PKCs pick through Ca\(^{2+}\)

Calcium signals destined for mitochondria are first screened by protein kinase C (PKC) isoforms, according to Pinton et al., on page 223. Different PKCs then adjust the organelles’ responses to their liking. PKC is a Ca\(^{2+}\)-activated kinase that comes in many flavors. Pinton et al. analyzed the contribution of several of these flavors to Ca\(^{2+}\) signaling by overexpressing or inhibiting individual isoforms in cells. Their effects were assessed by stimulating cells with an extracellular agonist to elicit Ca\(^{2+}\) stores from the ER into the cytoplasm.

One flavor, PKCa, limited all Ca\(^{2+}\) signaling by dampening this ER release. Others, however, worked specifically at the mitochondria. PKC\(_{\varepsilon}\) increased mitochondrial Ca\(^{2+}\) uptake, whereas PKCB and \(\beta\) reduced it. Thus, activation of PKC upon initial stimulation may alter the effect of subsequent Ca\(^{2+}\) spikes. Mitochondria are known to respond less to the second of two consecutive stimuli. The authors now show that PKCB is needed for this dampening. This function might make cells less sensitive to apoptotic signals, for example, which induce mitochondrial Ca\(^{2+}\) influx.

The PKC isoforms that decrease Ca\(^{2+}\) uptake also decrease mitochondrial membrane potential. There may be a causal link, but mitochondrial Ca\(^{2+}\) transporters have not been cloned, so identifying the relevant PKC substrates will require the purification of mitochondrial proteins that are phosphorylated in response to Ca\(^{2+}\).

Next vesicle SNAP’d up

Secretory vesicles wishing to play follow-the-leader use a particular SNARE to show them where the leader went, as shown by Takahashi et al. on page 255.

Vesicles heading to the plasma membrane sometimes selectively bind to another that has already fused there. This process, called sequential exocytosis, is efficient at large-scale secretion because vesicles in the cytosol can be mobilized without being transported all the way to the plasma membrane. Using 2-photon imaging, the authors show that sequential exocytosis is directed by a plasma membrane SNARE called SNAP25.

Sequential exocytosis was examined in insulin-secreting pancreatic b cells, in which SNAP25 diffused into the bulge where the leading exiting vesicle had fused with the plasma membrane. SNAP25 rarely diffused into spots where only one vesicle exited, but was seen at the majority of sequential exocytosis sites.

Although sequential exocytosis is common in many exocrine or endocrine cell types (which contain SNAP25), it accounted for only a small fraction of b cell exocytosis. Cholesterol depletion freed SNAP25 for easier diffusion and increased sequential exocytosis several fold. Restricting SNAP25 to lipid rafts might thus be one way to prevent exhausting insulin reserves, which are doled out steadily in small quantities.

Tracking transcripts

Mobile mRNAs rebrighten (left to right) a bleached speckle (circled). mRNAs do not travel willy-nilly through the nucleus, according to Molenaar et al. (page 191). Instead, they are transported by an energy-dependent mechanism that may bring them to quality control sites before they are exported to the cytoplasm.

Random diffusion from transcription sites to nuclear pores was generally accepted as the travel mode of preference for polyadenylated mRNAs. Based on the high mobility of oligo(T) probes, transcripts were assumed to be moving through the nucleoplasm at rates comparable to diffusion. But Molenaar and colleagues find that these speeds were probably overestimates resulting from free probe. Using a tighter-binding oligo(U) probe, they find that mRNA moves 10-fold more slowly than previous estimates.

This movement is energy dependent, indicating that an active process transports the mRNAs, perhaps by a motor or along chromatin fibers. The group now plans to inhibit nuclear mRNA-binding proteins to identify those that are essential for transport.

Transcripts were mobile even at speckles—putative nuclear storage sites for RNA-processing enzymes. This dynamic association suggests that transcripts are not important structural elements of speckles. Most transcripts passed through speckles at least briefly, so transcripts might instead be sent there to be checked for proper splicing. Since speckles contain splicing factors, they might even fix mRNAs that fail inspection, thus accounting for the small fraction of transcripts that were immobile in speckles.