



Endoplasmic reticulum involvement in yeast cell death

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Yeast cells undergo programmed cell death (PCD) with characteristic markers associated with apoptosis in mammalian cells including chromatin breakage, nuclear fragmentation, reactive oxygen species generation, and metacaspase activation. Though significant research has focused on mitochondrial involvement in this phenomenon, more recent work with both *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* has also implicated the endoplasmic reticulum (ER) in yeast PCD. This minireview provides an overview of ER stress-associated cell death (ER-SAD) in yeast. It begins with a description of ER structure and function in yeast before moving to a discussion of ER-SAD in both mammalian and yeast cells. Three examples of yeast cell death associated with the ER will be highlighted here including inositol starvation, lipid toxicity, and the inhibition of *N*-glycosylation. It closes by suggesting ways to further examine the involvement of the ER in yeast cell death.

Keywords: BX11, endoplasmic reticulum, ER stress, IRE1, UPR, yeast cell death

INTRODUCTION

In recent years, it has become increasingly clear that yeast cells undergo programmed cell death (PCD) in response to a variety of intrinsic and extrinsic stimuli, with characteristic markers associated with apoptosis in mammalian cells (Carmona-Gutierrez et al.,

Molecular components involved in regulating ER structure have recently been identified. Regions of high membrane curvature including the edges of the sheets and the tubules are stabilized by interactions between members of the reticulon family (Rtn1p and Rtn2p in budding yeast) and members of the DP1/Yop1p

2002), the yeast Atf1 homolog, Atf1p (Wissing et al., 2004), and the endonuclease G homolog, Nuc1p (Buttner et al., 2007), have been identified and linked to yeast cell death suggesting that a core machinery driving PCD is conserved in unicellular eukaryotes (Madeo et al., 2009).

Though significant research has focused on mitochondrial involvement in yeast PCD (Braun and Westermann, 2011), recent work with both *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* has implicated the endoplasmic reticulum (ER) in yeast PCD. This minireview provides an overview of ER stress-associated cell death (ER-SAD) in yeast. It begins with a description of ER structure and function in yeast before moving to a discussion of ER-SAD in both mammalian and yeast cells. It closes by suggesting ways to further examine the involvement of the ER in yeast cell death.

ENDOPLASMIC RETICULUM STRUCTURE IN YEAST

The ER is the largest membrane-bound organelle in the eukaryotic cell (Friedman and Voeltz, 2011; Hu et al., 2011). It consists of the nuclear envelope and the peripheral ER, a single network of interconnected sheets and tubules, which in yeast is located close to the plasma membrane where it is referred to as the cortical ER. A recent study that imaged the budding yeast ER by transmission electron microscopy and dual-axis electron tomography revealed that it can be divided into three structurally distinct major domains: the plasma membrane-associated ER (pmaER), the central cisternal ER (cecER), and the tubular ER (tubER; West et al., 2011).

then mammalian counterparts, stabilize the high curvature of ER tubules by using their double hairpin structure to form wedges and arc-like scaffolds that mold the lipid bilayer into tubules (Shibata et al., 2009, 2010).

Once ER tubules are shaped and formed, they need to be connected to the ER network via homotypic fusion between two identical but apposing membranes. In yeast, homotypic fusion appears to be mediated by the Sey1p protein, the ortholog of the mammalian atlastins, a class of GTPases that belong to the dynamin family (Hu et al., 2009; Anwar et al., 2012). Given Sey1p's structure, the data suggest that the fusion reaction could be mediated by conformational changes in the Sey1p GTPase domains that pull the apposing membranes together forcing them to fuse (Orso et al., 2009; Anwar et al., 2012).

ENDOPLASMIC RETICULUM FUNCTION IN YEAST

In all eukaryotic cells, the ER performs a variety of functions including protein translocation and folding, lipid synthesis, and calcium homeostasis. In yeast cells, protein transport into the ER can occur via either the signal recognition particle (SRP)-dependent (cotranslational translocation) or the Hsp70p-dependent (post-translational translocation) pathway (Zimmermann et al., 2011). Membrane insertion and completion of translocation involve the heterotrimeric Sec61p complex and the ER-luminal chaperone, Kar2p (or BiP). Kar2p appears to facilitate post-translational insertion of the polypeptide into the Sec61p complex and its translocation via a ratcheting mechanism (Lyman and Schekman, 1996). Once ER client proteins

have been translocated, they can be folded, modified, and packaged into ER-to-Golgi COPII transport vesicles that form at ER exit sites (ERES; Duden, 2003; Watanabe and Riezman, 2004; Watson and Stephens, 2005). In yeast, ER sheets have a markedly higher ribosome density than tubules suggesting that sheets may be better suited for ribosome binding and protein translocation (West et al., 2011).

Next, the ER serves as the main site for synthesis of three major classes of membrane lipids: sphingolipids, phospholipids, and sterols (Carman and Henry, 2007; Henry et al., 2012). For example, in yeast, most of the biosynthetic steps for triacylglycerols occur in the ER: Gat1p and Gat2p, which are the major glycerol-3-phosphate acyltransferases (GPATs) that catalyze the first step in the synthesis of almost all membrane phospholipids and neutral glycerolipids, localize to both the perinuclear and the cortical ER (Bratschi et al., 2009). Additionally, the two ER membrane proteins, Orm1p and Orm2p, have been shown to be involved in sphingolipid synthesis and phospholipid homeostasis (Han et al., 2010). These are only a few of numerous ER-localized gene products known to be involved in lipid biosynthesis in yeast.

Finally, the creation of a specifically targeted version of the Ca^{2+} -sensitive photoprotein, aequorin, to the lumen of the yeast ER revealed that this organelle is involved in calcium storage and homeostasis with a steady-state concentration of 10 μM free Ca^{2+} in wild-type yeast cells (Strayle et al., 1999). It is also known that two P-type ATPases are involved in regulating the levels of Ca^{2+} in the ER including the yeast high-affinity $\text{Ca}^{2+}/\text{Mn}^{2+}$ P-type ATPase, Pmr1p, which pumps cytosolic Ca^{2+} into the ER and the Golgi (Sorin et al., 1997; Strayle et al., 1999), and the ER-localized P-type ATPase, Cod1p/Spf1p, which appears to work with Pmr1p to maintain ER function and homeostasis (Vashist et al., 2002). Significantly, Ca^{2+} levels in the ER have been implicated in retention of resident luminal proteins, in export of secretory proteins, in protein folding and degradation, and in the association of the ER chaperone Kar2p with misfolded proteins (Durr et al., 1998).

ER STRESS-ASSOCIATED DEATH IN MAMMALIAN CELLS

In mammalian cells, a diverse range of factors can disrupt ER function and lead to ER stress, which if left unchecked can trigger ER-SAD. These include increases in ER-luminal protein levels that exceed the capacity of ER-resident chaperones, exposure to long-chain saturated fatty acids (SFA), alterations in calcium levels in the ER lumen, and disturbances to the ER redox balance (Ron and Walter, 2007; Parmar and Schroder, 2012). In animal cells, ER stress is sensed by three upstream signaling pathways driven by three effector proteins, IRE1, ATF6, and PERK, which are collectively called the unfolded protein response (UPR; Wang et al., 1998; Harding et al., 1999; Urano et al., 2000; Walter and Ron, 2011). Activation of the UPR can alleviate ER stress by synthesizing novel components of the protein folding machinery and by expanding the ER itself (Cox et al., 1997; Schuck et al., 2009). This activated UPR can be divided into three phases: the adaptive, the alarm, and the apoptotic phase. The adaptive phase begins with an immediate and fast response that decreases protein influx into the ER followed by a slower transcriptional response involving

downstream transcription factors that upregulate genes encoding ER-resident chaperones, components of the ER-associated protein degradation (ERAD) machinery, and regulators of ER size (Trusina et al., 2008). In many scenarios, the adaptive phase can restore equilibrium between protein load and chaperone capacity within the ER, dampening the UPR. However, in cases of chronic or unresolved ER stress, the UPR continues to a second alarm phase that involves several signal transduction events that move the cell from a pro-survival to a pro-apoptotic state (Tabas and Ron, 2011; Woehlbier and Hetz, 2011). This ends in the final apoptosis phase involving the transcriptional and post-translational activation of the BH3-only proteins and other BCL2 protein family members that trigger the canonical mitochondrial cell death pathway. Additionally, the BCL2 proteins have been implicated in linking ER Ca^{2+} homeostasis and apoptosis (Oakes et al., 2003; Bassik et al., 2004).

Mechanistically, in mammalian cells, the ER-SAD program is mediated largely by the UPR signaling molecules and endonuclease IRE1 α , which can transmit both pro-survival and pro-death signals. Indeed, in my view, ER-SAD can be defined as the cell death process that involves IRE1 function. In light of this, it is significant that there are pro- and anti-apoptotic effectors assembled around IRE1 α that are able to control the amplitude and duration of IRE1 α signaling (Woehlbier and Hetz, 2011). For example, IRE1 α signaling can be enhanced at the ER membrane by the formation of a complex between the cytosolic domains of IRE1 α and the BAX–BAK complex, two pro-apoptotic members of the BCL2 family of proteins (Scorrano et al., 2003; Zong et al., 2003). In contrast, IRE1 α signaling can be attenuated by the binding of the ER-localized anti-apoptotic protein, BAX inhibitor-1 (BI-1; Lisbona et al., 2009; Bailly-Maitre et al., 2010; Castillo et al., 2011). Late-phase UPR signaling of IRE1 α can lead to changes in the expression and activity of BCL2 protein family members and therefore to the activation of apoptosis.

Finally, we should note two emerging areas of inquiry involving the role of the ER in cell death. First, several studies in mammalian cells have begun exploring the links between ER and mitochondrial function during PCD. Both organelles form interconnected membrane networks that can influence various cellular processes including cell death (Csordas et al., 2006). More recently, Cardenas and colleagues have shown that Ca^{2+} transport between the ER and the mitochondria is regulated by the inositol triphosphate receptor, IP₃R, to modulate mitochondrial bioenergetics (Cardenas et al., 2010), a process involving BI-1, an ER-resident protein known to be involved in autophagy and apoptosis (Sano et al., 2012). This may explain the earlier observation that mitochondria preferentially accumulate Ca^{2+} in regions called mitochondria-associated microdomains (MAMs) where the ER and mitochondria are found in close proximity (Rizzuto et al., 1998). Next, there have been a few published reports that describe the fragmentation of the ER during ER stress and ER-SAD in mammalian cells (Brough et al., 2005; Kucharz et al., 2011a,b; Howarth et al., 2012). Though there is evidence that the loss of the GTPase atlastin 1 can cause ER fragmentation in *Drosophila* (Orso et al., 2009), the mechanism behind the ER fragmentation associated with ER stress in the mammalian system is still not known.

ER STRESS-ASSOCIATED DEATH IN YEAST CELLS

As they do in mammalian cells, a range of intrinsic and extrinsic triggers can disrupt ER function and lead to ER stress and to ER-SAD in yeast (Table 1). Notably, however, in yeast cells, ER stress is only sensed by a single signaling pathway driven by Ire1p, which is the most ancient of the three parallel UPR pathways found in the metazoan (Sidrauski and Walter, 1997). Three examples of yeast cell death associated with the ER will be highlighted here, including inositol starvation, lipid toxicity, and the inhibition of *N*-glycosylation.

First, Guerin et al. (2009) reported that the fission yeast, *S. pombe*, undergoes cell death with apoptotic-like features when it is deprived of inositol, a precursor of numerous phospholipids and signaling molecules. Deleting either *pca1*⁺, the gene for the only caspase-like protein in *S. pombe*, or *ire1*⁺, the gene for the only IRE1 homolog, enhanced cell survival in media lacking inositol, suggesting that both genes are involved in the cell death pathway. Interestingly, the ER transmembrane chaperone, calnexin, encoded by the *cnx1*⁺ gene, has also been implicated in inositol-starvation-induced ER-SAD since overexpressing different portions of the Cnx1p protein can alter the number of dying cells in inositol-starved conditions as measured by several assays (Guerin et al., 2009).

Next, feeding the budding yeast, *S. cerevisiae*, with extracellular SFA like palmitate (C16:0) triggers ER stress and leads to growth arrest and death (Pineau et al., 2009). Addition of palmitate to the cell culture also alters ER morphology with swelling of the organelle, detachment of the pmaER from the plasma membrane,

and in certain cells, the replacement of pmaER by electron-lucent clefts extending throughout the cytoplasm that are visible in the electron microscope. Both the induction of the UPR and the cell death associated with lipid toxicity were abrogated with the addition of the molecular chaperone 4-phenyl butyrate, suggesting that lipid-induced ER stress overburdens the folding machinery in the ER. Notably, lipid toxicity is known to induce apoptosis in mammalian cells (Kharroubi et al., 2004; Diakogiannaki et al., 2008). One paper reports that palmitate induces apoptosis in pancreatic beta cells by activating the IRE1 α , PERK, and ATF6 pathways (Cunha et al., 2008).

Finally, Hauptmann et al. (2006) reported that preventing the *N*-glycosylation of yeast proteins, either by mutating critical subunits of the oligosaccharyltransferase (OST) complex in the ER lumen, or by treating the cells with tunicamycin, a drug known to block the ER enzyme UDP-*N*-acetylglucosamine-1-*P* transferase (Alg7p) that is necessary for *N*-glycosylation, induced an apoptotic-like death in wild-type *S. cerevisiae* cells. The dying cells contained condensed nuclei, fragmented DNA, and externalized phosphatidylserine. Defects in *N*-glycosylation also led both to the appearance of a caspase-like activity that did not require functional yeast metacaspase, Yca1p, and to the production of reactive oxygen species (ROS) that could be diminished by heterologous expression of the human anti-apoptotic protein, Bcl-2. Two years later, the same team reported that the Golgi-localized Kex1p protease is involved in the apoptotic-like cell death linked to defects in *N*-glycosylation (Hauptmann and Lehle, 2008). Deletion of *KEX1* diminished the appearance of the caspase-like activity and decreased ROS accumulation in cells cultured in tunicamycin. Notably, the cell death described in these experiments was blocked by the addition of osmotic stabilizers to the culture media.

Strikingly, these studies disagreed with previous findings that had shown that tunicamycin does not induce cell death in wild-type cells unless the calcium-dependent phosphatase, calcineurin, had previously been inactivated (Bonilla et al., 2002; Bonilla and Cunningham, 2003). To resolve this disagreement, Dudgeon et al. (2008) used improved staining methods using both propidium iodide (PI) and FITC-VAD-FMK together instead of FITC-VAD-FMK alone, to analyze the cell death associated with growth in media containing tunicamycin. Their data showed that tunicamycin can induce cell death, but only in cells grown in low osmolyte yeast-peptone-dextrose (YPD) media, and not in cells grown in synthetic media. They also demonstrated that this dying process is not apoptotic in nature. The dying cells lacked two critical hallmarks of apoptosis – both chromatin fragmentation and phosphatidylserine externalization – suggesting that there may have been methodological problems in past efforts to characterize the cell death induced by tunicamycin in *S. cerevisiae*.

Instead, tunicamycin appeared to trigger two different forms of death in wild-type budding yeast cells, one that is partially dependent on a functional electron transport chain (ETC) and another that is independent of ETC function. Active calcineurin signaling could prevent the former, which is why it has been called calcineurin-less death, but not the latter form of cell death. Significantly, calcineurin-less death in response to tunicamycin

Table 1 | ER-Associated Cell Death in Mammalian and Yeast Cells.

ER function	Organism	Triggers of cell death (select list)	ER proteins involved
Protein translocation and folding	Mammalian	Protein aggregation	IRE1 α
		Ischemia reperfusion	ATF6
		Beta-mercaptoethanol (BME)	PERK
		Tunicamycin	BI
	Yeast	Dithiothreitol (DTT)	Grp78/BiP
		Heat shock	Ire1p
		Beta-mercaptoethanol (BME)	Bxi1p
		Tunicamycin	Kar2p/BiP
Lipid synthesis	Mammalian	Elevated free fatty acids (FFA)	IRE1 α
			ATF6
	Yeast	Elevated saturated fatty acids (SFA) inositol starvation	PERK
			Ire1p
Calcium dynamics	Mammalian	Thapsigargin	Cnx1p
		Calcium overload	PERK
	Yeast	Calcium starvation	SERCA
			Calcium chelators
			Pmr1p

did not involve any of the apoptosis-associated factors, Yca1p, Nuc1p, Nma111p, or Ste20p, strengthening the claim that this death is not apoptotic in nature. Rather, the dying process was regulated by Cmk2p, one of the two Ca^{2+} /calmodulin-dependent protein kinases, and by Hsp90p, one of the major heat shock chaperones in budding yeast. Finally, a very recent study from the same research team has concluded that tunicamycin leads to cell death by permeabilizing the vacuolar membranes of yeast cells and that this cell death program involves the V-ATPase that acidifies the vacuole (Kim et al., 2012). This tunicamycin-induced cell death involving vacuole membrane permeabilization could be blocked by calmodulin.

In light of the cumulative evidence, in my view, it is clear that tunicamycin leads to cell death, but that this dying process is not apoptotic in nature as had been previously reported. One possible reason for the discrepancy in the literature is the earlier study's failure to distinguish living apoptotic cells from dead necrotic cells, which are known to stain non-specifically with FITC-VAD-FMK (Wysocki and Kron, 2004; Hauptmann et al., 2006). Moreover, the observation reported in the earlier paper that the addition of an osmotic stabilizer like sorbitol is able to block some of the *N*-glycosylation-linked cell death suggests that this cell death may be lytic rather than apoptotic in nature (Hauptmann and Lehle, 2008). This is not surprising since protein *N*-glycosylation is crucial for cell wall assembly (Lesage and Bussey, 2006; Levin, 2011). Defects in this biochemical pathway would be expected to weaken the cell's ability to maintain its structural integrity.

Finally, can this tunicamycin-induced calcineurin-less cell death in *S. cerevisiae* properly be called ER stress-associated cell death? It is not clear. As I noted above, in mammalian cells, ER-SAD has been linked to the activation of the UPR and IRE1 function. Though tunicamycin does induce the UPR in budding yeast, it is also apparent that Ire1p is not required for either the pro-death activity of tunicamycin in calcineurin-deficient cells or

the anti-death activity of calcineurin in these cells (Bonilla et al., 2002). This is in stark contrast to the single published report suggesting that tunicamycin induces an apoptotic-like cell death in *S. pombe* that appears to partially require the fission yeast Ire1p (Guerin et al., 2008).

FUTURE DIRECTIONS

The study of the ER's role in yeast cell death is in its infancy. It would be interesting to determine if other physiological triggers of yeast cell death like acetic acid or ethanol – triggers not directly linked to ER function – involve the ER. Recently, my laboratory has begun characterizing the yeast BI protein, Bxi1p, an ER-localized protein that links the UPR to PCD in *S. cerevisiae* (Cebulski et al., 2011). Cells lacking *BXI1* are not only more sensitive both to ethanol-induced and to glucose-induced PCD, but also have a diminished UPR. Studies linking Bxi1p and Ire1p function in yeast are ongoing in my lab. Finally, it will be important to check if PCD alters the yeast's ER structure, and conversely, if mutants that modify ER structure alter the dynamics of yeast cell death. These investigations should uncover the mechanistic links between ER structure, ER function, and cell death in yeast.

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