The *Multiple Multicellular Prototype* Framework

Silica-Based Biomineralization and Early Eukaryotic Diversification

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Abstract:

Current models of early eukaryotic evolution encounter persistent anomalies: sophisticated silica biomineralization appearing across supposedly unrelated lineages (glass sponges, radiolaria, diatoms), electrical conduction in organisms lacking nervous systems, and phylogenetic inconsistencies in basal animal groups that resist resolution despite decades of molecular analysis. These issues stem from a core assumption that a single *Last Eukaryotic Common Ancestor* (LECA) gave rise to all multicellular life.

This paper identifies this as a fundamental modeling constraint that creates artificial bottlenecks in evolutionary explanation. By allowing multiple post-LUCA lineages to have independently developed multicellularity, resulting in several Multicellular Prototypes rather than a single LECA, these anomalies resolve into logical patterns. The Multiple MCP Framework proposes distinct ancient lineages: the *Silicarian* MCP (glass sponges, radiolaria, diatoms sharing silica biomineralization), the *Cnidarian* MCP (neural network specialists), the *Hijacker* MCP (parasitic and manipulative strategies from viruses to *Cordyceps*), and others, each representing parallel solutions to multicellular organization.

This framework eliminates the need for impossible convergent evolution scenarios, naturally explains the Cambrian period as a convergence event rather than an evolutionary explosion and reframes symbiosis as a fundamental innovation mechanism rather than a secondary adaptation. The paper introduces testable predictions, demonstrates how carnivorous plants may cluster with ctenophore rapid-response mechanisms rather than photosynthetic plant lineages, and predict that glass sponges will show closer molecular relationships to certain radiolarians than to sponges in silica-processing genes.

To facilitate immediate testing, we provide comprehensive MCP-organized sequence databases through the Open Science Framework, enabling researchers to conduct BLAST analyses against functional strategies rather than, or in combination with, traditional taxonomic categories. This represents a systems-level debugging of evolutionary models that preserves decades of molecular data while revealing the ancient multicellular experimentation that current frameworks have obscured.

Keywords:

Evolution, multicellular evolution, LECA, LUCA, glass sponges, silica biomineralization, *Silicarian* lineage, evolutionary convergence, basal animals, symbiosis, cambrian explosion, phylogenomics, multiple multicellular prototypes, glass sponges (*Hexactinellida*), radiolaria, diatoms, silica biomineralization, convergent evolution, phylogenetic bias, post-LUCA experimental period, multicellularity, evolutionary innovation, structural biology, electrical conduction without neurons, ancient lineages, evolutionary framework, evolutionary convergence, skeletal nanotechnology.

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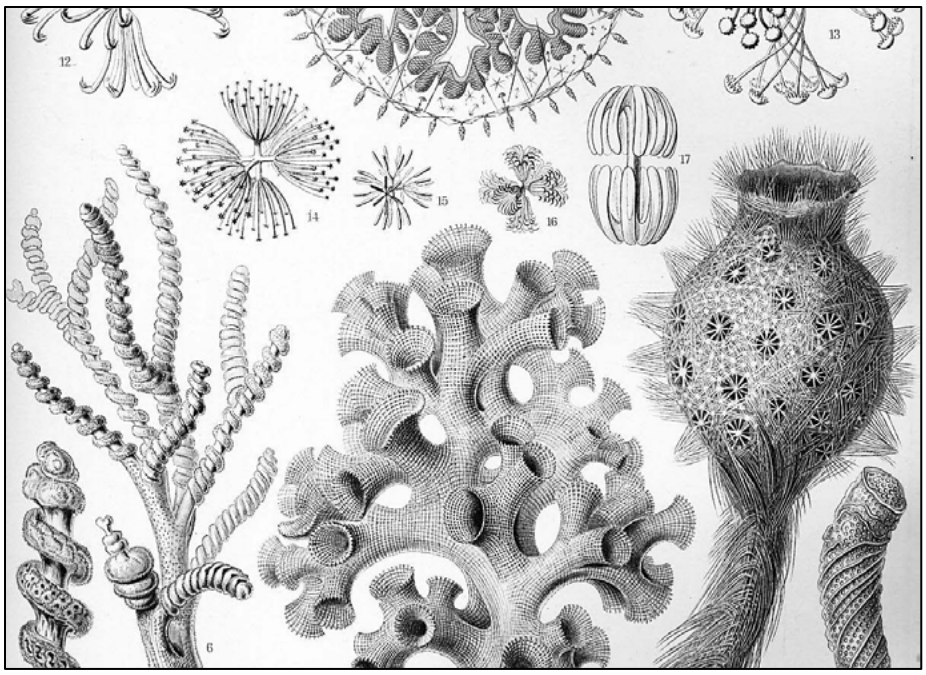

[Haeckel, E. *Kunstformen der Natur,* Plate 35, *Hexactinellae*, 1904].

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Prologue

A Systems Perspective on Evolutionary Models

The evolutionary biology community has built extraordinary foundational work over the past century. Molecular phylogenetics, genomic analysis, and sophisticated theoretical frameworks have generated a wealth of robust data and insights. However, like any complex system, sometimes a single architectural assumption can create persistent issues that resist debugging through incremental fixes.

The single-LECA model represents such a constraint. For decades, researchers have encountered the same recurring issues: glass sponges that conduct electricity without neurons, radiolaria with impossible architectural precision, phylogenetic trees that refuse to resolve despite additional data, and symbiotic relationships so fundamental that they seem baked into the system architecture rather than added later. Each anomaly has been handled individually through increasingly complex workarounds (*"convergent evolution," "secondary simplification," "horizontal gene transfer"*), but the underlying pattern suggests a deeper systems issue.

These explanations became entrenched not because they were inherently flawed, but because they were the only logical responses available within the single-LECA framework. When molecular phylogenies consistently showed glass sponges clustering apart from other animals, or when silica biomineralization appeared across supposedly unrelated lineages, convergent evolution was the most parsimonious explanation available. The data itself was accurate and valuable; the interpretive framework was simply constrained by assuming all multicellular complexity had to trace back through a single evolutionary bottleneck.

Established molecular phylogenies remain robust datasets under the Multiple MCP Framework—they simply require reinterpretation. Where current trees show *"problematic"* long branches or *"anomalous"* clustering patterns, the MCP framework predicts these represent authentic ancient divergences rather than phylogenetic artifacts requiring correction. When BLAST analyses return unexpected cross-kingdom matches, these become evidence of MCP relationships rather than contamination to be filtered out. The molecular data has been telling us about multiple ancient lineages all along; we have been forcing it into a single-lineage interpretation.

In software engineering terms, this resembles a race condition deep in the codebase. The application launches fine, handles most operations smoothly, but consistently hangs at certain execution points. Individual patches might work around specific crashes, but the core constraint remains, generating new exceptions whenever the system encounters certain data patterns.

The MCP framework makes specific predictions that differ from current models: glass sponges should cluster with radiolaria and diatoms in silica metabolism genes rather than with other sponges; carnivorous plants should show closer molecular relationships to cnidarian neural pathways than to photosynthetic plant lineages; and parasitic organisms across kingdoms should share host manipulation mechanisms that current taxonomy treats as unrelated convergences. Where traditional phylogenetics predicts these patterns should not exist or should be explained as independent innovations, the MCP framework predicts they represent deep vertical inheritance from ancient, shared strategies.

We propose that the constraint lies in forcing all multicellular evolution through a single bottleneck—one LECA event. By allowing multiple independent multicellular transitions, the system runs as intended. Glass sponges conducting electricity makes perfect sense if they're specialized electrical engineers from an 850-million-year-old *Silicarian* lineage. (Mills, 2017). Radiolaria architectural precision makes sense if they're part of the same structural engineering lineage. The Cambrian fauna patterns make sense as a convergence event rather than an explosion.

This isn't a revolutionary rewrite of evolutionary theory: it's a systems-level debugging that preserves all the excellent foundational work while fixing a core architectural constraint that prevented the full program from running smoothly. The molecular data, phylogenetic methods, and genomic insights developed over decades remain valuable; they simply reveal a more complex and ancient evolutionary landscape than previously recognized.

Introduction

The Glass Sponge Paradox

When we observe a radiolarian under the microscope, we witness architecture that rivals human engineering: elaborate silica lattices, elegant radial symmetries, and nanostructural precision beyond current materials science. Traditional evolutionary theory insists these intricate forms emerged independently of the silica frameworks found in glass sponges (*Hexactinellida*); a position that demands convergent evolution of extreme biochemical complexity across vastly different lineages.

Glass sponges themselves pose one of the most persistent puzzles in modern biology. These sessile animals build crystalline silica skeletons with micron-level precision, conduct electrical signals without neurons, and may persist for over 10,000 years while forming reef structures kilometers in scale. (Bawazer, 2012).

Their biology combines neural-like coordination with plant-like architectural precision, all without clear phylogenetic precedent. Each year adds new layers of complexity to their story, yet the evolutionary models remain flat: their innovations are routinely written off as isolated, convergent accidents.

Meanwhile, diatoms and radiolaria—also masters of silica biomineralization—are likewise treated as evolutionary outliers, despite displaying many of the same structural features found in glass sponges. The prevailing phylogenetic assumption that such architectures evolved independently in each lineage is not only statistically suspect, but also biologically inconsistent. This paradox exposes a deeper flaw in how current models interpret early multicellularity and complex traits.

This paper proposes a new framework—*Multiple Multicellular Prototypes (MCPs)*—to explain the shared architectural, biochemical, and organizational strategies observed across otherwise unrelated groups. Rather than invoking improbable convergence, we suggest that early multicellular evolution was not a linear path from a single eukaryotic common ancestor (LECA), but a branching experimental period following LUCA, during which multiple lineages independently explored multicellular strategies. Within this context, the silica-based architectures of radiolaria, diatoms, and glass sponges may represent not isolated events, but the preserved record of a coherent evolutionary lineage: the *Silicarian* Lineage.

This shift in perspective reframes convergent anomalies as coherent histories. It suggests that many current phylogenetic categories—shaped by terrestrial bias and morphological assumptions—obscure deeper evolutionary relationships rooted in biochemical strategy and material specialization. It is time we consider that the marvels of silica biology are not convergent curiosities, but signatures of a parallel evolutionary tradition that began in Earth's earliest multicellular experiments.

The Single-LECA Limitation

The concept of a single *Last Eukaryotic Common Ancestor* (LECA) has dominated molecular phylogenetics for decades, often presented as a universal progenitor from which all eukaryotes descend. However, this model imposes a structural constraint on evolutionary reasoning: it presumes a linear descent from a single organismal lineage, even when the data suggest complex, overlapping modular systems across early eukaryotic history (Roger and Simpson 2009; Koonin 2006).

Genomic evidence increasingly points to a plurality of ancient lineages—not a single surviving trunk but a landscape of deep-branching, parallel prototypes. These lineages exhibit mosaic combinations of cellular features such as phagocytosis, endomembrane systems, and cytoskeletal scaffolding (Doolittle 2021; Dagan et al. 2010). Many of these traits appear in non-tree-consistent distributions, implying lateral inheritance, independent innovation, or convergent recruitment rather than single-lineage descent.

The LECA model also relies heavily on reconstructed consensus sequences and tree-based topologies, which inherently filter out polyphyletic or reticulate signals. As a result, molecular toolkits that do not conform to a single bifurcating origin are either misattributed or discarded (Gribaldo et al. 2010; Martin et al. 2015). This filtering reinforces a false clarity, privileging monophyly over modular inheritance and obscuring lineage diversity at the base of eukaryotic life.

Instead of a singular LECA, we propose that multiple ancient cellular systems, modular cellular prototypes, contributed to the genetic and structural architecture of modern eukaryotes. These MCPs may have coexisted, hybridized, and radiated independently, some going extinct while others gave rise to recognizable eukaryotic lineages. Within this view, "*LECA*" is not an ancestor but an artifact of phylogenetic compression—a projection of survivorship bias onto a complex evolutionary past.

When we examine the five major animal groups recognized today (*Bilateria, Cnidaria, Ctenophora, Placozoa,* and *Porifera*), we find organizational principles so fundamentally different that they appear to represent parallel solutions to the challenge of multicellularity rather than modifications of a shared ancestral design.

Consider the implications: if these groups shared a recent multicellular ancestor, we must explain how:

- Glass sponges developed sophisticated electrical conduction without neurons.
- *Ctenophores* evolved unique collision-detection combs found nowhere else.
- *Placozoans* simplified to such an extreme degree while maintaining viability.
- Multiple lineages independently mastered complex silica biomineralization.

The single-LECA model forces all this diversity through an impossible evolutionary bottleneck.

In traditional phylogenetics, extinct lineages are treated as invisible: once a lineage leaves no direct descendants, it is presumed to have no ongoing influence. This assumption ignores a key reality of evolutionary systems: functional modules can persist beyond the death of their original lineage. Under a modular cellular prototype framework, lineages may disappear while specific molecular, structural, or behavioral toolkits survive by being transferred, assimilated, or convergently re-evolved within other lineages.

This phenomenon is well illustrated in the early eukaryotic record. For example, gene families involved in endomembrane trafficking, cytoskeletal dynamics, and phagocytosis are found in diverse eukaryotic clades, even those otherwise divergent in form and ecology (Koonin 2006; Dacks and Field 2007). These toolkits appear to have been modular and portable, capable of spreading via symbiosis, horizontal gene transfer, or convergent modular reassembly (Martin et al. 2015; Dagan et al. 2010).

When phylogenetic reconstruction methods attempt to pin such toolkits to a single surviving lineage, they often force artificial bottlenecks, creating the illusion of a single LECA when in fact the data more naturally reflect a field of extinct lineages with surviving molecular scaffolds. These *"ghost MCPs"* —now unrepresented by intact organisms — still echo through present-day eukaryotic architecture. Recognizing these modular survivors reframes evolution not as a tree with lost branches, but as a dynamic lattice of system inheritance where lineage extinction does not imply innovation loss.

The Multiple MCP Framework

This paper proposes that multicellularity evolved multiple times through distinct modular cellular prototypes: independent lineages that explored different solutions to the challenge of complexity. This framework retains support for a singular LUCA (Woese and Fox 1977), while offering a more parsimonious explanation for the radical organizational diversity observed in early multicellular life.

The key insight is that the transition from unicellular to multicellular life is not a trivial scaling of form, but a deep architectural shift in energy management, control systems, and structural logic. (*Evolution "On Purpose",* 2023). Evolutionary principles suggest that multiple viable solutions to this challenge would have emerged in the rich experimental space of early eukaryotic evolution. (Shapiro, 1992, 1999).

Each MCP lineage developed its own biochemical toolkits, organizational principles, and ecological strategies—divergent enough that subsequent evolution within each system became canalized along different paths (Koonin 2006; Martin et al. 2015).

The single-LECA model requires that profoundly different biological systems—such as the electrical syncytia of *Hexactinellid* sponges and the neural networks of cnidarians—derive from a single ancestral logic, differing only by subsequent elaboration. This is analogous to claiming that both analog and quantum computers derive from the same digital switchboard architecture: theoretically possible, but mechanistically implausible.

We instead propose that these divergent biological architectures are the legacy of parallel, modular experiments that followed LUCA. These MCPs likely shared raw molecular components but assembled them into qualitatively distinct control structures. This is consistent with findings across modern genomes, where many core modules (e.g., cytoskeletal proteins, membrane-trafficking systems), are reused in incompatible system-level architectures (Dacks and Field 2007; Doolittle 2021).

The post-LUCA, pre-lineage period likely represents the most intense phase of biological experimentation in Earth's history. During this window, unicellular systems had reached sufficient complexity to support multicellular transitions but had not yet been constrained by lineage-specific developmental programs. In this context, the diversity of modern animal phyla may reflect not divergence from a shared architecture, but survival of a subset of ancient modular strategies.

The Post-LUCA Experimental Period

Following the emergence of the *Last Universal Common Ancestor* (LUCA) approximately 3.5 to 4 billion years ago, Earth likely experienced a prolonged period of biological experimentation, spanning hundreds of millions of years, during which multiple lineages explored divergent solutions to the challenges of complex multicellular life. This "*post-LUCA experimental period"* formed the ecological and biochemical backdrop for the emergence of distinct modular cellular prototypes, each evolving in response to unique environmental constraints and symbiotic configurations (Koonin 2006; Dagan et al. 2010).

Environmental Partitioning: Different MCP lineages evolved in distinct geochemical settings. For example, lineages that emerged in silica-rich hydrothermal systems likely evolved specialized biomineralization toolkits for silicon metabolism, as seen in the elaborate skeletal systems of radiolarians and hexactinellid sponges (Uriz and

Maldonado 2020; Müller et al. 2009). In contrast, coastal or photosynthetic environments favored organisms optimized for organic carbon processing or phototrophic symbiosis.

Symbiotic Integration: Early lineages appear to have incorporated a wide variety of symbiotic partners—bacteria, archaea, and potentially even early eukaryotes. These partnerships shaped fundamental metabolic features, including mitochondrial origin, chemosynthesis, and silica templating strategies (Margulis 1993; Martin et al. 2015). Distinct MCPs likely stabilized around different partner combinations, which in turn constrained their evolutionary trajectories.

Organizational Strategies: Biological organization during this period was not standardized. Some lineages developed syncytial architectures capable of rapid material transport and electrical conduction (as in glass sponges), while others relied on cellular partitioning and chemical signaling (as in early bilaterians and cnidarians). These foundational choices shaped everything from developmental logic to energy transfer mechanisms (Leys et al. 2007; Dunn et al. 2015).

Resource Specialization: Specialization in resource use (particularly silica manipulation, oxidative metabolism, and symbiotic energy harvesting), allowed lineages to exploit distinct ecological niches. These resource alignments were not minor adaptations but deep, system-level commitments that made cross-lineage convergence unlikely beyond shared molecular parts.

Proposed Core MCP Lineages

The MCP framework offers an evolutionary architecture that aligns with widely recognized (but poorly integrated) stem-level divergences across early animal life. Rather than interpreting groups like *Porifera, Cnidaria, Ctenophora*, and *Placozoa* as variants on a shared template, we propose that they represent distinct multicellular prototypes that survived from a broader field of post-LUCA experimentation. This reframing resolves long-standing inconsistencies in molecular phylogenies and system-level biology (Simion et al. 2017; Moroz et al. 2014).

The ***Cnidarian*** **MCP** represents a lineage that integrated choanoflagellate-style epithelial coordination with early electrical signaling systems. This innovation led to the first neural networks, enabling rapid, distributed environmental response and laying the groundwork for true sensory integration. Modern cnidarians and bilaterians descend from this architectural prototype, which established the fundamental principles of neuron-mediated control systems. Interestingly, analogous strategies appear to have evolved convergently in neuroactive plants (such as *Dionaea muscipula*) and filamentous fungi, further supporting the idea that electrical control is a modular strategy, not a lineage-specific inheritance (Dunn et al. 2015).

In contrast, the ***Silicarian*** **MCP** ("glass sponge lineage") embodies a syncytial, non-neural approach to structural and signaling complexity. This lineage mastered silica-based biomineralization and developed syncytial tissues capable of conducting electrical signals across vast networks without neurons (Leys et al. 2007).

The architectural precision and longevity of organisms like *Hyalonema*, *Oopsacas minuta*, and *Aphrocallistes vastus*, combined with genomic matches to radiolarian forms such as *Actinomma boreale* and *Spongodiscus resurgens*, suggest an ancient and continuous lineage defined by its control of silicon, not by its animal affiliation (Uriz and Maldonado 2020; Müller et al. 2009). Diatoms, testate amoebae, and structural plants such as horsetails may represent echoes or convergent analogs of this MCP's silica architecture.

The ***Poriferan*** **MCP**, encompassing demosponges and calcareous sponges, reflects an entirely different multicellular logic: one based on cellular pumps and filtration efficiency. These organisms developed coordinated archaeocyte-based systems for water processing, optimizing nutrient acquisition in nutrient-poor marine environments. Unlike their silicarian cousins, poriferans are cell-based rather than syncytial, and lack electrical conduction systems. Their collagen-based matrices and decentralized coordination make them a blueprint for passive but highly effective biological filtration, a strategy seen in both ancestral and convergently evolved filter feeders such as bivalves (Dunn et al. 2015).

The ***Ctenophore*** **MCP** pursued yet another multicellular pathway: high-precision motion and sensory integration for active predation. These organisms developed unique structures (comb rows powered by synchronized cilia) and independent sensory systems optimized for collision detection and spatial awareness. Their nervous systems are structurally and genetically distinct from those of cnidarians and bilaterians, suggesting either deep parallelism or independent neural origins (Moroz et al. 2014). While often considered a "*basal*" lineage in molecular trees, ctenophores may also represent a separately rooted system of movement and control.

Finally, the ***Placozoan*** **MCP** shows that multicellularity does not require organizational complexity. Organisms such as *Trichoplax adhaerens* demonstrate that minimal cellular differentiation, external feeding, and simple contractile movement are sufficient for persistence in stable marine environments (Eitel et al. 2013). This lineage may represent not a simplified descendant of more complex organisms, but

a retained prototype from the experimental era of multicellular emergence—optimized for low energy expenditure and structural flexibility.

Collectively, these MCPs represent not variants of one body plan, but surviving nodes from a diversified field of multicellular strategies, each structured around a distinct systems logic. Rather than being "*early animals*," they are better understood as parallel results of post-LUCA modular exploration—the surviving solutions from an era in which complexity itself was being prototyped.

Extended MCP Framework: Beyond Traditional Animals

The Multiple MCP Framework naturally extends beyond the artificial animal-plant-fungi divisions imposed by traditional terrestrial-focused taxonomy. Rather than categorizing life by gross morphology or ecological role, this framework proposes that many extant organisms are the inheritors or combinations of ancient experimental strategies (*Multicellular Prototypes* or MCPs), developed in the post-LUCA era.

Many of these strategies parallel known stem groups but reinterpret them not as simplifications or divergences from a single LECA-derived tree, but as foundational blueprints refined in distinct evolutionary contexts.

Plant-Strategy MCPs

The canonical "*plant*" lineage rooted in chloroplast endosymbiosis, can be understood as one of several terrestrial adaptations that refined photosynthetic and modular growth strategies. This lineage likely crystallized around environmental partitioning mechanisms, such as root-shoot modularity, and tight partnerships with fungi (e.g., mycorrhizal symbioses), which remain critical for nutrient acquisition in terrestrial environments.

However, many lineages traditionally placed within the plant kingdom may, under the MCP framework, represent convergent or hybrid adaptations from other MCPs:

Carnivorous plants, such as *Dionaea* (Venus flytrap) and *Drosera* (sundews), show predatory behavior and mechanical coordination systems analogous to ctenophore MCP features—suggesting an organizational template adapted for collision detection and rapid prey response.

Structural plants, like bamboo and cacti, appear to follow the *Silicarian* blueprint by emphasizing architectural stability, modular repetition, and efficient material use akin to silica-based skeletal systems seen in radiolaria and glass sponges.

Bryophytes, including mosses and liverworts, lack complex vascular or signaling systems, and mirror placozoan MCP features of minimal multicellularity, environmental simplicity, and limited cell differentiation.

Parasitic plants, such as *Cuscuta* and *Orobanche*, embody the *Hijacker* MCP strategy: leveraging host signaling systems and resources rather than investing in independent functional infrastructure.

Fungal MCP Lineages

Modern *"fungi"* represent not a monophyletic kingdom but a suite of highly specialized MCPs, optimized for different modes of environmental interaction:

Partnership Specialist MCPs (e.g., lichens) formed some of the earliest stable mutualisms with photosynthetic microbes, predating many other multicellular strategies. These lineages have integrated molecular machinery for managing dual genomes and symbiotic interface systems.

Networking MCPs include mycorrhizal fungi and soil-wide communication specialists, which form resource and signal-sharing networks. These organisms emphasize environmental integration and long-distance coordination—a form of distributed multicellularity.

Chemical Conversion MCPs, such as yeasts, evolved around rapid metabolic reprogramming, particularly fermentation and energy capture through substrate-level phosphorylation.

Decomposer MCPs specialized in extracellular digestion and organic matter recycling, a strategy optimized for ecosystems built on complex carbon substrates.

These fungal lineages show deep divergence not just in function but in fundamental organization, and may derive from distinct post-LUCA experimental strategies, unified later under functional similarity rather than true common descent.

Hijacker MCP: Parasitism as Foundational Innovation

The ***Hijacker* MCP** proposes that multicellular influence does not require full cellular infrastructure. Instead, this strategy solves the problem of survival and reproduction through exploitation of other MCP architectures via manipulation, infiltration, or parasitism.

Unlike other MCPs, *Hijackers* evolved to leverage the cellular and metabolic investments of other organisms, evolving increasingly sophisticated machinery for host targeting, genome integration, and behavioral control.

Far from being latecomers, viruses are now widely recognized as deeply ancient entities, possibly predating LUCA itself (Koonin et al. 2006). The Viral Eukaryogenesis Hypothesis (VEH), proposed by Bell and

supported by genome data from giant viruses, posits that the eukaryotic nucleus originated from a DNA virus (likely *Tectilviruses*) that established a replication factory inside an Asgard archaeon.

This hybrid system led to the compartmentalization of transcription and translation: one of the defining features of eukaryotic cells (Bell 2001; Fischer and Suttle 2011). This interpretation casts viruses not as *"minimal life forms,"* but as architects of cellular innovation, whose parasitic logic produced the nuclear envelope and spurred endosymbiotic mergers.

Further supporting this are reduction models of viral evolution, which propose that large DNA viruses (such as *Pandoraviruses*) descend from parasitic cells that lost their metabolic independence. These viruses retain unique protein folds and core genes absent in extant cellular life, suggesting they are not degenerate cells but survivors of ancient lineages (Forterre 2006; Koonin and Yutin 2020). Their genomes hint at a once-independent metabolic logic now fully subordinated to host exploitation.

As genetic parasites, viruses are also key evolutionary drivers. They facilitate horizontal gene transfer, promote genome innovation, and shape host evolution through selective pressure and co-option. Retroviruses, in particular, have contributed massively to eukaryotic genome content (much of the human genome shows viral origin) and have been implicated in crucial innovations like placental development and immune regulation (Koonin 2006; Forterre and Krupovic 2012).

The **Hijacker MCP** thus spans a continuum of complexity:

1. **Simple viruses** hijack cellular machinery through minimal genomes.
2. **Giant viruses** maintain semiautonomous transcription systems within host cells.
3. **Parasitic fungi** such as *Cordyceps*, manipulate host behavior through small-molecule and epigenetic influence.
4. **Protozoan parasites** like *Toxoplasma gondii* alter host neurochemistry to influence behavior.
5. **Parasitic wasps** and some plants (e.g., fruit-bearing species that influence animal vectors) employ manipulation to advance reproduction and dispersal.

In all these cases, the strategy is the same: minimal self, maximal host leverage. This architecture may be older and more successful, in total biomass and persistence, than most cell-autonomous lineages.

Finally, the ecological ubiquity of viruses (outnumbering cellular life by an order of magnitude in most environments) suggests that parasitism was not a rare divergence from autonomy, but a foundational solution.

Viruses have shaped evolution not just through conflict, but by introducing new information regimes and architectural innovations, such as the separation of transcription/translation or the modularization of genomes (Forterre 2010).

In the MCP framework, the *Hijacker* lineage is not an outlier, but a primary form of post-LUCA experimentation: an evolutionary logic that sidesteps the costs of multicellularity by becoming its manipulator, not its builder.

MCP Interaction and Hybridization

Modern life forms frequently represent mergers, partnerships, or co-residences of multiple MCP lineages. Rather than being exceptions, these combinations may have driven key evolutionary advances:

- **Lichens** result from long-term co-organization of a fungal MCP with a photosynthetic MCP.
- **Corals** are derived from a cnidarian MCP incorporating photosynthetic symbionts.
- **Plants with chloroplasts** reflect a merger between a root-shoot structural MCP and a photosynthetic MCP—possibly of independent bacterial descent, as evidenced by the endosymbiotic origin of chloroplasts.

These *"merger events"* are not late-stage embellishments but primary evolutionary mechanisms, as suggested by the ancient molecular signatures found in partnership integration genes. Even contemporary biological phenomena such as microbiomes, parasitic manipulation, and symbiotic dependency echo these ancient partnership logics—ongoing iterations of MCP hybridization and specialization.

Evidence and Implications

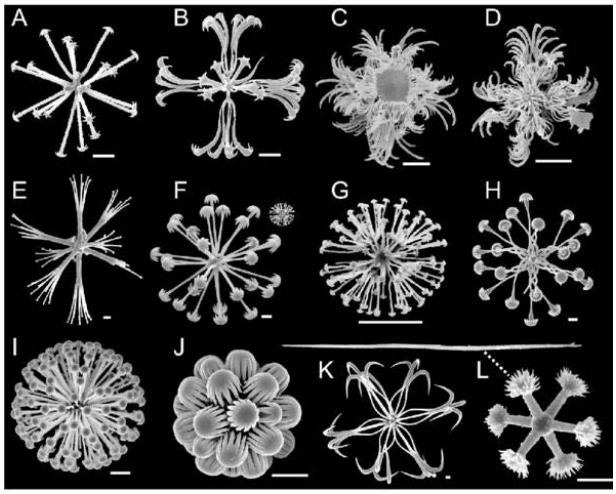
The *Silicarian* Lineage

Among the strongest empirical cases for the Multiple MCP Framework is the hypothesis of a shared evolutionary lineage uniting glass sponges (*Hexactinellida*), radiolarians, and diatoms: collectively proposed here as the *Silicarian* Lineage. These organisms exhibit extraordinarily precise silica-based biomineralization, complex scaffolding, and often nanometer-scale architectural sophistication that far exceeds what would be expected from single-celled or traditionally simple multicellular forms.

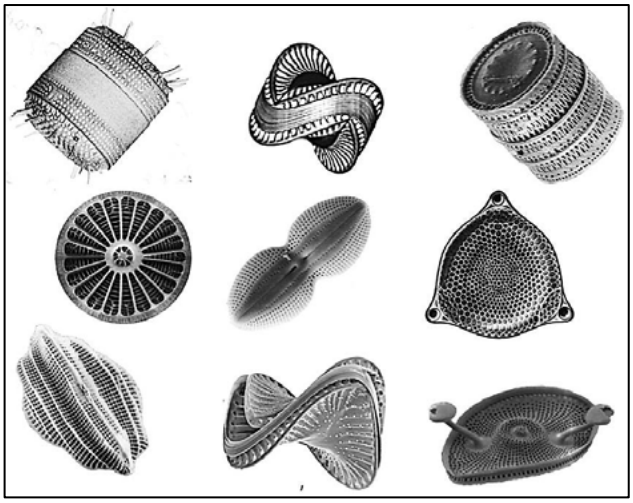
The alternative explanation (i.e., convergent evolution across these lineages) has become increasingly untenable. Radiolarians display lattice-like symmetry and intricate

shell construction; diatoms similarly repeat complex morphological patterns across vast taxonomic distances. Glass sponges exhibit syncytial organization, bioelectric conduction without neurons, and silica nanostructures with unprecedented geometrical regularity. The repeated emergence of such complexity, involving common biochemical pathways for silica metabolism, suggests not independent invention but shared ancestry—most parsimoniously, a distinct MCP lineage that mastered silicon biochemistry early in Earth's history.

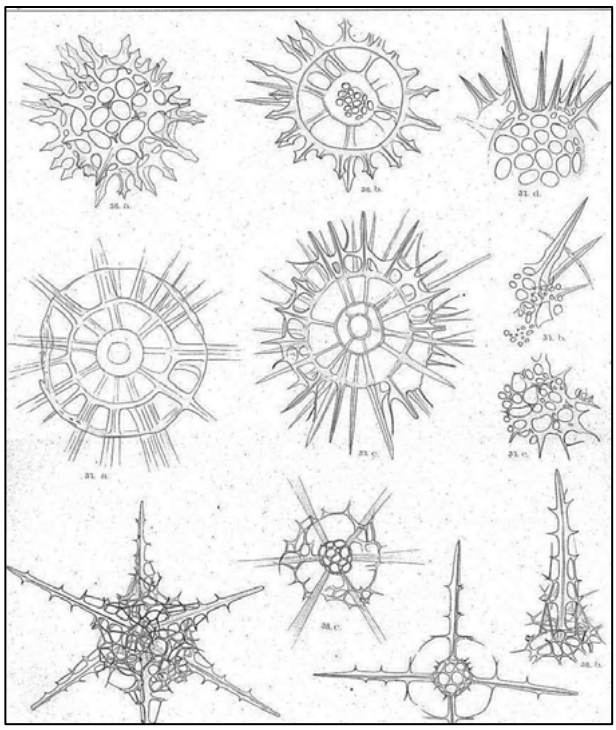
Preliminary genomic comparisons support this. Shared silica-processing pathways and regulatory modules are beginning to emerge across these groups, and future comparative genomics is likely to reveal conserved sequences indicating vertical inheritance of silica-specialization strategies.



[images of Hexactinellida hexasters, Dohrmann, 2017].



[images of Diatoms, Livage; 2018].



[diagrams of Radiolaria; Jørgensen. 1905]

Reframing the Cambrian *"Explosion"*

Traditionally interpreted as a sudden evolutionary burst, the Cambrian period (when most major animal phyla appear in the fossil record) has long puzzled evolutionary biologists. The Multiple MCP Framework offers an alternative view: the Cambrian was not an *"explosion"* of innovation but a convergence event.

It marked the ecological intersection of distinct multicellular prototypes that had evolved independently over hundreds of millions of years during the post-LUCA experimental period, finally brought together by a confluence of environmental and geological changes.

The convergence was likely triggered by multiple environmental shifts operating simultaneously during the late Ediacaran and early Cambrian periods. Rising atmospheric oxygen levels reached thresholds that enabled larger, more metabolically active organisms to survive in previously uninhabitable regions, while changing ocean chemistry (particularly increased calcium and phosphate availability) provided the raw materials for widespread biomineralization.

Tectonic reorganization during this period fundamentally altered ocean circulation patterns, breaking down long-standing biogeographic barriers that had kept different MCP lineages isolated in separate ocean basins or depth zones for hundreds of millions of years. The end of *Snowball Earth* glaciation events created massive ecological

disruptions that forced organisms from previously stable, isolated environments into contact with one another.

Ocean currents shifted dramatically as continental configurations changed, mixing water masses that had remained separate throughout the Proterozoic and bringing deep-sea MCP lineages into shallow water environments where they encountered coastal and photosynthetic MCPs for the first time.

These environmental upheavals eliminated the stable ecological partitions that had allowed different MCP strategies to evolve in isolation—the Silicarian lineage in deep, silica-rich environments, the Cnidarian MCP in coastal zones, and various other lineages in geochemically distinct niches.

In this model, the Cambrian fossil record reveals a mixing of pre-established architectures rather than their spontaneous emergence. Complex body plans, neural networks, and metabolic specializations did not suddenly appear; they were instead the result of long-separated MCPs coming into ecological proximity and beginning to interact, compete, and hybridize.

This convergence led to intense niche competition, rapid co-evolutionary arms races, and the disappearance of incompatible forms. This explains both the apparent innovation and rapid extinction that characterize the period. The *"explosion"* represents not the invention of complexity, but its sudden juxtaposition and interaction after eons of independent development.

This framework makes specific predictions about pre-Cambrian fossil patterns: we should find evidence of MCP lineages in geographically isolated deposits throughout the Proterozoic, with each region showing only a subset of the total MCP diversity that later appears together in Cambrian assemblages. Pre-Cambrian fossils should demonstrate sophisticated individual MCP architectures (such as *Silicarian* biomineralization or *Cnidarian* neural coordination) but lack the complex inter-MCP ecological relationships that characterize Cambrian communities. A

s we approach the Cambrian boundary, fossil assemblages should show increasing MCP diversity within single locations, gradual breakdown of geographic partitioning, and evidence of the environmental barriers that previously maintained MCP separation begin to disappear.

Cryptic Preservation and the Missing Record

A critical limitation in evaluating the Multiple MCP Framework lies in our bias toward calcium carbonate-based fossil preservation. Traditional paleontology focuses on shells, bones, and other structures that fossilize through familiar pathways, but many MCP lineages would have left entirely different preservation signatures, or none at all.

The *Silicarian* lineage, specialized for silica biomineralization, would fossilize as crystalline formations, agates, cherts, and silica deposits that are routinely interpreted as purely geological rather than biological in origin. (Ehrlich, 2024; Post, 1999; Rasmussen, 2024).

Complex radiolarian-like lattices and glass sponge architectures could be preserved as intricate silica formations in the geological record and misclassified as mineral specimens. This is particularly plausible for the Precambrian and Ediacaran periods, where high dissolved silica levels and limited morphological recognition criteria contributed to an underrepresentation of early biomineralizing MCPs in the fossil record. (Ehrlich, 2023; Mader, 2024; Müller, 2024).

Similarly, MCPs specialized in other biomineralization pathways (such as hydromanganese nodule formation, iron oxide precipitation, or complex sulfate minerals)would create preservation signatures that fall outside traditional paleontological analysis. (Afanasieva, 2014; Ghosh, 2021; Zhaoliang, 2023).

Many early MCPs were likely entirely soft-bodied, particularly those following the *Placozoan* strategy of minimal multicellularity or the Hijacker strategy of manipulating other organisms' structures rather than building their own. The Fungal networking MCPs, operating primarily through underground mycorrhizal networks and extracellular enzyme systems, would likewise be invisible to conventional fossil preservation. These lineages would leave no direct fossil record, existing only as ecological influences on the organisms they parasitized or manipulated.

This preservation bias fundamentally skews our interpretation of the Cambrian *"explosion."* What appears as sudden innovation may actually represent the convergence moment when calcium carbonate-biomineralizing MCP lineages (which preserve well) first encountered the full diversity of other MCPs (which preserve poorly or not at all).

The apparent sudden appearance of complex interactions and ecosystems reflects not evolutionary innovation but the first time that both fossilizable and non-fossilizable lineages came together in the same environments.

The framework predicts that re-examination of Proterozoic mineral formations—particularly complex agates, crystalline structures, and biomineralized deposits currently attributed to purely chemical processes—may reveal biological architectures consistent with ancient MCP

activity.

Advanced imaging techniques and geochemical analysis could potentially identify biological signatures in mineral formations that predate the Cambrian by hundreds of millions of years, revealing the true antiquity and diversity of multicellular experimentation that traditional fossil analysis has missed.

Symbiosis as Fundamental Strategy

Another implication of the Multiple MCP Framework is a redefinition of symbiosis—not as a secondary evolutionary convenience but as a primary mode of complexification. In the post-LUCA period, distinct MCPs likely engaged in metabolic and structural partnerships that persisted across evolutionary timescales. These symbiotic strategies became central to their survival, not optional adaptations.

Lichens, for instance, combine fungal and photosynthetic MCP elements into a stable dual-organism. Coral reef systems depend on the intimate partnership between cnidarian and algal MCPs. The acquisition of chloroplasts by early plant cells represents another deep merger of two formerly distinct lineages. Even the vertebrate gut microbiome can be seen as a vestige of ancient, ongoing symbiotic experiments that began in the early eukaryotic world.

This interpretation aligns closely with Lynn Margulis's symbiogenetic theory of eukaryogenesis (Margulis 1970) and expands it: symbiosis is not the exception but the mechanism through which complexity arises.

Testable Predictions

The Multiple MCP Framework makes several testable predictions, providing immediate avenues for empirical verification. If MCPs represent deeply divergent multicellular strategies, then each lineage should contain unique molecular markers—genetic fingerprints of their developmental pathways, signaling architectures, and environmental specializations.

The *Silicarian* lineage should display shared silica metabolism genes among radiolaria, diatoms, and glass sponges, particularly silicateins, silicon transporters, and silica templating proteins, with identity levels indicating ancient, shared ancestry rather than convergent evolution. These organisms should also share syncytial organization genes and gap junction proteins absent in cellular sponges, revealing their fundamental architectural differences.

The *Cnidarian* MCP should possess neural development genes that trace back to shared ancestry with choanoflagellates, including neurogenesis factors, voltage-gated ion channels, and neurotransmitter synthesis pathways showing conservation across cnidarians and bilaterians. The *Hijacker* MCP should reveal homologous host manipulation modules across viruses, parasitic fungi such as Cordyceps, and behavior-altering protozoa like Toxoplasma gondii, with conserved effector delivery systems and neural hijacking mechanisms showing substantial identity despite their apparent taxonomic diversity.

Carnivorous plants should exhibit convergent or retained features resembling those of the *Ctenophore* MCP, particularly in rapid-motion genes, mechanosensitive channels for collision detection, and electrical conduction pathways that enable their sophisticated prey responses. Glass sponges should cluster with radiolaria and diatoms in genes related to silica processing rather than with other sponges, while lichen-forming fungi should diverge molecularly from traditional fungal clades, retaining ancient integration modules from early symbiotic MCPs.

To facilitate immediate testing of these predictions, the author has compiled taxonomically organized reference sequence databases that enable researchers to conduct MCP-focused BLAST analyses. These datasets allow direct comparison of unknown sequences against proposed MCP members rather than broad groups, providing immediate opportunities to identify unexpected molecular relationships that support or refute the framework.

Many of these predictions can be tested immediately using existing sequence data, with targeted sequencing and comparative genomics providing validation within 1-2 years. The framework may be falsified if proposed MCP members fail to show expected molecular clustering or if they align more closely with current taxonomic groupings than with functional strategies.

Broader Implications

Adopting the MCP model means moving away from morphology-based taxonomy (a framework shaped largely by human perception and terrestrial familiarity) and toward one grounded in evolutionary strategy.

Rather than defining life forms by superficial appearance, we organize them by architectural logic: mobile individualist (*Cnidarian* MCP), sessile modular (*Silicarian* MCP), ecological networker (Fungal MCP), viral (*Hijacker* MCP), or minimalist (*Placozoan* MCP).

This reorganization not only clarifies deep evolutionary relationships but also unlocks applied potential:

- The silica biomineralization strategies of the *Silicarian* lineage could inspire new materials in nanotechnology and construction.

- *Hijacker* mechanisms may offer insights into targeted drug delivery or gene editing platforms.
- Ancient symbiotic strategies could enhance microbial-based agriculture or environmental remediation.

Finally, recognizing life on Earth as a collection of independently derived solutions to multicellularity rather than variants of a single ancestor dramatically broadens our search criteria for extraterrestrial life. If evolution can explore multiple architectures for complexity under Earth's constraints, we should expect the diversity of life beyond Earth to be even greater.

Future Directions

The Multiple MCP Framework lays the groundwork for a wide array of novel research trajectories. As a testable, integrative model, it invites empirical evaluation across disciplines ranging from evolutionary genomics to synthetic biology. There are at least five avenues of investigation.

Genomic Validation: Comparative genomic analyses can test the framework's core claim: that each MCP lineage retains distinct molecular signatures reflecting its evolutionary architecture. By isolating lineage-specific toolkits (e.g., silica metabolism, neural patterning, symbiotic integration), researchers can evaluate whether these features cluster by function or reflect true shared ancestry.

Environmental Correlation: If MCPs emerged during a post-LUCA diversification phase, then their foundational innovations may retain geochemical imprints. Analyses of isotope signatures, trace element usage, and inferred habitat types can help reconstruct the ecological contexts in which each MCP evolved.

Synthetic Biology: The framework offers a blueprint for engineering modular lifeforms that recapitulate ancient organizational principles. For example, synthetic syncytial systems could simulate *Silicarian* architectures, while distributed signaling systems might replicate early cnidarian coordination.

Paleobiological Reinterpretation: Fossil records, especially from the Cambrian and Ediacaran periods, should be reassessed not through a strict phylogenetic lens but as evidence of MCP convergence, integration, and extinction. Morphological oddities may be better understood as momentary hybridization events or isolated MCP branches.

Partnership Ecology: Modern ecosystems host complex inter-MCP collaborations from plant-mycorrhizal interactions to microbiome-host symbioses. Mapping these relationships may reveal echoes of ancient evolutionary partnerships and offer clues about which strategies were most resilient.

Together, these approaches provide a roadmap for reconstructing life's deep history, not as a linear tree, but as a web of modular strategies developed in parallel and frequently merged.

Conclusion

The *Silicarian* lineage exemplifies a fundamentally different evolutionary strategy from the cnidarian-rooted pathway that ultimately led to humans. Mainstream cnidarian pathways prioritized dynamic responsiveness, neural computation, and environmental manipulation. (Moroz, 2014).

However, the *Silicarians* mastered a radically different toolkit: silica nanofabrication, architectural precision, and life at stable low-energy multicellularity. These two strategies represent divergent answers to the same ancient questions—how to organize matter, harness energy, and persist across time.

Crucially, neither approach is superior. Each arose from specific environmental contexts, biochemical constraints, and evolutionary experiments. The *Silicarians*, far from being evolutionary curiosities, are survivors of a highly successful lineage whose principles may hold the key to future advances in material science, biotechnology, and environmental design.

By embracing the idea that multicellularity was not a single, linear innovation but a suite of independently derived solutions, we replace the narrowing lens of phylogenetic orthodoxy with a richer, more explanatory model. This perspective not only clarifies puzzling observations in modern biology but also expands our imagination of what life could be—on Earth and beyond.

Recognizing multiple MCPs does not abandon the unity of life's origins; rather, it refines our understanding of what that unity entails. LUCA provided the toolkit. The MCPs built the architectures.

The diversity of life we see today is the result of billions of years of modular innovation, recombination, and specialization; a tapestry far too complex to be understood through the lens of a single ancestor alone.

Data Availability

All sequences referenced are publicly available through NIH/NCBI and ENA databases. To facilitate immediate testing of MCP predictions, we have compiled comprehensive reference sequence databases organized by proposed MCP relationships rather than traditional taxonomy. These datasets are freely available through the Open Science Framework (OSF) at DOI 10.17605/OSF.IO/69WHF.

The MCP reference collection includes curated sequence datasets for key representatives of each proposed lineage, including: *Hexactinellida* (glass sponges, >50 MB), *Stramenopiles* including diatoms (>200 MB), comprehensive *Cnidaria* collections (> 800 MB total across all cnidarian groups), *Ctenophores* (>20 MB), *Placozoans* (>100 MB), multiple sponge classes (*Calcarea, Demospongiae, Homoscleromorpha*), viral sequences, and additional comparative groups including *Alveolata, Foraminifera, Bryozoa, Tunicata*, and others. Each dataset includes both FASTA sequence files and unique header identification files for streamlined analysis.

These reference databases enable immediate BLAST analysis of unknown sequences against MCP-organized datasets rather than traditional taxonomic categories, providing researchers with practical tools to test the framework's core predictions. Custom database FASTA files and complete sequence listings with methodological documentation are provided as supplementary materials within the OSF repository.

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