Supplemental Results

Because Hmg2p degradation proceeds by the HRD quality control pathway, we wondered if NSG levels had any general effects on ER quality control. As a gauge of such actions we tested the effects of overexpression or removal of NSG proteins on the unfolded protein response (UPR), the conserved signaling pathway that monitors and responds to levels of misfolded ER proteins. We used an integrated GFP reporter of UPR activity (Patil and Walter, 2001), that allows the effects of drugs or genetic perturbations to be measured in vivo by flow cytometry (Bays et al., 2001b; Cronin et al., 2002). Overexpression of either NSG protein caused no change on the basal levels of the UPR, nor any alteration of the dose-response curve for DTT, an agent that stimulates the UPR (Fig. 1S, A). Similarly the presence of either single deletion or the double null mutation *nsg1nsg2* had no discernable effects on the basal or stimulated UPR when compared to otherwise isogenic wild-type strains (control, Fig. 1S). Thus, despite its profound effects on Hmg2p stability, an absence or overabundance of NSG proteins had no effect on the tone or responsiveness of the UPR pathway.

Supplemental Materials and Methods

Reagents

Restriction enzymes and T4 DNA ligase were obtained from New England Biolabs (Berverly, MA). KOD HotStart DNA polymerase was obtained from Novagen Inc., Madison, WI. Anti-myc antibody was used as cell culture supernatant obtained by growing the 9E10 hybridoma cell line (CRL 1729 American Type Culture Collection) in RPMI1640 culture medium (GIBCO BRL, Grand Island, NY) with 10% fetal calf serum and supplements. Anti-HA.11 monoclonal antibodies were purchased as ascites fluid or affinity-matrix coupled from Covance Inc., Berkeley, CA. HRP-conjugated goat antimouse antibodies were purchased from Jackson Immuno Research. Chemiluminscence immunodetection reagents were obtained from Perkin Elmer. Serva Blue G was purchased from Serva Electrophoresis GmbH, Heidelberg, Germany. Digitonin was obtained from Fluka AG, Buchs, Switzerland, or Sigma. All other chemical reagents were obtained from Sigma, St. Louis, MO or Fisher Scientific, Fairlawn, NJ (chemicals) Hampton, NH (headquarters).

Plasmids and DNA

pRH1238 (*YIp/LEU2*, expressed *NSG2* from a *TDH3* promoter) was constructed by PCR amplification of NSG2 from genomic DNA and subcloning into expression vector pRH983 (YIp, *LEU2*). pRH1246 (*YIp/LEU2*, expressed *hemi-HRD1* from the *TDH3* promoter) was constructed by subcloning the region encoding the transmembrane domain of Hrd1p, referred to as hemi-Hrd1p (Gardner et al., 2000), into expression vector pRH981 (*YIp/LEU2*). pRH1574 (*YCp/ADE2/LEU2*, expressed *SEC61* from a *TDH3* promoter) was made by subcloning a BsaI-NarI fragment containing *ADE2* and *TDH3-SEC61* from pRH1348 (*YIp/ADE2*, expresses *SEC61* from a *TDH3* promoter) into pRS415 (*YIp/LEU)*. pRH1774, used for disruption of the *NSG1(YHR133c)* open reading frame, by PCR amplifying kanMX-deleted *nsg* allele from genomic DNA of the *YHR133c/yhr133c* \triangle Research Genetics heterozygous diploid strain (strain 21961, Invitrogen, Carlsbad, CA). The resulting product, containing long flanking sequences upstream and downstream of the *nsg1::kanMX* coding region, was cloned into the SmaI

site of pRS406. The disrupting fragment was cut out of the plasmid and used for transformation to create the $nsg1\Delta$ null allele. pRH1775, used for disruption of the *NSG2(YNL156c)* open reading frame, was prepared in an identical manner, using the *YNL156c/ynl156c* Research Genetics heterozygous diploid strain (strain 22056, Invitrogen, Carlsbad, CA). pRH1791 (*YIp/ADE2*, expressed *NSG1* from a *TDH3* promoter) was constructed by PCR amplification of the coding region from genomic DNA followed by subcloning into pRH1579 (*YIp/ADE2*, with *TDH3* promoter upstream of MCS). pRH1805 (*YIp/ADE2*, expressed *NSG1-3HA* from *TDH3* promoter) was constructed by addition of an in-frame 3HA coding region by SOEing and recloning into pRH1791 to create the tagged version of the coding region. pRH399, which is a promoterless version of 1myc-Hmg2p, was used to insert a single *myc* epitope tag into *HMG2* CDS expressed from its genomic locus by single site integration into the *hmg2::HIS3* null allele (Hampton and Rine, 1994). pDN431 (*YCp/URA3*, expresses *CPY*-HA*) was a gift from Davis Ng, Penn State. pDN431 (*YCp/URA3*, expresses *CPY*- HA*) was a gift from Davis Ng, Penn State.

In vitro ubiquitination of Hmg2p

In vitro ubiquitination of Hmg2p was evaluated in isolated microsomes by an assay characterized in detail in a separate publication (Garza et al., 2005). Briefly, microsomes from a $ubc7\Delta$ null yeast strain expressing $Hmg2p-GFP$ and $Hrd1p$ from the TDH3 promoter were prepared by glass bead lysis of 20 $OD₆₀₀$ units of log-phase cells in 400 ml of MF buffer (20 mM Tris pH 7.5, 100 mM NaCl, 300 mM sorbitol, with the following protease inhibitors: 1mM PMSF, 260µM AEBSF, 100 µM leupeptin hemisulfate, 76 μM pepstatin A, 5mM ε-aminocaproic acid, 5mM benzamidine, and 142 μ M TPCK) at 4°C, using hand vortexing for 6 x 1 minute intervals with 1 minute intervals on ice between each vortexing. The lysate was collected and pooled with 2 x 400 ml rinses of the beads with MF to give 1.2 ml of crude microsomal lysate. The crude lysate was next briefly microfuged using full speed (14,000 x g) 5 second pulses to remove large cellular debris. Next the microsomes were pelleted by 30 minute, 21,000 g spin at 4 oC and then resuspended in B88 buffer (20 mM Hepes pH 6.8, 250 mM sorbitol 150 mM KOAc, 5mM MgOAc, 1mM DTT, and the same cocktail of protease inhibitors used in the lysis buffer), to a final volume of 125 microliters. At the same time, cytosol from a Ubc7p overexpressing, $hrdI\Delta$ null strain was prepared in the manner of Spang and Schekman (Spang and Schekman, 1998). Control cytosol was prepared in parallel from an otherwise identical $ubc7\Delta$ null strain. Briefly, 500 OD equivalents of cells were pelleted, rinsed once with water, once with B88 buffer, and resuspended in 500 ml of B88 buffer. The resulting suspension was poured into a liquid nitrogen-containing mortar, and the resulting fast-frozen pellet was ground with a pestle until a fine powder. The frozen powder was next transferred to a microfuge tube, raised to 1mM ATP with a 500 mM stock solution in H20 ph 7.5, and allowed to thaw on ice. The thawed cytosol lysate was centrifuged at 3000 x g for 5 min, to remove debris, and the resulting supernatent was removed and centrifuged at 20,000 x g for 15 minutes. Finally, the resulting 20,000 supernatent was removed and ultracentrifuged (100,000 x g) for 1 hr. The resulting supernatent was collected and measured for protein, and adjusted to 25 mg/ml protein for use in the ubiquitination assay.

The *in vitro* ubiquitination assay was initiated by addition of 20 µl of microsomes (with Hrd1p and Hmg2p), 12 µl of cytosol, and sufficient concentrated stock of ATP to yield 30 mM ATP (with Ubc7p, E1, ATP, and ubiquitin), followed incubation at 30 °C, typically for an hour. The assay is then terminated by solubilization with 200 ml of SUME with protease inhibitors and 5mM N-ethylmaleimide, followed by addition of 600 ml of IP buffer, and subsequent immunoprecipitation of Hmg2p and immunblotting for Hmg2p-GFP with anti-GFP monoclonal antibodies, or for ubiquitin using anti-ubiquitin (Zymed Laboratorie, South San Francisco) or anti-GFP monclonals as described (Bays et al., 2001b).

4

References for Supplemental Material

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- Spang, A. and Schekman, R. (1998) Reconstitution of retrograde transport from the Golgi to the ER in vitro. J Cell Biol, 143, 589-599.

Figure legend Supplemental

Figure 1S Overexpressed NSGs (A), or $nsg\Delta$ null mutations (B) did not cause or alter UPR signaling. A) A reporter strain expressing the UPREx4-GFP reporter, with either empty vector or plasmids overexpressing the indicated NSGs from the TDH3 promoter, were subjected to flow cytometry after a 4 hour incubation with 0, 0.5, or 2 mM DTT to examine the basal and stimulated UPR. Vertically placed histograms have identical fluorescence axes allowing visual comparison. B) The same experiment was performed on the reporter strain, with normal NSG genes or the indicated null mutations.

Table of yeast strains used in studies

Table 1. List of strain, and figures of usage

Strain	Genotype	Figure
RHY3119	MATα ade2-101 met 2 lys2-801 his3Δ200 leu2Δ::LEU2 ura3-	Fig $2\overline{A}$
	52::URA3::pTDH3-HMG2-GFP hmg2A::HIS3::pTDH3-	left
	<i>ImvcHMG2</i>	column
RHY3120	MATa ade2-101 met 2 lys2-801 his3A200 leu2A::LEU2-	Fig 2A
	pTDH3-NSG2 ura3-52::URA3::pTDH3-HMG2-GFP	left
	hmg2 Δ ::HIS3::pTDH3-1mycHMG2	column
RHY3121	MATa ade2-101 met 2 lys2-801 his3A200 leu2A::LEU2-	Fig 2A
	pTDH3-hemiHRD1 ura3-52::URA3::pTDH3-HMG2-GFP	left
	hmg2A::HIS3::pTDH3-1mycHMG2	column
RHY3127	MATα ade2-101:: ADE2 met 2 lys2-801 his3Δ200 leu2Δ ura3-	Fig 2A
	52::URA3::pTDH3-HMG2-GFP hmg2A::HIS3::pTDH3-	right
	1mvcHMG2	column
RHY3128	MATa ade2-101::ADE2::pTDH3-NSG1 met 2 lys2-801	Fig $2\overline{A}$
	his3 \triangle 200 leu2 \triangle ura3-52::URA3::pTDH3-HMG2-GFP	right
	hmg2 Δ ::HIS3::pTDH3-1mycHMG2	column
RHY3213	MATα ade2-101::ADE2::pTDH3-NSG1-3HA met 2 lys2-801	Fig 2A
	his3 Δ 200 leu2 Δ ura3-52::URA3::pTDH3-HMG2-GFP	right
	hmg2A::HIS3::pTDH3-1mycHMG2	column
RHY3219	MATa ade2-101::ADE2 met 2 lys2-801 his3 Δ 200 leu2 Δ ura3-	Fig 2B
	52 hmg2A::HIS3::pTDH3-1mycHMG2	Fig 7A, B
RHY3220	MATa ade2-101::ADE2::pTDH3-NSG1 met 2 lys2-801	Fig. 2B
	his3A200 leu2A ura3-52 hmg2A::HIS3::pTDH3-1mycHMG2	
RHY3221	MATa ade2-101::ADE2::pTDH3-NSG1-3HA met 2 lys2-801	Figure 2B
	his3A200 leu2A ura3-52 hmg2A::HIS3::pTDH3-1mycHMG2	Fig 7A, B
RHY3472	MATα ade2-101 met 2 lys2-801 his3Δ200 leu2Δ::LEU2 ura3-	Figure 2B
	52 hmg2 Δ ::HIS3::pTDH3-1mycHMG2	
RHY3473	MATa ade2-101 met 2 lys2-801 his3Δ200	Figure 2B
	leu2A::LEU2::pTDH3-NSG2 ura3-52 hmg2A::HIS3::pTDH3-	
	1mycHMG2	
RHY3474	$MAT\alpha$ ade2-101 met 2 lys2-801 his3 Δ 200	Figure 2B
	leu2A::LEU2::pTDH3-hemiHRD1 ura3-52	
	hmg2A::HIS3::pTDH3-1mycHMG2	
RHY3254	MATa ade2-101::ADE2 met 2 lys2-801 his3 Δ 200 leu2 Δ ura3-	Figure 3A
	52 hmg2A::HIS3::pTDH3-1mycHMG2 [pDN431] (expressing	
	$CPY^*-HA)$	
RHY3255	MATa ade2-101::ADE2::pTDH3-NSG1 met 2 lys2-801	Figure 3A
	his3A200 leu2A ura3-52 hmg2A::HIS3::pTDH3-1mycHMG2	
	[pDN431] (expressing CPY*-HA)	
RHY3475	MATa ade2-101 met 2 lys2-801 his3A200 leu2A::LEU2 ura3-	Figure 3A
	52 hmg2 Δ ::HIS3::pTDH3-1mycHMG2 [pDN431] (expressing	
	$CPY^*-HA)$	
RHY3476	MATa ade2-101 met 2 lys2-801 his3Δ200	Figure 3A
	leu2A::LEU2::pTDH3-NSG2 ura3-52 hmg2A::HIS3::pTDH3-	
	ImycHMG2 [pDN431] (expressing CPY*-HA)	
RHY3477	MATa ade2-101 met 2 lys2-801 his3Δ200	Figure 3A
	leu2A::LEU2::pTDH3-hemiHRD1 ura3-52	
	hmg2A::HIS3::pTDH3-1mycHMG2 [pDN431] (expressing	
	$CPY^*-HA)$	
RHY3322	MATa ade2-101::ADE2 met 2 lys2-801 his3 A200 leu2A ura3-	Figure 3B
	52:: URA3::pTDH3-6mycHMG2-GFP hmg2A::HIS3::pTDH3-	
	1mycHMG2	

 \overline{a}

Figure 1S