

The spindle assembly checkpoint

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The spindle assembly checkpoint monitors proper chromosome attachment to spindle microtubules and is conserved from yeast to humans. Checkpoint components reside on kinetochores of chromosomes and show changes in phosphorylation and localization as cells proceed through mitosis. Adaptation to prolonged checkpoint arrest can occur by inhibitory phosphorylation of Cdc2.

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Current Opinion in Cell Biology 1996, 8:773-780

© Current Biology Ltd ISSN 0955-0674

Abbreviations

APC	anaphase-promoting complex
BUB	budding inhibited by benzimidazole
MAD	mitotic-arrest deficient
MPS	monopolar spindle
SPB	spindle pole body

Introduction

The survival of cells and organisms requires accurate chromosome segregation. Chromosome loss can kill cells, and chromosome loss or gain can cause birth defects or contribute to tumor progression [1]. The spindle assembly checkpoint detects defects in spindle structure or in the alignment of chromosomes on the spindle, and delays the onset of chromosome segregation (anaphase) until these defects are corrected. Disruption of the spindle with microtubule-depolymerizing drugs such as nocodazole and colchicine arrests cells in mitosis (reviewed in [2]), and this arrest depends on the integrity of the spindle assembly checkpoint. More subtle defects, such as the presence of a single kinetochore (the protein complex assembled on the centromeric DNA that attaches chromosomes to microtubules) that is not attached to spindle microtubules, can also activate the checkpoint [3]. Genetic analysis in budding yeast has identified components of the spindle assembly checkpoint [4,5], making it possible to determine which defects arrest cells in mitosis by activating the checkpoint, and which induce arrest by other means. This analysis shows that the checkpoint detects spindle depolymerization [4,5], the presence of multiple minichromosomes and dicentric chromosomes [6,7], and defects in the spindle pole body (SPB, the budding yeast centrosome) [8,9], microtubules ([10]; C Mistrot, K Hardwick, A Murray, unpublished data), kinetochore proteins [11], centromeric DNA [12], or microtubule motors ([4]; C Mistrot, K Hardwick, R Li, A Murray, unpublished data) (Table 1).

Below, we discuss: the importance of kinetochore-microtubule interactions in activating the spindle assembly checkpoint; the protein components of the checkpoint, some of which reside on the kinetochore; the potential targets of the checkpoint; and a novel pathway out of mitosis that may be used by cells to adapt to a checkpoint arrest.

The role of the kinetochore in the spindle assembly checkpoint

All of the defects that the spindle assembly checkpoint detects can affect the ability of kinetochores to attach to spindle microtubules (reviewed in [13]; see Table 1), suggesting that kinetochores that are not attached to the spindle generate an inhibitory signal that halts the cell cycle. Exit from mitosis cannot depend on a positive signal from correctly attached kinetochores, as a spindle that lacks chromosomes (and thus also kinetochores) undergoes anaphase-like movements with no delays [14].

Direct support for the existence of an inhibitory signal from kinetochores comes from experiments on mammalian tissue culture cells. Anaphase will not begin until the last kinetochore attaches to the spindle, even if attachment takes many hours [3]. This delay can be abolished if the last unattached kinetochore is destroyed by a laser microbeam [15]. Low doses of microtubule-polymerization inhibitors and taxol, a microtubule stabilizer, also activate the checkpoint in animal cells [15,16,17]. In both of these situations, normal bipolar attachment of chromosomes occurs and the spindle appears normal. It is thought, however, that in the presence of drugs the number of microtubules attached per kinetochore is less than normal and that the attachment is less stable than in the absence of drugs.

In some meiotic cells, the checkpoint also monitors the tension on the kinetochore-microtubule linkage. In a fraction of insect spermatocytes, one of the sex chromosomes loses its attachment to its partners [18]. As a result, this chromosome is attached to only one spindle pole (centrosome) and the cell arrests in mitosis for many hours. Using a microneedle to apply tension to the mono-oriented chromosome induces anaphase [19]. Tension may directly control the activity of the checkpoint, or it may stabilize the kinetochore-microtubule attachment [20], with the checkpoint responding to unoccupied microtubule-binding sites on the kinetochore. In mammalian cells and budding yeast, a single attached kinetochore that lacks a sister kinetochore does not activate the checkpoint [15,21,22], suggesting that in these cells tension may be applied by forces that move the chromosome arms away from the spindle pole.

Table 1

Treatments and defects that activate the spindle assembly checkpoint.

Treatment or defect	Organism	Description
High doses of microtubule-depolymerizing drugs	Many	Causes complete spindle depolymerization. Strength of mitotic arrest and speed of recovery varies [2,4,5,23].
Low doses of microtubule-depolymerizing drugs	Budding yeast, sea urchin embryos, HeLa cells	Bipolar spindle forms, but anaphase is delayed [16]. In budding yeast, the <i>BUB2</i> gene is not required for this delay [11*].
Taxol	Mammalian tissue culture cells	Stabilization of spindle microtubules delays anaphase [15**,17].
Defects in microtubules	Budding yeast	Some <i>tub2</i> (β -tubulin) mutants cause <i>MAD</i> -dependent arrest in mitosis ^(a) and some <i>tub1</i> (α -tubulin) mutants are suppressed by additional copies of <i>BUB</i> genes [10].
Excess or defective centromeres	Budding yeast	Excess circular or linear centromeric plasmids [6*], dicentric chromosomes [7] and centromeric DNA mutations [12] all cause <i>MAD</i> - or <i>BUB</i> -dependent delays in mitosis.
Defects in centromere-binding proteins	Budding yeast	Some <i>ctf13</i> and <i>cbf1</i> mutants cause <i>MAD</i> - and <i>BUB</i> -dependent delays in mitosis [11*] ^(a) . Some <i>cep3</i> , <i>ndc10</i> and <i>skp1</i> mutants also delay in mitosis [61–63].
Injection of antibodies to kinetochore components	Mammalian tissue culture cells	Injection of 3F3/2 antibodies causes delays in mitosis [27]. Injection of antibodies to CENP-C and CENP-E also causes delays in mitosis [64,65] that may depend on the spindle assembly checkpoint.
Monopolar attachment of chromosome homologs	Insect spermatocytes	Causes 5–7 hour delay in mitosis unless tension is applied to kinetochore [19**].
Single unattached kinetochore	Mammalian tissue culture cells	Delays the initiation of anaphase [3].
Defects in SPB	Budding yeast	<i>kar1</i> , <i>ndc2</i> , <i>mps2</i> and <i>cdc31</i> mutants arrest in mitosis with monopolar spindles [35]. The <i>cdc31</i> and <i>mps2</i> arrest is <i>MAD</i> -dependent [9**].
Defects in microtubule motors	Budding yeast, sea urchin embryos, mammalian tissue culture cells	Mutants in the budding yeast <i>Kar3</i> , <i>Cin8</i> and <i>Kip1</i> kinesins delay in mitosis [66]. The <i>kar3</i> and <i>cin8</i> delay is <i>MAD</i> -dependent ^(a) . Injection of antibodies to the kinesin CHO1 into sea urchin embryos or tissue culture cells causes delays in mitosis [67,68] that may depend on the spindle assembly checkpoint.
Defects in B-type cyclins	Budding yeast	Deletion of <i>CLB3</i> and <i>CLB4</i> (two budding yeast B-type cyclins) causes a <i>MAD2</i> -dependent delay in mitosis [69].
Meiotic cross-overs	<i>Drosophila</i> oocytes	Tension caused by meiotic cross-overs between chromosome homologs is required for metaphase I arrest. This arrest may require the spindle assembly checkpoint [70].

^(a)C Mistrot, K Hardwick, R Li, A Murray, unpublished data. CENP, centromere protein.

Do other cells have different sources for the checkpoint signal? In sea urchin embryos, partial or complete spindle depolymerization [23], or ripping the spindle in two with a microneedle [24], delays the cell cycle. In contrast, the presence of multiple unattached kinetochores causes no delay in the cell cycle [25]. Thus, in these cells, a spindle assembly checkpoint exists, but cannot be activated by unattached kinetochores. One possibility is that passage through mitosis in these cells requires the presence of overlapping antiparallel microtubules that exist only in a spindle with more than one pole. This requirement may define a novel checkpoint in embryonic cells.

Checkpoint proteins on the kinetochore

The chemistry of the kinetochore changes when it becomes attached to the spindle. The 3F3/2 antibody recognizes a phosphoepitope at the kinetochore of animal cells that is present in prophase and prometaphase [26]. Injecting the antibody into cells delays both anaphase and the loss of the phosphoepitope [27]. These correlations suggest that the 3F3/2-labeled epitope is a component of the spindle assembly checkpoint, and that its dephosphorylation occurs when kinetochores attach to the spindle and the checkpoint is turned off. In insect spermatocytes, kinetochores that are not under tension stain brightly with

3F3/2 and prevent the onset of anaphase. Applying tension to these kinetochores with a microneedle reduces 3F3/2 staining and allows cells to enter anaphase [28**].

The vertebrate homolog of the budding yeast checkpoint gene *MAD2* (mitotic-arrest deficient) codes for a protein that behaves like the 3F3/2-labeled epitope [4,29**,30**] (Table 2). *XMAD2* and *hsMAD2* (the *Xenopus* and human homologs) localize to kinetochores in tissue culture cells during prophase and prometaphase. Just like 3F3/2, the anti-*XMAD2* antibody recognizes an epitope that is present in high levels only on kinetochores that have not attached to the spindle. *XMAD2* is unlikely to be the 3F3/2-labeled epitope, as it is not phosphorylated. Like its yeast homolog, *XMAD2* is required for the spindle assembly checkpoint. When *XMAD2* is depleted from checkpoint-arrested frog egg extracts [31], a rapid exit from the checkpoint arrest ensues.

The conservation of *MAD2* suggests that the spindle assembly checkpoint is conserved from yeast to vertebrates. It also suggests that the putative vertebrate homolog of the

yeast protein Mad1 might be the 3F3/2-labeled epitope: Mad1 binds tightly to Mad2 (R-H Chen, K Hardwick, A Murray, unpublished data), so it is probably localized to the kinetochore, and conditions that activate the spindle assembly checkpoint induce its hyperphosphorylation ([32*]; Table 2).

Checkpoint kinases

Checkpoint-induced hyperphosphorylation of Mad1 depends on four proteins: Bub1, Bub3, Mps1 and Mad2 ([9**,32*]; Table 2). The *BUB* (budding uninhibited by benzimidazole) genes, like the *MAD* genes, were isolated in a screen for checkpoint-defective mutants [4,5]. Bub1 is a protein kinase that can bind to and phosphorylate Bub3 [33]. The *mps1* (monopolar spindle) mutation results in a defect in SPB duplication [34], but, unlike other mutations involved in SPB duplication [35], fails to arrest in mitosis [8*]. The arrest of these mutants, and that due to spindle depolymerization, requires a functional *MPS1* gene. Thus, *MPS1* functions at two points in the cell cycle, in G₁ phase to ensure proper SPB duplication and spindle assembly, and in mitosis to respond to spindle defects.

Table 2

Checkpoint components. (a) Budding yeast spindle assembly checkpoint components. (b) Other known checkpoint components.

Gene/protein	Function and properties
(a)	
<i>MAD1</i>	Encodes a coiled-coil protein. Biochemical function of protein unknown. Nonessential. Protein hyperphosphorylated during checkpoint activation [4,32*]. Protein binds to Mad2 ^(a) .
<i>MAD2</i>	Biochemical function of protein unknown. Nonessential. Protein binds to Mad1 ^(a) and required for Mad1 hyperphosphorylation [4,32*]. <i>Xenopus</i> and human homologs (<i>XMAD2</i> and <i>hsMAD2</i>) localize to unattached kinetochores. <i>XMAD2</i> is required for maintenance of checkpoint in frog egg extracts [29**,30**].
<i>MAD3</i>	Encodes a 60 kDa protein whose biochemical function is unknown. Nonessential. Protein has homology with amino terminus of Bub1 [4] ^(b) .
<i>BUB1</i>	Encodes a protein kinase which binds to and phosphorylates Bub3 [5,33]. Protein required for Mad1 hyperphosphorylation [32*]. Nonessential, but mutants have growth defects. Mouse homolog of Bub1 localizes to kinetochores ^(c) .
<i>BUB2</i>	Biochemical function of protein unknown [5]. Nonessential. Fission yeast homolog, <i>cdc16</i> , is required for the spindle assembly checkpoint and has essential function in cytokinesis [71].
<i>BUB3</i>	Protein binds to and is phosphorylated by the Bub1 protein kinase [5,33]. Bub3 required for Mad1 hyperphosphorylation [32*], but mutants have growth defects.
<i>MPS1</i>	Encodes a protein kinase [8*,36]. Essential for SPB duplication [34]. Required for Mad1 hyperphosphorylation. Phosphorylates Mad1 <i>in vitro</i> [9**].
<i>CDC55</i>	Encodes a B-regulatory subunit of PP2A [59]. Nonessential, but mutants have growth defects. <i>cdc55</i> mutants have increased tyrosine phosphorylation on Cdc28 ^(d) .
(b)	
p42-ERK2	A MAP kinase that is required for activation of the checkpoint in <i>Xenopus</i> egg extracts [31].
p53	Tumor suppressor protein that is required for the DNA-damage checkpoint in vertebrate cells [38]. Possible role in the spindle assembly checkpoint [37*]. Mutants may have additional checkpoint defects in centrosome duplication [39] and S-phase restraint [72].

(a)R-H Chen, K Hardwick, A Murray, unpublished data. (b)K Hardwick, A Murray, unpublished data. (c)S Taylor, F McKeon, personal communication. (d)J Minshull, A Straight, A Rudner, A Dernburg, A Murray, unpublished data; see Note added in proof; J Wang, D Burke, personal communication. ERK, extracellular signal regulated kinase; MAP, mitogen-activated protein.

Mps1 is likely to be the physiological Mad1 kinase [9**,36]. *MPS1* encodes a protein kinase that can phosphorylate a fragment of Mad1 *in vitro*. Overexpression of Mps1 causes a mitotic arrest and hyperphosphorylation of Mad1. This arrest is not due to spindle defects but reflects a constitutive activation of the checkpoint: mutations in the *MAD1-3* or *BUB1-3* genes prevent this arrest, confirming that these six checkpoint proteins act in a single pathway.

A vertebrate homolog of Bub1 can also be found at the kinetochore (S Taylor, F McKeon, personal communication), raising the possibility that Bub1, Bub3, Mad1, Mad2 and Mps1 form a multiprotein signaling complex at the kinetochore. Even if this appealing speculation is true, however, we know nothing about how the complex converts information about kinetochore-microtubule interactions into changes in protein phosphorylation.

p53 and the spindle assembly checkpoint

Mammalian cells that lack a functional p53 gene increase in ploidy when cultured in nocodazole or colcemid [37*], phenotypes identical to those of mutants in the budding yeast spindle assembly checkpoint genes. This result has been interpreted as indicating a role for p53 in this checkpoint. An alternative explanation is that wild-type and p53-deficient cells leave mitosis at similar rates, but that the wild-type cells either die or arrest in G₁ phase. Such behavior might reflect a novel checkpoint that monitors cell ploidy and prevents cells that have passed through aberrant mitosis from passing from G₁ phase into S phase, a cell cycle transition that p53 is known to regulate in response to DNA damage (reviewed in [38]). Passage through this checkpoint after an abortive mitosis would also lead to the increase in centrosome number that has been observed in p53-deficient cells [39].

Targets of the checkpoint

How does the spindle assembly checkpoint prevent anaphase? The cyclin-proteolysis machinery causes the destruction both of cyclin B [40] (and thus of the kinase activity of Cdc2/28-cyclin B complexes) and of proteins that regulate the separation of sister chromatids [41]. Two candidates for these regulatory proteins are Pds1 from budding yeast and Cut2 from fission yeast. These two proteins are degraded by the cyclin-proteolysis machinery as cells exit mitosis, and their degradation is required for sister chromatid separation [42*,43*,44**]. When *mad* mutants leave mitosis in the presence of spindle damage, B cyclins are degraded and sister chromatids separate, as would happen in a normal mitosis (J Minshull, A Straight, A Rudner, A Dernburg, A Murray, unpublished data; see Note added in proof). Thus, a likely target of the spindle assembly checkpoint is the cyclosome/APC (anaphase-promoting complex), the protein complex that ubiquitinates cyclin B, Pds1 and Cut2 (Fig. 1).

The cyclosome/APC has been purified from clam and frog eggs and is a 20S complex containing eight major subunits

([45*,46*]; J-M Peters, R King, C Höög, M Kirschner, personal communication; see Note added in proof), including homologs of the yeast proteins Cdc16, Cdc23 and Cdc27, all of which are required for the degradation of yeast B cyclins [47]. Unlike other components of the destruction machinery, the activity of the cyclosome/APC is regulated during the cell cycle and four of its components show changes in protein phosphorylation during the cell cycle.

Is there any direct evidence that the cyclosome/APC is the target of the checkpoint? Yeast extracts made from nocodazole-arrested cells (in which anaphase is prevented and the checkpoint is turned 'on') have no *in vitro* ubiquitination activity against Clb2 (the major budding yeast B-type cyclin) [48*]. In addition, *cdc16*, *cdc23*, and *cdc27* mutants arrest in mitosis, with high Cdc2/28-cyclin B activity and unseparated sister chromatids even in the absence of a functional *MAD*- and *BUB*-dependent checkpoint ([47]; A Rudner, A Murray, unpublished data).

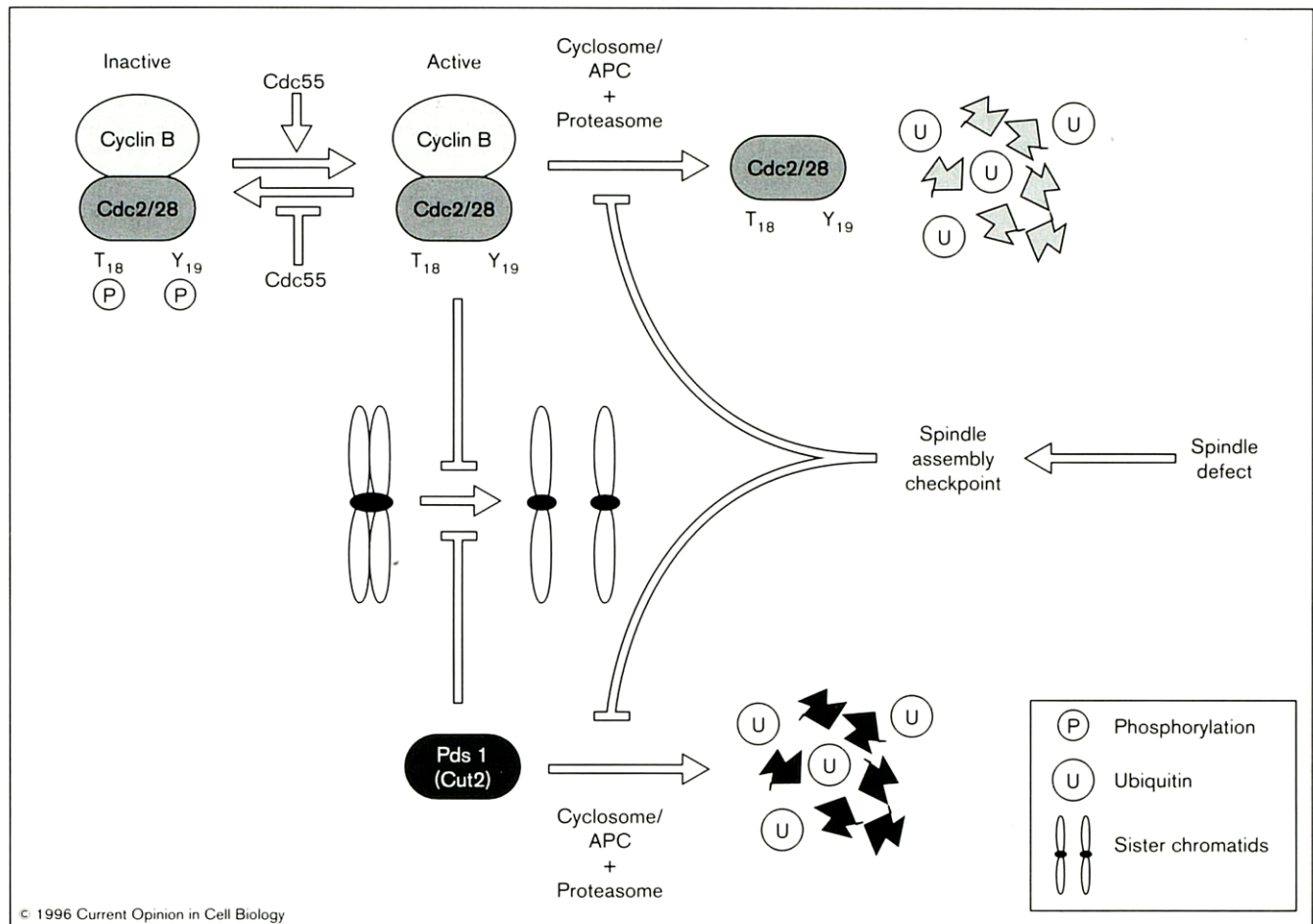
Are there other potential targets of the checkpoint? Accessibility or recognition of substrates by the ubiquitination and proteolytic machinery might be regulated. Although free cyclin B can be ubiquitinated *in vitro* [45*,46*], *Xenopus* cyclins A1, B1 and B2 require Cdc2 binding for their destruction [49]. Xe-p9 is the *Xenopus* homolog of the Cdc2-binding protein Suc1 from fission yeast [50]. Xe-p9, which binds tightly to Cdc2, is also required for the destruction of cyclin B in egg extracts [51*]. In addition, a large group of budding yeast mutants allow sister chromatid separation without cyclin B degradation [52–56], suggesting that the accessibility of different substrates to the cyclosome/APC might be differentially regulated during mitosis.

Is there regulation after cyclin ubiquitination? One report shows that the number of ubiquitin molecules on cyclin is the same in extracts in which cyclin is stable as it is in extracts in which cyclin is being rapidly degraded [57*]. Interpreting this observation is complicated by the probability that cyclin molecules that carry more than a threshold number of ubiquitins are rapidly degraded, and are thus excluded from this steady-state analysis.

Adaptation to checkpoint arrest

In many cell types, the duration of the mitotic arrest induced either by treatment with anti-microtubule drugs or by other spindle defects is not indefinite [2,58]. Cells eventually separate their sister chromatids and return to interphase despite the absence of a mitotic spindle. Continued activation of the checkpoint prevents proliferation and may be lethal. Thus, cell division in the face of the checkpoint signal produced by a persistent spindle defect (adaptation) may be beneficial because it allows a chance for survival as opposed to the certainty of death. In animals, where aneuploidy can initiate tumorigenesis [1], apoptosis may replace adaptation as the fate of cells that cannot correct their spindle defects.

Figure 1



A model for the control of the exit from mitosis in budding yeast. For a successful mitosis, the sister chromatids must separate and Cdc2/28–cyclin B must be inactivated. Sister chromatid separation is inhibited by Pds1 and the presence of active Cdc2/28–cyclin B. Both of these inhibitory influences are required to maintain sister chromatid linkage. Activation of the cyclin-proteolysis machinery (which involves ubiquitination of the target proteins by the cyclosome/APC and proteolysis of the target proteins by the proteasome) induces the ubiquitin-dependent destruction of cyclin B and Pds1, thus removing both forms of inhibition and inducing sister chromatid separation. Cdc2/28–cyclin B can also be inactivated by inhibitory phosphorylations on threonine 18 (T18) and tyrosine 19 (Y19) of Cdc2/28. (Activating phosphorylation occurs at threonine 169 of Cdc2/28 [not shown]). Cdc55, a B-type regulatory subunit of protein phosphatase 2A, normally restrains the use of this alternative pathway leading out of mitosis by ensuring that Cdc2/28–cyclin B remains active. Prolonged arrest in mitosis inhibits Cdc55 activity (not shown) and leads to adaptation from the arrest. The *MAD*- and *BUB*-dependent part (not shown) of the spindle assembly checkpoint (center right) acts to inhibit the activity of the cyclin-proteolysis machinery in cells with spindle defects. For Pds1, the name of the fission yeast counterpart is indicated in parentheses.

Adaptation could occur by inactivating the checkpoint and allowing a normal exit from mitosis. An alternative possibility is that there is a second pathway out of mitosis that is turned on during periods of prolonged arrest (Fig. 1). The recent discovery that mutations in *CDC55* are checkpoint-defective supports the latter possibility (J Minshull, A Straight, A Rudner, A Dernburg, A Murray, unpublished data; see Note added in proof; J Wang, D Burke, personal communication). Like the *mad* mutants, *cdc55* mutant cells cannot maintain Cdc2/28-associated kinase activity and sister chromatid cohesion in the presence of spindle defects. The drop in Cdc2/28-associated kinase activity in *cdc55* cells is

due to inhibitory phosphorylation of Cdc28 on the residues threonine 18 and tyrosine 19, rather than to cyclin proteolysis (see Fig. 1). *CDC55* encodes a B-type regulatory subunit of protein phosphatase 2A (PP2A) [59]. PP2A activity regulates Cdc2/28-associated kinase activity by regulating both Cdc25 and Wee1, the phosphatase and kinase responsible for removing and adding the inhibitory phosphorylations on Cdc2/Cdc28 [60].

The checkpoint defect of *cdc55* mutants is quite different from that of any of the *mad* or *bub* mutants and might reflect a role not in the initial response to spindle damage, but rather in an adaptive pathway. This theory

would propose that the absence of *CDC55* causes cells to immediately adapt to spindle damage and exit mitosis independently of proteolysis (Fig. 1).

Conclusions and future directions

Molecular details of the spindle assembly checkpoint are conserved from yeast to humans. Sensing and transducing proteins of the checkpoint reside on the kinetochores of chromosomes. Many details, though, remain to be elucidated. For example, what are the identities of the 3F3/2-labeled epitope and its kinase? Are all of the yeast checkpoint proteins conserved in larger eukaryotes and do they reside on the kinetochore? Is the cyclosome/APC the target of the checkpoint? The *cdc55* mutation serves as a starting point for the investigation of adaptation to prolonged checkpoint arrest. This novel pathway that leads out of mitosis may also allow a deeper understanding of the normal exit from mitosis.

Note added in proof

The paper referred to in the text as J Minshull, A Straight, A Rudner, A Dernburg, A Murray, unpublished data, has now been accepted for publication [73].

The paper referred to in the text as J-M Peters, R King, C Höög, M Kirschner, personal communication, has now been accepted for publication [74].

Acknowledgements

We thank W Wells, S Biggins, A Szidon, K Hardwick and M Shonn for comments on the manuscript, and C Mistrot, K Hardwick, R-H Chen, Y Wang, D Burke, S Taylor, F McKeon, J-M Peters, R King, C Höög and M Kirschner for permission to cite unpublished work. AD Rudner is supported by a Howard Hughes Medical Institute predoctoral fellowship.

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