Abstract. Yeast calmodulin (CaM) is required for the progression of nuclear division (Ohya, Y. and Y. Anraku. 1989. Curr. Genet. 15:113–120), although the precise mechanism and physiological role of CaM in this process are unclear. In this paper we have characterized the phenotype caused by a temperature-sensitive lethal mutation (cmdl-101) in the yeast CaM. The cmdl-101 mutation expresses a carboxyl-terminal half of the yeast CaM (Met72-Cys147) under the control of an inducible GALI promoter. Incubation of the cmdl-101 cells at a nonpermissive temperature causes a severe defect in chromosome segregation. The rate of chromosome loss in the cmdl-101 mutant is higher than wild-type cell even at permissive temperature. The primary visible defect observed by immunofluorescence and electron microscopic analyses is that the organization of spindle microtubules is abnormal in the cmdl-101 cells grown at nonpermissive temperature.

Majority of budded cells arrested at the high temperature contain only one spindle pole body (SPB), which forms monopolar spindle, whereas the budded cells of the same strain incubated at permissive temperature all contain two SPBs. Using the freeze-substituted fixation method, we found that the integrity of the nuclear morphology of the cmdl-101 mutant cell is significantly disturbed. The nucleus in wild-type cells is round with smooth contours of nuclear envelope. However, the nuclear envelope in the mutant cells appears to be very flexible and forms irregular projections and invaginations that are never seen in wild-type cells. The deformation of the nuclear becomes much more severe as the incubation at nonpermissive temperature continues. The single SPB frequently localizes on the projections or the invaginations of the nuclear envelope. These observations suggest that CaM is required for the functions of SPB and spindle, and the integrity of nucleus.
eukaryotic microorganism is well suited for this endeavor, first because it possesses CaM with properties physiologically similar to those of higher organisms (Ohya and Anraku, 1989b, Davis and Thorner, 1989). Second, the yeast mitotic apparatus has been studied intensively by both cytological analysis and genetic dissection (Byers, 1981a, Winne and Byers, 1992).

Recently we have reported that the essential function of the yeast CaM in cell proliferation can be carried out by its derivatives, the half CaMs. Either the amino-terminal or carboxyl-terminal half of CaM complements the cmdl null mutation when they are expressed under a strong promoter, but not the authentic CMD1 promoter (Sun et al., 1991). Cells depending solely on these half CaMs all show a temperature-sensitive phenotype for growth. This temperature-sensitive growth is rescued specifically by addition of 50 mM CaCl$_2$ to the medium (Sun et al., 1991).

In this paper, we describe the characterization of a temperature sensitive cmdl-101 mutant expressing the carboxyl-terminal half CaM (Met$^{72}$-Cys$^{147}$). The cmdl-101 mutant showed a severe defect in chromosome segregation. Immunofluorescence and electron microscopic analyses have revealed that the half CaM mutation affected the spindle organization, SPB functions and nuclear morphology.

**Materials and Methods**

**Stains and Microbial Techniques**

Yeast strains used in this work are listed in Table I. Yeast media and general genetic manipulations were carried out essentially as described in Rose et al. (1990). Yeast cultures were grown in YP (1% yeast extract [Difco Laboratories Inc., Detroit, MI], 2% polypeptone [Nihon Seiyaku, Tokyo, Japan]) supplemented with 5% glucose (YPD) or with 5% galactose and 0.2% sucrose (YPGS).YPD and YPGS supplemented with 100 mM SGS) supplemented with appropriate nutrients were used to select for plasmids. Plasmid integrations at the chromosomal locus, the plasmid pGCAMTC1 for integration was constructed as follows. The 0.8-kb HindIII-StuI fragment of TRP1 gene from TRP/SK + (Sun et al., 1991) was inserted into the Sinai gap on pRSCAMCTI, creating plasmid pRSCAMCT1. A BamHI linker (pCGGATCCG) was inserted into the Sinai gap on pRSCAMCTI, creating plasmid pCAM106 (Sun et al., 1991) was replaced by the 2.4-kb BamHI fragment carrying the carboxyl-terminal half of CaM complements the cmdl/null mutant expressing the carboxyl-terminal half CaM (Met$^{72}$-Cys$^{147}$). The cmdl-101 mutant showed a severe defect in chromosome segregation. Immunofluorescence and electron microscopic analyses have revealed that the half CaM mutation affected the spindle organization, SPB functions and nuclear morphology.

**Flow Cytometry**

Yeast cells were prepared for flow cytometry essentially as described by Hutter and Eipel (1979) using propidium iodide (Sigma Chemical Co., St. Louis, MO). The culture of yeast strain GHGC1501 (cmdl-101/cmdl-101) in early-exponential phase was shifted to 37°C. Cells (5×10$^6$) were collected, fixed in 70% ethanol and washed with 0.2 M Tris-CI (pH 7.5) solution. The activities were sonicated thoroughly, and treated with 1 mg/ml RNase A. Before analysis, the cells were stained with 5 µg/ml propidium iodide for 15 min on ice, then analyzed on an Epics C system (Coulter Corp., Hialeah, FL).

**Measurements of Chromosome Loss**

Analysis of chromosome loss was performed using the chromosome fragment method as described by Sher et al. (1991). For color sectoring assay, strains GHGC300 and GHW300 were grown to early-exponential phase in SGS (-ura) to prevent outgrowth of cells that had lost the marker chromosome. These cells were plated onto the YPGS solid medium, which is a condition allowing the loss of the marker chromosome. For quantitation of chromosome loss, the strains GHGC300 and GHW300 were first grown to early-exponential phase in the selective medium. These cells were then transferred to fresh YPGS medium and incubated for 4 h at 23°C or 30°C, or 3 h at 23°C and then 1 h at 37°C. Viability was determined by plating out a portion of the culture on YPGS plates. The remaining cells were collected from culture and plated on SGS plate containing 1 mg/ml 5-FOA (Sigma Chemical Co.) to select cells lacking a URA3 chromosome fragment as described (Shero et al., 1991). The frequency of chromosome loss equals the number of Ura- cells divided by the number of viable cells.

**Immunofluorescence Microscopy**

Immunofluorescent staining of yeast cells was performed using a method of Stearns and Botstein (1988) with modifications. Cells were fixed in 5% formaldehyde in YPGS for 30 min at room temperature. The cells were then collected and fixed in 3.7% formaldehyde in 0.1 M KPO$_4$, pH 7.5 for an additional 30 min. The fixed cells were speroplasted in 0.1 M KPO$_4$, pH 7.5 for 45 min at 37°C. Fixed cells were then permeabilized with 0.1% Triton X-100, 0.5 mg/ml RNase A and 0.5 mg/ml proteinase K. The cells were then washed with 2× saline-sodium citrate buffer (SSC) and fixed in 3.7% formaldehyde. The cells were permeabilized, washed and incubated with 10 µg/ml propidium iodide (PI) and 0.5 µg/ml 4',6'-diamidino-2-phenylindole (DAPI) for 30 min at room temperature. The cells were then washed with 2× SSC and embedded in 1:3 glycerol (v/v). A coverslip was placed on the sample and sealed with nail polish. Samples were photographed with a Zeiss Universal microscope equipped with a cooled charge-coupled device camera.

**Table I. Strain List**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genetic Composition</th>
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<tr>
<td>YPH499</td>
<td>MATa ura3-53 lys2-80 ade2-101 trpl-Δ63 his3-Δ200 leu2-Δ1</td>
</tr>
<tr>
<td>YPH500</td>
<td>MATa ura3-53 lys2-80 ade2-101 trpl-Δ63 his3-Δ200 leu2-Δ1</td>
</tr>
<tr>
<td>YPH501</td>
<td>MATa ura3-53 lys2-80 ade2-101 trpl-Δ63 his3-Δ200 leu2-Δ1</td>
</tr>
<tr>
<td>GHGC1499</td>
<td>MATa ura3-53 lys2-80 ade2-101 his3-Δ200 ade2-101 cmdl::GALIp-cmdl-101-TRP1</td>
</tr>
<tr>
<td>GHGC1500</td>
<td>MATa ura3-53 lys2-80 ade2-101 his3-Δ200 ade2-101 cmdl::GALIp-cmdl-101-TRP1</td>
</tr>
<tr>
<td>GHGC1501</td>
<td>MATa ura3-53 lys2-80 ade2-101 his3-Δ200 ade2-101 cmdl::GALIp-cmdl-101-TRP1</td>
</tr>
<tr>
<td>GHGC1502</td>
<td>MATa ura3-53 lys2-80 ade2-101 his3-Δ200 ade2-101 cmdl::GALIp-cmdl-101-TRP1</td>
</tr>
<tr>
<td>GHGC300</td>
<td>MATa lys2-80 ade2-101 his3-Δ200 ade2-101 cmdl::GALIp-cmdl-101-TRP1 SUP11::URA3</td>
</tr>
<tr>
<td>GHW300</td>
<td>MATa lys2-80 ade2-101 trpl::Δ63 his3-Δ200 ade2-101 SUP11::URA3</td>
</tr>
</tbody>
</table>
Freeze-substituted Fixation Method of EM

Preparation of thin section of yeast cells by the freeze-substituted fixation method was carried out as described (Kanbe and Tanaka, 1989) with minor modifications. Diploid cells grown in YPGS medium at 23°C were shifted to 37°C. After incubation for a certain period, the cells were collected by centrifugation. Pellets of cells were mounted on the copper meshes to form a thin layer and plunged into liquid propane cooled with liquid N2. The spheroplasts were then applied to the wells of multiple freezemicroscope (Olympus Corp., Tokyo, Japan) and photographed on Kodak Extachrome 400 film (Eastman Kodak Co., Rochester, New York).

Three-dimensional Reconstitutions

Computer-aided reconstructions from images of serial thin sections were made using OSMOZONE 2AS (Nikon Inc., Tokyo). Briefly, prints of serial 100-nm sections were enlarged to a final magnification of 18000 by xerographic copy. For each section, profiles of the nuclear envelope, the plasma membrane, and the microtubules were drawn on the sheets of xerographic copy. The sheets were then aligned by best fit of the profiles. These profiles were put into a computer (PC9801 Vm, NEC Co., Tokyo) using a digitizing tablet, and a profile-stack reconstruction was made. After the best viewing angle was established and shaded, solid-model views were made. The x- and y-axes of each three-dimensional reconstruction were equivalent to those obtainable by standard transmission electron microscopy, but in the z-axis it was limited to the section thickness (i.e., 100 nm). The three-dimensional image of type I cell was constructed based on 41 serial sections and that of type III cell was based on 29 serial sections that covering the entire nucleus.

Pulse-Labeling, Chase, and Immunoprecipitation

Cells were grown to 0.2 O.D.600 (1 O.D.600 unit = 1 × 10^8 cells) in synthetic minimal minus sulfate medium containing 100 μM (NH4)2SO4. One O.D.600 unit of cells was harvested, washed once with distilled water and resuspended in 720 μl of SGS minus sulfate medium. After incubation for 10 min at 30°C, 400 μCi Tran35S label (ICN Biomedicals, Inc., Costa Mesa, CA) was added. The labeling time is 10 min. The chase was initiated with the addition of 80 μl of a solution containing 10 mM (NH4)2SO4, 0.03% L-cysteine, and 0.04% of L-methionine and 650 μl of YPGS medium. Immediately after initiating the chase, equivalent aliquots (150 μl) of the suspension were transferred to fresh YPGS or YPGS plus 100 mM CaCl2 media, and chased in the two media at either 30 or 37°C. Equivalent aliquots (1 ml) were removed at the indicated time point and added to equal volumes of ice-cold 20 mM sodium acetate to terminate the chase. Labeled cells were washed with 1 ml of ice-cold 20 mM sodium acetate, and resuspended in 200 μl of TBS containing 1% SDS, 1 mM PMSF, and 5 μg/ml each of leupeptin, antipain, pepstatin A, and chymostatin. Glass beads (200 mg) were added and the suspensions were vortexed at top speed for 2 min and then heated on a 100°C heat block for 5 min. Extracts were adjusted to a volume of 1 ml by addition of 2% Triton X-100 in TBS and clarified by centrifugation at 12,000 g for 15 min at 4°C. The supernatants were incubated with 1 μl IgG fraction of anticalmodulin polyclonal antibody (Ohyama et al., 1987) on ice for at least 12 h and then with 20 μl of 50% (vol/vol) protein A-Sepharose CL-4B (suspension in TBS) with gentle agitation at room temperature for 2 h. The immunoprecipitates were collected by centrifugation and washed twice with 1 ml of 1% Triton X-100, 0.2% SDS, 150 mM NaCl, 5 mM EDTA, and 10 mM Tris-HCl, pH 8.0, twice with 1 ml of 2 M urea, 1% Triton X-100, 0.2% SDS, 150 mM NaCl, 5 mM EDTA, and 10 mM Tris-HCl, pH 8.0, and once with 1 ml of 150 mM NaCl, 5 mM EDTA, and 10 mM Tris-HCl, pH 8.0. The immunoprecipitates were eluted from the beads by heating at 100°C for 5 min in SDS gel sample buffer and subjected to SDS-PAGE as described (Laemmli, 1970). After electrophoresis, the gels were treated with Amplify (Amerham Corp., Arlington Heights, IL), dried and exposed to Kodak X-Omat AR film for 1-3 d at −80°C. The level of the CaM or half CaM was measured on a Shimazu Model CS-900 densitometer (Shimazu, Tokyo, Japan).

Results

Construction of the cmdl-101 Mutant

To characterize the phenotype of a mutant expressing the half CaM, the wild type CMD1 genes of strains YPH499 (MATα) and YPH500 (MATα) were replaced with the fusion gene GALlp-cmdl-101 (Sun et al., 1991) expressing the half CaM (Met7-Cys147). The strategy for this gene replacement is schematically shown in Fig. 1. A 2.4-kb DNA fragment carrying the GALlp-cmdl-101 fusion gene and TRPL gene with 0.3 kb and 0.4 kb flanking the CMD1 gene-replacing fragment was used to transform trpl haploid strains. Because depletion of the half CaM causes a lethal phenotype (Sun et al., 1991), cells carrying the integrated cmdl-101 gene do not grow on medium containing glucose, where the GALI promoter is switched off (Johnston and Davis, 1984). Therefore, we selected Glc Trp transformants. The correct fragment replacement at the CMD1 locus was verified by Southern analysis using endonuclease digested DNA from seven individual transformants of each strain. In all the Glc Trp transformants the CMD1 gene was replaced with the fusion gene (data not shown). The expressions of the half CaM from the strains carrying the fusion gene were confirmed by immunoprecipitation with antiyeast CaM antibody (see below). The diploid strain (GHGC1501) was obtained by mating GHGC1499 (MATα, cmdl-101) and GHGC1500 (MATα, cmdl-101), which were derived from YPH499 and YPH500, respectively.

We have examined whether the deletion of the region adjacent to the CMD1 gene (see Fig. 1) had any effect on the phenotype of the cmdl-101. First, we transformed the cmdl-101 cells with a plasmid pGCAM105 expressing the coding region of the native CaM under the GALI promoter: pGCAM105 complemented completely the temperature sensitive defects observed in the cmdl-101 mutant (data not shown).

Figure 1. Scheme of the strategy for construction of the cmdl-101 mutant. The 2.4 kb BamHI fragment of pGC-A1MTC1 was used to transform haploid strains YPH499 (MATα CMD1) and YPH500 (MATα CMD1). The Glc Trp transformants were picked and the integrations of the GALI-pcmdl-101 fusion gene into the chromosomal CMD1 locus were verified by Southern analysis.
shown). We have also examined another deletion construction (cmd1-Δl) which deletes 3/4 of the CMD1 gene within its coding region (Sun et al., 1991). Cells containing cmdl-Δl and a centromere-based plasmid pRSGCAMC1 (Sun et al., 1991) expressing the half CaM under the GAL1 promoter showed a temperature sensitive phenotype and aberrant microtubule organization (see below) similar to the cmdl-101 mutant cells. These results confirmed that the phenotype exhibited in the cmdl-101 mutant was due to the mutations in the CMD1 gene.

The cmdl-101 Mutant Shows Defects in Mitosis at Nonpermissive Temperature

The cmdl-101 cells were capable of growth at 23, 30, and 33°C on YPGS medium. However, the cmdl-101 cells did not grow at 37°C (Fig. 2). Upon shift to 37°C, the cmdl-101 cells (GHGC1501) stopped growth within 3 h (Fig. 3 A). Cell division ceased within two rounds, as judged by the number of cells in microcolonies formed from single cells on agar medium using time lapse photomicroscopy (Hartwell, 1971, 1978). The cmdl-101 mutation is lethal at the restrictive temperature; cells transferred to 37°C for 4 h yield <10% viable cells when returned to the permissive temperature (23°C) (Fig. 3 B). Microscopic examination of the GHGC1501 (cmdl-101/cmdl-101) cells after the shift to 37°C for 4 h revealed that ~90% of cells appeared with buds; 80% containing large buds and 10% small buds (Fig. 4 B). DAPI staining of nuclear DNA showed that >98% of cells incubated at the nonpermissive temperature were arrested with a single nucleus (see below: Fig. 7 C-E).

In S. cerevisiae, cell morphologies are good measures for distinguishing the stage of cell cycle. However, this measure alone cannot determine a specific defect either in chromosome segregation or in DNA synthesis, because both defects cause growth arrest as mononucleated large budded cells. The point of accumulation in the cell cycle can be more precisely determined by flow cytometric analysis of DNA content of the arrested cells. Diploid cells (GHGC1501) grown in YPGS medium at 23°C generated two peaks, one corresponding to the fraction of cells in the population with 2c content of DNA, and the other to cells with 4c content of DNA (Fig. 5, top). Upon shift to 37°C, the proportion of 4c cells increased while that of 2c cells decreased. After incubation at 37°C for 5 h, almost all the cells were arrested with 4c DNA content (Fig. 5, bottom). The increased fluorescence at the later time points was due to the contribution of mitochondrial DNA to the fluorescent signal, because the...
Figure 5. Flow cytometric analysis of the DNA contents of the *cmdl-101* cells grown in YPGS medium at 37°C. Cells of diploid strain GHGC1501 (*cmdl-101/cmdl-101*) grown to early-exponential phase in YPGS medium at 23°C were shifted to 37°C. Cells were withdrawn at intervals, fixed, stained with propidium iodide, and subjected to flow cytometric analysis. For each sample, 20,000 fluorescent events were measured. The *cmdl-101* mutant cells arrested with G2/M DNA content.

Figure 4. Cell cycle arrest morphology caused by the *cmdl-101* mutation. Exponential phase cultures of *cmdl-101* diploid strain (GHGC1501) in YPGS at 23°C were shifted to 37°C. (A) The morphology of the *cmdl-101* cells incubated in YPGS at 23°C; (B) the *cmdl-101* cells incubated in YPGS 4 h after shift to 37°C.

The *cmdl-101* Mutant Has a Defect in Chromosome Segregation

The effects of the *cmdl-101* mutation on chromosome stability were examined using the colony color sectoring assay (Shero et al., 1991). Yeast cells with a nonsense mutation *ade2-101* in the *ADE2* gene accumulate a red pigment and turn red upon growth on solid medium. This red color is not detected when the cell contains a tRNA suppressor that can suppress the *ade2-101* nonsense mutation. The loss of the tRNA suppressor during colony development allows the accumulation of pigment in the resulting clonal lineage. A 10-kb plasmid p300-1KMC (*SUP11, CEN4, and URA3*) linearized with EcoRI and BglII was used to transform the *cmdl-101* mutant (GHGC1500) as well as its isogenic wild-type strain (YPH500). This manipulation generated a non-essential marker chromosome carrying the *CEN4, URA3, SUP11*, and a part of the chromosome VI. After growing cells containing the marker chromosome to exponential phase in selective medium, the cells were plated onto YPGS medium (see Materials and Methods). The sectoring patterns are shown in Fig. 6. A portion of colonies of the mutant cells were red or containing red sectors (Fig. 6 B), whereas wild-type colonies were almost all white (Fig. 6 A). This result clearly showed that the half CaM mutant cell lost the marker chromosome at a higher frequency than the wild-type cell did.

Next, we examined the rate of chromosomal loss by counting the colonies formed on plates containing 5-fluoro-orotic acid (5-FOA). This compound is converted to a toxic product, 5-fluorouracil, through the action of the decarboxylase, which is encoded by the *URA3* gene. Therefore, *ura3* cells are resistant to 5-FOA, whereas *URA3* cells are killed on the 5-FOA plate. This method is used to select cells lacking the marker chromosome fragment carrying the *URA3* gene (Boeke et al., 1987; Shero et al., 1991). The strains containing the marker chromosome were first grown to early-exponential phase in selective medium at 23°C and then transformed to fresh YPGS medium for 4 h at different temperatures before plating onto 5-FOA plates. The *cmdl-101* mutant showed an increased frequency of chromosome loss after being incubated at the nonpermissive temperature for 1 h (Table II). In addition, the half CaM mutant had a 50-fold higher rate of chromosome loss compared to the wild-type strains even at the permissive temperature. These results indicate that the half CaM mutant has a defect in accurate chromosome segregation.
The Strain Containing cmdl-101 Produces a Monopolar Spindle

The stage of the cell cycle at which the cmdl-101 mutant cells were arrested was examined in more detail by examining the microtubule organization in the cmdl-101 diploid strain incubated at 37°C by immunofluorescence microscopy. As seen in Fig. 7 A, the microtubules in wild-type cells were found to be associated exclusively with the SPB(s) and the cytoplasmic microtubules were not prominent. The staining patterns of microtubules in the cmdl-101 cells grown in YPGS medium at 23°C (Fig. 7 B) were almost indistinguishable from that seen in wild-type cells (Fig. 7 A). However, the microtubule organization observed in the cmdl-101 cells incubated at the nonpermissive temperature was apparently disturbed. Fig. 7, C-E, show three typical staining patterns of microtubules observed in the large-budded cells of the cmdl-101 mutant 3 h after transfer to 37°C. In the first class (type I), the mutant cells contained one focus of microtubules that was associated with the nuclear DNA (Fig. 7 C). The second form (type II) is the cells containing one cluster of microtubules that was not associated with the nuclear DNA (Fig. 7 D). Both type I and type II cells apparently did not exhibit any spindelike structures. The third type is the cells containing a very short spindle or a microtubule organization that appeared like a short spindle (Fig. 7 E). The distribution and temporal relationship of the three staining patterns in the population are shown in Fig. 8. We found that only a small fraction of the cells exhibited short spindle (or type III) morphology, and fewer type III cells were observed as the incubation at the nonpermissive temperature continued. After incubation at 37°C for 4 h, only 6.4% of cells displayed such morphology. Furthermore, in the mutant cells arrested at high temperature, the length of cytoplasmic microtubules was longer and exhibited brighter fluorescent staining (Fig. 7, C and E) than those seen in the
Table II. cmdl-101 Mutant Increases Chromosome Loss

<table>
<thead>
<tr>
<th>Culture condition</th>
<th>Wild-type</th>
<th>cmdl-101 mutant</th>
</tr>
</thead>
<tbody>
<tr>
<td>23°C 4 h</td>
<td>1.3</td>
<td>68.9</td>
</tr>
<tr>
<td>30°C 4 h</td>
<td>1.9</td>
<td>108.6</td>
</tr>
<tr>
<td>23°C 3 h, 37°C 1 h</td>
<td>1.3</td>
<td>165.7</td>
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</table>

Frequencies of chromosome loss for cells that had been incubated in YPGS at 23, 30, or 37°C. The strains GHGC300 and GHW300 were first grown to early-exponential phase in the selective medium. These cells were then transferred to fresh YPGS medium and incubated for 4 h at 23°C or 30°C, or 3 h at 23°C and then 1 h at 37°C. Viability was determined by plating out a portion of the culture on YPGS plates. The remaining cells were collected from culture and plated on SG6 plate containing 1 mg/ml 5-FOA to select cells lacking a URA3 chromosome fragment as described (Shem et al., 1991). The frequency of chromosome loss equals the number of Ura- cells divided by the number of viable cells.

Wild type cells (Fig. 7 A) or mutant cells grown at the permissive temperature (Fig. 7 B), suggesting that the cytoplasmic microtubules are abnormally developed. Moreover, some of the microtubules appeared to be unassociated with the spindle plaque (Fig. 7 D). The apparent disruption of microtubule organization is consistent with gross defects in chromosome segregation.

The defects in microtubule organization and chromosome segregation seen in the cmdl-101 (GHGC1501) cells were found to result from the formation of a monopolar spindle. Serial sections through the entire nucleus in each of 37 large budded cells arrested at high temperature were examined by electron microscopy. In 32 nuclei (87%), only a single SPB was observed. No other structure resembling to a spindle plaque with or without attached microtubules was found. We have also examined the serial sections through the whole cell of four of the cells containing a single SPB, and no SPB that detached from the nuclear envelope was observed. The distribution of large budded cells containing a single SPB in such a high frequency was never observed in wild-type cells (YPH501). In wild-type cells, as the SPB duplication occurs early in cell cycle, budded cells in exponentially growing cultures should contain two SPBs at various stages of mitosis (Byers and Goetsch, 1975, also see Fig. 9 C). We found that all the budded cells (n = 13) of the cmdl-101 GHGC1501 strain grown at 23°C contained two SPBs per nucleus (Fig. 9, D–F), each acting as a pole of the mitotic spindle as that seen in the wild cell (Fig. 9 C).

According to the number of SPB and the position of SPB localized, we found that the morphology of cells observed under electron microscope still could be divided into three types (Fig. 9, G–M; Fig. 10). These three types of microtubule organizations are corresponding to those observed by immunofluorescence microscopy, respectively (Fig. 7, C–E; Fig. 8).

We found that both the cells of type I and type II contained...
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Figure 8. Cells from an exponential-phase culture of strain GHG-Cl501 (cmdl-101) grown in YPGS at 23°C were shifted to 37°C. At the indicated time point, samples were fixed and processed for antitubulin immunofluorescence and DAPI staining as described in Materials and Methods. The staining patterns of microtubules and nuclear DNA in the cells were examined and counted under a fluorescence microscope. Type I indicates morphology of a cell exhibiting a cluster of microtubules associated with the nuclear DNA; type II indicates a cell carrying a focus of microtubules unassociated with the nuclear DNA; type III shows a cell displaying a short spindle or spindle-like structure. "n" is the number of the total cells examined from three independent preparations of samples.

The morphology of the nucleus in cmdl-101 cells appeared abnormal. When observed by the freeze-substituted fixation method, the morphology of the nucleus in wild-type cells always appears round and the nuclear contour is smooth (Fig. 9 A; also see Kanbe and Tanaka, 1989; Baba and Osumi, 1989). However, we found that the nuclear envelopes of the mutant cell formed invaginations even when the cmdl-101 mutant. There are 13% of the cells (5/37) containing two SPBs (type III) 4 h after incubation at 37°C. Fig. 10 (E and F) show the typical morphology observed in the type III cells. The direction of the spindle was distorted from the long axis of nuclear elongation in all the five cells examined. Cells displaying type III morphologies were minor in cell specimens prepared after incubation for 4 h at 37°C. This result is consistent with the fluorescence microscopic observation. Majority of cells were arrested with a single SPB that formed a monopolar spindle (Fig. 8). These observations suggest that the spindle organization is inhibited in the cmdl-101 mutant.

The multi-plaque structure of the single SPB in the three types appeared normal. The SPB was not enlarged as those observed in cdc31 (Byers, 1981b) and karl mutants (Rose and Fink, 1987), and did not contain an enlarged half bridge or an abnormal SPB without attached microtubules as those observed in mps1 and mps2 mutants (Winey et al., 1991). However, the perturbed association of microtubules with the spindle plaque and the altered location of the SPB on the nuclear envelope suggest that the function of SPB is affected in the cmdl-101 mutant.

The Integrity of the Nucleus Is Apparently Disturbed in cmdl-101 Mutant

The morphology of the nucleus in cmdl-101 cells appeared abnormal. When observed by the freeze-substituted fixation method, the morphology of the nucleus in wild-type cells always appears round and the nuclear contour is smooth (Fig. 9 A; also see Kanbe and Tanaka, 1989; Baba and Osumi, 1987, Baba et al., 1989). However, we found that the nuclear envelopes of the mutant cell formed invaginations even when the cells were incubated at the permissive temperature, although the morphology and duplication of SPB still appeared normal (Fig. 11, A and B) The deformation of the nucleus became more severe 2 h after shift to 37°C (Fig. 11, C and D). As the incubation at the nonpermissive temperature con-
Figure 11. The morphology of nucleus in the cmdl-101 mutant. The nuclear envelope observed in cmdl-101 cells (GHGC1501) incubated at 23°C (A and B) forms invaginations using the freeze-substituted fixation method. The nuclear envelope deforms more severe after incubation at 37°C for 2 h (C and D). As the incubation at 37°C continues (5.5 h), the nuclear envelope becomes more intricate and the fragmentation of the nucleus begins (E and F). Arrows indicate the invagination of nuclear envelope; arrowheads indicate the nuclear envelope. N, nucleus.

Figure 10. Three-dimensional reconstruction from serial thin sections. (A–D) The three-dimensional image of the type I cell shown in Fig. 9, G and H. (E–F) The three-dimensional image of the type III cell. The plasma membranes are represented by dotted lines (white), the nuclear envelope was represented by a nontransparent surface (red, A, B, and E) or semitransparent surface (C, D, and F). The microtubules appear as solid lines (green in A–D and yellow in E–F). The vacuole is represented by a nontransparent (E) or transparent surface (F, blue). A, C, E, and F are top views of the cell, D is a view from the side. B is the top view of the section phase where the SPB located. Arrows indicate the positions of the SPB.
uniform: a large bud and a G2/M DNA content (Figs. 4 B and 5). These phenotypes indicate that the expression of CaM under the control of a strong promoter. The half CaM expressed under the authentic CMD1 promoter does not complement the cmdl null mutation (Sun et al., 1991). Thus, this mutant allele can not be isolated like a typical cdc mutation.

Several lines of evidence indicate that the cmdl-101 mutation inhibits the normal functions of SPB and mitotic spindle. Genetic studies show that the cmdl-101 temperature sensitive mutation increases the frequency of chromosome loss, a phenotype resulting from defects in chromosome segregation (Table II). Immunofluorescence analysis of the mutant cells arrested at high temperature strongly suggests that the SPB fails to form a normal mitotic spindle (Fig. 7, C and D; see also Fig. 8). Electron microscopic analyses of serial sections of arrested mitotic cells showed that in these cells, only a single SPB is observed and the location of the SPB on the nuclear envelope is abnormal. Furthermore, the association of nuclear microtubules with the SPB is also affected (Fig. 9, K-L). In addition, we have also examined the phenotype of cells depleted of the half CaM: electron microscopy revealed that all the cells (n = 5) depleted of the half CaM had a single SPB and formed monopolar spindle (Sun, G.-H., A. Hirata, Y. Ohya, and Y. Anraku, unpublished data). Taken together, these results suggest an essential role of CaM in spindle organization and SPB functions.

A number of mutations in yeast, for instance, cdc31 (Baum et al., 1986), ndcl (Thomas and Botstein, 1986), kar1 (Rose and Fink, 1987), esp1 (Baum et al., 1988), mps1 and mps2 (Winey et al., 1992) have been reported to cause defects in the duplication and functions of SPB. The cmdl-101 mutant shares many characteristic phenotypes with the cdc31, kar1, and mps1 mutants including formation of a monopolar spindle, abnormal localization of SPB in the invagination of the nuclear envelope. There are still some distinct phenotypes: the morphology or the size of the SPB appears to be affected in these three mutants, while these features of the SPB in the cmdl-101 appear normal. In addition, the orientation of the SPB on the nuclear envelope and the association of microtubules with the SPB are not interfered in the cmdl-101 mutant. Among these previously reported genes, the CDC31 gene which is required for SPB duplication has been found to encode a Ca2+-binding protein similar to CaM (Baum et al., 1986). We found that overexpression of the half CaM in the cdc31 mutant, or combination of the cmdl-101 with the cdc31 mutations showed no synthetic phenotype (G.-H. Sun, Y. Ohya, and Y. Anraku, unpublished data).

We have shown that the cmdl-101 mutation caused defects at the G2/M phase of the cell cycle. Unlike all previously described cdc mutants (Johnston et al., 1977; Pringle and Hartwell, 1981), this conditional CaM mutant contains two unique features: the first is the large deletion mutation within the structure of the CaM (half CaM), and the second is that the mutant CaM is designed to be expressed under the control of a strong promoter. The half CaM expressed under the authentic CMD1 promoter does not complement the cmdl null mutation (Sun et al., 1991). Thus, this mutant allele can not be isolated like a typical cdc mutation.

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We have shown that the cmdl-101 mutation caused defects

**Table:**

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<th>Media</th>
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**Fig. 12.** Pulse-chase experiment of the carboxyl-terminal half CaM with antibody against yeast CaM. Diploid strain GGC1502 (cmdl-101/CMD1) which expresses both the carboxyl-terminal half CaM and the native CaM was used. The pulse and chase were performed as described in Materials and Methods. The immunoprecipitates were resolved by 15% sodium dodecyl sulfate polyacrylamide gel electrophoresis. After electrophoresis, the gel was dried and exposed to film overnight. The file was then scanned with a densitometer. The "fold" is the rate of expression level of the half CaM over that of the wild-type CaM (mol/mol) at each indicated time point.
in SPB functions and formed abnormal monopolar spindles at the nonpermissive temperature. How do these monopolar spindles arise? Which step(s) in the process of spindle organization require CaM functions? There are several considerable possibilities. First, it is possible that the CaM function is required for SPB duplication. The failure in SPB duplication results in a high percentage of cells containing a single SPB which forms monopolar spindle. We found that the size of the single SPB in the cmdl-101 cells was not significantly enlarged, and the morphology was similar to that of SPB in G0 phase of the cell cycle. These observations suggest that execution of the CaM functions is at an early step in the pathway of SPB duplication. It is also possible that CaM has more than one execution point during the formation of mitotic spindle. Indeed, there are ~10% of cells exhibiting bipolar short spindle (type III). These cells are probably the population that has escaped the critical point(s) at the early step of SPB duplication that requires the CaM function. We found that the organizations of the short spindle in these cells are abnormal: (a) one of the two SPBs was frequently embedded in the deep invagination of the nuclear envelope (Fig. 11, C and D), and (b) the orientation of the short spindle was always different from the direction of nuclear elongation (Fig. 10, E and F). These abnormal organizations suggest that functions of the SPB in the bipolar spindle are also affected by the cmdl-101 mutation. Finally, we have found that the cell number did not increase after incubation for 3 h at 37°C (Fig. 5). However, the type III cells were falling, whereas the type I cells with the monopolar spindle were increasing (Fig. 8). These observations may indicate that some cells with bipolar spindle have converted into cells exhibiting monopolar spindle without cell division. This result suggests that CaM may be also required for the integrity and stability of SPB. It is possible that the SPB duplication in type III cells is interfered by a loss of CaM function. Thus, a defective SPB is formed and then broken down at the nonpermissive temperature. It is experimentally difficult to follow and examine the morphological changes of the same SPB at different time points. It must be informative to examine the morphology of SPB using a synchronized culture, or the synthetic phenotypes of the cmdl-101 with the other mutations causing defects in SPB duplication.

The carboxyl-terminal and the amino-terminal halves of CaM show very high homology to each other. Each of the half domains forms a lobe of the dumbbell structure of the entire CaM molecule (Babu et al., 1985, 1988). Functional complementation of the cmdl null mutation with both the half molecules suggests that the function of CaM involved in SPB functions and organization of microtubules might depend only on one of its two structurally similar domain, not its global structure. We have found that cells expressing only the amino-terminal half CaM show a similar phenotype with that observed in cells expressing the carboxyl-terminal half (Sun, G.-H., Y. Ohya, and Y. Anraku, unpublished data). It is possible that the half CaM regulates the process of PBS duplication and spindle formation through activation of CaM-dependent enzymes. It is also possible that each of the half domains might perform as a temporal component of the spindle or SPB structure.

The cytoplasmic microtubules also appear abnormally developed in the cmdl-101 mutant incubated at the nonpermissive temperature. The abnormal development and organization of cytoplasmic microtubules are consistent with previous studies that have shown that CaM has a protective effect on microtubules. Microinjection of CaM into PtK cells has a stabilizing effect on kinetochore microtubules (Swee et al., 1988). The 145-K STOP protein, a CaM-binding protein described by Margolis and co-workers (1986) confers cold-stability to brain microtubules (Pabion et al., 1984). We have found that combination of the cmdl-101 mutation with tub2-150 mutation (Stearns et al., 1990), which stabilizes microtubules and requires benomyl for mitotic growth at high temperature, caused more strict Ts growth than with other tubulin mutation alleles (G.-H. Sun, Y. Ohya, and Y. Anraku, unpublished data). This result is consistent with the aberrant organization of cytoplasmic microtubules seen in the cmdl-101 cells, suggesting that the mutant CaM may have an effect causing an excessive stabilization or incorrect assembly of microtubules.

Immunofluorescent staining studies have shown that CaM localizes to the centriolar region and to the kinetochore-to-pole microtubules in various cells (Welsh et al., 1978, 1979). Fluorescent CaM, microinjected into cells, appears at the same sites (Zavortnik et al., 1983). This concentrated localization of CaM in the mitotic apparatus suggests an important role for CaM in the corresponding process. The formation of monopolar spindle observed in the cmdl-101 mutant allele is consistent with the distribution of CaM observed in higher organisms. In S. cerevisiae, it is still not clear whether the yeast CaM is a component of SPB or temporally associated with the mitotic apparatus. The immunofluorescence staining with antibody against yeast CaM reveals that CaM is present throughout the cytoplasm at all stages of the cell cycle and is concentrated in the site of bud growth (Sun et al., 1992). The immunolocalization of the half CaM in the cmdl-101 cells grown at permissive temperature is similar to that of native CaM observed in wild-type cells (data not shown). It may be possible that the concentration of CaM required for SPB and spindle functions is lower than that for bud growth. The immunofluorescence microscopy alone cannot specify a precise localization of yeast CaM in the mitotic apparatus. It must be informative to examine the localization of yeast CaM in the mitotic apparatus using immunoelectron microscopy.

The mitotic arrest phenotypes, including specific arrest at G2/M phase and an elevated rate of chromosome loss observed in the cmdl-101 mutant, are consistent with the phenotypes observed in a CaM depleted mutant (Ohya and Anraku, 1989a). As CaM is a stable protein and requires 12-15 h (approximately six generations) to remove the protein completely, we found that the terminal phenotype of the CaM depleted mutant is not as uniform as that caused by the cmdl-101 temperature sensitive mutation. The percentage of cells arrested with small bud is higher in the CaM depleted cells than in the cmdl-101 cells. It is possible that other processes (e.g., bud growth) which require CaM functions are also affected in the CaM depleted mutant.

Using the freeze-substituted fixation method, combined with a sufficient number of serial sections of better preserved nuclei, we were able to dissect the nuclear morphology in the cmdl-101 mutant (Fig. 11). We found that the integrity of the nuclear envelope in the cmdl-101 mutant cells at nonpermissive temperature was significantly perturbed (Figs. 10 and 11). One possibility is that the alteration in normal SPB
and spindle function may develop abnormal morphologies of the nuclear envelope. Similar phenotype has also been observed with the kar1 mutation, which causes a defect in SPB duplication (Rose and Fink, 1987). It may also be possible that CaM is simultaneously required for maintenance of nuclear envelope integrity. We found that the cmdl-101 mutant loses the viability rapidly upon shift to nonpermissive temperature. This phenotype is different from the cdc31 and mps2 mutants that also form monopolar spindle at the nonpermissive temperature. These two mutants exhibit good viability at the transient arrest and increase the ploidy upon the return to permissive conditions (Schild et al., 1981, Winey et al., 1991). We presume that the perturbed integrity of the nuclear envelope may also affect the viability of the cmdl-101 cells at high temperature.

The pulse chase experiment showed that the stability of the half CaM at the nonpermissive temperature (37°C) was not very different from that at 30°C, a temperature at which the cmdl-101 cells still grow well (see Fig. 2). One possibility for the Ts- growth phenotype is that a very little decrease causes a severe defect. If this is true, an increase in the expression level of the mutant CaM should rescue the temperature sensitive phenotype. To verify this possibility, we have transformed the cmdl-101 strain with plasmid pRSGCAM1 which is a high copy plasmid carrying the GALp-cmdl-101 fusion gene. Even though the expression level of the half CaM was elevated, the cells still exhibited a temperature sensitive phenotype similar to those without the expression plasmid (data not shown). These results suggest that the instability of the mutant protein may not be the primary cause of the temperature sensitive phenotype. We presume that the high temperature may block the functional interaction of CaM with its target proteins. The high concentration of extracellular Ca2+ ion partially rescued the Ts- growth of the cmdl-101 cells, but did not show any effect on the growth of the cells depleted of the half CaM (data not shown). The degradation of the half CaM was still faster than that of the native protein when cells were grown in medium containing CaCl2 supplement. These results suggest that the addition of Ca2+ ion may activate the interaction of the mutant CaM with its targets (Anraku et al., 1991). Future investigations on the crucial targets of CaM will determine the molecular mechanisms of CaM involved in spindle organization and SPB functions.

We are grateful to Dr. Teruhiko Beppu, Dr. Minoru Yoshida and Dr. Takeo Usui for their kind instruction and technical help on flow cytometric analysis, to Dr. David Bottstein for the nab mutants, and to Dr. Tsuneyoshi Kuroiwa for his detailed instruction and help in carrying out the three-dimensional reconstruction and VIMPCS measurement. We thank Dr. Mark Rose for general discussions and criticism, Dr. Rebecca Bernat, Dr. Akihiko Nakano, and Dr. Yoh Wada for critical reading of the manuscript. This work was supported in part by Grant-in-Aid 0325612 (Y. Ohya) for Scientific Research on Priority Areas from the Ministry of Education, Science, and Culture of Japan, and a grant from the Japan Society for the Promotion of Science for Japanese Young Scientists to G.-H. Sun. 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