Endosymbiosis and horizontal gene transfer

Mitochondria and plastids, which evolved by way of symbiogenesis, have over time come under the control of nuclear genes. It is still not known how the expression of genes encoded in the nucleus and mitochondrion is coordinated to make them functional. Model systems such as highly specialized plastid-incorporating marine slugs can be used to help clarify such issues.

According to current knowledge, two endosymbiotic events led to the development of mitochondria and plastids in eukaryotic cells: early on during the development of life on earth, an anaerobic prokaryotic host cell engulfed an alpha proteobacterium, and some time later a cyanobacterium was incorporated into this proto-eukaryotic cell (see "Symbiogenesis of mitochondria and plastids"). During the gradual conversion of the endocytosed bacteria into cell organelles which are unable to subsist outside the host cell (e.g. mitochondria, plastids), many endosymbiont genes were transferred into the nuclear genome of the host cell, while others underwent functional changes or were lost altogether. This means that the genomes of mitochondria and plastids are highly reduced compared to the genomes of their free-living relatives. Nevertheless, the mitochondrial and plastid genomes still have a sufficiently large number of characteristic sequences to show that they evolved from free-living bacteria. Nobody really doubts this. However, there is less agreement when it comes to the assumption that the prokaryotic host cells that engulfed the bacteria are archaea rather than bacteria. However, some elementary nuclear genes and biochemical parameters of eukaryotes suggest that these organelles descended from archaea. Archaea form a large and diverse group of unicellular organisms that also includes strictly anaerobic methanogens (microorganisms that produce methane as a metabolic byproduct) that can live in extreme environments.

Genomes are undergoing constant change

A team of researchers led by Dr. Peer Bork from the European Molecular Biology Laboratory (EMBL) in Heidelberg has studied the distribution of genes in the genomes of modern-day microorganisms and reconstructed the putative number of genes and genome-altering processes in the ancestors of proteobacteria and archaea. Examples of such genome-altering processes are gene loss, gene duplication, horizontal gene transfer and the de novo development of genes. The EMBL researchers estimate that the common ancestor of proteobacteria had around 2,500 genes, many of which have been lost during evolution. Their research also led them to assume that the ancestor of archaea had around 2,050 genes. This is a relatively low number compared to many other organisms. However, the
mitochondrial genomes (mt genomes) of modern organisms are even smaller: the circular mitochondrial DNA of humans is just 16,569 base pairs long and contains only 13 protein-coding genes, all of which encode proteins of the respiratory chain (electron transport chain). These genes code for cytochrome b, the cytochrome c oxidase (3 subunits), NADH dehydrogenase (7 subunits) and ATP synthase (3 subunits) enzymes, as well as two genes coding for ribosomal RNAs, 13 mRNAs and 22 tRNAs. The majority of genes that are required for the maintenance of mitochondrial function are localized in the cell nucleus.

The nuclear genome plays a predominant role in maintaining mitochondrial function in all eukaryotes, although the gene content and size of mitochondrial DNA varies considerably among species. It is assumed that this variability is due to the fact that mitochondrial genomes have a much higher mutation rate than nuclear genomes. The mitochondrial genomes of plants are quite big; they are several hundred thousand base pairs (bp) long while, as mentioned above, mammalian mtDNA molecules are between 15,000 and 17,000 bp long. Professor Dr. Andres Jäschke from Universität Heidelberg, who is specifically focused on mitochondrial protein synthesis and cellular respiration, assumes that the extreme reduction of the animal mitochondrial genome is the result of the high energy requirement of animals that needs to be covered by way of a process known as oxidative phosphorylation, which takes place on the inner mitochondrial membrane. “Due to the fundamental importance of oxidative phosphorylation for the production of cellular ATP, any impairment of citric acid cycle enzymes leads to severe metabolic disorders,” explains Jäschke (ed. note: the citric acid cycle, which occurs in the mitochondria, is a series of chemical reactions that lead to the generation of the energy-rich substrates required for the production of ATP). Pathogenic mutations that lead to defects in the function of mitochondria and prevent them from fulfilling the energy requirements of tissue can cause neuromuscular disorders (known as mitochondrial myopathies). Although such mutations have been identified in nuclear as well as in mitochondrial genomes, the number of harmful mitochondrial mutations is much higher than the number of nuclear mutations.

Gene transfer between organelles and organisms

So the question arises as to how the cell nucleus can control the mitochondrial metabolism. So far, little is yet known about this. However, what is known is that the enzymes required for the mitochondrial energy metabolism that are encoded by the nuclear DNA need to cross the inner mitochondrial membrane, a process for which they need molecules known as chaperones (see "Cellular chaperones").

A specific chaperone protein family, i.e. cpn60, is quite common in mitochondria, plastids and bacteria. However, cpn60 proteins have also been found in anaerobic microorganisms, which do not possess mitochondria (e.g. in Entamoeba histolytica, which causes amoebiasis, a gastrointestinal infection with symptoms ranging from mild diarrhea to dysentery that can even be fatal). The E. histolytica cpn60 gene is contained in the nuclear genome and is closely related to the cpn60 gene of free-living proteobacteria and mitochondria. This relationship can be best explained by assuming that although Entamoeba protozoans lost their mitochondria as they evolved an anaerobic parasitic way of life, they did not lose all their mitochondrial genes. Investigations involving other mitochondria-deficient eukaryotic cells have led to the discovery of nuclear genes that are assumed to have a proto-bacterial origin and that are taken as an indication for the early symbiosis with bacterial cells. Prof. Andrew H. Knoll from Harvard University, who is a leading expert in the evolution of life on earth, believes that the incorporation of chaperone protein genes into the nuclear genome of the host cells is a relatively common mechanism and potentially also a prerequisite for the endosymbiosis of bacteria.

What has just been described for mitochondria is also true in principle for chloroplasts. In addition to cpn60, the nuclear genome also contains genes encoding other chaperone proteins, as Prof. Dr. Irmgard Sinning from the Biochemistry Centre at Universität Heidelberg has shown. These chaperones are used for example to ensure that the light-harvesting proteins (ed. note: biological solar collectors in the chloroplasts) reach their final destination in the chloroplast membrane of green plants.

Kleptoplast slugs

Some marine slugs are excellent examples of how plastid genes can be transferred between two completely different organisms. The green sea slug Elysia chlorotica that lives off the Atlantic coast in North America eats green algae of the genus Vaucheria and incorporates the algal chloroplasts into the spaces between its own cells. The slug turns green and photosynthesizes when exposed to sunlight, thus making its own food. It was previously assumed that Elysia chlorotica lived in an endosymbiotic relationship with the algae, such as the relationship that is known to exist between corals and some mussel species. However, the truth about the slug’s strategy is somewhat stranger.
Elysia eats and digests the green algae, but not the algae’s photosynthetic plastids. The slug sequesters the plastids and manages to maintain their functionality. The plastids are phagocytosed by the slug’s intestinal epithelial cells and distributed across the entire, widely branched intestine. The chloroplasts are able to continue dividing and accumulating in the subepidermal cell layer on the slug’s body surface. The plastids photosynthesize and provide Elysia with oxygen and carbohydrates. If there is enough sunlight, the sea slug is able to live exclusively from photosynthesis for around 10 months. The plastids then die and the slug has to replenish its plastid store and eat more algae.

This phenomenon can hardly be called symbiosis, which is defined as a partnership that is beneficial to both partners. Instead, the term kleptoplasty was coined to describe the phenomenon whereby host species like Elysia steal chloroplasts from their food (i.e. algae). Although Elysia is more a thief than an equal symbiotic partner, the slug is nevertheless a fascinating model for showing how an unstable endosymbiotic relationship might turn into a permanent one. As is the case for all algae and green plants, the majority of Vaucheria plastid proteins are encoded by nuclear genes. So the question arises as to how the slug manages to keep the plastids functional for such a long period of time. It seems unlikely that Elysia manages to conserve the nuclear genome and in this way gain access to the nuclear genes required for maintaining the function of the chloroplasts. The first clue for solving the puzzle might be the algal gene that was discovered in the nuclear genome of Elysia. It is assumed that this gene was horizontally transferred to Elysia from Vaucheria. This algal gene, which is known as PsbO, encodes a protein that is involved in a key process of photosynthesis, namely the light-dependent hydrolysis of water (photolysis). While the slug passes PsbO on to its offspring, each slug generation nevertheless needs to take up the photosynthetic plastids by eating Vaucheria in order to be able to carry out photosynthesis.

It is assumed that additional Vaucheria plastid genes have been incorporated into the Elysia genome. However, this has not yet been clarified because there are certain questions that still need to be answered relating to the mechanisms by which the genes were incorporated into the slug genome, the modification of the gene promoters that enable the slug to activate the genes required for photosynthesis and how the gene products are transported from the slug into the plastids.