The Mitotic Exit Network integrates temporal and spatial signals by distributing regulation across multiple components

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Abstract

GTPase signal transduction pathways control cellular decision making by integrating multiple cellular events into a single signal. The Mitotic Exit Network (MEN), a Ras-like GTPase signaling pathway, integrates spatial and temporal cues to ensure that cytokinesis only occurs after the genome has partitioned between mother and daughter cells during anaphase. Here we show that signal integration does not occur at a single step of the pathway. Rather, sequential components of the pathway are controlled in series by different signals. The spatial signal, nuclear position, regulates the MEN GTPase Tem1. The temporal signal, commencement of anaphase, is mediated by mitotic cyclin-dependent kinase (CDK) phosphorylation of the GTPase’s downstream kinases. We propose that integrating multiple signals through sequential steps in the GTPase pathway represents a generalizable principle in GTPase signaling and explains why intracellular signal transmission is a multi-step process. Serial signal integration rather than signal amplification makes multi-step signal transduction necessary.
Introduction

Accurate chromosome segregation is essential for genome maintenance and viability of the organism. Central to this accuracy is the integration of temporal and spatial signals by the cell cycle machinery. Deciphering the molecular mechanisms that bring about signal integration is thus critical to understanding how organisms are built.

In eukaryotes, a family of protein kinases, known as cyclin-dependent kinases (CDKs) drive progression through the cell cycle. G1 CDKs promote cell cycle entry, S phase CDKs initiate DNA replication, and mitotic CDKs drive entry into mitosis (reviewed in ref. 1). Events during mitosis are controlled by a ubiquitin ligase known as the Anaphase Promoting Complex or Cyclosome (APC/C; Figure 1A; reviewed in ref. 2,3). The APC/C together with its specificity factor Cdc20 degrade the anaphase inhibitor Securin (Pds1 in budding yeast; ref. 4) to allow the protease Separase (Esp1 in budding yeast) to cleave cohesins, the proteins that hold the duplicated sister chromatids together. Cleavage of cohesins initiates anaphase. APC/C-Cdc20 not only targets Securin for degradation, the ubiquitin ligase also ubiquitinylates S phase and mitotic cyclins$^5$–$^8$. In budding yeast, APC/C-Cdc20 promotes the complete destruction of the S phase cyclin Clb5 and degradation of approximately half the pool of the mitotic cyclin Clb2$^4$. This partial degradation of cyclins is a prerequisite for execution of the final cell cycle transition - exit from mitosis.

During exit from mitosis mitotic events are reversed. The mitotic spindle is disassembled, chromosomes decondense and cytokinesis ensues. Mitotic CDK inactivation brings about this transition$^9$,$^{10}$. In mammals, CDK inactivation occurs in a single step initiated at the metaphase to anaphase transition. In budding yeast CDK inactivation is a two-step process (reviewed in ref. 11). CDK inhibition begins at the metaphase to anaphase transition when APC/C-Cdc20 targets all S phase cyclins and a fraction of mitotic cyclins for destruction. Then, in a second step, APC/C bound to a specificity factor related to Cdc20 - Cdh1 - brings about the complete degradation of mitotic cyclins and hence complete mitotic CDK inactivation. This results in mitotic exit. APC/C-Cdh1 is aided in mitotic CDK inactivation by the CDK inhibitor Sic1$^{12}$.

APC/C-Cdh1 and Sic1 activity are controlled by the essential protein phosphatase Cdc14. Cdc14 dephosphorylates Cdh1 and Sic1 thereby activating them$^{13}$–$^{16}$. Given the central role of Cdc14 in control of exit from mitosis it is not surprising that the phosphatase is tightly regulated. For most of the cell cycle Cdc14 is bound to its inhibitor Cfi1/Net1 in the nucleolus$^{17}$,$^{18}$. During anaphase the phosphatase dissociates from its inhibitor spreading through the nucleus and cytoplasm to dephosphorylate many proteins including Sic1 and Cdh1.
Two signaling pathways have been identified that control the interaction between Cdc14 and its inhibitor. The Cdc14 Early Anaphase Release (FEAR) network releases Cdc14 from its inhibitor in the nucleolus upon anaphase entry. The FEAR network only transiently releases Cdc14 from its inhibitor. Cdc14 will return to the nucleolus unless the mitotic exit network (MEN) becomes active. Activation of the MEN in late anaphase causes the sustained release of Cdc14 from the nucleolus, resulting in exit from mitosis.

The FEAR network is comprised of some of the same proteins that control chromosome segregation at the onset of anaphase (Figure 1A). Separase not only cleaves cohesins, the protease also associates with Slk19 which leads to the phosphorylation of the Cdc14 inhibitor Cfi1/Net1 by an unknown mechanism. Cfi1/Net1 phosphorylation combined with activation of the FEAR network protein Spo12 then leads to Cdc14 release from its inhibitor in the nucleolus. While Cdc14 released from Cfi1/Net1 by the FEAR network has many roles in facilitating anaphase chromosome segregation, the network is not essential for exit from mitosis. Inactivation of the FEAR network only causes a 20 minute delay in exit from mitosis.

The Mitotic Exit Network (MEN) is activated during anaphase and promotes the sustained release of Cdc14 from the nucleolus. Released Cdc14 then triggers complete CDK inactivation and hence exit from mitosis. The MEN is essential. Cells lacking MEN function arrest in late anaphase failing to exit from mitosis. The signaling pathway resembles a Ras-like GTPase signal transduction cascade and is comprised of the GTPase Tem1, the protein kinases Cdc15 and Dbf2-Mob1, and the signaling scaffold Nud1 (see Figure 7A for a MEN diagram; reviewed in ref. 41). MEN components are scaffolded onto spindle pole bodies (SPBs), the yeast equivalents of centrosomes, by Nud1. Tem1 recruits Cdc15 to SPBs during anaphase. Cdc15 then activates Dbf2-Mob1. Active Dbf2-Mob1 promotes the release of Cdc14 from the nucleolus.

One function of the MEN is to ensure that sustained Cdc14 activation only occurs when the nucleus moves into the bud during anaphase. Asymmetric localization of MEN activators and inhibitors causes the MEN to react to spindle position. Kin4, which activates the Tem1 GTPase activating protein (GAP) complex Bub2-Bfa1 and hence maintains Tem1 in the GDP bound form, localizes to the mother cell. Lte1, which inhibits Kin4 and hence activates Tem1, localizes to the bud. Thus, Kin4 and Lte1 create a MEN inhibitory zone in the mother cell and a MEN activating zone in the bud, respectively (Figure 1B). This setup ensures that the MEN can only be activated when a SPB carrying the MEN GTPase translocates into the bud during anaphase, hence making the MEN responsive to spindle position.
While an appealing model for how cells sense spindle position, this zone model of MEN activation fails to explain how mitotic exit is coordinated with cell cycle progression. It has previously been observed that when cells experience a prolonged metaphase arrest the nucleus moves into the bud\textsuperscript{61}, yet these cells do not exit from mitosis. Why does the MEN not promote exit from mitosis in these metaphase arrested cells despite a MEN GTPase-bearing SPB moving into the bud (Figure 1B)? We show here that high mitotic CDK activity prevents MEN activation in metaphase, even when a MEN GTPase-bearing SPB moves into the bud. We further show that APC/C-Cdc20 dependent cyclin degradation and activation of Cdc14 by the FEAR network lowers mitotic CDK activity to permit MEN activation upon movement of the SPB into the bud. Surprisingly, antagonism by CDKs does not inhibit the MEN GTPase Tem1, but rather causes phosphorylation of downstream components of the MEN, the protein kinases Cdc15 and Mob1-Dbf2. CDK inhibition of the MEN kinase cascade prevents the feedback loops that would otherwise be initiated upon movement of a MEN GTPase-bearing SPB into the bud. Our study shows that the MEN integrates spatial and temporal signals at different steps of the signaling pathway, demonstrating logical “AND gate” control of the pathway. This signal integration logic ensures that exit from mitosis only occurs after anaphase entry AND after partitioning of the genetic material between mother and daughter cell. Utilizing multi-point regulation explains how GTPase pathways perform signal integration and provides a rationale for why signaling pathways are multi-step processes.

Results

\textit{MEN activity is confined to anaphase in the strain W303}

The MEN promotes exit from mitosis. This activity of the MEN is confined to anaphase. During this cell cycle stage movement of a SPB into the bud leads to the association of the MEN kinase Cdc15 with SPBs where it phosphorylates the scaffold Nud1\textsuperscript{45,47}. This promotes the association of Dbf2-Mob1 with SPBs, resulting in activation of the kinase\textsuperscript{44}. Dbf2-Mob1 then activates Cdc14 to trigger exit from mitosis.

A recent study reported that the MEN kinases Cdc15 and Dbf2-Mob1 are active prior to anaphase and prior to a SPB moving into the bud, but that this activity cannot be measured by conventional kinase activity assays\textsuperscript{62}. This metaphase-specific MEN activity was reported to affect spindle positioning\textsuperscript{63,64} by controlling the localization of the spindle positioning factor Kar9. When the MEN was inactivated, Kar9 localization to astral microtubules emanating from the old, daughter bound SPB was impaired, resulting in the aberrant inheritance of the newly synthesized SPB by the daughter cell. These results raised the interesting possibility that low levels of SPB-localized MEN activity promote spindle positioning during metaphase but are insufficient to bring about exit
from mitosis. A key question arising from this observation is how MEN activity is controlled in a manner that allows the pathway to fulfill its spindle orientation function in metaphase, yet does not promote exit from mitosis even when a MEN-bearing SPB transiently moves into the bud during metaphase.

To address this question we examined Kar9 localization in cells either harboring a temperature sensitive (cdc15-2) or an analog sensitive (cdc15-as1) allele of the MEN kinase CDC15. Kar9 association with astral microtubules is asymmetric. Kar9 preferentially binds to microtubules that emanate from the old SPB, that is destined to move into the bud during anaphase. Hotz et al. (2012) reported that Kar9 localization becomes symmetric when the MEN is inactive, associating almost equally well with microtubules emanating from both, the new and old SPB. We found that Kar9 localization was not affected by MEN inhibition. Kar9 localization in cdc15-2 and cdc15-as1 cells was indistinguishable from that of wild-type cells (Figure 1 – figure supplement 1A-M). Because Kar9 localization is highly dynamic we also performed short-term (100s, 10s per frame; Figure 1 – figure supplement 1I-J) and long-term imaging studies (4h, 5m per frame; Figure 1 – figure supplement 1K-M). Inactivation of the MEN did not affect Kar9 localization in either experimental set up.

The changes in Kar9 localization found in MEN mutants was reported to cause spindle pole body inheritance defects. In wild-type cells, the old SPB is inherited by the daughter cell, whereas the newly synthesized SPB remains in the mother cell. In MEN mutants this stereotypic inheritance pattern was reported to be perturbed. To measure SPB inheritance we fused the SPB protein Spc42 to the slow folding mCherry fluorophore. This fusion makes the old SPB appear brighter than the newly synthesized one, allowing us to follow SPB inheritance (Figure 1 – figure supplement 1O). As previously reported, we found that deletion of KAR9 randomized SPB inheritance (Figure 1 – figure supplement 1N). However, inactivation of CDC15 using the cdc15-as1 allele, did not affect SPB inheritance (Figure 1 – figure supplement 1N). We conclude that in our strain background, W303, there is no evidence for MEN activity prior to anaphase onset. We propose that strain background differences could be the reason why our results differ from those reported by Hotz et al. (2012). Based on a lack of evidence for MEN activity outside of anaphase in our strain background, we will define “MEN activity” by its ability to promote mitotic exit throughout the remainder of the paper.

**APC/C-Cdc20 activity is required for MEN activation**

The nucleus has been observed to make transient excursions into the bud prior to anaphase. This is particularly evident in APC/C mutants that arrest in metaphase. Cells harboring a temperature sensitive allele of the APC/C subunit encoding gene CDC23 (cdc23-1) arrest in metaphase. During the arrest 97% of cells move part or the
entirety of the undivided nucleus into the bud. To determine whether MEN activation occurs in cdc23-1 cells in which the nucleus translocated into the bud, we analyzed Mob1 localization. In wild-type cells, Mob1 associates with SPBs when the MEN is activated during anaphase (Figure 1C; Figure 1 – figure supplement 2). Following MEN activation, Cdc14 is released into the cytoplasm (Figure 1D Figure 1 – figure supplement 2). Exit from mitosis and entry into the next cell cycle ensues, as judged by cells forming a new bud (referred to as rebudding; Figure 1E).

In metaphase-arrested cdc23-1 mutants neither MEN activation nor exit from mitosis occurred. SPB movement into the bud caused only weak, inconsistent Mob1 association with SPBs, Cdc14 was not released from the nucleolus, and cells failed to enter the next cell cycle (Figure 1C-E; Figure 1 – figure supplement 2). It is, however, noteworthy that some Mob1 associated weakly with SPBs when the nucleus moved into the bud in cdc23-1 mutants (Figure 1C; Figure 1 – figure supplement 2). This observation suggests that the MEN retained at least some ability to respond to spindle position. Yet, the low level of Mob1 association with SPBs combined with lack of Cdc14 release from the nucleolus and lack of rebudding indicates that MEN activation is suppressed during metaphase. We conclude that movement of a SPB into the bud causes MEN activation only when it occurs during anaphase.

Spindle elongation is not sufficient to activate the MEN

Which aspect of anaphase is critical for MEN activation? Previous work has established that APC/C-Cdc20 has two essential functions in promoting anaphase onset: cyclin degradation and Securin degradation (Figure 1A). Cyclin degradation reduces CDK activity during anaphase. Securin degradation activates the FEAR network and causes cohesin cleavage, which in turn leads to spindle elongation and chromosome segregation. Any or all of these anaphase events could be required for MEN activation during anaphase.

We first tested the role of anaphase spindle elongation in MEN activation. To render spindle elongation independent of APC/C-Cdc20 activity we introduced a temperature sensitive cohesin allele known as mcd1-1 into cdc23-1 cells. This double mutant undergoes spindle elongation during a metaphase arrest because sister chromatids are no longer held together due to the loss of cohesin function. Inactivation of cohesins activates the spindle assembly checkpoint (SAC). To prevent interference of the SAC with anaphase events we deleted the SAC gene MAD1. Analysis of the cdc23-1, mcd1-1, mad1Δ strain revealed that spindle elongation was not sufficient to activate the MEN in metaphase. Mob1 only weakly associated with SPBs, Cdc14 was not released from the nucleolus, and cells failed to enter the next cell cycle (Figure 1C-E; Figure 1 – figure supplement 2).
Similar results were obtained when we inactivated the APC/C-Cdc20 by depleting Cdc20. We arrested cells in G1 using alpha factor pheromone and synchronously released them into the cell cycle under conditions that inactivated cohesin and depleted Cdc20. We measured MEN activity by assaying for Cdc15 activity. The protein kinase phosphorylates Nud1 on Threonine 78, which can be detected using a phospho-specific antibody (Figure 1F)\(^{47}\). In mcd1-1 mad1Δ control cells Nud1 T78 phosphorylation occurred during anaphase. Mitotic exit followed as judged by the disassembly of the anaphase spindle. In cells deplete for Cdc20, T78 phosphorylation was greatly delayed and diminished, irrespective of whether or not spindle elongation occurred (Figure 1F). Furthermore, cells failed to exit from mitosis as judged by the persistence of anaphase spindles in cells. We conclude that movement of a SPB into the bud is a prerequisite for MEN activation but spindle elongation is not.

Cdc14 activated by the FEAR network contributes to MEN activation in anaphase.

Degradation of Securin by APC/C-Cdc20 not only triggers cohesin cleavage and hence spindle elongation, it also leads to activation of the FEAR network (Figure 1A). The FEAR network transiently releases Cdc14 from the nucleolus during early anaphase. Previous studies showed that Cdc14 release from the nucleolus mediated by the FEAR network is required for the timely activation of the MEN\(^{19,36,37}\). In the absence of FEAR network function MEN activation is delayed by approximately 15 – 20 minutes. We confirmed these previous findings using the mad1Δ mcd1-1 experimental set-up, because the use of a cohesin mutant ensured delivery of a MEN bearing SPB into the bud to allow for activation of Tem1 by Lte1.

Inactivation of the FEAR network led to a highly consistent 15 minute delay in MEN activation (Figure 2). Upon release from a pheromone induced G1 arrest, overexpression of a non-degradable form of Pds1 caused a 15 minute delay in Nud1T78 phosphorylation and anaphase spindle break-down (Figure 2A). In contrast, arrest of cells in metaphase using the microtubule depolymerizing drug nocodazole completely prevented MEN activation and mitotic exit. The same result was obtained with an additional assay for MEN activity: an IP-kinase assay to measure activity of the Dbf2-Mob1 kinase (Figure 2B)\(^{44}\). A similar 15 minute delay in Nud1 T78 phosphorylation, Dbf2 kinase activation, and anaphase spindle breakdown was observed in cells harboring a temperature sensitive allele of Sepasise (esp1-1) and in two other FEAR network mutants: slk19Δ and spo12Δ bns1Δ (Figure 2C, D; 3A-D; Figure 3 – figure supplement 1).

To determine whether the FEAR network promotes MEN activity by activating Cdc14 we measured MEN activity in cells carrying the temperature sensitive cdc14-3 allele. cdc14-3 cells synchronously released from a pheromone-induced G1 arrest exhibited a 30
minute delay in Nud1 T78 phosphorylation and Dbf2 kinase activation (Figure 3E, F). We conclude that activation of the FEAR network at the metaphase – anaphase transition contributes to the timely activation of the MEN.

High CDK activity inhibits MEN activation

Lack of FEAR network activity in metaphase cannot explain why MEN activation does not occur when a MEN bearing SPB moves into the bud. This is evident when comparing MEN activity of Cdc20-depleted cells with that of cells expressing a non-degradable version of Securin (Figure 4A). Cdc20-depleted cells neither activated the MEN as judged by a lack of Nud1T78 phosphorylation nor exited mitosis as judged by the persistence of anaphase spindles. In contrast, cells in which FEAR network activity was inhibited by expressing a non-degradable version of Pds1 delayed MEN activation and exit from mitosis by only 20 minutes. This result demonstrates that the APC/C-Cdc20 must have an additional role in MEN activation separate from activation of the FEAR network.

We hypothesized that APC-Cdc20’s function in promoting the degradation of S phase and mitotic cyclins could explain why MEN activity is restricted to anaphase. To test this hypothesis we analyzed the consequences of overexpressing a non-degradable form of Clb2 (Clb2dBΔ). We found that overexpression of Clb2dBΔ prevented MEN activation during anaphase as judged by reduced Mob1 association with SPBs (Figure 4B; Figure 4 – figure supplement 1). Exit from mitosis also did not occur as judged by the inability of cells to form a new bud (Figure 4C). Combining overexpression of Clb2dBΔ with the cdc14-3 allele completely abolished Mob1 binding to SPBs (Figure 4B; Figure 4 – figure supplement 1). These data demonstrate that high CDK activity is sufficient to inhibit the MEN.

APC-Cdc20 degradation of Clb2 is essential for MEN activation

The observation that high mitotic CDK activity in anaphase is sufficient to prevent MEN activation suggested that high mitotic CDK activity prevents MEN activation during metaphase. To test this possibility, we examined the consequences of lowering mitotic CDK activity during metaphase. We arrested cells in metaphase without APC/C activity using the temperature sensitive cdc20-1 or cdc23-1 mutations. To lower mitotic CDK activity we introduced the temperature sensitive clb2-VI allele into these strains and examined exit from mitosis. To measure exit from mitosis we analyzed Cdc3 localization. Cdc3 is a component of the septin ring that dissociates from the structure in response to mitotic CDK inactivation during exit from mitosis69. Loss of Cdc3 from the bud neck is thus a sign that mitotic CDKs have been completely inactivated and exit from mitosis has occurred.
Analysis of Cdc3 localization led to the discovery that exit from mitosis depends on both the state of mitotic CDK activity and spindle position. *cdc20-1* single mutants arrested in metaphase and did not exit from mitosis as judged by persistent Cdc3 localization at the bud neck (Figure 5A, D). Next, as a positive control, we examined the effects of deleting *BUB2*, which encodes a subunit of Tem1’s two-component GAP. Deletion of *BUB2* leads to premature MEN activation and, after a significant delay, exit from mitosis in metaphase-arrested cells (reviewed in ref. 70). We confirmed this result and further found that mitotic exit occurred in a partially spindle position independent manner (Figure 5A). 78% of cells in which the spindle migrated into the bud exited from mitosis. In mother cells this number was smaller. Only 36% of cells in which the spindle remained in the mother cell exited mitosis. Interestingly, mitotic exit was delayed in both categories of cells. Time from the onset of budding to exit from mitosis took on average 283 minutes in *cdc20-1 bub2Δ* cells compared to 86 minutes in wild-type cells (Figure 5B). This delay confirms that a MEN inhibitor, presumably CDK activity, prevents MEN activation in a manner that is GAP independent.

We also noted that some *cdc20-1 bub2Δ* cells elongated their spindles prior to cytokinesis (Figure 5C). This observation suggests that activation of APC/C-Cdh1 by the MEN not only causes mitotic cyclin degradation but that APC/C-Cdh1 can also induce Securin degradation. Consistent with this interpretation is the observation that deletion of *BUB2* neither caused exit from mitosis nor spindle elongation in *cdc23-1* mutants (Figure 5A-D). In this mutant both forms of the APC are inactive and neither mitotic cyclins nor Securin can be degraded.

Next, we examined the effects of lowering mitotic CDK activity in the two APC/C mutants. Inactivating the mitotic cyclin Clb2 using the *clb2-VI* allele caused mitotic exit in *cdc20-1* mutants (Figure 5A, D). Importantly, this exit from mitosis depended on spindle position. Mitotic exit only occurred in cells in which the nucleus had moved into the bud during the arrest. A similar dependence was observed when analyzing the ability of *cdc23-1* cells to exit from mitosis (Figure 5A). *cdc20-1* mutants were more likely to undergo mitotic exit than *cdc23-1* mutants (Figure 5A), most likely because *cdc20-1* mutants can still activate the APC/C-Cdh1, whereas *cdc23-1* mutants cannot. We note that unlike in *cdc20-1 bub2Δ* mutants spindle elongation did not occur in either *cdc20-1 clb2-VI* or *cdc23-1 clb2-VI* mutants. Spindle elongation requires mitotic CDK activity71. The *clb2-VI* allele likely lowers mitotic CDK activity below the level necessary to accomplish this task.

To determine whether the exit from mitosis we observed in *cdc20-1 clb2-VI* mutants was due to activation of the MEN, we examined MEN activity in this strain. As mitotic exit did not occur in all cells we developed a live cell assay for MEN activation that was
compatible with co-observation of Cdc3 localization. To selectively measure MEN activity we took advantage of the finding that the MEN kinase Dbf2-Mob1 phosphorylates the NLS of Cdc14, increasing cytoplasmic Cdc14 when the MEN is active\(^{48}\). We fused the C-terminus of Cdc14, which contains the NLS, to a fluorescent reporter (NLS\(_{\text{Cdc14}}\)). Release of NLS\(_{\text{Cdc14}}\) from the nucleus into the cytoplasm depended on MEN activity, validating this novel MEN assay (Figure 5 – figure supplement 1A-C).

Furthermore, in the FEAR network mutant slk19\(^{\Delta}\), export of NLS\(_{\text{Cdc14}}\) from the nucleus was delayed by 20 minutes, which is consistent with the 20 minute delay in MEN activation observed in slk19\(^{\Delta}\) mutants. (Figure 5 – figure supplement 1A – E). Most importantly, the analysis of slk19\(^{\Delta}\) mutants demonstrated that the NLS\(_{\text{Cdc14}}\) localization assay specifically reports on MEN-dependent control of Cdc14. When we compared the release of full-length Cdc14 from the nucleolus with export of the NLS\(_{\text{Cdc14}}\) from the nucleus we found that the time difference between the two was smaller in FEAR network mutants than in wild-type cells (Figure 5 – figure supplement 1F). This is due to the fact that release of full length Cdc14 from the nucleolus only depends on MEN activity in FEAR network mutants, delaying its release. As release of the NLS\(_{\text{Cdc14}}\) is not mediated by the FEAR network, the time delay between the two events is smaller. We conclude that NLS\(_{\text{Cdc14}}\) localization specifically reports on MEN activity.

cdc20-1 single mutants arrested in metaphase did not release NLS\(_{\text{Cdc14}}\) into the cytoplasm when a SPB translocated into the bud which is consistent with their failure to disassociate Cdc3 from the bud neck and to exit from mitosis (Figure 5E, F). Deletion of BUB2 caused release of NLS\(_{\text{Cdc14}}\) into the cytoplasm in metaphase-arrested cells (Figure 5E, F). In cdc20-1 clb2-VI mutants in which exit from mitosis occurred (Cdc3 delocalized from the bud neck), we also observed translocation of NLS\(_{\text{Cdc14}}\) from the nucleus into the cytoplasm (Figure 5E, F), indicating that exit from mitosis in this strain was preceded by MEN activation. Indeed, we found that spindle position dependent exit from mitosis in cdc20-1 clb2-VI cells required MEN activity. cdc20-1 clb2-VI cdc15-2 triple mutants failed to exit mitosis upon translocation of a SPB into the bud (Figure 5A). Together, our results demonstrate that MEN activation requires two signals: (1) movement of a MEN GTPase-bearing SPB into the bud and (2) a lowering of mitotic CDK activity by APC/C-Cdc20 at the onset of anaphase.

**DNA damage inhibits the MEN by additional mechanisms**

In budding yeast, activation of the DNA damage checkpoint causes cell cycle arrest in metaphase\(^{72}\). We therefore asked whether high mitotic CDK activity also prevented MEN activation in this arrest. We used three methods to trigger activation of the DNA damage checkpoint: the temperature sensitive cdc13-1 and cdc9-1 alleles as well as hydroxyurea (HU). CDC13 is required for telomere function. In its absence large amounts of single stranded DNA accumulate at telomeres, which causes activation of the DNA damage
checkpoint\textsuperscript{73–75}. CDC9 mutants fail to join Okazaki fragments, causing double strand breaks to form which in turn activate the checkpoint\textsuperscript{76,77}. HU inhibits ribonucleotide reductase thus causing nucleotide depletion and replication stress.

As in our analysis of cdc20-1 and cdc23-1 mutants we first examined the effects of deleting BUB2 on the DNA damage-induced metaphase arrest. Deletion of BUB2 increased the percentage of cells exiting mitosis in all three DNA damage-inducing conditions (Figure 5G). Presumably, as in cdc20-1 bub2Δ mutants, deletion of BUB2 activates the MEN in the DNA damage checkpoint arrest causing APC/C-Cdh1 to promote exit from mitosis.

Interestingly, unlike cdc20-1 clb2-VI cells, combining the clb2-VI allele with the DNA damage-inducing conditions did not cause more cells to exit from mitosis upon movement of the nucleus into the bud (Figure 5G). This finding indicates that mechanisms in addition to high mitotic CDK activity prevent MEN activation in cells arrested in metaphase due to DNA damage. Indeed, previous reports have shown that DNA damage inhibits the MEN by activating the MEN inhibitory GAP complex, Bub2-Bfa1\textsuperscript{78–80}. Consistently deleting BUB2 allows cdc13-1, cdc9-1 and HU-treated cells to exit from mitosis (Figure 5G). We conclude that at least one mechanism in addition to spindle position and high mitotic CDK activity prevents MEN activation in response to DNA damage. This additional inhibitory mechanism is likely to be activation of the MEN GAP Bub2-Bfa1 by DNA damage.

\textit{Mitotic CDKs inhibit the MEN by phosphorylating components of the kinase cascade}

Previous work had established that the MEN kinase Cdc15 has 7 CDK phosphorylation sites\textsuperscript{81}; Mob1 has 2\textsuperscript{82}. Mutation of these sites to alanine (cdc15-7A and mob1-2A) prevents their phosphorylation by mitotic CDKs.

To determine whether CDK phosphorylation of Cdc15 and/or Mob1 was responsible for restricting MEN activity to anaphase we examined the ability of cdc15-7A and mob1-2A mutants to exit from mitosis in a cdc20-1 metaphase arrest. We found that 21\% of cdc15-7A cdc20-1 double mutants were able to exit from mitosis (Figure 6A). Importantly, as seen when lowering mitotic CDK activity, exit from mitosis depended on movement of a SPB into the bud.

Replacing MOB1 with mob1-2A had a more pronounced effect on exit from mitosis. 52\% of cdc20-1 mob1-2A cells exited mitosis (Figure 6A). Exit from mitosis largely depended on movement of the nucleus into the bud. 52\% of cells with the spindle in the daughter cell exited mitosis, whereas only 6\% of cells exited mitosis in which the spindle remained
in the mother cell (Figure 6A). We hypothesize that a transient, unobserved excursion of a MEN-bearing SPB into the bud activated the MEN in this small fraction of cells.

As observed in cdc20-1 bub2Δ cells, mitotic exit in cdc20-1 cdc15-7A and cdc20-1 mob1-2A was slow and proceeded by spindle elongation (Figure 6B-C). APC/C-Cdh1 likely triggers Pds1 degradation in these cells. Importantly, exit from mitosis in cdc20-1 mob1-2A cells was accompanied by MEN activation. cdc20-1 mob1-2A cells that exited mitosis exported NLS_{Cdc14} from the nucleus into the cytoplasm (Figure 6D; Figure 5 – figure supplement 2).

Combining the cdc15-7A and mob1-2A allele was additive. 80% of cdc15-7A mob1-2A cdc20-1 triple mutants exited from mitosis during the metaphase arrest and cells exited mitosis more rapidly than either of the single mutants (Figure 6A, B). In contrast, only 15% of cells where the nucleus remained in the mother cell exited mitosis, presumably due to unobserved, transient excursions by a MEN-bearing SPB into the bud. We conclude that CDK activity inhibits the MEN during metaphase by phosphorylating multiple MEN kinases. At the onset of anaphase APC/C-Cdc20 attenuates mitotic CDK activity by (1) targeting a fraction of mitotic cyclins for destruction and (2) inducing FEAR-network mediated release of Cdc14 from its inhibitor in the nucleolus. These two mechanisms restrict MEN activation to anaphase, preventing premature exit from mitosis.

**Discussion**

Our results demonstrate that signal integration in the Mitotic Exit Network occurs through the regulation of multiple signaling elements rather than a central signaling hub. Regulation of the GTPase by spindle position and regulation of the downstream kinase cascade by CDK activity creates a logical “AND gate”. MEN activation only occurs when (1) a SPB enters the bud and (2) mitotic CDK activity has decreased. We propose that regulating the MEN signaling cascade in series decreases susceptibility to noise; a downstream dependence on CDK inactivation insulates the MEN against spindle movement. Our work also provides an explanation for why signaling pathways are multi-step processes. Signal integration rather than signal amplification may be the reason for why signal transduction pathways are multi-step processes.

**CDK regulation of the MEN creates anaphase specific ultrasensitivity**

Positive feedback loops, such as the mutual regulation between Cdc14 and the MEN (Figure 7A, B) as well as double-negative feedback loops, such as exist between CDKs and the MEN (Figure 7A, C), create ultrasensitive, switch-like responses (reviewed in ref. 83–85). In MEN regulation this ultrasensitivity is isolated to anaphase because of its dependence on APC/C-Cdc20 activity. APC/C-Cdc20 activates Cdc14 through the FEAR
network and decreases mitotic CDK activity through mitotic cyclin degradation. This
primes the MEN for robust, anaphase specific signaling.

Observations of MEN activation prior to anaphase clarify the importance of the feedback
loops governing MEN activity. When a SPB moves into the bud during metaphase a
slight, but appreciable MEN activation occurs. Small amounts of Mob1 localize to the
SPBs, yet signaling strength (as judged by Mob1 association with SPBs) is weak and
inconsistent, never leading to release of Cdc14 from the nucleolus. This emphasizes the
importance of the FEAR network and mitotic cyclin degradation at the metaphase –
anaphase transition. Without the FEAR network, the Cdc14 positive feedback loop is
disrupted, slowing MEN activation by 20 minutes. Likewise, without APC/C-Cdc20
degradation of Clb2 and Clb5 at the metaphase – anaphase transition, the double-negative
feedback loop between mitotic CDKs and the MEN is too heavily weighted towards
CDK activity, preventing MEN activation.

Signal integration across multiple serial MEN signaling elements.
The initial characterization of MEN regulation focused on the MEN GTPase Tem1.
Tem1 was found to make the MEN responsive to spindle position and DNA
damage. Our work has revealed that MEN regulatory signals control not just
Tem1 but also every subsequent step in the pathway (Figure 7A). The protein kinase
Cdc15 is regulated by the polo-like kinase Cdc5 and CDK activity (ref. 81,88; this
study). The Mob1-Dbf2 kinase is regulated by CDK activity (ref. 82; this study). These
observations raise an important question. Why is the MEN regulated via a serial process
rather than integrating all signals through the GTPase?

The phenotype of the cdc15-7A mobl-2A double mutant indicates that control of the
MEN kinases protects cells from spindle movements into the bud such as occur when
cells arrest in metaphase for prolonged periods of time. It is worth emphasizing that
movement of the nucleus into the bud during metaphase arrests is not merely a byproduct
of cell cycle arrests brought about by mutations in genes critical for anaphase entry. DNA
damage or microtubule – kinetochore attachment defects can arrest cells in metaphase for
hours. Indeed, our live cell analyses show that wild-type cells arrest in metaphase at an
appreciable frequency presumably due to light-induced DNA damage. In 67% of these
arrested cells the spindle moves in the bud. Our data further suggest that even transient
excursions of the spindle into the bud during metaphase could lead to inappropriate Tem1
activation. 15% of cdc15-7A mobl-2A double mutants exited mitosis during the
metaphase arrest without obvious and hence inferred transient movement of the nucleus
into the bud. However, we cannot exclude the possibility that the mitotic exit observed in
these 15% of cells is due to partial loss of spindle position sensing. In either case our
findings indicate that inhibition of the MEN kinase cascade by mitotic CDKs prevents inappropriate mitotic exit prior to anaphase.

Although the phenotype of the cdc15-7A mob1-2A double mutant was similar to that of the clb2-Val mutant, it is possible that mitotic CDKs regulate additional MEN components. Mass spectrometry studies have detected phosphorylation consistent with modification by CDKs on many MEN components and regulators including Bfa1, Cdc5, Cdc14, Lte1, Nud1, Tem1, and Dbf2\(^{89-91}\). The MEN GTPase Tem1 harbors five putative, minimal CDK consensus motifs (S/T-P), but mutation of these sites caused partial loss of Tem1 function (I.W.C. unpublished observations). Other MEN components could however be inhibited by CDKs.

Serial signal integration beyond the Mitotic Exit Network.

The MEN is a member of the Hippo pathway family (Reviewed in ref. \(^{92,93}\)). While the core components of the Hippo pathway are highly conserved across eukaryotes, the signaling cascade appears to be fast evolving as judged by the differences in activating signals and targets across species. In budding and fission yeast, the Hippo pathway regulates cytokinesis\(^ {94}\), in animals it controls cell growth\(^ {95}\). Is serial signal integration a common feature of Hippo signaling despite the fast-evolving nature of the pathway? In the fission yeast MEN equivalent, the Septation Initiation Network (SIN), this may be the case. Like in budding yeast the SIN GTPase Spg1 responds to spindle position\(^ {96}\). In addition, the SIN is inhibited by CDK activity\(^ {97,98}\). Likewise, the mammalian Hippo pathway responds to multiple signals including cell polarity, GPCR signaling, and mechanical signals from the extracellular matrix (reviewed in ref. \(^ {99}\)). The MEN offers a paradigm for how signal integration could occur in mammalian Hippo signaling.

Materials and methods

Yeast strains and growth conditions

All S. cerevisiae strains in this study are derivatives of W303 (A2587) and are listed in Supplementary file 1. Growth conditions are described in the figure legends. Strains were constructed and manipulated as previously described in reference \(^ {100}\).

Plasmid Construction

Plasmids used in this study are listed in Supplementary file 2.

Live Cell Microscopy

The growth conditions for live cell imaging are described in the figure legends. Cells were imaged on agarose pads (2% agarose, synthetic complete (SC) medium containing 2% glucose, unless otherwise noted) affixed to a glass slide and covered with a coverslip. The microscope platform was a DeltaVision Elite (GE Healthcare Bio-Sciences,
Pittsburgh, PA) consisting of an InsightSSI solid state light source, an UltimateFocus hardware autofocus system and a model IX-71, Olympus microscope controlled by SoftWoRx software. A 60X Plan APO 1.42NA objective and CoolSNAP HQ2 camera were used for image acquisition. 6 z sections 1μm apart were acquired and maximally projected.

Image processing was performed using Volocity (PerkinElmer) software. Twenty non-mitotic cells that subsequently move at least one SPB into the bud (Figure 1C-E), reached anaphase (Figure 3B-D; 4B), or exited mitosis (Figure 5E, F, except cdc20-1 which never exit mitosis; Figure 6D) were randomly chosen for analysis. Length of analysis is described in the figure legends. Mob1 intensity was quantified by manually segmenting the SPBs, as identified by Spc42-mCherry localization, and measuring maximum Mob1 intensity within the segmented region [max(SPB)]. Cellular background was subtracted from the maximum intensity at the SPB [max(SPB)-mean(cell)]. Cdc14 release from the nucleolus and NLS\textsubscript{Cdc14} translocation into the cytoplasm was quantified by manually segmenting the cell and measuring the coefficient of variation (CV=stdev/mean) of intensities within the cell as previously described\textsuperscript{101}, normalized and centered as indicated in the figure legends.

*Nud1pT78 immunoblot*

Nud1-3V5 immunoprecipitation, Nud1pT78 detection, and Nud1-3V5 detection were performed as previously described\textsuperscript{47} with the following modifications: Denaturing immunoprecipitations were performed on approximately 15 ODs of cells using 30μl of anti-V5 agarose affinity gel (Sigma). Primary antibodies: Nud1pT78 was detected with a polyclonal antibody (rabbit 41040, 1:1000 dilution)\textsuperscript{47}, Nud1-3V5 was detected with a monoclonal anti-V5 antibody (Invitrogen, 1:2000 dilution).

*Dbf2 kinase assays*

Dbf2 kinase assays were performed as previously described\textsuperscript{44} with the following modifications: Immunoprecipitations were performed with an anti-Myc agarose affinity gel (Sigma). Kinase reactions were incubated for 1 hour with gentle mixing and separated by SDS PAGE. Histone H1 phosphorylation was quantified using the phosphorImaging system. Prior to this analysis, the top part of the gel was cut off the kinase assay gel and processed for Dbf2 Western blot analysis. Proteins were transferred onto nitrocellulose using semi-dry blotting. The membrane was probed with an anti-c-Myc [9E10] antibody (abcam, 1:500 dilution) and imaged using the ECL Plus system (GE Healthcare).

*Fixed cell microscopy*

Indirect in situ immunofluorescence microscopy to detect Tub1 was performed as previously described\textsuperscript{102} using a rat anti-α-tubulin (YOL1/34, oxford biotechnology, 1:100
dilution). An anti-rat Cy3 antibody (Jackson Laboratory) was used as a secondary antibody. Cells were scored on a Zeiss Axio Observer Z1 inverted microscope (Zeiss. Thornwood, NY). ≥100 cells were counted per time point.

**Antibody Information**

Primary antibody and dilution are listed under individual experimental procedures. Secondary anti-mouse and anti-rabbit antibodies were used at a 1:5000 dilution (GE).

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Competing Interests Statement

The authors declare no competing interests.
Figure 1: MEN activation requires APC/C activity.

A. APC/C-Cdc20 cascade:
- Cyclin degradation
- Securin degradation
- FEAR network
- Cdc14 activation
- CDK inactivation
- Chromosome segregation

B. MEN activation:
- Anaphase
  - MEN: OFF
  - MEN: ON
- Metaphase
  - MEN: OFF
  - MEN: ?

C. Graph showing Mob1 intensity at SPBs over time:
- Wild type
- cdc23-1 mcd1-1
- cdc23-1 mcd1-1 maf1Δ

D. Graph showing Cdc14 release over time:
- Time since SPB entered bud (min.)

E. Graph showing % cells budded over time:
- Time (min.)
Figure 1. MEN activation requires APC/C activity.

(A) Control of the metaphase–anaphase transition. APC/C<sup>Cdc20</sup> has three roles in activating the MEN: cyclin degradation (1); activating the FEAR network (2) and triggering chromosome segregation (3). See text for more details.

(B) The zone model explains spatial regulation of the MEN. Anaphase spindle elongation along the mother-bud axis drives one Tem1 bearing SPB into the bud. This removes the MEN GTPase from the inhibitory effect of Kin4 and brings it into contact with the MEN activator Lte1, activating the MEN. If spindle elongation fails to translocate a SPB into the bud the MEN does not become active. During metaphase SPBs can make excursions into the bud. We assayed MEN activity during these pre-anaphase excursions.

(C, D, E) Wild type (A39323), cdc23-1 (A39374), cdc23-1 mcd1-1 (A40568), and cdc23-1 mcd1-1 mad1Δ (A39461) cells containing MOB1-eGFP, SPC42-mCherry, and CDC14-tdTomato were grown at 34°C and imaged every 3 min for 4-6 hours. Curves show mean and stdev. (n=20 cells per condition; see figure supplement 2 for individual traces and sample images). Data were normalized to the average intensity measured during the 15 minutes prior to anaphase. Data were centered at the frame where at least one SPB had moved into the daughter for the first time. This centered timepoint was designated t=3min. (C) Mob1-eGFP intensity at mother and daughter cell SPBs [max(mSPB)+max(dSPB)]. (D) Cdc14 release from the nucleolus measured as coefficient of variation (CV=stdev/mean) of Cdc14 intensity within the cell. (E) Percent cells that exited mitosis and entered a new cell cycle as judged by their ability to form a new bud (rebudding).

(F) MET-CDC20 mad1Δ (A37828), MET-CDC20 mad1Δ mcd1-1 (A37907), and mad1Δ mcd1-1 (A37739) cells containing NUD1-3V5 were arrested in G1 with α-factor (5μg/ml) pheromone at room temperature in synthetic medium lacking methionine. After 3 hours cells were released into pheromone free YEPD medium supplemented with 8mM methionine at 37°C. Methionine was re-added every hour. The percentage of cells with buds (black), metaphase spindles (blue), and anaphase spindles (red) was determined at the indicated times. Nud1 T78 phosphorylation and total Nud1 levels were determined.
Figure 2: Securin degradation and Separease function promote MEN activation.

A

B

C

D

Nocodazole

GAL-PDS1dBA

mad1Δ mcd1-1

esp1-1 mcd1-1

mad1Δ mcd1-1

Time (min.)

% Cells

budding

meta. spindle

ana. spindle

Ddc-3-Myc

Nud2-Y56

p77B/A5 (AU)

Time (min.)

0

30

60

90

120

Time (min.)

0

30

60

90

120

Time (min.)

0

30

60

90

120

Time (min.)

0

30

60

90

120

kinesin-MYc (AU)

esp1-1

mad1Δ mcd1-1

mad1Δ mcd1-1
Figure 2. Securin degradation and Separase function promote MEN activation.

(A, B) GAL-PDS1ΔBA mad1Δ mcd1-l and mad1Δ mcd1-l cells containing (A) NUD1-3V5 (A37904 and A37739) or (B) DBF2-3MYC (A37497 and A37523) were arrested in G1 with α-factor pheromone at room temperature in YEP medium containing raffinose. After 3 hours cells were released into pheromone free YEP medium containing raffinose and galactose at 34°C. A control sample was released from the G1 arrest into medium containing nocodazole (15μg/ml) to arrest cells in metaphase.

(C, D) esp1-l mad1Δ mcd1-l and mad1Δ mcd1-l cells containing (C) NUD1-3V5 (A38079 and A37739) or (D) DBF2-3MYC (A37500 and A37523) were arrested in G1 with α-factor pheromone at room temperature in YEPD medium. After 3 hours cells were released into pheromone free YEPD medium at 37°C. A control sample was released from the G1 arrest into medium containing nocodazole.

(A-D) Percentage of cells with buds (black), metaphase spindles (blue), and anaphase spindles (red) was determined at the indicated times. (A, C) Nud1 T78 phosphorylation and total Nud1 levels were determined. (B, D) Dbf2 kinase activity and Dbf2 protein levels were determined.
Figure 3: The FEAR network promotes MEN signaling by activating Cdc14

A

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B

\[
\text{Wild type} \quad \text{sil19Δ} \quad \text{cdc15-2}
\]

C

\[
\text{Mdt} \quad \text{Gpr} \quad \text{Spg}
\]

D

\[
\text{Cdc4} \quad \text{Mdt} \quad \text{Gpr}
\]

E

Time (min.)

% Cells

- budding
- meta spindle
- ana spindle

F

Time (min.)

% Cells

- budding
- meta spindle
- ana spindle
Figure 3. The FEAR network promotes MEN signaling by activating Cdc14

(A) spo12Δ bns1Δ mad1Δ mcd1-1 (A38127) and mad1Δ mcd1-1 (A37739) cells containing NUD1-3V5 were arrested in G1 with α-factor pheromone at room temperature.

(E, F) cdc14-3 mad1Δ mcd1-1 and mad1Δ mcd1-1 cells containing (E) NUD1-3V5 (A38112 and A37739) or (F) DBF2-3MYC (A37714 and A37523) were arrested in G1 with α-factor pheromone at room temperature. (A, E, F) After 3 hours cells were released into pheromone free medium at 37°C. A control sample was released from the G1 arrest into medium containing nocodazole. The percentage of cells with buds (black), metaphase spindles (blue), and anaphase spindles (red) was determined at the indicated times. (A, E) Nud1 T78 phosphorylation and total Nud1 levels were determined. Note, Nud1 is hyperphosphorylated in cdc14-3 cells. Samples were therefore treated with Lambda Phosphatase to detect the protein (Nud1-V5+Pase, Western). (F) Dbf2 associated kinase activity and Dbf2 protein levels were determined.

(B, C, D) Wild type (A39323), slk19Δ (A39378), and cdc15-2 (A39353) cells containing MOB1-eGFP, SPC42-mCherry, and CDC14-tdTomato were grown at 34°C and imaged every 3 min for 4 hours. Curves show mean and stdev. (n=20 cells; see figure supplement 1 for individual traces). Data were normalized to the average intensity measured during the 15 minutes prior to anaphase. Data were centered at the first frame where anaphase onset (spindle >3μm) was detected. This centered timepoint was designated t=3min. (B) Mob1-eGFP intensity at the daughter bound SPB[max(dSPB)]. (C) Cdc14 coefficient of variation (CV=stdev/mean) within the cell. (D) Percent cells that rebudded, indicating exit from mitosis and entry into the next cell cycle occurred.
Figure 4: Mitotic CDKs antagonize the MEN

A

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| Nud1p7T8 | | | |
| Nud1pV5 | | | |
| % Cells | meta. spindle | ana. spindle | |

B

C

% cells budded

Time since anaphase onset (min.)
Figure 4. Mitotic CDKs antagonize the MEN.

(A) MET-CDC20 mad1Δ mcd1-1 (A37907), GAL-PDS1dΔ mad1Δ mcd1-1 (A37904), and mad1Δ mcd1-1 (A37739) cells containing NUD1-3V5 were arrested in G1 with α-factor pheromone at room temperature in synthetic medium lacking methionine and supplemented with raffinose. After 3 hours cells were released into pheromone free YEP medium containing raffinose, galactose and 8mM methionine at 34°C. Methionine was re-added every hour. The percentage of cells with buds (black), metaphase spindles (blue), and anaphase spindles (red) as well as Nud1 T78 phosphorylation and total Nud1 levels were determined at the indicated times.

(B,C) Wild type (A33715), GAL-CLB2dΔ (A39542), cdc14-3 (A39541), and GAL-CLB2dΔ cdc14-3 (A39540) cells containing MOB1-eGFP and SPC42-mCherry were grown at 34°C in SC medium containing raffinose and galactose and imaged every 3 min for 5 hours. Curves show mean and stdev. (n=20 cells; see figure supplement 1 for individual traces). Data were normalized to the average intensity measured during the 15 minutes prior to anaphase. Data were centered at the first frame where anaphase onset (spindle >3μm) was detected. This centered timepoint was designated t=3min. (B) Mob1-eGFP intensity at daughter bound SPB [max(dSPB)] was determined. (C) Percent cells that rebudded, indicating that exit from mitosis and entry into the next cell cycle had occurred.
Figure 5: Mitotic CDKs prevent MEN activation in metaphase

A

% exit mitosis

B

Time from budding to mitotic exit (min.)

C

% elongated spindle

D

Tub1 Cdc3

E

Release of NLS_5(Cy3) (CFU)

F

Wild type

cdc20-1

cdc20-1 bub2Δ

cdc20-1 cib2-VI

G

% exit mitosis
Figure 5. Mitotic CDKs prevent MEN activation in metaphase.

(A-D, G) The indicated strains containing mCherry-Cdc3 and GFP-Tub1 were grown at 37°C and imaged every 5 minutes for 5 (WT) or 8 (remaining strains) hours.

(A) Spindle position was monitored and cells were apportioned by whether the spindle had entered the daughter cell (daughter) or remained in the mother cell (mother). Mitotic exit was measured by loss of Cdc3 from the bud neck.

(B) Time from bud emergence until mitotic exit for the cells shown in (A).

(C) Percent of cells from (A) that elongated their spindles (>3 μm).

(D) Sample images for (A-C). Cdc3 is shown in red, microtubules in green.

(E, F) Wild type (A40293), cdc20-1 (A40295), cdc20-1 bub2Δ (A40296), and cdc20-1 clb2-VI (A40292) cells containing mCherry-Cdc3, Spc42-mCherry, and NLS<sub>Cdc14</sub>-GFP were grown at 37°C and imaged every 5 minutes for 4 (WT), or 8 (remaining strains) hours. Curves in (E) show mean and stdev. (n=20 cells; see figure supplement 2 for individual traces). Data were normalized to the average intensity measured during the initial 20 minutes of the analysis. Data were centered so that loss of Cdc3 from the bud neck represents t=0. cdc20-1 cells do not lose Cdc3 from the bud neck. We therefore analyzed cells for 2.5 hours after the spindle first moved into the bud. NLS<sub>Cdc14</sub>-GFP localization was measured as coefficient of variation (CV=stdev/mean) within the cell. Sample images are shown in (F). Cdc3 is shown in red, microtubules in green.

(G) Spindle position was monitored and mitotic exit was measured by loss of Cdc3 from the bud neck. 5mg/ml hydroxyurea (HU) was used in indicated samples.
Figure 6: CDK activity inhibits the MEN by phosphorylating Cdc15 and Mob1.

A

% exit mitosis

Cdc15-WT
cdc15-TA
MOB1-WT
mob1-2A
Cdc15-WT
MOB1-WT
mob1-2A
Cdc15-WT
MOB1-WT
mob1-2A

B

Time from budding to mitotic exit (min.)

CDC15-WT
cdc15-TA
MOB1-WT
mob1-2A
CDC15-WT
MOB1-WT
mob1-2A

C

% elongated spindle

Cdc15-WT
cdc15-TA
MOB1-WT
mob1-2A
Cdc15-WT
MOB1-WT
mob1-2A

D

Release of NLS

Wild type
cdc20-1 mob1-2A

Time since loss of Cdc3 at budneck (min.)
Figure 6. CDK activity inhibits the MEN by phosphorylating Cdc15 and Mob1.

(A-C) The indicated strains containing mCherry-Cdc3 and GFP-Tub1 were grown at 37°C and imaged every 5 minutes for 8 hours.

(A) Spindle position was monitored and cells apportioned by whether the spindle entered the daughter cell (daughter) or remained in the mother cell (mother). Mitotic exit was measured by loss of Cdc3 from the bud neck.

(B) Time from bud emergence until mitotic exit for the cells shown in (A).

(C) Percent of cells from (A) that elongated their spindles (>3μm).

(D) Wild type (A40293), or cdc20 mob1-2A (A40292) cells containing mCherry-Cdc3, Spc42-mCherry, and NLS<sub>Cdc14</sub>-GFP were grown at 37°C and imaged every 5 minutes for 4 (WT), or 8 (cdc20-1 mob1-2A) hours. Curves show mean and stdev. (n=20 cells; see Figure 5 – figure supplement 2 for individual traces). Data were normalized to the average intensity measured during the initial 20 minutes of the analysis. Data were centered so that loss of Cdc3 from the bud neck represents t=0. Release of NLS<sub>Cdc14</sub>-GFP was measured as coefficient of variation (CV=stdev/mean) of NLS<sub>Cdc14</sub>-GFP intensity within the cell.
Figure 7. Temporal and spatial signals distribute regulation across multiple MEN components.

(A) The Mitotic Exit Network and its regulators. Direct positive regulators are shown in green, direct negative regulators in red. See text for details.

(B) The MEN and Cdc14 act in a positive feedback loop to make mitotic exit ultrasonic.

(C) CDK and the MEN regulate each other through a double-negative feedback loop isolating mitotic exit ultrasonic sensitivity to anaphase.
Figure 1 – figure supplement 1. CDC15 mutants do not exhibit Kar9 localization and SPB inheritance defects.

(A-D, I, L) Wild type (A40512) and cdc15-as1 (A40524) cells containing an mCherry-TUB1 and KAR9-GFP fusion were treated with 10μM 1-Na-PP1 for the indicated time period at 25°C on agar pads.

(E-H, J, M) Wild type (A40530) and temperature sensitive cdc15-2 (A40529) cells containing the mCherry-TUB1 and KAR9-GFP fusions were heat shocked for the indicated period of time at 37°C on agar pads.

(A, E) Cells were imaged and metaphase cells were identified by spindle morphology. Astral microtubule associated Kar9 intensity was determined for both SPBs in metaphase. The two SPBs in each metaphase cell were placed into one of two categories: SPB with high levels of Kar9 bound to emanating microtubules (strong) or the pole with low levels of Kar9 bound to emanating microtubules (weak). Mean and stdev are shown (n > 90 cells).

(B, F) Quantifications from (A) and (E) were used to create a weak SPB/strong SPB localization ratio in (B) and (F), respectively. Mean, stdev, and results of t-test are shown.

(C, G) Qualitative classification of Kar9 localization for cells quantified in (A) and (E).

(D, H) Sample images of Kar9 localization categories quantified in (C) and (G).

(I, J) Cells were imaged every 10s for 100s. Metaphase cells were identified by spindle morphology and Kar9 localization was quantified using the classifiers described in (H; n > 45 cells).

(K-M) Cells were imaged every 5m for 4h. G1 cells were followed until anaphase and Kar9 intensity was measure on astral microtubules 10 minutes prior to anaphase onset. Mother and daughter bound SPBs were identified during anaphase. Kar9 intensity and Kar9 symmetry index [(dSPB-mSPB)/(dSPB+mSPB)] was determined. Mean, stdev, and results of t-test are shown (n > 60 cells).

(N, O) Wild type (A40559), cdc15-as1 (A40556), or kar9Δ (A40562) cells containing SPC42-mCherry and GFP-TUB1 were treated with 10μM 1-Na-PP1 for 45 minutes at 25°C on agar pads. Cells were then imaged every 15m for 3h. SPB inheritance was determined by the brightness of the Spc42-mCherry signal entering the bud (N; Mean and stdev of three experiments are shown, t-test). Sample images of Spc42-mCherry signal are shown in (O).
Figure 1 – figure supplement 2. Mob1 localization to SPBs and release of Cdc14 from the nucleolus depends on the APC/C.

(A) Sample images. SPBs are marked with white arrowheads. Mob1 localization is shown in green, Spc42 and Cdc14 in red.

(B, C) Traces of 20 individual cells from Figure 1C and D, respectively
Figure 3 – figure supplement 1. Deletion of SLK19 delays MEN activation and Cdc14 release from the nucleolus.

(A, B) Traces of 20 individual cells from Figure 3B and C, respectively. The FEAR network mutant slk19Δ delayed Mob1 localization to the daughter SPB (A) and delayed release of Cdc14 from the nucleolus (B). The MEN mutant cdc15-2 failed to localize Mob1 to the daughter SPB (A) and only transiently released Cdc14 from the nucleolus (B).
Figure 4 – figure supplement 1. Clb2 degradation and Cdc14 released from the nucleolus by the FEAR network activate the MEN.
Related to Fig 4B-C.
Traces of 20 individual cells from Figure 4B. GAL-CLB2ΔΔ and cdc14-3 cells prevented Mob1 localization to the daughter SPB.
Figure 5 – figure supplement 1. NLS\textsubscript{Cdc14} is a live-cell MEN activity reporter.

Related to Figure 5E and Figure 6D.

(A) Representative images of Cdc14 (\textit{Cdc14-eGFP}) and NLS\textsubscript{Cdc14} (\textit{NLS\textsubscript{Cdc14}-TagRFP}) release throughout the cell cycle in wild type (A39895), \textit{slk19A} (A40177) and cells harboring the analog sensitive \textit{cdc15-as1} (A40095) treated with 1-NA-PP1. Arrows indicate the time-point when the nucleus enters the bud.
(B) Quantification of Cdc14 release from the nucleolus and NLS\textsubscript{Cdc14} release into the cytoplasm of cells shown in (A). Release was quantified as the coefficient of variation (CV) of the signal intensity within the cell. Dashed lines indicate the time point when the nucleus enters the bud.

(C) The extent of release of Cdc14 from the nucleolus (left) and NLS\textsubscript{Cdc14} translocation into the cytoplasm (right) in FEAR network (\textit{slk19Δ}) and MEN (\textit{cdc15-as1}) mutants. Relative changes in release is calculated as $\frac{CV_{\text{max}} - CV_{\text{min}}}{CV_{\text{max}}}$. NLS\textsubscript{Cdc14} release depended only on the MEN and not the FEAR network.

(D) Comparison of relative changes in CV $\frac{(CV_{\text{max}} - CV_{\text{min}})}{CV_{\text{max}}}$ for a canonical nuclear localization signal NLSSV40 (2xmCherry-NLSSV40) and NLS\textsubscript{Cdc14} (NLSCdc14-GFP) during cell cycle in Wild type (\textit{CDC15}, A40339) and MEN mutant (\textit{cdc15-as1}, A40371) cells. The observed low level of relative changes in CV for NLSSV40 in both cases and NLSCdc14 in cdc15-as1 is due to nuclear division.

(E) Time of Cdc14 and NLS\textsubscript{Cdc14} release relative to the time the nucleus enters the bud for Wild type and FEAR mutant (\textit{slk19Δ}). The data points are set to a transparency value of 0.2 and thus the shade correlates with number of observations. The dashed line represents the identity line. Both releases were delayed in the FEAR network mutant.

(F) Time delays between maximum release of Cdc14 and NLS\textsubscript{Cdc14} for Wild type and FEAR mutants (\textit{slk19Δ}, \textit{spo12Δ}, \textit{spo12Δbns1Δ}). Red lines represent mean values. The reduced delay (increased correlation) between the two release events in FEAR network mutants is consistent with the interpretation that without the FEAR network both processes are the result of MEN activity.
Figure 5 – figure supplement 2. Clb2 degradation and Mob1 dephosphorylation promote MEN activation.

Related to Figure 5E, F and Figure 6D.

Traces of 20 individual cells from Figure 5E and Figure 6D. In wild type cells diffusion of NLS$_{\text{Cdc14}}$ into the cytoplasm coincides with Cdc3 loss from the bud neck indicating MEN activation. cdc20-1 cells never lost Cdc3 from the bud neck and did not release the NLS$_{\text{Cdc14}}$ into the cytoplasm. cdc20-1 bub2Δ, cdc20-1 clb2-VI, and cdc20-1 mob1-2A cells which lost Cdc3 from the bud neck also released NLS$_{\text{Cdc14}}$. 
Supplementary files.

Supplemental File 1: Yeast strains. Yeast strains used in this study.
Supplemental File 2: Plasmids. Plasmids used in this study.