A role for Rab5 in structuring the endoplasmic reticulum

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The endoplasmic reticulum (ER) is a contiguous network of interconnected membrane sheets and tubules. The ER is differentiated into distinct domains, including the peripheral ER and nuclear envelope. Inhibition of two ER proteins, Rtn4a and DP1/NogoA, was previously shown to inhibit the formation of ER tubules in vitro. We show that the formation of ER tubules in vitro also requires a Rab family GTPase. Characterization of the 29 Caenorhabditis elegans Rab GTPases reveals that depletion of Rab-5 phenocopies the defects in peripheral ER structure that result from depletion of RET-1 and YOP-1, the C. elegans homologues of Rtn4a and DP1/NogoA. Perturbation of endocytosis by other means did not affect ER structure; the role of RAB-5 in ER morphology is thus independent of its well-studied requirement for endocytosis. RAB-5 and YOP-1/RET-1 also control the kinetics of nuclear envelope disassembly, which suggests an important role for the morphology of the peripheral ER in this process.

Introduction

The ER is a single contiguous compartment (Terasaki and Jaffe, 1991; Cole et al., 1996; Terasaki, 2000) that is differentiated into at least three functionally distinct domains: rough ER, smooth ER, and nuclear envelope (Palade, 1955; Watson, 1955; Baumann and Walz, 2001). Cumulatively, these ER domains partition the nuclear contents from the cytoplasm and direct the synthesis of lipids, as well as membrane and secretory proteins (Estrada de Martin et al., 2005; Hetzer et al., 2005; Margalit et al., 2005; Shibata et al., 2006; Vedrenne and Hauri, 2006). The ER is also a signaling organelle that serves as a storage site for intracellular calcium and regulates its uptake and release into the cytoplasm (Papp et al., 2003).

Structurally, the ER network consists of membrane tubules, flattened sheets, and cisternae. The thickness of ER sheets is similar to the diameter of ER tubules, typically 60–100 nm, suggesting that common structural elements underlie these morphologically distinct forms (Shibata et al., 2006). The differing morphologies exhibited by ER domains likely contribute to their distinct functions. Rough ER, specialized for protein synthesis and folding, is often found in ribosome-studded sheets. In contrast, smooth ER, a site for lipid synthesis, contact with other organelles, and vesicle budding and fusion, lacks ribosomes and is often tubular (Baumann and Walz, 2001). The nuclear envelope, perhaps the most highly differentiated region of the ER, is a polarized sheet that regulates the movement of macromolecules between the nuclear space and the cytoplasm (Hetzer et al., 2005; Prunuske and Ullman, 2006). The membrane on one side of the sheet, the outer nuclear membrane (ONM), faces the cytoplasm, and on the opposite side of the lumen, the inner nuclear membrane (INM) faces the chromatin. Nuclear pores, gated channels between the cytoplasm and the nuclear interior, pass through both membrane bilayers and are sites where the INMs and ONMs are fused to each other (Salina et al., 2001; Hetzer et al., 2005; Tran and Wente, 2006). Resident INM proteins pass from the ONM to the INM by diffusion or active transport through the nuclear pores and concentrate in the INM as a result of interactions with the underlying chromatin and the nuclear lamina (Gerace and Burke, 1988; Soullam and Worman, 1995; Ellenberg et al., 1997; Holmer and Worman, 2001; Ohba et al., 2004; Gruenbaum et al., 2005; King et al., 2006).

Visualization in living cells has revealed the dynamic nature of the ER network. ER tubules in the periphery of mammalian cells continuously form and fuse, generating a meshwork characterized by the presence of “three-way” junctions between tubules that can move relative to one another (Lee and Chen, 1988; Waterman-Storer and Salmon, 1998; Estrada de Martin et al., 2005). The ER is also structurally reorganized during cell...
cycle progression. One prominent example is in animal cells, where the nuclear envelope disassembles during mitotic entry to promote spindle assembly. After the chromosomes separate in anaphase, nuclear envelopes reform around each of the separated chromatin masses (Mattaj, 2004; Margalit et al., 2005; Prunuske and Ullman, 2006). The peripheral ER also undergoes cell cycle–dependent changes. In eggs from a variety of vertebrate and invertebrate species, there is a dramatic clustering of the peripheral ER network during mitosis (Bobinnec et al., 2003; Poteryaev et al., 2005; Strickler, 2006). This has been particularly well characterized in *Xenopus laevis* oo cytcs, where electron microscopy revealed the formation of “mitotic ER clusters” between 1 and 5 μm in diameter composed of packed smooth ER tubules and cisternae (Terasaki et al., 2001).

Relatively little is known about the factors that shape ER tubules and sheets, how the domains within the contiguous ER network maintain their distinct morphologies, or how transitions in the organization of the ER network during cell cycle progression are orchestrated. However, the development of systems for assembly of ER tubules from vesicles in vitro has led to some molecular insight. The reticulum family member Rtn4a was identified based on its modification by sulfhydryl reagents that inhibit the assembly of ER tubules (Voeltz et al., 2006). Inhibition of Rtn4a by antibody addition to the in vitro reaction did not block vesicle fusion but prevented the fused vesicles from adopting an elongated tubule-like morphology. These results suggest that ER tubule formation requires both homotypic vesicle fusion and factors, including Rtn4a, that confer a tubular, rather than spherical, geometry. Rtn4a interacts with a second integral membrane protein called DP1/NogoA, and in *Saccharomyces cerevisiae*, Ret1p and Yop1p, homologues of Rtn4a and DP1/NogoA, localize to the ER and play a functionally redundant role in the maintenance of peripheral ER tubules (Voeltz et al., 2006). The mechanisms that drive homotypic fusion during the assembly of ER tubules remain unclear. In vitro, fusion requires GTP and is inhibited by a nonhydrolyzable GTP analogue (Dreier and Rapoport, 2000). In addition, a previous study demonstrated that the homotypic fusion of mammalian ER microsomes could be blocked by Rab GDP-dissociation inhibitor (GDI), implicating a Rab-type GTPase in the fusion reaction (Turner et al., 1997).

Here, we used the *Caenorhabditis elegans* embryo as a model system to explore the molecular requirements for ER structure and dynamics. We show that simultaneous inhibition of YOP-1 and RET-1, the *C. elegans* homologues of DP1 and Rtn4a, results in a defect in ER morphology that is most pronounced during mitosis, when the ER is coalesced. Using this phenotype as a guide, we examined embryos depleted of each of the 29 *C. elegans* Rab family GTPases. Surprisingly, we found that specific depletion of the endosomal Rab-type GTPase, RAB-5, resulted in a defect in ER morphology that closely resembled depletion of YOP-1/RET-1. Both RAB-5 and YOP-1/RET-1 are also required for timely disassembly of the nuclear envelope during mitosis. Cumulatively, these results suggest that the morphology of the peripheral ER is important for nuclear envelope disassembly during mitotic entry.

**Results**

**RET-1 and YOP-1 are redundantly required for ER morphology**

To explore the molecular requirements for ER structure, we used the first division of the *C. elegans* embryo as a model system. In *C. elegans* (Poteryaev et al., 2005), as in eggs from other vertebrate and invertebrate species (Kline, 2000; Terasaki et al., 2001; Bobinnec et al., 2003), the ER coalesces during mitosis into a reticular network of thick tubules and “mitotic ER clusters.” Because the interphase network of fine ER tubules is difficult to resolve at the light microscopic level, examination of the ER in its coalesced mitotic state provides a convenient means to identify defects in ER structure. We monitored ER dynamics by imaging embryos expressing a GFP fusion with the luminal signal peptidase SP-12 (Poteryaev et al., 2005). After fertilization, the oocyte- and sperm-derived pronuclei migrate toward each other. The two pronuclei meet, and the nuclear/centrosome complex moves to the embryo center and rotates onto the long axis of the cell. Subsequently, the nuclear envelopes become permeable, and the mitotic spindle assembles (Fig. 1 A). During interphase, before pronuclear migration, GFP:SP-12 was present in the pronuclear envelopes as well as in a network of fine tubules and punctate structures dispersed throughout the cytoplasm. As the embryos entered mitosis, the ER coalesced to form a reticular network of thicker tubules and mitotic clusters (Fig. 1, B and D; and Video 1, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1; Poteryaev et al., 2005). The clusters began to form ∼80 s before the onset of nuclear envelope disassembly and were enriched around the centrosomes and mitotic spindle (Fig. 1, B and C, 0-s time point). The first embryonic division in *C. elegans* is polarized, and mitotic ER clusters were concentrated near the cortex in the embryo anterior (Fig. 1 B, 0-s time point, cortical plane), similar to the cortical actomyosin cytoskeleton. After chromosome segregation in anaphase, the thick tubules and clusters abruptly dispersed, and nuclear envelopes re-formed around the separated chromosome masses, returning the ER to its interphase state (Video 1).

Rtn4a and its associated protein DP1/NogoA have been implicated in ER tubule assembly in vitro (Voeltz et al., 2006). We therefore characterized the localization and depletion phenotypes for their *C. elegans* homologues, RET-1 and YOP-1. Both endogenous RET-1 (Fig. 1 E) and a GFP fusion with YOP-1 (Fig. S1, A and B, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1) localized to the ER. Like their vertebrate and yeast homologues (Voeltz et al., 2006), RET-1 and YOP-1 concentrate in the peripheral ER and are largely excluded from the nuclear envelope, where they are de-enriched relative to the luminal ER marker SP-12 (Fig. 1 E and Fig. S1 A). Consistent with their redundant functions in budding yeast, embryos depleted of YOP-1 or RET-1 alone exhibited no appreciable defects in embryo viability or ER structure (unpublished data). However, simultaneous depletion of YOP-1 and RET-1 dramatically altered ER morphology and reduced embryonic
viability to ~40% (473 of 1191 embryos survived to hatching).

The ER morphology defect was particularly evident during mitosis, when the network is normally coalesced. In YOP-1/RET-1-depleted embryos, there were fewer thick tubules that appeared shorter and more poorly organized than in control embryos, and no mitotic ER clusters were formed (Fig. 1, B and C; and Video 1). We conclude that YOP-1/RET-1 play a critical role in ER structure. In addition, their simultaneous inhibition results in a phenotype that is easily detected by monitoring ER organization in mitotic embryos using light microscopy.

Depletion of RAB-5 results in an ER morphology defect similar to YOP-1/RET-1 depletion

A visual assay for formation of a tubular ER network from salt-washed ER-enriched membranes isolated from X. laevis oocytes revealed that tubule assembly requires GTP, in addition to Rtn4a and DP1/NogoA (Dreier and Rapoport, 2000; Voeltz et al., 2006). To investigate the origin of this GTP requirement, we compared the ability of X. laevis ER-enriched membranes to form tubules after incubation with either Rab or Rho GDI, which
inhibit Rab or Rho family GTPases, respectively. Although Rho GDI failed to have any effect, addition of Rab GDI potently blocked ER tubule formation in vitro (Fig. 2 A). This result suggested that, in addition to YOP-1 and RET-1, ER structure is controlled by a Rab family GTPase.

To investigate whether a Rab GTPase contributes to ER structural dynamics in vivo, we systematically depleted each of the 29 C. elegans Rabbs (Table S1, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1). This analysis identified six Rab activities necessary for embryo production and/or early embryogenesis (Fig. 2 B). Of these, only reduction of RAB-5 levels resulted in an effect on ER structure similar to depletion of YOP-1/RET-1 (compare Fig. 2 C with Fig. 1, B and C; Video 1). Depletion of RAB-5, which resulted in 100% embryonic lethality, inhibited both the formation of a reticular network of thick tubules and the appearance of mitotic ER clusters (Fig. 2, C, E, and F; and Videos 1 and 2). In contrast to the dramatic effect on ER structure, staining of control and RAB-5–depleted fixed embryos with antibodies against a Golgi marker, the glucuronyltransferase SQV-8, revealed that Golgi size and distribution were not altered by RAB-5 depletion (Fig. 2 D).

Figure 2. Depletion of RAB-5 results in an ER morphology defect similar to depletion of YOP-1/RET-1. (A) Salt-washed membrane vesicles isolated from X. laevis eggs were incubated in the absence (top left) or presence of GTP (top right) or in the presence of GTP and 30 μM Rho GDI (bottom left) or 10 μM Rab GDI (bottom right). Data are representative of four independent experiments for each condition. Bar, 5 μm. (B) A rooted phylogenetic tree based on a sequence comparison of selected Rab-type GTPases from S. cerevisiae, C. elegans, and Homo sapiens. Asterisks denote redundancy between RAB-8 and RAB-10 or RAB-6.1 and RAB-6.2, which must be codepleted to observe a phenotype. Lethality of the embryos produced by the dsRNA-injected mother (Emb) and/or the failure of the injected mother to produce a normal number of embryos (Ste) is indicated. (C) Spinning-disk confocal optics were used to image RAB-5–depleted embryos (rab-5[RNAi]; n = 21) expressing the ER marker GFP:SP-12, as in Fig. 1 B. Bar, 10 μm. Higher magnification (2 ×) views of a portion of the adjacent cortical sections are shown to the right. Bar, 5 μm. (D) Metaphase control (left) and rab-5[RNAi] (right) embryos were fixed and stained with antibodies to the endosome marker RAB-5 (top) and the Golgi marker SQV-8 (bottom). Images are projections of deconvolved 3D datasets. Bar, 10 μm. (E) The number of mitotic ER clusters (>0.5 μm in diameter) measured in a cortical section of embryos expressing GFP:SP-12 collected 10 s before anaphase onset is plotted for at least 16 embryos for each condition. (F) Representative cortical sections used for the quantification in E showing GFP:SP-12 in control (left), RAB-5–depleted (middle), and YOP-1– and RET-1–depleted (right) embryos 10 s before anaphase onset. Bar, 10 μm.
The role of RAB-5 in ER structure is independent of its requirement during endocytosis

Rab5 has an established role in endocytosis and early endosome fusion (Somsel Rodman and Wandinger-Ness, 2000; D’Hondt et al., 2000; Pfeffer, 2001; Zerial and McBride, 2001). Previous work in C. elegans has shown that these functions are mediated by two RAB-5 guanine nucleotide exchange factors (GEFs), RME-6 and RABX-5, which have overlapping functions (Sato et al., 2005). Examination of the ER in embryos mutant for rabx-5 in which RME-6 was depleted by RNAi revealed a structural defect essentially identical to that in rab-5(RNAi) embryos.
(Fig. 3, A and E), indicating that the role of RAB-5 in ER structure is also mediated by RME-6 and RABX-5.

To determine whether the effect of RAB-5 depletion on ER structure is an indirect consequence of its effect on endocytosis, we inhibited endocytosis by depleting other proteins that function in the early endocytic pathway, including clathrin heavy chain (CHC-1; Fig. 3 B), dynamin, and α-adaptin (not depicted). Depletion of CHC-1 redistributed clathrin light chain into the cytoplasm (not depicted) and resulted in a dramatic decline in cytoplasmic yolk granule density (Fig. 3 B), a hallmark of a pronounced defect in endocytosis during oocyte development (Grant and Hirsh, 1999). However, despite a reduction in yolk density similar to that in RAB-5–depleted embryos, ER morphology was not perturbed by CHC-1 depletion (Fig. 3 B). RAB-5 still localized to punctate endosomal structures in CHC-1–depleted embryos (Fig. 3 C), although the RAB-5 structures were enlarged and relatively more concentrated in the embryo anterior compared with controls. Examination of ER structure in embryos individually depleted of candidate RAB-5 effector proteins, including the C. elegans homologues of EEA-1, Rabenosyn-5, Rabaptin-5, and the catalytic subunit of a type 3 PI 3-kinase, hVps34 (Deneka et al., 2003), also failed to reveal any detectable alteration in ER morphology (Fig. 3, D and E).

Depletion of RAB-5 also did not substantially alter the appearance of the microtubule cytoskeleton (Fig. S1 C), which has been shown to play a role in the distribution of the ER within cells (Du et al., 2004; Vedrenne and Hauri, 2006). In addition, mitotic ER tubules and clusters still formed in nocodazole-treated embryos that lacked detectable microtubule polymer (Fig. S1 D). As previous work suggested that the actomyosin cytoskeleton also plays a role in ER structure (Poteryaev et al., 2005), we examined the distributions of GFP fusions with myosin II (GFP:NMY-2; Nance et al., 2003) and the actin binding domain of moesin (GFP:Moe), an established probe for filamentous actin in the C. elegans embryo (Motegi et al., 2006). In the period leading up to metaphase, the actin cytoskeleton appeared similar in control and depleted embryos (Fig. S1 E). A comparison of the distribution of GFP:NMY-2 in control, rab-5::RNAi, and chc-1::RNAi embryos revealed that during the establishment of polarity, the organization of cortical myosin II was also similar under all three conditions (Fig. S1 F). During mitosis, the organization of GFP:NMY-2 in rab-5::RNAi embryos, although distinct from that in controls, was similar to that in the chc-1::RNAi embryos (Fig. S1 G). These results suggest that although compromised endocytosis, which is common to both rab-5::RNAi and chc-1::RNAi embryos, does alter the organization of cortical NMY-2, this mild perturbation is not responsible for the impact of RAB-5 depletion on ER structure.

Cumulatively, these findings indicate that the defect in ER structure in RAB-5–depleted embryos is not a consequence of a general perturbation of membrane trafficking, a disruption of microtubule–ER interactions, or a defect in the organization of the actomyosin cytoskeleton, and instead support the conclusion that RAB-5 has a specific and previously unappreciated role in ER morphology.
YOP-1/RET-1 would not enhance the effect of RAB-5 depletion on ER morphology. However, simultaneous depletion of YOP-1/RET-1 with RAB-5 resulted in a dramatic synergistic defect evident throughout the cell cycle (Fig. 4, D and E). In the triple-depleted embryos, ER morphology was aberrant in interphase, when GFP:SP-12 was present in numerous loop-shaped structures. These ER loops accumulated around the spindle poles as the triple-depleted embryos entered mitosis, leaving the embryo periphery nearly devoid of ER (Fig. 4 D). In addition, as in the individual depletions, the ER failed to coalesce into a network of thick tubules and clusters (Fig. 4 D and Video 4, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1). Although it is possible that RAB-5 and YOP-1/RET-1 are on a single pathway and the synergistic defect in ER structure is due to a greater effectiveness in inhibiting this pathway when two of its constituents are depleted by RNAi, we favor the idea that the strong synergistic phenotype indicates that RAB-5 and YOP-1/RET-1 make distinct essential contributions to ER structure. It is worth pointing out, however, that the idea that RAB-5 and YOP-1/RET-1 each retain some function when the other is absent does not rule out the possibility that RAB-5 exerts its effect in part by altering the function of YOP-1/RET-1.

Both RAB-5 and YOP-1/RET-1 promote nuclear envelope disassembly

The ER is a single contiguous compartment that includes the nuclear envelope. We were therefore interested in whether, in addition to the peripheral ER, inhibition of RAB-5 or YOP-1/RET-1 altered nuclear envelope dynamics. One clue that this might be the case came from the observation that depletion of either RAB-5 or YOP-1/RET-1 resulted in a characteristic...
“four-eyes” phenotype at the end of the first division, in which two nuclei instead of one re-formed in each daughter cell. In the C. elegans zygote, after the two pronuclei meet, the nuclear envelopes are permeabilized and cleared from the region near the centrosomes, allowing spindle microtubules to interact with and align chromosomes before their segregation (Fig. 5 A; Oegema and Hyman, 2005). After anaphase chromosome segregation, a single nuclear envelope reforms around each of the separated chromatin masses, thereby mixing the haploid sperm and oocyte genomes. In embryos in which either RAB-5 or YOP-1/RET-1 was depleted, separate nuclear envelopes formed around the sperm- and oocyte-derived chromosomes after their segregation, resulting in two nuclei in each daughter cell (Fig. 5 B).

To understand the basis for this phenotype, we filmed embryos coexpressing a GFP fusion with the INM protein LEM-2 and an RFPmCherry fusion with histone H2B. This analysis revealed that ~35 s before anaphase onset, the juxtaposed oocyte and sperm pronuclear envelopes in control embryos undergo a scission event in close proximity to the aligned chromosomes and are cleared from the region between the chromosomes, allowing the chromosomes from the two pronuclei to mix and form a single nucleus after segregation (Fig. 5 C and Video 5, left, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1). In embryos in which either RAB-5 or YOP-1/RET-1 were depleted, this scission event never occurred, and the oocyte- and sperm- derived chromosomes remained separate during their segregation on the spindle (Fig. 5, D and E; and Video 5, right). Consequently, two nuclei were formed in each daughter cell, and the mixing of the genomes derived from the two gametes failed.
Depletion of NPP-12 phenocopies
the nuclear envelope disassembly defect resulting from RAB-5 or YOP-1/RET-1 depletion without disrupting peripheral ER structure

The four-eyes phenotype observed in YOP-1/RET-1– or RAB-5–depleted embryos is highly unusual. Functional genomic analysis of cell division in C. elegans identified only one other protein, the nuclear pore component NPP-12, whose depletion reproducibly results in this phenotype (Sönnichsen et al., 2005). NPP-12 is the C. elegans homologue of gp210, one of two integral membrane proteins associated with the nuclear pore (Holaska et al., 2002; Hetzer et al., 2005). Imaging of embryos coexpressing GFP:LEM-2 and RFP:histone confirmed that depletion of NPP-12 results in a defect in nuclear envelope disassembly similar to that resulting from depletion of RAB-5 or YOP-1/RET-1 (Fig. 5 F). However, analysis of GFP:SP-12 indicated that, in contrast to depletion of YOP-1/RET-1 or RAB-5, depletion of NPP-12 does not noticeably perturb peripheral ER structure (Fig. 5, G and H). These results indicate that the defect in nuclear envelope disassembly in the YOP-1/RET-1– and RAB-5–depleted embryos is likely to be a consequence rather than a cause of the defect in ER structure. They also point to an interesting functional connection between the role of peripheral ER structure in nuclear envelope disassembly and events occurring at nuclear pores.

Figure 6. RAB-5 depletion delays nuclear envelope permeabilization, nuclear pore removal, and lamina disassembly. (A) Time-lapse spinning-disk confocal sequences of control, rab-5(RNAi), and npp-12(RNAi) embryos expressing GFP:histone were used to measure the timing of nuclear envelope breakdown relative to chromosome condensation. Representative sequences of individual nuclei are shown. Times are with respect to condensation onset. Bar, 5 μm. (B) Plot of the mean value of the condensation parameter versus time for control (gray circles; n = 5), rab-5(RNAi) [red squares; n = 5], and npp-12(RNAi) [green diamonds; n = 5] embryos. Traces are displayed with the onset of condensation as t = 0. Arrows mark the timing of nuclear envelope permeabilization for each dataset. Error bars indicate SEM. (C and D) Time-lapse sequences of control and rab-5(RNAi) embryos expressing RFP:histone and either GFP:NUP-155 (C) or YFP:LMN-1 (D) were acquired using spinning-disk confocal optics (n = 5 for each condition). Images from representative sequences are shown for control (left) and rab-5(RNAi) (right) embryos. Times are in seconds relative to the onset of chromosome segregation. Bar, 5 μm. (E) The total fluorescence intensity of nuclear LMN-1 was measured at each time point for control (n = 7), rab-5(RNAi) [n = 6], and npp-12(RNAi) [n = 6] embryos. The mean value for this measurement is plotted versus time. Error bars indicate SEM. Sequences were time aligned with respect to onset of anaphase chromosome segregation.
Depletion of RAB-5 or NPP-12 delays multiple steps in nuclear envelope disassembly

Diffusion of membrane proteins between the peripheral ER and INM is proposed to require energy-dependent restructuring that creates transient channels through the nuclear pore membrane (Ohba et al., 2004). Antibodies to gp210 inhibit diffusion between the peripheral ER and INM, suggesting that gp210 plays a role in this restructuring (Ohba et al., 2004). A role in promoting the diffusion of integral membrane proteins between the peripheral ER and INM would provide a plausible explanation for why perturbing gp210 or peripheral ER structure has a similar effect on nuclear envelope disassembly. To explore the phenotypic similarity of these two very different perturbations further, we used a series of assays to compare nuclear envelope disassembly in NPP-12- and RAB-5-depleted embryos. Nuclear envelope disassembly is accompanied by several distinct events: (1) loss of the peripheral pore components, which renders the nuclear envelope permeable to macromolecules of progressively larger diameter (Terasaki et al., 2001; Lenart et al., 2003); (2) removal of pores from the membrane; (3) disassembly of the nuclear lamina; and (4) release of resident INM proteins back into the peripheral ER (Hetzer et al., 2005; Prunuske and Ullman, 2006). Because the dependencies between these different events are not clear, we compared the effects of RAB-5 and NPP-12 depletion on all of them.

To determine if nuclear envelope permeabilization was affected, we filmed embryos expressing GFP:histone H2B and measured the timing of nuclear envelope permeabilization with respect to the kinetics of chromosome condensation. Permeabilization was followed by monitoring the diffusion of free GFP: histone out of the nucleus, which occurs within 60 s of the entry of cytoplasmic 70-kD dextran into the nucleus (Portier et al., 2007). We refer to the time point when the free nuclear GFP: histone fluorescence has equilibrated with the cytoplasm as nuclear envelope permeabilization. To analyze chromosome condensation, we used a recently developed image analysis method that can be used to quantitatively compare condensation kinetics between control and specifically perturbed embryos (Maddox et al., 2006). This analysis revealed that the kinetics of chromosome condensation were not altered by depletion of either RAB-5 or NPP-12. However, both perturbations resulted in a 50–60-s delay between the completion of chromosome condensation and nuclear envelope permeabilization (Fig. 6, A and B).

Timing the release of a NLS-containing GFP fusion protein (GFP-LacI) from the nucleus relative to anaphase onset provides independent support that permeabilization is delayed by approximately 50 s in RAB-5– or NPP-12-depleted embryos (Fig. S4, A–C, available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1).

To analyze the removal of nuclear pores from the envelope, we filmed embryos expressing a GFP fusion with NUP-155, a stable component of the pore wall (Franz et al., 2005). Redistribution of NUP-155 from the nuclear rim to the cytoplasm was delayed by approximately 50 s in RAB-5– and NPP-12-depleted embryos (Fig. 6 C and not depicted). Disassembly of the nuclear lamina was also similarly delayed by both perturbations. Although a YFP fusion with the C. elegans B-type lamin LMN-1 is nearly completely removed from the nuclear envelope by anaphase onset in control embryos, substantial amounts of LMN-1 remained at anaphase onset in RAB-5– or NPP-12-depleted embryos (Fig. 6 D). Fluorescence intensity measurements revealed that until anaphase onset, lamin disassembly is quantitatively similar between RAB-5– and NPP-12–depleted embryos (Fig. 6 E).

We next investigated the effect of depletion of RAB-5 and NPP-12 on the release of resident INM proteins into the peripheral ER. In the C. elegans embryo, the INM protein LEM-2 is present in the peripheral ER throughout the cell cycle. As the nuclear envelope forms in telophase, LEM-2 becomes selectively enriched in this ER domain (Fig. S4 E). Because the presence of LEM-2 in ER concentrated around mitotic spindle poles interfered with visualization of LEM-2 associated with the nuclear envelope, we examined the effect of RAB-5 depletion in spd-5(RNAi) embryos, which lack functional centrosomes and fail to build mitotic spindles (Fig. 7 A). In embryos depleted of SPD-5 alone, the peripheral ER exhibits normal dynamics and coalesces during mitosis to form a network of thick tubules and clusters (Fig. 7 B). As expected, when both SPD-5 and RAB-5 were depleted, there was a profound defect in the formation of thick tubules and clusters during mitosis (Fig. 7 B). In embryos depleted of SPD-5 alone, LEM-2 is completely dispersed into the surrounding ER and then reaccumulates around the chromatin as it begins to decondense. In contrast, in embryos codepleted of either RAB-5 or NPP-12 with SPD-5, the redistribution of LEM-2 failed to occur (Fig. 7, C–E).

Cumulatively, these results indicate that depletion of RAB-5 or NPP-12 results in a similar, broadly based defect in nuclear envelope disassembly, in which the release of INM proteins into the peripheral ER is blocked and nuclear envelope permeabilization, pore removal, and lamina disassembly are delayed. These results highlight a central importance of peripheral ER structure in ensuring timely nuclear envelope disassembly.

Discussion

A role for Rab5, the canonical endocytic Rab GTPase, in ER structure

Here, we show that ER morphology is sensitive to both depletion and activation of RAB-5, exhibiting opposing responses to the two perturbations. The effect of RAB-5 depletion on ER structure phenocopies the depletion of YOP-1/RET-1, two ER proteins previously implicated in the assembly of ER tubules in vitro. Experiments in human cells expressing a dominant-active mutant form of Rab5A suggest that the role of Rab5 in controlling ER structure is likely to be conserved. We discuss the nature of the defects in peripheral ER structure and nuclear envelope disassembly observed in RAB-5– and YOP-1/RET-1–depleted embryos and speculate on underlying mechanisms.

The defects in ER morphology in RAB-5– and YOP-1/RET-1–depleted embryos are most prominent during mitosis and could therefore reflect a specific role for RAB-5 and YOP-1/RET-1 in restructuring the interphase peripheral ER network during mitotic entry. Alternatively, YOP-1/RET-1 and RAB-5 may be required to maintain a normal ER network during interphase,
which is then the substrate for mitotic coalescence. We favor the later possibility for three reasons. First, in embryos that are simultaneously depleted of YOP-1/RET-1 and RAB-5, obvious defects in ER structure are apparent in interphase (Fig. 4, D and E). Second, reticulon/Rab-dependent assembly of ER tubules in vitro from X. laevis oocyte membranes is inhibited by mitotic but not interphase cytosol (Dreier and Rapoport, 2000). Third, defects in ER structure are apparent when Yop1p and the reticulons are deleted in budding yeast, regardless of cell cycle state (De Craene et al., 2006; Voeltz et al., 2006).

Previous work has identified >20 different effectors that link Rab5 to a variety of cellular activities (Christoforidis et al., 1999). However, technical difficulties have prevented the isolation of integral membrane proteins that respond to Rab5 signaling. The fact that depletion of YOP-1/RET-1 has an effect on ER structure that is similar to that of depletion of RAB-5, and the requirement for YOP-1/RET-1 for RFP:RAB-5Q78L to exert a dominant effect, make YOP-1 and RET-1 attractive candidates for integral membrane effectors that link RAB-5 to the ER. Interestingly, the budding yeast homologue of YOP-1, Yop1p, was identified based on the fact that a short amino acid stretch in its N terminus interacts with Yip1, a protein implicated in the dissociation of Rab GTPases from GDI. In addition, Yop1p was found to interact with multiple Rab-type GTPases in yeast, potentially via their prenylation motifs (Calero et al., 2001). Although a conventional in vitro approach using GST:RAB-5 isolated from bacteria failed to uncover evidence for a direct interaction between RAB-5 and either YOP-1 or RET-1 (Fig. S3 C), it is possible that this interaction requires prenylation of RAB-5 and/or membrane association of YOP-1/RET-1, and hence a different approach may be needed to uncover an interaction. In addition to YOP-1 and RET-1, our data suggest the existence of additional effectors, as simultaneous depletion of RAB-5 exacerbates the defect in ER morphology present in embryos depleted of YOP-1/RET-1 alone (Fig. 4, D and E). A combination of genetic analysis in C. elegans with in vitro biochemical reconstitution of ER tubules using X. laevis membranes will likely be useful to uncover these important factors.

Control of ER structure by trans-acting small GTPases—an emerging theme?

RAB-5 was the only Rab GTPase whose depletion phenocopied the effect of YOP-1/RET-1 depletion on ER structure. This finding was surprising because RAB-5 localizes to endosomes and has well-studied functions in endocytosis and early endosome fusion (for reviews see D’Hondt et al., 2000; Somsel Rodman and Wandinger-Ness, 2000; Pfeffer, 2001; Zerial and McBride, 2001). Inhibition of endocytosis by other means, such as CHC-1 depletion, does not affect ER structure but also does not abolish localization of RAB-5 (Fig. 3 C), indicating that endosomes, although abnormal, are still present. In contrast to CHC-1 depletion, simultaneous inhibition of the two characterized RAB-5 GEFs, RME-6 and RABX-5, redistributes RAB-5 to the cytoplasm (Sato et al., 2005) and phenocopies the effect of RAB-5 depletion (Fig. 3, A and E). These results suggest that endosomal RAB-5 acts in trans to control ER structure.
work suggests a role for the Rab24 GTPase during starvation-induced autophagy, although its precise function in this process remains unknown (Munafo and Colombo, 2002). Why would ER structure be controlled by trans-acting GTPases? One possibility is that trans-action restricts homotypic ER fusion to specific times and places within the cell to facilitate the formation of a network or envelope as opposed to large membrane aggregates.

A connection between peripheral ER morphology and nuclear envelope disassembly

We show that depletion of YOP-1/RET-1 or RAB-5 leads to a defect in nuclear envelope disassembly in addition to disrupting the morphology of the peripheral ER. Further characterization of this defect revealed a striking phenotypic similarity to depletion of NPP-12, the C. elegans homologue of the nuclear pore-associated integral membrane protein, gp210. Although both perturbations delay nuclear envelope permeabilization, pore removal, and lamina disassembly, the most pronounced consequence of either depletion is an essentially complete block in the release of INM components into the peripheral ER.

RAB-5 and YOP-1/RET-1 may directly restructure the nuclear envelope in addition to the peripheral ER. However, we suspect that the contribution of RAB-5 and YOP-1/RET-1 to nuclear envelope disassembly occurs indirectly via their function in structuring the peripheral ER. Consistent with this idea, YOP-1/RET-1 and their homologues in other organisms are selectively enriched in the peripheral ER relative to the nuclear envelope (Fig. 1 E; Fig. S1 A; Voeltz et al., 2006). Previous work has shown that INM components disperse into the peripheral ER during mitosis after their release from chromatin and the nuclear lamina (Yang et al., 1997; Mattaj, 2004). We therefore propose that disruption of peripheral ER morphology in RAB-5– and YOP-1/RET-1–depleted embryos prevents the diffusion of INM proteins, trapping them in the spindle region (Fig. 8 B). In this context, the fact that depletion of NPP-12/gp210 phenocopies the effect of disruption of the peripheral ER on nuclear envelope disassembly would support the previous suggestion that NPP-12/gp210 acts as a gatekeeper that positively regulates the diffusion of membrane proteins between the INM and peripheral ER (Ohba et al., 2004). We would like to emphasize that although depletion of RAB-5 or YOP-1/RET-1 results in defects in both mitotic clustering of the peripheral ER and in nuclear envelope breakdown, our data do not demonstrate that these phenotypes are linked (i.e., cluster formation stimulates nuclear envelope breakdown). It remains equally likely that these two phenotypes are independent consequences of disruption of peripheral ER structure.

In summary, our results suggest that trans-acting mechanisms involving small GTPases play an integral role in structuring the distinct domains, including the peripheral ER and nuclear envelope, within the contiguous ER network. In addition to identifying a new role for Rab5 in ER structure, our analysis also supports a role for peripheral ER structure in nuclear envelope disassembly.
Materials and methods

The generation of C. elegans strains expressing fluorescent fusions with histone H2B (Oegema et al., 2001), LEM-2 (Galy et al., 2003), SP-12 (Poteryaev et al., 2005), and NUP-155 (Franz et al., 2005) has been described previously. Other fluorescent fusions with YOP-1 et al., 2003), SP-12 (Poteryaev et al., 2005), and NUP-155 (Franz et al., 2003) were generated by cloning the entire genomic locus of C. elegans (Cheeseman et al., 2004) or pAA64 (RePCrew, McNally et al., 2006). The activated form of RAB-5 (Q78I) was generated by subjecting the spliced genomic locus of F26H9.6 to site-directed mutagenesis before cloning into pAA64. Constructs were integrated into DF38 [unc-119(ed3)] as described previously (Prattis et al., 2001) using a particle delivery system (Biologic PDS-1000/He; Bio-Rad Laboratories, Inc.). All strains used in this study are listed in Table S2 [available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1]. The strains expressing GFP:2xFYVE and GFP:NUP-155 were provided by B. Grant (Rutgers University, Piscataway, NJ) and P. Askaer (Parc Científic de Barcelona, Barcelona, Spain), respectively.

RNA-mediated interference and antibody production

Double-stranded RNA (dsRNA) was prepared as described previously (Oegema et al., 2001) from templates prepared by using the primers listed in Table S3 [available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1] to amplify N2 genomic DNA. For complete and partial depletions, L4 hermaphrodites were injected with dsRNA and incubated at 20°C for 45 or 22–24 h, respectively, before analysis. Antibodies against RAB-5 and RET-1 were generated by cloning nucleotides 124–612 of F26H9.6 (RAB-5) and the entire coding sequence of W06A2.3b (RET-1) amplified from cDNA libraries into pGEX6P-1 (GE Healthcare). Purified GST fusion proteins were outsourced for injection into rabbits (Covance). Both antibodies were affinity purified from serum as described previously (Desai et al., 2003) by binding to columns of the same antigen after removal of the GST tag by cleavage with PreScission protease. Antibodies directed against SQV8 and GFP have been described previously (Audhya et al., 2005; Sato et al., 2006).

Microscopy and condensation analysis

For analysis of fixed embryos, images were acquired using a 100x, 1.35 NA UPlan-apo objective lens (Olympus) mounted on a DeltaVision microscope system (Applied Precision) equipped with an Olympus IX70 base and a charge-coupled device camera (CoolSnap; Roper Scientific). Immuno-fluorescence of fixed embryos was performed as described previously (Desai et al., 2003), using the following rabbit antibodies at a concentration of 1 μg/ml: a-RAB-5 (Cy3 labeled), the mouse monoclonal antibody DM1a (Oregon green 488 labeled; Sigma-Aldrich), a-SQV8 (Cy3 labeled), and the goat polyclonal GFP antibody (Oregon green 488 labeled). For live analysis, embryos were mounted as described previously (Oegema et al., 2001) and imaged at 20°C on a spinning-disc confocal microscope (Eclipse TE2000E; Nikon) equipped with a Nikon 60×, 1.4 NA Planaplo objective lens and a charge-coupled device camera (Orcara ER; Hamamatsu). To depolymerize microtubules, meiotic embryos were dissected directly into meioisis media (25 mM Hapes, pH 7.4, 60% Leibovitz L-15 Media, 20% fetal bovine serum, and 500 μg/ml insulin) containing 10 μg/ml nocodazole and imaged in a depression slide sealed with petroleum jelly. Quantification of ER cluster formation and lamin and Lc3 fluorescence intensity measurements were performed using MetaMorph software. Analysis of chromosome condensation was performed as described previously (Maddox et al., 2006). The mean value of the condensation parameter was calculated after aligning the image sequences with respect to nuclear envelope permeabilization. To simplify presentation, the plots of the condensation parameters are displayed aligned with respect to the onset of condensation.

In vitro ER tubule assembly

A light membrane fraction from X. laevis egg extracts was prepared as described previously (Voeltz et al., 2006), stained with octadecyl rhodamine dimer labeled and mounted on glass slides to visualize the tubule formation. To test the effect of GDI addition, membranes were preincubated for 10 min with either 10 μM Rab GDI or 30 μM Rho GDI, followed by the addition of 1 mM ATP and 0.5 mM GTP. Reactions were allowed to proceed for 60 min before staining and pipette transfer onto slides. Purified Rho GDI was provided by G. Bokoch (The Scripps Research Institute, La Jolla, CA), and the construct to express Rab GDI was a gift from W. Balch (The Scripps Research Institute).

Online supplemental material
Fig. S1 shows that YOP-1 localizes to the ER and nuclear envelope, reorganization of the ER during mitosis does not require microtubules, and the defect in ER organization observed after RAB-5 depletion is not caused by a perturbation in the actomyosin cytoskeleton. Fig. S2 shows that RAB-5-depletion containing late endosomes contact the ER more frequently than RAB-5–containing early endosomes, and EEA-1 localization is lost after RAB-5 depletion but only subtly perturbed upon RAB-5Q78L expression. Fig. S3 shows that Rab5A79T overexpression potentiates ER cluster formation in HeLa cells, and neither YOP-1 nor RET-1 binds to GFP-loaded GST:RAB-5. Fig. S4 shows that nuclear envelope permeabilization is delayed in embryos depleted of RAB-5, GFP:2xFYVE does not localize to the nuclear envelope, and LEM-2 is present in the peripheral ER throughout the cell cycle. Table S1 lists the putative Rab-type GTPases in C. elegans. Table S2 lists the strains used in this study. Video 1 shows the ER morphology in embryos depleted of RAB-5 or YOP-1/RET-1. Video 2 shows that RAB-5 is required for ER structure and dynamics. Video 3 shows that expression of activated RAB-5T74N potentiates ER clustering. Video 4 shows that codepletion of RAB-5 and YOP-1/RET-1 leads to a synergistic defect in ER morphology. Video 5 shows that RAB-5 depletion blocks nuclear envelope disassembly. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200701139/DC1.

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A role for Rab5 in structuring the endoplasmic reticulum

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We mistakenly referred to the human homologue of the Caenorhabditis elegans protein YOP-1 as DP1/NogoA. NogoA is another name for Rtn4a, which functions redundantly with DP1 in ER restructuring. The human homologue of YOP-1 is DP1.