Aurora A phosphorylation of TACC3/maskin is required for centrosome-dependent microtubule assembly in mitosis

Kazuhisa Kinoshita, 1 Tim L. Noetzel, 1 Laurence Pelletier, 1 Karl Mechtler, 2 David N. Drechsel, 1 Anne Schwager, 1 Mike Lee, 3 Jordan W. Raff, 3 and Anthony A. Hyman 1

1 Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG), 01307 Dresden, Germany
2 Research Institute of Molecular Pathology, A-1030 Vienna, Austria
3 The Wellcome Trust/Cancer Research UK Gurdon Institute, Cambridge CB2 1GN, England, UK

Centrosomes act as sites of microtubule growth, but little is known about how the number and stability of microtubules emanating from a centrosome are controlled during the cell cycle. We studied the role of the TACC3–XMAP215 complex in this process by using purified proteins and Xenopus laevis egg extracts. We show that TACC3 forms a one-to-one complex with and enhances the microtubule-stabilizing activity of XMAP215 in vitro. TACC3 enhances the number of microtubules emanating from mitotic centrosomes, and its targeting to centrosomes is regulated by Aurora A–dependent phosphorylation. We propose that Aurora A regulation of TACC3 activity defines a centrosome-specific mechanism for regulation of microtubule polymerization in mitosis.

Introduction

In animal cells, microtubules are nucleated from centrosomes and grow out with their plus ends that lead into the cytoplasm (for review see Howard and Hyman, 2003). The number and stability of microtubule plus ends growing from centrosomes changes through the cell cycle, which is concomitant with assembly of the mitotic spindle (Hannak et al., 2001; Kline-Smith and Walczak, 2004; Piel et al., 2004). One obvious mechanism controlling microtubule assembly at centrosomes is modulation of the microtubule nucleation rate (for review see Job et al., 2003). Indeed, the amount of γ-tubulin increases at centrosomes as cells enter mitosis (Khodjakov and Rieder, 1999; Hannak et al., 2002). However, another equally plausible mechanism is modulation of the stability of nucleated plus ends. The stability of microtubule plus ends is dependent on the rate at which microtubules interconvert between growing and shrinking (called the catastrophe rate) and between shrinking and growing (called the rescue rate; Walker et al., 1988; Howard and Hyman, 2003).

Xenopus laevis egg extracts have been particularly useful for studying the regulation of microtubule polymerization from centrosomes. Because meiotic spindles in Xenopus egg extracts can form without centrosomes by nucleation and stabilization of microtubules around chromosomes (Heald et al., 1996; Karsenti and Vernos, 2001; Sampath et al., 2004), it is possible to study separately the regulation of microtubule polymerization around mitotic centrosomes or chromosomes. In Xenopus egg extracts, the dynamic behavior of microtubules in the cytoplasm is regulated, in large part, by the activity of XMAP215, which is a member of a conserved family of microtubule-associated proteins (Kinoshita et al., 2002; Gard et al., 2004). XMAP215 both stimulates the growth rate and opposes catastrophe activity of XKCM1/XLMCAK, which is member of the Kin I/kinesin-13 family (Walczak et al., 1996; Tournebize et al., 2000; Noetzel et al., 2005). Physiological microtubule dynamics can be reconstituted in vitro by a mixture of XMAP215 and mitotic centromere-associated kinesin (MCAK) together with tubulin (Kinoshita et al., 2001). Although XMAP215 and MCAK clearly have a central role in determining microtubule dynamics in Xenopus egg extracts, we know little about how these proteins are regulated during cell cycle progression. However, these proteins are localized to centrosomes, suggesting that they could be involved in the regulation of microtubule growth from centrosomes (Kinoshita et al., 2002; Gard et al., 2004).

A clue as to the possible mechanisms regulating XMAP215 family proteins at centrosomes came from the...
discovery that the *Drosophila melanogaster* member of the XMAP215 family is associated with D-TACC (Cullen and Ohkura, 2001; Lee et al., 2001). Mutants in TACC family members reduce microtubule number and prevent the localization of XMAP215 family proteins to centrosomes or spindles in *D. melanogaster* (Cullen and Ohkura, 2001; Lee et al., 2001), *Caenorhabditis elegans* (Bellanger and Gönczy, 2003; Le Bot et al., 2003; Srayko et al., 2003), yeasts (Usui et al., 2003; Sato et al., 2004), and human cells (Gergely et al., 2003). Beyond the fact that TACC family members are required to localize XMAP215 family members to centrosomes, we know little about the role of TACC in the modulation of microtubule dynamics and in regulating the activity of XMAP215. In this study, we investigated these issues by using purified proteins and *Xenopus* egg extracts.

**Results**

**TACC3 forms a complex with and stimulates the activity of XMAP215**

To look at the role of the TACC3–XMAP215 complex in microtubule assembly, we studied the activity of the complex in vitro. We first confirmed via immunoprecipitation that native TACC3 and XMAP215 form a protein complex in *Xenopus* egg extracts (Fig. 1 A). When coexpressed in baculovirus-infected insect cells, recombinant TACC3 and XMAP215 pro-

**Figure 1.** TACC3 forms a complex with XMAP215 in *Xenopus* egg extracts and in vitro. (A) Coimmunoprecipitation in *Xenopus* egg extracts. Immunoprecipitation (IP) was performed using control IgG (lane 1) or anti-TACC3 antibody (lane 2). The blots were probed with anti-TACC3 (top) or anti-XMAP215 (bottom). (B) Coimmunoprecipitation in the extracts of baculovirus-infected insect cells. Total lysates of TACC3 baculovirus single infected cells and TACC3 (lane 1) and XMAP215 virus double infected cells (lane 2) were prepared for immunoprecipitation. In each cell lysate, immunoprecipitation were performed using anti-TACC3 (lanes 3 and 4) or control IgG antibody (lanes 5 and 6). Total cell lysate and immunoprecipitates that were dissolved in sample buffer were subjected to SDS-PAGE, and the gel was stained with Coomassie brilliant blue. (C) Fractions from the top and bottom of a continuous sucrose density gradient centrifugation with purified proteins. Fractions collected after 3–15% continuous sucrose gradient centrifugation with TACC3 alone (top), XMAP215 alone (middle), or a mixture of TACC3 and XMAP215 (bottom) were subjected to SDS-PAGE. The gels were stained with Coomassie brilliant blue.

**Figure 2.** TACC3 increases the antagonizing activity of XMAP215 against MCAK. (A) Sedimentation analysis to monitor MCAK-dependent microtubule destabilization activity. 2.5 μM GMPCPP microtubules were mixed with 125 nM MCAK (lanes 3–14) or control buffer (lanes 1 and 2) in presence of ATP. 500 nM XMAP215 (lanes 5–14) and increasing concentrations of TACC3 from 250 (lanes 7 and 8), 500 (9 and 10), and 1,000 (11 and 12) to 1,500 nM (13 and 14) or control buffer (5 and 6) were added in reactions. Reaction mixtures were sedimented after a 38-min incubation at 30°C, supernatants (S) and pellets (P) were subjected to SDS-PAGE, and the gel was stained with Coomassie brilliant blue.

(B) Sedimentation assay to monitor XMAP215 affinity to microtubules. 2.5 μM GMPCPP microtubules were mixed with 1,250 nM TACC3 (lanes 1 and 2), 500 nM XMAP215 (3 and 4), or 500 nM XMAP215 in addition to increasing concentrations of TACC3 from 250 (lanes 5 and 6), 500 (7 and 8), 750 (9 and 10), and 1,000 (11 and 12) to 1,250 nM (13 and 14) or control buffer (5 and 6) were added in reactions. Reaction mixtures were sedimented after a 38-min incubation at 30°C, supernatants (S) and pellets (P) were subjected to SDS-PAGE, and the gel was stained with Coomassie brilliant blue.
proteins also form a complex (Fig. 1 B). By mixing purified recombinant proteins and performing sucrose gradient centrifugation as well as gel filtration, we showed that TACC3 and XMAP215 form a one-to-one complex with a native molecular mass of 366 kD (Fig. 1, C and D).

Using a mixture of these purified proteins, we monitored the ability of the TACC3–XMAP215 complex to oppose the microtubule-destabilizing activity of MCAK by using a microtubule sedimentation assay (Desai et al., 1999a). In the presence of MCAK, microtubules were completely destabilized (Fig. 2 A, lanes 1 and 2) as reported previously (Desai et al., 1999a). The addition of 500 nM XMAP215 resulted in a slight reduction of MCAK’s microtubule-destabilizing activity (Fig. 2 A, lanes 3 and 4). However, XMAP215 that complexed with TACC3 more efficiently opposed the destabilizing activity of MCAK (Fig. 2 A, lanes 3–6; Δ TACC3) with adding back of TACC3 (lanes 5 and 6) or control buffer (lanes 1–4). The blots of interphase (lanes 1, 3, and 5) and mitotic extracts (lanes 2, 4, and 6) were probed by anti-TACC3 (top; TACC3) and anti-XMAP215 (bottom; XMAP215). Δ TACC3 did not have detectable effect on MCAK activity (not depicted). One possibility is that TACC3 increases the microtubule-stabilizing activity of XMAP215 by enhancing the affinity of XMAP215 for microtubules. Indeed, microtubule sedimentation analyses that were performed in the absence of MCAK indicated that the TACC3–XMAP215 complex has a higher affinity for microtubules than XMAP215 alone (Fig. 2 B). We have previously shown that XMAP215 opposes MCAK in a dose-dependent manner (Kinoshita et al., 2001). Therefore, we conclude that TACC3 stabilizes microtubules in vitro by forming a complex with XMAP215, increasing the affinity of XMAP215 for microtubules, and, thus, enhancing the antagonizing activity against MCAK.

**TACC3 is required for mitotic microtubule assembly around centrosomes by opposing the activity of MCAK**

To confirm that TACC3 regulates microtubule growth under physiological conditions, we analyzed meiotic spindle assembly in cycling extracts (cycled spindles; Murray, 1991; Desai et al., 1999b). Specifically, we used antibodies to immunodeplete TACC3 from *Xenopus* egg extracts and examined spindle assembly in the depleted extracts. To our surprise, meiotic spindles that assembled in the absence of TACC3 were indistinguishable from spindles that assembled in mock-depleted extracts (Fig. S1, available at http://jcb.org/cgi/content/full/jcb.200503023/DC1) despite the depletion of TACC3 to undetectable levels. Under similar depletion conditions for XMAP215, no spindles were observed. This was unexpected because TACC mutants have phenotypes in mitotic systems that were previously studied (see Introduction; Raff, 2002).

In all systems in which localization has been examined, TACC and XMAP215 are found at centrosomes, suggesting that TACC3 could have a centrosome-specific role in mitosis. Accordingly, we looked specifically at the role of TACC3 in...
microtubule growth from mitotic centrosomes. Traditionally, centrosomal microtubule assembly has been examined in *Xenopus* egg extracts by adding human centrosomes directly to mitotic extracts (Belmont et al., 1990). However, the formation of a mitotic centrosome is likely to be a complex process involving cell cycle transition. To create mitotic centrosomes, we added isolated centrosomes to interphase extracts and drove the extracts into mitotic (M) phase by the addition of a nondegradable cyclin B (cyclin B Δ90; Glotzer et al., 1991). In mock-depleted extracts, microtubule assembly around centrosomes was activated by the induction of M phase (Fig. 3 A, left). In TACC3-depleted extracts, the microtubule number around centrosomes was decreased to 15% of that in control extracts (Fig. 3 A, right; and B). Importantly, adding back recombinant TACC3 protein to depleted extracts increased microtubule assembly from mitotic centrosomes, returning it to the levels that were found in control extracts (Fig. 3, C–E). In contrast to M phase–induced extracts, no detectable effect of TACC3 depletion was observed on microtubule assembly in interphase extracts (Fig. 3 A, top). We confirmed that TACC3 was localized to these mitotic centrosomes in mock-depleted and TACC3 add-back extracts but not in TACC3-depleted extracts (Fig. 3 D, insets). We conclude that TACC3 is required specifically for microtubule assembly around mitotic centrosomes in *Xenopus* egg extracts.

The in vitro characterization of TACC3 activity suggested the possibility that in the absence of TACC3, microtubules cannot grow from mitotic centrosomes because of high MCAK activity. To test this idea, we examined the effect of MCAK inhibition on microtubule growth in TACC3-depleted extracts. We found that the addition of inhibitory MCAK antibodies to TACC3-depleted extracts stimulated the growth of microtubules from mitotic centrosomes (Fig. 3, F and G). This led to the conclusion that the likely function of TACC3 is to antagonize the microtubule destabilization by MCAK, presumably by increasing XMAP215 activity on centrosomes in M phase but not in interphase.

**Aurora A-phosphorylated TACC3 is enriched at mitotic centrosomes**

The results argue that TACC3 activity at centrosomes is specifically required for M phase microtubule growth and poses the question as to whether cell cycle–specific modulation of TACC3 activity could regulate the growth of microtubules from centrosomes. Experiments in *D. melanogaster* and *C. elegans* suggested a role of the mitotic kinase Aurora A in TACC3 localization to centrosomes (Giet et al., 2002; Bellanger and Gönczy, 2003; Le Bot et al., 2003) but could not distinguish between a specific role of the kinase in modulating TACC3 activity at centrosomes and a more general role in regulating centrosome assembly and maturation. Therefore, we decided to investigate the specific role of Aurora A in the regulation of TACC3 localization and activity. TACC3 has three consensus Aurora A sites (Cheeseman et al., 2002) that are conserved between *Drosophila* and *C. elegans* (Ser33, Ser620, and Ser626) and humans (Ser34, Ser552, and Ser558; Fig. 4 A). Recent experiments have shown that TACC3 is an in vitro substrate of Aurora A in *Xenopus* (at Ser626; Pascreau et al., 2005) and humans (Tien et al., 2004). We confirmed by mass spectrometry that Xenopus TACC3 is indeed phosphorylated by Aurora A at these three consensus sites (Fig. S2, available at http://jcb.org/cgi/content/full/jcb.200503023/DC1). Furthermore, we mutated these three conserved sites to alanine and showed that the incorporation of labeled 32P into the alanine-mutated protein (3A mutant; TACC3-3A) is reduced to 3% compared with the wild-type (WT) protein (TACC3-WT; Fig. 4 B). We raised phosphospecific antibodies to the three conserved Aurora A sites (Fig. 4 C). Because of the limitations of cytology in *Xenopus* systems and in order to use RNA interference as a control for antibody specificity, we examined the localization of phosphorylated TACC3 in human tissue culture cells. Interestingly, phospho-TACC3, which was stained by antibodies against P-Ser626 (in *Xenopus*; Ser558 in humans), localized specifically to mitotic centrosomes, whereas the general population of TACC3, which was stained by polyclonal antibodies against the fragment of TACC3 protein (73–265 amino acids), localized throughout the mitotic spindle as previously reported (Fig. 5 A; Gergely et al., 2000, 2003). siRNA of TACC3 greatly reduced
the staining of phospho-TACC3 as well as that of nonspecific TACC3 (Fig. 5 B). Phospho-TACC3 antibodies recognized a band of ~130 kD molecular mass specifically in mitosis-arrested tissue culture cells (Fig. 5 C) as well as a band of the same molecular mass that disappeared after the immunodepletion of either TACC3 (see Fig. 6 D) or Aurora A (Fig. S3, available at http://jcb.org/cgi/content/full/jcb.200503023/DC1) from Xenopus egg extracts in mitosis. Therefore, we conclude that TACC3 protein on centrosomes is specifically phosphorylated during M phase by Aurora A.

**Phosphorylation of TACC3 by Aurora A is required for its targeting to mitotic centrosomes**

To test whether phosphorylation is required to target TACC3 to centrosomes, we examined the localization of the nonphosphorylatable mutant of TACC3 in Xenopus egg extracts. By adding back WT (TACC3-WT) versus alanine-mutated TACC3 (TACC3-3A) to the depleted extracts (Fig. 6 D), we found that centrosomes contained 10% of TACC3-3A compared with TACC3-WT (Fig. 6 A, insets; and B). We confirmed that the TACC3-3A mutant could still interact with XMAP215 both in vitro and in Xenopus egg extracts (Fig. S4, available at http://jcb.org/cgi/content/full/jcb.200503023/DC1). Furthermore, TACC3-3A still enhanced the affinity of XMAP215 for microtubules (Fig. 6 E). Importantly, TACC3-3A cannot target XMAP215 to mitotic centrosomes as efficiently as TACC3-WT (Fig. S5, available at http://jcb.org/cgi/content/full/jcb.200503023/DC1), and this argues that TACC3 phosphorylation by Aurora A is required for efficient centrosomal localization of the TACC3–XMAP215 complex in M phase.

To test whether targeting of TACC3 to centrosomes is required for its activity, we assayed centrosome-mediated microtubule assembly in TACC3-depleted extracts that were reconstituted with either WT or alanine-mutated TACC3. Compared with the WT protein, the alanine-mutated TACC3 could only poorly rescue the effect of TACC3 depletion (Fig. 6, A and C). We confirmed that, after addition to the extract, TACC3-WT was phosphorylated, whereas TACC3-3A was not (Fig. 6 D). Thus, the targeting of TACC3 to centrosomes by Aurora A phosphorylation is required to stimulate microtubule growth from mitotic centrosomes. We were unable to detect any effect of Aurora A phosphorylation of TACC3-WT on its ability to enhance the affinity of XMAP215 for microtubules (Fig. 6 E). This implies that the likely function of Aurora A phosphorylation of TACC3 is targeting of the TACC3–XMAP215 complex to mitotic centrosomes rather than directly regulating its activity toward microtubules.

**Discussion**

**Activation of microtubule assembly by the TACC3–XMAP215 complex on mitotic centrosomes**

Previous studies have shown that the combination of XMAP215 and XKCM1/MCAK is essential to promote the dynamic properties of mitotic microtubule assembly (Kinoshita et
Phosphorylation of TACC3 by Aurora A is required for centrosomal localization of TACC3 and its microtubule-stimulating activity. [A] Localization of WT versus phosphorylation mutant of TACC3 on mitotic centrosomes. Microtubules around mitotic centrosomes were visualized by the addition of fluorescent tubulin in add-back experiments. Bar, 10 μm. Insets show immunolocalization of TACC3 on centrosomes in immunodepleted extracts with add back of WT versus the phosphorylation mutant of TACC3. Bar, 1 μm. [B] Quantification of immunostaining of TACC3 on centrosomes in A. Relative fluorescence intensity of TACC3 staining on centrosomes (within 1.079 μm radius) was measured. [B and C] Values shown are the means ± SD. [D] Immunoblotting of depleted extracts in add-back experiments. Mitotic extracts were immunodepleted with control IgG (lane 1; mock dep) or anti-TACC3 antibody (lanes 2–4; Δ TACC3) with adding back of control buffer (lanes 1 and 2; + buffer), TACC3-WT (lane 3; + TACC3-WT), or phosphorylation mutant TACC3 (lanes 4; + TACC3-3A). [E] Sedimentation assay to monitor XMAP215 affinity to microtubules in the presence of WT or phosphorylation mutant TACC3. 2.5 μM GMPCPP microtubules were mixed with 0.5 μM XMAP215 alone (lanes 1, 2, 7, and 8), 0.5 μM XMAP215 + 1.0 μM TACC3-WT (lanes 3, 4, 9, and 10), or 0.5 μM XMAP215 + 1.0 μM TACC3-3A (lanes 5, 6, 11, and 12) in the absence (lanes 1–6) or presence (lanes 7–12) of Aurora A. Mixtures were incubated for 38 min at 30°C and sedimented, and supernatants (S) and pellets (P) were subjected to SDS-PAGE. The gels were stained with Coomassie brilliant blue (top; CBB staining) or transferred onto nitrocellulose membrane for immunoblotting (IB) using the phosphospecific TACC3 antibody (antiphospho-Ser626; bottom).

Aurora A regulates centrosomal microtubule assembly in mitosis

The targeting of TACC3 to centrosomes defines a potential mechanism for regulating the polymerization of microtubules from centrosomes in mitosis. Previous data in other systems has shown that Aurora A is required to target TACC to centrosomes (Giet et al., 2002; Bellanger and Gönczy, 2003; Le Bot et al., 2003). However, the specific role of TACC3 phosphorylation has been unclear, as Aurora A has general roles in both centrosome assembly and cell cycle progression (Hannak et al., 2001; Giet et al., 2002; Hirota et al., 2003). Our data show that targeting of TACC3 to centrosomes specifically requires...
Aurora A phosphorylation. Furthermore, targeting is essential for TACC activity at centrosomes. Because Aurora A activity increases as cells enter M phase, this would account for the increase in microtubule polymerization that was observed as centrosomes mature during the cell cycle. Consistent with this idea, the protein level of both TACC3 and Aurora A as well as the kinase activity of Aurora A are all highly cell cycle regulated (Bischoff et al., 1998; Gergely et al., 2003). In Xenopus egg extracts, the increase of Aurora A kinase activity may be sufficient to trigger the activation of centrosomal microtubule polymerization in mitosis. Thus, the phosphorylation of TACC3 provides a mechanism for Aurora A to specifically modulate the growth of microtubules from centrosomes. However, Aurora A regulates processes other than microtubule assembly at centrosomes. Identification of the other Aurora A substrates will be essential for understanding the mechanisms of mitotic spindle assembly.

Materials and methods

Expression and purification of recombinant proteins

Full-length Aurora A cDNA was subcloned into pET21 vector (CLONTECH Laboratories, Inc.) for Xenopus Aurora A expression in bacteria (pET21 Aurora A; a gift from J. Swedlow, University of Dundee, Dundee, UK). TACC3 was expressed both in bacteria and insect cells. Full-length TACC3 cDNA was subcloned into pET30 vector (CLONTECH laboratories, Inc.) for expression in bacteria (pET30a maskin; a gift from J. Richert, University of Massachusetts, Worcester, MA). The mutations with an alanine substitution of Aurora A target sites were introduced by PCR. Bacterially expressed Histagged proteins were purified by using Ni-nitrotriacetic acid (QIAGEN). For the expression of TACC3 in insect cells, we used the Bac-to-Bac baculovirus expression system (Invitrogen). Full-length TACC3 cDNA was subcloned into pFastbac vector for the preparation of bacmid DNA (NH4-terminal His6 tagged). TACC3 baculovirus-infected expressSF+ cells (Protein Sciences) were pelleted after a 42-h incubation at 27°C and were resuspended in ice-cold lysis buffer (50 mM Hepes, pH 7.5, 0.1% Triton X-100, 200 mM NaCl, 10 mM CaCl2, 25 U/μl benzonase [Novagen], 10 μg/ml nucodazole [Sigma-Aldrich], and 1× protease inhibitor mix). The inhibitor mix consisted of 10 μg/ml antipain-HCl, 10 μg/ml APMASF, 6 μg/ml chymostatin, 0.5 μg/ml leupeptin, 2 μg/ml aprotinin, 0.7 μg/ml pepstatin, and 3.6 μg/ml E64 (all protease inhibitors were purchased from Sigma-Aldrich except for E64, which was obtained from BIOMOL Research Laboratories, Inc.). The resuspended pellets were dounced 20 times on ice using a Dounce homogenizer. The lysate was cleared by centrifugation, loaded onto a column (HiTrap Q FF; GE Healthcare), and equilibrated in 20 mM anion exchange buffer [Tris, BisTris-propane, and HCl], pH 7.5. The peak containing full-length TACC3 was supplemented with 3 mM imidazole (Sigma-Aldrich) and loaded onto a HiTrap chelating HP column (GE Healthcare), 25 mM Tris-HCl, 8.0, 300 mM NaCl, 3 mM imidazole, and 20% glycerol. The column was washed stepwise with binding buffer supplemented with 5 mM ATP, 1.5 M NaCl, and 30 and 60 mM imidazole and was eluted with 300 mM imidazole. The peak containing full-length TACC3 was pooled and desalted with a column (NAP25; GE Healthcare) into 20 mM anion buffer (Tris, BisTris-propane, and HCl), pH 7.5. Protein concentration was determined by using the Bradford assay and the molecular extinction coefficient at OD280.

Immunoprecipitation, sucrose density gradient centrifugation, and gel filtration

For immunoprecipitation using insect cell lysates, protein A-Sepharose beads that bound control rabbit IgG or anti-TACC antibodies were incubated with lysate from insect cells that were infected either with TACC3 baculovirus or with both TACC3 and XMAP215 baculovirus. Eluted immunoprecipitates were separated by SDS-PAGE and stained by Coomassie brilliant blue.

Sucrose gradients (3–15%) were poured as step gradients (five steps of equal volume) in 1× PBS, 0.1% Tween 20, 1 mM DTT, and 0.2× protease inhibitor mix. Gradients were incubated at 4°C for 24 h to allow diffusion into a continuous gradient. Equal concentrations of TACC3 and XMAP215 were mixed in vitro, incubated for 10 min on ice, diluted into gradient buffer to a final concentration of 1% glycerol, loaded onto the gradient, and spun for 6.5 h at 4°C and 120,000 g. Gradients were fractionated from the top by hand with a cut pipette tip. Fractions were analyzed by 4–12% SDS-PAGE (NuPage; Invitrogen) and stained by Coomassie brilliant blue. Standard proteins with known sedimentation values were run in parallel and scanned, band intensities were quantified, and peak fractions were assigned. Standard curves of peak fractions versus sedimentation coefficient were used to estimate the S value of proteins. Standard proteins that were used in sucrose gradients are listed as follows (sedimentation values are indicated in parentheses): chymotrypsinogen [2.6 S]; ovalbumin [3.5 S]; BSA [4.6 S]; aldolase [7.3 S]; and catalase [11.3 S].

Gel filtration chromatography was performed using a column (model G5000PWXL; Tosoh) in 1× PBS, 0.1% Tween 20, 1 mM DTT, 5% glycerol, and 0.2× protease inhibitor mix. The column was calibrated with standard proteins of known Stokes radii: 125 μM XMAP215 and increasing concentrations of prepolymerized GMPCPP microtubules was added to the reaction mix that was supplemented with 125 mM MCAK or control buffer in 1× BBR80 (80 mM Pipes, pH 6.8, 1 mM MgCl2, and 1 mM EGTA) containing 125 mM KCl and 1.5 mM Mg-ATP. 500 nM XMAP215 and increasing amounts of TACC3 or control buffer were added to reactions. Reactions were sedimented after 30 min at 30°C through a glycerol cushion. Equilibrium sedimentation of the supernatant and pellets were analyzed by 4–12% SDS-PAGE followed by Coomassie brilliant blue staining. For sedimentation
assays to monitor the affinity of XMAP215 to microtubules, 2.5 μM of prepolymerized GMPCPP microtubules were incubated with 500 nM XMAP215 or control buffer in 1× BRB80 containing 125 mM KCl in the presence of TACC3 or control buffer. In each condition, we confirmed that all proteins were in the supernatant after sedimentation without GMPCPP microtubules.

Preparation of Xenopus egg extracts and immunodepletion
Xenopus egg extracts were prepared as described previously (Murray, 1991; Desai et al., 1999b). Interphase extracts were prepared by the addition of calcium to cytoskeletal factor extracts. Cycloheximide was added to 100 μg/ml to avoid translation of cyclin B messenger in extracts and to arrest them in interphase. To generate mitotic extracts, a purified, nondegradable cyclin B fragment (cyclin BΔ90) and a final concentration of 20 nM siRNA against either TACC3 (purchased from Ambion; Gergely et al., 2003) or a control siRNA (control siRNA#1; Ambion) according to the manufacturer’s recommendations. After transcription, cells were incubated in fresh media for 72 h before analysis by immunofluorescence.

Hela S3 cells were grown in suspension in MEM that was modified for suspension cultures (Biochrom) containing 10% serum supplemented with nonessential amino acids (GIBCO BRL) and were grown using standard procedures. For RNA interference, Hela cells were seeded onto glass coverslips 16 h before transfection. Cells that were grown to ~40% confluence were transfected for 6 h using the OligofectAMINE reagent (Invitrogen) and to final concentration of 20 nM siRNA against either TACC3 (purchased from Ambion; Gergely et al., 2003) or a control siRNA (control siRNA#1; Ambion) according to the manufacturer’s recommendations. After incubation, cells were incubated in fresh media for 72 h before analysis by immunofluorescence.

Immunofluorescence and microscopy for culture cells
Transfected Hela cells that were grown on coverslips were fixed and permeabilized in methanol at −20°C for 8 min. Cells were washed with PBS and incubated 10 min in PBS containing 0.2% fish skin gelatin (PBS-FSG; Sigma-Aldrich) to prevent nonspecific binding of antibodies. Cells were incubated 20 min with primary antibody. Antibodies that were used were anti-α-tubulin (DM1A; Sigma-Aldrich), anti-TACC3 (Gergely et al., 2000), and anti-phospho-TACC3 (anti-P-Ser626 in this study) diluted to 1 μg/ml in PBS-FSG. After washing in PBS, cells were incubated for 20 min at 37°C in 1 μg/ml (in PBS-FSG) of donkey secondary antibodies that were labeled with either Texas red, FITC, or Cy5 (Jackson ImmunoResearch Laboratories) and were washed in PBS before mounting in the presence of 1 μg/ml DAPI to visualize chromatin. Three-dimensional datasets were acquired on an imaging system (DeltaVision; Applied Precision) that was equipped with a microscope (model IX70; Olympus), a camera (CoolSNAP; Roper Scientific), and a 100× NA 1.4 plan-Apochromat objective. Images were computationally deconvolved by using the SoftWorx software package (Applied Precision) and were shown as two-dimensional projections.

Online supplemental material
Fig. S1 shows spindle assemblies in mock-depleted versus TACC3-depleted Xenopus egg extracts. Fig. S2 shows in vitro phosphorylation sites in TACC3/maskin as determined by mass spectrometry. Fig. S3 shows TACC3 phosphorylation in Aurora A–depleted extracts. Fig. S4 shows the characterization of phosphorylation mutant TACC3 in Xenopus egg extracts and in vitro. Fig. S5 shows centrosomal localization of XMAP215-GFP in Xenopus egg extracts. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200503023/DC1.

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