The nucleoporins Nup170p and Nup157p are essential for nuclear pore complex assembly

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We have established that two homologous nucleoporins, Nup170p and Nup157p, play an essential role in the formation of nuclear pore complexes (NPCs) in Saccharomyces cerevisiae. By regulating their synthesis, we showed that the loss of these nucleoporins triggers a decrease in NPCs caused by a halt in new NPC assembly. Preexisting NPCs are ultimately lost by dilution as cells grow, causing the inhibition of nuclear transport and the loss of viability. Significantly, the loss of Nup170p/Nup157p had distinct effects on the assembly of different architectural components of the NPC. Nucleoporins (nups) positioned on the cytoplasmic face of the NPC rapidly accumulated in cytoplasmic foci. These nup complexes could be recruited into new NPCs after reinitiation of Nup170p synthesis, and may represent a physiological intermediate. Loss of Nup170p/Nup157p also caused core and nuclear-plemmically positioned nups to accumulate in NPC-like structures adjacent to the inner nuclear membrane, which suggests that these nucleoporins are required for formation of the pore membrane and the incorporation of cytoplasmic nups into forming NPCs.

Introduction

Molecules travel across the nuclear envelope (NE) through nuclear pore complexes (NPCs). The NPC (~66 MD in yeast) possesses eightfold rotational symmetry perpendicular to the plane of the NE and can be divided in three parts: a central core or annulus, the nuclear basket, and cytoplasmic filaments. Structural analyses have revealed that the central core consists of distinct cytoplasmic, luminal spokes, and nucleoplasmic rings (Yang et al., 1998; Beck et al., 2004; Beck et al., 2007). Movement of macromolecules through the NPC is controlled by nuclear transport receptors, which bind to nuclear localization signals (NLSs) or nuclear export signals on these molecules. Karyopherins (kaps) are a family of structurally related proteins, of which there are 14 in yeast, that bind to different signals and function as importers (importins) or exporters (exportins; Wozniak et al., 1998). Kaps interact with a subset of nuclear proteins (termed nucleoporins [nups]) containing phenylalnine-glycine repeats (termed FG-nups) that populate the translocation channel. Distinct models suggest that the FG-nups form a hydrophobic barrier (hydrogel; Frey et al., 2006; Frey and Gorlich, 2007) or, by the rapid Brownian motion of unstructured FG domains, a virtual gate (Rout et al., 2003). By binding FG-nups, kaps overcome this barrier and progress through the channel.

The FG-nups are attached to the symmetrical core that forms the architectural framework of the NPC. The core is composed largely of nups that lack FG repeats (Hetzer et al., 2005; Tran and Wente, 2006). Several of these are transmembrane proteins (termed poms), which probably function by anchoring the NPC to the NE. The structural organization of nups that contribute to the rings and spokes of the NPC has been investigated using various biochemical, genetic, and cytological techniques (for review see Suntharalingam and Wente, 2003). Seminal contributions have included the isolation and characterization of subcomplexes. In yeast, these include the heptameric Nup84p subcomplex, the Nup188p–Nic96p–Pom152p subcomplex, and the Nup170p–Nup53p–Nup59p subcomplex (Nehrbass et al., 1996; Marelli et al., 1998; Lutzmann et al., 2002; Lutzmann et al., 2005). Recently, through an elegant biochemical and computational study, Alber et al. (2007a,b) proposed a structure...
of the NPC that provides a view of how nups are likely organized within the NPC. A growing body of crystal structures of nups, among them the structure of a Sec13–Nup145 complex (Hsia et al., 2007), have also led to predictions for the structure of the NPC. These varied approaches are likely to provide a high-resolution map of the NPC core in the near future.

The assembly of subcomplexes likely plays a role in the formation of mature NPCs. This process occurs both when the NE is intact and during NE reassembly in the final stages of mitosis. Postmitotic NPC assembly occurs in organisms that undergo an open mitosis, and at the end of mitosis, when membrane vesicles and NPC components are recruited back to the chromatin surface. Studies using in vitro Xenopus NE assembly assays and tissue culture cells show that NPC formation occurs through the ordered assembly of nup subcomplexes on the chromatin surface together with coordinated interactions with the NE membrane (for reviews see Hetzer et al., 2005; Tran and Wente, 2006). First, the Nup107–160 subcomplex (vertebrate equivalent of the yeast Nup84p subcomplex) is recruited to chromatin through its interactions with ELYS/Mel28 (Rasala et al., 2006, 2008; Franz et al., 2007; Gillespie et al., 2007). These preproteins act as binding sites for membrane vesicles containing Ndc1 and Pom121 (Antonin et al., 2005; Rasala et al., 2008). This step is functionally linked to the incorporation of Nup155 and Nup53 (Franz et al., 2005; Hawryluk-Gara et al., 2008) and precedes a cascade of events that ultimately leads to the formation of mature NPCs.

NPCs are also formed across an intact NE. In higher eukaryotic cells, the number of NPCs appears to double during S phase (Maul et al., 1972). Accordingly, NPC assembly has been observed across an intact NE of nuclei reconstituted in vitro using Xenopus egg extracts and in vivo using HeLa cells (D’Angelo et al., 2006). The assembly of NPCs across the NE is likely the only mechanism functioning in unicellular eukaryotes that undergo closed mitoses (i.e., the NE remains intact during mitosis). In Saccharomyces cerevisiae, the number of NPCs increases throughout the cell cycle (Winney et al., 1997), allowing NPC numbers to be maintained in both the mother and daughter. A recent study suggests that the process may be more complicated, with new NPC formation being the primary source of NPCs in the daughter nucleus (Shcheprova et al., 2008).

A requisite step in the formation of NPCs across the NE is the fusion of the inner and outer nuclear membranes to form transisternal nuclear pores. Poms and nups located close to the membrane are likely to play a role in this and accompanying steps of NPC assembly. In higher eukaryotes, three poms—gp210, Pom121, and Ndc1—have each been implicated in NPC assembly (Antonin et al., 2005; Mansfeld et al., 2006; Stavrú et al., 2006a,b; Funakoshi et al., 2007). Three S. cerevisiae poms—Pom152p, Pom34p, and Ndc1p—also appear to share a redundant function in NPC assembly (Chial et al., 1998; Lau et al., 2004; Madrid et al., 2006; Miao et al., 2006). In addition to poms, analyses of several yeast nups have lead to the conclusion that they are required for NPC assembly. Mutants in NTC96, NUP192, or NSP1 cause a decrease in NPC numbers (Mutvei et al., 1992; Zabel et al., 1996; Kosova et al., 1999; Gomez-Ospina et al., 2000). Studies using Xenopus egg extracts have also implicated nuclear and cytoplasmic pools of the Nup107–160 subcomplex in forming NPCs within intact nuclei (D’Angelo et al., 2006). Intriguingly, NPC assembly also employs soluble components of the nuclear transport machinery including Ran, Kap121p, and Kap95p (Lusk et al., 2002; Ryan et al., 2003, 2007; D’Angelo et al., 2006).

The NUP170 gene family is conserved among eukaryotes and is essential for growth in various species (Gigliotti et al., 1998; Kiger et al., 1999; Galy et al., 2003). The S. cerevisiae genome encodes two homologous genes—NUP170 and NUP157—one or the other of which is required for growth (Aitchison et al., 1995). Both genetic (Aitchison et al., 1995; Tcheperegine et al., 1999; Miao et al., 2006) and structural studies (Alber et al., 2007a,b) suggest that Nup170p and Nup157p are located close to the pore membrane, where they could interact with poms and the membrane. Nup170p and Nup157p are predicted to contain β-propeller and α-solenoid domains that are reminiscent of membrane coat proteins such as clathrin (Devos et al., 2004, 2006). To uncover their functions, we constructed a conditional lethal strain that allowed repression of NUP170 in the absence of NUP157. We found that loss of these proteins caused a decrease in NPC density due to a defect in new NPC assembly. In the absence of Nup170p and Nup157p, newly synthesized nups accumulated in cytoplasmic foci and inner nuclear membrane-associated structures, which is suggestive of stalled NPC assembly intermediates. Importantly, reinitiation of Nup170p synthesis induces the dissociation of the cytoplasmic foci and their incorporation into the NE. We conclude that Nup170p and Nup157p are required for the assembly of subcomplexes within the forming NPC at a step that likely coincides with the fusion of the outer and inner nuclear membranes and the formation of the nuclear pore.

Figure 1. Depletion of Nup170p in the nup157Δ background causes a defect in cell growth. [A] The strains TMY1098 (Pmet-HA-NUP170) and TMY1269 (NUP170 HA) were grown in medium lacking methionine. Methionine was added to induce NUP170 shut-off and incubated for the indicated times. Samples were analyzed by Western blotting using anti-HA and anti-Gsp1p (load control) antibodies. [B] The yeast strains TMY1098 (Pmet-HA-NUP170) and TMY1269 (Pmet-HA-NUP170 nup157Δ) were streaked on CM (−Met) and CM (+Met) plates, and grown for 2 d at 30°C.
**Results**

Loss of Nup170p and Nup157p causes a decrease in the number of the NPCs

One of the major lineages that comprise the *S. cerevisiae* complex shares a common ancestor that underwent a whole genome duplication (Scannell et al., 2007). The duplicated *S. cerevisiae* genome retains ~551 duplicate pairs, including the nup genes *NUP170* and *NUP157*. Nup170p and Nup157p have both redundant and distinct functions (Aitchison et al., 1995; Kerscher et al., 2001). Neither gene is essential for growth, but deletion of the pair is lethal, which suggests that they share essential functions.

To investigate the molecular basis underlying the synthetic lethality of *nup170* and *nup157* null alleles, the endogenous *NUP170* promoter was replaced by a repressible *MET3* promoter in backgrounds containing or lacking *NUP157* (*PMET3-NUP170 NUP157* and *PMET3-NUP170 nup157Δ*). In the absence of methionine, the *MET3* promoter is active, leading to levels of Nup170p that are similar to those of wild-type (WT) cells (Fig. 1A). Upon addition of methionine, the promoter is repressed and levels of Nup170p decrease. By 4 h after methionine addition, Nup170p levels are barely detectable (Fig. 1A). In strains containing Nup157p (*P_{MET3-NUP170 NUP157}*, depletion of Nup170p had little effect on growth. However, strains lacking Nup157p and depleted of Nup170p (which we will refer to as depleted of Nup170p [*nup157Δ*]) failed to form colonies on plates (Fig. 1B).

To understand the functional basis for the growth inhibition observed in the absence of Nup170p and Nup157p, we examined the morphology of the NE after repression of *NUP170* in the *PMET3-NUP170 nup157Δ* strain. Samples were harvested at various time points after the addition of methionine, postfixed with potassium permanganate, and analyzed by thin-section transmission EM (TEM). With this method, membranes are darkly stained while proteinaceous structures
are not highlighted. Thus, the NE membrane is clearly visible and nuclear pores appear as gaps of defined size in the continuity of the NE. WT or cells depleted of only Nup170p (P_MET nitrogen, NUP170, NUP157) contained largely spherical nuclei with visible nuclear pores (unpublished data). Similarly, P_MET nitrogen, NUP170 nup157Δ cells showed no striking changes in the number of their nuclei through 8 h after the addition of methionine (Fig. 2 A). However, these nuclei contained fewer pores. We quantified the number of NPCs by counting the number of pores per micrometer of linear distance along the NE in multiple sections. A linear density of 0.54 ± 0.03 pores/µm was observed upon loss of Nup170p and Nup157p as a consequence of NPC depletion.

The loss of Nup170p and Nup157p causes the mislocalization of other nups

The reduction in NPCs detected upon depletion of Nup170p and Nup157p is likely to arise from an inhibition of new NPC assembly, either exclusively or in conjunction with the destabilization of existing NPCs. To more closely evaluate the role of these nups in NPC assembly, we examined the consequences of depleting Nup170p and Nup157p on the association of individual nups with the NE. To visualize each nup, a GFP tag was introduced at the 3' end of its open reading frame (ORF). In most cases, the NUP-GFP allele did not affect cell growth. However, strains containing the GLE2-GFP, NUP192-GFP, NUP57-GFP, NUP49-GFP, NPS1-GFP, and NIC96-GFP alleles exhibited severe growth defects upon depletion of Nup170p even in the presence of Nup157p (unpublished data), which suggests that the C-terminal GFP compromises the function of these nups and causes a synthetically lethal interaction with reduced NUP170 expression. As a consequence, these nups were omitted from further analysis.

The localization of each nup-GFP fusion was examined 6 h after methionine-induced repression of NUP170. Nups belonging to various subdomains of the NPC were examined, including those positioned on the cytoplasmic or nucleoplasmic face (here referred to as cytoplasmic or nucleoplasmic nups), and within the core, integral membrane proteins. The most dramatic effects of Nup170p (nup157Δ) depletion were on nups positioned exclusively on the cytoplasmic face of the NPC, including Nup82-GFP and Nup159-GFP. Upon depletion of Nup170p (nup157Δ; 6 h), the NE localization of Nup82-GFP and Nup159-GFP was largely lost, and the proteins were found in foci located in the cytoplasm and occasionally adjacent to the NE (Fig. 4). Generally, 3–7 foci were visible per cell. In contrast, the nucleoplasmic nups Nup1-GFP, Nup2-GFP, Nup60-GFP, and Mlp1-GFP, and the membrane protein Pom152p retained their nuclear rim localization over the same time period (Fig. 4). Nups that contribute to the central core of the NPC showed a mixed phenotype upon depletion of Nup170p (nup157Δ). For example, components of the Nup84 complex (Nup84-GFP, Nup85-GFP, and Nup133-GFP), Gle1-GFP, Nup100-GFP, and Ndc1-GFP were still visible at the NE but generally exhibited a weaker signal than seen at the time of 0 h. In addition, these nups were detected in punctate cytoplasmic structures (Fig. 4). Cytoplasmic foci were also visible, but less abundant, when we examined a group of more centrally located core nups and poms including Nup188-GFP, Nup59-GFP, Nup53-GFP, and Pom34-GFP (Fig. 4). Each of these retained an NE signal at 6 h after Nup170p (nup157Δ) depletion.

To determine whether the mislocalized nups coassembled into foci with other nups, we examined the localization of Nup159–monomeric RFP (mRFP) in cells coproducing Nup188-GFP, Nup82-GFP, Nup2-GFP, or Ndc1-GFP. All of the double-tagged strains grew normally when either Nup157p or Nup170p was present, which suggests that the tags did not alter the functions of these nups. 4 h after addition of methionine, both Nup159-mRFP...
and Nup82-GFP colocalized to the same cytoplasmic foci adjacent the NE (Fig. 5). In contrast, Nup188-GFP, Nup2-GFP, and Ndc1-GFP were generally restricted to the NE at the 4-h time point (Fig. 5). By 8 h, Nup188-GFP and Ndc1-GFP began to accumulate in cytoplasmic foci (Fig. 5). The Nup188-GFP cytoplasmic foci generally colocalized with Nup159-mRFP, which suggests that Nup188-GFP can associate with structures containing the cytoplasmic nups. Similarly, overlapping Ndc1-GFP and Nup159-mRFP spots were detected. However, distinct Ndc1-GFP and Nup159-mRFP foci were also seen: the Ndc1-GFP-specific foci that likely represent spindle pole body–associated protein, and the Nup159-mRFP-specific foci perhaps arising from their positioning away from membrane containing Ndc1-GFP. Finally, little or no colocalization of Nup2-GFP and Nup159-mRFP was detected in cells at 4 or 8 h after depletion (Fig. 5). These results suggest that the depletion of Nup170p
foci and its normal NE association was lost, a pattern largely similar to that observed in the cytoplasmic nups. Consistent with this, we observed that the Kap95-GFP signal colocalized with Nup159-mRFP (Fig. 6 B). Kap121-GFP and Kap123-GFP were less frequently seen in cytoplasmic foci and remained concentrated at the nuclear periphery at the 4-h time point.

(nup157Δ) causes the mislocalization of cytoplasmically positioned nups into foci, which at later time points also contain detectable amounts of core nups and certain poms.

The distributions of certain importins were also affected by Nup170p (nup157Δ) depletion (Fig. 6). By 4 h after methionine addition, Kap95-GFP was visible primarily in cytoplasmic foci and its normal NE association was lost, a pattern largely similar to that observed in the cytoplasmic nups. Consistent with this, we observed that the Kap95-GFP signal colocalized with Nup159-mRFP (Fig. 6 B). Kap121-GFP and Kap123-GFP were less frequently seen in cytoplasmic foci and remained concentrated at the nuclear periphery at the 4-h time point.

Figure 4. The loss of Nup170p and Nup157p has distinct effects on the localization of NPC components. (A) The endogenous gene encoding the indicated nup was tagged with GFP in the TMY1098 and TMY1126 strains, and the fusion proteins were examined at the indicated times after repression of NUP170 expression using an epifluorescence microscope. Pom152p localization was analyzed by indirect immunofluorescence using an anti-Pom152p antibody (mAb118C3). Note, the brighter Ndc1-GFP foci of seen at the NE at 0 h likely reflect the shared spindle pole body association of Ndc1p (Chial et al., 1998). Diagrams adjacent to the images depict the general localization of each nup within the NPC (red). Nup100p is present on both faces of the NPC but is biased to the cytoplasm. Bars, 5 µm.
depletion, in contrast to what is seen in cycling cells (Fig. 7B). Moreover, Nup82-GFP also accumulated in cytoplasmic foci, which is consistent with the inhibition of new NPC biogenesis. These foci were not detected in arrested cells expressing NUP170 (Fig. 7B).

The fates of existing NPCs and the formation of new ones in the absence of Nup170p and Nup157p was also examined using nups tagged with the fluorescent protein Dendra. Dendra undergoes a photoconversion from green to red fluorescent states in response to visible blue or UV light (Gurskaya et al., 2006). This allows one to distinguish the pool of Dendra-tagged protein present at the point of photoconversion from that synthesized after exposure. We used this tag to follow the fates of existing and newly synthesized Nup82-Dendra and Nup60-Dendra after depletion of Nup170p (nup157Δ). These nups were selected as they represent different NPC substructures, and they exhibited different localization patterns after depletion of Nup170p (nup157Δ). After addition of methionine, cells were flashed with UV light to induce conversion of Nup-Dendra-green to Nup-Dendra-red. After conversion, no Nup82-Dendra-green signal was visible, and Nup82-Dendra-red appeared along the NE in an NPC-like pattern (Fig. 8A). By 6 h after repression of NUP170 (nup157Δ), the Nup82-Dendra-red signal showed a striking decrease (Fig. 8A), which is consistent with our observed decrease in NPCs (Fig. 2B). In most cells, the remaining Nup82-Dendra-red signal was largely localized in a roughly spherical pattern, which is consistent with its continued presence in the NE.

This distribution pattern appeared to have more similarity to that seen with core nups such as Nup53 (Fig. 4). Finally, cellular distribution of Kap104-GFP appeared unaffected by depletion of Nup170p (nup157Δ).

The decrease in NPC density upon loss of Nup170p and Nup157p is caused by a defect in NPC assembly

Our data are consistent with a model in which the loss of Nup170p and Nup157p inhibits new NPC assembly, and preexisting NPCs, being largely stable, are diluted out between mother and daughter cells during repeated cell cycles. Based on this model, we predict that the inhibition of the cell cycle would prevent the loss of preexisting NPCs. To test this idea, we inhibited cell cycle progression using α-factor to arrest cells in G1 phase, and TEM analysis was performed to determine NPC density (Fig. 7A). When Nup170p was present in the nup157Δ background, the linear density of NPCs in the NEs of cells arrested with α-factor for 6 h was estimated at 0.49 NPC/µm, which was similar to cycling cells (0.51 NPC/µm; Fig. 7A). In cells incubated for 6 h in the presence of α-factor and methionine, in order to inhibit Nup170p synthesis, NPC density decreased slightly (to 0.37 NPC/µm) when compared with cells expressing NUP170 but was significantly higher than that seen in cycling cells depleted of Nup170p (nup157Δ) for 6 h (0.17 NPC/µm). Consistent with these data, Nup82-GFP remained visible at the NE in α-factor–arrested cells after 6 h of Nup170p (nup157Δ) depletion, in contrast to what is seen in cycling cells (Fig. 7B). Moreover, Nup82-GFP also accumulated in cytoplasmic foci, which is consistent with the inhibition of new NPC biogenesis. These foci were not detected in arrested cells expressing NUP170 (Fig. 7B).

The fates of existing NPCs and the formation of new ones in the absence of Nup170p and Nup157p was also examined using nups tagged with the fluorescent protein Dendra. Dendra undergoes a photoconversion from green to red fluorescent states in response to visible blue or UV light (Gurskaya et al., 2006). This allows one to distinguish the pool of Dendra-tagged protein present at the point of photoconversion from that synthesized after exposure. We used this tag to follow the fates of existing and newly synthesized Nup82-Dendra and Nup60-Dendra after depletion of Nup170p (nup157Δ). These nups were selected as they represent different NPC substructures, and they exhibited different localization patterns after depletion of Nup170p (nup157Δ). After addition of methionine, cells were flashed with UV light to induce conversion of Nup-Dendra-green to Nup-Dendra-red. After conversion, no Nup82-Dendra-green signal was visible, and Nup82-Dendra-red appeared along the NE in an NPC-like pattern (Fig. 8A). By 6 h after repression of NUP170 (nup157Δ), the Nup82-Dendra-red signal showed a striking decrease (Fig. 8A), which is consistent with our observed decrease in NPCs (Fig. 2B). In most cells, the remaining Nup82-Dendra-red signal was largely localized in a roughly spherical pattern, which is consistent with its continued presence.
Nup60p is one of the nups whose association with the NE was unaffected after 6 h of Nup170p (nup157Δ) depletion (Fig. 4). Because NPC formation is inhibited under these conditions, we were interested in comparing existing Nup60-Dendra to that synthesized after depletion of Nup170p (nup157Δ). 6 h after photoconversion and repression of NUP170 (nup157Δ), newly synthesized Nup60-Dendra-green was visible along the NE in foci that were, in many cases, distinct from Nup60-Dendra-red in preexisting NPCs (Fig. 8 B). Because few NPCs are formed in the absence of Nup170p and Nup157p, the nature of these deposits was of interest.

Loss of Nup170p and Nup157p induces the formation of proteinaceous structures adjacent to the inner nuclear membrane

As the loss of Nup170p and Nup157p inhibits NPC formation, we were perplexed by the continued localization of core and nucleoplasmic nups at the NE after 6 h of Nup170p (nup157Δ) depletion. To further investigate the basis for these observations,
we examined Nup170p (nup157Δ)-depleted cells using TEM techniques (osmium tetroxide fixation and uranyl acetate staining) that highlight NPCs. In addition to NPCs, we observed electron-dense structures adjacent to the nucleoplasmic face of the inner nuclear membrane at 4 h after repression of NUP170 (nup157Δ; Fig. 9, B and C, white arrowheads). The inner and outer NE membranes were clearly distinguishable at these sites, with no connecting pore membrane domain. Measurements of the width and thickness of these structures (71 ± 7 nm wide and 34 ± 9 nm thick; n = 32) revealed that they are similar in dimension to those of native NPCs (75 ± 7 nm wide and 33 ± 4 nm thick; n = 32). Similar structures were not detected before repression of NUP170 (nup157Δ; 0 h) or in strains lacking only Nup170p or Nup157p (Fig. 9 A and not depicted). We propose that these structures arise from core and nucleoplasmic nups forming NPC assembly intermediates at the inner membrane. To further test this conclusion, we performed immunoelectron microscopy analysis using mAb414, a monoclonal antibody that binds to several XFXFG repeats containing nups but mainly the core and nucleoplasmic nups Nsp1p and Nup2p (Kenna et al., 1996). We detected mAb414 binding to NPCs, as defined by discontinuities in the lumen of the NE (Fig. 9 D, black arrowheads). After Nup170p (nup157Δ) depletion, however, a significant number of gold particles were also observed at sites apart from NPCs (Fig. 9 D, white arrowheads; and Table I) and adjacent to the inner nuclear membrane. These results support the conclusion that core and nucleoplasmic nups contribute to the proteinaceous structures accumulating along the inner nuclear membrane.

Reinitiation of Nup170p synthesis induces targeting to the NE of cytoplasmic pools of mislocalized nups

If the structures observed upon depletion of Nup170p (nup157Δ) represent an accumulation of intermediates in NPC assembly, it is possible that these nups could be used in new NPC formation after reinitiation of Nup170p synthesis. To test this idea, Nup82-Dendra-green was induced to accumulate in cytoplasmic foci by a 5-h depletion of Nup170p (nup157Δ), then converted to Nup82-Dendra-red. Cells were then switched to media lacking methionine to induce Nup170p synthesis. As shown in Fig. 8 C, Nup170p production induced both the disassembly of the cytoplasmic foci and the relocation of Nup82-Dendra-red to the NE in a pattern consistent with its localization to NPCs, which suggests that nups in the cytoplasmic foci remain competent to assemble into NPCs.

Table I. Quantification of mAb414 immunogold labeling of Nup170p (nup157Δ)-depleted cells

<table>
<thead>
<tr>
<th>+Met (h)</th>
<th>Total number of gold particles</th>
<th>Gold particles at NPCs</th>
<th>Gold particles at the inner nuclear membrane</th>
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<tr>
<td>0</td>
<td>98</td>
<td>82 (84%)</td>
<td>16 (16%)</td>
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<tr>
<td>4</td>
<td>110</td>
<td>54 (49%)</td>
<td>56 (51%)</td>
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The +Met (h) column shows time after addition of methionine to the TMY1126 strain. Gold particles present at discontinuities in NE lumen of a size consistent with NPCs were scored as NPC associated. Gold particles at the inner nuclear membrane but distinct from NPCs were scored as inner membrane associated. Percentages of the total number of particles counted are given in parentheses.
consistent with the predicted stability of these structures (Daigle et al., 2001; Rabut et al., 2004a,b). However, the loss of these nups leads to the arrest of NPC formation and small foci composed of distinct groups of nups accumulated in either the cytoplasm or the nucleus adjacent to the inner nuclear membrane. We demonstrate that the cytoplasmic foci represent pools of Structures similar to the cytoplasmic foci seen in Nup170p (nup157Δ)-depleted cells have also been observed in strains lacking Aqp12p (Scarcelli et al., 2007). This ER membrane protein has been proposed to play a role in the biophysical properties of the nuclear membrane and the formation of NPCs. An apq12Δ strain at 23°C accumulates cytoplasmic foci containing nups, including Nup82-GFP. The addition of benzyl alcohol to the medium disperses these nups and promotes their association with the NE and incorporation into NPCs (Scarcelli et al., 2007). Similarly, we observed that the incubation of apq12Δ cells with another alcohol, 3% hexane-1, 6-diol, also induced the dispersion of Nup82-GFP–containing cytoplasmic foci and localization to the nuclear periphery (Fig. 10). This alcohol has been demonstrated to disrupt nup–nup interactions in various contexts, including dispersing cytoplasmic aggregates of FG-nups (Patel et al., 2007). Treatment with 3% hexane-1, 6-diol also partially dispersed Nup82-GFP–containing foci formed upon loss of Nup170p and Nup157p, but Nup82-GFP failed to relocalize to the nuclear rim (Fig. 10) and remained diffusely distributed throughout the cytoplasm. Thus, although hexane-1, 6-diol can bypass the requirement for Aqp12p and induce reassembly of cytoplasmic nups onto the NE, this latter process requires the presence of Nup170p and Nup157p.

Discussion

The assembly of NPCs across an intact NE requires the fusion of the inner and outer NE and the assembly of nups within the newly forming NPC. Here, we show that the related nups Nup170p and Nup157p are required for the assembly of subcomplexes within the forming NPC at a step before or coinciding with the membrane fusion and pore formation. Depletion of these nups does not appear to affect existing NPCs, which is consistent with the predicted stability of these structures (Daigle et al., 2001; Rabut et al., 2004a,b). However, the loss of these nups leads to the arrest of NPC formation and small foci composed of distinct groups of nups accumulated in either the cytoplasm or the nucleus adjacent to the inner nuclear membrane. We demonstrate that the cytoplasmic foci represent pools of structures similar to the cytoplasmic foci seen in Nup170p (nup157Δ)-depleted cells have also been observed in strains lacking Aqp12p (Scarcelli et al., 2007). This ER membrane protein has been proposed to play a role in the biophysical properties of the nuclear membrane and the formation of NPCs. An apq12Δ strain at 23°C accumulates cytoplasmic foci containing nups, including Nup82-GFP. The addition of benzyl alcohol to the medium disperses these nups and promotes their association with the NE and incorporation into NPCs (Scarcelli et al., 2007). Similarly, we observed that the incubation of apq12Δ cells with another alcohol, 3% hexane-1, 6-diol, also induced the dispersion of Nup82-GFP–containing cytoplasmic foci and localization to the nuclear periphery (Fig. 10). This alcohol has been demonstrated to disrupt nup–nup interactions in various contexts, including dispersing cytoplasmic aggregates of FG-nups (Patel et al., 2007). Treatment with 3% hexane-1, 6-diol also partially dispersed Nup82-GFP–containing foci formed upon loss of Nup170p and Nup157p, but Nup82-GFP failed to relocalize to the nuclear rim (Fig. 10) and remained diffusely distributed throughout the cytoplasm. Thus, although hexane-1, 6-diol can bypass the requirement for Aqp12p and induce reassembly of cytoplasmic nups onto the NE, this latter process requires the presence of Nup170p and Nup157p.

Figure 9. NPC-like structures accumulate at the inner nuclear membrane after the loss of Nup170p and Nup157p. (A–C) The strains TMY1098 (Pmet3-NUP170; A) and TMY1126 (Pmet3-NUP170 nup157Δ; B and C) were harvested at 4 h after NUP170 repression. The cells were then examined by TEM. Black arrowheads indicate structures attached on the inner nuclear membrane with similar size and staining properties of NPCs. White arrowheads indicate structures attached on the inner nuclear membrane. Bars, 0.2 µm.

Figure 10. Hexane-1, 6-diol suppresses the NPC assembly defect of the apq12Δ strain but not that of cells lacking Nup170p and Nup157p. apq12Δ (TMY1290) and Pmet3-NUP170 nup157Δ (TMY1135) strains expressing Nup82-GFP were grown in YPD overnight at 23°C, and for 6 h in media containing methionine to induce NPC assembly defects and accumulation of Nup82-GFP foci. Hexane-1, 6-diol (+HD; final 3% wt/vol) was then added to the media, and samples were taken at the indicated times. Images of Nup82-GFP were acquired using an epifluorescence microscope. Bar, 5 µm.
nups that remain competent to assemble into NPCs after re-initiation of \textit{NUP170} expression.

Other nup mutants also show a decrease in NPC numbers, including \textit{nec96-1} and \textit{nup192-15} (Zabel et al., 1996; Kosova et al., 1999). In these mutants, the overall NE structure, protein import, and mRNA export are not significantly altered at early times after transfer into a nonpermissive condition; however, the number of the NPCs is significantly reduced (Zabel et al., 1996; Kosova et al., 1999; Gomez-Ospina et al., 2000). Thus, much like cells lacking Nup170p and Nup157p, these mutations are likely to affect NPC assembly but not the function of intact NPCs. This difference is not always discernible, and, in the case of several other nup mutants, it has been difficult to discriminate between those mutations that affect the integrity or function of the NPC versus those inhibiting assembly. Among the most interesting phenotypes observed are those of nup mutants that induce NE herniations that seal over NPCs (e.g., Wente and Blobel, 1993). It is not clear, however, whether this phenotype arises as a consequence of assembly defects or represents a cellular response to damaged NPCs.

Of the various nup mutants that have now been examined, only cells lacking both Nup170p and Nup157p exhibit the unique feature of accumulating putative NPC assembly intermediates. These intermediates were revealed by the inspection of individual nups after loss of Nup170p and Nup157p. Nups that contribute to defined NPC subcomplexes or are positioned at a common location in the NPC (e.g., the nucleoplasmic face of the NPC) exhibited one of three distinct localization patterns. For example, the cytoplasmic nups Nup82p and its binding partner Nup159p (Belgareh et al., 1998) rapidly accumulated in cytoplasmic foci after loss of Nup170p and Nup157p (Fig. 4). In a second phenotype, nups associated with the symmetrical core of the NPC showed a mixed distribution between the cytoplasmic foci and structures along the NE. Several nups thought to be closely associated with Nup82p in the NPC, including Glec1p, Nup100p, and members of the Nup84p complex (Alber et al., 2007a,b), showed a clear association with the cytoplasmic foci as well as the NE. Other core nups including Nup188p and Nup35p exhibited a weaker, but detectable, signal in cytoplasmic foci. Similarly, Ndc1p and Pom34p were seen in a subset of the cytoplasmic foci, presumably those at or near the NE or ER membrane. Each of these core nups and poms also exhibited a significant punctate NE localization (Fig. 4). In contrast, nucleoplasmic nups were found exclusively at the NE after the loss of Nup170p and Nup157p (6 h; Fig. 4). These results, coupled with the results of the Nup60-Dendra and the immunoelectron microscopy experiments (Fig. 8 and 9), have led us to conclude that association of the core and nucleoplasmic nups with the NE reflected their presences in the inner membrane–associated, NPC-like structures.

The nup localization patterns seen after the loss of Nup170p and Nup157p provide important insights into their role in NPC assembly. We conclude that the removal of Nup170p and Nup157p does not inhibit the targeting of core and nucleoplasmic nups to the nuclear periphery or their assembly into structural precursors of the NPC, which are what we interpret the inner nuclear membrane–associated structures to represent. In contrast, Nup170p and Nup157p appear essential for the incorporation of the cytoplasmically positioned nups into NPCs. Although displaced from the NE, these nups appear to associate with known binding partners (e.g., the interaction of the Nup82p/Nup159p with the Nup84p complex) within cytoplasmic foci. These foci are likely composed of assembly intermediates, not nonspecific aggregates, as their nups remain competent to target to the NE after derepression of \textit{NUP170}, and appear to assemble into NPCs (Fig. 8 C).

We propose that Nup170p and Nup157p function at the NE membrane, where they facilitate insertion of the core and cytoplasmic structures into the forming nuclear pore, potentially by assisting in the fusion of the inner and outer nuclear membranes. Alternatively, these factors could be required for the bending and stabilization of the incipient nuclear pore, which may form but collapse in their absence. These activities would necessitate the positioning of these proteins at or near the membrane. A growing number of observations support these ideas; among these are synthetic lethal interactions between mutations in \textit{NUP170} and \textit{POM152} or \textit{POM34} (Aitchison et al., 1995; Tcheperegine et al., 1999; Miao et al., 2006). These interactions appear to be based, in part, on physical associations. Nup170p binds directly to the pore-exposed region of Pom152p (Fig. S1) and is detected in subcomplexes with Ndc1p, Pom34p, and Pom152p; Nup157p is detected bound to Pom34p (Alber et al., 2007b; see Onischenko et al. on p. 475 of this issue). Also, based on their analysis, Alber et al. (2007a,b) have positioned Nup170p and Nup157p adjacent to the membrane in their proposed architecture of the NPC (Alber et al., 2007a,b).

The placement of Nup170p at or near the pore is also consistent with functions suggested by its structural features. Like members of the Nup84p complex, Nup170p and Nup157p are predicted to contain an N-terminal β-propeller and a C-terminal α-solenoid domain, features they also share with membrane vesicle coatomer proteins such as clathrin (Devos et al., 2004, 2006). By analogy to clathrin, these regions of Nup170p and Nup157p provide surfaces for interactions with membrane proteins and perhaps a means for these proteins to influence the curvature of the pore membrane. In support of this idea, near the N-terminal end of the α-solenoid region of Nup170p lies a predicted membrane-binding, amphipathic α-helix, or ALPS, domain (Drin et al., 2007). An ALPS domain has also been detected in Nup133p, and its ability to preferentially bind curved membranes has been documented in vitro (Drin et al., 2007).

In addition to their own membrane binding potential, Nup170p and Nup157p also directly interact with Nup53p (Fig. S1; Lusk et al., 2002; Alber et al., 2007a,b; Onischenko et al., 2009; unpublished data). Nup53p contains a C-terminal amphipathic helix that mediates membrane binding and is required for the formation of inner membrane–derived tubular vesicular structures induced by the overexpression of Nup53p (Marelli et al., 2001; Patel and Rexach, 2008). We envisage that the complexes formed between Nup53p–Nup170p–Nup157p are likely capable of interacting with the membrane at multiple interfaces and by various mechanisms, which are properties consistent
with a role for these proteins in steps that promote membrane curvature and fusion during NPC assembly.

It remains to be determined whether the mammalian counterpart of Nup170p and Nup157p, Nup155, would play a similar role in interphase NPC assembly. However, Nup155 is essential for postmitotic NPC assembly, and its function has been linked to events at the membrane (Franz et al., 2005). Depletion of Nup155 from Xenopus extracts inhibits NPC and NE assembly at a step after vesicle binding to chromatin. This phenotype is similar to that observed upon depletion of the membrane proteins POM121 or NDC1 (Antonin et al., 2005; Mansfeld et al., 2006) and the Nup155 binding partner Nup53 (Hawryluk-Gara et al., 2008), but is distinct from phenotypes seen after depletion of other nups, including members of the Nup107–Nup160 complex (Harel et al., 2003; Walther et al., 2003). These results have been interpreted to suggest that the functions of Nup155 and Nup53 in NPC assembly are tightly linked to those of POM121 or NDC1, which is consistent with a potential role for these proteins in influencing pore membrane structure (Hawryluk-Gara et al., 2008).

The steps that lead to pore formation in yeast, including changes in membrane structure and fusion, are also likely to be controlled by additional factors, including non-NPC proteins and lipids (Schneider et al., 1996). In this regard, mutations in Kap95p and Apq12p have been described that exhibit the accumulation of NPC intermediates similar to those we have documented in the Nup170p- and Nup157p-depleted cells. The phenotype of the kap95 mutant may be particularly relevant to our observations, as it disrupts the localization of Nup170p, thus raising the possibility that the phenotype of the kap mutant is, at least in part, caused by a defect in the targeting of Nup170p to its site of function in pore formation. Importantly, the kap95 mutant also exhibits a synthetic sick phenotype in combination with a functionally compromised nup170-GFP allele (Ryan et al., 2007). We have previously proposed the idea that kaps play an important role in NPC assembly through their targeting of nups to the inner nuclear membrane, where assembly intermediates would be formed (Marelli et al., 2001). In these studies, Kap121p was shown to assist in the targeting of Nup53p to NPCs, and it was required for the inner membrane proliferation induced by overexpression of NUP53. In light of the phenotypic similarities between the kap95 mutant and the Nup170p- and Nup157p-depleted cells, a similar role for Kap95p in targeting Nup170p and possibly other nups, including Nup2p (Dilworth et al., 2001), to the nucleoplasm seems reasonable.

In addition to contributing a nuclear targeting function, it has been suggested that Kap95p may play a role in the assembly of the cytoplasmic face of the NPC, functioning here to regulate the fusion of putative nup-containing vesicles to the outer nuclear membrane (Ryan et al., 2007). Consistent with a cytoplasmic role for Kap95p, we also detected Kap95-GFP in association with the cytoplasmic nup foci formed after the loss of Nup170p and Nup157p (Fig. 6). The time course of the appearance of Kap95-GFP foci after depletion paralleled that of cytoplasmic nups, which suggests that the association of Kap95 with these foci is linked to this group of nups. Whether or not these cytoplasmic foci are membrane-associated remains to be addressed.

Null mutants lacking the integral ER and NE membrane protein Apq12p also contain mislocalized cytoplasmic nups and inner nuclear membrane–associated, NPC-like structures when grown at a semipermissive temperature (Scarcelli et al., 2007). Moreover, combinations of apq12Δ and mutations in several NPC components, including Pom34p, Ndc1p, and Nup170p, exhibit synthetic growth defects, with an apq12Δ nup170Δ mutant showing especially strong defects in nuclear membrane structure. Although the role of Apq12p in NPC assembly remains to be clearly established, it has been proposed that it contributes to membrane fluidity by modulating the lipid composition of the NE (Scarcelli et al., 2007). This conclusion is based, in part, on the observation that benzyl alcohol treatment of apq12Δ cells can induce the dispersion of the cytoplasmic nup foci and the recruitment of their nups to the NE, presumably stimulating their assembly into NPCs. We observed a similar effect using hexane-1, 6-diol treatment of apq12Δ cells. Thus, alcohols can suppress the defects caused by the loss of Apq12p. However, hexane-1, 6-diol treatment of cells depleted of Nup170p and Nup157p, although capable of dispersing cytoplasmic nup foci, did not induce their incorporation into the NE. Based on the phenotypic similarities caused by the loss of either Apq12p or Nup170p and Nup157p, we conclude that they likely function at a similar point in NPC assembly, but that their different responses to alcohol suggest they contribute to distinct aspects of the process. The relationships between these proteins are again consistent with a role for Nup170p and Nup157p in mediating structural changes in the NE membrane that drive formation of the pore membrane and contribute to its stability. Although they required for these essential processes, Nup170p and Nup157p are expected to function in concert with pore membrane proteins, Apq12p, and other proteins that may interact with these guides. Understanding the physical relationships between these proteins and the pore membrane will be a key step in further understanding the mechanisms of nuclear pore formation.

Materials and methods

**Yeast strains, media, and plasmids**

Yeast strains used in this study are shown in Table S1. All strains were grown in YPD (1% yeast extract, 2% bactopeptone, and 2% glucose) or synthetic media containing 0.17% yeast nitrogen base (without amino acids and ammonium sulfate), 0.5% ammonium sulfate, 2% glucose, and the appropriate supplements at 30°C. Cell transformations were performed using a lithium acetate method (Soltz and Schiestl, 2007) and a PCR-based, one-step gene modification method (Longtine et al., 1998). The plasmid used for the PAF6-NUP170 integration, pTM1046, was constructed by the replacement of the BglII–PacI region of pFA6a-kanMX6-PGAL1-3HA (Longtine et al., 1998) with a BglII–PacI fragment containing a promoter region of the MET3 gene, which was made by PCR using BY4742 genomic DNA as a template and the primers 5’TGGCGAGATCCTTTAGTACTAACAGAGAC-3’ and 5’TGGCCTCAATGAAAGCAGTCTTCTTTGACTAAGACAGAC-3’. The following NLS reporter plasmids were used: pGAD-GFP (pML-NLS-GFP; Shluga et al., 1996), pEB0836 (Pho4-NLS-GFP; Koffman et al., 1998), pNaB2[200–249]-GFP (rG-NLS-GFP; Lee and Aitchison, 1999), and pBT008 (rpL25-NLS-GFP). The following plasmids were used for protein expression in Escherichia coli: pGST-170 (full-length NUP170 ORF cloned in pGEX-4T1), pGST-152N (coding region POM152 corresponding to amino acid residues 1–111 in pGEX-6P1), and pET53 (full-length NUP53 ORF cloned into pET9d).
For repression of MET3-NUP170, cells were grown in the supplemented minimal media lacking methionine to a mid-logarithmic growth phase. Methionine (from the 20-µg/ml stock) was then added into the media to a final concentration of 200 µg/ml and incubated at 30°C for the indicated times. For α-factor arrest experiments, α-factor was added into the media to a final concentration of 20 ng/ml at the same time as the methionine addition and incubated for 6 h.

Fluorescence microscopy
Yeast strains synthesizing various GFP and mRFP fusion proteins were taken from cultures at various time points after methionine addition. The locations of GFP and mRFP fusion proteins in live cells were visualized using either an epifluorescence or confocal microscope. Epifluorescence images were obtained with either a microscope (BX50; Olympus) using a UPlanS-Apochromatic 100×/1.40 NA oil objective lens (Olympus) and a charge-coupled device (CCD) camera (AxioCam HRm; Carl Zeiss, Inc.) controlled by AxioVision software (Carl Zeiss, Inc.), or with a microscope (IX70; Olympus) using a UPlanS-Apochromat 100×/1.30 oil objective lens (Olympus) with a CCD camera (CoolSNAP HQ; Photometrics) controlled by Axiviva software (Media Cybernetics). Confocal images were obtained with a microscope (Axiovert 200M; Carl Zeiss, Inc.) equipped with a confocal scanning system (LSM 510 META; Carl Zeiss, Inc.) using a Plan-Apochromat 63×/1.44 NA oil objective lens (Carl Zeiss, Inc.). Image processing (cropping, background subtraction, and linear normalization of images) was performed with the Image software (National Institutes of Health).

Immunofluorescence microscopy using anti-Pom152p (mAb118C3 at 1:200 dilution; Strambio-de-Castillia et al., 1995) and Alexa Fluor 594-labeled anti-mouse IgG (1:200 dilution; Invitrogen) was performed as described previously (Nishikawa et al., 2003). FISH analysis was performed as described previously (Amberg et al., 1992; Cole et al., 2002) using Texas red-labeled oligo (dT50) as a probe.

Kinetic nuclear import assay of NLS reporter proteins
For the kinetic nuclear import assay, the yeast strains expressing a Nls2-2-NLS-GFP reporter protein were harvested from cultures at various time points after methionine addition. Nucleoplasmic equilibration of the reporter protein was achieved by energy depletion using sodium azide and deoxyglucose. Nuclear import of the reporter was initiated by removal of the metabolic poison and addition of media containing glucose, and cells were examined at the indicated times as described previously (Shulga et al., 1996).

Photoconversion of Dendra fusion proteins
We performed two sets of photoconversion experiments using Dendra fusion proteins. In the first set, we examined the localization of Dendra fusion proteins after loss of Nup170p and Nup157p. Yeast cells expressing Dendra fusion proteins were harvested from cultures cells grown in media lacking methionine. Methionine (from the 20 mg/ml stock) was then added to repuppose the Nup170p expression, and cells were immediately placed on a slide-mounted agarose pad (2% low-melt agarose containing the supplemented minimal medium and 200 µg/ml methionine) and then on the fluorescence microscope (BX61 with a UPlanFl 100×/1.30 oil objective; Olympus). Cells were then allowed to grow on the agarose pad for 2 h at 30°C, and images of the Dendra-red signal were imaged just after photoconversion. Cells were then washed with media lacking methionine and then placed on an agarose pad (2% low-melt agarose containing the supplemented minimal medium and 200 µg/ml methionine) and then on the fluorescence microscope (BX61 with a UPlanFl 100×/1.30 oil objective; Olympus) and a CCD camera (AxioCam HRm; Carl Zeiss, Inc.) controlled by AxioVision software (Carl Zeiss, Inc.), or with a microscope (IX80; Olympus) using a UPlanS-Apochromat 100×/1.40 NA oil objective lens (Olympus) and a charge-coupled device (CCD) camera (AxioCam HRm; Carl Zeiss, Inc.) controlled by AxioVision software (Carl Zeiss, Inc.). Image processing (cropping, background subtraction, and linear normalization of images) was performed with the Image software (National Institutes of Health).

Immunoelectron microscopy was performed as described previously (Wente et al., 1992), with modifications. Spheroplasts were incubated in 0.6 M sorbitol and 100 mM potassium phosphate, pH 6.5 (buffer A), for 15 min on ice, and then fixed with 4% formaldehyde and 0.05% glutaraldehyde in buffer A for 1 h on ice. The samples were dehydrated twice in 50% ethanol for 10 min, twice in 80% ethanol for 10 min at room temperature, and then incubated with LR white resin for infiltration at 4°C overnight. The resin was polymerized using UV light for 23 h at 4°C. Thin sections were cut on a Leica Ultracut S microtome. The sections were mounted on nickel grids. The samples were blocked with 1% BSA in TBST and then incubated with mAb14 (Covance) diluted 1:2,000 in 1% BSA in TBST at room temperature for 1 h. After washing with 1% BSA in TBST, the grids were incubated with 12 nm of colloidal gold-conjugated goat anti-mouse IgG (Jackson ImmunoResearch Laboratories) diluted 1:30 in 1% BSA in TBST. After final washes, the samples were contrasted with 2% aqueous uranyl acetate for 5 min.

Isolation of recombinant proteins expressed in bacteria and in vitro binding assays
An E. coli strain BL21 (DE3) containing plasmids expressing GST, Nup53p, GST-Nup170p, and GST-Pom152p1–111 was grown to an OD of 0.6–1.0 at 37°C, and induced with 1 mM IPTG for 2 h at 37°C for GST, Nup53p, and GST-Pom152p1–111, and overnight at room temperature for GST-Nup170p. GST and GST fusion proteins were purified on glutathione Sepharose 4B beads (GE Healthcare), according to the manufacturer’s instructions, in lysis buffer (50 mM Tris HCl, pH 7.5, 300 mM NaCl, 150 mM potassium acetate, 2 mM MgCl2, 0.1% octylglucoside, 1 mM DTT, and complete protease inhibitor cocktail [Roche]).

Nup170p was separated from GST and released from the beads by incubation with 0.6 units of thrombin (Sigma-Aldrich) per 10 µl of beads for 4 h at room temperature.

For in vitro binding assays examining the interactions of Nup170p and GST-Pom152p1–111, 25 µl of purified Nup170p in buffer B (50 mM Tris HCl, pH 7.5, 150 mM potassium acetate, 2 mM MgCl2, 0.1% octylglucoside, 10% glycerol, 1 mM DTT, and complete protease inhibitor cocktail [Roche]) was incubated with 25 µl of glutathione Sepharose 4B beads preloaded with either purified GST or purified GST-Nup152p1–111 for 2 h at 4°C. The unbound fraction was obtained from the supernatant after the incubation. After washing, proteins were eluted from the beads with SDS-PAGE sample buffer and analyzed by SDS-PAGE and Coomassie blue staining.

For in vitro binding assays examining the interactions of Nup53p and GST-Nup170p, 15 µl of bacterial lysate containing Nup53p in lysis buffer was supplemented with 2 mM ATP and 10 mM MgSO4, and then incubated with 100 µl of glutathione Sepharose 4B beads preloaded with purified GST-Nup170p for 20 min at 4°C. The unbound fraction was obtained from the supernatant just after the incubation. After washing, proteins were released from the beads by incubation with 0.6 units of thrombin. Proteins in the various fractions were analyzed by SDS-PAGE and Coomassie blue staining.

Online supplemental material
Fig. S1 shows that recombinant Nup170p directly binds an N-terminal fragment of Pom152p and Nup53p. Table S1 lists the strains used in this study. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200810029/DC1.

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References


Figure S1. **Nup170p directly interacts with Pom152p and Nup53p.** (A) Nup170p directly binds an N-terminal fragment of Pom152p. Recombinant Nup170p (N), GST-Pom152p1-111 (P), and GST (G) were purified (input). GST-Pom152p1-111 and GST were bound to glutathione Sepharose 4B beads and incubated with Nup170p (T). Bead-bound proteins (B) and the unbound flow through (UB) were then separated. Proteins in the various fractions were analyzed by SDS-PAGE and Coomassie blue staining. (B) Recombinant Nup170p binds directly to recombinant Nup53p. Recombinant GST-Nup170p was bound to glutathione Sepharose 4B beads and incubated with E. coli lysates containing recombinant Nup53p. Bound and unbound fractions were examined directly, or the Nup170p–Nup53p complex was released from the beads by incubation with thrombin. Fractions were analyzed by SDS-PAGE and Coomassie blue staining. The positions of Nup170p and Nup53p are indicated. The identity of Nup53p was conferred by Western blotting (not depicted).
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