The mitotic spindle in mammalian somatic cells are focused at spindle poles, a process thought to include direct capture by astral microtubules of kinetochores and/or noncentrosomally nucleated microtubule bundles. By construction and analysis of a conditional loss of mitotic function allele of the nuclear mitotic apparatus (NuMA) protein in mice and cultured primary cells, we demonstrate that NuMA is an essential mitotic component with distinct contributions to the establishment and maintenance of focused spindle poles. When mitotic NuMA function is disrupted, centrosomes provide initial focusing activity, but continued centrosome attachment to spindle fibers under tension is defective, and the maintenance of focused kinetochore fibers at spindle poles throughout mitosis is prevented. Without centrosomes and NuMA, initial establishment of spindle microtubule focusing completely fails. Thus, NuMA is a defining feature of the mammalian spindle pole and functions as an essential tether linking bulk microtubules of the spindle to centrosomes.

Introduction

The mitotic spindle is a bipolar array of microtubules required for the alignment and segregation of chromosomes during mitosis. The poles of the spindle are major focal points for the minus ends of spindle microtubules and serve as the final destination for chromosomes segregated in anaphase (Compton, 1998). In animal somatic cell mitosis, spindle poles are coincident with centrosomes, the major cellular microtubule-organizing structures. However, centrosomes are required for the formation of the spindle or the pole. In vitro, DNA-coated beads catalyze the formation of bipolar microtubule spindles in acentrosomal Xenopus laevis egg extracts (Heald et al., 1996). Additionally, bipolar spindles also form in somatic mitotic cells in which centrosomes have been destroyed by laser ablation or prevented from forming normally by depletion of essential centrosomal components (Khodjakov et al., 2000; Mahoney et al., 2006). Previous studies in Xenopus extracts in vitro have established a role for the abundant spindle pole–localized nuclear mitotic apparatus (NuMA) protein in centrosome-independent spindle pole formation (Heald et al., 1996; Mendoza et al., 2000). However, the relative contributions of NuMA and centrosomes in the establishment and maintenance of spindle pole integrity remain to be determined.

The attachment and movement of chromosomes on the mitotic spindle is mediated by kinetochore fibers, bundles of microtubules that link spindle poles to the kinetochores of each chromosome. Microtubules are nucleated in both a centrosome-dependent and -independent manner. Many are initiated directly at the pole by γ-tubulin–dependent nucleation, whereas others are nucleated adjacent to kinetochores through the local activation of components such as Tpx2 (Tulu et al., 2006). In the mitotic cytoplasm, these components are inactive as the result of binding to the importins but can be released by a chromosome-generated gradient of Ran-GTP (Gruss and Vernos, 2004). Under these conditions, microtubules nucleated in the vicinity of kinetochores are elongated and captured by centrosomal microtubules (Dasso, 2001; Khodjakov et al., 2003; Maiato et al., 2004). How these kinetochore-associated bundles are captured and focused toward centrosomes has not been determined. In addition, the means for sustained anchoring of kinetochore fibers at spindle poles and the role of centrosomes in both active focusing and the maintenance of spindle pole integrity are not established.

NuMA, along with cytoplasmic dynein, has been proposed to participate in focusing microtubules toward the poles of the mitotic spindle and physically tethering centrosomes to
spindle microtubules (Merdes et al., 1996; Khodjakov et al., 2003). The foundation for our current mechanistic understanding of the role for NuMA during mitosis was established by work in cell-free extracts. Compared with typical mammalian spindles, those formed in Xenopus egg extracts are much larger, undergo substantially greater microtubule flux, and have limited astral microtubules and no cortical attachments (Ganem and Compton, 2006). Furthermore, spindles formed in egg extracts rely significantly more on a gradient of Ran-GTP emanating from chromosomes to contribute to spindle assembly and have relatively few bundled microtubules comprising kinetochore fibers (Kalab et al., 2002, 2006).

Investigations of NuMA function in mammalian mitosis have previously used antibody microinjection approaches, which have yielded contradictory outcomes. An early study reported spindle collapse to monopolarity (Yang and Snyder, 1992), and subsequent efforts demonstrated unfocused spindle poles and an extended mitotic delay (Gaglio et al., 1995). The difficulty in using siRNA to remove the abundant and long-lived NuMA protein has confounded strategies to determine mitotic NuMA function in the mammalian context (Elbashir et al., 2001; Chang et al., 2005). In addition, during interphase, NuMA accumulates in the nucleus, where it has been proposed to participate in aspects of nuclear structure and/or function, which might also be disrupted during extended siRNA treatment (Merdes and Cleveland, 1998; Harborth et al., 1999). To specifically test the principles of mammalian spindle assembly, particularly the mechanisms of pole focusing and the maintenance of pole integrity, we now use gene replacement to engineer mice and cells in which NuMA’s mitotic function can be selectively disrupted by administration of the small molecule 4-hydroxytamoxifen (4-OHT).

We tested the localization of GFP-tagged versions of the 410 amino acid C-terminal globular tail of the mouse NuMA protein that were either wild-type or deleted for residues encoded by exon 22 (Fig. S2, A and B, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). The C-terminal tail was used to avoid association of tagged NuMA with endogenous NuMA through the central coiled-coil dimerization domain (Harborth et al., 1995). As expected, a wild-type NuMA tail fragment tagged with GFP localized appropriately to nuclei in interphase and was present in the crescent-shaped pattern typical of endogenous NuMA at spindle poles during mitosis (Fig. S2 C). The same GFP tail fragment, but lacking the 59 amino acids encoded by exon 22, was also nuclear during interphase but was severely compromised in localization to spindle poles during mitosis (Fig. S2, C and D).

Therefore, we generated a targeting construct designed to produce an allele of NuMA in which exon 22 could be conditionally deleted through the action of the Cre recombinase. Homologous recombination in mouse ES cells was used to flank exon 22 with loxP sites to create a NuMANeo allele in which the Neo gene was itself deletable by the action of the flipase (Flp) recombinase (Fig. 1 A). ES clones were screened by PCR and DNA blotting for homologous recombination at 5′ and 3′ ends of the exon 22 targeting construct, and multiple targeted clones were identified (Fig. 1, B–D). Two independently targeted ES cell lines were used to generate mice. These animals were crossed to an Flp-enhanced deleter strain (Rodriguez et al., 2000) to remove the Flp recombinase target (FRT)–flanked neomycin gene from intron 22, thereby generating a conditional allele, NuMAdeo. Subsequent mating to the ZP3-Cre mouse line expressing the Cre recombinase in the female germ line (Lewandoski et al., 1997) produced animals heterozygous for the NuMA deletion allele, NuMA22 (Fig. 1 A). Genotypes were confirmed using a three-primer PCR reaction capable of

**Results**

**Creation of mice with a conditional exon 22 deletion allele of NuMA**

Immunoblotting of extracts from a panel of mouse tissues indicated that NuMA was expressed at similar levels in most tissues examined (Fig. S1 A, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). In contrast, Mad2, BubR1, and centromere protein E (CENP-E), which are thought to be primarily or exclusively functional during mitosis, were only detected in the testes and spleen, which contain large numbers of dividing cells. Expression of the nuclear proteins lamin A and C was detected in all tissues examined and closely mirrored the expression of NuMA (Fig. S1 A). Examination of NuMA localization by immunostaining of terminally differentiated motor or Purkinje neurons demonstrated that NuMA was exclusively nuclear but excluded from nucleoli (Fig. S1 B). The near-ubiquitous expression pattern and accumulation of NuMA in nuclei of long-lived postmitotic cells supports the possibility of a nonmitotic interphase function of NuMA.

To test a mitotic role for NuMA without disrupting putative nuclear functions, we used gene targeting in mouse embryonic stem (ES) cells to create a conditional loss of mitotic function allele of NuMA. To do this, we identified an in-frame deletion within the NuMA gene that eliminated its microtubule binding without affecting intranuclear accumulation in interphase.

The tubulin-binding domain of NuMA is comprised of an ∼100 amino acid region in the C-terminal globular tail of NuMA, which interacts directly with tubulin in vitro and mediates its localization to spindle poles in vivo (Haren and Merdes, 2002). Mouse and human NuMA share 88% of amino acid identity in this domain, which is partially encoded by nucleotides comprising the 22nd exon of the mouse NuMA gene. We tested the localization of GFP-tagged versions of the 410 amino acid C-terminal globular tail of the mouse NuMA protein that were either wild-type or deleted for residues encoded by exon 22 (Fig. S2, A and B, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). The C-terminal tail was used to avoid association of tagged NuMA with endogenous NuMA through the central coiled-coil dimerization domain (Harborth et al., 1995). As expected, a wild-type NuMA tail fragment tagged with GFP localized appropriately to nuclei in interphase and was present in the crescent-shaped pattern typical of endogenous NuMA at spindle poles during mitosis (Fig. S2 C). The same GFP tail fragment, but lacking the 59 amino acids encoded by exon 22, was also nuclear during interphase but was severely compromised in localization to spindle poles during mitosis (Fig. S2, C and D).

Therefore, we generated a targeting construct designed to produce an allele of NuMA in which exon 22 could be conditionally deleted through the action of the Cre recombinase. Homologous recombination in mouse ES cells was used to flank exon 22 with loxP sites to create a NuMANeo allele in which the Neo gene was itself deletable by the action of the flipase (Flp) recombinase (Fig. 1 A). ES clones were screened by PCR and DNA blotting for homologous recombination at 5′ and 3′ ends of the exon 22 targeting construct, and multiple targeted clones were identified (Fig. 1, B–D). Two independently targeted ES cell lines were used to generate mice. These animals were crossed to an Flp-enhanced deleter strain (Rodriguez et al., 2000) to remove the Flp recombinase target (FRT)–flanked neomycin gene from intron 22, thereby generating a conditional allele, NuMAdeo. Subsequent mating to the ZP3-Cre mouse line expressing the Cre recombinase in the female germ line (Lewandoski et al., 1997) produced animals heterozygous for the NuMA deletion allele, NuMA22 (Fig. 1 A). Genotypes were confirmed using a three-primer PCR reaction capable of
CONDITIONAL INACTIVATION OF NuMA 
Silk et al.

reduction in NuMA protein levels relative to wild-type cells and animals (Fig. 1 F), most likely the result of reduction in correctly spliced NuMA mRNA caused by the presence of the intronic neomycin cassette (Fig. S3, A–D, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). Taking advantage of this hypomorphic expression from NuMANeo, we tested distinguishing wild type and each of the engineered NuMA alleles (Fig. 1 E).

**NuMA is essential for early development**

Assessment of NuMA levels in ES cells and multiple tissues from mice heterozygous for the NuMANeo allele demonstrated a
the requirement for NuMA in embryonic development and viability and found that the NuMANeoNeo allele could not be bred to homozygosity. No NuMANeoNeo live pups or early embryos were ever recovered (0/88 pups and 0/50 embryos; Table I). As expected, the conditional Nu Mafia allele, produced by Flp-mediated removal of the neomycin marker, was readily bred to between loxP sites. Table I. Genotype incidence and frequencies of pups and embryos from NuMANeo/+ , NuMafia/+ , and NuMA22/+ heterozygous crosses

| Parental genotypes | Progeny | Progeny genotypes |
|--------------------|---------|------------------|
|                    | +       | Neo  | Neo Neo | fl ox | fl ox | Δ22  | Δ22  |
| Neo/+ × Neo/+      | Pups7   | 23 [26%] | 65 [74%] | 0     | NA    | NA    | NA    |
|                    | Embryos8| 21 [42%] | 29 [58%] | 0     | NA    | NA    | NA    |
| fl ox/+ × fl ox/+  | Pups    | 34 [31%] | NA     | NA    | 53 [47%] | 25 [22%] | NA    |
|                    | Embryos | 7 [32%]   | NA     | NA    | NA    | 28 [67%] | 0     |

NuMA Neo, NuMA Neo; fl ox, NuMA fl ox; Δ22, NuMA22; +, wild-type NuMA allele; NA, not applicable.

Mating NuMA fl ox/+ , Cre-ER TM to NuMA fl ox/+ mice was used to obtain embryonic day 14.5 embryos that were wild type, heterozygous, or homozygous for the conditional NuMA allele and that also carried the Cre-ER TM transgene. Mouse embryo fibroblasts (MEFs) were prepared from embryos of each genotype. To confirm that addition of 4-OHT would drive efficient recognition and recombination of loxP sites within the NuMA gene, contact-inhibited cells were treated with 4-OHT for 48 h in low serum. 4-OHT was subsequently washed out, and cells were maintained under growth arrest conditions for an additional 48 h to allow turnover of endogenous NuMA (Fig. 2 A). Multiple independent NuMA fl ox/fl ox, Cre-ER TM cell lines showed highly efficient deletion of the loxP-flanked region after 48 h of 4-OHT treatment (Fig. 2 B).

Quantification of recombination by quantitative PCR (qPCR) showed time and 4-OHT dose-dependent efficiency to exon 22 excision with a maximum effect observed after 48 h, resulting in a fibroblast population with 90% conversion of NuMA fl ox alleles to NuMA22 by day 4 (Fig. 2 C). Immunoblotting revealed that NuMA22 accumulated to a lower than wild-type level (Fig. 2 D). Remaining NuMA protein in NuMA22/22 cells could not be eliminated by doubling the duration of cell cycle arrest after 4-OHT washout, suggesting that all wild-type NuMA had been completely turned over. As expected, the amino acids encoded by exon 22 were dispensable for nuclear accumulation of NuMA but were necessary for efficient spindle pole localization. We conclude that wild-type NuMA protein is absent from NuMA22/22 MEFs 4 d after 4-OHT treatment and that the mutant protein accumulates to ~30% of the level of the wild-type NuMA polypeptide.

NuMA is required for proliferation of primary fibroblasts

To directly assess the consequences of preventing NuMA accumulation at spindle poles, population growth curves were generated for NuMA Neo Neo, NuMA fl ox/fl ox, and NuMA fl ox fl ox MEFs, each carrying the Cre-ER TM transgene. After treatment with 4-OHT to convert the NuMA fl ox allele to NuMA22, NuMA Neo, and NuMA Neo22 cells grew normally after release from low serum arrest, demonstrating that there are no dominant effects on cell cycle progression of mutant protein produced from the NuMA22 allele. Strikingly, NuMA22/22 MEFs failed to increase in number after release from growth arrest (Fig. 2 E), demonstrating that removal of exon 22 results in cell-autonomous growth defects. These conclusions are consistent with cell-intrinsic defects, causing early embryonic lethality in NuMA22/22 mice and the lack of dominant effects or haploinsufficiency observed in NuMA22Neon animals, which develop and age normally.

To determine whether loss of NuMA from spindle poles provoked extended delays in mitosis, as has been previously reported from antibody microinjection-mediated disruption of the

**Table I. Genotype incidence and frequencies of pups and embryos from NuMANeo/+ , NuMafia/+ , and NuMA22/+ heterozygous crosses**

| Parental genotypes | Progeny | Progeny genotypes |
|--------------------|---------|------------------|
|                    | +       | Neo  | Neo Neo | fl ox | fl ox | Δ22  | Δ22  |
| Neo/+ × Neo/+      | Pups7   | 23 [26%] | 65 [74%] | 0     | NA    | NA    | NA    |
|                    | Embryos8| 21 [42%] | 29 [58%] | 0     | NA    | NA    | NA    |
| fl ox/+ × fl ox/+  | Pups    | 34 [31%] | NA     | NA    | 53 [47%] | 25 [22%] | NA    |
|                    | Embryos | 7 [32%]   | NA     | NA    | NA    | 28 [67%] | 0     |

*Mouse pups were genotyped at postnatal day 21.

Embryos were collected between embryonic days 9.5 and 14.5.
Spindle defects caused by loss of NuMA function

Despite normal timing of progression through mitosis, NuMA<sup>Δ22/Δ22</sup> primary cells displayed obvious spindle defects, most striking of which was the detachment of microtubule-nucleating structures from the ends of mitotic spindles. Cytoskeletal staining with a γ-tubulin antibody provided strong evidence that the dissociated structures were bona fide centrosomes, whereas in others, even poles with associated centrosomes lacked a discernable microtubule focus (Fig. 3 A). Greater than 50% of metaphase-like cells in the NuMA<sup>Δ22/Δ22</sup> population had at least one centrosome that was clearly not protein, the mitotic index of NuMA<sup>Δ22/Δ22</sup>, NuMA<sup>Δ22/Δ22</sup>, and NuMA<sup>+/+</sup> MEFs was determined (Gaglio et al., 1995). There was no increase in the percentage of cells in mitosis after NuMA disruption (Fig. 2 F). Mitotic timing was reexamined even more directly in NuMA<sup>Δ22/Δ22</sup>,Cre-ER<sup>TM</sup> and NuMA<sup>Δ22/Δ22</sup>,Cre-ER<sup>TM</sup> immortalized fibroblasts, which were treated with 4-OHT, and the duration of mitosis was determined by phase-contrast time-lapse microscopy. After 4-OHT treatment, NuMA<sup>Δ22/Δ22</sup> was converted to NuMA<sup>ΔΔ22</sup> with the same efficiency as seen in primary cells. Mitosis was defined as the period between the first stage of cell rounding and the point at which cells had completely flattened back onto the substrate. Consistent with the failure of NuMA disruption to alter mitotic index, no significant difference in the duration of mitosis was observed between NuMA<sup>Δ22/Δ22</sup> and control cells (Fig. 2 G).
associated with a spindle pole (apolar centrosome), and a similar frequency had at least one pole in which microtubules did not converge to a single focal point (unfocused kinetochore fibers; Fig. 3 C). These phenotypes contrasted sharply with metaphases observed in wild-type and NuMA4Δ22 cells, which showed typical spindle architecture with focused microtubule arrays terminating near centrosomes (Fig. 3, A and C). In addition to centrosome–spindle coupling and microtubule-focusing defects, metaphase spindle lengths in MG132-arrested NuMAΔ22Δ22 cells were on average 30% longer than either wild-type or NuMA4Δ22 controls (Fig. 3 D).

The spindle defects observed in NuMAΔ22Δ22 cells were also present in anaphase (Fig. 3 B). However, immunostaining of unperturbed fibroblasts with a cyclin B1 antibody confirmed that the apolar centrosome and pole-defocusing phenotypes in NuMAΔ22Δ22 fibroblasts occurred before anaphase onset (Fig. S4 B). In addition, cells arrested in metaphase by blocking cyclin B and securin degradation by treatment with the proteasome inhibitor MG132 showed similar spindle defects at high frequency, corroborating this interpretation (Fig. S4 A). Tension between sister kinetochores in pole-defocused spindles was reduced by ~33% compared with normal cells (Fig. 4, A and B), and chromosome alignment defects were observed more frequently in metaphase NuMAΔ22Δ22 than control NuMA4Δ22 fibroblasts (Fig. 4, C and D). Therefore, spindles in NuMAΔ22Δ22 cells are deficient in their ability to apply or retain tension.

Figure 3. Spindle defects in primary NuMAΔ22Δ22 fibroblasts. Primary fibroblasts were processed for immunofluorescence on experimental day 5, as shown in Fig. 2 A. (A) Example of metaphase in a control cell (NuMA4+/+) and two exon 22–deleted (NuMA4Δ22/Δ22) primary fibroblasts. Arrows indicate centrosomes. (B) Anaphase in wild-type and two NuMA4Δ22/Δ22 primary cells. Each image represents a maximum intensity projection of a deconvolved series of z sections spanning the entire cell in 0.2-μm intervals. Arrows indicate centrosomes. Tubulin is shown in green, and phosphorylated histone H3 is shown in purple. (C) Frequencies of spindle–centrosome dissociation and pole splaying defects seen in control and NuMA-depleted metaphase cells. Cells were scored as phenotypic if at least one centrosome was nonpolar or at least one pole displayed an obvious lack of microtubule focusing. Two independent cell lines were examined per genotype, with >50 cells counted for NuMA4+/+ and >130 cells for each of NuMA4Δ22 and NuMA4Δ22Δ22 controls. (D) Spindle length in MG132-arrested primary fibroblasts measured as the linear distance between spindle poles or the approximate position of most spindle microtubule ends in defocused poles. At least 20 spindles per genotype were examined. *, P < 0.01 using Bonferroni’s multiple comparison test and compared with NuMA4Δ22Δ22; **, P < 0.001. Error bars indicate SEM.
across sister kinetochores and align chromosomes in a metaphase alignment.

Spindle abnormalities were likely not caused by a failure of the dynein–dynactin complex to localize appropriately. A component of dynactin, p150, localized to centrosomes independent of spindle attachment, suggesting that failure of centrosome–spindle coupling and loss of kinetochore fiber focusing did not result from mislocalization of dynein–dynactin, the major mitotic binding partner of NuMA (Fig. S4 C). Cold treatment to preferentially depolymerize dynamic microtubules confirmed that kinetochore fibers remained stably attached to kinetochores in NuMA-disrupted cells even when completely defocused at poles and detached from centrosomes (Fig. S4 D).

From these results, we conclude that spindle pole integrity is defective in the absence of NuMA and more specifically that NuMA is required at spindle poles to couple centrosomes to kinetochore fibers. We also note that although kinetochore–microtubule attachments are apparently intact, tension across sister kinetochores is reduced, and chromosome alignment is defective in NuMAΔ22Δ22 cells.

The displacement of centrosomes from kinetochore fibers in metaphase could arise either from an initial failure of NuMAΔ22Δ22 cells to focus microtubules at the poles of the spindle or from an inability to maintain centrosome attachment to a fully formed spindle. To distinguish these possibilities, we followed spindle formation and mitotic progression in live NuMAΔ22Δ22 MEFs. Primary cells were transduced with a retrovirus encoding tubulin-YFP 2 d before the initiation of Cre recombinase activity with 4-OHT and arrest in G0/G1 with low serum. Cells were subsequently released from arrest and filmed by time-lapse fluorescence microscopy. NuMAΔ22Δ22 cells always formed bipolar spindles and maintained centrosomes at spindle poles throughout mitosis (6/6 morphologically normal spindles; Fig. 5 A; and Video 1, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). In contrast, NuMAΔ22Δ22 fibroblasts exhibited a high frequency of pole defocusing and centrosome detachment phenotypes (9/13 spindles aberrant) (Fig. 5 B). Live cell imaging showed clearly that in NuMAΔ22Δ22 cells, microtubules can establish focusing at centrosomes during the initial across sister kinetochores and align chromosomes in a metaphase alignment.

Figure 4. Reduced spindle tension and efficiency of chromosome alignment in the absence of NuMA. (A) Distance between sister kinetochores in cells arrested in metaphase with MG132 and incubated on ice for 10 min to selectively depolymerize nonkinetochore fiber microtubules. Images represent maximum intensity projections of a deconvolved series of z sections spanning the entire cell in 0.2-μm intervals [projection] or single deconvolved z sections. Kinetochores were identified in single z sections by the relative positioning of kinetochores and orientation of associated kinetochore fibers. Blue, DNA; green, microtubules; red, kinetochores. Bars: (left) 5 μm; and (right) 2.5 μm. (B) Interkinetochore distances of paired sister chromatids in NuMAΔ22Δ22 and nocodazole (Noc)-treated control cells. The boxes represent the interquartile (middle 50%), and the whiskers represent the full range. Horizontal lines represent the median value. (C) Examples of NuMAΔ22Δ22 cells with fully aligned chromosomes and NuMAΔ22Δ22 fibroblasts with chromosome alignment defects. Cells were treated as in A and processed for immunofluorescence to visualize DNA (purple) and tubulin (green). Bars, 5 μm. (D) Percentage of spindles showing chromosome alignment defects. ***, P < 0.0001. Error bars indicate SEM.
in NuMA/H900422 cells was not responsible for the subsequent mitotic deficits, we performed an in vivo test for retention of nuclear function of the NuMA/H900422 protein. To do this, wild-type NuMA was replaced with NuMA/H900422 protein in spinal cord motor neurons, a cell type in which NuMA is known to be present in nuclei in adult neurons (Fig. S1B). These cells were chosen for two reasons: first, defects in motor neuron function give rise to characteristic and easily scorable motor deficits, including gait alterations and paralysis. Second, the lifetimes of individual neurons extend for the full life span of the organism, allowing access to any age-dependent features of loss of interphase NuMA function.

NuMA was deleted specifically from motor neurons by crossing the NuMA flox allele with animals carrying the vesicular acetylcholine transporter (VAcHT)–Cre transgene. This transgene has previously been demonstrated to direct Cre recombinase expression exclusively in motor neurons after the final division of motor neuron progenitors, ensuring that any phenotypes would arise exclusively from postmitotic loss of NuMA (Misawa et al., 2003). NuMA flox/flox, VAcHT-Cre, NuMA+/flox, VAcHT-Cre, and NuMA flox/flox littermate controls were obtained, and animals of all genotypes and genders were produced in expected Mendelian ratios. Activity of the Cre recombinase and restriction of expression to motor neurons in VAcHT-Cre mice was confirmed by mating to the ROSA26R reporter strain (Soriano, 1999). Examination of spinal cord and sagittal brain sections from VAcHT-Cre, ROSA26R mice for β-galactosidase activity confirmed that Cre expression

stages of spindle assembly but that as cells progress through mitosis, maintenance of centrosome–spindle coupling is lost, and poles subsequently defocus.

Despite these defects, completion of mitosis appeared normal, daughter cells formed morphologically normal nuclei, and cytokinesis, including abscission, also occurred (Video 2, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). We also measured the duration of mitosis in tubulin-YFP–expressing MEFs, which we defined as the length of time between nuclear envelope breakdown and the first observable stage of midbody formation. Consistent with our previous observations, mitotic timing was similar for control (33 ± 9 min, n = 6) and NuMA22/22 cells that experienced spindle defects (27 ± 5 min, n = 5). Additionally, the kinetics of spindle bipolarization were similar in control (12 ± 4 min, n = 6) and phenotypic NuMA22/22 cells (13 ± 3 min, n = 5). These observations indicate that loss of NuMA function during mitosis does not prevent the initial timely establishment of focused bipolar spindles but results in centrosome loss from the spindle poles before anaphase followed by microtubule defocusing. Surprisingly, despite these defects, bulk chromosome segregation proceeds largely as normal in NuMA22/22 cells (Fig. 3B and Video 2).

The NuMA22 allele supports potential interphase functions of NuMA

The ability of NuMA22/22 cells to enter mitosis and the spindle phenotypes observed were consistent with specific defects in spindle pole integrity. To confirm that a potential nuclear defect

Figure 5. Bipolar spindle formation precedes centrosome detachment in the absence of mitotic NuMA function. (A and B) Selected images from videos of primary embryo fibroblasts transduced with retrovirus encoding tubulin-YFP, either heterozygous (A; Video 1, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1) or homozygous (B; Video 2) for NuMA22/22, undergoing the first mitosis after 4-OHT treatment and release from growth arrest. Arrows indicate centrosomes, and each time point shows a maximum intensity projection of five confocal fluorescence z sections acquired in 2-μm intervals.
was restricted to motor neurons (Fig. S5 A, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1).

Extensive visual observation demonstrated that NuMA^fl ox/fl ox, VαCHT-Cre animals showed no behavioral defects indicative of motor neuron dysfunction, even up to 2 yr of age. Weight gain was also similar in control and NuMA^fl ox/fl ox, VαCHT-Cre mice, providing no evidence for motor neuron dysfunction or muscle denervation (Fig. S5 B). Finally, counting of cresyl violet–stained motor neuron cell bodies in spinal cord sections of 200-d-old animals revealed no effect on motor neuron numbers (Fig. S5 C). Thus, the exon 22–deleted mutant complements all potential nuclear functions of NuMA and does so for extended periods in vivo. Alternatively, NuMA may perform limited or redundant interphase functions in these cells.

**NuMA is required for the maintenance of centrosome-spindle coupling in bipolar spindles under tension**

Live imaging of tubulin-YFP–marked spindles in unperturbed fibroblasts demonstrated that in the absence of NuMA, initial microtubule focusing at the pole appeared normal. This strongly supports a maintenance rather than establishment role for NuMA in the attachment of centrosomes to kinetochore fibers. To further test this, we arrested NuMA wild-type, NuMA^+/−/H9004^22, and NuMA^22/22/H9253^ cells in mitosis with the Eg5 inhibitor S-trityl-l-cysteine (STLC; Skoufias et al., 2006). Eg5 is a bipolar, homotetrameric, kinesin-related motor protein that is required during mitosis to both establish and maintain separation of centrosomes. It is thought to function by cross-linking and sliding apart antiparallel microtubules from opposing centrosomes, thereby pushing centrosomes apart (Kapitein et al., 2005). STLC inhibits activity of Eg5, causing collapse of bipolar spindles. Regardless of genotype, in the absence of STLC, monopolar spindles were observed with equally low frequency in all cell lines, but upon STLC treatment, all MEF cell lines produced a high frequency of monopolar spindles that appeared almost exclusively as chromosome rosettes surrounding a central γ-tubulin–positive pole (Fig. 6, A and B). This indicates that in monopolar spindles, centrosomes continue to dictate the location of spindle pole formation when NuMA function is disrupted. Furthermore, under these conditions, kinetochore fibers do not require NuMA for active focusing toward centrosomes.

Throughout the extended mitotic delay caused by treatment with STLC, centrosomes persisted at the center of monopolar spindles in NuMA^22/22/H9253^ cells. How can this be reconciled with a maintenance role of NuMA in centrosome–spindle coupling? Relative to bipolar metaphase spindles, monopolar spindles have reduced tension forces acting between centrosomes and kinetochores. Thus, the spindle defects produced in cycling NuMA^22/22/H9253^ cells likely reflect a requirement for NuMA in maintaining centrosomes at poles of spindles experiencing typical metaphase forces. To directly test this possibility, STLC was washed out from monopolar-arrested cells to reintroduce tension into spindles with kinetochore fibers focused toward a monopole. 1 h after release, cells were fixed for immunofluorescence. In control cells, anaphases always had one centrosome at each pole (Fig. 6 C). In contrast, NuMA^22/22/H9253^ cells displayed anaphase figures in which chromosomes had segregated normally, but spindle poles were defocused, and centrosomes (detected as discrete foci of strong γ-tubulin staining) had failed to separate.

These results were corroborated by following the recovery of spindle bipolarity in retrovirally transduced α-tubulin-YFP–expressing fibroblasts. After release from STLC, control cells were uniformly observed to recover from monopolarity by separating centrosomes and forming bipolar spindles with well-focused poles (7/7 cells; Fig. 6 D; and Video 3, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1). However, after the reestablishment of tension, NuMA^22/22/H9253^ fibroblasts often formed spindles with one well-focused pole and one splayed spindle pole lacking a centrosome (8/13 cells; Fig. 6 D and Video 4). We conclude that mitotic NuMA function is required to maintain centrosome–spindle attachments under conditions in which tension is applied across the spindle.

Adjacent centrosomes that failed to separate in NuMA^22/22/H9253^ cells were always initially observed at the spindle end with focused microtubules. As NuMA^22/22/H9253^ cells progressed through mitosis, the paired centrosomes often dissociated from the pole. These cone-shaped spindles were not arrested monopolar spindles observed in profile because they uniformly proceeded into anaphase, indicating that mitotic checkpoint signaling was silenced. These data demonstrate that normal NuMA function is required for centrosome separation after recovery from a monopolar state. In addition, because the centrosome distal half of each NuMA-deficient spindle forms a splayed pole after release from STLC, we conclude that in the absence of centrosomes, NuMA is required for the establishment of microtubule focusing.

**Stable kinetochore-microtubule interactions are required for centrosome separation after recovery from monopolarity**

The aforementioned evidence demonstrates a requirement for NuMA in the physical tethering of centrosomes to kinetochore fibers and reveals the surprising finding that centrosome–spindle connections are required for centrosome separation after recovery from monopolarity. This finding has important implications for the mechanism of centrosome separation during reestablishment of spindle bipolarity in prometaphase. Therefore, we specifically tested whether stable microtubule–kinetochore attachments are also required for centrosome separation in recovering monopolar spindles. The Ndc80 complex, a heterotetramer composed of the Ndc80, Nuf2, Spc24, and Spc25 proteins, is a key component involved in the stable attachment of microtubule bundles at kinetochores (Cheeseman and Desai, 2005). To directly test the requirement for kinetochore–microtubule attachment in centrosome separation, we used siRNA to deplete Nuf2 in HeLa cells stably expressing fluorescently tagged tubulin and histone H2B (Fig. 7 A). These cells were arrested with monopolar spindles using STLC, the drug was removed, and time-lapse fluorescence microscopy was used to observe recovery of spindle bipolarity. 90 min after STLC washout, all but 3% of control siRNA-treated cells had separated their centrosomes and formed bipolar spindles. However, in the same period of time, 35% of Nuf2-depleted
allele with a prolonged G0/G1 arrest, we were able to achieve nearly quantitative turnover of accumulated wild-type NuMA protein before the first mitotic division. Strikingly, we show that in the absence of functional NuMA, and despite apparently normal initial bipolar spindle formation, centrosomes are unable to maintain attachment to the ends of kinetochore fibers. The subsequent defocusing of microtubules at spindle poles reveals a distinct requirement for NuMA in the maintenance of mammalian centrosome–spindle attachments.

Discussion

In this study, we describe the creation of a separation of function allele of NuMA by specific deletion of exon 22 of the mouse NuMA gene. Removal of exon 22 produces a mutant protein that is unable to efficiently localize to spindle poles during mitosis but is able to perform all essential interphase functions of NuMA. By combining inducible inactivation of this

spindles failed to resolve their centrosomes and form bipolar spindles (Fig. 7, B and C). We conclude that efficient centrosome separation after recovery from monopolar spindles relies on the two-point attachment of kinetochore fibers at centrosomes and kinetochores.

Figure 6. Prometaphase centrosome separation and centrosome-independent spindle pole focusing require NuMA. (A) Primary MEFs were arrested in mitosis by treatment with STLC and processed for immunofluorescence. Green, α-tubulin; blue, DNA; red, γ-tubulin. (B) Frequencies of monopolar spindles as shown in A. Two independent cell lines per genotype were used, and >200 mitoses per genotype were counted. (C) Anaphase in NuMA+/Δ22 control and NuMA+Δ22/Δ22 cells 1 h after washout of STLC. In merged images, DNA is shown in purple and γ-tubulin in green. Arrows indicate centrosomes. (D) Stills from videos of NuMA+/Δ22 (Video 3, available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1) and NuMA+Δ22/+Δ22 (Video 4).
This has been proposed to occur through the capture of kinetochore fibers by NuMA (Khodjakov et al., 2003), which itself is transported toward spindle poles, likely on centrosomal/astral microtubules by dynein (Merdes et al., 2000). However, centrosomes are not required for microtubule focusing or NuMA localization to spindle poles (Khodjakov et al., 2000). Our efforts in this study have extended this to demonstrate that in the absence of functional NuMA, initial bipolar spindle formation proceeds normally. However, after the establishment of tension across kinetochores, centrosomes subsequently detach from the spindle, and microtubules defocus. This demonstrates that NuMA is required to physically tether kinetochore fiber minus ends at the poles of bipolar spindles under tension and provides the first evidence that an essential function of NuMA during mitosis is in the maintenance and not establishment of mammalian centrosomal–spindle connections.

The normal initiation of bipolar spindle formation in the absence of NuMA suggests the existence of alternative processes involved in establishing focused spindle poles. These are likely to be dependent on the presence of centrosomes, which might function in cooperation with components such as HSET in mammals and Ncd in Drosophila melanogaster (Gordon et al., 2001; Goshima et al., 2005). This interpretation is corroborated by our observation that after recovery from monopolarity, microtubules in NuMA<sup>Δ22</sup> MEFs are severely defocused in the acentrosomal spindle half. The formation of these monoaxial, bipolar cone-shaped spindles provides clear evidence that NuMA is required for spindle pole focusing in the absence of centrosomes. Thus, NuMA and centrosomes function redundantly in establishing spindle poles by contributing independently to initial microtubule focusing. It is likely that mammalian acentrosomal spindle systems, including mouse oocytes, rely heavily on NuMA for the establishment of spindle poles, which is a question now testable with the NuMA<sup>Δ22</sup> allele.

Disruption of dynein function gives rise to defects similar to those we have observed in NuMA<sup>Δ22</sup> MEFs, including centrosome–spindle uncoupling and, to a lesser extent, a mild degree of kinetochore fiber defocusing during metaphase (Heald et al., 1997; Goshima et al., 2005). In multiple contexts, dynein inhibition causes NuMA to redistribute from spindle poles to along the length of spindle microtubules. This suggests that a major function of spindle-localized dynein in mitosis may be to transport NuMA as a cargo to microtubule minus ends (Gaglio et al., 1997; Merdes et al., 2000). The rapid kinetics of

---

**Figure 7. Kinetochore–microtubule attachments are required for centrosome separation in prometaphase.** (A) Immunoblot of an extract of HeLa cells 48 h after transfection with siRNA oligos against glyceraldehyde 3-phosphate dehydrogenase (GAPDH) or Nuf2. (B) Still images from videos of HeLa cells coexpressing H2B–monomeric RFP and tubulin-YFP. Cells were transfected with siRNA oligos against GAPDH or Nuf2 and 48 h later were arrested with STLC. Time is given in minutes relative to STLC washout. Images are maximum intensity projections of five confocal z sections spaced 2 μm apart. Green, tubulin; purple, histone H2B. (C) Frequency of spindles that remained monopolar 90 min after release from STLC in cells treated with siRNA to GAPDH or Nuf2. Error bars represent the mean and SEM of three separate experiments; n = 192 cells GAPDH siRNA; n = 228 cells Nuf2 siRNA; ***, P < 0.0001 by Fisher’s exact test.
NuMA localization to spindle poles and the kinetochore fiber–independent nature of NuMA accumulation at poles (unpublished data) is consistent with this interpretation. Therefore, much of the phenotype caused by inhibition of dynein function may be a direct result of a failure to properly localize NuMA.

**Function of Eg5 in prometaphase centrosome separation**

In mitotic prophase before nuclear envelope breakdown, two duplicated centrosomes move across the nuclear envelope in a dynein-dependent manner to diametrically oppose each other in anticipation of bipolar spindle formation (Gonczy et al., 1999). Maintenance of centrosome separation after nuclear envelope breakdown requires activity of the plus end–directed motor Eg5, which acts to slide apart antiparallel microtubules that emanate directly from centrosomes. Inhibition of Eg5 activity causes centrosome collapse after nuclear envelope breakdown, triggering an extended mitotic delay (Kapitein et al., 2005; Skoufias et al., 2006). Surprisingly, we demonstrate that centrosome separation fails after restoration of Eg5 activity in monopolar NuMA<sup>Δ22/Δ22</sup> cells, indicating a novel function for NuMA in mitosis. Anchoring of kinetochore fibers at the spindle pole may be critical to allow Eg5 to drive initial separation of juxtaposed centrosomes. Once this occurs, overlapping antiparallel arrays of microtubules are formed between centrosomes, providing forces to drive further centrosome separation. Consistent with this interpretation, in the absence of stable kinetochore–microtubule interactions, centrosome separation after release from monopolarity is also inhibited. Thus, we provide a demonstration that Eg5-dependent centrosome separation requires the two-point attachment of microtubules at kinetochores and centrosomes.

**Chromosome segregation in the absence of focused poles**

The striking spindle defects observed in NuMA<sup>Δ22/Δ22</sup> fibroblasts did not delay progression through mitosis. Because a single unattached kinetochore is capable of delaying anaphase onset (Rieder et al., 1994), this indicates that microtubule capture by kinetochores occurs efficiently in the absence of functional NuMA. Furthermore, bulk chromosome segregation was observed to occur normally on spindles with detached centrosomes and defocused poles. These observations indicate that pole focusing is not an absolute requirement for (a) all kinetochores to be attached to spindle microtubules and (b) the bulk of chromosomes to be aligned and segregated in anaphase. Indeed, plant cells carry out faithful mitoses without centrosomes, using spindles without discernibly focused poles (Franklin and Cande, 1999). Additionally, mechanical severing of kinetochore fibers between spindle poles and kinetochores has been shown to not prevent continued poleward chromosome movements (Nicklas, 1989).

Although bulk chromosome segregation occurs normally, most NuMA<sup>Δ22/Δ22</sup> cells exhibited modest chromosome alignment defects, such as an elongated spindle and reduced tension across sister kinetochores. These defects are likely to result in chromosome segregation errors that explain the requirement of NuMA-dependent pole focusing for mouse embryonic viability and normal cellular proliferation. This is consistent with chromosome mis segregation driving embryonic lethality (e.g., from loss of the centromere motor/tether CENP-E; Putkey et al., 2002). Alternatively, the early lethality of NuMA<sup>Δ22/Δ22</sup> embryos may result from mis segregation of centrosomes or centrioles as spindle cargo (Pickett-Heaps 1969), which are not required for mitotic spindle function but are essential for normal embryonic development (Chatzimeletiou et al., 2008). Therefore, our evidence collectively demonstrates that NuMA and its role in focusing spindle poles is a required component of normal mammalian mitotic progression and embryonic development.

**Materials and methods**

**Construction of NuMA-targeted mice**

A mouse 129S6/SvEtvTac bacterial artificial chromosome genomic library (RPCI-22; Children’s Hospital Oakland Research Institute, Oakland, CA) was screened for the NuMA gene with a probe to the largest exon of NuMA. A single clone was identified and confirmed by PCR to contain the entire NuMA gene. An 8-kb EcoRV–Scal fragment containing exons 16–25 was subcloned into pBluescript (Agilent Technologies). A loxP sequence and 3’ Scal restriction site were introduced upstream of exon 22 by cloning an oligonucleotide linker into a BatEll site. A loxP-FRTPGKNeo-FRT fragment from pK-11 (Meyers et al., 1998) was inserted downstream of exon 22. Finally, the diphertheria toxin negative selection marker (Yanagawa et al., 1999) was introduced downstream of the short homology arm. The targeting vector was linearized with NotI before electroporation into ES cells. ES cell culture and transfection was performed as described previously (Putkey et al., 2002). DNA from G418-resistant ES cells was cloned using PCR and genomic DNA blotting. The probe for targeting of exon 22 was amplified from R1 ES cell DNA using primers pr13 forward (5’-TTTGGTTGTTGTTGTGTGC-3’) and pr13 reverse (5’-TGATAGGGAGGACGACCCAGG-3’). Mice, ES cells, and embryos were genotyped as shown in Fig. 1 A with primers i (5’-AACCCCATCGCAGGTTGAC-3’), ii (5’-ATGCTCCCGAATGCTGACG-3’), iii (5’-GGAGGTGTTGTCGACACCTGTA-3’), and iv (5’-GGAGGTGTATTCTACTGGGAG-3’). ES clones carrying the appropriate genetic modification were injected into C57/Bl6 embryos at the Transgenic Mouse and Gene Targeting Core facility (University of California, San Diego, La Jolla, CA). Pups from chimeric mice were screened by coat color, and PCR was used to identify germline transmission.

**Mouse embryonic fibroblast preparation and culture**

Mouse embryonic fibroblasts were prepared as previously described (Putkey et al., 2002). Primary fibroblasts were maintained and passaged in an incubator set at 10% CO<sub>2</sub> at 37 °C and maintained at 3% O<sub>2</sub> by a continuous flow of nitrogen gas to increase replicative lifespan as described previously (Parrinello et al., 2003). In all experiments using primary cells, fibroblasts were grown for no more than two cumulative weeks in culture after derivation. To induce growth arrest, MEFs were cultured to confluence and shifted to media containing 2% serum. In fibroblasts carrying the Cre-ER<sup>TM</sup> transgene, 4-OHT (10 mg/ml stock in ethanol; Sigma-Aldrich) was added to a final concentration of 0.1 μM (unless otherwise indicated) to cause nuclear translocation of Cre.

**Retrovirus preparation and infections**

Retroviral plasmids (pBABE variants) were prepared as described previously (Shah et al., 2004). For retroviral infection of primary MEFs, cells grown in 12-well plates were washed with PBS and incubated for 15 min in a humidified incubator with retroviral supernatant mixed with 8 μg/ml polybrene (Sigma-Aldrich). Plates of cells were wrapped in parafilm and spun at 1,100 g for 30 min at room temperature, after which the supernatant was replaced with primary MEF media, and cells were returned to the incubator.

**Preparation and analysis of DNA, RNA, and cDNA**

For analysis of splicing defects in NuMA<sup>Neo/</sup> cells and tissues, RNA was prepared from mouse fibroblasts using the RNaseasy Mini kit (QIAGEN) and from cells and tissues using TRIzol reagent (Invitrogen). cDNA was prepared from total RNA and used in quantitative RT–PCR with SYBR Green reaction mixture on a Step One Plus (Applied Biosystems). PCR was performed using the following conditions: 1 cycle of 95°C for 10 min followed by 40 cycles of 95°C for 15 s, 60°C for 30 s, and 72°C for 30 s. Sequences of primers are located in Table I.
preparing with the SuperScript III First-Strand Synthesis kit (Invitrogen). Splicing events were detected in NuMAαααα-/- cells and tissues by PCR amplification from cDNA with primers pr4 forward (5'-GGTTCCGAAGACTCGC-CCG-GACGG-3') and Neo33 (5'-GGATCTCATCGTGGCCGCTGGGT-3'). The C-terminal half of the NuMA cDNA was amplified from the NuMAα allele as a control, using primers pr4 forward and ex2 reverse (5'-GGACTGGAAGGGCCAGCAACCTG-3'). For use in qPCR, RNA from cells and tissues was treated with the RNase-Free DNase set (QIAGEN) before reverse transcription. The loss of full-length NuMA mRNA from NuMAααααα-/- cells and tissues was measured with primers 22F2 (5'-AAGCCGATCG-CAGATGTGC-3') and 22 R (5'-TACGCCTCTACATCGCCGTC-3'). Cyclophilin A was amplified as a normalizer using primers cycloA forward (5'-GAGAGAAAGGATT-3') and cycloA reverse (5'-AGCACTG-GAGTGGGTCTCAGAGGAAACTCG-3'). The degree of mRNA loss was calculated using the comparative cycle time method by normalizing the signal produced from cDNA with primers pr4 forward (5'-CTGCTCTAATAGTGGGCCG-3') and 22 reverse (5'-GGTGGGTCTCAGAGGAAACTCG-3'). The mouse γ-actin gene was amplified as a normalizer using primers 6590 (5'-TGGAATCTCAAGAGCAGGAATGATG-3') and 6591 (5'-CTCCGAATCTCATCCATGAAGC-3'). Reactions were performed using 40 ng genomic DNA and the SYBR Green Supermix qPCR reagent (Bio-Rad Laboratories). The degree of splicing was calculated by normalizing the signal produced from an experimental sample to the unexonised gene γ-actin and comparing experimental samples to DNA extracted from NuMAααααα-/- MEFs as described previously (Paffoni, 2001). All qPCR reactions were run using the iCycler (Bio-Rad Laboratories).

Live cell microscopy

HeLa and MEF cells were seeded onto 35-mm glass-bottom dishes (MatTek) and incubated in CO2-independent medium (Invitrogen) supplemented as described previously (Moever et al., 2007). Dishes were placed in a heat-controlled stage set at 37°C. Fluorescence imaging was conducted using a spinning disk confocal (McBain Instruments) attached to an inverted microscope (TE2000e; Nikon) equipped with a 60x/1.4 NA objective lens. Fluorescence excitation was controlled by Metamorph software (MDS Analytical Technologies). Z-series images were acquired using a camera (Orco-ER; Hamamatsu Photonics) at 3- or 5-min intervals. Z stacks were compiled by maximum intensity projection for presentation.

Immunofluorescence

For indirect immunofluorescence analysis of frozen tissue sections, brain and spinal cord were prepared and processed as described previously (Lobsiger et al., 2005). Antibody staining was performed overnight at room temperature. Sections were mounted on slides (Superfrost Plus; Thermo Fisher Scientific) in a solution of 0.2% gelatin in PBS, dried overnight, and covered with antifade reagent (ProLong; Invitrogen) and glass coverslips before imaging.

For immunofluorescence analysis of cultured cells, cells were grown on hydrochloric acid–washed, poly-lysine (Sigma-Aldrich)–coated 18-mm glass coverslips and fixed in either ice-cold methanol for 10 min (γ-tubulin and cyclin B1 staining) or 4% formaldehyde in PBS for 10 min and processed using standard conditions. DNA was visualized by staining with DAPI. Images of fixed cells were acquired using a 100x oil objective on a DeltaVision-modified inverted microscope (IX70; Olympus) using SoftWorx software (Applied Precision, LLC) and were deconvolved unless otherwise indicated. Rabbit polyclonal antibodies used in this study included anti-Xenopus NuMA tail (1:250; Merdes et al., 1996), anti-human NuMA tail (1:500; Gaglio et al., 1995), anti-CENP-E Hpx (1:200; Yao et al., 1997), anti-lamin A/C (1:500; provided by L. Gerace, Scripps Research Institute, San Diego, CA), and anti-Mad2 (1:250).

Monoclonal antibodies used include SMI-32 (1:1,000; Sternberger Monoclonals), GTU88 (1:1,000; Sigma-Aldrich), DMA1 (1:1,000; Abcam), G9N1 (1:100; Santa Cruz Biotechnology, Inc.), p15GSK1 (1:100; BD), and S9F (1:500; Taylor et al., 2001). These antibodies identify neurofilaments, γ-tubulin, α-tubulin, cyclin B1, dynein complex component p15GSK1, and Bub1, respectively. Additionally, antibodies isolated from human autotransplant available as anticentromeric antibodies (1:100; Antibodies Inc.) were used to identify kinetochores. Secondary antibodies (Jackson ImmunoResearch Laboratories) labeled with FITC, Texas red, or Cy3 were used at final dilutions of 1:200.

Online supplemental material

Fig. S1 shows the expression pattern of NuMA in mouse tissues and the localization of NuMA in adult mouse neurons. Fig. S2 provides data characterizing the localization of GFP-tagged NuMA tail fragments. Fig. S3 provides data demonstrating splicing defects underlying hypomorphic expression from the NuMAαααα allele. Fig. S4 provides additional data characterizing the phenotype of NuMAααααα-/- cells, including timing of centromosome detachment, dynactin localization, and kinetochore fiber stability. Fig. S5 includes data that characterize VachT-Cre transgenic mice and show the phenotype of animals with deletion of NuMA exon 22 in motor neurons. Videos 1 and 2 illustrate spindle formation and integrity throughout mitosis in cycling NuMAααααα and NuMAαααααααα-/- primary fibroblasts. Videos 3 and 4 show mitotic spindle structure and centromere positioning during the degree of STU-induced monopolarity in NuMAααααα and NuMAαααααααα-/- primary fibroblasts. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200810091/DC1.

We thank A. Desai and K. Oegema for helpful comments and access to imaging equipment. We also acknowledge members of the Cleveland laboratory for invaluable support and helpful discussion throughout the duration of this work.

This work was supported by a grant (GM29253) from the National Institutes of Health to D.W. Cleveland, who receives salary support from the Ludwig Institute for Cancer Research. A.J. Holland is supported by a European Molecular Biology Organization Long-Term Fellowship.

Submitted: 14 October 2008
Accepted: 4 February 2009

Note added in proof. Since the final submission of this manuscript, an independent study also identified a role of kinetochore-dependent forces in prometaphase centrosome separation (Fiso et al., 2009).

References

Chang, W., J.N. Dynnek, and S. Smith. 2005. NuMA is a major acceptor of poly(ADP-ribosylation) by tankyrase 1 in mitosis. Biochem. J. 391:177–184.
Chatzimelianos, K., E.E. Morrison, N. Prapas, Y. Prapas, and A.H. Handyside. 2008. The centromere and early embryogenesis: clinical insights. Reprod. BioMed. Online. 16:485–491.
Cheeseman, I.M., and A. Desai. 2005. A combined approach for the localization and tandem affinity purification of protein complexes from metazoans. Sci. STKE.
Compton, D.A. 1998. Focusing on spindle poles. J. Cell Sci. 111(Pt 11):1477–1481.
Dasso, M. 2001. Running on Ran: nuclear transport and the mitotic spindle. Cell. 104:321–324.
Elbashir, S.M., J. Harborth, W. Lendeckel, A. Yalcin, K. Weber, and T. Tuschl. 2001. Duplexes of 21-nucleotide RNAs mediate RNA interference in cultured mammalian cells. Nature. 411:494–498.
Franklin, A.E., and W.Z. Cande. 1999. Nuclear organization and chromosome segregation. Plant Cell. 11:523–534.
Gaglio, T., A. Saredi, and D.A. Compton. 1995. NuMA is required for the organization of microtubules into aster-like mitotic arrays. J. Cell Biol. 131:693–708.
Gaglio, T., M.A. Dionne, and D.A. Compton. 1997. Mitotic spindle poles are organized by structural and motor proteins in addition to centrosomes. J. Cell Biol. 138:1055–1066.
Ganem, N.J., and D.A. Compton. 2006. Functional roles of poleward microtubule flux during mitosis. Cell Cycle. 5:481–485.
Gonczy, P., S. Pichler, M. Kirkham, and A.A. Hyman. 1999. Cytoplasmic dynein is required for distinct aspects of MTOC positioning, including centrosome separation, in the one cell stage Caenorhabditis elegans embryo. J. Cell Biol. 147:135–150.
Gordon, M.B., L. Howard, and D.A. Compton. 2001. Chromosome movement in mitosis requires microtubule anchorage at spindle poles. J. Cell Biol. 152:425–434.
Goshima, G., F. Nedelec, and R.D. Vale. 2005. Mechanisms for focusing mitotic spindle poles by minus end-directed motor proteins. J. Cell Biol. 171:229–240.
Gruss, O.J., and J. Vernos. 2004. The mechanism of spindle assembly: functions of Ran and its target TPX2. J. Cell Biol. 166:949–955.
Harborth, J., K. Weber, and M. Osborn. 1995. Epitope mapping and direct visualization of the parallel, in-register arrangement of the double-stranded coiled-coil in the NuMA protein. EMBO J. 14:2447–2460.
Harborth, J., J. Wang, C. Gueth-Hallonet, K. Weber, and M. Osborn. 1999. Self assembly of NuMA: multiamer oligomers as structural units of a nuclear lattice. EMBO J. 18:1689–1700.
