The unfolded protein response (UPR) monitors the protein folding capacity of the endoplasmic reticulum. One of the UPR branches includes an unusual cytoplasmic splicing reaction leading to removal of an intron from an mRNA encoding a key UPR transcription factor. The cleavage step of the process is well characterized in both yeast and animals, but the animal enzyme responsible for exon ligation remains a mystery. Recent reports, including a paper in this issue of The EMBO Journal, identify RTCB as the RNA ligase during UPR in mammals and C. elegans.

See also: J Jurkin et al, SG Kosmaczewski et al and Y Lu et al

The unfolded protein response (UPR) is an intracellular signaling pathway activated by endoplasmic reticulum (ER) stress that arises from the accumulation of unfolded proteins in the ER lumen (Walter & Ron, 2011; Moore & Hollien, 2012). In metazoan animals, UPR is mediated by three different ER transmembrane proteins that monitor conditions in the lumen: (i) IRE1 initiates cytoplasmic splicing of mRNA encoding a transcription factor X-box binding protein 1 (XBP1); (ii) protein kinase PERK phosphorylates translation initiation factor eIF2-α; and (iii) ATF6, a transcription factor precursor that is activated by proteolysis. Together, these three UPR branches induce transcriptional and translational responses that increase protein folding capacity and decrease the folding load in the ER. IRE1 is the only branch operating in Saccharomyces cerevisiae and is consequently the most studied and molecularly best-understood UPR pathway. The intra-lumenal sensor domain of IRE1 detects unfolded proteins and promotes lateral oligomerization of IRE1 in the ER membrane, which results in activation of the IRE1 cytoplasmic endoribonuclease domain (Fig 1). When activated, IRE1 excises an intron in XBP1 mRNA (or its yeast counterpart HAC1), initiating an unusual splicing reaction distinct from the nuclear spliceosome-mediated processing. In S. cerevisiae, exons resulting from XBP1/HAC1 cleavage are joined by RNA ligase TLR1, a multi-functional enzyme also involved in splicing of intron-containing tRNAs. XBP1/HAC1 splicing allows the synthesis of functional proteins that direct removal of an intron from an mRNA (or its spliceosome-mediated processing. In S. cerevisiae, exons resulting from XBP1/HAC1 cleavage are joined by RNA ligase TLR1, a multi-functional enzyme also involved in splicing of intron-containing tRNAs. XBP1/HAC1 splicing allows the synthesis of functional proteins that directly express tRNA splicing also impaired accumulation of the spliced (s) mRNA form and its translation product XBP1s. This was accompanied by lower expression of established XBP1s target genes including XBP1 itself, as XBP1s influences its own expression through a positive feedback loop. Importantly, this phenotype was rescued by re-expression of wild-type but not catalytically inactive RTCB. Demonstration that XBP1 mRNA splicing can be reconstituted in vitro with recombinant RTCB and the IRE1 nuclease domain provided the final evidence for the ligase’s role in UPR.

Similarly, Jurkin et al (2014) first looked for evidence of RTCB activity in XBP1 mRNA splicing in HeLa cells and extracts and found that lysates of cells with RNAi knockdown of RTCB or archease were deficient in the ligation of XBP1 mRNA exons. However, consistent with the data of Iwawaki and Tokuda (2011), depletion of RTCB alone had almost no effect on XBP1 mRNA splicing in intact cells. Marked repression of its maturation and the occurrence of downstream effects of XBP1 depletion required the simultaneous knockdown of RTCB and archease. Hence, archease is a generic RTCB co-factor, active in both tRNA and XBP1 mRNA splicing. In its presence, even the low RTCB levels
stimulation, RTCB-deficient B cells failed to activate the reporters in mutant B-cell types. In response to lipopolysaccharide (LPS) (Moore & Hollien, 2012). Jurkin et al. generated a conditional mouse model in which RTCB was deleted specifically in all mature B cells. Use of antibodies to antibody-producing plasma cells is a part of a physiological developmental program. Differentiation of B cells to antibody-producing plasma cells is part of a physiological developmental program. Differentiation of B cells results in a reduction in immunoglobulin secretion due to ER stress with tunicamycin (Anderson & Ivanov, 2014). A further possibility is that artificially created intron-less tRNA^{Leu(CAA)} and tRNA^{Tyr(GUA)} are not fully functional due to lack of certain nucleoside modifications. Some modifications are introduced into tRNAs at the level of intron-containing precursors (Grosjean et al., 1997), and deficiencies in modification could affect tRNA performance, possibly in a cell- or mRNA-specific fashion (Gu et al., 2014).

XBP1 mRNA splicing is unusual with respect to not only the hairpin-like exon/intron borders (Fig 1) and the proteins involved but also its cytoplasmic localization. Previous work demonstrated the ER association of HAC1/XBP1 mRNA and thus its availability for rapid processing upon activation of IRE1. All three reports verify the presence of RTCB, and also archease, in the cytoplasm with considerable fractions associated with ER, all consistent with a role in XBP1 splicing. Lu et al. also demonstrated that RTCB and IRE1 interact with each other even in the absence of UPR induction.

The physical association of IRE1 with RTCB raises interesting possibilities. In animals, IRE1 not only acts in the processing of XBP1 mRNA but also in a process known as RIDD (regulated IRE1-dependent decay), remaining after knockdown were sufficient to catalyze effective XBP1 exon ligation.

Jurkin et al. also investigated the importance of RTCB in vivo, in the situation when the UPR pathway is part of a physiological developmental program. Differentiation of B cells to antibody-producing plasma cells is associated with large XBP1-dependent expansion of ER in anticipation of massive antibody secretion (Walter & Ron, 2011; Moore & Hollien, 2012). Jurkin et al. generated a conditional mouse model in which RTCB is deleted specifically in all mature B-cell types. In response to lipopolysaccharide stimulation, RTCB-deficient B cells failed to induce XBP1. They also had a lower percentage of plasmablasts with significantly affected immunoglobulin secretion due to the disorganized ER structure. Moreover, immunization of mice carrying RTCB-deficient B cells resulted in a reduction in cells secreting antibodies and in antibody titers in the serum.

Kosmaczewski et al. (2014) investigating the role of RTCB in Caenorhabditis elegans found that RTCB loss-of-function worms grow to mature but sterile adults. Use of reporters dependent on IRE1/XBP1 showed that induction of ER stress with tunicamycin failed to activate the reporters in mutant worms. ER stress in the mutants did not induce XBP1 mRNA accumulation, but this defect was rescued by expression of wild-type but not inactive RTCB.

Like the authors of the other two papers, Kosmaczewski et al. were concerned with distinguishing the roles of RTCB in UPR and in tRNA splicing: Depletion of tRNAs could impact both translation and growth. In C. elegans, all genomic copies of tRNA^{Leu(CAA)} and tRNA^{Tyr(GUA)} contain introns. By constructing transgenic animals expressing intron-less copies of these tRNA genes, the authors reversed the effects of RTCB deletion on worm lifespan and growth under unstressed conditions. Unexpectedly, RTCB−/− worms expressing intron-less tRNAs still had highly penetrant phenotypes independent of UPR: They were defective in vulval development and were sterile due to the failure of germ cells to mature to oocytes. The authors speculate that these UPR- and tRNA splicing-independent phenotypes are due to additional substrates of RTCB ligase or to tRNA fragments accumulating in RTCB-deficient worms, for example, tRNA halves originating from intron-containing tRNA genes present in the genome. tRNA-derived fragments were found recently to have strong deleterious effects on various aspects of cell activity (Anderson & Ivanov, 2014). A further possibility is that artificially created intron-less tRNA^{Leu(CAA)} and tRNA^{Tyr(GUA)} are not fully functional due to lack of certain nucleoside modifications. Some modifications are introduced into tRNAs at the level of intron-containing precursors (Grosjean et al., 1997), and deficiencies in modification could affect tRNA performance, possibly in a cell- or mRNA-specific fashion (Gu et al., 2014). XBP1 mRNA splicing is unusual with respect to not only the hairpin-like exon/intron borders (Fig 1) and the proteins involved but also its cytoplasmic localization. Previous work demonstrated the ER association of HAC1/XBP1 mRNA and thus its availability for rapid processing upon activation of IRE1. All three reports verify the presence of RTCB, and also archease, in the cytoplasm with considerable fractions associated with ER, all consistent with a role in XBP1 splicing. Lu et al. also demonstrated that RTCB and IRE1 interact with each other even in the absence of UPR induction.
mediates degradation of ER-associated mRNAs encoding membrane and secretory proteins, which relieves the folding burden of the ER (Walter & Ron, 2011; Moore & Hollien, 2012). Recently, Cho et al (2013) found that the RIDD-derived mRNA fragments produced in response to intra-lumenal activation of IRE1 by cholera or Shiga toxins activate the RIG-1 innate immunity pathway, stimulating expression of NF-kB and inflammatory cytokines. Similar effect, depending on phosphorylated 3’-ends, was previously described for RNA fragments generated by the IRE1-related ribonuclease RNase L (Malathi et al, 2007). Irrespective of whether induced by toxins or regular UPR, the RIDD-generated mRNA fragments bear 5’-OH and 2’,3’-cyclic phosphate termini, which makes them ideal substrates for RTCB. Since RTCB has a very relaxed specificity and can efficiently ligate any RNA with the proper termini (Filipowicz et al, 1983; Popow et al, 2011), it is possible that it also functions to mitigate innate immune signaling by catalyzing intramolecular ligation (circularization) of RIDD RNA fragments.

In summary, the three studies provide convincing evidence that RTCB not only processes intron-containing tRNAs in animals but also splices XBP1, a key regulator of UPR that is also important for priming specific cells for high secretory activity, such as plasma cells. As always, such studies also raise many new questions. Is RTCB indeed involved in the ligation of substrates other than tRNAs and XBP1 mRNA, and is it possibly involved in repair/religation of RNAs incidentally cleaved by cellular endoribonucleases? Do other components of the RTCB complex also play a role in XBP1 (and tRNA) splicing? If so, what are their specific functions? It would be nice if answering these questions takes less than the decade or so consumed in the search for the mysterious RNA ligase carrying XBP1 splicing.

References

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Witold Filipowicz

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