The yeast nuclear pore complex functionally interacts with components of the spindle assembly checkpoint

Tatiana Iouk,1 Oliver Kerscher,2 Robert J. Scott,1 Munira A. Basrai,2 and Richard W. Wozniak1

1Department of Cell Biology, University of Alberta, Edmonton, Alberta, T6G 2H7 Canada
2Genetics Branch, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD 20889

A physical and functional link between the nuclear pore complex (NPC) and the spindle checkpoint machinery has been established in the yeast *Saccharomyces cerevisiae*. We show that two proteins required for the execution of the spindle checkpoint, Mad1p and Mad2p, reside predominantly at the NPC throughout the cell cycle. They are associated with a subcomplex of nucleoporins containing Nup53p, Nup170p, and Nup157p. The association of the Mad1p–Mad2p complex with the NPC requires Mad1p and is mediated in part by Nup53p. On activation of the spindle checkpoint, we detect changes in the interactions between these proteins, including the release of Mad2p (but not Mad1p) from the NPC and the accumulation of Mad2p at kinetochores. Accompanying these events is the Nup53p-dependent hyperphosphorylation of Mad1p. On the basis of these results and genetic analysis of double mutants, we propose a model in which Mad1p bound to a Nup53p-containing complex sequesters Mad2p at the NPC until its release by activation of the spindle checkpoint. Furthermore, we show that the association of Mad1p with the NPC is not passive and that it plays a role in nuclear transport.

**Introduction**

A defining feature of eukaryotic cells is the encapsulation of their genome by the nuclear envelope (NE)* membrane. Replication of the genome and the regulation of transcriptional activity require the exchange of massive amounts of macromolecules between the cytoplasm and the nucleoplasm across the NE. This transport occurs through channels formed by nuclear pore complexes (NPCs). These highly conserved structures are composed of multiple repetitive subunits that form an elaborate eightfold symmetrical structure (for review see Rout and Aitchison, 2001).

In budding yeast, the NPC is believed to be composed of ~30 nucleoporins, or nups (Rout et al., 2000). 12 of these contain phenylalanine-glycine repeats. These “FG-nups” play a direct role in transport through the NPC by binding a family of proteins (termed karyopherins) that carry cargo molecules through the NPC (for reviews see Wozniak et al., 1998; Wente, 2000; Macara, 2001; Rout and Aitchison, 2001).

Several observations also point to a role for specific nucleoporins in chromosome segregation that may be independent of their functions in mediating transport through the NPC. Most notably in yeast, we have shown that strains containing mutations in the gene encoding Nup170p, an evolutionarily conserved nup, exhibit a chromosome loss phenotype. Moreover, in these mutants, transcription of a reporter gene through an assembled kinetochore was detected, suggesting a defect in kinetochore integrity (Kerscher et al., 2001). These defects were not seen in deletion mutants of *NUP157*, a paralogue of *NUP170*, suggesting they are specifically linked to *NUP170* and not a general defect in nuclear transport.

Other links between chromosome segregation and nups have been uncovered by two localization studies conducted in vertebrate cells. In these papers, three nucleoporins, Nup107p, Nup133p (Belgareh et al., 2001), and Nup358 (RanBP2; Joseph et al., 2002) were found to be associated with kinetochores during mitosis. The functional relevance of recruiting nups to the kinetochores during mitosis is not clear. However, a clue may come from another work showing that two human proteins, hsMad1p and hsMad2p, are associated with the NPC during interphase (Campbell et al., 2001). These proteins are members of an evolutionarily con-
served group of spindle checkpoint mediators that were first identified in *Saccharomyces cerevisiae* and include Mad1p, Mad2p, Mad3p, Bub1p, Bub2p, Bub3p, and Mps1p (for review see Millband et al., 2002). Subcellular localization studies in *Xenopus laevis* and humans have shown that Mad1p and Mad2p localize to kinetochores before chromosome alignment at the metaphase plate (Chen et al., 1996, 1999; Li and Benezra, 1996). These proteins and other checkpoint mediators transmit a signal that prevents anaphase entry and chromosome segregation by inhibiting the anaphase-promoting complex/cyclosome from targeting key proteins for ubiquitin-mediated proteolysis until all chromosomes have formed functional spindle attachments, thus preventing aneuploidy (for reviews see Hardwick, 1998; Shah and Cleveland, 2000; Hoyt, 2001). In vertebrates, a key player in this process is a complex containing Mad3p (BubR1), Bub3p, Cdc20p, and perhaps Mad2p, that inhibits the anaphase-promoting complex in early mitosis and during checkpoint activation (Sudakin et al., 2001; Tang et al., 2001; Fang, 2002). This complex in its active form could also be isolated from interphase cells (Sudakin et al., 2001), suggesting it is stored, perhaps at the NPC, in preparation for its role during mitosis.

In *S. cerevisiae*, little is known about the subcellular distribution of the checkpoint proteins or how their dynamic associations with kinetochores and possibly NPCs influence their function. In this paper, we begin to address this question by focusing on two checkpoint proteins, Mad1p and Mad2p. We show that both Mad1p and Mad2p are associated with NPCs through a subcomplex of nups, consisting of Nup53p, Nup59p, Nup157p, and Nup170p (termed the Nup53p-containing complex; Marelli et al., 1998). On activation of the spindle checkpoint, distinct changes are detected in the molecular interactions between components of the Nup53p-containing complex, Mad1p, and Mad2p that lead to the release of Mad2p, but not Mad1p, from the NPC and the subsequent recruitment of Mad2p to kinetochores. Biochemical and genetic data are presented that demonstrate the significance of these interactions both in checkpoint and NPC functions. These findings represent the first report that the significance of these interactions both in checkpoint and NPC functions. These findings represent the first report that the significance of these interactions both in checkpoint and NPC functions.

**Results**

**Mad1p and Mad2p are associated with *S. cerevisiae* NPCs**

Mad1p and Mad2p are members of a group of at least seven conserved yeast proteins that are critical for executing a mitotic checkpoint in response to kinetochore and spindle integrity defects. We have investigated the subcellular localization of these two proteins by attaching a GFP tag to the COOH terminus of the endogenous protein. Three observations suggest that the Mad1-GFP and Mad2-GFP proteins are functional in checkpoint control. First, cells expressing these proteins grew at similar rates to isogenic wild-type (WT) cells in the presence of the microtubule-depolymerizing drug benomyl (Fig. 1 A). This was in contrast to strains containing null mutations in *MAD1* or *MAD2* (Fig. 1 A; *mad1Δ* and *mad2Δ*), which exhibited a severe growth deficiency due to a defect in mitotic checkpoint arrest. Second, Mad1-GFP, but not Mad2-GFP, was hyperphosphorylated in a manner similar to the WT protein when the spindle...
checkpoint was activated by the microtubule-destabilizing drug nocodazole (Fig. 1 B; for review see Hardwick and Murray, 1995). Finally, chromosome segregation defects observed in mad1Δ and mad2Δ mutants were not detected in the MAD1-GFP– and MAD2-GFP–containing strains (unpublished data).

Fluorescence microscopy of asynchronously growing cells revealed that Mad1-GFP and Mad2-GFP were predominately visible along the NE in a distinct punctate pattern reminiscent of proteins associated with NPCs (Fig. 1 C). Mad2-GFP also exhibited low levels of a diffuse signal throughout both the cytoplasm and the nucleoplasm. To confirm that the NE localization of Mad1-GFP and Mad2-GFP reflects their association with NPCs, we examined their distribution in a nup120Δ strain where NPCs cluster within a single region of the NE and, as a consequence, signals derived from NPC-associated proteins can be discriminated from other NE proteins (Aitchison et al., 1995a). In nup120Δ strains, both the Mad1-GFP and Mad2-GFP signals were clustered within a single patch of the NE, further supporting the conclusion that they are associated with the NPC (Fig. 1 C). Consistent with these data, subcellular fractionation experiments showed that Mad1-GFP was enriched in nuclear and NE fractions (Fig. 1 D). Both of these fractions also contained Mad2p; however, significant levels of Mad2p were also present in a cytosolic fraction (Fig. 1 D).

Spindle checkpoint activation induces the release of Mad2p, but not Mad1p, from NPCs and its accumulation at kinetochores
Numerous studies have shown that the mammalian orthologues of Mad1p and Mad2p are recruited to kinetochores during mitosis (Chen et al., 1996; Gorbsky et al., 1998). To explore whether Mad1p and Mad2p exhibit similar dynamics in yeast cells, we monitored the localization of Mad1-GFP and Mad2-GFP in an asynchronously growing cell population. We observed that the bulk of both Mad1-GFP and Mad2-GFP remained associated with the NPCs throughout the cell cycle (unpublished data), including mitosis (Fig. 2 A, representative images), with no detectable redistribution of either protein to kinetochore clusters (Fig. 2, B and C, Log) as judged by comparison to the CFP-tagged kinetochore protein Mtw1p (Goshima and Yanagida, 2000).

Vertebrate homologues of Mad1p and Mad2p are recruited to kinetochores during mitosis. We reasoned that in yeast their association with kinetochores might depend on activation of the spindle checkpoint. To test this, we examined the distribution of Mad1-GFP or Mad2-GFP in cells expressing MTW1-CFP after nocodazole treatment. As shown in Fig. 2 B, checkpoint arrest had no effect on the NPC localization of Mad1-GFP and little or no overlap was observed with the Mtw1-CFP signal. In contrast, checkpoint activation had a striking effect on Mad2-GFP. In nocodazole-arrested cells, Mad2-GFP was no longer visible at the NPC and instead colocalized with Mtw1-CFP at the kinetochores in >94% of cells that showed signals from both proteins (Fig. 2 C). Mad2-GFP was not detected at spindle pole bodies under these same conditions as judged by colocalization with the spindle pole body protein Bub2-CFP (unpublished data).
These observations led us to investigate whether Mad1p and Mad2p could be detected in association with Nup170p and Nup157p after their purification from disassembled NPCs. For these experiments, protein A (pA)–tagged versions of either nup (Nup157-pA or Nup170-pA) were purified from nuclear extracts derived from either logarithmically growing or α-factor–arrested cultures. Associated proteins were eluted with a step gradient of increasing MgCl₂. Results from α-factor–arrested cultures are shown in Fig. 3, and are similar to those obtained with logarithmically growing cells (unpublished data). Consistent with our previous results, Nup170p was associated with Nup53p (Fig. 3 A; Nup170-pA, α-factor) (Marelli et al., 1998), Nup53p was also present in eluates from Nup157-pA (Fig. 3 A). Moreover, we detected Mad1p and Mad2p in association with both Nup170p and Nup157-pA. By comparison, neither protein was detected in experiments using strains lacking a pA tag or containing another tagged nup, Nup60-pA (Fig. 3 B), which interacts with Nup2p (Dilworth et al., 2001; Fig. 3 B).

Because Nup53p is associated with both Nup157p and Nup170p, we also tested whether Mad1p and Mad2p could be detected in this complex by immunoprecipitating Nup53p from cells expressing MAD1-GFP or MAD2-GFP. As shown in Fig. 3 C (Nup53 IP, α-factor), both the Mad1-GFP and Mad2-GFP proteins were detected in association with Nup53p. Moreover, reciprocal immunoprecipitations performed with anti-GFP antibodies also detect Nup53p and Mad2p bound to Mad1-GFP (Fig. 3 D).

Changes in molecular interactions between the Mad1p–Mad2p complex and the NPC on spindle checkpoint activation

The activation of the spindle checkpoint leads to the release of Mad2-GFP from NPCs and its recruitment to kinetochores (Fig. 2 B), but does not affect the NPC association of Mad1p (Fig. 2 B) or Nup53p, Nup157p, and Nup170p (unpublished data). To investigate the biochemical basis for these events, we analyzed the effects of spindle checkpoint activation on interactions between these proteins. As predicted, after checkpoint activation induced by either nocodazole (Fig. 3 A, noc) or benomyl (unpublished data), Mad2p was no longer associated with affinity-purified Nup157pA, Nup170pA, or Nup53p (Fig. 3, A and C). In contrast, Mad1p remained associated with Nup53p; however, neither Mad1p nor Nup53p were detected in association with Nup170-pA or Nup157-pA (Fig. 3, A and C, noc). These results suggest that a complex containing Nup53p and Mad1p is no longer bound to Nup170p and Nup157p. We excluded the possibility that these were nonspecific effects caused by nocodazole or benomyl because the mere addition of benomyl to either factor (Fig. 3 A, noc) or nocodazole (Fig. 3 A, noc) did not induce these changes (unpublished data). Moreover, checkpoint activation did not affect the association of Nup60p or Nup170p with Mad2p, even though Nup2p appears to be modified in these cells (Fig. 3, A and B), possibly by phosphorylation (Ficarro et al., 2002).

Because strains lacking individual members of the Nup53p–Nup170p–Nup157p complex are viable, we examined the localization of Mad1-GFP and Mad2-GFP in

Mad1p and Mad2p are associated with a specific subset of nucleoporins

To further understand the functional significance of the associations of Mad1p and Mad2p with the NPC and the dynamics of Mad2p’s localization to kinetochores, we focused on identifying nups that anchor Mad1p and Mad2p to the NPC. Clues as to the identity of these nups came from two previous observations. First, it was recently demonstrated that mutations that affect the function of Nup170p lead to defects in chromosome segregation and kinetochore integrity (Kerscher et al., 2001). Second, a paralogue of Nup170p (Nup157p) was shown to interact with Mad2p in a genomewide two-hybrid screen (Uetz et al., 2000).

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the deletion mutants. The localization of Mad1-GFP to the NPC in strains lacking NUP170 (nup170Δ), NUP157 (nup157Δ), or NUP59 (nup59Δ), a gene encoding a nup structurally similar to Nup53p, was not altered in asynchronous or nocodazole-treated cells (Fig. 4 A). In contrast, asynchronous cultures of cells lacking Nup53p (nup53Δ) ex-
hibited reduced levels of NE-associated Mad1-GFP (Fig. 4 A). This effect was further exacerbated by nocodazole treatment where >80% of arrested cells exhibited weak or barely visible amounts of Mad1-GFP at the NPCs.

As noted above, in WT strains, Mad2-GFP is localized to the NPC in asynchronous cultures (Fig. 1 C and Fig. 2 A) and to kinetochores on checkpoint activation. A similar localization pattern for Mad2-GFP was observed in a nup170Δ strain (Fig. 4 B). However, in a nup53Δ strain, as was the case with Mad1-GFP, the levels of Mad2-GFP at the NPC were visibly reduced in asynchronous cultures (Fig. 4 B). Moreover, when this strain was treated with nocodazole, the accumulation of Mad2-GFP at kinetochores was attenuated, with many cells (~63%) showing barely visible or nondetectable kinetochore signals. This effect did not appear to be a function of altered kinetochore localization as the signal intensity of Mtw1-CFP in a nup53Δ strain was the same as observed in WT cells (unpublished data).

The Mad1p–Mad2p complex associates with the NPC through Mad1p
We investigated whether Mad1p, Mad2p, or both proteins interacted with the Nup53p-containing complex. To do this, Nup53p was immunoprecipitated from WT, mad1Δ, and mad2Δ strains, and the eluates were probed with antibodies directed against Mad1p and Mad2p. As shown in Fig. 5 A,
Genetic interactions between MAD1 and MAD2 and nucleoporin genes

We investigated genetic interactions between MAD1 and MAD2 and four nup genes (NUP170, NUP157, NUP53, and NUP59) to further assess the functional significance of the association of Mad1p and Mad2p with the NPC. Initially, we assayed the growth characteristics of each single deletion strain on rich media at 27 and 37°C. Our analysis revealed that all the strains showed growth characteristics similar to the WT strain with the exception of the nup170Δ strain, which grew slower at both temperatures (Fig. 6 A).

Each of the nup null haploids was crossed with the mad1Δ and mad2Δ deletion strains. We tested the growth characteristics of the haploid double deletion strains, and all of these strains showed similar growth characteristics (Fig. 6 A). Exceptions were the nup170Δ mad1Δ, nup170Δ mad2Δ, and nup59Δ mad2Δ deletion strains, which grew slower than the parents and exhibited impaired growth at 27°C and either slow (nup170Δ mad2Δ) or barely detectable (nup170Δ mad1Δ) growth at 37°C.

The benomyl sensitivity of various null mutants was also tested. As expected, benomyl inhibited growth of the mad1Δ and mad2Δ strains (Fig. 6, A and B). However, null mutants of NUP170, NUP157, NUP53, and NUP59 grew better than WT cells on benomyl-containing plates (Fig. 6, A and B). This was also the case for the viable double null strains nup59Δ nup53Δ, nup53Δ nup157Δ, and nup59Δ nup157Δ (unpublished data). Resistance to benomyl appears to be specific for these nups as several other nup null mutants, including two (nup188Δ and pom152Δ) that genetically interact with members of the Nup53p-containing complex (Aitchison et al., 1995b; Marelli et al., 1998), were not resistant (Fig. 6 B).

To determine whether the benomyl resistance of the nup null mutants required a functional checkpoint, we examined the growth of the mad/nup double mutants on benomyl-containing plates. As shown in Fig. 6 A, the mad1Δ and mad2Δ deletions eliminated the benomyl-resistant phenotype of the nup nulls. Most of the double null strains exhibited growth characteristics similar to the mad1Δ and mad2Δ mutants. The nup170Δ mad2Δ and nup59Δ mad2Δ strains were somewhat more resistant to benomyl than the mad2Δ mutant, with the nup170Δ mad2Δ strain growing similar to WT cells. From these analyses, we conclude that the increased benomyl resistance of the tested nup deletions is dependent on Mad1p and Mad2p. Thus, these genetic analyses suggest an important functional interplay between Mad1p, Mad2p and Nup53p, Nup59p, Nup170p, and Nup157p in spindle dynamics.

Nup53p is required for the hyperphosphorylation of Mad1p in nocodazole-treated cells

In response to checkpoint activation, Mad1p is hyperphosphorylated. Because Nup53p appears to play a role in anchoring Mad1p to the NPC during checkpoint activation, we examined the effects of removing Nup53p on the nocodazole-induced hyperphosphorylation of Mad1p. WT, nup53Δ, and nup170Δ strains containing Mad1-GFP or Mad2-GFP were treated with or without nocodazole. In the presence of nocodazole, each of these strains arrested with a 2C DNA content, suggesting that the spindle checkpoint was functional (Fig. 7 A). As shown in Fig. 7 B, a reduction in the mobility of Mad1-GFP, diagnostic of its phosphorylation, was visible in arrested samples from WT and nup170Δ...
strains. However, under the same conditions, no change in the mobility of Mad1-GFP was seen in the nup53Δ/H9004 strain, suggesting that it was not hyperphosphorylated in nocodazole-arrested cells. These results suggest that the Nup53p-dependent association of Mad1p with the NPC is critical for its hyperphosphorylation.

Mad1p plays a role in NPC function

The association of Mad1p with the NPC raises the question of whether it plays a role in nuclear transport. To address this, we used an in vivo nuclear import assay developed by Shulga et al. (1996) to evaluate the effects of MAD1 deletion on transport. In this assay, a nuclear reporter is allowed to equilibrate across the NE by treatment of cells with inhibitors of glycolysis and mitochondrial respiration. After their removal and reinitiation of transport, the relative import rates can be assessed by counting the number of cells showing nuclear accumulation of the reporter at various time points. We examined the import of a reporter protein, Pho4-GFP that is imported by karyopherin Kap121p. Kap121p has been shown to specifically interact with the Nup53p-containing complex. As shown in Fig. 8, WT and mad2Δ strains exhibited similar rates of import, with ~40% of the cells showing nuclear accumulation of the Pho4-GFP reporter after ~6 min. Surprisingly, however, the mad1Δ and nup170Δ strains required 13 and 16 min, respectively. This reporter accumulation defect was further exacerbated in the mad1Δ nup170Δ strain, where 23 min were required for 40% of the cells to show a nuclear accumulation of the reporter. Similar results were also obtained when cells were first incubated at 37°C for 3 h before performing the assay (Fig. 8 B).

The nup170Δ and mad1Δ deletions also appear to affect the stability of the Nup53p-containing complex. When we examined the localization of Nup53-GFP in the mad1Δ, nup170Δ, and nup170Δ mad1Δ strains at 27°C, Nup53-GFP was clearly associated with the nuclear periphery (Fig. 9). However, after shifting to 37°C for 3 h, the levels of Nup53-GFP associated with the NE were decreased to barely detectable levels in each strain. This effect was specific, as temperature shift had no effect on the localization of two other nups, Nup49-GFP and Nup188-GFP. Moreover, shifting WT or mad2Δ cells to 37°C had no effect on the localization of Nup53-GFP.

Discussion

We have identified a functional link between components of the S. cerevisiae NPC and the mitotic checkpoint machinery. By a variety of criteria, we have shown that the checkpoint proteins Mad1p and Mad2p reside largely at the NPC throughout the cell cycle. Their association with the NPC occurs through a previously identified nup subcomplex containing Nup53p, Nup59p, and Nup170p (Marelli et al.,
The interactions between these nups and mads were detected by reciprocal affinity purification of the nup complex, Mad1p (Fig. 3), or Mad2p (unpublished data). Our data are consistent with a model in which the association of Mad2p with these nups is dependent on Mad1p (Fig. 10). In the absence of Mad1p, Mad2p fails to associate with NPCs and is dispersed throughout the cell. Nup53p plays an important role in either directly or indirectly tethering the Mad1p–Mad2p complex to the NPC. Removal of Nup53p causes a reduction in levels of Mad1p and Mad2p associated with NPCs (Fig. 4), but no significant changes in the cellular levels of either protein (unpublished data). It remains to be determined what nups, in the absence of Nup53p, would support the reduced levels of Mad1p and Mad2p at the NPC. One explanation is that their association is partially maintained by lower affinity interactions with other members of the Nup53p-containing complex. However, this remains an open question because null mutations of NUP59, NUP157, and NUP170 (Fig. 4) have no readily visible effects on the NPC association of Mad1p. Another candidate is the karyopherin Kap121p, which is also associated with Nup53p-containing complex. However, we fail to detect any effect on the localization of Mad1p and Mad2p in strains containing temperature-sensitive alleles of KAP121 (Anderson, A., and R. Wozniak, personal communication).

Our observation that S. cerevisiae Mad1p and Mad2p remain associated with NPCs throughout the cell cycle differs from the events described in vertebrate cells. Recent data have
shown that vertebrate homologues of these proteins are also associated with NPCs during interphase (Campbell et al., 2001). However, in these cells, upon entering mitosis, the NE and NPCs are disassembled and Mad1p and Mad2p accumulate at unattached kinetochores during prometaphase. This situation does not occur in \textit{S. cerevisiae} where the NE and NPCs remain intact during mitosis. Moreover, after replication of centromeric DNA, kinetochores are assembled and rapidly engaged by microtubules (for review see Winey and O'Toole, 2001). This may partially explain why Mad1p and Mad2p remain at the NPC during mitosis. Consistent with these predictions, only on activation of the spindle assembly checkpoint is Mad2p released from the NPCs (Fig. 2). In contrast, the bulk of Mad1p remains at the NPC and we fail to detect a discernible accumulation of Mad1p at the kinetochores. It is possible that a portion of Mad1p is also recruited to kinetochores but that it is either below the level of detection, obscured by the NPC signal, or its association with the kinetochores is transient, with Mad1p being quickly recycled back to the NPCs.

In addition to the release of Mad2p, checkpoint arrest induced by nocodazole also results in profound effects on the molecular interactions between members of the Nup53p-containing complex and Mad1p–Mad2p. In nocodazole-arrested cells, Nup53p, Mad1p, and Mad2p are no longer detected in association with Nup157p or Nup170p (Fig. 3). These changes are accompanied by the phosphorylation of Nup53p (Marelli et al., 1998; unpublished data) and Mad1p (Fig. 3; Hardwick and Murray, 1995). However, Nup53p and Mad1p remain associated, and this interaction is likely important for maintaining WT levels of Mad1p at the NPC after spindle checkpoint activation (Fig. 4). By analogy to higher eukaryotes where extensive changes in protein–protein interactions between nups occur during mitosis, these experiments suggest that distinct molecular rearrangements also occur within the yeast NPC. However, in yeast, these specific changes do not lead to NPC disassembly. Ourselves and others have not observed changes in the NPC localization of any nups during mitosis, including those that are part of the Nup53p-containing complex (Copeland and Snyder, 1993; Aitchison et al., 1995b; Marelli et al., 1998; Kerscher et al., 2001). We propose that in yeast, specific changes in protein–protein interactions occur during mitosis that alter the functional properties of the NPC, including its association with the checkpoint machinery.

Several observations suggest that the association of the Mad1p–Mad2p complex with the NPC plays an important role in the function of these checkpoint proteins and the NPC. We have shown that the checkpoint-induced hyperphosphorylation of Mad1p does not occur in the absence of Nup53p, suggesting that the physical association of Mad1p with Nup53p promotes the phosphorylation of Mad1p, an event that is believed to be mediated by the kinase Mps1p in response to spindle damage (Hardwick et al., 1996). This observation reiterates that the phosphorylation of Mad1p is not required for spindle checkpoint function (Farr and Hoyt, 1998), as the \textit{nup53Δ} strain does not exhibit a readily detectable checkpoint defect, and raises the question of whether phosphorylation of Mad1p plays a role in NPC function.

The association of Mad2p with the NPC is dependent on Mad1p and consistent with this idea, both proteins show a decreased association with the NPC in asynchronous cultures of a \textit{nup53Δ} strain (Fig. 4). We also detected a decrease in kinetochore associated Mad2p in the \textit{nup53Δ} strain after checkpoint activation. Because the cellular levels of Mad1p are not altered in the \textit{nup53Δ} strain, these results suggest that the association of the Mad1p–Mad2p complex with the NPC is an important prerequisite for the association of Mad2p with the kinetochores. Moreover, our results would suggest the checkpoint functions of Mad2p may not be tightly linked to the amount of Mad2p bound to kinetochores, as the \textit{nup53Δ} strain exhibits no checkpoint defects.

Because Nup53p and Mad1p do not appear to leave the NPC or accumulate at the kinetochores during checkpoint activation, it seems unlikely that they play a direct role in the association of Mad2p to the kinetochores. A role of Mad1p and Nup53p in this process could be explained if we consider a model in which the NPC acts as a platform for regulating the assembly of checkpoint complexes that then associate with kinetochores. Our data, showing that Mad2p (but not Mad1p) is present in a cytoplasmic fraction, are consistent with the idea that a free pool of Mad2p exists in the cytoplasm and that formation of the Mad1p–Mad2p complex may occur at the NPC. Recent reports also place \textit{Schizosaccharomyces pombe} Mad2p at the nuclear periphery (Ikuh et al., 2002). It would also seem possible that the formation of other complexes that have been shown to be dependent on Mad1p, including, for example, the Mad2p–Mad3p–Bub3p–Cdc20p complex (Hardwick et al., 2000, Fraschini et al., 2001), could occur at the NPC. Such complex formation involving Mad2p could contribute to its function at kinetochores. Similar events may instead occur at kinetochores in vertebrate cells. For example, Chung and Chen (2002) have recently shown that a Mad1p-free pool of Mad2p is required for checkpoint function, and that this pool may cycle through a kinetochore-bound Mad1p intermediate. Conceptually, one could envision that these latter events occur at the NPC in yeast. It is possible that in vertebrates, kinetochore-bound Mad1p may also be associated with NPC components that are recruited there after NE disassembly, perhaps as defined subcomplex similar to that observed in yeast. This idea is supported, in theory, by recent data showing that several NPC proteins are detectable at kinetochores after disassembly of the NPCs during mitosis (Belgareh et al., 2001).

It still remains to be determined whether the interactions between the Nup53p-containing complex and Mad1p and Mad2p are critical for their checkpoint functions or whether this association plays another role, such as regulating the level of the checkpoint response. The functional redundancy between members of the Nup53p-containing complex makes this difficult to test directly. However, a potential functional link is the benomyl-resistant phenotype of the nup null mutants, which is dependent on a functional spindle checkpoint, as the deletion of \textit{MAD1} or \textit{MAD2} suppressed this phenotype (Fig. 6). The mechanistic basis for this phenotype is not clear, but one possibility is that deletion of any one of its members alters the ability of the Nup53p-containing complex to regulate the level of the checkpoint response. The
The benomyl resistant phenotype of the nup mutants could reflect an up-regulation of the checkpoint response that prolongs mitotic arrest and increases cell survival in the presence of elevated levels of benomyl. Alternatively, the benomyl resistance of these mutants may reflect a separate, as yet undefined, role for these nups in regulating spindle dynamics.

Our data also support the idea that Mad1p plays an active role in NPC function. Import assays using a reporter protein imported by Kap121p show that both the mad1Δ and mad1Δ nup170Δ strains exhibit import defects (Fig. 8). The functional basis for this defect remains to be determined, as does the extent to which other karyopherin-mediated pathways are affected. One possibility is that the function of Mad1p is linked to Nup170p and its role in establishing the NPC sets the stage for our further understanding of genome stability in model organisms and humans.

Materials and methods
Yeasts, strains, and plasmids
Media for yeast growth and sporulation were as described previously (Adams et al., 1997) except where indicated. Benomyl-containing plates were used for subsequent crosses. Strains exhibit import defects (Fig. 8). The functional basis for this defect remains to be determined, as does the extent to which other karyopherin-mediated pathways are affected. One possibility is that the function of Mad1p is linked to Nup170p and its role in establishing the NPC sets the stage for our further understanding of genome stability in model organisms and humans.

Production of NUP and MAD deletions
Unless otherwise noted, complete chromosomal deletions were constructed in WT strains DF5α, DF5α, or DF5. Deletions were confirmed by PCR and marker segregation in subsequent tetrad analysis.

Deletions of nup and checkpoint genes were produced by two similar PCR-mediated gene deletion techniques (Baudin et al., 1993). In the first technique, we used a PCR product derived from 40 bp of sequences immediately upstream of the start and downstream of the stop codon of the gene to be deleted and 20 bp of sequence homologous to pRS303 (HIS3) or pRS400 (KAN) (Sikorski and Hieter, 1989; Brachmann et al., 1998) immediately adjacent to the vector selectable marker. The second technique utilizes genomic DNA of an existing deletion strain to PCR amplify a deletion cassette module containing ~200 bp upstream of the start and downstream of the stop codon of the deleted gene of interest plus the deletion marker.

The NUP170 ORF was replaced with the HIS3 marker in the DF5α strain (YMB1482) and with the KAN marker in the strain YMB1451. Heterozygous mad1Δ::KAN/MAD1 (YMB1488) and mad1Δ::HIS3/MAD2 (YMB1496) deletions were made in diploid WT strain DF5 using a mad1Δ::KAN strain (YFS1120) provided by F. Spencer, The Johns Hopkins School of Medicine, Baltimore, MD) or a mad2Δ::HIS3 strain (YKH447; provided by K. Hyland and P. Hieter, University of British Columbia, British Columbia, Canada) to PCR amplify the respective deletion module. The resulting strain mad1Δ::KAN/MAD1 (YMB1488) was transformed with a MAD1/URA3 plasmid (pKH130; Hardwick and Murray, 1995), and mad2Δ::HIS3/MAD2 (YMB1498) was transformed with a MAD2/URA3 containing plasmid pCD2; Warren et al., 2002). PK1130 and pCD2 are gifts from F. Spencer. The diploid strains were sporulated and the haploid deletion mutants (YMB1908 and YMB1911) and mad2Δ::HIS3 strains (YMB1900 and YMB1906) were used for subsequent crosses.

For double deletion mutants, mad1Δ::KAN (YMB1908 and YMB1911) or mad2Δ::KAN (YMB1900 and YMB1906) was mated to nup170Δ::HIS3 (YMB1484), nup157a::URA3 (NP157–21), nups3::HIS3 (from NP53/ NP157–21), and nups157::HIS3 (from NP9–23). Haploid meiotic progeny of the diploids was analyzed. Similarly, nup170Δ::URA3 MAD1-GFP (NP12014) and nup157-2::URA MAD2-GFP (NP11202M) haploid strains were derived from diploids made by crossing NP120–25–4 with M1GFP or M2GFP, respectively. Strains with nup gene deletions containing MAD1-GFP or MAD2-GFP are described below.

Construction of tagged MAD1, MAD2, and MTW1 genes
MAD1 and MAD2 were tagged with GFP after their last amino acid codon using an integrating PCR-based transformation procedure. Primers and the GFP/HIS5 template plasmid pGFP (Wigge et al., 1998) were supplied by Dan Burke (University of Virginia, Charlottesville, VA). In brief, GFP, and the HIS5 marker were PCR amplified from plasmid pGFP using a sense primer containing a region of the MAD1/MAD2 just before the termination codon and an antisense primer containing a region of MAD1/MAD2 just past the termination codon. PCR products were transformed into a WT strain (YPH728) and His+ transformants were screened for in-frame fusions of MAD1-GFP and MAD2-GFP by PCR and Western blot analysis. Strains MAD1-GFP/HIS5 (YMB1299) and MAD2-GFP/HIS5 (YMB1296) were used for subsequent studies.

For the examination of Mad1p-GFP protein in nup deletion mutants, a MAD1-GFP/HIS5 module (from strain YMB1299) was PCR-amplified and transformed into the WT strain DFS to generate MAD1-GFP/HIS5 strains (YMB2018 or YMB2020). Subsequently, these MAD1-GFP/HIS5 strains were crossed with NP53/HIS3 strains were derived from NP53/HIS3 (from strain no. 10734) and the MAD1-GFP module was derived from strain no. 3785 (Research Genetics); the nup53::KAN deletion module was derived from strain no. 10734 (Research Genetics); and the mad1Δ::KAN deletion module was derived from YMB1979.

The gene encoding the centromere associated protein Mtw1p (Goshima and Yanagida, 2000) was tagged with the gene-encoding GFP or the CFP as follows: Mtw1p and the adjoining promotor sequences were amplified from genomic DNA with the following primers: OMB338 (YMB1908 and YMB1911) or OMB339 (YMB1900 and YMB1906) was mated to nup170Δ::HIS3 (YMB1482), nup157a::URA3 (NP157–21), nups3::HIS3 (from NP53/ NP157–21), and nups157::HIS3 (from NP9–23). Haploid meiotic progeny of the diploids was analyzed. Similarly, nup170Δ::URA3 MAD1-GFP (NP12014) and nup157-2::URA MAD2-GFP (NP11202M) haploid strains were derived from diploids made by crossing NP120–25–4 with M1GFP or M2GFP, respectively. Strains with nup gene deletions containing MAD1-GFP or MAD2-GFP are described below.

Cell cycle arrest
For cell cycle arrest, we used early logarithmic phase cultures grown at 30°C. For G1 arrest, cells were incubated with 1 μg/ml a-factor (T6901; Sigma-Aldrich) for 90 min. For G2/M arrest, cells were incubated with 15 μg/ml nocodazole (M-1404; Sigma-Aldrich) or 30 μM benomyl (Sigma-Aldrich) for 90–120 min (Hardwick and Murray, 1995). Cell cycle arrest was monitored by microscopic examination of cells and FACScan analysis (Basti et al., 1996).

Cell fractionation, affinity purification, and Western blotting procedures
Cell fractionation of the strain M1GFP was performed as described previously (Stambro-Mi-Castilla et al., 1995). The cytosol and crude nuclei fractions are the supernatant and pellet fractions, respectively, from a low speed centrifugation.
speed centrifugation (10,000 g for 15 min) of lysed spheroplasts. Purified nuclei were used to produce a NE fraction. Nuclei were digested with 20 μg/ml DNase I-EP and then diluted with an equal volume of buffer to a final concentration of 200 mM NaCl, 10 mM Bis-Tris, pH 6.5, and 0.1 mM MgCl₂ and incubated on ice for 15 min. Samples were then centrifuged at 200,000 g for 15 min at 4°C to produce a pellet fraction containing crude NEs and a supernatant fraction (containing histone proteins) designated as the nucleoplasmic fraction.

Immunoprecipitations and affinity purification of nup–pA fusion proteins were performed on nuclear extracts derived from crude nuclear fraction isolated from a 250-ml culture (Tcherepenev et al., 1999). The nuclear fraction was digested with 10 μg/ml DNAse and then diluted with 1 vol of extraction buffer to a final concentration of 1% Triton X-100, 20% dimethyl sulfoxide, 150 mM NaCl, 0.1 mM MgCl₂, 1 mM DTT, 50 mM Tris-HCl, pH 7.5, and containing a protease inhibitor cocktail (50 mM NaF, 0.2 mM PMSF, 2 μg/ml leupeptin, 2 μg/ml aprotinin, and 0.4 μg/ml pepstatin A), Samples were clarified by centrifugation at 200,000 g for 15 min at 4°C. The supernatant fraction containing the nuclear extract was incubated with IgG-Sepharose beads (Amersham Biosciences), using 10 μl of bead slurry per 1 ml of extract for 3 h at 4°C. Alternatively, extracts from strains were precipitated with 10% trichloroacetic acid.
M1GFP or M2GFP cells were incubated with rabbit polyclonal anti-GFP antibodies (provided by L. Berthiaume, University of Alberta, Edmonton, Alberta, Canada) or polyclonal anti-Nup53p antibodies (Marelli et al., 1998) followed by the addition of 20 μl protein G-Sepharose beads (Amer- sham Biosciences). Beads were washed extensively in wash buffer (0.1% Tween 20, 150 mM NaCl, 0.1 mM MgCl₂, 1 mM DTT, 50 mM Tris-HCl, pH 7.5, and a protease inhibitor cocktail and then with wash buffer containing 50 mM MgCl₂. Bound proteins were eluted with a MgCl₂ step gra- dient (0.1 M, 0.5 M, 1 M, and 2.0 M for protein A fusions and 0.1 M, 0.5 M, and 2 M for anti-Nup53p and anti-GFP) and a final wash with 0.5 M acetic acid, pH 3.4.

For the analysis of whole cell lysates, samples were prepared as de- scribed previously (Marelli et al., 2001) and proteins were separated by SDS-PAGE. For the examination of phosphorylated Mad1-GFP, proteins from whole cell lysates were separated by double-inverted gradient gel electrophoresis as described previously (Zardoya et al., 1994). Immuno- blotting was performed as described previously (Marelli et al., 1998). Pro- tein A fusions were detected with rabbit anti-mouse IgG (ICN Biomed- icals). Polyclonal anti-GFP antibodies were a gift from Michael Rout (The Rockefeller University, New York, NY). Anti-Mad1 pAb was provided by Kevin Hardwick (University of Edinburgh, Edinburgh, UK). Anti-Mad2 polyclonal antibodies were a gift from Rei-Hui Chen (Cornell University, Ithaca, NY; Chen et al., 1999). Nup2p was detected using anti-Nup2p pAbs provided by John Aitchison (Institute for Systems Biology, Seattle, WA; Dilworth et al., 2001). Immune complexes were detected with HRP- conjugated secondary antibodies and the ECL system (Amersham Bio- sciences).

Nuclear transport assays
Nuclear import of a Pho41-CFP-GFP reporter was assessed in the strains DFS5, YMB1482, YMB1906, and YMB1979 transformed in the plasmid EB0836 (Kaffman et al., 1998), provided by O. E. O’Shea, University of California, San Francisco, San Francisco, CA using a previ- ously described assay (Shulgina et al., 1996, 2000) with modifications. Cells were treated with a metabolic poison cocktail of 100 mM 2-deoxyglucose and 10 mM sodium azide for 45 min at 30°C. Cells were then washed and resuspended in CM-Ura media at RT. Recovery was allowed to proceed at RT on a slide and confocal images were captured at the indicated times and scored for nuclear accumulation of the reporter. For 37°C-treated cells, cultures were grown for 3 h at 37°C before metabolic poisoning.

Fluorescence microscopy
Strains containing both GFP- and CFP-tagged proteins were examined on a microscope (AxioScope 2; Carl Zeiss MicroImaging, Inc.) fitted with an HBO100 W/12 lamp (Carl Zeiss MicroImaging, Inc.) and a Leica (Wetzlar, Germany) MicroImaging, Inc.). Fluorescence was captured using an optical CFP filter set (model XF114–2; Omega Optical, Salem, NH) and an optical GFP filter set (model XT114–2; Omega Optical, Salem, NH). Images were obtained using a fluorescence microscope (Axioscope 2; Carl Zeiss MicroImaging, Inc.) equipped with an AxioCam MRm digital camera (Carl Zeiss MicroImaging, Inc.). All confocal images discussed in the results were obtained using a confocal microscope (model LSM510; Carl Zeiss MicroImaging, Inc.).

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