PERSPECTIVES: EVOLUTIONARY BIOLOGY

A Powerhouse Divided

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Comparing the genomes of mitochondria and α-proteobacteria has yielded many sequence similarities. This finding strongly supports the view that these energy-generating organelles of eukaryotic cells were once free-living bacteria (*1*). About 2 billion years have passed since free-living α-proteobacteria developed a beneficial (symbiotic) relationship with their host cells and became permanent passengers (*2*). As eukaryotic cells diversified into the myriad forms seen today, their mitochondria also became more diverse, with different mitochondrial lineages retaining different traces of their free-living bacterial past. On page 1276 of this issue, Beech *et al.* (*3*) report the exciting discovery of a bacterial relic in the mitochondria of the unicellular alga *Mallomonas splendens*. They find that the alga has two forms of a cell division protein, FtsZ: one in chloroplasts and the other, bearing a strong resemblance to bacterial FtsZ, in mitochondria.

Bacterial FtsZ forms a scaffold for cell division by polymerizing, in a guanosine triphosphate (GTP)–dependent manner, to form a ring at the site where constriction of the cell wall occurs (*4*). Removal of a phosphate group from GTP is thought to pull the ring tighter so that the dividing cell is squeezed into two daughter cells (*5*). Although found in all bacteria, archaea, and chloroplasts, FtsZ has not been found in the mitochondria of yeast or other eukaryotic cells. Beech and colleagues set out to plug this gap, discovering two homologs of the bacterial FtsZ protein in *Mallomonas*. The first, found in chloroplasts of the alga, strongly resembles the FtsZ of cyanobacteria and plant chloroplasts, and is almost certainly involved in division of these light-trapping organelles (*6*). The second, a splendid find and aptly named FtsZ-mt, is located in algal mitochondria. This second cell division protein is very similar to the FtsZ of α-proteobacteria.

Antibodies raised against FtsZ-mt combined with confocal immunofluorescence microscopy allowed the authors to track the progress of this nuclear-encoded protein. They found that it homed to mitochondria where it formed a ring-like structure that is strikingly similar to the rings formed by bacterial FtsZ during division. They also showed that the amino-terminal sequence of FtsZ-mt contains the signal that ensures this protein is imported into mitochondria. The findings support the view that FtsZ-mt carries out the same task in mitochondrial division as its relative does in bacterial division, revealing yet another piece in the puzzle of mitochondrial origins.

Given this, one might think that all eukaryotes should possess mitochondrial FtsZ homologs. But this is not so. Although probably ubiquitous among prokaryotes (bacteria and archaea), FtsZ is notably absent from the mitochondria of yeast and higher eukaryotic cells (*4*). As Beech *et al.* explain, the yeast genome does not contain the *ftsZ* gene. Instead of FtsZ-like proteins, yeast apparently commandeer GTP-dependent dynamin proteins to constrict their mitochondria during division. Intriguingly, dynamin, like FtsZ, also polymerizes into ring structures at the points of mitochondrial constriction.

This finding led the authors to suggest that early in eukaryotic evolution, the α-proteobacterial ancestor of mitochondria donated its *ftsZ* gene to the nucleus of its host cell. The gene became a fixed feature of the genome, and its product, FtsZ-mt, acquired a signal to ensure that it got targeted back to mitochondria. In yeast and higher eukaryotes such as the worm *Caenorhabditis elegans*, the function of FtsZ in mitochondrial division has apparently been replaced by members of the dynamin family and, as a consequence, the mitochondrial-specific FtsZ has been lost. If this is so, the chances are that other groups of one-celled eukaryotes will have kept their mitochondrial FtsZ.

The alga *Mallomonas* belongs to a diverse assemblage of one-celled eukaryotes (derived from a single ancestor) known as the stramenopiles. This group includes both photosynthetic (heterokonts) and nonphotosynthetic (oomycetes) members. Heterokonts acquired their chloroplasts by secondary symbiosis, that is, by engulfing a eukaryotic alga. The chloroplast-associated FtsZ sequence reported by Beech *et al.* hints that the symbiont of *Mallomonas* was probably a red alga (its nucleus having been lost). In other groups of simple photosynthetic organisms, a remnant of the secondary symbiont's nucleus (the nucleomorph) has been retained and itself has some involvement in organelle division. The recent sequencing of nucleomorph chromosomes from the cryptomonad *Guillardia thea*—a unicellular organism with two flagella that has a photosynthetic organelle acquired by secondary symbiosis—reveals that surprisingly few of its proteins are targeted to plant organelles (plastids) (*7*); intriguingly, its FtsZ protein is one of the few that is.

A vexing evolutionary facet of the organelle and bacterial division story is its connection to the major components of the eukaryotic cytoskeleton, tubulin and actin. The structures formed by prokaryotic FtsZ are strikingly similar to the protofilaments formed by eukaryotic tubulins (*5*). Although the sequence similarity between FtsZ and tubulin is slight (*8*), the three-dimensional structures of the proteins are quite similar (*9*). Moreover, a further component of the prokaryotic cell division machinery, FtsA, is very similar to actin (*8*). Because a true cytoskeleton is one of the attributes that distinguishes eukaryotes from prokaryotes, the transition of these two prokaryotic proteins into their eukaryotic counterparts is unanimously agreed by biologists to be one of the crucial steps in eukaryotic evolution (*8, 10*). Yet with newer data pushing the origin of mitochondria possibly as far back as the origin of eukaryotes themselves (*1, 10*), there is less unanimity as to which came first: the cytoskeleton or the mitochondrion. Although FtsZ seems to be present in all prokaryotes, FtsA is found only in eubacteria (not in archaea), and more specifically in those that possess peptidoglycan (murein) in their cell walls (*4*). This indicates an intriguing eubacterial connection (albeit a loose one) to the origin of actin.

Genes that regulate organelle division in the earliest eukaryotes may provide further clues. Also likely to point the way are hydrogenosomes—anaerobic forms of mitochondria that usually lack DNA and are common among one-celled organisms that may represent an early branch of the evolutionary tree (*10, 11*). Some hydrogenosomes have been shown to undergo division (*12*), and it will be exciting to see how they have solved their division dilemma. Will they have chosen to divide in the same way as the mitochondria of *Mallomonas* or those of yeast, or will they have developed their own unique method? We shall just have to wait and see.

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