The Pseudocolus Stinkhorn and the Survival of Ediacaran Architecture:

A Genomic & Structural Reassessment of a Misclassified Proto-Animal

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Abstract:

This study presents genomic and morphological evidence challenging the classification of *Pseudocolus* species as terrestrial fungi and instead supports their identification as living representatives of ancient marine metazoan lineages. Using an extended BLAST alignment pipeline (REBLAST), this study identified high-confidence genomic matches between *Pseudocolus* and basal marine taxa, including sponges (Porifera), cnidarians, and unicellular holozoans.

Alignments consistently exceeded 1,750 base pairs with >85% identity and E-values of zero, indicating deep evolutionary conservation rather than convergent similarity. The strongest matches occurred with demosponges (*Axinella, Geodia*) and calcareous sponges (Clathrinida), exhibiting triradial spicule arrangements, as well as with predatory flagellates (*Tunicaraptor*) showing 87% identity over 2,116 base pairs.

Morphological analyses further demonstrate that *Pseudocolus* displays features inconsistent with fungal biology: triradial symmetry, manganese-rich biomineralization, hydrogel-supported modular architecture, and a volatile chemical profile resembling marine stress-response signaling rather than terrestrial spore dispersal. These traits align with Ediacaran fossil forms and suggest a scaffold-based developmental logic predating bilaterian patterning systems.

Based on this converging genomic and structural evidence, we propose reclassifying *Pseudocolus* as *Tribrachia fusiformis* (Demospongiae, incertae sedis) and introduce the provisional clade *Triquadrozoa*, defined by triradial morphogenesis and mineral-organic scaffold formation. This lineage represents a living archive of pre-bilaterian body plan logic, offering novel insights into early metazoan evolution and the persistence of ancestral developmental architectures.

Keywords:

Pseudocolus; Triquadrozoa; triradial symmetry; modular body plans; long-read BLAST alignment; REBLAST; scaffold morphogenesis; Ediacaran biota; Porifera; Cnidaria; Amoebozoa; choanoflagellates; MCP framework; prebilaterian development; mineral scaffolds; biomineralization; manganese gels; morphodynamic logic; deep homology; cryptic genomic signal; discovery-oriented genomics; non-canonical body plans; evolutionary bioinformatics.

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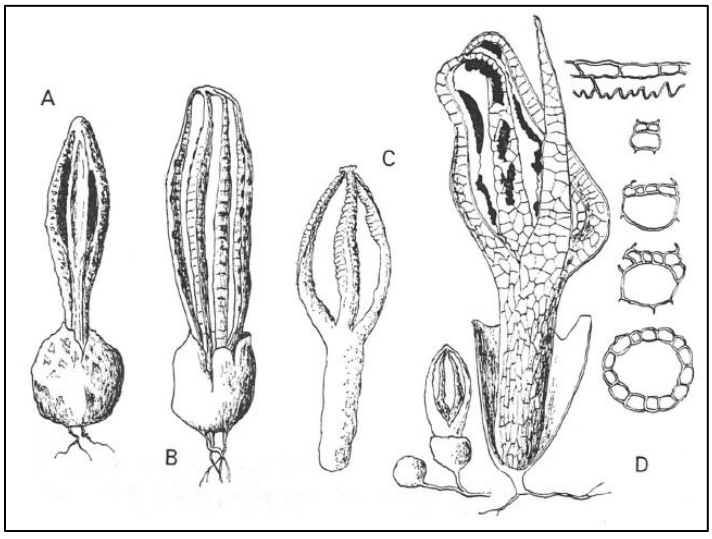
Introduction

The organism traditionally identified as *Pseudocolus fusiformis*, a member of the Phallaceae (Stinkhorns), has long been classified as a terrestrial saprobic fungus, notable for its unusual morphology and pungent volatile emissions. However, long-read genomic analyses and comparative structural studies reveal striking homologies between *Pseudocolus* and basal marine metazoans and pre-metazoan lineages, including sponges (Porifera), cnidarians, and unicellular eukaryotes. These findings challenge the current taxonomic placement of *Pseudocolus* and raise the possibility that it represents a surviving lineage of Ediacaran-grade multicellular life.

This study integrates extended-sequence genomic alignments, biomineralization patterns, developmental observations, and morphological comparisons to reassess *Pseudocolus* not as a fungus, but as a marine modular organism with conserved prebilaterian body plan features. Using the REBLAST alignment framework, optimized for detecting structurally conserved regions across distant taxa, we recovered high-confidence alignments with triactine sponge scaffolds, cnidarian body modules, and unicellular protist morphotypes. These alignments consistently exceeded 1,800 base pairs with ≥85% identity and E-values of zero.

The data suggest that *Pseudocolus* embodies a lineage defined by a conserved morphogenetic architecture rooted in recursive scaffold construction, mineral-organic interfaces, and environmental responsiveness. This paper proposes that this organism—here reassessed under the provisional designation *Tribrachia fusiformis* (Demospongiae, incertae sedis)—provides a living model for studying scaffold-based multicellularity, modular inheritance, and the persistence of early developmental logics across geological time.



Pseudocolus fusiformis (Dring, 1980).

Taxonomic Context: The Case of *Pseudocolus*.

Pseudocolus is a genus within the family *Phallaceae*, distinguished by its compact, branched fruiting body that emerges from a volval "egg" and rapidly expands into a structure typically composed of three or four upright arms. These arms are fused at the base and diverge upward, sometimes forming a loose arch or open framework, with the gleba deposited along the inner surfaces. (Dring 1980).

The bright coloration (often orange, red, or pink) combined with the mucilaginous, foul-smelling gleba, contributes to its classification among the Stinkhorn fungi. The odor is widely interpreted as an adaptation for attracting insects, particularly flies, which are presumed to aid in spore dispersal. (Dring 1980).

Ecologically, *Pseudocolus* species are described as saprotrophic and are commonly found in nutrient-rich substrates such as decaying wood, compost, and garden mulch. Fruiting bodies typically appear after rainfall and in humid conditions and are ephemeral (collapsing within a day or two after emergence).

The genus is regularly observed in human-altered landscapes including urban parks, landscaped beds, and compost piles, suggesting a preference for high-organic, disturbed environments.

Species of *Pseudocolus* have been documented in lowland coastal forests, garden soils, volcanically enriched terrains, and semi-urban mulched environments, frequently in regions where moisture fluctuations, organic matter accumulation, and intermittent disturbance occur. It is particularly common in sheltered forest clearings, woodchip piles, and horticultural beds where the substrate is loose and decay is actively underway. Reports have also placed it near tidal forest margins, floodplain habitats, and disturbed roadside verges, especially in subtropical and temperate climates.

Methodology

Dataset Construction and Sequence Filtering

A curated dataset of DNA gene sequences was assembled to evaluate the evolutionary landscape of non-fungal eukaryotes. Sequences were derived from high-throughput similarity search outputs, with alignment metrics including alignment length (bp), bit score, percent identity, and E-value recorded for each hit.

Given gaps in current sequence databases (particularly for early-diverging eukaryotes) taxa not observed were

interpreted as unsampled or unresolvable, not absent. Orphan sequences and long-branch outliers were retained in ancillary datasets for future analysis under relaxed parameters or alternate markers.

Molecular Engineering Framework

To formalize exploratory alignments into evolutionary hypotheses, this paper developed the Molecular Engineering Framework for Evolutionary Fact Inference (MEEF). This model allows alignment-derived relationships to be expressed as logic-based ancestry statements, especially in cases involving underclassified or morphologically ambiguous taxa.

Key Operational Definitions

- **Molecular Fact**: A consistently reproducible high-confidence sequence alignment (≥1500 bp, ≥70% identity, ≥1800 bit score, E-value = 0), not attributable to noise or convergence.
- **Vertical Ancestry Signal (VAS)**: A Molecular Fact linking two distantly related taxa, implying inheritance from a shared common ancestor.
- **Ancestral Module**: A gene or domain found across divergent lineages, likely derived from an early multicellular toolkit (e.g., MCPs).

MEEF Logic Engine: Transitive Inference

Once Molecular Facts are established, a transitive logic model is applied:

1. If rel(A, B) and rel(B, C), infer rel(A, C)
2. If A and C are placed in separate taxonomic groups but rel(A, C) is supported, propose a Taxonomic Reconciliation Hypothesis (TRH):
    - A and C may belong to the same ancestral clade, misclassified by morphology
    - Or, A and C share a deep ancestral module lost in other lineages.

This framework is particularly useful for interpreting relationships between scaffold-driven taxa, where tree-based models fail due to irregular divergence or missing intermediates.

REBLAST Protocol and Sequence Coverage

At time of publication, NIH and ENA listed 18 *Pseudocolus* sequences, all ≤908 bp except one:

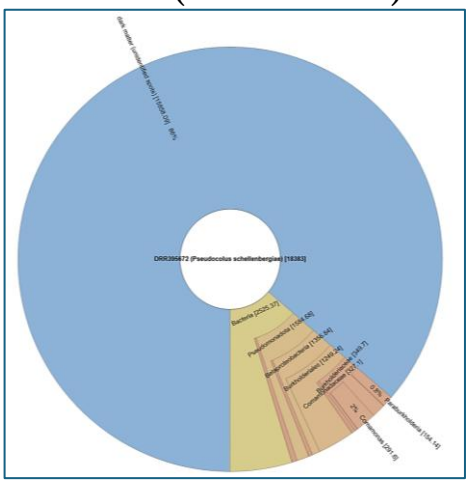
- **AF026623.1** (1773 bp, Harvard, 1997), used as the primary REBLAST query.

This sequence was also analyzed using REBLAST against core_nt, nt_euk, nt_others, nt_virus, and nt_prok. Notably:

- The virus database yielded 77 hits, including a strong alignment to White Spot Syndrome Virus (bit score = 895, E = 0).
- nt_prok returned matches to archaea (*Hyperthermus*) and bacteria (e.g., *Pseudomonadota*, *Bacillota*, *Cyanobacteriota*).

An additional 2024 mycorrhizal dataset (SAMD00515458) listed *Pseudocolus schellenbergiae* with 86.26% unassigned "dark matter" sequences and 13.74% bacterial sequences.

Krona (SAMD00515458):



Alignment Limitations and Justification of Approach

While BLASTn excels at detecting local sequence similarity, it lacks an evolutionary model and is not suited for placing scaffold divergent or taxonomically anomalous organisms. Tree-based methods (e.g., NCBI BLAST Tree Viewer) failed to resolve topologies across the dataset, largely due to:

1. **Sequence length constraints**: ~1800 bp is informative but insufficient for deep branching models.
2. **Cross-kingdom match profiles**: Hits span protists, basal animals, and holozoans—beyond the scope of neighbor-joining tools.
3. **Missing intermediates**: Many relevant lineages are extinct or poorly sequenced, undermining stable node resolution.

These limitations justify our scaffold-logic approach. High-confidence alignments (E = 0, bit score >1800, >1750 bp) are interpreted as structural affinity events, not taxonomic

placements. Each such match represents a distinct evolutionary clue and should be published and interrogated even in the absence of broader phylogenetic synthesis.

Genomic Results: Homology Clusters and Scaffold Logic

Conventional BLAST-based taxonomic assignment methods aim to identify the single closest known match to a novel sequence. While effective for organisms within well-characterized clades, this approach breaks down when applied to taxa with deep divergence from established phyla. *Pseudocolus* exemplifies this limitation: its high fraction of unannotated genomic content preclude meaningful placement within a single lineage.

To address this, this paper adopts a multi-vector alignment strategy. Rather than seeking a singular taxonomic assignment, this paper evaluates a constellation of high-confidence alignments—each representing conserved architectural features across distantly related organisms. The emphasis shifts from taxonomic proximity to structural logic: a morphogenetic thread uniting organisms with modular, radial, or scaffold-driven emergence, including sponges, cnidarians, and unicellular eukaryotes.

Top Matches

Species	Len.	Bit	Id.	E-Val.
Axinella sp. (*Demospongiae, Porifera*)	1812	1825	85.4	0
	1811	1831	85.5	0
	1808	1834	85.5	0
	1802	1964	85.0	0
	1796	1973	85.1	0
Colpophyllia sp. & Favia sp. (*Hexacorallia*, *Cnidria*)	1858	1710	80.6	0
	1824	1810	82.6	0
Chrysaora sp., Atolla sp., & Mastigias sp., Nausithoe sp. *(Scyphozoa, Cnidaria)*	1794	1982	85.2	0
	1808	1882	83.8	0
	1793	1970	84.9	0
	1780	1984	85.2	0
Clathrinida (*Calcarea*, *Porifera*)	1787	1997	85.5	0
	1787	2024	85.8	0
	1787	2002	85.5	0
	1787	2002	85.5	0
	1788	2000	85.6	0

This paper focuses on alignments that combine high identity, long length, and structural coherence with related taxa. The table below summarizes representative hits exceeding 1750 bp, with bit scores above 1800 and E-values of 0—criteria consistent with deep homology rather than stochastic or repetitive domain similarity.

Where multiple hits occurred within a lineage, representative midpoints were selected to reflect structural continuity across related taxa. This prevents overemphasis on numerical extremes and highlights evolutionary coherence at the modular level.

Alignment metrics prioritized long matches (≥1750 bp), high identity (≥85%), bit scores exceeding 1900, and E-values of 0. Sequence match hits meeting these criteria were grouped into five major scaffold-affinity clusters.

Scaffold Homology Across Basal Marine Lineages

Porifera: Calcarea (Clathrinida, Leucosolenida)

Multiple matches were recovered to *Clathrinida*, a calcified sponge order distinguished by triactine spicules with 120° symmetry. These matches displayed long alignments (up to 1791 bp) with bit scores >2000 and identity percentages reaching 85.8%.

The consistent triactine symmetry of these organisms (a direct mineral embodiment of tripartite structural logic) supports the view that *Pseudocolus* shares regulatory or structural domains responsible for spatial orientation and mineral scaffold deployment. Similar alignments were also recorded to Leucosolenida, an order with free-floating spicule matrices and early skeletal plasticity.

These results indicate that *Pseudocolus* may retain ancestral codebases linked to sponge spicule axis generation, particularly those aligned to triplet body geometry and spatially patterned mineralization.

Porifera: Demospongiae (*Axinella*, *Geodia*)

The *Axinella* genus of demosponges produced the longest continuous alignments in this category (up to 1973 bp) with identity percentages around 85.5%. Notably, one of the highest-confidence matches originated from an *Axinella* species exhibiting a 3-point expansion morphology, wherein its major body lobes deploy symmetrically from a central axis. This match sits at the confluence of both sequence and structural logic: a tripartite morphogenetic phenotype backed by direct genomic alignment.

The presence of these features in *Axinellid* sponges (known for their canal systems, scaffold plasticity, and three-dimensional mineral architecture) further supports a deep, vertically inherited morphogenetic logic between *Pseudocolus* and this lineage.

Similarly, demosponges like *Geodia barretti* use sclerocyte-mediated spiculogenesis with cytoplasmic sheaths and ECM deposition—systems that may analogously guide lobe mineralization in *Pseudocolus*. Geodia also had strong matches with *Pseudocolus*.

Cnidaria: Anthozoa (*Favia*, *Colpophyllia*, *Xenia*)

Multiple long alignments (1858–1960 bp, ~85.2% identity) were found with anthozoans, particularly lobed stony corals and sea anemones.

While Anthozoans typically exhibit radial symmetry, many species display lobed arrangements that organize around triplet or quadruple structural centers, particularly in tentacle emergence and internal mesenterial patterns.

In stony corals with fixed skeletons, the presence of regular four- or six-lobed mineralization planes may reflect recursive iterations of a more ancient threefold scaffold logic — a pattern consistent with the ability of *Pseudocolus* to variably express 3- or 4-lobed forms without disrupting its base body plan.

Cnidaria: Scyphozoa (*Chrysaora*, *Cephea*, *Atolla*, *Nausithoe*)

Within the Scyphozoan medusae, high-confidence alignments were found with Rhizostomeae and Coronatae, both large-bodied jellyfish lineages with flow-mediated tentacle placement and lobed bell structures. Sequence matches approached 1984 bp with 85.2% identity. These organisms often use radial lobes to orchestrate water flow for feeding and propulsion — paralleling the active lobe-pumping system used by *Pseudocolus* to regulate fluid motion across its arm surfaces.

The functional use of lobes to manipulate water gradients reinforces the shared scaffold logic with cavity-based fluid dynamics, and diffusion-optimized surface area.

Protist Scaffold Systems: Modular and Lobed Unicellular Eukaryotes

The BLAST alignment results from *Pseudocolus* revealed a notable cluster of high-confidence matches to unicellular eukaryotes, especially among scaffold-generating amoeboid and flagellated protists within Holozoa, Filasterea, and Choanoflagellata. These organisms, while taxonomically diverse, share a core structural behavior: the deployment of modular extensions from a central or stalk-like body via fluid dynamics, ciliary flow, or membrane-based scaffolding.

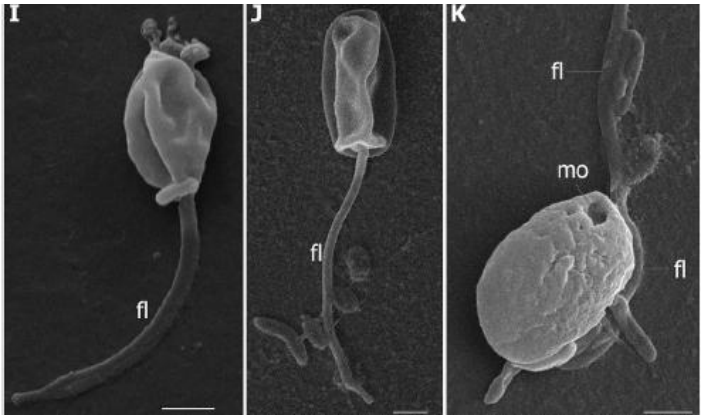
Across this group, alignment lengths consistently exceeded 1775 base pairs, with bit scores between 1930 and 2116, and percent identities ranging from 84% to 87.2%. E-values were universally 0.0, confirming that these are not low-complexity artifacts but statistically meaningful genomic affinities.

The strongest hits included:

Species	Length	Bit Score	Id. No.	E Value
Pigoraptor chileana	1795	1910	86.3	0
Diaphanoeca grandis	1789	2002	85.5	0
	1789	1988	85.2	0
Tunicaraptor unikontum	1785	2006	87.2	0
	1782	2116	86.9	0
Corallochytrium limacisporum	1784	1968	85.4	0
Pigoraptor vietnamica	1783	1957	85.1	0
Savillea micropora	1778	1961	85.1	0
Acanthocorbis unguiculata	1778	1958	85.1	0

One of the most striking alignments came from *Tunicaraptor,* a predatorial flagellate that yielded a 2116 bp alignment at 87.2% identity with an E-value of 0. Additional matches from the species or related organisms included:

- *Tunicaraptor unikontum* (Holozoa): Two alignments at 1785 bp (87.2%) and 1782 bp (86.9%) with bit scores >2000
- *Pigoraptor vietnamica* (Filasterea): 1783 bp, 85.1% identity
- *Corallochytrium limacisporum* (Teretosporea): 1784 bp, 85.4% identity



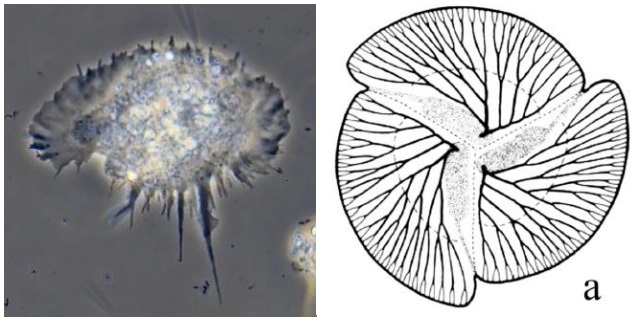
Tunicaraptor unikontum, "cell with posterior flagellum" & "with small break of the theca at the anterior." (Tikhonenkov, 2020).

These lesser-known lineages are basal to animals and fungi. Many of them exhibit fluidic predatory behaviors, adhesive stalk formation, or cytoskeletal-driven emergence. The repeated appearance of *Tunicaraptor*, especially with 87.2% identity and 2116 bp length, marks it as a structurally and genetically significant match. It supports the conclusion that *Pseudocolus* may conserve ancient unicellular scaffold domains, now deployed in a multicellular configuration.

The choanoflagellates matches are also highly relevant due to their position as the closest known unicellular relatives of animals. Structurally, they often express three-part collar complexes, silica basket scaffolds, and symmetrical ciliary feeding flows. The depth and breadth of matches to these organisms strongly implicate *Pseudocolus* as a modular scaffold body whose emergence logic is continuous with pre-metazoan architectures.

Other strong matches included:

- *Flabellula* (1882 bp, 76.9%)
- *Pompholyxophrys punicea* (1778 bp, 85.0%)



Flabellula sp. "specimen with some long trailing filaments." Criloo, Netherlands. Microworld (2019); *Albumares brunsae* (triradial fossil with glide locomotion, and triparts resembling *Flabellula*). (Ivantsov, A., 2021).

Taken together, this group of alignments forms a cohesive signal: *Pseudocolus* is genetically affiliated with a deep lineage of lobed and scaffold-based unicellular eukaryotes, particularly those that operate through tripartite or radial emergence from central body plans. These relationships suggest that *Pseudocolus* retains functional elements of a shared scaffold genome that existed before tissue-based developmental programs, and that structured form through fluid, mineral, and membrane constraints.

The convergence of choanoflagellate collar logic, lobose pseudopodial mechanics, and flagellated stalked emergence in this alignment cluster validates a key hypothesis of the *Triquadrozoa* framework: that triradial morphogenesis arises from recursive inheritance of eukaryotic scaffold systems, now integrated into a persistent multicellular lineage.

The recurrence of tripartite or radially symmetric behaviors in choanoflagellates, filastereans, and lobose amoebae suggests that the core functional logic of MCP — namely, lobe emergence from a centralized scaffold, spatial symmetry maintenance, and mineral or polysaccharide templating was already operational at the unicellular level.

The fact that *Pseudocolus* aligns with over a dozen such protists in both sequence and structure supports the view that MMCP represents a conserved material and genomic scaffold that has persisted across the transition to multicellularity. *Pseudocolus* thus exemplifies a lineage where the MCP architecture has been retained and elaborated, rather than overwritten, offering a rare living window into the transitional logic that structured early metazoan emergence.

Morphological & Structural Correlates

Reinterpreting Pseudocolus as a Crown, Marine, Modular Organism

Anatomical and Ecological Anomalies

The genus *Pseudocolus*, long classified among the Phallaceae (Stinkhorn fungi), displays a suite of morphological, biochemical, and developmental traits that fundamentally conflict with its placement in terrestrial fungal lineages. Comparative evidence instead supports its reinterpretation as a modular marine metazoan, potentially representing a cryptic survivor of a basal, scaffold-forming clade now occupying terrestrial margins.

The fruiting body of *Pseudocolus* emerges from a volva-like cyst, analogous to sponge gemmules or cnidarian planulae. Its vertical arms are hollow, porous, and chambered—architecturally similar to the aquiferous systems of hexactinellid sponges or the gastrovascular canals of colonial cnidarians. Rhizomorphs display mineralized sheaths with angular crystals morphologically consistent with spicule-forming tissues. These architectural features suggest that *Pseudocolus* retains ancestral marine morphogenetic logic, now deployed under terrestrial constraints.

Volatile Organic Compounds (VOCs): Necrobiotic Signaling

Studies of *Pseudocolus*' volatile emissions (Kakumyan et al., 2020) reveal a VOC profile highly uncharacteristic of terrestrial fungi. Mature stages emit sulfurous compounds such as dimethyl trisulfide (DMTS) and 4-methylphenol, while lacking the C8 alcohols and ketones typical of fungal VOC cascades. These emissions peak post-emergence, suggesting an internally regulated biochemical trigger.

Rather than functioning as insect attractants for spore dispersal (as assumed in fungal models) these compounds resemble stress-induced death signals used by marine sponges, cnidarians, and tunicates to initiate microbial recycling, deter predation, and revert to unicellular survival states. Their role may be ecological, not reproductive, constituting part of a regulated necrobiotic module suited for aqueous environments.

The high presence of reduced sulfur compounds suggests metabolic pathways consistent with chemolithotrophic or chemoautotrophic metabolisms, wherein manganese and iron serve as electron donors or cofactors in anaerobic respiration. This signature is reinforced by the near-absence of typical fungal volatiles such as alcohols, aldehydes, and esters (Zhang et al., 2010).

These compounds are integral to anaerobic microbial consortia thriving in serpentinization systems, further reinforcing ecological parallels between these terrestrial emergents and deep crustal life forms.

VOC production in *Pseudocolus* is developmentally regulated, absent in the egg stage and initiated only upon morphogenic expansion. This aligns with marine regenerative systems, not fungal sporulation. The presumed "spores" may instead be unicellular modules akin to sponge archaeocytes, cnidarian larvae, or placozoan propagules—misinterpreted through terrestrial and mycological lenses.

In its current terrestrial context, the full emergence and VOC emission of *Pseudocolus* appears to backfire. The VOC blend, which under marine conditions may have orchestrated an efficient ecological transition to unicellular survival, now functions as an attractant for terrestrial insects (flies, beetles) that parasitize the organism instead of enabling regeneration.

This inversion of signal interpretation underscores the likelihood that *Pseudocolus*'s biochemical logic was adapted to underwater microbial and chemical dynamics, not aerial dispersal biology. The organism may, in fact, be failing its emergence process—initiating a biochemical death mode meant for aquatic decay and recovery, but instead triggering exploitation in dry terrestrial ecosystems.

This reinterpretation suggests that *Pseudocolus* is a cryptic marine metazoan lineage that has survived through ecological marginalization, possibly by adopting fungal-like strategies for dormancy and emergence in high-moisture terrestrial zones (e.g., rainforests, mulch beds). It may represent a surviving fragment of a once fully aquatic modular clade, misread due to the overlap of convergent traits with terrestrial fungi.

Developmental Parallels

The fruiting body of *Pseudocolus* emerges from a volva-like structure resembling a cyst or periderm, similar to marine resting stages or larval envelopes (e.g., cnidarian planulae or sponge gemmules). The vertical arms of the mature body are hollow, spongey, and chambered—mirroring the aquiferous canal systems found in glass sponges (Hexactinellida) and the gastrovascular systems of some colonial cnidarians.

Internal hyphal structures exhibit pseudoparenchymatic tissue architecture, reminiscent of the parenchymal matrix in sponges — where functional compartments emerge through minimal tissue differentiation. The volva, gleba, and hollow lobes of *Pseudocolus* closely parallel sponge oscula, canal systems, and choanocyte-lined chambers. These correspondences suggest, but shared organization.

Rhizomorphs, often assumed to be feeding hyphae, exhibit biomineralized sheaths and angular crystals soluble in KOH, suggesting the presence of silicate or calcite analogs common in sponge spicules. These structures are more consistent with structural elements of sessile marine invertebrates than with terrestrial fungal hyphae (Abbamondi et al. 2021).

Biomineralization Mechanisms

This organism's arms are deeply infiltrated with manganese — a metal with unique redox properties and a long association with hydrothermal and sedimentary systems. Manganese precipitates, particularly manganese oxides often grow in dendritic, radial, or triradial morphologies under non-equilibrium conditions.

Quantitative assays of related taxa (such as *Clathrus ruber*, *Phallus impudicus*, and *Clathrus archeri*) revealed Mn levels up to 1900 mg/kg, wit corresponding elevated Fe concentrations (Stijve, 1997; Schmitt, 1977). In these organisms, manganese appears to support enzymatic activity and gel-phase transformation during emergence and liquefaction processes, including manganese peroxidase and laccase production (Kuhar et al., 2016).

These mineral patterns are widely observed in natural *"chemical gardens,"* where metal salts introduced into alkaline silicate-rich solutions spontaneously self-organize into branching tubes and fans (Cartwright et al. 2002; Barge et al. 2015). Such mineral dendrites are not simply beautiful — they are logical structures. They arise from constraints: from the way ions diffuse, how pH gradients form, and how growing crystals deform the space around them. And crucially, these systems do not require biological instructions. They encode their own pattern as they grow.

In modern vent ecosystems, manganese is used by microbial communities and invertebrates to form skeletons, to mediate

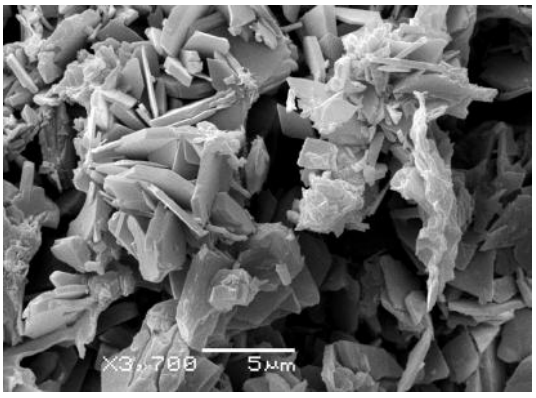
redox reactions, and to create reactive or defensive surfaces (Tebo et al. 2005). The same materials (manganese oxides) form thin black surface gels like those seen on this organism's arms. These structures may act as both scaffolds and signaling interfaces.

In this organism, its mineral phase appears embedded within a polysaccharide matrix — likely similar to alginate, chitin, or other glycosaminoglycans known from sponges and soft-bodied marine animals. These biological gels bind metal ions, modulate local stiffness, and create hydrogel frameworks capable of dynamic behavior.

Polysaccharides are widely used in biomineralization as templates and buffers. They slow down crystal growth, guide its direction, and create the soft-to-hard gradients found in many invertebrate skeletons (Weiner and Dove 2003). In this case, the soft fractal arms may represent a living composite: part sponge, part mineral, part soft robot. Their flexibility, fractality, and manganese content suggest feedback-sensitive form generation — a kind of shape memory not driven by cells, but by materials.

Scanning electron microscopy of *Pseudocolus* reveals crystalline incrustations on the surface of rhizomorphs and hyphae (Sulzbacher, 2013; Mykchaylova, 2022), structurally analogous to the spicules formed by sclerocytes in Calcarea and Demospongiae.

In sponges, spicules form via protein-mediated mineral aggregation around a central organic axial filament — a process possibly co-opted or re-expressed in *Pseudocolus*.



Pseudocolus garciae, "rhizomorphs covered by crystals" (Sulzbacher, M.; 2013)

This leads to a radical but coherent proposition: that form came before inheritance. That recursive morphologies (triradial, branching, pump-like) stabilized themselves through chemical and mechanical feedback long before nucleic acids encoded development. In this model:

- The first bodies were mineral-gel systems capable of sustaining and modifying their shape.
- Triradiality was not an evolutionary oddity, but a solution to flow and stability.
- Heritability emerged only after form was already stable and repeatable.

The organism presented here with its Mn-rich arms, triradial-to-quadralateral switching, and deep-sea emergence behavior, may be a living descendant of such a system. Or perhaps more accurately, it is a re-expression: an organism that retains or reactivates these deep material logics in modern form.

It invites us to reconsider the assumptions of body plan evolution. Not all morphology is inherited genetically. Some may still arise, as it once did, from the inherent logic of matter and flow — and from the recursive geometries that shape themselves.

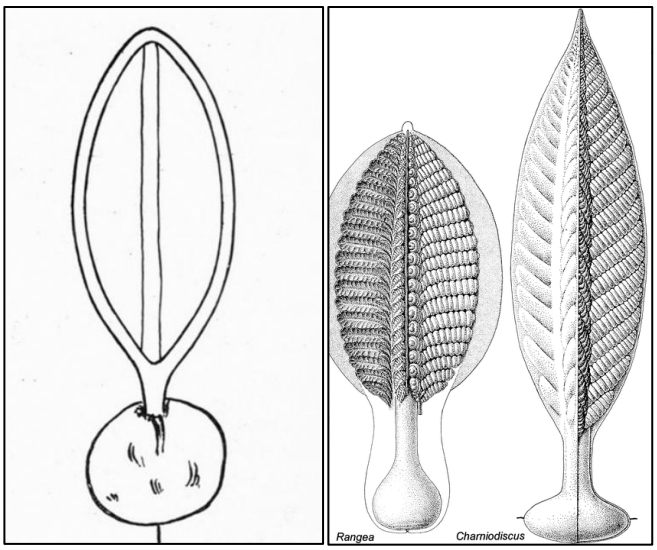
Evolutionary Implications: Triradial Morphogenesis and Deep Scaffold Lineages

Life builds bodies through many mechanisms. In modern animals, most development is guided by genetic instructions, regulatory gene cascades, and tissue-layer organization. But these systems evolved from simpler, more physical architectures that shaped form through scaffold, gradient, and feedback before genetic segmentation arose. *Pseudocolus* presents compelling evidence for the persistence of such a scaffold-driven lineage.

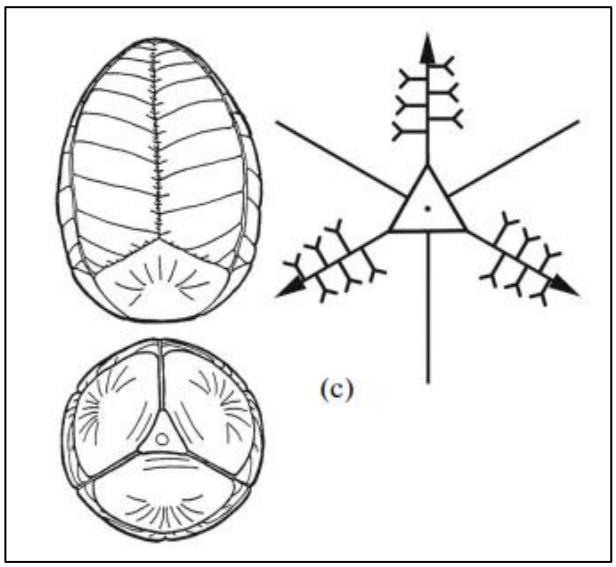
Long-read BLAST alignments of *Pseudocolus* sequences reveal high-confidence matches across basal metazoans and scaffold-bearing protists. The consistent reappearance of three-lobed and scaffold-organized body plans across these high-confidence hits supports the existence of a morphogenetic lineage that predates the bilaterian radiation. This paper designates this lineage *Triquadrozoa*: a group unified by tripartite emergence logic, modular recursion, and scaffold-driven development.

Some of the most compelling matches involved calcareous sponges (Calcarea), particularly *Clathrina* spp., which build their internal skeletons from triactine and tetractine spicules arranged with precise 120° symmetry (Wörheide 2012). These spicules define radial structural axes and scaffold water flow systems, effectively acting as early morphogenetic regulators. Similarly, in demosponges like *Axinella*, body expansion often occurs along three recursive growth fronts aligned with underlying spicule symmetry (Uriz et al. 2003).

Where six-rayed spicules appear, particularly in Hexactinellida, they often result from recursive doubling of triactine bases rather than independent morphological innovations, reinforcing the primacy of the threefold scaffold as a developmental template (Uriz et al. 2003).



Pseudocolus. Drawing. Lloyd C. G. 1907;
Rangea and *Charniodiscus*. Ediacaran biota. (Dzik, J., 2003).



Ventogyrus chistyakovi (Ivantsov and Zakrevskaya, 2020).

Cnidarian matches were strongest among colonial hydrozoans such as *Obelia dichotoma* and *O. longissima*, which develop modular colonies through tripartite budding and radial polyp arrangement (Buss and Burch 1989). The gastro- and gonozooid modules of these colonies function as independent radial domains, suggesting an underlying morphogenetic logic that is modular rather than fixed, and which may reflect an ancient body plan logic unrelated to bilaterality.

Significant matches also included amoeboid protists such as *Flabellula*, known for its naked with locomotive form altering from a flattened expanded or reticulate one, when slowly moving, to a subcylindrical monopodial one when in rapid movement or under specific conditions. (Adl, S.M., 2013). These lobes are stabilized by cytoplasmic–gel feedback systems and can express persistent spatial patterning (Smirnov and Goodkov 2007).

Their presence in the alignment results implies conservation of symmetry-stabilizing domains that may have predated multicellularity altogether, supporting the idea that triradial logic emerged first as a physical constraint solution, later becoming scaffolded into modular multicellular forms.

Triradial symmetry is not common in extant animals but is well documented in Ediacaran fossils such as *Tribrachidium*, *Albumares*, and *Anfesta* (Ivantsov & Zakrevskaya, 2020). These organisms, like *Pseudocolus*, display radially distributed lobes, centralized stalks or chambers, and no signs of bilaterian segmentation. These forms appear to use recursive lobe patterning, possibly to modulate flow or distribute mechanical stress.

The organism *Pseudocolus* represents a direct, extant member of the Ediacaran biota. This statement is based on structural morphology, scaffold emergence, biomineral logic, and long-read genomic alignment, *Pseudocolus* conforms to the criteria that define the Ediacaran body architecture: triradial modular symmetry, scaffold-based morphogenesis, non-bilaterian emergence logic, and recursive pattern formation unconstrained by modern developmental segmentation. It is a living representative of an architectural lineage that predates the bilaterian body plan.

Pseudocolus does not mimic early life — it preserves it. Its architecture, genome, and mineral logic offer a rare, extant instance of a morphogenetic scaffold older than modern developmental pathways. Rather than evolving new strategies, this lineage conserved a functional body plan capable of withstanding geological time through modular logic and material feedback.

Proposed Taxonomic Reclassification: Tribrachia (Demospongiae incertae sedis)

The convergence of genomic, morphological, and biochemical evidence supports the reclassification of the organism currently known as *Pseudocolus* from terrestrial Basidiomycota to marine Demospongiae. We propose the new combination *Tribrachia fusiformis* (comb. nov.), reflecting both the organism's defining triradial morphology and the establishment of a new genus within Demospongiae incertae sedis.

The genomic evidence provides the clearest support for demosponge affinity. Alignments with *Axinella* species consistently exceeded 1800 bp with identities above 85% and E-values of zero, representing some of the strongest matches in the entire dataset. Additional high-confidence alignments

with *Geodia barretti, Ectyoplasia ferox,* and other demosponges reinforce this pattern. These sequence similarities span regulatory regions likely involved in scaffold-based morphogenesis, suggesting deep conservation of developmental machinery characteristic of basal Demospongiae.

Morphologically, *Tribrachia fusiformis* exhibits the defining characteristics of demosponge organization: a porous, modular body plan built around organic scaffolding, pseudoparenchymatic tissue architecture, and biomineralized structural elements. The absence of true organs, combined with the presence of chambered internal architecture and mineral-organic composite materials, aligns with basal sponge body plans rather than any known fungal morphology. The triradial emergence pattern that defines the genus *Tribrachia* represents a distinctive architectural feature within Demospongiae.

Formal nomenclature:

- **Kingdom:** Animalia
- **Phylum:** Porifera
- **Class:** Demospongiae
- **Order:** *incertae sedis*
- **Family:** *Triquadrozoa*
- **Genus:** *Tribrachia* (*Pseudocolus fusiformis*)

The placement within Demospongiae *incertae sedis* acknowledges both the clear demosponge affinities and the unusual characteristics that preclude assignment to existing orders. This classification provides a framework for continued research while correcting the fundamental misplacement within terrestrial fungi.

The *incertae sedis* designation appropriately reflects our current understanding that strong demosponge relationships are evident, but the precise phylogenetic position within Demospongiae requires additional investigation.

This reclassification positions *Tribrachia fusiformis* as potentially representing an early-diverging demosponge lineage that has retained ancestral characteristics obscured in other modern sponge groups, offering unique insights into the evolutionary history of the oldest metazoan phylum.

Conclusion

The discovery and analysis of *Pseudocolus* compel a reevaluation of long-held assumptions about body plan evolution, multicellular emergence, and the boundaries of known biological architecture. Through high-confidence genomic alignments, mineral-morphogenetic analysis, and structural comparison with both extant and extinct organisms, this paper proposes that *Pseudocolus* is not simply a taxonomic outlier — it is a material and genetic archive of pre-bilaterian morphogenesis.

Multiple lines of biological evidence align these taxa with deep biosphere life strategies. Mineral concentrations far exceeding those of typical fungi and aligning with marine endoliths and vent organisms. Emissions of hydrogen sulfide and thiols indicative of anaerobic, metal-driven metabolic pathways. Hydraulic pressurization mirroring biomechanical strategies employed by deep biosphere biofilms and vent communities to modulate internal chemical gradients

These adaptations are coherent with survival in high-pressure, anoxic, metal-rich environments characteristic of deep-sea and sub-crustal ecosystems. The rapid maturation and collapse cycle observed in these organisms is incompatible with sustained life in terrestrial surface environments. It reflects a terminal metabolic discharge: a physiological legacy of dispersal or emergency emergence mechanisms from their original subsurface habitats.

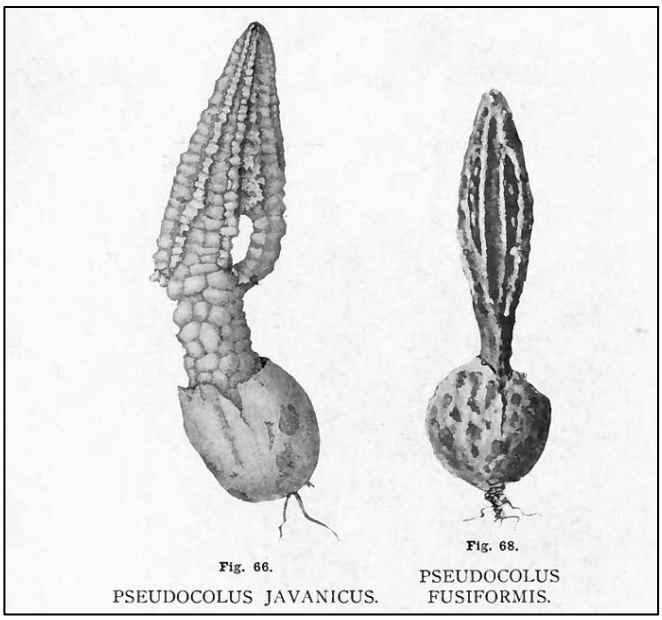
In natural deep biosphere contexts, such pressurization and expansion would facilitate pore colonization or dispersal through mineral matrices, allowing colonization of new rock microenvironments (Staudigel et al., 2008). However, upon accidental exposure to oxygen-rich surface conditions, these mechanisms fail, leading to rapid exhaustion of internal reserves, VOC emission, and tissue collapse.

Its triradial-to-quadralateral symmetry, lobed scaffold emergence, and manganese-rich polysaccharide matrix place it squarely within a developmental tradition older than modern animal phyla. The evidence reveals continuity and a persistent scaffold logic conserved across billions of years, encoded not in canonical genes, but in modular geometry, mineral chemistry, and feedback-mediated emergence.

The proposed *Triquadrozoa* clade reframes our understanding of multicellular ancestry. It positions *Pseudocolus* as a living descendant of the same architectural lineage that produced the triradial Ediacaran forms (*Tribrachidium*, *Albumares*, and *Rangea*) and connects it materially to basal sponges, lobose amoebae and other organisms.

Taken together, the data and models presented suggest that modern developmental biology has obscured — rather than replaced — a deeper stratum of morphogenetic order. This order is not theoretical. It is scaffolded in gel and metal, in flow and curvature, in feedback and recursion — and it is still alive, emerging from the seafloor or soil to remind us that life did not begin with the genome. It began with form.

This study underscores the value of long-alignment comparative frameworks and morphogenetic logic as complementary tools to classical phylogenetics, especially when confronting lineage-defying organisms.



Pseudocolus (Lloyd, C.G. 1909).

Data Availability

All sequences referenced are publicly available through NIH/NCBI and ENA databases. Custom database FASTA files and complete sequence listings with methodological documentation are provided as supplementary materials within the OSF repository. These datasets are freely available through the Open Science Framework (OSF) at DOI 10.17605/OSF.IO/69WHF.

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Appendix A: Summary of BLAST Results

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Onchidoris bilamellata	**Sea Slug** *(Doridacea, Nudibranch, Gastropoda).*	AJ224783.1	1887	1289	75.7	0
Flabellula sp.	**Amoeba** (*Elardia*, *Tubulinea, Amoebozoa)*	LC340976.1	1882	1379	76.9	0
Haliommilla capillacea	**Radiolaria** (*Spumellaria, Polycystinea, Rhizaria)*	MT670487.1	1863	1378	77.2	0
Colpophyllia natans	**Stony Coral** *(Scleractinia, Hexacorallia, Anthozoa, Cnidaria)*	LT631261.1	1858	1710	80.6	0
Hartmannella sp.	**Amoeba** (*Elardia*, *Tubulinea, Amoebozoa)*	EF205324.1	1853	1477	78.4	0
Obelia longissima	**Colonial Hydrozoan** (*Leptothecata, Hydrozoa, Cnidaria)*	KM603469.1	1841	1695	81	0
Nanomia septata	**Siphonophore** (*Siphonophorae, Hydrozoa, Cnidaria)*	CM107577.1	1826	1752	82.0	0
Favia fragum	**Stony Coral** *(Scleractinia, Hexacorallia, Anthozoa, Cnidaria)*	LT631268.1	1824	1810	82.6	0
Favia fragum	**Stony Coral** *(Scleractinia, Hexacorallia, Anthozoa, Cnidaria)*	LT631269.1	1823	1811	82.5	0
Diploria labyrinthiformis	**Stony Coral** *(Scleractinia, Hexacorallia, Anthozoa, Cnidaria)*	LT631262.1	1817	1804	82.7	0
Obelia dichotoma	**Colonial Hydrozoan** (*Leptothecata, Hydrozoa, Cnidaria)*	KX665387.1	1815	1828	82.9	0
Bebryce sp.	**Soft Coral** *(Octocorallia, Anthozoa, Cnidaria)*	PP410842.1	1812	1824	82.1	0
Axinella damicornis	**Sponge** *(Axinellida, Demospongiae, Porifera)*	OZ007509.1	1812	1825	85.4	0
Axinella damicornis	**Sponge** *(Axinellida, Demospongiae, Porifera)*	OZ007506.1	1811	1831	85.5	0
Obelia dichotoma	**Colonial Hydrozoan** (*Leptothecata, Hydrozoa, Cnidaria)*	KX665396.1	1810	1822	83	0
Xenia sp.	**Soft Coral** *(Octocorallia, Anthozoa, Cnidaria)*	NW_025813507	1809	1851	83.6	0
Ectyoplasia ferox	**Sponge** *(Axinellida, Demospongiae, Porifera)*	EU702415.1	1809	1829	85.4	0
Mastigias albipunctata	**Jellyfish** (*Rhizostomeae, Scyphozoa, Cnidaria)*	PQ647264.1	1808	1882	83.8	0
Bebryce sp.	**Soft Coral** *(Octocorallia, Anthozoa, Cnidaria)*	PP410839.1	1808	1872	83.9	0
Gorgonia flabellum	**Soft Coral** *(Octocorallia, Anthozoa, Cnidaria)*	PP410861.1	1808	1855	83.6	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Cephea cephea	**Jellyfish** (*Rhizostomeae, Scyphozoa, Cnidaria)*	PQ647263.1	1807	1898	84	0
Tubipora musica	**Soft Coral** *(Octocorallia, Anthozoa, Cnidaria)*	AF052909.1	1807	1853	83.5	0
Axinella corrugata	**Sponge** *(Axinellida, Demospongiae, Porifera)*	EF092264.1	1807	1827	85.5	0
Plectroninia neocaledoniense	**Sponge** *(Lithonida, Calcarea, Porifera)*	AM180979.1	1804	1810	85.2	0
Atolla vanhoeffeni	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	AF100942.1	1803	1868	85.8	0
Axinella damicornis	**Sponge** *(Axinellida, Demospongiae, Porifera)*	OZ007509.1	1803	1957	85	0
Geodia barretti	**Sponge** (*Tetractinellida Demospongiae, Porifera)*	CASHTH010003473	1803	1831	85.4	0
Axinella damicornis	**Sponge** *(Axinellida, Demospongiae, Porifera)*	OZ178462.1	1802	1964	85	0
Ectyoplasia ferox	**Sponge** *(Axinellida, Demospongiae, Porifera)*	EU702415.1	1802	1955	85	0
Edwardsiella lineata	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KF155691.1	1802	1925	84.4	0
Pachycerianthus fimbriatus	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	AF358111.1	1802	1901	84.2	0
Axinella corrugata	**Sponge** *(Axinellida, Demospongiae, Porifera)*	AY737637.1	1800	1948	84.8	0
Axinella polypoides	**Sponge** *(Axinellida, Demospongiae, Porifera)*	U43190.1	1800	1948	84.8	0
Spirastrella sp.	**Sponge** *(Clionaida, Demospongiae, Porifera)*	KX894463.1	1800	1904	84.3	0
Eurypon clavatum	**Sponge** *(Heteroscleromorpha, Demospongiae, Porifera)*	AJ621547.1	1799	1957	84.9	0
Agelas clathrodes	**Sponge** *(Agelasida Demospongiae, Porifera)*	AY769087.1	1799	1957	84.9	0
Stephanoeca diplocostata	**Flagellated Eukaryote** (*Choanoflagellata*)	AF084235.1	1799	1931	84.3	0
Tethya wilhelma	**Sponge** *(Tethyida, Demospongiae, Porifera)*	OX175333.1	1799	1929	84.7	0
Cyanea nozakii	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria*)	MT813455.1	1799	1915	84.1	0
Geodia barretti	**Sponge** *(Tetractinellida Demospongiae, Porifera)*	CASHTH010003473	1798	1966	84.9	0
Axinella corrugata	**Sponge** *(Axinellida, Demospongiae, Porifera)*	EF092264.1	1798	1957	85	0
Stephanoeca diplocostata	**Flagellated Eukaryote** (*Choanoflagellata*)	AY149899.1	1798	1957	84.7	0
Plectroninia neocaledoniense	**Sponge** *(Lithonida, Calcarea, Porifera)*	AM180979.1	1798	1947	84.5	0
Soleniscus radovani	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AF452017.1	1797	1925	84.4	0
Axinella polypoides	**Sponge** *(Axinellida, Demospongiae, Porifera)*	OZ178462.1	1796	1973	85.1	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Aurelia sp.	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	IADZ01000102.1	1796	1937	84.4	0
Tethya californiana	**Sponge** *(Tethyida, Demospongiae, Porifera*	OZ123596.1	1796	1926	84.6	0
Salpingoeca kvevrii	**Flagellated Eukaryote** (*Choanoflagellata*)	EU011930.1	1795	1956	85	0
Pigoraptor chileana	**Sponge** *(Axinellida, Demospongiae, Porifera)*	MF190553.1	1795	1910	86.3	0
Petrobiona massiliana	**Sponge** *(Baerida, Calcarea, Porifera)*	AF452026.1	1795	1923	84.6	0
Achramorpha ingolfi	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	MH385157.1	1794	1952	84.8	0
Atolla vanhoeffeni	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	AF100942.1	1794	1982	85.2	0
Metridium senile	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	OX459095.1	1794	1953	85.2	0
Aurelia solida	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	MZ788653.1	1794	1920	84.1	0
Axinella polypoides	**Sponge** *(Axinellida, Demospongiae, Porifera)*	EF092266.1	1794	1951	84.89	
Achramorpha ingolfi	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	MH385157.1	1794	1952	84.8	0
Chrysaora pacifica	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	KY212123.1	1793	1970	84.9	0
Echinospongilla brichardi	**Freshwater Sponge** (*Spongillidae, Demospongiae, Porifera*)	EF095192.1	1792	1954	84.9	0
Cyanea sp.	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria*)	AF358097.1	1792	1949	84.6	0
Bunodeopsis (Viatrix) globulifera	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KJ483025.1	1792	1940	85.1	0
Galatheanthemum	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KJ483012.1	1791	1960	85.2	0
Baeria nivea	**Sponge** *(Baerida, Calcarea, Porifera)*	AF182191.1	1791	1939	84.7	0
Leucosolenia sp.	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	AF100945.1	1791	1961	85	0
Edwardsia timida	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	GU473315.1	1791	1952	85.1	0
Chrysaora melanaster	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	AF358099.1	1791	1938	84.4	0
Sycon ciliatum	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	OZ025892.1	1790	1956	84.9	0
Chrysaora colorata	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	AF358098.1	1790	1953	84.6	0
Vosmaeropsis sp.	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	AF452018.1	1790	1952	84.9	0
Sycettusa tenuis	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	AM180975.1	1790	1947	84.8	0
Aiptasia insignis	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	AY046885.1	1790	1942	85	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Sycon ciliatum	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	NC_088643.1	1790	1956	84.9	0
Diaphanoeca grandis	**Flagellated Eukaryote** (*Choanoflagellata*)	AF084234.1	1789	2002	85.5	0
Diaphanoeca grandis	**Flagellated Eukaryote** (*Choanoflagellata*)	DQ059033.1	1789	1988	85.2	0
Grantessa sp.	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	JQ272313.1	1789	1961	84.9	0
Actinoscyphia plebeia	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	FJ489437.1	1789	1960	85.2	0
Phyllospongia foliascens	**Sponge** *(Dictyoceratida, Demospongiae, Porifera)*	OZ156448.1	1789	1957	85.1	0
Peachia cylindrica	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KJ483015.1	1789	1975	85.4	0
Syconessa panicula	**Sponge** *(Leucosolenida, Calcarea, Porifera)*	AM180976.1	1789	1957	84.9	0
Stichopathes sp.	**Thorn Soft Coral** (*Antipatharia*, *Hexacorallia, Anthozoa, Cnidaria*)	PP410996.1	1789	1955	85	0
Soleneiscus stolonifer	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180955.1	1788	2000	85.6	0
Clathrina cerebrum	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180957.1	1788	1978	85	0
Chrysaora sp.	**Jellyfish** (*Semaeostomeae*, *Scyphozoa, Cnidaria)*	AY920769.1	1788	1961	84.8	0
Bathypathes sp.	**Thorn Soft Coral** (*Antipatharia*, *Hexacorallia, Anthozoa, Cnidaria*)	MT318865.1	1788	1957	85	0
Leucascus ap.	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180954.1	1787	2024	85.8	0
Pericharax heteroraphis	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180967.1	1787	2002	85.5	0
Leucetta villosa	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180966.1	1787	2002	85.5	0
Leucetta sp.	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180964.1	1787	1997	85.5	0
Leucetta microraphis	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180965.1	1787	1993	85.3	0
Clathrina sp.	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180960.1	1785	1980	85.4	0
Tunicaraptor unikontum	**Predatorial Flagellate Protist** (*Holozoa*)	MT611055.1	1785	2006	87.2	0
Clathrina luteoculcitella	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180959.1	1785	1967	85.2	0
Leiopathes glaberrima	**Thorn Soft Coral** (*Antipatharia*, *Hexacorallia, Anthozoa, Cnidaria*)	PP411001.1	1785	1954	85	0
Corallochytrium limacisporum	**Non-Flagellated Protist** *(Teretosporea, Holozoa)*	L42528.1	1784	1968	85.4	0
Pigoraptor vietnamica	**Ameboid Eukaryote** (*Filasterea*)	MF190552.1	1783	1957	85.1	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Clathrina helveola	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AM180958.1	1783	1983	85.3	0
Tunicaraptor unikontum	**Predatorial Flagellate Protist** (*Holozoa*)	MT611055.1	1782	2116	86.9	0
Leucetta sp.	**Sponge** *(Clathrinida, Calcarea, Porifera)*	AY737644.1	1782	1989	85.4	0
Korsaranthus sp.	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KJ483017.1	1782	1960	85.1	0
Preactis millardae	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KJ483018.1	1782	1965	85.1	0
Antipathes sp.	**Thorn Soft Coral** (*Antipatharia*, *Hexacorallia, Anthozoa, Cnidaria*)	LT631294.1	1782	1957	84.9	0
Halcurias hiroomii	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	LC768581.1	1781	1945	84.8	0
Vaceletia sp.	**Sponge** *(Dictyoceratida, Demospongiae, Porifera)*	EU702425.1	1781	1942	85.1	0
Distichoptilum gracile	**Sea Pen** (*Octocorallia, Anthozoa, Cnidaria*)	OL741694.1	1781	1942	84.9	0
Parazoanthidae	**Zoanthids** (*Hexacorallia, Anthozoa, Cnidaria*)	MZ329696.1	1780	1941	84.8	0
Nausithoe werneri	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	MT603628.1	1780	1984	85.2	0
Savillea micropora	**Flagellated Eukaryote** (*Choanoflagellata*)	EU011928.1	1778	1961	85.1	0
Acanthocorbis unguiculata	**Flagellated Eukaryote** (*Choanoflagellata*)	L10823.1	1778	1958	85.1	0
Pompholyxophrys punicea	**Amoeba**, scale-bearing filose *(Nucleariid, Holomycota)*	MK547175.1	1778	1957	85	0
Atolla gigantea	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	OM260068.1	1778	1957	85.2	0
Atolla vanhoeffeni	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	OM260085.1	1778	1957	85.2	0
Periphylla periphylla	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	OM201141.1	1776	1957	85	0
Chrysaora sp.	**Jellyfish** (*Semaeostomeae, Scyphozoa, Cnidaria)*	KY610821.1	1776	1942	84.7	0
Nausithoe werneri	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	MT603630.1	1775	1980	85.2	0
Periphylla periphylla	**Jellyfish** (*Coronatae, Scyphozoa, Cnidaria)*	OM201140.1	1775	1955	85	0
Heterodactyla hemprichii	**Sea Anemone** (*Hexacorallia, Anthozoa, Cnidaria*)	KC812194.1	1775	1939	84.8	0

Appendix B: *Pseudocolus* Making it Work.

Pseudocolus (unverified), Hartford Co., Maryland.
(iNaturalist Observation. No. 288601088, © Joshua Jones).

Pseudocolus (unverified), Norfolk Co., Massachusetts.
(iNaturalist Observ. No. 284094233, © Lindsay Blevins).

Pseudocolus (unverified), Pennsylvania, USA.
(iNaturalist Observation No. 288849521).

Pseudocolus (unverified), Victoria, Australia.
(iNaturalist Observ. No. 288904335, © Talia Fitzgerald).

Pseudocolus (unverified), Leesburg, Virginia, USA.
(iNaturalist.org Observation No. 281490214, © Tara Holt).

Pseudocolus (unverified), Sydney, Australia.
(iNaturalist.org Observ. No. 254711135, © Sofia Zvolanek).

Pseudocolus (unverified), Jawa Tengah, Indonesia
(iNaturalist.org Observation No. 256603849,
© Eka Maulida Cahyaningsih)

Pseudocolus (unverified), Hsinchu Co., Taiwan.
(iNaturalist.org Observation No. 231009188, © 唐銘澤)

Pseudocolus (unverified), New Castle Co., Delaware.
(iNaturalist.org Observation No. 245557018)

Pseudocolus (unverified), Harwinton, CT, USA.
(iNaturalist.org Observ. No. 179031041, © Sarah Wilson)

Pseudocolus (unverified), Keelung, Taiwan.
(iNaturalist.org Observ. No. 270376393, © Chen Alice)

Pseudocolus (unverified), Nantou, Taiwan.
(iNaturalist.org Observation No. 270152158)

Pseudocolus (unverified), Jefferson Co., Kentucky.
(iNaturalist.org Observation No. 238792895)

Pseudocolus (unverified), Nova Scotia, Canada.
(iNaturalist.org Observation No. 241490278)

Pseudocolus (unverified), Cartago, Costa Rica.
(iNaturalist.org Observation No. 254727238)

Pseudocolus (unverified), Norfolk Co., Massachusetts.
(inaturalist.org Obs. No. 284094233, © Lindsay Blevins)

Pseudocolus (unverified), Wellington, Victoria, Australia.
(inaturalist.org Observation No. 197684486,
© Barry Langdon-Lassagne)

Pseudocolus (unverified), New South Wales, Australia.
(iNaturalist.org Observation No. 251368234)

Pseudocolus (unverified), New South Wales, Australia.
(iNaturalist.org Observation No. 166599395)

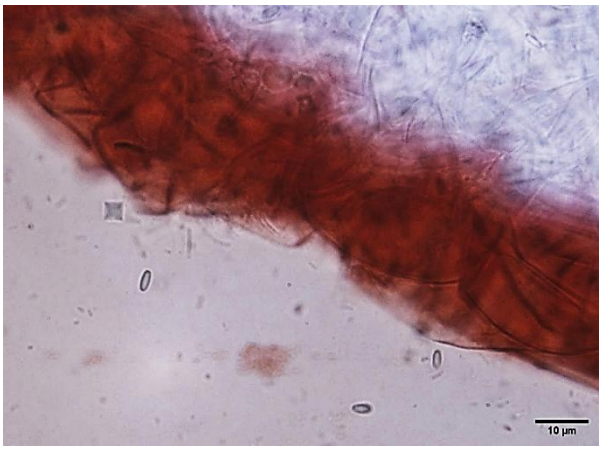
Pseudocolus (unverified), Queensland, Australia.
(inaturalist.org Observation No. 219670370)

Pseudocolus (unverified), Guilford Co., North Carolina. (iNaturalist.org Observation No. 134342935, © Frank Hackl)

Pseudocolus (unverified), Guilford Co., North Carolina. (iNaturalist.org Observation No. 134342935, © Frank Hackl)

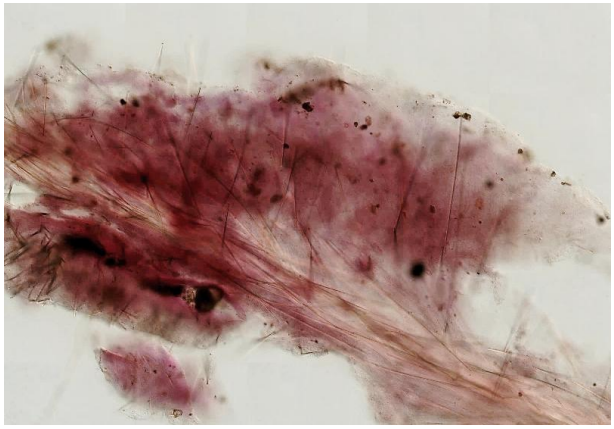
Appendix C: Morphological Images

Tissue (Microscopic)

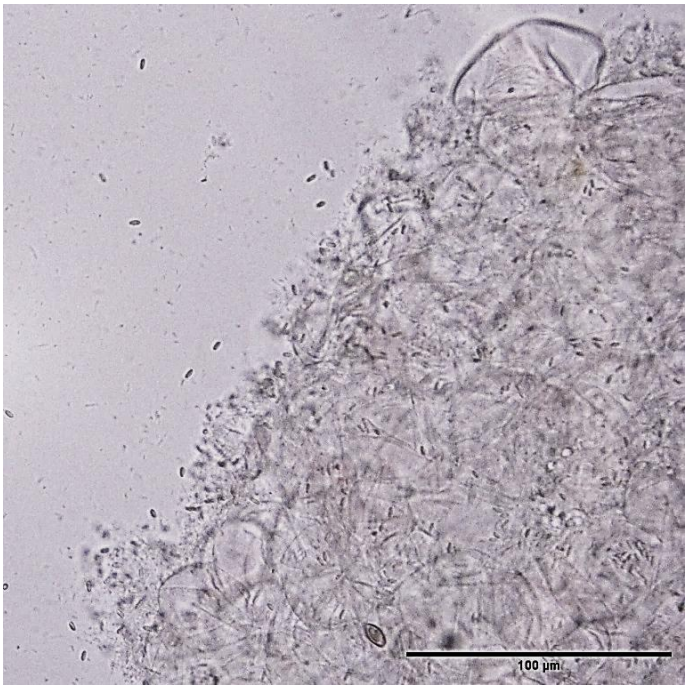


Pseudocolus (unverified), bar = 10 µm.
iNaturalist Observation No. 238792895,
Louisville, Kentucky, USA, 2024.

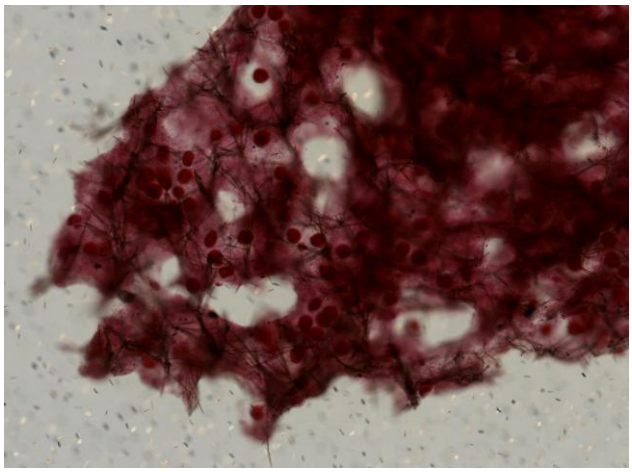
Soleneiscus intermedius, lumen of a tube with the apical actine of tetractines. (Klautau, M., 2022).



Axinella sp., 70% alc.; Cat. No. IZ.006386.PR,
Atlantic Ocean; Caribbean Sea; Jamaica, Discovery Bay;
Yale Peabody Museum, (photo by Calderon, K., 2017).

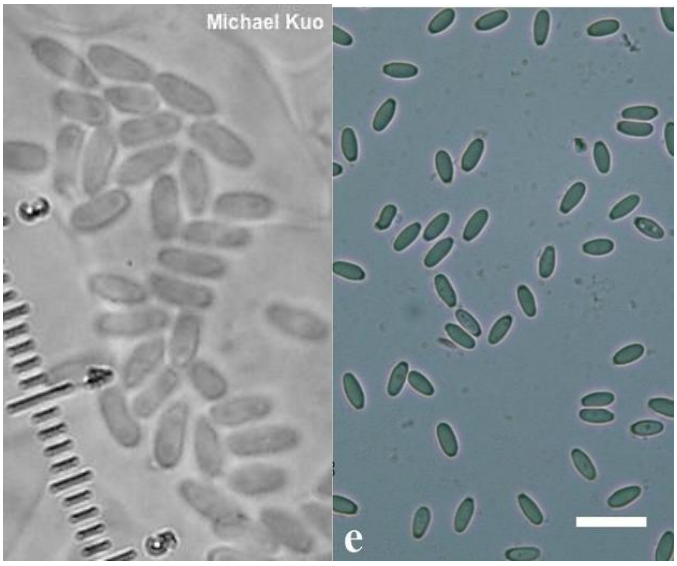


Pseudocolus (unverified), bar = 100 µm.
iNaturalist Observation No. 238792895,
Louisville, Kentucky, USA, 2024.

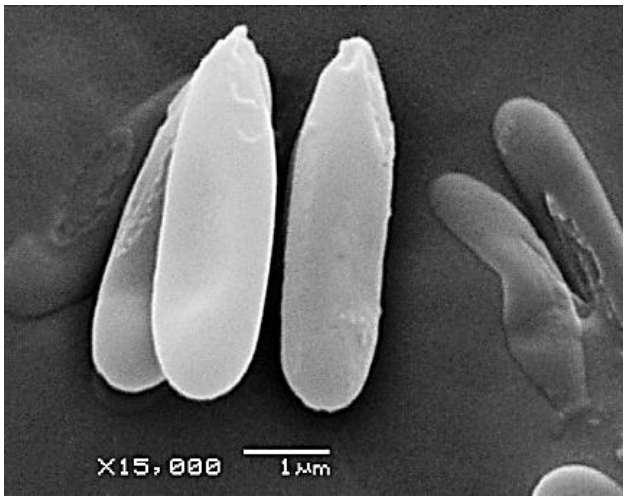


Axinella polypoides; Cat. No. IZ.084484.PR,
Naples, Italy, Atlantic Ocean.
Yale Peabody Museum, (photo by Fortunato, A. M., 2017).

Reproduction (Microscopic)

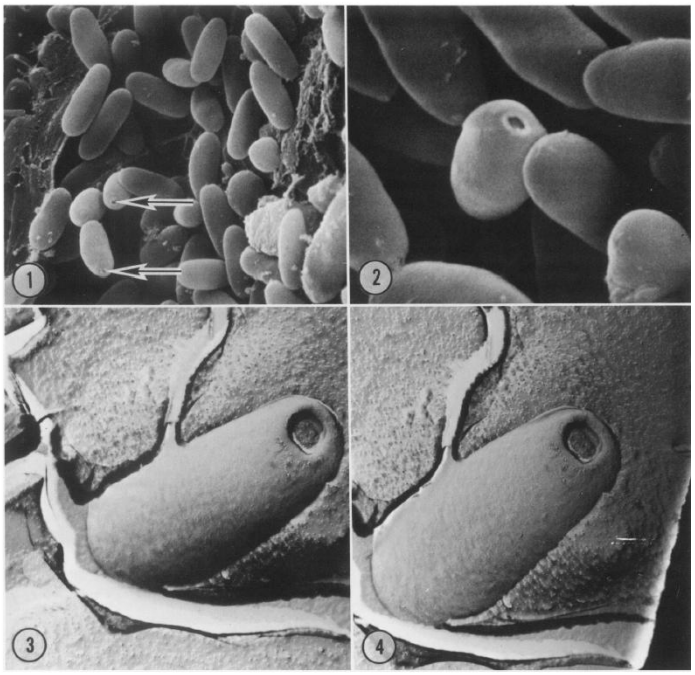


Pseudocolus, "spores" (Kuo, 2021; Yakar, 2019).



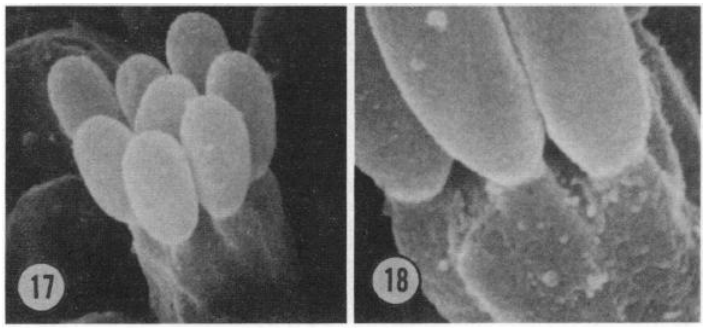
Pseudocolus garciae "basidiospores" (Sulzbacher, M.; 2013)

Pseudocolus "spores" (Blanton, R.L. 1976)

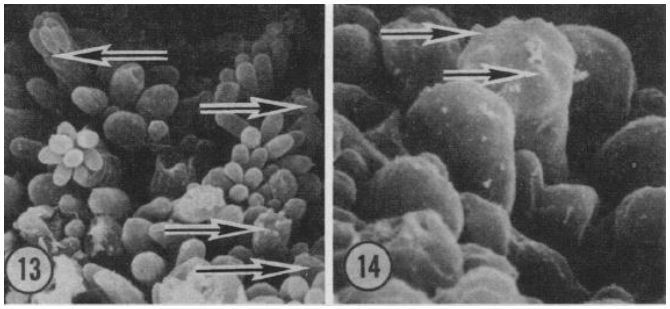


Figs. 1–4. *Mutinus caninus*. 1. Cluster of spores showing (arrows) hilar scars. SEM, ×4600. 2. Single spore showing hilar scar. SEM, ×13,800. 3, 4. Stereopair transmission electron micrographs of freeze-fracture replica of spore showing a hilar scar, ×23,000.

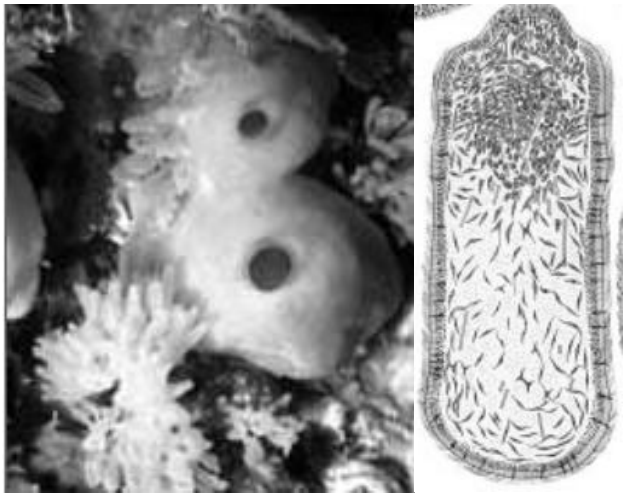
Mutinus canis (basal Stinkhorn). SEM of "spores" with "hilar scars." (Flegler, S. L. 1980).



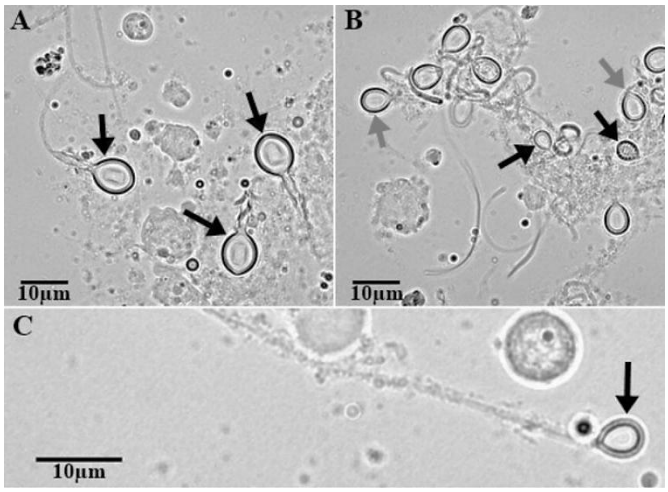
Mutinus canis (basal Stinkhorn). "basidium" and "mature badiospores." (Flegler, S. L. 1980).



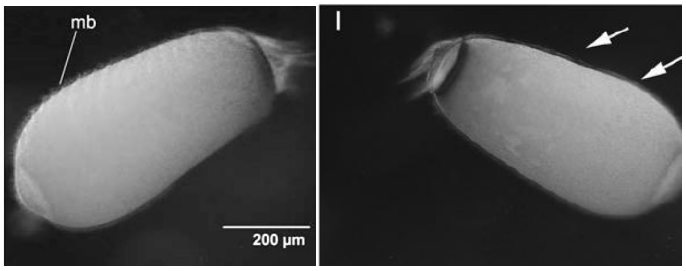
Mutinus canis (basal Stinkhorn). "Glebal chamber" with "badiospore development." (Flegler, S. L. 1980).



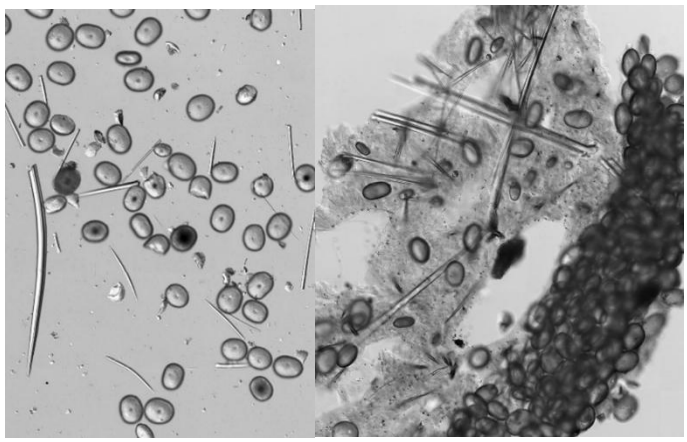
Pericharax heteroraphis. Sponge. (Hooper, John, 1999);
Axinella crista-galli, Parenchymella larvae. (Leys, S.P., 2003).



Nausithoe, Cnidaria. "Nemocysts," "euryteles," and "isorhiza capsules." (Molinari, C.G., et al, 2020).

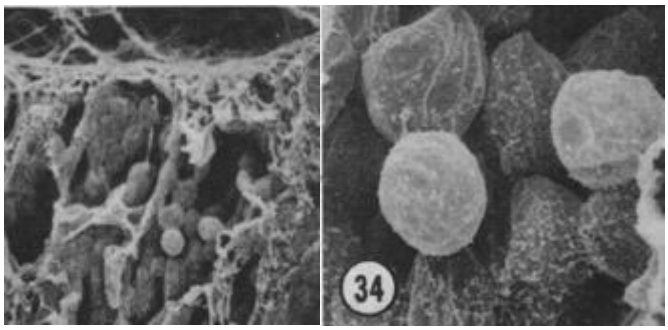


Cacospongia sp. and *Ircinia*. *oros* sponge larvae.
(Maldonado, M., 2006).

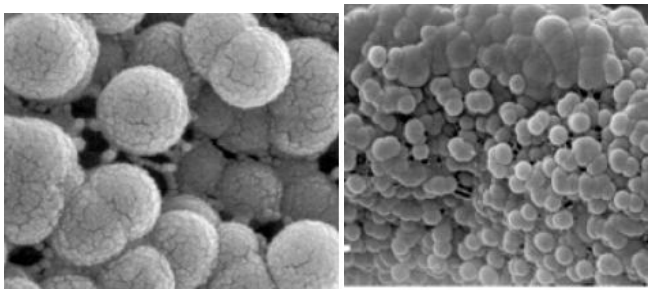


Geodia sp., *Demospongiae*, Cat. No. IZ.084236,
Cordell Bank, California, USA, Pacific Ocean.
Yale Peabody Museum, (photo by Fortunato, A. M., 2017).

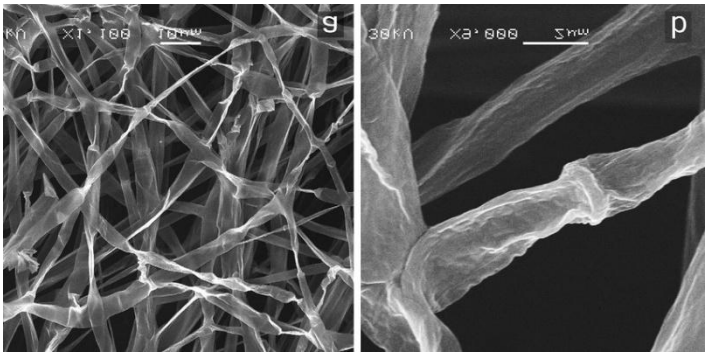
Extracellular Matrix and Formations



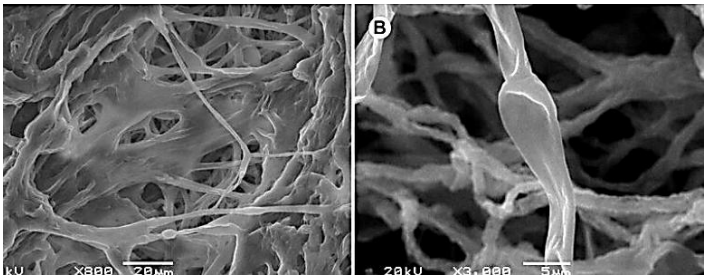
Mutinus canis (basal Stinkhorn), SEM photo of "cells."
(Flegler, S. L. 1980).



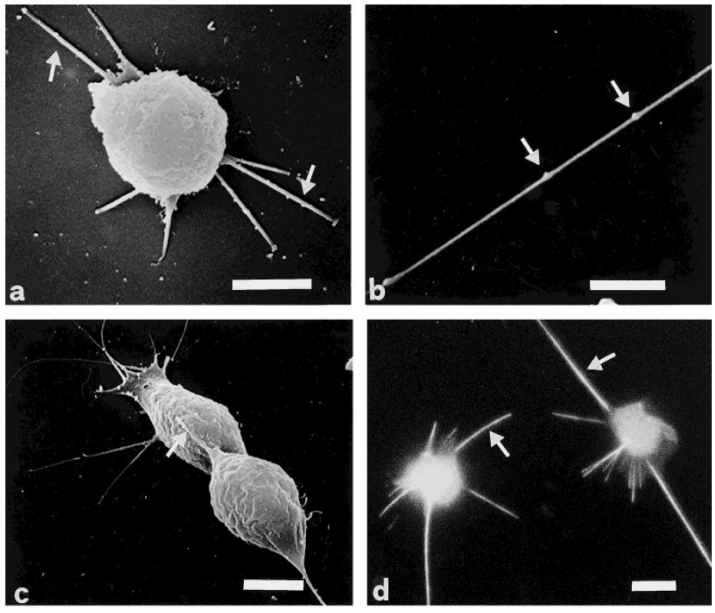
Porifera. Early silification process; formation of silica nanospheres. (Uriz, 2006).



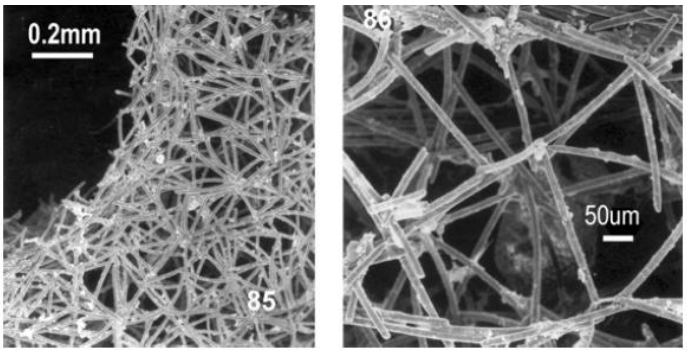
Clathrus archeri (basal Stinkhorn).
"Clampless mycelia" and "collapsed hypha."
(Mykchaylova, Oksana; 2022).



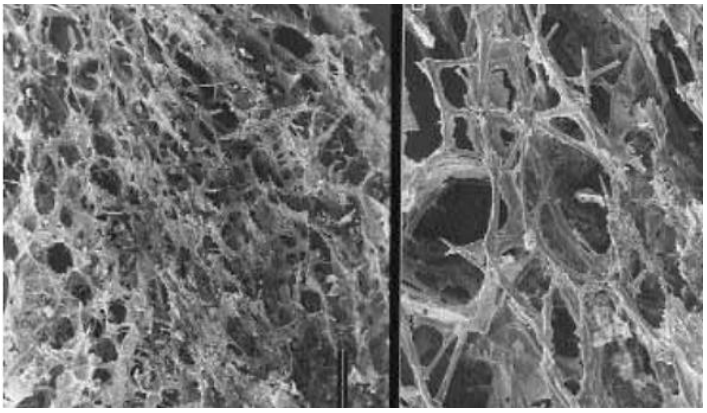
Clathrus ruber (Stinkhorn).
"Vegetative mycelium" and "young intercalary cells."
(Sukhomyln M., 2021).



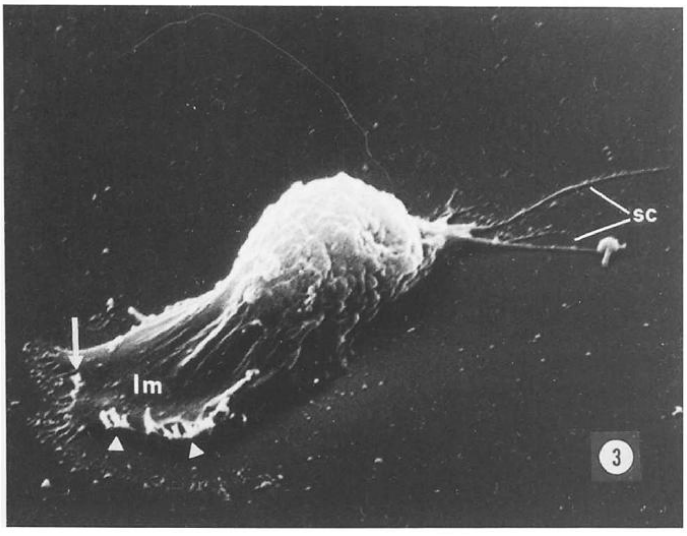
Clathrina cerebrum. SEM of choanocytes.
(Gaino, E. and Magnino, G., 1999).



Demosponge. "Plumose arrangement of the skeleton of demosponges." (Uriz, 2006).



Axinella polypoides. "Choanosomal skeleton."
(Alvarez, Belinda & Hooper, John; 2002).



Clathrina. Cell spreading on polylysine substratum; note a large lamellipodium (lm) showing microspikes (arrowheads) and ruffles (arrow). x6800. (Gaino, E., et al, 1993).