The Saccharomyces cerevisiae Spindle Pole Body Duplication Gene MPS1 Is Part of a Mitotic Checkpoint

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Abstract. M-phase checkpoints inhibit cell division when mitotic spindle function is perturbed. Here we show that the Saccharomyces cerevisiae MPS1 gene product, an essential protein kinase required for spindle pole body (SPB) duplication (Winey et al., 1991; Lauze et al., 1995), is also required for M-phase checkpoint function. In cdc31-2 and mps2-1 mutants, conditional failure of SPB duplication results in cell cycle arrest with high p34\textsuperscript{CDC28} kinase activity that depends on the presence of the wild-type MAD1 checkpoint gene, consistent with checkpoint arrest of mitosis. In contrast, mps1 mutant cells fail to duplicate their SPBs and do not arrest division at 37°C, exhibiting a normal cycle of p34\textsuperscript{CDC28} kinase activity despite the presence of a monopolar spindle. Double mutant cdc31-2, mps1-1 cells also fail to arrest mitosis at 37°C, despite having SPB structures similar to cdc31-2 single mutants as determined by EM analysis. Arrest of mitosis upon microtubule depolymerization by nocodazole is also conditionally absent in mps1 strains. This is observed in mps1 cells synchronized in S phase with hydroxyurea before exposure to nocodazole, indicating that failure of checkpoint function in mps1 cells is independent of SPB duplication failure. In contrast, hydroxyurea arrest and a number of other cdc mutant arrest phenotypes are unaffected by mps1 alleles. We propose that the essential MPS1 protein kinase functions both in SPB duplication and in a mitotic checkpoint monitoring spindle integrity.

The essential processes of cell division are vulnerable to environmental perturbation and are prone to error to some degree. Eukaryotic cells have “checkpoint” mechanisms that can negatively regulate cell division when critical processes or structures are perturbed, allowing time for corrective mechanisms to respond to such forces of disorder (Hartwell and Weinert, 1989). Progress from S phase into mitosis, for example, is inhibited by a checkpoint mechanism when DNA is damaged or incompletely replicated in many cell types. In the budding yeast Saccharomyces cerevisiae, this response requires a number of gene products; lesions in these products eliminate cell cycle response to errors in DNA metabolism, leading to lethal division when such events occur. Some of these genes, such as RAD9, are not essential for growth in the absence of insult (Weinert and Hartwell, 1988; Weinert et al., 1994). Others, such as SAD1 and DNA polymerase ε itself, are essential for normal growth (Allen et al., 1994; Navas et al., 1995; Weinert et al., 1994). Checkpoint regulation of cell division likely works by affecting the oscillations of cyclin/cyclin-dependent kinase complex activity that are critical for cell cycle transitions, although the actual mechanisms by which they do this are still unclear (for review see Forsburg and Nurse, 1991; Luca, 1993; King et al., 1994; Nurse, 1994). Just as a cell's genetic material must be fully replicated and intact before segregation for division to be productive, so must the mitotic spindle be able to segregate duplicated chromosomes to the daughter cells accurately. Mitotic progress is sensitive to perturbations of the spindle apparatus, and it is becoming clear that mitotic checkpoint regulation plays an important role in linking mitotic progress to the structural and functional integrity of the spindle. Careful observation of mitosis in PtK~ cells and large newt pneumocytes (Reider and Alexander, 1989; Reider et al., 1994) and studies using antimicrotubule drugs (Jacobs et al., 1988; Jordan et al., 1992; Andreassen and Margolis, 1994) suggest that mitotic progress is negatively regulated when spindle structure is compromised. Micromanipulation of chromosomes and spindles has shown that mechanical tension on chromosomes may be a critical parameter monitored by mitotic checkpoints (Nicklas and Ward, 1994). In budding yeast, checkpoint regulation of mitosis in response to spindle disruption depends on the products of at least three MAD genes and three BUB genes (Hoyt et al., 1991; Li and Murray, 1991). When any one of these six gene products is disrupted, yeast cells cannot arrest...
passage though M phase upon treatment with the microtubule-depolymerizing drug nocodazole. None of the genes is essential for growth under normal conditions, suggesting that their only role in the cell is in a mitotic checkpoint ensuring that progress through M phase does not occur in the absence of a functional mitotic spindle.

Centrosome duplication is among the earliest morphological signs that eukaryotic cells have begun the process of division. In animal cells, the process is marked by G1 duplication of the centrioles (Vanderey and Borisy, 1989). Precise duplication of this microtubule-organizing center generates the two poles of the mitotic spindle, thereby setting up a bipolar spindle apparatus (Mazia, 1978, 1985). The cycle of centrosome duplication can proceed independently of cell cycle progress (Gard et al., 1990; Sluder et al., 1990; Balczon et al., 1995), and the regulatory pathways that link the centrosome duplication and the cell cycle remain unclear. A number of studies suggest that some factor critical in cell cycle regulation may reside at the centrosome or require centrosome duplication. For example, microsurgical removal of centrosomes from tissue culture cells prevents entry into mitosis (Maniotis and Schliwa, 1991). Removal of the structure, however, may not be equivalent to disrupting its function; deletion of the *Aspergillus nidulans* gene encoding the centrosome-associated protein γ-tubulin disrupts centrosome function and mitotic spindle formation, but does not lead to M-phase arrest despite the absence of a functional mitotic spindle (Oakley et al., 1990). To investigate how mitotic checkpoints monitor centrosome duplication, we have examined cell cycle phenotypes associated with *S. cerevisiae* conditional mutations that disrupt duplication of the spindle pole body (SPB),1 which is the centrosome-equivalent structure in budding yeast.

The SPB is a trilaminar disk-shaped structure embedded in the nuclear envelope, which remains intact throughout cell division (Byers, 1981a; Winey et al., 1991). Microtubules emanate from the cytoplasmic and nucleoplasmic faces of the structure, and a thickened region of nuclear envelope called the “half bridge” is often observable adjacent to the SPB proper. SPBs are duplicated in late G1, as cells proceed from START to S phase (Byers, 1981a). The conditional mutations *cdc31-2, mpsl-1*, and *mps2-1* disrupt distinct steps of SPB duplication at restrictive temperatures, leading to the formation of monopolar spindles with distinctive SPB morphologies (Byers, 1981b; Winey et al., 1991). The *cdc31-2* mutation disrupts an early step in the duplication process. The single SPB in *cdc31-2* strains is enlarged and has little or no half-bridge structure (Byers, 1981b). *CDC31* function is required before START, while both *MPSl* and *MPS2* gene functions are required at or immediately after START. The *mps1-1* lesion likely disrupts an intermediate stage of SPB duplication. In *mps1-1* strains, SPBs enlarge and develop a very large half-bridge structure but do not duplicate. The *mps2-1* mutation disrupts a late step in SPB duplication, resulting in the formation of an aberrant second SPB that is not inserted into the nuclear envelope. The *mps1-1* mutation is epistatic to *mps2-1* for SPB morphology (Winey et al., 1991). Five other distinct *mps1* alleles have subsequently been identified that share the *mps1-1* phenotype (Schutz, A., and M. Winey, personal communication); in this study we used *mps1-1* as a representative allele.

When both *cdc31-2* and *mps2-1* mutants are exposed to restrictive temperatures, they arrest division after failure of SPB duplication, resulting in cells with monopolar spindles, large buds, and G2 DNA content (Byers, 1981b; Schild et al., 1981; Winey et al., 1991). In marked contrast, strains carrying the *mps1-1* mutation fail to duplicate their SPBs at restrictive temperatures but do not arrest division. Rather, these cells proceed through monopolar mitosis and cytokinesis without pausing, and eventually go on to further DNA synthesis resulting in accumulation of cells with aberrantly high DNA content (Winey et al., 1991). Both *cdc31-2* and *mps2-1* strains maintain high viability at restrictive temperatures, while viability falls rapidly in *mps1-1* cultures at restrictive temperatures (Byers, 1981b; Schild et al., 1981; Winey et al., 1991). This phenotypic difference indicates that a monopolar spindle need not always cause mitotic arrest.

Our investigation of the *cdc31-2* and *mps2-1* mutant phenotype indicates that yeast with monopolar spindles generally arrest the cell cycle with high levels of p34*cdc28* activity, similar to the arrest phenotype observed upon treatment with nocodazole. We have found that this arrest depends upon the presence of the wild-type *MAD1* gene, indicating that a mitotic checkpoint is involved. We also found that the essential *MPSl* gene product is involved in this checkpoint. Alleles of *mpsl* interfere with the *cdc31-2* arrest phenotype without affecting the characteristic *cdc31-2* mutant SPB morphology and also make cells conditionally unable to arrest in nocodazole. This latter phenotype is independent of conditional SPB duplication failure caused by *mpsl* alleles and indicates that the essential protein kinase encoded by *MPSl* (Lauze et al., 1995) has roles in both SPB duplication and mitotic checkpoint function.

### Materials and Methods

#### Strains, Cell Culture, and Genetic Techniques

The yeast strains used in this study are listed in Table I. Yeast media, genetic techniques, and molecular techniques were as described by Ausubel et al. (1994). Yeast cells were arrested in G1 with α-factor (7–10 μM) produced by custom peptide synthesis using Fmoc chemistry on a peptide synthesizer (model 488; Applied Biosystems, Inc., Foster City, CA). Hydroxyurea and nocodazole were purchased from Sigma Chemical Co. (St. Louis, MO). Hydroxyurea was used at 0.1 M. Nocodazole was used at 15 μg/ml, a concentration reported to disrupt microtubules (Jacob et al., 1986), and added from a 1.5 mg/ml DMSO stock. The efficiency of a given arrest was monitored by determination of the budding index (proportion of budded cells in a sample of 200 cells) of briefly sonicated aliquots. G1 α-factor arrests were considered adequate when 95% of the cells were unbudded and were subsequently confirmed by flow cytometry to show that the population contained primarily cells with G1 DNA content. Early S-phase arrest was induced by releasing α-factor–arrested cultures into rich media containing 0.1 M hydroxyurea. Hydroxyurea arrests were considered adequate when >95% of the cells were budded, and 75–85% were large budded such that mother and daughter cell bodies were of equal size; arrest was later confirmed by flow cytometry to show that the population predominantly contained cells with G1/S DNA content. Cultures synchronized by treatment with α-factor or hydroxyurea were released from these blocks by rinsing with growth medium equilibrated to the appropriate temperature or drug content for the experiment. In these experiments, entry into and progression through the cell cycle were monitored.

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1. Abbreviation used in this paper: SPB, spindle pole body.
Table I. Yeast Strains*

| Name            | Genotype | Source                  |
|-----------------|----------|-------------------------|
| WX241-2         | a, mps1-1, ura3-52, leu2-3,112, his3Δ200 | This study               |
| WX237-5c        | a, ura3-52, his3Δ200, leu2-3,112, trp1Δ1 | This study               |
| WX266-2         | a/a, ura3-52/ura3-52, leu2-3,112/leu2-3,112, his3Δ200/his3Δ200, trp1Δ1/trp1Δ1 | This study               |
| WX178-3c        | a/a, mps1-2, ura3-52, leu2-3,112, trp1Δ1 | This study               |
| ELW65-9d        | a/a, cdc31-2/cdc31-2, ura3-52/ura3-52, leu2-3,112/leu2-3,112, trp1Δ1/trp1Δ1 | This study               |
| ELW78-7c        | a/a, cdc31-2/cdc31-2, mps1-1/mps1-1, ura3-52/ura3-52, leu2-3,112/leu2-3,112, trp1Δ1/trp1Δ1 | This study               |
| ELW112-3a       | a/a, cdc31-2/cdc31-2, mad1-1/mad1-1, ura3-52/ura3-52, leu2-3,112/leu2-3,112, trp1Δ1/trp1Δ1 | This study               |
| ELW92           | spontaneous diploid, WX241-2b | This study               |
| DRL139-7b       | a/a, mad1-1, ura3-52, leu2-3,112 | Li and Murray            |
| AS127-1a        | a, mps1-K412, ura3-52, leu2-3,112, his3Δ200, trp1Δ1 | Schurz                   |
| AS132-3a        | a, mps1-1237, ura3-52, leu2-3,112, his3Δ200, trp1Δ1 | Schutz                   |
| AS126-5a        | a, mps1-3796, ura3-52, leu2-3,112, his3Δ200, trp1Δ1 | Schutz                   |
| AS131-2d        | a, mps1-757, ura3-52, his3Δ200, trp1Δ1 | Schutz                   |
| ELW132-32b      | a, cdc31-2, mps1-737, ura3-52, leu2-3,112, trp1Δ1 | This study               |
| ELW134-6c       | a, cdc31-2, mps1-K412, ura3-52, leu2-3,112 | This study               |
| ELW136-2a       | a, cdc31-2, mps1-1237, ura3-52, trp1Δ1 | This study               |
| ELW138-14c      | a, cdc31-2, mps1-3796, ura3-52, trp1Δ1 | This study               |
| H9C1A5          | a, cdc9-1, his7, hom3, can1' | Hartwell                 |
| 4078-13-3       | a, cdc13-1, ura3, leu2, his7, can1' | Hartwell                 |
| H16C1A5         | a, cdc16-1, his7, ura1, can1' | Hartwell                 |
| H20C1A1         | a, cdc20-1, his7, ura1, can1' | Hartwell                 |
| H2C1AX          | a, cdc23-1, adel1, his7, can1' | Hartwell                 |
| WX258-1b        | a, cdc7-1, mps1-1, his7, can1' | This study               |
| WX259-1c        | a, cdc13-1, mps1-1, can1, ura-3, his7, can1' | This study               |
| WX265-1b        | a, cdc16-1, mps1-1, ura3-52 | This study               |
| WX261-1a        | a, cdc20, mps1-1, ura-, his- | This study               |
| WX262-1b        | a, cdc23, mps1-1, ura-, ade-, his- | This study               |

*Where precise identity of markers are unknown, auxotrophies are indicated.

by budding index (relative percentages of different budding morphologies) and flow cytometry.

**Analysis of p34cdc28 Activity**

H1 was prepared from calf thymus by extracting blended tissue with 0.74 N HCl and flow cytometry.

**Preparation of whole cell lysates and H1 kinase activity assays were performed essentially as described by Langan et al. (1989) with some modifications.** Cells washed with cold 70% acetone, resolubilized in H2O and buffered to pH 7-7.5 by addition of 1 M Tris base, pH 9.0, to a final concentration of ~85 mM Tris. 700 g of thymus tissue yielded ~0.8 g protein. Final stock protein concentration was adjusted to 10 mg/ml with 85 mM Tris, pH 7.5. PAGE analysis of this protein preparation showed that it is primarily histone H1.

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**Results**

*cdc31-2 and mps2-1 Strains Arrest Mitotic Progress with High p34cdc28 H1 Kinase Activity**

Nocodazole arrest, generally considered a block to mitotic

Yeast cells were fixed for determination of budding morphology by addition of formaldehyde to 3.7%. Immediately before scoring, samples were sonicated briefly. In scoring budding morphology, cells without obvious buds were considered unbudded, cells with buds less than approximately one-third the volume of the mother cell were considered small budded, and cells with buds of greater size were considered large budded. Cells that had multiple buds or other unusual morphologies were scored as aberrant. Yeast cells were prepared for flow cytometry by the method of Hutter and Eipel (1979) using the DNA stain propidium iodide (Sigma Chemical Co.). Stained cells were analyzed on a FACScan® flow cytometer using the CELLFIT and LYSYS software packages (Becton Dickinson Immunocytometric Systems, San Jose, CA) to obtain and analyze data. Yeast cells were prepared for EM by procedures described by Byers and Goetsch (1975), and serial 70-80-nm thin sections were viewed on an electron microscope (JEOL USA, Peabody, MA).
progression, occurs with sustained elevation of mitotic p34\(^{CDC28}\) H1 kinase activity (Langan et al., 1989; Hadwiger et al., 1989). To determine the status of p34\(^{CDC28}\) activation at the cdc31-2 arrest, we made crude extracts of cdc31-2 (ELW65-9d) cultures arrested in G1 by addition of mating pheromone, in M by addition of nocodazole, or at the cdc31-2 arrest by incubation at 37°C for 4 h, and assayed the H1 kinase activity in these extracts. Extracts of restrictive temperature-arrested cdc31-2 cells had H1 kinase activity comparable to that observed in extracts of nocodazole-arrested cells, and significantly higher than observed in α-factor–arrested cells (Fig. 1, left). Most of the H1 kinase activity present in extracts of nocodazole and 37°C-arrested cdc31-2 cells could be depleted with p13\(^{Suc1}\) sepharose, a reagent that specifically precipitates p34\(^{CDC28}\) kinase complex (Hadwiger et al., 1989). As in crude extracts, material precipitated from extracts of nocodazole and 37°C-arrested cdc31-2 cells could be depleted with p13\(^{Suc1}\) Sepharose. This experiment shows that progress through mitosis is blocked at the cdc31-2 arrest, with elevated p34\(^{CDC28}\) kinase activity. To determine if other parts of the cell cycle are affected in cdc31-2 strains, we compared synchronous cdc31-2 cultures with similarly treated wild-type cells. After synchronizing wild-type (WX266-2b) and cdc31-2 (ELW65-9d) strains in early S phase with hydroxyurea (see Materials and Methods), we released the cultures into drug-free medium at 37°C, sampling at regular intervals to measure H1 kinase activity, percentage of large-budded cells, and DNA content. Because budding yeast cells synchronized in early S phase have duplicated their SPBs (Byers and Goetsch, 1975), the cdc31-2 cells in this experiment should divide normally once and fail to duplicate their SPBs in G1 of the subsequent cell cycle. After release at 37°C, both cdc31-2 and wild-type cells went through one division. After this first cycle, cdc31-2 cells arrested with large buds while wild-type cells completed a second division (Fig. 2 C). H1 kinase activity rose and fell during the first division in both cultures, as expected during normal mitosis. In the second cycle, this activity rose at about the same time in the wild-type and cdc31-2 cultures. After this, H1 kinase activity dropped in wild-type cells but remained high in cdc31-2 cells, coincident with large-budded arrest.

**Figure 1.** H1 kinase activity in extracts of variously treated cdc31-2 cultures. The left panel shows H1 kinase activity from whole cell lysates of cdc31-2 (ELW65-9d) cells. The major phosphorylated band is histone H1. In the left panel, extracts were treated with sepharose or p13\(^{Suc1}\) sepharose. Lanes α, kinase activity in extracts of α-factor–arrested cdc31-2 (ELW65-9d) cells; lanes NZL, kinase activity in extracts of such cells arrested in 15 μg/ml nocodazole; and lanes 4 h 37°C, kinase activity in extracts of cells incubated at 37°C for 4 h. The right panel shows H1 kinase activity associated with p13\(^{Suc1}\) sepharose precipitates from extracts of α-factor–arrested (α), nocodazole-treated (NZL), or 37°C-incubated (4 h 37°C) cdc31-2 (ELW65-9d) cells.

**Figure 2.** Cell cycle events in synchronized cdc31-2 and wild-type cultures at 37°C. (A) H1 kinase activity in whole cell extracts of cdc31-2 (ELW65-9d) and wild-type (WX266-2b) cultures synchronized in early S phase and then released into 37°C medium. (B) Raw data for A. (C) The percentages of large budded cells in these cultures at successive times.
(Fig. 2, A and B). Flow-cytometric analysis showed that cells with G2 DNA content appeared in both wild-type and cdc31-2 cultures at similar times, indicating that DNA synthesis was not slowed in cdc31-2 cells as they came to arrest (not shown). Therefore, progress through S phase into mitosis, with coincident activation of p34\(^{CDC28}\), is apparently not affected by failure of SPB duplication due to the cdc31-2 allele.

To determine if the features of cdc31-2 monopolar arrest are restricted to the cdc31-2 lesion, we performed a similar set of experiments on an mps2-1 mutant strain. The mps2-1 mutation disrupts insertion of the nascent SPB into the nuclear envelope, a late step in SPB duplication. As with cdc31-2, the mps2-1 lesion leads to accumulation of cells with large buds and G2 DNA content at restrictive temperatures (Winey et al., 1991). Synchronized mps2-1 (WX178-3c) cells at restrictive temperatures behaved as cdc31-2 cells did, arresting with large buds and elevated H1 kinase activity (not shown).

cdc31-2, mad1-1 Cells Fail to Arrest at 37°C

Failure of SPB duplication gives rise to an aberrant monopolar spindle. In this case, mitotic arrest may depend on the function of a mitotic checkpoint that monitors spindle structure. To test this idea, we examined the cell cycle phenotype of a cdc31-2, mad1-1 double mutant. The mad1-1 mutation renders cells unable to arrest mitosis upon nocodazole treatment, and is thought to disrupt the checkpoint monitoring mitotic spindle function. (Li and Murray, 1991). Asynchronous cdc31-2 (ELW65-9d) and double mutant cdc31-2, mad1-1 (ELW112-3a) cells were shifted to 37°C for 4 h. Double mutant cdc31-2, mad1-1 cells exhibited no evidence of cell cycle arrest. After this shift, budding morphology was as follows: in the cdc31-2 culture, 94% of the cells were large budded, and 6% were un budded; in the cdc31-2, mad1-1 culture, 47% were un budded, 29% were large budded, 5% were small budded, and 19% were multiply budded. In contrast to the flow-cytometric profile of cdc31-2 cells exposed to 37°C for 4 h, flow cytometry of the 37°C-treated cdc31-2, mad1-1 culture revealed that this culture contained cells with higher than normal DNA content as well as cells with apparently lower than normal DNA content (Fig 3). The latter cells were most likely aploid or hypoploid daughter cells resulting from monopolar mitosis followed by cytokinesis; Winey et al. (1991) and Baum et al. (1988) showed that such cells are produced when cytokinesis occurs in cells with malformed spindles. Taken together with the lack of morphologically defined arrest, these data suggest that cytokinesis occurred in many of the cdc31-2, mad1-1 cells without proper chromosome segregation and that such divisions were followed by subsequent DNA replication in the cell bodies that received chromosomal DNA. The presence of multiply budded cells suggests that cytokinesis was not completely efficient, however. The rise and fall of H1 kinase activity in synchronous cdc31-2, mad1-1 (ELW112-3a) cells at 37°C resembled that of wild-type cells (not shown), in contrast to the sustained elevated activity seen in cdc31-2 single mutant cells. Therefore, the MAD1 checkpoint function is required for cdc31-2 arrest as it is for nocodazole arrest, although mad1-1 strains do not undergo cytokinesis efficiently in nocodazole (see Fig. 8).

mps1-1 Cells Fail to Duplicate Their SPBs and Do Not Arrest the H1 Kinase Activity Cycle

The cell cycle phenotype of mps1-1 cells is strikingly different from the cdc31-2 and mps2-1 phenotypes. Winey et al. (1991) showed that mps1-1 cells conditionally failed in SPB duplication without apparent cell cycle arrest. If this phenotype reflects a failure of checkpoint control, mps1-1 cells should go through S phase, M phase, and cytokinesis with wild-type timing, and p34\(^{CDC28}\) activity should rise and fall as in wild-type cells. Wild-type (WX257-5c) and mps1-1 (WX241-2b) cultures synchronized in G1 with a-factor were released into 30°C medium (restrictive for mps1-1) and sampled at intervals for measurement of bulk H1 kinase activity, flow-cytometric measurement of DNA content, and scoring of budding morphology. The rise and fall of H1 kinase activity in a synchronized mps1-1 culture was similar to wild-type in both amplitude and timing (Fig. 4, A and B). The percentages of large-budded cells present in the wild-type and mps1-1 cultures rose until ~115 min after release from pheromone arrest. After this, the percentage of large-budded cells fell in both cultures (Fig. 4 C), as percentage of un budded cells rose (Fig. 4, legend), suggesting that cytokinesis occurred with similar timing in mps1-1 and wild-type strains. Flow cytometry showed that aploid/hypoploid cell bodies appeared in the mps1-1 culture after 115 min and that cells with greater than normal ploidy subsequently emerged (not shown); this is consistent with previously reported analysis of the mps1-1 phenotype (Winey et al., 1991). These results demonstrate that mps1-1 cells do not inhibit mitotic progress or the cycle of p34\(^{CDC28}\) activity when SPB duplication fails, as cdc31-2 or mps2-1 cells do.
mps1-1, cdc31-2 Cells Have the cdc31-2 SPB Phenotype but Do Not Arrest Mitosis

The mps1 phenotype shows that failure of SPB duplication does not always lead to cell cycle arrest. However, the mps1 cell cycle phenotype could be due to structural features of SPBs in mps1 strains at restrictive temperatures. The aberrant unduplicated SPB formed in mps1 cells at restrictive temperatures has a distinctive, enlarged half-bridge structure relative to SPBs found in wild-type or cdc31-2 cells when viewed in the electron microscope (Winey et al., 1991). Alternatively, the MPS1 gene product may itself play an important role in signaling mitotic

arrest after SPB duplication failure. To distinguish these possibilities, we examined SPB morphology and cell cycle phenotypes of cdc31-2, mps1-1 double mutants. To ensure that phenotypes observed are not specific to the mps1-1 allele, we examined the cell cycle phenotypes of double mutants between cdc31-2 and four other distinct mps1 alleles.

In these experiments, the synchronization protocol is important. The cdc31-2 execution point precedes that of mps1-1, and both execution points precede $S$ phase (Winey et al., 1991). Upon release into 37°C medium, an mps1-1, cdc31-2 culture synchronized in $S$ should be affected first by the cdc31-2 mutation. If cdc31-2 is epistatic to mps1-1 with respect to SPB phenotype, all cells in this culture should have an unduplicated SPB characteristic of cdc31-2 single mutants. In contrast, an asynchronous double mutant culture should contain some cells that have passed the cdc31-2 execution point but not the mps1-1 execution point. Asynchronous mps1-1, cdc31-2 cells shifted to restrictive temperatures should exhibit a mixture of cdc31-2

Figure 4. Cell cycle events in synchronized mps1-1 and wild-type cultures at 30°C. (A) H1 kinase activity in whole cell extracts of mps1-1 (WX241-2b) and wild-type (WX257-5c) cultures synchronized at START. (B) Raw data for A. (C) The percentage of cells in these cultures that had large buds at successive times. The percentage of cells in the mps1-1 culture that were unbudded following release at 30°C rose from 11.5% at 75 min to 71% at 105 min; the percentage of cells in the wild-type culture that were unbudded rose from 18% at 75 min to 72.5% at 105 min.

Figure 5. EM of SPB structure in a cdc31-2, mps1-1 double mutant strain (ELW78-7c) at 37°C. (A) Electron micrographs of SPBs from an asynchronous culture shifted to 37°C. Most SPB morphologies are characteristic of cdc31-2 single mutants, lacking pronounced half-bridge structures. More rarely, SPBs exhibit pronounced half bridges (arrowhead), as in mps1-1 single mutants. (B) Electron micrographs of SPBs from cells synchronized by hydroxyurea treatment before transfer to 37°C. Such cells uniformly exhibit SPB structure characteristic of cdc31-2 single mutants. In both cultures, pole morphology characteristic of cdc31-2 single mutants predominates.
Figure 6. Flow-cytometric analysis of DNA content in double mutant *cdc31-2, mps1-1* and single mutant *cdc31-2* and *mps1-1* cells at restrictive temperature. Unlike *cdc31-2* (ELW65-9a) cells, neither *cdc31-2, mps1-1* (ELW78-7c) nor *mps1-1* (ELW92) cells exhibit cell cycle arrest. Note presence of cells with higher and lower than normal DNA content. The x-axis is relative DNA content, and the y-axis indicates cell number; each histogram represents 10,000 cells. The approximate positions of the centers of G1 and G2 DNA content peaks in the cultures before shift to 37°C (arrows) are labeled G1 and G2.

Figure 7. Cell cycle events in synchronized *cdc31-2, mps1-1* and *mps1-1* cultures at 37°C. (A) H1 kinase activity in whole cell extracts of *cdc31-2, mps1-1* (ELW78-7c) cells and *mps1-1* (ELW92) cultures synchronized in early S phase and released into 37°C medium, and sampled at intervals after release. Flow-cytometric analysis showed that both cultures failed to arrest with G2 DNA content (Fig. 6). After 4 h at 37°C, both cultures contained aaploid or hypoploid bodies and cells with higher than normal ploidy, similar to *mps1-1* single mutant strains (Winey et al., 1991) and *cdc31-2, mad1-1* cells at 37°C (see Fig. 3). H1 kinase activity in the synchronized *cdc31-2, mps1-1*
double mutant culture rose and fell in concert with budding and cytokinesis (Fig. 7), much as in mps1-1 or wild-type strains (see Figs. 2 and 4). Hence, mps1-1 is epistatic to cdc31-2 with respect to cell cycle phenotype. Because the SPBs in synchronized cdc31-2, mps1-1 cells after failure of SPB duplication are characteristic of a cdc31-2 single mutant, the mps1 cell cycle phenotype cannot be attributed to abnormal SPB morphology. The cell cycle phenotypes of double mutants carrying cdc31-2 and one of four distinct mps1 alleles (ELW132-32b, ELW134-6c, ELW136-2a, ELW138-14c) were also examined. They behaved similarly to cdc31-2, mps1-1 cells, failing to arrest mitosis (not shown).

**mps1 Cells Are Conditionally Unable to Arrest in Nocodazole**

Given our observation that mps1 cells do not arrest division when the mitotic spindle is malformed due to SPB duplication failure, we asked if mps1 strains fail to arrest when the spindle is destroyed by the microtubule-depolymerizing drug nocodazole. While mps1-1 cells arrested upon treatment with nocodazole at 25°C (not shown), they did not arrest in nocodazole containing medium at 37°C. Wild-type (WX257-5c), mps1-1 (WX241-2b), and mad1-1 (DRL139-7b) cultures synchronized at 25°C in G1 with α-factor were split four ways and released into four different media conditions: nocodazole-containing medium at 25°C and 37°C, and drug-free medium at 25°C or 37°C. The distributions of budding morphologies present after 4 h in 25°C nocodazole-containing medium are shown in the left side of Fig. 8. Wild-type and mps1-1 cells arrested with large buds, while mad1-1 cells became multiply budded. Flow cytometry indicated that wild-type and mps1-1 cultures arrested with G2 DNA content, while mad1-1 cells went on to higher ploidy, indicating that S phase had been reinitiated in the absence of chromosome segregation (not shown). In contrast, after 4 h in 37°C medium containing nocodazole, mps1-1 strains behaved as mad1-1 cells did, becoming mostly multiply budded (Fig. 8, right). Flow-cytometric analysis showed that while wild-type cells arrested with G2 DNA content at 37°C (Fig. 8 A), mps1-1 and mad1-1 cells did not (Fig. 8 B and C). Instead, mps1-1 and mad1-1 cells went on to reduplicate their DNA, evidenced by the appearance of cells with higher ploidy in later time points. This experiment was repeated with strains carrying four other distinct mps1 alleles (AS127-1a, AS132-3a, AS126-5a, AS131-2d). None of these mps1 mutant strains exhibited cell cycle arrest in the presence of nocodazole at 37°C that could be detected by flow cytometry or examination of budding morphology (not shown).

Winey et al. (1991) and Baum et al. (1988) demonstrated that aploid and hypoploid cells are generated when cytokinesis occurs in cells with malformed mitotic spindles. It appears that cytokinesis, as evidenced by the appearance of unbudded aploid and hypoploid cell bodies, does not occur efficiently in nocodazole-treated mad1-1 and mps1 strains in this experiment. Although the mps1 cells at restrictive temperature and mad1-1 cells clearly re-budded and went on to subsequent rounds of DNA synthesis in the presence of nocodazole, neither strain produced a large number of aploid or hypoploid cell bodies. Instead, both mad1-1 and mps1-1 strains mostly formed multiply budded polyploid cells. This phenotype is com-
Figure 9. Failure of mps1-1 cells to arrest in nocodazole at 37°C. Flow-cytometric profiles of (A) wild-type (WX257-5c) cells, (B) mps1-1 (WX241-2b), and (C) mad1-1 (DRL139-7b) cells sampled at intervals after release from α-factor arrest into 37°C medium containing nocodazole. Note the appearance of polyploid cells at later times (B and C). Sampling times after release from α-factor arrest are noted on the left side of C. The x-axis is relative DNA content, and the y-axis indicates cell number; each histogram represents 10,000 cells. The approximate positions of centers of G1 and G2 DNA content peaks from asynchronous cultures of these strains (arrows) are labeled G1 and G2.

Figure 10. Failure of hydroxyurea-synchronized mps1-1 cells to arrest in nocodazole at 37°C. Flow-cytometric profiles of (A) wild-type (WX257-5c), (B) mps1-1 (WX241-2b), and (C) mad1-1 (DRL139-7b) cells sampled at intervals after release from hydroxyurea arrest into 37°C medium containing nocodazole. As in Fig. 9, B and C, note the appearance of polyploid cells at later times (B and C). Sampling times after release from α-factor arrest are noted on the left side of C. Same strains released from hydroxyurea arrest into 37°C medium containing nocodazole. Notation and cell number are as in Fig. 9.
pleted SPB duplication and formed short bipolar mitotic spindles (Byers and Goetsch, 1974). Upon release from hydroxyurea arrest into nocodazole containing medium at 37°C, wild-type strains arrested with large buds and G2 DNA content (Fig. 10 A). In contrast, neither mpsl nor mad1-1 strains arrested in the presence of nocodazole, instead rebudding and going on to subsequent DNA synthesis (Fig. 10, B and C). As above, the appearance of cells with high ploidy is evidence of this failure to arrest mitosis in the absence of a functional mitotic spindle. Four other mpsl alleles (AS127-1a, AS132-3a, AS126-5a, AS131-2d) shared this phenotype upon release from hydroxyurea arrest into 37°C medium containing nocodazole (not shown). Hence, conditional failure of mitotic arrest in nocodazole-treated mpsl cells is apparently not caused by failure of SPB duplication.

**Wild-type MPS1 Is Not Required for Hydroxyurea Arrest or Various cdc Arrests**

To determine if mpsl alleles disrupt cells’ ability to arrest division in response to inhibition of DNA synthesis, we examined how mpsl cells at restrictive temperatures responded to hydroxyurea. Wild-type (WX257-5c) and mpsl-1 (WX241-2b) cells were synchronized in G1 with α-factor at 25°C and then released from this arrest into 25°C and 37°C medium containing or lacking hydroxyurea. Wild-type and mpsl cultures released in the presence of hydroxyurea arrested with large buds (Fig. 11) and G1/S phase DNA content (not shown). H1 kinase activity in hydroxyurea-treated wild-type and mpsl-1 cultures rose relatively slowly, reaching a peak ~3.5 h after release from α-factor arrest into hydroxyurea-containing medium (not shown). Therefore, the wild-type MPS1 gene product is not required for hydroxyurea arrest.

We examined the interaction of mpsl-1 with cdc9, cdc13, cdc16, cdc20, and cdc23 mutations and found no evidence that mpsl-1 affects the cell cycle arrest phenotypes associated with these mutations. The behavior of cdc16, mpsl-1 double mutant cells is representative of the phenotypes observed in these double mutant strains. Asynchronous cdc16 (H16ClA5) and cdc16, mpsl-1 cells (WX265-1b) were shifted from 25°C to 37°C, and the culture was

![Figure 11. Response of wild-type and mpsl-1 cells to hydroxyurea at 37°C. Wild-type and mpsl-1 strains (WX257-5c, WX241-2b) were released from α-factor arrest into 37°C medium either containing 0.1 M hydroxyurea (HU) or lacking drug. Accumulation of large budded cells over time is shown.

![Figure 12. Cell cycle phenotypes of various cdc mutants in combination with mpsl-1. (A) Flow-cytometric profiles of cdc16 (H16ClA5) and cdc16, mpsl-1 (WX265-1b) strains shifted to 37°C for 4 h. (B) Percentages (rounded to the nearest integer) of cells with un budded and large-budded morphology after a 4-h incubation at 37°C in various mutant strains. Percentages of cells with small budded or aberrant morphology are not shown.]
sampled hourly for 6 h. Cells with G2 DNA content (Fig. 12 A) and large buds (Fig. 12 B) accumulated, indicating that the cdc16 arrest phenotype is epistatic to the mps1-1 cell cycle phenotype. Double mutant budding phenotypes are summarized in Fig. 12 B. It is worth noting that cdc9 and cdc13 arrests are dependent on the RAD9 checkpoint (Weinert and Hartwell, 1993), indicating that the mps1-1 lesion does not interfere with that checkpoint.

Discussion

The experiments reported here demonstrate that the wild-type MPS1 gene product is required for an M-phase checkpoint that allows yeast cells to arrest division when the mitotic spindle is disrupted or malformed. This defines a novel role for the MPS1 gene product, an essential protein kinase also required for SPB duplication in G1 (Lauze et al., 1995; Poch et al., 1994; Winey et al., 1991). We have shown that failure of SPB duplication normally results in arrest of mitosis with high p34cdc28 activity. In mps2-1 and cdc31-2 strains, cell cycle arrest occurs after DNA replication is complete and p34cdc28 kinase activity rises, suggesting that events leading to the fall of p34cdc28 kinase activity are inhibited when SPB duplication fails. In contrast, cdc31-2, mad1-1 cells fail to arrest mitosis, indicating that the MAD1-dependent mitotic checkpoint (Li and Murray, 1991) is required for mitotic arrest after failure of SPB duplication. A priori, it seems reasonable that some of the same cell cycle regulators are involved in both nocodazole arrest and mitotic arrest in the presence of a monopolar spindle, because both conditions are fundamentally defects in spindle integrity. These findings suggest that the MPS1 gene product acts in the MAD1-dependent mitotic checkpoint as well as in SPB duplication, the earliest structural step in bipolar spindle formation.

In mps1 mutants, both conditional SPB duplication failure and checkpoint defects are evident. Cultures of mps1-1 cells synchronized in G1 and released at restrictive temperatures go through budding, DNA replication, rise and fall of H1 kinase activity, and cytokinesis with essentially normal timing, ultimately committing aberrant monopolar cell division. A number of experiments performed here attempt to separate these phenotypes. Analysis of the cdc31-2, mps1-1 double mutant phenotype is particularly informative, showing that lack of mitotic arrest in cells carrying the mps1-1 lesion cannot be attributed to structural defects of the SPB visible in the electron microscope. Furthermore, we have found that mps1 mutant cells are conditionally unable to arrest mitosis in the presence of nocodazole. This phenotype is shared by mad1-1 cells, although mad1-1 is not a conditional mutation. It is perhaps most telling that mps1-1 cells conditionally fail to arrest in nocodazole after synchronization in S phase with hydroxyurea. Because SPB duplication and short spindle formation are complete in hydroxyurea-arrested cells, this treatment separates the mps1-1 SPB duplication and mitotic checkpoint phenotypes. When mps1-1 cells were released from hydroxyurea arrest into restrictive temperature medium, they appeared to undergo one normal division, suggesting that the mps1-1 mutation does not adversely affect spindle function after SPB duplication is complete. We propose that after SPB duplication is complete, Mps1p activity is also required for checkpoint-mediated restraint of M-phase progress upon disruption of the mitotic spindle. Because both MAD1 and MPS1 gene products are required for mitotic arrest in the presence of a malformed or disrupted mitotic spindle, it is possible that these two proteins are involved in the same pathway linking cell cycle progress to the status of the mitotic apparatus.

MPS1's cell cycle regulatory role appears to be specifically within the mitotic checkpoint monitoring spindle integrity. Hydroxyurea arrest and cdc mutant arrests that depend on RAD9 and other S-phase checkpoint activities are unaffected by the mps1-1 mutation. It is also interesting that the cdc16 and cdc23 mutations are epistatic to mps1-1 with respect to cell cycle phenotype, considering that the CDC16 and CDC23 gene products are required for ubiquitin-mediated proteolysis that accompanies M-phase exit (Irniger et al., 1995). This suggests that the effects of mps1-1 on checkpoint regulation are upstream of cyclin degradation. Although it functions in a different checkpoint, MPS1 is comparable to the SAD1/MEC3 gene, which is essential for viability and required for arrest of cell division specifically when DNA is damaged or unreplicated (Allen et al., 1994; Weinert et al., 1994).

MPS1 is apparently among a class of checkpoint components that serve dual roles: one in an essential process and another in regulation of the cell cycle when that process is perturbed. Li and Deshaies (1993) propose three classes of checkpoint regulators. One class of gene products might originate a signal to arrest when processes are disturbed. These proteins might also participate in critical processes or be components of structures important for cell division. Such gene products would likely be essential for normal growth and interact with a second class of “transducer” proteins that relay and amplify a signal to arrest the cell cycle. Ultimately, a signal would be relayed to a third class of effector proteins that can directly inhibit cell cycle progression. DNA polymerase ε itself is an example of the first class of checkpoint regulators: mutations in the COOH-terminal region of S. cerevisiae POL2 disrupt S-phase checkpoint activity (Navas et al., 1995). The Schizosaccharomyces pombe cut5 and cdc18 gene products, which are critical for S-phase progression and required for arrest of the cell cycle when DNA metabolism has gone awry, also define this first class of checkpoint elements (Saka and Yanagida, 1993; Kelly et al., 1993; Saka et al., 1994).

In contrast, checkpoint components that transduce information need not be essential for growth under ideal conditions because the signals they pass might never be generated in the absence of perturbation. The RAD9 and MAD1 gene products, for example, are both dispensable unless specific problems arise and are thought to fall into this transducer class (Li and Deshaies, 1993). The MPS1 gene product is essential for viability, involved in SPB duplication, and required for inhibition of mitotic progress when spindle structure is disrupted. Therefore, the MPS1 protein likely stands among the class of checkpoint components that both participate in an essential process and originate a signal to arrest division when the process fails. In this case, we propose that the MPS1 gene product acts in both the G1 process of SPB duplication and the mitotic checkpoint monitoring spindle integrity.
The MPS1 gene product is a protein kinase that phosphorylates itself on serine, threonine, and tyrosine and exogenous substrates on serine and threonine in vitro (Lauze et al., 1995). The *mps1* mutant lesion falls within the kinase domain, as do four other known alleles that exhibit the same SPB duplication and cell cycle phenotypes as *mps1*-1 (Schutz, A., and M. Winiey, personal communication). We predict that Mps1p's enzymatic activity is of key importance to both the protein's SPB duplication and mitotic checkpoint functions. For example, if Mps1p's kinase activity normally rises in G1 to drive SPB duplication and is inhibited once a bipolar spindle is assembled, failure or delay of SPB duplication would result in prolonged activation of the enzyme and cell cycle arrest. Alternatively, there may be a burst of Mps1p kinase activity at the time of SPB duplication, with the enzyme activated to inhibit mitosis if the process fails or if the spindle is destroyed by other insult. In either case, MPS1 kinase activity might work in G2/M to inhibit mitotic progress in a MAd1-dependent manner, while continuing to drive processes that promote SPB duplication. Phosphorylation of MAd1 correlates with mitotic arrests requiring that protein (Hardwick and Murray, 1995). It will be interesting to see if Mps1p phosphorylates Mad1p or other proteins believed to transduce cell cycle arresting signals when mitotic spindle integrity is compromised.

E. Weiss thanks T. Giddings for thin sectioning and assistance with EM operation, A. Jackson for assistance with H1 kinase assays, J. Muller for p13**(K)** beads, and S. Dutcher and C. Nislow for critical input on this manuscript. R. Nicklas and K. Hardwick provided MAd1 strains and helpful data before publication, and A. Schutz provided outcrossed mps1 alleles, initially isolated and kindly provided by J. Kilmartin, T. Haffaker, and E. Siewert. Grateful acknowledgment is due to L. Backhus, J. Baschent, S. Biggs, H. Dlott, K. Hardwick, F. Luca, L. Pilus, B. T. Roberts, and B. Wells for illuminating discussions.

The investigators involved in this work have been supported by a National Institutes of Health (NIH) training grant (GM07135, E. Weiss), and an American Cancer Society Junior Faculty Research award (A70760, M. Winiey). This work was initiated with support from an American Cancer Society Research grant (MV63940) and was completed with support from the NIH (GM51312). Additional support was from the Pew Scholars Program in the biomedical sciences (PO205SC).

Received for publication 1 September 1995 and in revised form 1 October 1995.

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