. In addition, the C-terminal sequence, which differs among isotypes, is the major MAP binding site. Thus, isotype composition of MTs is involved in dynamics regulation. Some tubulin isotypes, such as class III  $\beta$  tubulin, were found to be overexpressed in tumors [28, 29]. This isotypic selection of tubulin in tumors may have important consequences for MT dynamics regulation and for the sensitivity or resistance to MTDs [29–34].

**Structural MAPs.** MT stability is promoted to a large degree by MAPs. One major family of MAPs, called

structural MAPs, which includes MAP1A, MAP1B, MAP2, MAP4 and Tau, is responsible for cross-linking and stabilizing MTs in the cytosol (table 1 and fig. 1). MAP1A and MAP1B are large, filamentous molecules found mainly in axons and dendrites of neurons [35, 36]. MAP2, MAP4 and Tau are characterized by the presence of three or four repeats of an 18-residue sequence in their MT binding domain. MAP2 is found in dendrites, where it forms fibrous cross-bridges between MTs, and it also associates MTs with intermediate filaments. MAP2 expression has also been reported in non-neuronal tissues such as hair follicles [37]. MAP4, the most ubiquitous MAP, is found in neuronal and non-neuronal cells. Tau, which is much smaller than most other MAPs, is present in both axons and dendrites but also in other cell types, such as endothelial cells [unpublished observation] [38]. Dhamodharan and Wadsworth demonstrated that MAP2 and partially purified preparation of brain MAPs drastically suppress MT dynamic instability by decreasing the rate and extent of MT growth and shortening events, increasing the percentage of time spent in pause and decreasing the catastrophe frequency [39]. MAP2 is distributed inhomogeneously along MT length by forming high-density regions, which is important for its function as stops of depolymerization occur at these cluster sites [40].

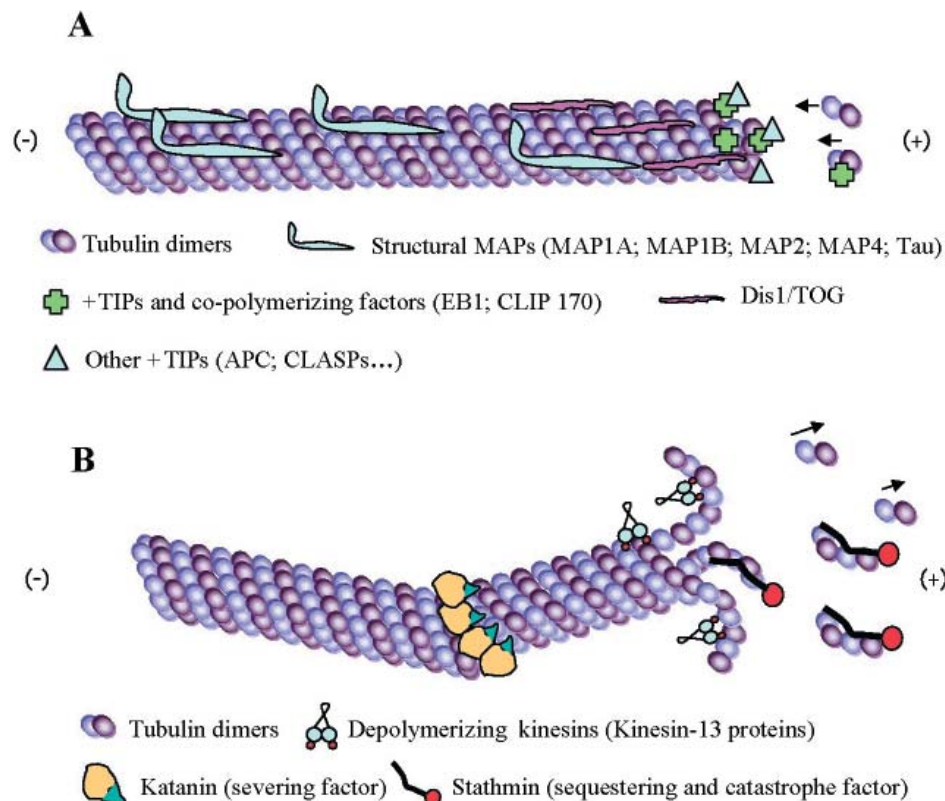


Figure 1. MT interactions with the major MT-related proteins. (A) A growing MT and various interactions with stabilizing factors. (B) A shortening MT and various interactions with destabilizing factors. (–) and (+) indicate the minus and the plus ends of the MT, respectively.

MAP effects on the dynamic instability parameters may, however, vary among the MAPs, and also among the different isoforms of a given MAP. For example, Tau protein exists in six isoforms derived from alternative splicing of a Tau messenger RNA (mRNA) and differs by the presence of either three- or four-repeat MT binding domains (3R and 4R, respectively). Bunker et al. demonstrated that 4R Tau reduced the rate and extent of both growth and shortening events in MCF7 cells expressing GFP tubulin, whereas 3R Tau was three-fold less potent than 4R Tau and had only a minimal ability to suppress shortening events [41]. This research group also analyzed the effects of 3R and 4R Tau proteins on MT growth rate *in vitro* [42]. First, the effects are dependent upon the tau: tubulin ratio. At low tau:tubulin ratio, 3R Tau isoforms reduced MT growth rate, whereas 4R Tau isoforms increased it. At high tau:tubulin ratio, both 4R and 3R Tau increased the growth rate. Altogether, these data show that the presence or absence of the exon 10-encoded sequence of Tau is important in the regulation of MT dynamics. Moreover, Tau is able to inhibit the destabilizing activity of XKCM1, a kinesin-13 family protein [43]. All these results illustrate the complexity of the regulation of MT dynamics by MAPs.

Expression, post-translational modifications and biological activities of various MAPs have been shown to be differentially regulated in tumor progression [44], probably resulting in differential regulation of MT dy-

namics. For example, Tau and MAP1B expression in a neuroblastoma cell line are increased upon differentiation [44] and MAP2 expression appears to be induced in primary cutaneous melanoma but absent in metastatic melanomas [45]. The consequences of these changes in MAP expression remain unclear. Indeed, during early tumor progression, MAP2 expression in melanoma inhibits cell division and metastasis [46] whereas a correlation between MAP2 expression and oral carcinogenesis was recently described [47].

**Plus end binding proteins (+TIPs).** A subset of MT binding proteins interacts specifically with MT plus ends. These proteins can be divided into MT destabilizing +TIPs, which belong to the kinesin-13 family [48, 49] and MT plus end tracking proteins, also termed stabilizing +TIPs (table 1).

Unlike most other kinesins, which are involved in MT-driven intracellular transport, kinesin-13 proteins concentrate at MT ends and can induce depolymerization *in vitro* [50] (fig. 1). These proteins influence MT dynamics in cells both during mitosis (e.g. XKCM1) [51] and interphase [52, 53]. Mennella et al. evaluated the interphase functions, location and dynamics of two *Drosophila* kinesin-13 family members termed KLP10A and KLP59C [54]. In *Drosophila* S2 cells, both proteins contribute to MT depolymerization but affect distinct parameters of dynamic instability. KLP10A stimulates catastrophe, whereas KLP59C suppresses rescue. The authors also



demonstrated that KLP10A and KLP59C targets polymerizing and depolymerizing MT plus ends, respectively. Moreover, KLP10A is concentrated at the MT plus end by the plus end tracking protein EB1 [54].

MT plus end tracking proteins represent a highly diverse group of proteins, such as EB1, 2, 3; APC; Dis1/TOG; CLIP-170/CLIP-115; CLASP 1, 2; ACF7; Dynactin (p150 Glued); LIS1; dynein [55–60] (fig. 1). Although these proteins can bind to MTs independently, evidence of interactions among them has led to the hypothesis of the existence of a plus end complex. By binding to the plus ends of MT, +TIPs influence MT structure and accessibility.

EB1 recruitment at MT plus ends plays an important role in the regulation of MT dynamics. Experiments with depletion or overexpression of EB1 in *Drosophila* S2 cells and frog egg extracts demonstrate that, during mitosis, EB1 localizes to elongating kinetochore MTs and stabilizes them, while in interphase it decreases pause duration [61, 62]. Moreover, EB1 interacts with dynactin, and overexpression of either of these two proteins induces MT bundles in cultured cells, suggesting that each may enhance MT stability. Dynactin has a potent MT nucleation effect, whereas EB1 has a potent elongation effect [55]. More recently, Wen et al. found that small amounts of EB1 are present at the tips of stable MTs (detyrosinated MTs) of fibroblasts where it forms a complex with APC and mDia [63].

The plus end binding Dis1/TOG family, which includes the human TOG, can bind directly to MTs and promote MT polymerization [64, 65]. Using purified TOG protein, Charrasse et al. showed that it increases the MT growth rate equally at both ends [65]. In this family, XMAP215, a frog homologue, suppresses MT catastrophe by opposing the activity of the destabilizing factor XKCM1, which belongs to the kinesin-13 family [66]. Studies in other systems, such as budding yeast, suggest that the antagonistic stabilizing/destabilizing effects of the Dis1/TOG family and depolymerizing kinesins have been conserved during evolution [67].

The proteins of the CLIP family, such as CLIP 170, are clearly involved in MT stabilization [68], acting as rescue factors [69, 70]. In addition, CLIP 170 and its homologues promote MT capture at cortical sites through direct interaction with dynein-dynactin [71–73] and the Rac1/Cdc42 effector IQGAP [74, 75]. The CLIP-associated proteins CLASP1 and CLASP2 stabilize MTs by promoting pauses and restricting MT growth and shortening events. They mediate interaction between the MT plus end and cell cortex and act as local rescue factors, probably through the formation of a complex with EB1 and MT tips [76]. The affinity of CLASPs for MTs is spatially regulated in cells [77]. The cooperation between CLIPs and CLASPs in the regulation of the MT network was recently reviewed [58].

Other +TIPs, such as ACF7, play a role similar to CLIP170 and CLASPs in the cortical capture and stabilization of MTs through interaction with the actin cytoskeleton [59].

**Stathmin.** The oncoprotein18 (op18)/stathmin belongs to a protein family involved in the regulation of MT dynamics in both interphase and mitosis [78]. Stathmin is a major MT-destabilizing phosphoprotein that promotes MT depolymerization by two distinct mechanisms [79] (table 1 and fig. 1). The first is a catastrophe-promoting activity involved in mitotic spindle regulation. The second is a tubulin-sequestering activity involved in the regulation of MT dynamics during interphase. Stathmin is inactivated by phosphorylation, which prevents its binding to tubulin [80]. Phosphorylation is mediated by a number of protein kinases, such as the Cdc2 kinase family [81, 82] and the small GTPases Rac and Cdc42 effectors, namely the p21-associated kinases (PAKs) [83, 84]. The activity of stathmin can also be regulated at the transcriptional level by p53 and E2F [85, 86]. Finally, stathmin has been reported to be overexpressed in various cancer malignancies, for example acute leukemia [87] and breast cancer [88]. Such stathmin overexpression can point to highly proliferative primary breast carcinomas [89], but the significance of this overexpression in cancer remains unclear.

**Regulation by kinases and phosphatases.** Phosphorylation has been shown to be a key regulatory posttranslational modification of most of the MAPs described so far. In general, MAP phosphorylation leads to their detachment from the MT lattice and/or tubulin, thus decreasing MT stability. The phosphorylation state of these MAPs is thus crucial for the regulation of MT dynamics in cells and relies entirely on the concerted action of protein kinases and phosphatases.

Kinases inhibitors are known to suppress MT dynamic instability [90]. The most important kinases that regulate MT dynamics are those that control the cell cycle, such as the Cdc2 kinase family [91–93] and Cdk 5 in neurons [94], and those that control centromere localization, such as Aurora kinases [95]. PAKs that control cell migration [24, 83, 96], the mitogen-activated protein kinases (ERK, JNK) and GSK-3 $\beta$ , which are targets of extracellular signals involved in cell proliferation [97–99], are also involved in the regulation of MT dynamics.

It is becoming increasingly evident that the functions of MT-regulating proteins are modulated both spatially and temporally by site-specific phosphorylation events. For example, stathmin phosphorylation by PAK1 inhibits its plus end catastrophe activity. However, *in vivo*, PAK1 activity is not sufficient to phosphorylate stathmin, indicating that additional pathways downstream of Rac 1 are required for stathmin regulation [100].

Phosphatases such as type 1 phosphatases (PP1) and type 2A phosphatases (PP2A), the major serine/threonine phosphatases in most cells [101], play a critical role in the regulation of MT dynamics in cells, as shown by the increase in MT dynamics induced by okadaic acid treatment [90]. Notably, PP2As are required to maintain the short steady-state length of MTs in mitosis by modulating catastrophe frequency through stathmin regulation. In contrast, PP1s are only required to control MT dynamics during transitions into and out of mitosis [102]. Interestingly, some specific PP2A isoforms are regulated by their binding to MTs [103, 104]. MT anchoring of PP2A may serve to sequester selective intracellular pools of enzymes in an inactive state, and to promote kinase-mediated phosphorylation of MAPs. MT depolymerization results in the release and activation of PP2A, and the dephosphorylation of MAPs such as Tau [105, 106]. Finally, it is of crucial importance to identify the protein kinases and phosphatases that regulate MAP phosphorylation *in vivo* as well as the signaling cascades that regulate them. Overall MT dynamics may result from a balance between the individual effects of these regulatory proteins.

### Cellular functions depending on microtubule dynamics

Among the various cell functions regulated by MT dynamics, the most important ones that are involved in tumor progression are the control of cell proliferation and migration. Besides being powerful anticancer agents, MTDs that either depolymerize the MT network, such as vinca alkaloids, or stabilize it, such as taxanes, are valuable tools for deciphering the roles of MT dynamics and the importance of their regulation in cellular contexts.

### Mitosis and cell proliferation

In eukaryotes, the mitotic spindle is composed of MTs extending from two opposing spindle poles: the minus ends, anchored to the poles, and the plus ends, extending away from them. Three distinct subsets of mitotic MTs can be characterized: kinetochore MTs (kMTs), whose plus ends attach to sister chromatids at the kinetochore, interpolar or pole-to-pole MTs, which overlap MTs from the opposite pole at the spindle midzone, and astral MTs, extending away from the spindle (fig. 2A). Direct analysis of MT dynamics and measurements of the dynamic instability parameters are hard to achieve during mitosis, due to the brief time window available and to image resolution problems at the central spindle. However, in spite of the significant complexity of this process, the intimate mechanisms of mitotic spindle dynamics and their regulation are increasingly being investigated. For a recent review, see Kline-Smith and Walczak [107]. Mathematical and computer modeling [108] demonstrate

that the cell predominantly regulates MT transition frequencies in order to reorganize the interphase array into a mitotic spindle. MT turnover is much higher in mitotic cells than in interphase cells [109, 110], and this is thought to be responsible for mitotic spindle establishment and its maintenance. During early prophase, it has been shown that MT nucleation at the centrosomes increases 4-fold [14]. The growth of these MTs is stabilized in the vicinity of the nuclear envelope [13]. MTs from the two developing poles can interact with each other to form overlapping associations (fig. 2A). Thus, formation of two MT subsets, interpolar and astral, starts prior to nuclear envelope breakdown (NEB). When the nuclear envelope is still intact, non-nuclear MT dynamics regulators are predicted to be responsible for early events involved in spindle assembly.

Upon NEB, as nuclear factors and mitotic chromosomes enter the cytoplasm, MT dynamics increase dramatically; this is the hallmark of the 'Search-and-Capture' model of spindle assembly. Indeed, during prometaphase, spindle MT plus ends probe the cytoplasm until linkage with a chromosomal kinetochore is established. Kinetochores, selectively stabilizing their associated MTs, enable the formation of mature and stable K fibers containing approximately 25 MTs in vertebrate metaphase cells [111, 112]. If dynamic instability is sufficient to explain chro-

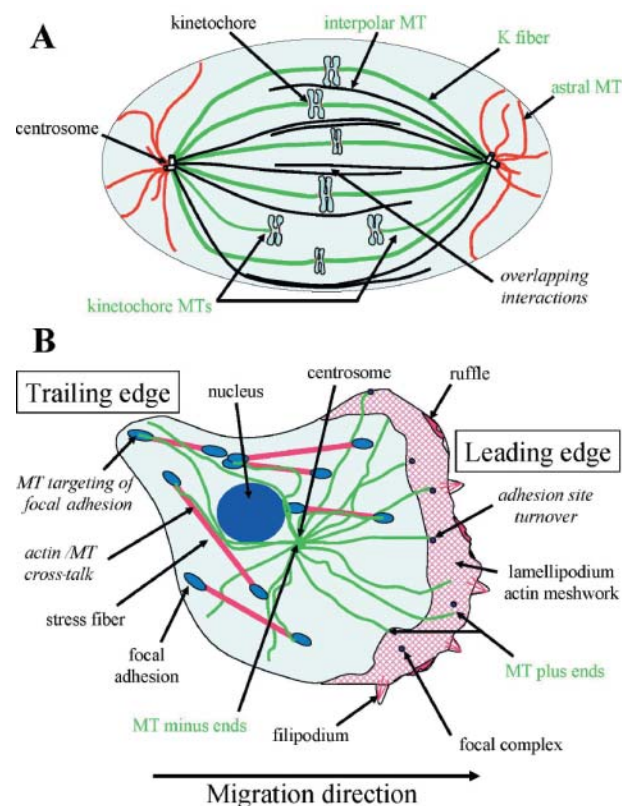


Figure 2. Structural organization of the MT network in mitotic cell at the prometaphase stage (A) and in migrating cell (B).

mosome capture within mitotic timescales, mathematical modeling predicts that MT dynamics may be biased toward the chromosomes by the presence of a spatial gradient of a 'stabilizing' factor (e.g. RanGTP gradient) to enable an accurate congression of chromosomes [113]. The availability and distribution of MT plus ends is a source of differential stability within the spindle. The majority of kMTs are continuous from the centrosome to the kinetochore [114]. In contrast, astral and interpolar MTs have many free plus ends that can be affected by the balance of cytoplasmic MT-regulating proteins (see above). Overall dynamicity of astral MT plus ends, in prometaphase or metaphase epithelial cells, is increased 4-fold as compared with interphase MTs [115]. This increase is mainly due to a decrease in rescue frequency and an increase in catastrophe frequency. In addition, the time spent in pause is dramatically decreased. In these experiments, no significant change in MT growth and shortening rates was observed. In contrast, Piehl and Cassimeris [13] demonstrated, by following EB1-GFP movement in living epithelial cells, a 1.5-fold increase in MT growth rate during prophase, prometaphase and metaphase, as compared with interphase. Elsewhere, MT growth rate does not seem to be spatially regulated during mitosis, as seen when comparing astral and spindle MTs in prometaphase and metaphase [13]. As combinations of regulatory factors are active during different phases of the cell cycle, they may be responsible for the similar MT growth and shortening rates observed throughout the cell cycle.

A subset of more stable astral MTs has been described in metaphase [115]. Interactions of their plus ends with the cell cortex might contribute to spindle positioning. Moreover, several events have been proposed to stabilize MT minus ends at poles during prometaphase: NuMA and TPX2 transport to spindle poles [116–118], increased levels of  $\gamma$  tubulin [14]; localized activation of MAPs; and activation of MT assembly promoters by small GTPase Ran [119]. Many proteins affect chromosome alignment: the kinetochore-associated kinesin CENP-E is required for stability of kinetochore-MT attachment [120], NuMA organization of poles is required for proper chromosome movement [117, 118] and centromere-associated MCAK is required for resolving improper kinetochore attachments that can disrupt chromosome congression and alignment [121–123]. Despite their overall increased stability, kMT plus ends exhibit highly regulated dynamics that are associated with chromosome movement in somatic cells [112, 124]. Chromosome-associated motors, called chromokinesins, may participate to force production at chromosome arms, helping chromosome alignment and orientation. Although chromokinesins and kinetochore-associated proteins certainly play a role in chromosome alignment, the detailed regulation of MT dynamics during congression is poorly under-

stood, partly due to the difficulties of imaging the highly varied movements of spindle MTs and chromosomes during prometaphase. Elsewhere, accurate regulation of MT dynamics prevents, at least in part, chromosome segregation defaults. For example, MT dynamics can be differentially regulated to counteract merotelical orientation of chromosomes [125].

During anaphase, two mechanisms of K fiber depolymerization exist to drive chromosome segregation. In somatic cells, kMT plus end depolymerization dominates, while treadmilling appears to play a minor role in force production for chromosome segregation. In parallel, overlapping MTs at the spindle midzone polymerize at their plus ends. These overlapping interactions participate in spindle elongation and pole removal, ultimately leading to cytokinesis. A recent study on metaphase-arrested budding yeast cells demonstrated that separase activation at anaphase onset, which triggers chromosome segregation through cohesin cleavage, induces MT stabilization, resulting in a 60% decrease in spindle MT turnover [126]. Separase also activates the phosphatase Cdc14, which is responsible for MT dynamics silencing. Altogether, these data show that MT dynamics are highly regulated during cell division by a combination of MT-regulating proteins, nuclear factors and cell cycle-related proteins.

### Cell migration

Cell migration is an essential process for all multicellular organisms. It is necessary for many physiological processes not only during development but also throughout life, including wound repair and immune surveillance. It is also involved in pathological processes such as tumor neoangiogenesis and metastasis. Directional cell migration is usually initiated in response to extracellular stimuli. A migrating cell is highly polarized, as shown by the asymmetrical distribution of signaling molecules, cytoskeleton, centrosome, golgi apparatus and directed membrane trafficking (fig. 2B).

Migration can be viewed as a periodically repeating sequence of events that includes formation of pseudopodial protrusions, attachment and translocation of the cell body in the direction of the new adhesion sites [127]. All these events can, theoretically, be served by the actin cytoskeleton, in the absence of MTs [128]. However, the pioneering work of Vasiliev [129] showed that a majority of cell types does require MTs for directional locomotion.

MT dynamic instability is important to generate an asymmetrical MT array and maintain cell shape [130–132]. In most undifferentiated and non-polarized mammalian cells, MT arrays are arranged radially and are composed of highly dynamic MTs. In many migrating cells, MT arrays become polarized by selective formation of a subset of unusually stable MTs at the leading edge [133–138]. This specific stabilization of MT plus ends is mediated



by EB1/APC [63] and by integrin- and focal adhesion kinase (FAK)-facilitated Rho-mDia signaling pathways [138]. These stable MTs have a long half-life and are capped at their plus ends [139]. They accumulate post-translationally modified tubulin, such as detyrosinated tubulin, in which the C-terminal tyrosine of the  $\alpha$  subunit is removed by tubulin carboxy peptidase [140]. Stabilized MTs may function as specialized tracks for vesicle and cytoskeletal trafficking. They also enable centrosome reorientation toward the leading edge. This centrosome reorientation is cell-type specific and is not required for directed cell migration [141]. It is becoming evident that MTs cannot act solely as tracks for directed delivery of motility-required components to the leading edge but that MT dynamics regulate cell migration.

The dependence on MTs for the locomotion of a particular cell type correlates with the presence of focal adhesions. Cells that form focal complex-type adhesions but do not convert them into focal adhesions can move independently of MTs. In contrast, cells that require MTs for migration are well-attached cells that demonstrate typical focal adhesions in addition to focal complexes [142]. On the one hand, MT depolymerization in such cells leads to a further increase in the number and size of focal adhesions [143–145], which impedes cell migration by increasing their adhesion to a level incompatible with locomotion [146]. Such processes arise through the activation of Rho GTPases [143–145]. On the other hand, recovery from treatment with an MT depolymerizing agent leads to MT regrowth toward and into the membrane ruffle and to activation of Rac1 [147]. It has been suggested that MT outgrowth activates Rac1 at the cell front to promote migration. Because Rac1 promotes MT growth through its effectors [100, 148, 149] and because MT growth stimulates the activation of Rac1 [147], MTs and Rac1 seem to be part of a feedback loop that maintains the activity of Rac1 for cell migration. Thus, a direct correlation exists between specific phases of MT dynamics and the activity of the Rho GTPase proteins that direct actin organization and substrate adhesion dynamics. MT dynamics might modulate the activity of Rho family GTPases by regulating GEFs such as RhoGEF-H1 [150].

Multiple targeting events of focal adhesion by MT plus ends induce their dissociation and release from the substrate to promote cell migration [20, 151, 152]. This regulation of adhesion site turnover appears to be dependent upon kinesin-1 [153], dynamin and FAK but independent of Rho and Rac activity [154]. The effect of MTs on cell migration might be imputed to their ability to regulate the turnover of adhesions, to enable protrusion and lamellipodium formation at the cell front, and to promote retraction at the rear of cells.

Even if MT involvement in cell migration is now evident, the relationship between the parameters of individual MT

dynamic instability and cell migration remains poorly described. Cell locomotion and lamellipodial size have been examined in migrating cells [155]. Faster cell movement and a larger lamellipodial area have been found to be correlated with MTs spending more time growing, a greater number of MT ends near the base of lamellipodia, and faster MT shortening rates. Slower movement and smaller lamellipodial area are associated with MTs spending more time in pause.

MT plus ends are regulated differently in the different subcellular regions of a migrating cell. At the leading edge, MTs tend to persist in growth, whereas in the cell body they spend more time pausing and shortening, and the catastrophe frequency is higher [156]. More recently, the same research group analysed MT dynamics in migrating CHO and LLC-PK cells at both the leading and the trailing edges [157]. MT dynamicity was 2- to 13-fold higher at the trailing edge than at the leading edge. Interestingly, no difference between MT growing rates at the leading edge and the trailing edge was observed. Nevertheless, MTs at the leading edge experienced a lower shortening rate, a lower catastrophe frequency and a higher duration of pauses as compared with the trailing edge. Thus, in migrating cells, a gradient of MT dynamic instability occurs from the leading edge to the trailing edge, and it appears to be crucial for cell polarity maintenance and the motility process.

### MT dynamics and cell signaling

Connections between the MT cytoskeleton and cell signaling remain complex and poorly understood. Intracellular signaling, as from Rho GTPases and MAPKs (mitogen-activated protein kinases), regulates many cellular processes, including MT network functions [158–164]. A pool of survivin, an apoptosis inhibitor (IAP), associates with MTs and participates in mitotic spindle function [165, 166]. Forced expression of survivin in epitheloid carcinoma cells profoundly influences MT dynamics, with reduction of pole-to-pole distance at metaphase and stabilization of MTs against nocodazole-induced depolymerization [167]. Inhibition of PI3K (phosphatidylinositol 3-kinase)/Akt and MAPK pathways diminishes survivin induction and sensitizes cells to taxane-mediated cell death [168].

Conversely, MT dynamics may influence cell signaling. Various proteins are associated with MTs, and modulation of MT dynamics is likely to affect their sequestration and/or activation. MTDs such as vinca alkaloids, nocodazole and paclitaxel activate the nuclear factor  $\kappa$ B (NF- $\kappa$ B) signaling pathway through the degradation of the NF- $\kappa$ B inhibitor (I $\kappa$ B), located on intact MTs [169–171]. Elsewhere, about 40% of total MAPKs are linked to MTs [172] via kinesin-related motor molecules [173]. Similarly, MTs probably regulate Rho GTPase activity by sequestering GEFs such as GEF-H1 [150]. Bim, a proap-



optotic factor of the Bcl-2 family, is also associated with MTs. It represents an important link between the MT network and the apoptotic machinery, as lymphocytes *bim*  $-/-$  are refractory to MT perturbations [174]. Upon disruption of MT network functions by MTDs, freed Bim translocates to the mitochondria where it constitutes an initiating event in apoptotic signaling [175, 176]. In response to DNA damage, the tumor suppressor protein p53 is transported to the nucleus via the interphase MT minus end-directed motor dynein [176–179]. Thus, the nuclear p53 activity depends on MT integrity [178–181]. These results suggest that MT dynamics also regulate intracellular transport in addition to motor proteins.

In eukaryotic cells, membrane-bounded vesicles, organelles such as mitochondria, RNA and proteins are frequently transported many micrometers along well-defined routes in the cytosol and delivered to particular addresses. The importance of MT-directed transport has been largely investigated in neuronal biology [182]. It is important for information transduction, such as MT-motor dependent transduction of neurotrophic signals. The basic components of the MT-dependent transport system are MT motor proteins, kinesin and dynein, and the polarized MT tracks along which they carry cargoes. Nearly all kinesins move cargo toward the MT plus ends (anterograde transport), whereas dyneins transport cargo toward the MT minus ends (retrograde transport) [183]. The net direction of transport depends on the balance between plus end-directed and minus end-directed motors. Several kinesins have been reported to alter MT dynamics, including kinesin-13 family proteins (e.g. MCAK), which trigger MT depolymerization (see above). Moreover, MAPs, which regulate MT dynamics, can profoundly affect patterns of motor activity [184]. For example, MAP2 can inhibit kinesin-driven MT sliding [185]. Most cytoplasmic MTs have a substantial complement of MT-related proteins, and their regulation, which in turn regulates MT dynamics, could thus profoundly modify patterns of MT-based intracellular transport.

### Microtubule dynamics as a therapeutic target in oncology

The critical role that MTs play in cell division makes them a very suitable target for the development of chemotherapeutic drugs against rapidly dividing tumor cells such as leukemias and lymphomas. In addition, these compounds are also broadly active against more slow growing tumors, such as some breast, lung and ovary cancers. MTs are thus the target for a large and chemically diverse group of molecules called MTDs. The effectiveness of MTDs has been validated by the successful use of several vinca alkaloids and taxanes for the treatment of a wide variety of human cancers. Their clinical success has

prompted a worldwide search for new compounds with improved characteristics (solubility, pharmacokinetics, oral route administration, non-Pgp-dependent and efficiency in tumor-resistant cells).

### Suppression of microtubule dynamics disturbs mitotic progression

MTDs exert their inhibitory effects on cancer cell proliferation primarily by blocking mitosis, which requires a finely regulated control of MT dynamics. MTDs are therefore referred as anti-mitotic drugs. They are usually divided into two groups when they are used at relatively high concentrations. MT-depolymerizing agents such as the vinca alkaloids, colchicinoids and estramustine inhibit MT polymerization, depolymerize MTs and decrease the MT polymer mass. In contrast, MT stabilizing agents, such as taxanes, promote MT polymerization, stabilize MTs and increase MT polymer mass in cells [186].

More recently, it has been proved that MTDs, at low but clinically relevant concentrations, potently suppress MT dynamics without affecting MT polymer mass [186–188]. This occurs through several ways, depending on cell types, on the tubulin binding site (i.e. colchicine, vinca alkaloid or paclitaxel binding site) but also on molecules [187, 189, 190]. Therefore, MTDs can suppress MT dynamics either by decreasing growth and shortening rates, or by affecting transition frequencies or even both [11, 186]. However, these diverse alterations of MT dynamics lead to very similar mitotic spindle abnormalities and usually result in mitotic block (fig. 3) [187, 189, 190]. The effects of MTDs on MT dynamics in tumor cells were measured in interphase cells. The question arises whether these measurements also reflect drug effects on the mitotic spindle. Indirect evidences suggest that MTDs also suppress spindle MT dynamics. First, the level of MT dynamics suppression by MTDs in interphasic cells correlates with the level of mitotic block in the cell population [187, 188, 191]. In addition, studies on the dynamics of centromeres, kinetochores and their attached spindle MTs in human osteosarcoma cells indicate that mitotic block is closely associated with suppression of centromere dynamics by paclitaxel and vinca alkaloids [192, 193]. Thus, it is reasonable to argue that the anti-mitotic and anti-cancer activity of MTDs is largely due to the suppression of spindle MT dynamics, instead of their effects on the MT polymer mass, as previously thought. The anti-tumor actions of MTDs appear to involve their capacity of MT dynamics suppression to levels below those necessary for MTs to achieve their mitotic functions, especially the transition from metaphase to anaphase.

Interestingly, a low suppression of MT dynamic instability by MTDs, which does not allow the accumulation of cells in mitosis, still inhibits cell proliferation and induces apoptosis in tumor cells [190]. This effect cor-

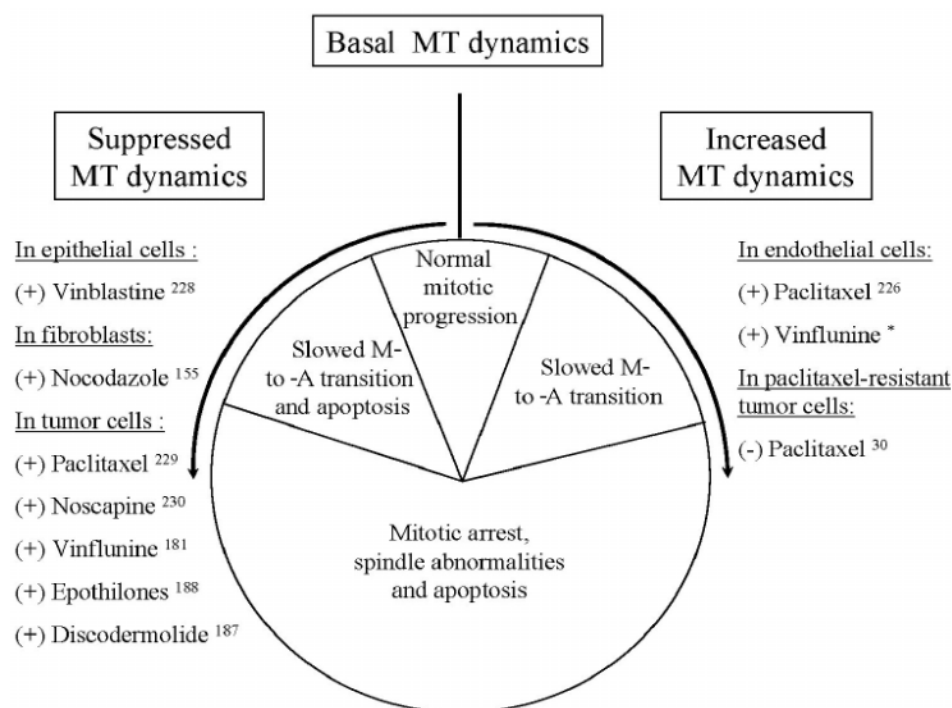


Figure 3. Consequences of MT dynamics modulation by MT-targeted drugs on mitotic progression. M-to-A transition = metaphase-to-anaphase transition. \*, unpublished observation.

relates with a slowing of the mitotic progression at the metaphase-to-anaphase transition and subsequent mitotic slippage [187, 194, 195]. During prometaphase, the plus ends of dynamic spindle MTs appear to probe the cytoplasm until linkage with a chromosomal kinetochore is established. Reduced MT dynamics in cells treated with MTDs may result in impaired probing of the intracellular space by MTs and to the attachment of a fewer number of MTs to kinetochores, thus delaying chromosome congression to the metaphase plate and also reducing the tension necessary for the metaphase-to-anaphase transition [192, 193, 196, 197]. Slowing of metaphase-to-anaphase transition usually lead to chromosome alignment defaults and a correlation between MT dynamics suppression and mitotic spindle abnormalities has been demonstrated [187].

Interestingly, A549-T12 and A549-T24 tumor cells, which are 9- and 17- fold resistant to paclitaxel, respectively, as compared with parental A549 cells, require low concentrations of paclitaxel for proliferation. In these cells, in the absence of added paclitaxel MT dynamic instability was drastically increased proportional to the resistance level [30]. Thus, the decreased paclitaxel sensitivity of these cells can be explained by their increased MT dynamics. More drug molecules are thus needed to suppress MT dynamics below the levels necessary to achieve their functions. Moreover, when grown without paclitaxel, A549-T12 cells were blocked at the metaphase/anaphase transition and displayed abnormal mitotic spindles with uncongressed chromosomes [30]. When grown with low paclitaxel concentrations, nor-

mal mitotic spindle is recovered, probably because MT dynamics were slowed to a range compatible with their functions. These results suggest that both excessively rapid dynamics as well as suppressed dynamics correlate with impaired mitotic spindle function and inhibition of cell proliferation (fig. 3).

### Suppression of MT dynamics induces apoptosis

It has been clearly demonstrated that MTDs induce apoptosis mainly through the intrinsic pathway, as reviewed by Carre and Braguer [198]. Apoptosis induction correlates with the suppression level of MT dynamics [191] through a mechanism which remains unclear. Interestingly, suppression of MT dynamics and alteration of mitochondrial parameters are two early and concomitant events. These early mitochondrial disturbances (i.e. reactive oxygen species [ROS] production, decrease in mitochondrial respiration rate, alteration of mitochondrial membrane potential) [199, 200] finally lead to the release of proapoptotic factors into the cytosol and ultimately caspase activation [201]. These MTD effects may be mediated by the presence of a pool of mitochondrial tubulin [202]. However, there is still no link between MT dynamics suppression and the mitochondrial apoptotic pathway.

Bim, a proapoptotic member of the Bcl-2 family, is sequestered by MTs and released upon MT network disruption (see above). In addition, it has been shown that p53 can translocate to the nucleus and also to the mitochondria, following suppression of MT dynamics by MTDs [178, 179, 181]. Elsewhere, C19ORF5, a sequence homologue of MAP1A and MAP1B, selectively

associates with MTs stabilized by paclitaxel or by the MT stabilizer RASSF1A, and it also binds to mitochondria-associated proteins [203, 204]. Thus, MT-regulating proteins as well as proteins that are sequestered or transported by MTs may represent an important link between MT dynamics suppression and apoptosis induction.

#### **MT dynamics suppression inhibits cell migration**

One of the main causes of failure in the treatment of patients with solid malignancies is the difficulty in controlling or preventing the spread of metastases. The process of tumor cell invasion and metastasis is conventionally understood as the migration of individual cells that detach from the primary tumor, enter lymphatic vessels or the bloodstream, and seed in distant organs.

The effects of MTDs on cell migration and invasion remain very controversial, probably due to different tumor cell line behaviors, different culture conditions, but most important to different drug concentrations [205–211]. Both paclitaxel and nocodazole, at concentrations that significantly suppress MT dynamics without modifying the MT polymer mass, reduced up to 60% the rate of locomotion of NRK fibroblasts [155, 209]. In these cells, inhibition of cell migration was correlated with MT dynamics suppression, limiting the number of MT plus ends that effectively reach the lamellipodium base to regulate its formation. Interestingly, Belotti et al. demonstrated that the anti-migratory effect of paclitaxel occurs at non-anti-proliferative concentrations in tumor cells [212].

The paucity of studies that effectively link MT dynamics and cell migration highlights the need of further experiments to decipher the exact role of MT dynamics in tumor cell migration, invasion and metastasis.

#### **Targeting MT dynamics in endothelial cells**

The tumor vasculature currently represents a new target for the development of cancer therapy, since functional vasculature is critical for both primary tumor growth and metastatic invasion [213, 214]. The vasculature is easily accessible to therapeutic agents. Two approaches are used to target the vascular functions in tumors: antivasular therapy, which aims at a rapid and extensive shutdown of the tumor vasculature, leading to tumor cell death [215, 216], and antiangiogenic therapy, which consists in an inhibition of new blood vessel formation.

**Antivasular therapy.** Historically, the MT-depolymerizing drug colchicine was the first MTD to show antivasular effects [217, 218]. Unfortunately, the therapeutic window was very limited due to the drug toxicity. Vinblastine and vincristine also induce vasculature damage in animal tumors but at concentrations close to the maximum tolerated doses [219]. Nevertheless, the ability of several novel MTDs (i.e. combretastatine, vinflunine and ZD 6126) to rapidly shut down existing tumor vascu-

lature, at doses well below the maximum tolerated doses, was recently demonstrated [216, 220]. Interestingly, these vascular targeting agents seem to damage tumor vasculature without significantly altering normal tissues [221]. The reason for this specificity is still unknown, but it was imputed to differences in the architecture, and cellular and biochemical composition between normal and tumor blood vessels [222, 223]. Finally, the anti-vascular effect of the MTDs relies on MT network disruption in tumor-derived endothelial cells rather than on MT dynamics alteration.

**Antiangiogenic therapy.** In contrast to the antivasular approach, the antiangiogenic approach is likely to be related to MTD effects on MT dynamics in endothelial cells. MTDs were among the first anti-cancer agents reported to have antiangiogenic properties at relatively low concentrations, as compared with those used for antitumor effects [212, 224]. Neo-angiogenesis is the formation of new blood vessels from the pre-existing vasculature toward and into tumors. This complex and dynamic process requires activation, proliferation, migration and differentiation of endothelial cells. Inhibition of one or more of these steps may dramatically alter neo-angiogenesis *in vivo*. Until recently, the majority of the research in this area focused on the antiproliferating impact of antiangiogenic therapy. Paclitaxel, at concentrations > 10 nM, inhibits endothelial cell proliferation through mitotic block and the mitochondrial apoptotic pathway [225]. This cytotoxic effect of paclitaxel classically correlates with MT dynamics suppression as observed in tumor cells [226]. In contrast, below 10 nM, paclitaxel inhibits endothelial cell proliferation without any accompanying mitotic arrest or apoptosis. This cytostatic effect correlates with a slowing of the metaphase-to-anaphase transition [225]. Unexpectedly, these cytostatic concentrations of paclitaxel cause a strong increase in MT dynamic instability in living endothelial cells (fig. 3) [226]. Increased MT dynamic instability correlates with angiogenesis inhibition, as measured by the inhibition of capillary-like tube formation on Matrigel. The antiangiogenic effect of paclitaxel also occurs at concentrations that do not inhibit endothelial proliferation. Elsewhere, it has been shown that taxanes can inhibit endothelial cell migration, probably through the impairment of centrosome reorientation toward the direction of migration [227]. Increased MT dynamics and antiangiogenesis at non-anti-proliferative concentrations have also been demonstrated for vinflunine, the newest vinca alkaloid in development [unpublished observation]. Interestingly, concentrations of vinflunine that increased MT dynamics in living endothelial cells also inhibited endothelial cell migration (unpublished observation). These results suggest that the increase in MT dynamics is a common feature of MTD, at non-cytotoxic concentrations and seems

to be specific to endothelial cells, as it is not observed in cancer cells [226]. Further studies are needed to better understand the mechanism by which MTDs increase MT dynamics in these cells, and the molecular link between the increase in MT dynamics and the antiangiogenic properties of MTDs.

## Conclusion

MT dynamics allow cell adaptation to rapid changes in their microenvironment. MT dynamics regulation by intracellular components, which directly interact with MTs, is beginning to be elucidated. However, little is known about how extra-cellular stimuli regulate the MT network. Development of potent new tools such as genomics and proteomics will improve the identification of proteins regulating the MT network. It will also lead to a better understanding of tumor progression regulators. Finally, identification of highly specific targets of MT dynamics will be very helpful for clinical research to improve cancer therapy.

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