Rafts and the evil amyloids

Lipid rafts are bad news for those with Alzheimer’s disease (AD). On page 113, Ehehalt et al. show that formation of the β-amyloid peptide (Aβ), which is tightly linked to AD, depends on the raft association of one of its creators.

The creating enzyme is β-secretase, which cleaves the amyloid precursor protein (APP) to release a product that is then processed into Aβ. Several recent lines of evidence suggest that cholesterol is somehow linked to Aβ production. For instance, high cholesterol levels are correlated with an increased likelihood of developing AD.

As cholesterol is found in membrane lipid rafts, the authors investigated whether APP and β-secretase were linked with these compartments. They found that, indeed, both proteins were found in lipid rafts. Further increasing the fraction of APP and β-secretase in lipid rafts (by oligomerizing each protein) released more Aβ.

The small size of lipid rafts makes it unlikely that both proteins are found within the same raft. The group demonstrates, however, that endocytosis is necessary for Aβ formation. Thus, endocytosis may lead to a clustering of rafts that puts β-secretase within striking distance of APP. The regulation and mechanism of this clustering await further studies.

Decreasing cholesterol levels in cells limited Aβ secretion, but how cholesterol is involved is also not yet clear. Perhaps specific lipids are required to activate β-secretase. The authors plan to use purified secretase and APP to determine whether raft lipids are needed for processing.

Prion scrapies are also formed in lipid rafts, so rafts seem to be conducive to the formation of amyloids. Potential therapeutic drugs should therefore function within raft environments if they are to be successful at preventing amyloid formation.

Caspases chew on electron transport

Caspases seem to have their hand in everything during apoptosis. They cleave and activate enzymes that degrade DNA, induce cell blebbing, and induce changes in the plasma membrane that make the dying cell attractive to phagocytes. Now, add another to the list—caspases disturb electron transport.

Ricci et al. (page 65) show that, in both isolated mitochondria and living cells, caspase-3 induces a loss of membrane potential in mitochondria that have been permeabilized by proapoptotic proteins. Inhibition of caspase activity prevented this loss in potential, which places membrane potential loss downstream of cytochrome c release and subsequent activation of caspases.

Mitochondria lost membrane potential because complexes I and II were injured. Caspase-treated permeabilized mitochondria did not consume oxygen in response to substrates used by complexes I and II, although the other complexes remained intact. The interference of the transfer of electrons by complexes I and II to complex III produced reactive oxygen species and is expected to limit ATP production and disturb mitochondrial metabolism. Together, these effects may be critical for dismantling the cell during death, although their importance has not been established. The authors are currently identifying caspase substrates within complexes I and II. They will then determine whether blocking cleavage of these substrates changes either mitochondrial responses to caspases or the pattern of cell death.

Even with fully functioning complexes I and II, apoptosis may still induce DNA damage and cytoskeletal and plasma membrane changes that lead to cell death. But life or death may not be the whole story when it comes to apoptosis. Given the widely conserved nature of various components of apoptosis, perhaps all the small effects are important because they add up to a dying cell that can be readily eaten and quickly discarded.
Sos-1 activation and the recruitment of both PI3K and PIP3 are crucial for growth factor responses, including two levels of membrane ruffling. The assembly of the tetrameric complex between PI3K and Rac are uncovered on page 17 in an article by Innocenti et al. that reveals the importance of complexes involving the GEF Sos-1.

Genetic evidence has supported the involvement of the GEF SOS-1 for stimulating Rac activity in response to growth factors. SOS-1 is found in complex with ABI1 and Eps8, and interference with any of these proteins is known to block actin remodeling in response to RTK activation. Innocenti et al. now show biochemically that SOS-1 is indeed the GEF that activates Rac in response to PDGF.

Full GEF activation was a stepwise process. The physical presence of PI3K itself stimulated low levels of the SOS-1 GEF activity, perhaps by inducing a conformational change in SOS-1. PI3K gets to the SOS-1 complex through ABI1. PI3K bound to ABI1 in vitro and colocalized with ABI1 and Eps8 in PDGF-induced membrane ruffles.

PIF3, the product of PI3K, further stimulated the basal SOS-1 GEF activity. Thus, strong GEF activity would be unleashed only by activation of PI3K by growth factor-stimulated RTKs. As expected, inhibition of SOS-1 GEF activity by interfering with the interaction of PI3K and ABI1 blocked PDGF-induced membrane ruffling. The assembly of the tetrameric complex therefore allows for a number of biological consequences important for growth factor responses, including two levels of SOS-1 activation and the recruitment of both PI3K and PIP3 to sites where they are most needed for actin reorganization.

Receptor tyrosine kinases (RTKs) that are bound to appropriate growth factors activate PI3K, which initiates Rac-induced cytoskeletal alterations. The signaling steps between PI3K and Rac are uncovered on page 17 in an article by Innocenti et al. that reveals the importance of complexes in activating guanine nucleotide exchange factors (GEFs).

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The complex life of a GEF

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On page 77, Farina et al. get a handle on RNA localization machinery by proving that an RNA-binding protein is essential for both mRNA transport and cell motility.

The cell motility connection comes about because localization of the β-actin mRNA to the lamellae is required for cell polarity and motility in fibroblasts. The new results show that this localization depends on ZBP1, a protein associated with cytoplasmic granules that contain the actin mRNA. ZBP1 bound to the mRNA through two COOH-terminal KH domains that were required for granule formation and attachment to the actin cytoskeleton. NH2-terminal regions of ZBP1 were necessary for granule localization in the lamellae.

Dominant-negative ZBP1 constructs that mislocalized actin RNA inhibited fibroblast motility. Since mRNAs for some actin-associated proteins, such as ARP3, also contain ZBP1-binding sequences, the authors believe that ZBP1 may link several messages involved in motility to a transport complex. But ZBP1 may be more than just a scaffold: a ZBP1 homologue has been linked to translational repression of the insulin-related growth factor. Perhaps ZBP1 also ensures that the actin mRNA is not translated until it reaches its ultimate destination.

The group plans to purify ZBP1-associated proteins in the complex to identify the motor responsible for actin-based transport. ZBP1 is also known to be associated with microtubules in neurons, so it may connect to different motors depending on the cell type.