

The Cell Within the Cell

QTC-026 · From Quarks to Consciousness

The Universe, Life, and How We Found Out

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Article Abstract

A eukaryotic cell is not the enlarged descendant of one simple lineage. Mitochondria preserve bacterial ancestry inside a host whose informational machinery is archaeal-related; plastids record a later cyanobacterial acquisition. Genomes, membranes, division systems and protein-import machinery make endosymbiosis established knowledge. The exact historical mechanism remains less certain. Competing models disagree over the host's complexity, the metabolism that joined the partners and whether mitochondria arrived before or after major eukaryotic innovations. Gene transfer then moved much organelle biology into the nucleus, while reduced organelles and secondary losses erased obvious traces. This article separates the secure merger from disputed reconstructions, follows plastids and Paulinella as comparative cases, and explains why eukaryotic ancestry is a network of joined histories rather than one uncomplicated tree.

In 60 Seconds

Mitochondria and plastids began as bacteria living inside other cells. Their reduced genomes, bacterial gene trees, membranes, division systems and nuclear-encoded protein import converge on that conclusion. The host lineage that produced eukaryotes is archaeal-related, with Asgard archaea among its closest known relatives. What remains unsettled is the sequence: did a complex, phagocytic host take in the mitochondrial ancestor, or did symbiosis help build eukaryotic complexity? Metabolic hypotheses, molecular clocks and ancient gene duplications give different answers. Integration moved many endosymbiont genes into the nucleus and made organelles dependent on imported proteins. Hydrogenosomes and mitosomes are modified mitochondrial relatives, while Monocercomonoides lost the organelle secondarily. Plastids arose from a cyanobacterium, then spread through further eukaryote-within-eukaryote mergers. Paulinella acquired a separate photosynthetic organelle much later. The central event is secure; its exact partners, metabolism and order of innovations remain a live reconstruction problem. The evidence supports one merger while leaving several pathways scientifically competitive.

Why This Question Matters

Every animal, plant, fungus and protist inherits a cell assembled through ancient partnership. That history matters because it changes what a lineage is: not a sealed thread, but a system capable of joining genomes, membranes and metabolisms. It also offers a model of scientific confidence. Multiple observations establish endosymbiosis, while the same evidence leaves room for disagreement over mechanism and timing. Keeping those layers separate prevents two opposite errors—treating the

merger as speculation, or presenting one elegant origin story as a recorded event. The cell within the cell is both a fact of ancestry and an unfinished reconstruction.

1. The Eukaryotic Cell Is a Historical Composite

The Question

A mitochondrion looks like a normal part of a cell. Why claim that it descends from a separate bacterium, and how can a merger remain visible after more than a billion years of shared evolution?

A eukaryotic cell contains histories that did not begin together. Its mitochondria descend from bacteria; in plants and algae, plastids descend from cyanobacteria.[1,3–5,25] The partners became one reproducing lineage, but their genes and molecular machines still retain different phylogenetic addresses. A cell can therefore be an organism and a record of an ancient association at once.

The conclusion does not rest on resemblance to a bean-shaped microbe. Organelle genomes, bacterial gene affinities, membrane chemistry, division systems and nuclear-controlled protein import converge on endosymbiosis.[3,4,22,23] Each line has limitations. Together they explain more than a model in which all compartments arose solely by folding one ancestral host membrane.

Lynn Sagan's 1967 paper assembled a broad symbiotic origin for eukaryotic cells and helped restore a tradition with earlier contributors.[1,2] Later molecular phylogenies changed the status of the mitochondrial and plastid claims from bold synthesis to established ancestry. Historical credit is therefore plural: proposing, integrating and testing were different achievements performed at different times.

The familiar cartoon—one bacterium swallowed by an already modern cell—is too finished at the start. Eukaryogenesis involved prolonged gene transfer, metabolic coupling and construction of trafficking systems.[3,18,33,36] Researchers disagree over how much complexity the host already possessed. The secure part is integration; the exact order of its cellular steps is reconstructed rather than observed.

That distinction sets this article's boundary. QTC-023 followed the common ancestry of all life, and QTC-024 showed that microbes still dominate planetary diversity and metabolism. Here the question is how joined microbial histories produced the eukaryotic cell. QTC-027 will ask what later lineages built from that cell.[3,4]

Where That Leaves Us

The eukaryotic cell is a composite without being a temporary alliance: integration made one durable lineage from histories that remain detectable. To see why that conclusion became secure, the next step is to inspect the evidence preserved inside organelles—especially their genomes, membranes, division and dependence on proteins encoded elsewhere.

2. Two Membranes and Bacterial Genomes

Mitochondria and plastids carry DNA, but not miniature copies of a bacterial genome. Their chromosomes are reduced, rearranged and differently organized across lineages.[3,4,25,27] Conserved ribosomal and protein genes nevertheless place mitochondrial sequences with bacteria

and plastid sequences with cyanobacteria.[7,25,29,31] Reduction records dependence, not loss of ancestry.

Early biochemical comparison connected *Paracoccus denitrificans* with mitochondrial respiration, while sequence phylogenies later placed mitochondrial genes among Alphaproteobacteria.[6,7] The first comparison was productive without making *Paracoccus* the ancestor. Living organisms are cousins sampled after immense divergence; an ancestor is a historical population, not whichever modern species looks most similar.

Two surrounding membranes fit an intracellular origin. Yet membrane number is not a mechanical replay of one engulfment.[24,25,28] Inner and outer membranes acquired new proteins, contacts and functions; some plastids gained additional membranes through later endosymbioses. Membrane topology supports a history only when combined with composition, targeting and phylogeny.

Organelle division contains bacterial-derived elements but is controlled by the host and remodelled differently among eukaryotes.[3,4,23,32] The same mosaic appears in bioenergetic membranes: ancient bacterial electron-transfer machinery operates beside proteins evolved or recruited after integration. Calling the entire organelle a bacterium would ignore most of its subsequent history.

No single observation carries the whole case. DNA alone could be transferred material; a double membrane has other causes; fission is widespread.[2,3,24] The power lies in their agreement with import pathways and gene trees. Endosymbiosis predicts a correlated package of bacterial inheritance and host control, and that package is what cells contain.

Where That Leaves Us

Genomes and cell biology make bacterial ancestry hard to escape, but ancestry is less specific than identity. The evidence locates mitochondria near Alphaproteobacteria without naming one living bacterium as their parent. That gap opens the next problem: how closely can phylogenies approach the vanished mitochondrial ancestor, and what metabolism did it possess?

3. The Mitochondrial Ancestor

The Question

If mitochondrial genes are bacterial, their branch should have relatives. Yet the deepest phylogeny changes with sampled genomes and evolutionary models. How much of the founding bacterium can a modern tree identify with confidence today?

Sequence data established an alphaproteobacterial relationship, but the exact branch remains unsettled.[5,7,8] One analysis placed mitochondria outside sampled Alphaproteobacteria; another, using models for variation across sites and branches, favoured mitochondria as their sister.[5,8] Both reject a literal descent from a named living species. Their disagreement is about a deep topology, not bacterial origin.

Deep phylogeny is difficult for predictable reasons. Mitochondrial genes are ancient, reduced and fast-changing; many moved to the nucleus or disappeared. Taxon sampling, long-branch attraction, compositional bias and gene selection can pull the branch differently.[4,5,8] A sophisticated model can improve fit without turning an unobserved ancestor into a sampled organism.

Earlier candidates still matter historically. *Paracoccus* illuminated respiratory similarity, and Rickettsiales seemed attractive because intracellular lifestyles resemble symbiosis.[6,8] Later sampling and bias-aware analyses weakened literal identifications. Superseded does not mean useless: those proposals generated comparisons that clarified which similarities are ancestral, convergent or consequences of intracellular life.

Metabolism is harder to reconstruct than placement. The founding bacterium may have been aerobic, facultatively anaerobic or metabolically flexible; modern mitochondria, anaerobic mitochondria and hydrogenosomes preserve different subsets.[4,13,21] Gene loss and retargeting obscure the starting inventory. A present pathway demonstrates possibility and inheritance, not the exact ecological bargain that began the association.

One conclusion is firmer: the common ancestor of living eukaryotes already possessed a mitochondrion or mitochondrial derivative.[3,4,19,21] Anaerobic and parasitic lineages repeatedly modified, reduced or lost functions. Even *Monocercomonoides*, which lacks a detectable mitochondrial organelle, descends from ancestors that had one. Secondary absence is not a surviving pre-mitochondrial stage.

Where That Leaves Us

The mitochondrial ancestor was alphaproteobacterial-related, but its nearest sampled cousin and physiology remain open. The other partner is reconstructed through a different archive: nuclear informational genes and archaeal genomes. Following that archive moves the story from the bacterium that entered the association to the host lineage whose identity has also changed with new sampling.

4. The Archaeal Host

Eukaryotic nuclear genes do not tell one simple ancestry. Systems for information processing—replication, transcription and translation—show strong archaeal affinity, while many metabolic genes have bacterial histories.[3,11,16,35] Transfer, duplication and differential loss complicate every percentage. The broad mosaic is robust; a tidy inventory split between exactly two donors is not.

Phylogenomic analyses increasingly place eukaryotes within Archaea in a two-domain tree.[9,10,12] This makes the host archaeal-related rather than a third primary lineage formed independently beside Bacteria and Archaea. Exact rooting and models still matter. 'Within Archaea' constrains ancestry without naming the host species or its cellular form.

Asgard archaea sharpened that constraint. Their genomes contain homologues of proteins involved in cytoskeleton, membrane remodelling and trafficking in eukaryotes, and their branches lie close to eukaryotes in many analyses.[9,10] These eukaryotic signature proteins are clues to ancestral capacities. They do not prove that an Asgard cell already possessed a nucleus or phagocytosis.

Prometheoarchaeum syntrophicum supplied the first cultivated Asgard representative after years of enrichment.[11] It grows slowly, depends on metabolic partners and forms protrusions, facts that made syntrophic models more physically imaginable. It is still a modern species separated

from the host by immense time. One culture constrains possibilities; it does not reenact eukaryogenesis.

The host therefore has an address but not a portrait. Asgard affinity, archaeal informational machinery and bacterial metabolic contributions define parts of the problem.[10,11,14,18] They leave open the exact lineage, partners and pre-merger complexity. New 2026 gene reconstructions also suggest associations with more microbial sources than a clean two-part formula captures. [15,16]

Where That Leaves Us

Asgard genomes and cultures narrowed the host from an abstraction to an archaeal-related lineage with testable cellular capacities. They did not reveal the merger's sequence. That is where models diverge most sharply: whether metabolism first bound simple partners, whether phagocytosis preceded entry, and whether mitochondrial energy was a cause or a consequence of growing complexity.

5. How the Merger Happened

The Question

The partners are constrained more tightly than their encounter. Without a fossil of the merger, can ancient genes, metabolism and membranes distinguish a host that swallowed prey from partners that first depended on one another?

No rock preserves the first mitochondrial endosymbiosis. Mechanisms must satisfy phylogeny, bioenergetics, membrane topology and the order of eukaryotic innovations.[3,18,33] That does not make them mere stories: each model risks different predictions. It does mean that naming a plausible pathway is not equivalent to observing the historical event.

The hydrogen hypothesis proposes an archaeal host dependent on hydrogen from a facultatively anaerobic bacterial partner.[13,34] Metabolic dependence would stabilize association before organelle integration. It is specific enough to test against ancestral pathways, but those pathways are reconstructed after transfer and loss. The hypothesis remains active, not a settled biography of the first eukaryote.

Host-first models give the archaeal-related cell substantial internal complexity or phagocytic capacity before mitochondrial entry. Mitochondria-early models make symbiosis central to building those features.[13–15,18,33] The camps contain variants, and words such as early and late require a reference event. A nucleus, endomembranes, cytoskeleton and import machinery need not have appeared together.

Gene-age analyses illustrate both promise and fragility. A 2016 study inferred late mitochondrial acquisition; work on ancient duplications in 2021 and 2026 reconstructed different sequences, including substantial host complexity before entry.[14,15,33] Root choice, hidden paralogy, transfer, loss and clock assumptions can change the order. A molecular estimate is not a photographed intermediate.

An energetic model argues that many internal bioenergetic membranes gave eukaryotes power per gene sufficient for genome expansion and complexity.[17,18] The proposal is influential and quantitative. Its necessity is contested because modern scaling may not reproduce ancestral

ecology and because energetic advantage does not establish timing. Mitochondria clearly transformed energy; whether that transformation was the required trigger remains open.

Where That Leaves Us

Mechanistic models turn an established merger into competing causal histories. Their disagreements are useful because they expose which observations still lack an order. Whatever route began the association, persistence required a second transformation: genes moved, proteins returned from the host cytosol, and formerly autonomous bacteria became organelles that could be reduced almost beyond recognition.

6. Genes Moved, Organelles Shrunk

Endosymbiotic gene transfer moved genes from organelle genomes into nuclear chromosomes. [22,24,31] A transferred gene became useful to the organelle only if its product could be expressed and returned to the correct compartment. Transfer therefore coupled genome reduction to a new logistical system. The nucleus did not simply confiscate DNA; cell biology had to rebuild delivery.

Today most mitochondrial and plastid proteins are nuclear encoded and imported through translocation complexes.[23,24,32] Targeting sequences route precursors through membranes, and host regulation coordinates their production with the residual organelle genome. Modern channels are derived systems. Their complexity records prolonged integration, not a complete apparatus already waiting before endosymbiosis.

Why any genes remain inside organelles is still unresolved. Redox control close to electron-transfer membranes, hydrophobicity of proteins, genetic-code changes and barriers to successful transfer may all contribute.[3,22,24] Different organelles retained different inventories. One attractive explanation need not govern every gene, and a small genome is not evidence for incomplete integration.

Some mitochondria changed so radically that they were first treated as absences. Entamoeba mitosomes and multiple hydrogenosomes lack familiar oxidative phosphorylation yet retain mitochondrial-related machinery or ancestry.[20,21] Reduction followed adaptation to anaerobic or parasitic life. These organelles show why searching only for oxygen-consuming powerhouses would systematically erase mitochondrial history.

Monocercomonoides goes farther: no mitochondrial organelle has been detected, and an essential iron–sulfur assembly function was replaced by a cytosolic system.[19] The lineage nevertheless nests within mitochondrion-bearing eukaryotes. It lost the organelle secondarily. The exception therefore strengthens the evolutionary distinction between ancestral absence and loss after deep integration.

Where That Leaves Us

Integration can hide its own evidence: transferred genes leave a tiny organelle genome, imported proteins blur origin, and secondary loss can erase the compartment. Plastids underwent the same broad conversion from endosymbiont to host-controlled organelle, then added another complication—photosynthesis spread when eukaryotic cells themselves became partners inside other eukaryotes.

7. Plastids Repeated the Logic

The Question

Mitochondria could seem like an evolutionary accident too ancient to compare under the same physical rules. Plastids and Paulinella provide other mergers. Which features repeat, and which belong only to one route into organelle dependence?

Primary plastids trace to a cyanobacterial endosymbiont integrated in the ancestor of Archaeplastida.[25–29] Plastid genomes and cyanobacterial genes in the nucleus preserve that ancestry. The exact closest cyanobacterial branch remains sensitive to sampling and early phylogeny. As with mitochondria, confidence is highest at the broad origin and lower at the precise donor.

Gene transfer and protein import again changed ownership. Thousands of nuclear genes have been assigned cyanobacterial histories in comparative analyses, while targeting systems return many products to plastids.[22,31,32] Counts vary because gene loss, other bacterial transfers and difficult trees complicate assignment. The process is established even when one gene's donor remains uncertain.

Photosynthesis then spread through secondary and later endosymbioses. A eukaryotic host retained a photosynthetic eukaryote, producing plastids surrounded by additional membranes and leaving host, plastid and sometimes remnant nuclear histories.[24–26,28] Different algal groups experienced acquisition, replacement and loss. One word—plastid—therefore covers organelles with unequal numbers of nested ancestors.

Paulinella chromatophora supplies an independent, much younger case. Its cyanobacterial-derived chromatophore has undergone genome reduction and integration with genes from the founding endosymbiont and other bacteria contributing to host functions.[30] Paulinella is not a halfway stage toward plant plastids. It is a separate experiment that makes early organellogenesis comparatively accessible.

The comparison reveals both recurrence and contingency. Stable inheritance, metabolic dependence, genome reduction, gene transfer and protein targeting recur; the partners, pathways and membrane outcomes differ.[25,30] A second primary photosynthetic organelle shows that organellogenesis is physically repeatable. It does not show that the mitochondrial merger followed the same mechanism.

Where That Leaves Us

Plastids and Paulinella turn one ancient event into a comparative science. They confirm recurring requirements for inheritance and host control while exposing multiple routes through membranes and gene transfer. The final consequence reaches beyond organelles: once lineages merge, different genes preserve different trees, and eukaryotic ancestry becomes a network that must still support a coherent history.

8. One Merger Changed the Tree

A nuclear ribosomal gene, a mitochondrial gene and a plastid gene can trace three different branches without contradiction.[3,16,35] Each tree answers a question about one inherited

component. A species history must explain how those components became linked. Treating one marker as the whole organism would turn genuine endosymbiotic structure into apparent conflict.

The shorthand 'archaeal host plus alphaproteobacterium' captures two central ancestries but not every nuclear gene.[15,16,35] Bacterial transfers, viral associations, ancient duplications and differential loss add layers. A 2026 analysis inferred diverse microbial associations during eukaryogenesis.[16] Association in a gene tree does not automatically identify another permanent endosymbiont, so the richer picture remains method-dependent.

Networks do not make trees obsolete. Vertical descent still connects parent and offspring, and rooted trees remain essential for individual genes and cellular lineages.[3,35] Networks add edges where inheritance crossed lineage boundaries. The task is to demonstrate those edges with compatible gene histories, cellular mechanisms and timing, not to replace every difficult branch with an unspecified merger.

Confidence must follow scale. One mitochondrial origin before living eukaryotes diversified is strongly supported; the exact host species, metabolic bargain and order of innovations are not.[4,18,21,36] The article's epistemic profile therefore rests at current scientific interpretation. Established observations support a composite cell, while its thesis includes a reconstruction whose internal sequence remains revisable.

That composite cell enabled later histories without dictating them. Mitochondria transformed metabolism, nuclei and endomembranes reorganized information and traffic, and plastids opened photosynthetic worlds. The merger also left different genes with different trees.[3,35] QTC-027 asks how descent remains traceable when transfer and viruses connect lineages.

Where That Leaves Us

The cell within the cell is established history at broad scale and unfinished reconstruction in detail. Independent genomes expose the merger; host control explains its durability; disagreement marks the vanished sequence, not ignorance of the event. From this integrated cell, the series turns to branching inheritance, gene transfer and viruses.

What We Know, and How

- Mitochondria and plastids have bacterial endosymbiotic origins supported by genomes, phylogeny and host-controlled import.[3,4,22–25]
- The eukaryotic host lineage is archaeal-related, with Asgard archaea among its closest known relatives.[9–12]
- The common ancestor of living eukaryotes already possessed a mitochondrion or mitochondrial derivative.[3,4,19,21]
- Gene transfer to the nucleus and protein import transformed endosymbionts into dependent organelles.[22–24,31,32]

What We Still Don't Know

- The exact closest bacterial lineage to the mitochondrial ancestor.
- The precise archaeal host lineage and its cellular complexity before the merger.
- Whether metabolic syntrophy, phagocytosis or another interaction initiated stable endosymbiosis.

- The relative order of mitochondria, nucleus, endomembranes, cytoskeleton and phagocytic machinery.
- Why particular genes remain in organelle genomes while others moved to the nucleus.

What Could Change Our Minds

- Broader bacterial and archaeal genome sampling that stabilizes the deepest phylogenetic branches.
- Independent ancient-duplication and molecular-clock analyses that converge on one order of innovations.
- Cultured Asgard diversity and experimental syntrophies that make a proposed merger physically implausible or likely.
- Gene-tree reconciliation showing that a thesis-bearing ancestry reflects contamination, hidden paralogy or later transfer.
- A demonstrably primitively amitochondriate eukaryotic lineage.

If You Remember Only One Thing

Mitochondria and plastids are integrated bacterial descendants. Their ancestry is established, while the host, metabolism and order of innovations that produced the first eukaryotic cell remain actively reconstructed in detail.

Related Articles

- QTC-023 — LUCA: The Ancestor We Reconstructed
- QTC-024 — The Microbial Planet
- QTC-027 — From Information to Inheritance: Tree, Web and Viruses

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