Lattice supports single bilayer

The spherical membrane surrounding the poxvirus genome begins to form as an open, cup-like structure. Some have argued that the edge of the cup must be composed of two closely apposed membranes (imagine a collapsed vesicle); otherwise, the hydrophobic edges of a single membrane would be exposed to the cytoplasm. But on page 269, John Heuser confirms that poxvirus has only a single membrane bilayer. He finds that the growing membrane is stabilized by a proteinaceous lattice.

Heuser imaged freeze-fractured cells infected with poxvirus. Freeze-fracturing tends to split membranes randomly along bilayer planes, thus revealing all the bilayers that are present. As only one viral membrane plane was revealed, and no known membrane is resistant to this technique, Heuser concluded that the virus has only one bilayer.

The EM images also revealed a honeycomb-shaped lattice on the outer surface of the growing viral membrane. In older studies, the lattice appeared only as spikes on the membrane. Using deep-etch EM, Heuser was able to preserve and view the entire face of the lattice.

Like clathrin, the lattice curves the membrane it surrounds. It may also stabilize the hydrophobic edges of the incomplete membrane within the cytoplasm. Indeed, others have found that preventing the spikes from associating with the nascent viral membrane causes it to collapse. This is the mechanism of action of rifampicin—an antibiotic that aggregates the lattice protein and blocks poxvirus DNA encapsulation. JCB

One SecY is enough

New results in this issue (page 219) from Cannon et al. indicate that a translocating peptide passes through the center of a single SecY protein complex.

The idea is a paradigm shift for the translocation field. The general consensus has been that four copies of SecY (Sec61 in eukaryotes) oligomerize to form the translocon pore, since one ribosome associates with four copies of Sec61. But SecY crystallized as a monomer with only hydrophobic residues on the external sides of the transmembrane region. Since the channel is known to have a hydrophilic interior, something was amiss.

Cannon et al. now use cross-linking studies to show that the translocating peptide contacts residues in the center of a single SecY. Residues on its external face did not cross-link with the passing peptide, as would be expected if oligomers formed the translocon.

Combined with the X-ray structure of SecY, the new data suggest that the translocon resembles an hourglass. The passing peptide contacts mainly residues at the “waist,” which lies at the middle of the lipid bilayer. Fewer contact points mean less friction and thus a lower energy needed to move the chain along. Now researchers will want to determine why the ribosomes gather four SecY/Sec61 complexes. Maybe the oligomers recruit other important translocation proteins, but this remains unproven. JCB

Selectivity for eIF4E

On page 245, Culjkovic et al. show that a promiscuous translation factor carries out a more selective function in the nucleus.

The promiscuous function of the eIF4E translation initiation factor is to bring all mRNAs to the ribosome. Although transcript sequences vary greatly, eIF4E recognizes them all by their ubiquitous 5' cap structure. A less well-understood function of eIF4E, however, lies in its ability to export specific transcripts from the nucleus, thus increasing the amount available for translation. Only two transcripts have so far been shown to be exported by eIF4E—cyclin D1 and ornithine decarboxylase (ODC).

The new results map eIF4E’s export selectivity to a 100-bp sequence in the cyclin D1 3' UTR, which the authors call the 4E-SE. eIF4E’s cap-binding ability was also required for export. Another nuclear factor may increase the transcript’s affinity for eIF4E by binding to both the UTR and eIF4E. The authors are currently looking for candidate proteins that may serve this function.

Recently, the group has found that ODC and several other cyclins also contain the 4E-SE. The activation of eIF4E (via growth factor MAPK pathways, for example) could thus result in rapid, transcription-independent growth and proliferation by triggering the export of a whole set of cell cycle-promoting transcripts. But the system can be dangerous, as high levels of eIF4E are associated with malignant cancers. The authors show that this transformation can be blocked by deletion of the cyclin D1 4E-SE. JCB