Molecular Characterization of *Trichophyton schoenleinii* Reveals Systematic Affinities with Ancient Eukaryotes

Genetic Evidence for Functional and Taxonomic Misclassification

Authors: Ashley Gjovik, B.S., J.D. (ashleymgjovik@protonmail.com) | **Date**: June 22 2025

Abstract

For over 150 years, *Trichophyton schoenleinii* has been classified as a "human fungal pathogen" causing scalp infections. This classification has driven decades of antifungal treatments and research approaches based on the assumption that it represents a derived specialist that evolved to parasitize human hosts.

Comprehensive genetic analysis reveals this classification to be fundamentally incorrect. High-resolution sequencing demonstrates that *T. schoenleinii* shares systematic molecular signatures with Earth's most ancient eukaryotic lineages—including choanoflagellates, basal metazoans, slime molds, tardigrades, and early-diverging protists—with >85% sequence identity and E-values of 0, while exhibiting poor phylogenetic integration with modern fungal taxa. Both nuclear ribosomal RNA and mitochondrial DNA show high-confidence matches to these ancient lineages, indicating genuine evolutionary relationships.

T. schoenleinii represents a genomic relic preserving primordial, marine biological architecture from before major eukaryotic divergence. Its sophisticated sulfur metabolism, keratin-degradation machinery, and biofilm-like colonization strategies mirror biochemical systems found in marine microbial mats and extremophile environments—not superficial pathogens. The organism's apparent "pathogenicity" reflects opportunistic biochemical compatibility with human substrates, not evolved parasitism.

These findings demonstrate systematic taxonomic misclassification driven by anthropocentric interpretive frameworks that prioritize human-relevant observations over deep evolutionary relationships. *T. schoenleinii* is not a fungal pathogen but a "chemical fossil"—an ancient marine organism that has persisted for hundreds of millions of years. This challenges fundamental assumptions about the boundaries between ancient and modern life, and the understanding of the human biome.

Keywords

Trichophyton schoenleinii, chemical fossils, genomic stasis, evolutionary biology, dermatophyte evolution, REBLAST, sulfur metabolism, anthropocentric classification, taxonomic misclassification, basal eukaryotes, Cnidaria, Porifera, Ctenophora, Stinkhorns, primordial genomic architecture, chemical-genetic integration, marine origins, ancient life, phylogenetic misclassification, biofilm architecture, marine biochemistry, Ediacaran, living fossils.

Citation

Gjøvik, Ashley M. "Molecular Characterization of *Trichophyton schoenleinii* Reveals Systematic Affinities with Ancient Eukaryotes: Genetic Evidence for Functional and Taxonomic Misclassification," *The Journal of Decolonized Ecology and Evolution* 1, no. 1 (June 22 2025). DOI 10.5281/zenodo.15717921

Project Data

Journal: https://osf.io/ur79d/ DOI 10.17605/OSF.IO/UR79D

Issue One Data: https://osf.io/69whf/ DOI 10.17605/OSF.IO/69WHF

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Introduction

The classification of *Trichophyton schoenleinii* as a specialized human fungal pathogen represents one of the most significant taxonomic errors in medical mycology. For over a century, this organism has been studied, treated, and understood through the lens of anthropocentric medicine as a derived specialist that evolved sophisticated mechanisms to parasitize human hosts. This interpretive framework has obscured its true biological significance.

T. schoenleinii exhibits a constellation of characteristics that are inexplicable under conventional pathogen models. The organism produces unique microscopic "favic chandeliers"—complex, branched hyphal structures unknown in other dermatophytes but strikingly similar to the fractal branching patterns seen in deep-sea microbial mats, biomineralized marine structures, and soft coral colonies. These three-dimensional branching networks resemble the growth patterns used by marine filter-feeders and sessile organisms to maximize surface area for nutrient capture in fluid environments—not the morphology expected from a specialized human pathogen.

Beyond its marine-like morphology, *T. schoenleinii* demonstrates minimal conidial production, characteristically slow growth rates, and employs sophisticated sulfur metabolism involving cysteine dioxygenase (CDO1) and sulfite efflux systems (SSU1) typically found in extremophile organisms rather than superficial pathogens. The organism's growth strategy prioritizes structural complexity and metabolic sophistication over rapid reproduction—again resembling marine organisms adapted to stable, resource-limited environments rather than opportunistic terrestrial fungi.

Most significantly, *T. schoenleinii* exhibits strict human specificity despite possessing metabolically expensive keratin degradation machinery that appears energetically inefficient for simple parasitism. Its sulfur-handling strategies—including sulfite secretion for disulfide bond reduction and coordinated cysteine detoxification—resemble biochemical systems found in marine microbial mats and sulfur-cycling extremophiles, not typical fungal biology.

These anomalies suggest that *T. schoenleinii* is not a derived human-adapted specialist, but an ancient lineage whose association with humans reflects opportunistic biochemical compatibility rather than evolved parasitism. The human body provides an environment remarkably similar to ancient marine conditions—rich in sulfur compounds, salt, and complex structural proteins—that may allow ancient organisms to persist using their original biochemical toolkit rather than requiring evolutionary adaptation.

This study hypothesized that comprehensive molecular analysis of *T. schoenleinii* would reveal systematic affinities with ancient eukaryotic lineages rather than modern terrestrial fungi, and that the organism's unusual biochemical capabilities represent retained ancestral functions rather than recent pathogenic adaptations.

The BLAST analysis of *T. schoenleinii* sequences against diverse taxonomic databases confirms this prediction, revealing systematic high-confidence matches with evolutionarily ancient representatives across multiple major eukaryotic lineages while showing poor integration within its supposed fungal relatives.

These findings demonstrate how anthropocentric classification systems can systematically obscure deep evolutionary relationships, mistaking ancient biological persistence for derived pathogenic specialization. Rather than representing a sophisticated human-adapted pathogen, *T. schoenleinii* appears to be an evolutionary relic—an organism that has retained its original biological architecture while most other lineages underwent major evolutionary transitions. The results necessitate fundamental reconsideration of the organism's taxonomic placement and challenge basic assumptions about the relationship between evolutionary age and ecological niche.

Trichophyton schoenleinii

Current Classification and Human Associations

Trichophyton schoenleinii represents a distinctive member of the dermatophyte lineage, exhibiting unique morphological, physiological, and molecular characteristics that distinguish it fundamentally from other species within the genus (Iwasa et al. 2019; Gao et al. 2019). *T. schoenleinii* belongs to the *T. megninii complex* and is classified within Arthrodermataceae. The current taxonomic framework recognizes sixteen species within the genus *Trichophyton* (de Hoog et al. 2017; Zhan et al. 2018).

The organism is currently found in association with chronic scalp infections in humans, characterized by distinctive inflammation. *T. schoenleinii* exhibits strict host specificity as an obligate human-associated organism with limited environmental survival capabilities (Gao et al. 2019). This anthropophilic lifestyle contrasts with the broader host ranges and environmental persistence observed in many other dermatophyte species, raising important questions about the evolutionary relationships between different ecological strategies within the group.

The organism's ability to establish chronic, minimally inflammatory infections distinguishes it from many dermatophytes that trigger more acute inflammatory

responses (Iwasa et al. 2019). This pattern suggests distinct mechanisms of host interaction that may reflect different evolutionary approaches.

Genomic Architecture and Gene Content

The first draft genome sequence of *T. schoenleinii* strain T2s, completed in 2021, consists of 11 scaffolds containing 7,474 predicted genes with a total genome size consistent with other dermatophyte genomes (Ge et al. 2021; Zhan et al. 2018).

Genomic and transcriptomic analyses reveal that *Trichophyton* possesses a large number of secreted proteases, particularly M36 metalloproteases and subtilisins, many of which are specifically upregulated in keratin-rich conditions (Qiu et al. 2022; Xu et al. 2017). Interestingly, *T. mentagrophytes* also encodes cysteine protease inhibitors (CPI), which can block endogenous protease activity (Bajuk et al. 2011). This regulatory complexity (including feedback inhibition and phase-specific expression) resembles environmental adaptation more than simple host exploitation.

Transcriptomic profiling demonstrates that *T. schoenleinii* exhibits differential gene expression when cultured in keratin-containing media compared to standard protein sources (Ge et al. 2021). Notably, genes encoding proteases, cysteine dioxygenase, and acetamidase show markedly elevated expression levels during keratin utilization, indicating coordinated metabolic adaptations for keratin degradation.

Morphogenetic Features

T. schoenleinii produces distinctive "favic chandeliers"—branched, antler-like hyphal structures that represent a unique morphogenetic program among dermatophytes (University of Adelaide, n.d.; Grumbt et al. 2013). These complex three-dimensional structures, while morphologically striking, remain functionally enigmatic, though they may play important roles in tissue colonization or nutrient acquisition strategies.

T. schoenleinii exhibits minimal conidial production compared to other dermatophytes (University of Adelaide, n.d.). This characteristic distinguishes it from species that rely heavily on asexual conidia for dispersal and suggests alternative reproductive and transmission strategies.

The species demonstrates characteristically slow growth rates even under optimal laboratory conditions, indicating distinct metabolic properties compared to faster-growing dermatophytes (University of Adelaide, n.d.). This growth pattern may reflect underlying differences in central metabolism and energy allocation strategies.

Culture of *Trichophyton schoenleinii* and microscopy showing favic chandeliers. (University of Adelaide, n.d.)

Sulfur Metabolism and Keratin Degradation Mechanisms

Cysteine-Sulfite Pathway

T. schoenleinii employs a sophisticated sulfur metabolism pathway central to its keratinolytic capabilities The organism produces sulfite from environmental cysteine through the action of cysteine dioxygenase (Cdo1), with sulfite secretion facilitated by the sulfite efflux pump Ssu1. This biochemical pathway serves dual functions: detoxification of cysteine, which becomes toxic at elevated concentrations during keratin breakdown, and production of reducing agents essential for keratin structure modification. (Grumbt et al. 2013).

The cysteine dioxygenase enzyme catalyzes the oxidation of cysteine to cysteine sulfinic acid, ultimately yielding sulfite, sulfate, and taurine as terminal metabolites. Importantly, CDO1 gene expression in *T. schoenleinii* shows significant upregulation following keratin exposure, indicating coordinated metabolic responses to substrate availability (Kasperova et al. 2013; Ge et al. 2021).

Perhaps the most striking anomaly is Trichophyton's extensive sulfur metabolism, including:

- Secretion of sulfite to reduce disulfide bonds (Grumbt et al. 2013)
- Expression of cysteine dioxygenase (CDO1) to detoxify free cysteine (Grumbt et al. 2013)
- Use of sulfite efflux transporters (SSU1) to regulate extracellular redox (Silva-Rocha et al. 2021)

These pathways are tightly regulated and energetically costly, yet they have no obvious precedent in other superficial organisms found on humans. They are typically

associated with sulfur-cycling systems found in sediments, extremophiles, or deep-sea microbial ecosystems—not human-associated fungi. This strongly suggests a legacy metabolism that has persisted across ecological transitions.

Keratin Degradation Strategy

At the molecular level, *Trichophyton* exhibits significant specialization for keratin degradation. Comparative genomics of dermatophytes reveal an expanded repertoire of secreted proteases, particularly serine proteases and M36 metalloproteases, used to hydrolyze host structural proteins (Qiu et al. 2022). These enzymes are often co-expressed with genes involved in stress response, pH regulation, and transport systems, reflecting a tightly integrated strategy for tissue colonization and nutrient acquisition (Silva-Rocha et al. 2021).

The degradation of keratin by *T. schoenleinii* follows a coordinated two-phase mechanism (Grumbt et al. 2013):

- **Phase 1: Structural Weakening** - Secreted sulfite acts as a reducing agent, cleaving disulfide bridges (cystine bonds) that maintain keratin's compact, cross-linked structure. This sulfitolysis process renders the normally recalcitrant keratin matrix accessible to enzymatic attack.
- **Phase 2: Proteolytic Hydrolysis** - Following structural relaxation, secreted proteases systematically degrade the loosened keratin matrix into oligopeptides and amino acids suitable for uptake and metabolism (Monod 2008).

Metabolic Integration

The keratin degradation pathway demonstrates remarkable metabolic integration, where cysteine released during proteolysis is rapidly converted via the Cdo1-Ssu1 system, preventing cytotoxic accumulation while generating reducing equivalents for continued keratin attack (Grumbt et al. 2013). This creates a self-sustaining cycle that enables efficient utilization of keratin as both carbon and nitrogen source.

Unlike many superficial organisms that rely on simple sugars or surface biofilms, *Trichophyton* employs a metabolically intensive process to degrade keratin. This involves the secretion of sulfite to reduce disulfide bonds, the release and detoxification of cysteine, and a coordinated array of proteases and peptidases (Grumbt et al. 2013; Ciesielska et al. 2021). Given the low energy yield of keratin relative to the enzymatic cost required for its breakdown, the question remains why this strategy would evolve unless the organism were adapted to such substrates at a more fundamental ecological level.

Sulfur metabolism is another defining feature. *T. rubrum* secretes sulfite via the SSU1 transporter, enabling it to cleave disulfide bonds in keratin and expose the protein for enzymatic digestion (Grumbt et al. 2013). The fungus also expresses cysteine dioxygenase (CDO1) to manage cysteine toxicity during keratin degradation (Grumbt et al. 2013; Ciesielska et al. 2021). These systems suggest a highly evolved sulfur-handling strategy not commonly found in related ascomycetes or superficial organisms found on humans.

Their high substrate specificity for keratin and sulfur-rich matrices may reflect ancient ecological specialization rather than co-evolution with vertebrate hosts.

Proteomic studies show that keratin contact triggers widespread metabolic reprogramming in *Trichophyton*, including upregulation of the TCA cycle, glutathione metabolism, and amino acid synthesis—particularly sulfur-containing amino acids These findings support the view that keratin is not merely a nutritional source, but also a powerful environmental signal for Trichophyton, initiating a complex transcriptional and post-translational cascade (Ciesielska et al. 2021; Xu et al. 2017).

Despite extensive study of *Trichophyton schoenleinii* as an organism associated with human scalp conditions (NIH MedGEN UIDs 697784 and 547545), several aspects of its biology remain poorly explained under the conventional host-associated model. These features point to an unusually complex metabolic and ecological history that does not fully align with its superficial role as a keratin colonizer.

Evolutionary Relationships and Ecology

Ecologically, *Trichophyton* species are traditionally categorized into geophilic (soil-adapted), zoophilic (animal-associated), and anthropophilic (human-restricted) groups. While geophilic and zoophilic species are frequently recovered from soil and animal fur, anthropophilic strains exhibit a narrow host range and are rarely found in the external environment (Junior et al. 2022; Orlandi et al. 2021).

The combination of slow growth rates, minimal conidial production, and human host specificity represents a coherent ecological strategy that differs fundamentally from the rapid-growth, high-dispersal approaches characteristic of other dermatophyte species (University of Adelaide, n.d.).

Transcriptomic analysis reveals upregulation of pH-responsive signal transduction pathways and transcription factors during keratin utilization, suggesting sophisticated environmental sensing capabilities (Ge et al. 2021). These regulatory networks likely coordinate the complex metabolic

transitions required for successful keratin colonization and may represent targets for understanding dermatophyte pathogenesis mechanisms.

Spores of *Trichophyton* exhibit stress tolerance and gene expression profiles suggestive of metabolic "priming," rather than true dormancy. Transcriptomic analysis of *T. rubrum* conidia reveals high expression of oxidative stress enzymes, signaling regulators, and membrane transporters even in resting phases (Zaugg et al. 2009). These features resemble spore-forming or mat-forming organisms in fluctuating environments, not obligate parasites confined to stable host surfaces.

The organism is known to be difficult to culture including collapsing, becoming downy, no reverse pigmentation, and no macroconidia and microconidia are seen in routine cultures. Colonies are reported to be slow growing, and providing waxy or suede-like texture, with a deeply folded honey-comb-like tissue. (University of Adelaide, n.d.).

This tissue is often cream-colored to yellow to orange brown. Numerous chlamydospores may be present in older cultures, presenting characteristic hyphae. A few distorted clavate microconidia may be formed by some isolates when grown on polished rice grains (University of Adelaide, n.d.).

While *Trichophyton* does not form classical bacterial biofilms, its tissue colonization strategy shows remarkable parallels. Hyphal networks form tight substrate associations, modulate extracellular pH, and secrete a suite of redox-active enzymes and transporters to manipulate local microenvironments (Silva-Rocha et al. 2021). This is consistent with biofilm logic (persistent colonization of a recalcitrant substrate) and may resemble behavior of marine microbial mats.

Biological Anomalies Requiring Explanation

The constellation of characteristics exhibited by *T. schoenleinii*—sophisticated sulfur cycling, metabolically expensive keratin degradation, biofilm-like colonization strategies, stress-tolerance mechanisms, and apparent ecological inflexibility—presents a coherent but highly unusual biological profile. These features suggest an organism adapted to environmental conditions and metabolic strategies that extend far beyond simple opportunistic association with human hosts.

The organism's apparent reliance on sulfur-rich, structurally complex substrates, combined with its sophisticated environmental sensing and stress-tolerance mechanisms, points to an evolutionary history that may involve fundamentally different ecological contexts than those implied by its current taxonomic classification. These biological anomalies prompted comprehensive genetic analysis to determine whether *T. schoenleinii* represents an unusual adaptation within established fungal lineages or indicates more fundamental questions about its evolutionary origins and systematic placement.

Methodology

Investigative Framework for Complex Evolutionary Relationships

This investigation employed a systematic recursive analysis approach designed specifically for uncovering complex evolutionary relationships that may challenge conventional taxonomic boundaries. The investigative process itself exhibits fractal architecture to properly trace deep evolutionary connections across multiple analytical scales. (Gjøvik, June 10 2025).

Effective evolutionary developmental research requires recursive, branching analytical approaches where each unexpected finding opens new investigative pathways that demand systematic exploration. The discovery of *T. schoenleinii's* ancient marine affinities emerged through precisely this kind of fractal methodology.

Initial BLAST searches against standard databases revealed anomalous matches, prompting construction of specialized databases targeting the specific niche areas where unexpected relationships appeared. When those custom databases confirmed systematic patterns, validation through NIH Web BLAST provided an independent analytical branch. Subsequently, REBLAST (Recursive BLAST) analysis of the aligned sequences from matched organisms created additional investigative branches, each prompting systematic analysis, and potentially additional NIH and REBLAST validations. (Gjøvik, June 10 2025).

This represents four recursive layers of investigation—each building on leads generated by the previous layer and opening new analytical pathways. The fractal nature of proper evolutionary genomic methodology means that genuine biological relationships typically require multiple branching levels of validation before their significance becomes apparent. Single-pass analytical approaches, no matter how sophisticated, lack the recursive depth necessary to uncover complex evolutionary relationships that span deep time.

The methodology itself should exhibit the same recursive, self-similar structure across scales of investigation that characterizes the biological systems under study.

Dataset Construction and Primary Sequence Analysis

Database Assembly and Sequence Selection

A curated dataset of DNA gene sequences was assembled to evaluate the evolutionary landscape of basal 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.

To investigate the genetic relationships of *Trichophyton,* representative nucleotide sequences were obtained from NCBI GenBank and the European Nucleotide Archive (ENA). The analysis compiled separate multi-FASTA reference files for each taxonomic group, with reference sequence selection representing well-characterized taxa within each group of interest. Sequences included full or partial 18S rRNA genes, internal transcribed spacer (ITS1/ITS2) regions, 5.8S and 28S/25S rRNA regions, and mitochondrial DNA.

BLAST Analysis Parameters

This analysis performed pairwise nucleotide comparisons using BLASTn to assess potential homology between Trichophyton and sequences of varied organisms. Two search strategies were employed for each comparison:

1. **Standard BLASTn:** with high-stringency parameters (-evalue 1e-10)
2. **Discontiguous MegaBLAST:** optimized for cross-species comparisons (-task dc-megablast, -evalue 1e-5)

All searches generated output in tabular format (-outfmt 6) with the following fields: query and subject IDs, alignment length, percent identity, bit score, e-value, mismatch count, query and subject coverage, alignment coordinates, and gap openings.

To prevent false-positive self-alignments, output underwent post hoc filtering using PowerShell with a logical condition excluding self-hits.

```
powershell
Where-Object { ($_ -split "`t")[0]
-ne ($_ -split "`t")[1] }
```

The resulting alignments were evaluated for biological significance using two primary thresholds: percent identity ≥ 70% and alignment length ≥ 100 bp. Alignments failing to meet both criteria were considered insufficient to suggest functional or evolutionary homology.

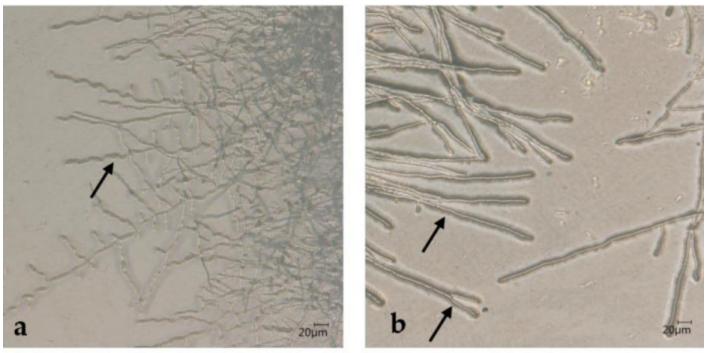
REBLAST Protocol and Recursive Validation

Sequence Selection for Analysis

At the time of publication, NIH and ENA listed 167 *Trichophyton schoenleinii* sequences, however only five exceed 1800 bp. The following were selected for systematic recursive analysis:

- **EF631620.1:** 5.8S 18S ITS1 ITS2 rRNA (2,316 bp, National Institute for Viral Disease Control and Prevention, Beijing China, 2016), used as the primary REBLAST query.
- **MT916930.1:** mtDNA complete genome (24,260 bp, Chinese Academy of Medical Sciences and Peking Union Medical College, 2024).
- **NC_082837.1 / OR361330.1:** mtDNA complete genome (24,260 bp, Universidade federal de Goias, 2023).
- **AJ430626.1:** mtDNA TRIS4 gene specific (2,525 bp, Charité – Universitätsmedizin Berlin, 2006).

The four largest remaining sequences (1509-1722 bp) were also included, representing gene-specific sequences related to sterol-14 alpha demethylase (ERG11B) genes. These returned only weak matches to *Neurospora crassa, Serpula lacrymans, Fusarium solani, and Fonticula alba* slime mold.



T. schoenleinii samples (Winter, P, et al 2023).

The matching ERG sequences were OQ536547.1 and OQ536548.1 collected in 1966 and 1972, then submitted in 2023. (Winter, P, et al 2023).

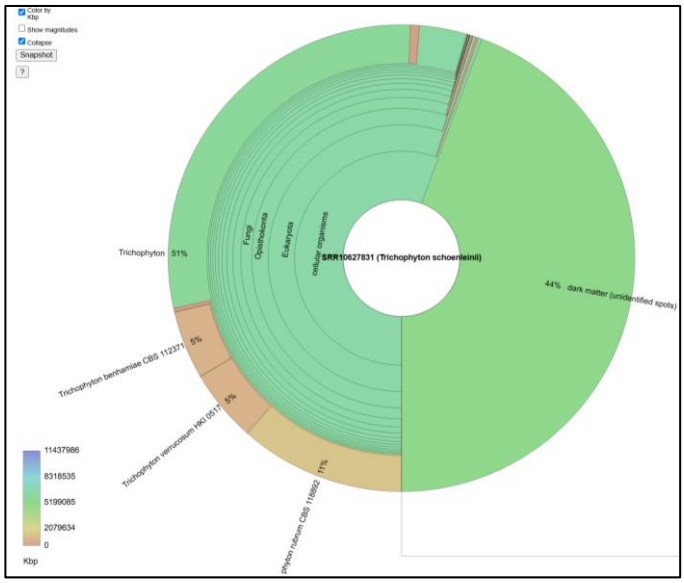
NIH Web BLAST Validation

The primary sequence (EF631620.1) was analyzed against core_nt, nt_euk, nt_others, nt_virus, and nt_prok databases. The virus database yielded 77 hits, including strong alignment to White Spot Syndrome Virus. The nt_prok database returned matches to archaea (*Hyperthermus*) and bacteria (e.g., *Pseudomonadota, Bacillota, Cyanobacteriota*).

Genome Run Analysis

Analysis included 15 SRA datasets for *Trichophyton schoenleinii* posted by the Chinese Academy of Medical Science and Peking Union Medical College in 2020-2021.

Genomes were sequenced with Illumina HiSeq X 10 4.4GB with 11.4G bases (SRX7319875) and PacBio Sequel 1.4GB sequence with 6.1G bases (SRX7319876). (Ge, et al, 2021).



Trichophyton schoenleinii SRA run SRR10627831.

Runs of these sequences returned self-hits, "dark matter," matches to humans, and less than 1% matches to various viruses, other fungi (*Aspergillus*), bacteria, amoeba (*Dictyostelia, Acytostelium*), Archaea (*Methanomicrobia* and *Thermoplasmata*), Stramenopiles (*Sargassaceae*), Choanoflagellata (*Salpingoeca*), Alveolata (*Eimeria, Plasmodium, Babesia, Ichthyophthirius*), plant (*Magnoliopsida*), and Cryptophyta (*Guillardia*). The genome runs reported results that were up to 44.4% "dark matter."

Analytical Framework and Limitations

Justification for Scaffold-Logic Approach

While BLASTn excels at detecting local sequence similarity, it lacks an evolutionary model and is not suited for placing taxonomically anomalous organisms. Tree-based methods (e.g., NCBI BLAST Tree Viewer) failed to resolve topologies across the dataset 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 the scaffold-logic approach employed. 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 requiring investigation even in the absence of broader phylogenetic synthesis. (Gjøvik, June 16 2025).

Comparative Analysis of Nuclear and Mitochondrial Sequences

Ribosomal DNA-ITS Locus Analysis

The focal sequences analyzed comprises a mitochondrial DNA and a contiguous stretch of ribosomal DNA, including partial 18S rRNA gene, complete internal transcribed spacer 1 (ITS1), complete 5.8S rRNA gene, and partial internal transcribed spacer 2 (ITS2). This locus is widely used in eukaryotic systematics due to its dual composition of highly conserved (18S, 5.8S) and rapidly evolving (ITS1, ITS2) regions, providing both deep and fine-scale phylogenetic signal.

BLAST analysis of this rDNA-ITS sequence revealed unexpectedly high sequence similarity (≥84% identity; bit scores ≥1800) across early-diverging eukaryotic lineages. Top hits were recovered from basal opisthokonts (*Capsaspora owczarzaki, Monosiga ovata, Aphelidiaceae spp.*), early-branching metazoans including demosponges (*Geodia barretti, Axinella polypoides*), cnidarians (*Hydra magnipapillata, Turritopsis spp.*), and ctenophores (*Beroe ovata*). Additionally, hits extended into deep protist lineages including *Trimastix, Jakoba,* and *Oxnerella micra*.

These observations support the hypothesis that the focal organism retains elements of an ancestral, less modularized genomic system—akin to a genomic "runtime environment"—which may predate the emergence of modern gene regulatory organization seen in derived animals. This fractal investigative approach proved essential for revealing the systematic ancient marine signature that conventional linear analytical workflows would have missed entirely.

Results

T. schoenleinii Exhibits Systematic Affinities with Ancient Marine Life

BLAST analysis of *T. schoenleinii* sequences revealed an unexpected pattern that challenges fundamental assumptions about this organism's evolutionary relationships. Rather than matching modern terrestrial fungi as predicted by its current taxonomic classification, *T. schoenleinii* shows systematic high-confidence genetic similarities to some of Earth's most ancient marine lineages.

The Ancient Marine Signature

The most striking finding is that *T. schoenleinii* consistently matches the same assemblage of evolutionarily ancient organisms across multiple independent genetic sequences. The organism exhibits greater than 85% genetic identity across alignments exceeding 1700 base pairs with ancient sponges, including both demosponges such as *Axinella polypoides, Geodia barretti,* and *Parahigginsia* species, as well as calcareous sponges from the *Clathrinida* order. These matches are characterized by bit scores exceeding 1900 and E-values of zero, indicating extremely high statistical confidence.

Strong genetic affinities also extend to early cnidarian lineages, including comb jellyfish (*Beroe ovata*), immortal jellyfish (*Turritopsis* species), sea anemones, and various coral species. Choanoflagellates (the single-celled protists most closely related to animals) show high-confidence alignments with *T. schoenleinii* sequences, as do tardigrades and slime molds.

Most significantly, these relationships are corroborated by mitochondrial DNA analysis, with extensive matches to tardigrade mitochondrial sequences extending up to 720 base pairs. The systematic appearance of this ancient assemblage across both nuclear ribosomal RNA and mitochondrial DNA indicates genuine evolutionary relationships rather than technical artifacts or random sequence similarity.

Modern Fungi Show Poor Integration with *T. schoenleinii*

In stark contrast to its affinities with ancient marine life, *T. schoenleinii* demonstrates remarkably poor integration with its supposed fungal relatives. This pattern becomes evident when examining the provenance and quality of apparent fungal matches. The strongest seeming fungal similarities consistently derive from environmental samples with complex biological contexts rather than well-characterized pure cultures.

Environmental Contamination Explains Apparent Fungal Matches

The top-scoring apparent fungal matches reveal a systematic pattern of environmental contamination or mixed biological samples. *Emydomyces testavorans*, which shows high sequence similarity to *T. schoenleinii,* was isolated from turtle lesion tissue containing microbial, fungal, and environmental DNA. *Aspergillus citrinoterreus* was sequenced from human lung mucus, inherently contaminated with multiple organismal sources. *Talaromyces rugulosus* was isolated from air samples with unknown co-isolated material, and subsequent genome analysis revealed 87.49% "dark matter" with only 2.04% matching the supposed organism identity.

When genome run data is examined systematically, these apparent fungal matches consistently show high proportions of unidentified sequences (44.4-92.9% "dark matter"), significant bacterial contamination, and frequent presence of archaeal sequences, particularly Thermoplasmatales. This pattern strongly suggests that apparent fungal similarity reflects contamination from the same ancient organisms that *T. schoenleinii* genuinely resembles, rather than legitimate fungal relationships.

Weak Affinities with Characterized Fungal Lineages

Standard BLAST+ analysis against curated fungal databases yielded limited matches primarily to other taxonomically problematic organisms. *T. schoenleinii* shows poor sequence similarity to well-characterized dermatophytes and weak integration within terrestrial ascomycete families. The organism's supposed classification within fungal lineages appears to reflect superficial morphological similarities rather than fundamental genetic relationships.

A Systematic Pattern Targeting Ancient Lineage Representatives

The genetic matches between *T. schoenleinii* and ancient organisms follow a distinctive systematic pattern that suggests deep evolutionary relationships rather than stochastic similarity. These alignments consistently target the most evolutionarily ancient representatives within each major taxonomic group, rather than derived or specialized modern forms.

Within sponge lineages, matches occur with basal demosponges and early calcareous sponges that represent some of the most ancient animal architectures. Among cnidarians, the strongest affinities appear with early-diverging forms like ctenophores and primitive hydrozoans rather than derived coral or jellyfish species. The choanoflagellate matches span multiple genera representing the base of the animal tree, while protist affinities extend to deep-branching eukaryotic lineages including *Trimastix*, *Jakoba*, and *Oxnerella micra*.

This systematic conservation across phylogenetically distant lineages cannot be explained through conventional vertical inheritance or horizontal gene transfer. The pattern suggests that *T. schoenleinii* preserves molecular architecture from before major eukaryotic divergences, consistent with retention of ancient chemical systems that preceded modern genetic organization.

Cross-Kingdom Molecular Conservation Indicates Ancient System Inheritance

Perhaps most significantly, identical molecular signatures

appear across taxonomically distant organisms within the ancient marine assemblage. The same ribosomal RNA sequences that match *T. schoenleinii* also appear in sponges, cnidarians, choanoflagellates, and ancient protists with remarkably similar identity values and alignment characteristics. This cross-kingdom conservation cannot be explained through recent evolutionary processes and suggests shared inheritance of molecular systems that predate modern taxonomic boundaries.

The mitochondrial DNA relationships provide independent validation of these patterns. Extensive mitochondrial similarity between *T. schoenleinii* and tardigrades, cnidarians, and basal eukaryotes confirms that the observed relationships reflect genuine systematic affinities rather than ribosomal conservation artifacts. The presence of both nuclear and mitochondrial molecular signatures pointing to the same ancient assemblage provides compelling evidence for deep evolutionary relationships that transcend current taxonomic classifications.

These results demonstrate that *T. schoenleinii* represents a fundamentally misclassified organism whose true evolutionary affinities lie with ancient marine lineages rather than modern terrestrial fungi, necessitating reconsideration of its biological identity and evolutionary significance.

Validation Through Independent REBLAST Analysis

To confirm these unexpected relationships and validate the systematic patterns observed, additional verification was performed using recursive BLAST approaches against NIH databases with key representative sequences.

REBLAST: Trichophyton

The top matching RNA sequence from *T. schoenleinii* (EF631620.1) was subjected to REBLAST analysis using NIH Web BLAST against specialized databases. When queried against the core_nt and nt_euk databases, this sequence matched primarily with Arthrodermataceae and showed limited hits to other Ascomycota across Onygenales and Aspergillaceae. Significantly, these results did not include the top fungal mitochondrial matches that emerged in the primary analysis.

More revealing patterns emerged when the same *T. schoenleinii* sequence was queried against broader databases. Results against the nt_other database returned a high-confidence match (1560 bit score, E-value of 0, 82.3% identity) to *Mallomonas*, a silica-adorned single-cell organism. Against the nt_virus database, the sequence showed substantial similarity (877 bit score, E-value of 0, 78.8% identity) to White Spot Syndrome Whispovirus.

The prokaryotic database (nt_prok) revealed extensive matches to marine-associated microorganisms, including uncultured archaea captured from Pacific Ocean depths of 120m and 790m, and various bacteria including *Edwardsiella, Lyngbya, Micrococcus, Vibrio, Hyperthermus, Klebsiella, Clostridium, Staphylococcus, Azotobacter,* and *Hydrogenophaga*. This prokaryotic signature aligns with deep marine environments rather than terrestrial fungal habitats.

REBLAST: *Beroe* and *Parahigginsia*

Reciprocal validation was performed using sequences from the ancient marine organisms that showed high similarity to *T. schoenleinii*. REBLAST of a top-matching *Beroe ovata* sequence (OR921247.1, RNA and ITS1) largely recapitulated the patterns observed with *T. schoenleinii*. Against core_nt and nt_euk databases, results returned only other comb jellies with no fungal matches, confirming the absence of fungal relationships in this ancient assemblage.

The nt_other database returned both *Mallomonas* and the fungus *Conlarium*, while prokaryotic matches (nt_prok) showed strong similarities to the same bacterial genera identified in *T. schoenleinii* analysis: *Klebsiella, Hydrogenophaga,* and *Clostridium*, with additional moderate matches to *Hyperthermus, Microcystis, Micrococcus, Lyngbya, Caldora, Staphylococcus, Ehrlichia, Vibrio, Halomonas, Azotobacter,* and *Citrobacter*.

REBLAST analysis of a representative *Parahigginsia* sequence (PP266643.1, RNA and ITS1) yielded similar results to both *T. schoenleinii* and *Beroe* analyses, with all nt_euk and core_nt results returning Demospongiae taxa including *Suberites, Spheciospongia, Halichondria, Tethya, Axos,* and *Spirastrella*. The prokaryotic signature remained consistent across all three organisms.

Genetic Affinities with Stinkhorn Lineages

BLAST+ analysis revealed high-confidence matches between *T. schoenleinii* rRNA and mtDNA sequences and various Stinkhorn taxa, including *Pseudocolus/Tribrachia*—a taxon previously reclassified as a marine demosponge (Gjøvik, June 16 2025). *T. schoenleinii* and *Pseudocolus/Tribrachia* share alignments up to 1704 bp, with bit scores reaching 2086, 88% identity, and e-values of 0.

T. schoenleinii exhibits strong matches with multiple Stinkhorn species with alignments exceeding 1600 bp, bit scores above 1900, e-values of 0, and identity percentages of 87% or greater. These include *Phallus impudicus, Mutinus caninus,* and *Aseroe coccinea,* as well as Bird's Nest fungi *Crucibulum laeve, Nidula niveotomentosa,* and *Mycocalia denudata*. Mitochondrial DNA similarities were confirmed with *Phallus indusiatus, Phallus dongsun,* and Bird's Nest fungi *Cyathus jiayuguanensis.*

Both *T. schoenleinii* and *Pseudocolus/Tribrachia* exhibit identical molecular signatures characterized by strong matches to non-metazoan opisthokonts, basal metazoans, Holozoa, Choanoflagellates, Tardigrada, and early-diverging fungal clades. Notably absent are strong matches to bilaterian animals, suggesting these organisms do not engage with compiled gene regulatory networks that characterize modern modular body plans.

The systematic appearance of this ancient marine assemblage (ctenophores, scyphozoans, demosponges, calcareous sponges, choanoflagellates, and related protists) in both organisms confirms the diagnostic genomic signature initially identified in *Pseudocolus/Tribrachia* analysis. This pattern occurs despite poor phylogenetic integration within their supposed taxonomic families.

Extended BLAST analysis confirmed that *T. schoenleinii* exhibits genomic alignments very similar to *Pseudocolus/Tribrachia* across four key categories: (1) Stinkhorn affinities with high-confidence matches to Phallaceae, (2) ancient marine assemblage alignments, (3) protist connections including choanoflagellates and Tunicaraptor, and (4) deep-sea indicators including extremophile and vent-associated organisms.

Cross-Validation Confirms Systematic Ancient Marine Signature

These REBLAST analyses provide crucial validation that *T. schoenleinii, Beroe,* and *Parahigginsia* share genuine molecular similarities that extend beyond superficial sequence matches. The consistent appearance of the same prokaryotic assemblage across all three organisms, combined with shared matches to *Mallomonas* (a silica-adorned protist) and absence of legitimate modern fungal relationships, confirms that these organisms represent components of an ancient biological system that predates modern taxonomic boundaries.

Discussion

Fundamental Misclassification Revealed by Molecular Analysis

The molecular analysis of *Trichophyton schoenleinii* reveals a genomic profile fundamentally inconsistent with its classification as a human fungal pathogen. Instead of matching terrestrial fungi as expected, *T. schoenleinii* shows systematic high-confidence genetic similarities with Earth's most ancient marine organisms—sponges, jellyfish, choanoflagellates, tardigrades, and early protists.

This pattern cannot be dismissed as coincidence. The matches include high-confidence alignments (>1800 bit scores, E-values of 0, >85% identity across >1700 base pairs) spanning multiple independent genetic systems. Critically, both nuclear ribosomal RNA and mitochondrial DNA show the same ancient marine signature. Since mitochondrial DNA evolves rapidly and rarely shows cross-phylum similarity without genuine evolutionary relationship, this provides independent confirmation of authentic ancient affinities.

A crucial validation comes from examining supposed "fungal" matches. The strongest apparent fungal similarities consistently derive from environmental samples, contaminated cultures, or host-associated isolates rather than pure fungal cultures. When these contaminated sources are excluded, *T. schoenleinii* shows poor integration within fungal lineages while maintaining strong affinities with ancient marine organisms. This suggests the organism has been systematically misclassified based on where humans encounter it rather than what it actually is.

Ancient Marine Heritage and Biochemical Specialization

The systematic pattern of ancient marine affinities explains *T. schoenleinii*'s unusual biology. The organism exhibits sophisticated sulfur metabolism, biofilm-like growth strategies, and complex branching morphology—all characteristics typical of marine environments rather than terrestrial fungi. Its metabolically expensive keratin-degradation machinery mirrors biochemical systems found in organisms that process sulfur-rich marine substrates.

The timing of these relationships provides decisive evidence. The organisms showing strongest genetic similarity to *T. schoenleinii* evolved during periods when terrestrial environments were largely uninhabitable. Marine origins therefore represents the most parsimonious explanation for these molecular affinities, rather than assuming independent evolution of identical biochemical systems.

Chemical Fossil Pattern Recognition

T. schoenleinii exhibits remarkable genetic similarity to Stinkhorn fungi, particularly *Pseudocolus*, which recent analysis revealed to be a misclassified marine sponge rather than a terrestrial fungus (Gjøvik, June 16 2025). Both organisms share nearly identical molecular signatures: high-confidence matches to ancient marine assemblages, poor integration within their supposed taxonomic families, and systematic affinities with the same ancient lineage representatives.

This parallel suggests both organisms represent "chemical fossils"—living systems that have preserved ancient

biological organization while most lineages underwent major evolutionary transitions. Rather than adapting to new environments through genetic reorganization, these organisms appear to have maintained their original biochemical toolkit, finding new ecological niches that match their ancient capabilities.

The concept emerges from recognizing that early life developed comprehensive chemical management systems before modern genetic organization evolved. Most lineages later streamlined these systems, but some preserved the original architecture. These chemical fossils retain access to ancient biochemical capabilities that compiled organisms have lost, explaining their often remarkable but puzzling abilities.

Implications for Evolutionary Biology and Classification

These findings reveal fundamental limitations in observation-based taxonomic frameworks that prioritize human-relevant characteristics over deep biological relationships. *T. schoenleinii*'s association with human scalp infections led to its interpretation as a "pathogen" with presumed modern origins, obscuring recognition of its ancient characteristics and evolutionary significance.

The systematic misclassification illustrates broader problems with anthropocentric science. Stinkhorns were named after human anatomy (*Phallaceae*) and classified as terrestrial fungi based on where humans found them, preventing recognition of their marine scaffold architecture for centuries. Similarly, many organisms currently classified as "human pathogens" may represent ancient lineages whose biochemical capabilities happen to be compatible with human biological systems.

T. schoenleinii's apparent "pathogenicity" likely reflects opportunistic biochemical compatibility rather than evolved parasitism. Human bodies provide environments remarkably similar to ancient marine conditions—rich in sulfur compounds, salt, and complex structural proteins—allowing ancient organisms to persist using their original biochemical toolkit without requiring evolutionary adaptation.

Toward Chemistry-Based Taxonomy

Moving beyond anthropocentric classification requires prioritizing biochemical capabilities, metabolic pathways, and genomic architecture over ecological associations or human interactions. Chemistry-based taxonomic frameworks could reveal additional ancient lineages currently misclassified based on superficial similarities rather than fundamental biological relationships.

The discovery of chemical fossils at both macroscopic (marine sponges misclassified as terrestrial fungi) and microscopic (*T. schoenleinii*) scales suggests this preservation of ancient architecture occurs across multiple environments and scales. Systematic application of chemical fossil diagnostic criteria—morphological anomalies, behavioral inconsistencies, and taxonomic isolation—could identify additional examples of preserved ancient biological organization.

The identification of *T. schoenleinii* as a chemical fossil also opens new avenues for understanding early eukaryotic evolution. If this organism genuinely preserves ancient biological organization, it represents a molecular window into evolutionary states that preceded modern biological modularity, potentially informing reconstruction of early eukaryotic biochemistry and developmental capabilities.

Revolutionary Implications for Biology

This research demonstrates that revolutionary biological discoveries can emerge from careful reexamination of familiar organisms using molecular rather than observational approaches. *T. schoenleinii* has been studied for decades as a medical curiosity, yet its true evolutionary significance remained hidden until approached through comprehensive genetic analysis rather than pathogen-focused frameworks.

The systematic discovery and characterization of chemical fossils promises to transform our understanding of early life, revealing that the transition from chemical to biological complexity may be preserved not only in geological records, but in the genomes of living organisms that never fully transitioned from ancient chemical systems to modern biological modularity.

Marine Origins and Ancient System Inheritance

Despite being classified and treated as a superficial pathogen, *Trichophyton* exhibits a range of molecular and ecological behaviors that align with ancient marine ecosystems rather than host-adapted parasitism. This section proposes that *Trichophyton* represents a legacy lineage originally adapted to metabolize disulfide-rich biological matrices in marine settings, and that its apparent "pathogenicity" reflects opportunistic biochemical compatibility rather than evolved parasitism.

Keratin as a Modern Surrogate for Ancient Substrates

Keratin, the primary target of *Trichophyton*, is structurally unusual among biological macromolecules. It is characterized by dense disulfide crosslinking, high cysteine content, and extreme mechanical resistance to enzymatic

digestion. These properties make it an unlikely substrate for terrestrial fungi unless they are specialized to handle oxidative sulfur chemistry (Grumbt et al. 2013; Ciesielska et al. 2021).

Marine organisms produce proteinaceous extracellular matrices that exhibit remarkably similar biochemical profiles. Cysteine-rich domains, disulfide-bonded structural peptides, and sulfur-modified secretions are common in marine ECMs and mucus sheaths (Agarwal et al. 2024; Liu et al. 2022). Certain marine peptides, such as fused bicyclic cysteine-knot toxins, mimic keratin's folding resistance and redox potential (Agarwal et al. 2024). Ancient keratinases likely evolved in marine contexts, targeting structural proteins with chemistries identical to modern keratin.

Sulfur Handling as Marine Ecological Legacy

The defining feature of *Trichophyton's* keratin degradation is its highly integrated sulfur metabolism—a sophisticated system with little parallel in typical terrestrial fungi. This includes sulfite secretion via SSU1 to break disulfide bridges, cysteine detoxification by CDO1, and tightly regulated redox stress responses (Grumbt et al. 2013; Ciesielska et al. 2021).

Marine microbial mats routinely operate under similar redox constraints, where sulfur species are used in both energy metabolism and structural modification (Wasmund et al. 2017; Vliet et al. 2020). Sulfate-reducing and sulfur-oxidizing bacteria inhabit disulfide-rich environments and display matrix-degrading behavior remarkably similar to *Trichophyton*. The presence of these capabilities in a supposed superficial pathogen suggests Trichophyton is not innovating—it is replaying ancient marine biochemistry triggered by structural similarity between keratin and ancestral substrates.

Morphological and Biochemical Echoes of Marine Life

Multiple lines of evidence support marine origins beyond sulfur metabolism. The organism's hyphal branching mirrors mat-forming organisms and sessile biofilm behavior (Silva-Rocha et al. 2021). Its stress-response gene expression in resting phases resembles organisms primed for transient colonization of redox-variable surfaces rather than stable parasitism (Zaugg et al. 2009). Most significantly, the distinctive "favic chandeliers" exhibit fractal branching patterns extremely similar to deep-sea microbial mats, biomineralized marine structures, and soft coral colonies—morphology designed for maximizing surface area in fluid environments, not terrestrial skin colonization.

Evolutionary Reinterpretation: Chemical Fossils and System Inheritance

The systematic molecular affinities between *T. schoenleinii* and ancient marine lineages represent a pattern consistent with organisms that have preserved their original biological architecture while most lineages underwent major evolutionary transitions. This concept—organisms functioning as "chemical fossils" that retain ancient biochemical systems—is detailed in a companion theoretical framework (Gjøvik, June 23 2025).

The identification of *T. schoenleinii* as a chemical fossil validates predictions that such organisms would exhibit characteristic molecular signatures: systematic high-confidence alignments with ancient marine assemblages despite poor integration within their supposed modern taxonomic families. This same pattern was recently confirmed in *Pseudocolus fusiformis*, which molecular analysis revealed to be the marine demosponge *Tribrachia fusiformis* rather than a terrestrial fungus (Gjøvik, June 16 2025).

From Parasitism to Biochemical Refugium

The apparent host specificity of *T. schoenleinii* likely represents structural compatibility rather than co-evolution. Human skin and nails offer a chemically familiar niche: keratin, sulfhydryl exposure, and mildly reducing microenvironments that biochemically resemble ancient marine conditions. Rather than a pathogen in the classical sense, *T. schoenleinii* appears to be an ecological refugee—a sulfur-adapted marine organism whose biochemical niche happens to overlap with human biology.

The persistent resistance of *T. schoenleinii* to standard antifungal therapies becomes comprehensible when viewed through the lens of its true evolutionary identity. Antifungal agents target cellular processes specific to true fungi—ergosterol synthesis, chitin formation, and fungal-specific metabolic pathways.

Given that *T. schoenleinii* exhibits genetic affinities with tardigrades and ancient marine organisms rather than terrestrial fungi, resistance to ergosterol-targeting antifungals like terbinafine and itraconazole represents predictable biochemical incompatibility rather than acquired resistance. Tardigrades are renowned for surviving extreme chemical exposures, radiation, and desiccation through cryptobiotic states and robust stress-response systems. An organism with substantial tardigrade genetic heritage would be expected to exhibit similar resilience to chemical intervention.

Current treatment protocols may inadvertently exacerbate

inflammation through biochemical antagonism rather than therapeutic effect. Standard treatments include selenium sulfide and zinc pyrithione shampoos, compounds that disrupt sulfur metabolism—precisely the biochemical pathway this analysis identifies as central to *T. schoenleinii*'s ancient marine heritage. Rather than eliminating the organism, these sulfur-disrupting agents likely trigger defensive metabolic responses in an organism whose fundamental biology revolves around sulfur chemistry.

The characteristic chronic inflammation may therefore reflect ongoing biochemical warfare between human immune responses and an organism defending its metabolic integrity against chemical attack, rather than active pathogenic aggression. Clinical observations consistently report that lesions become more inflamed and painful during treatment periods, a pattern more consistent with defensive stress responses than therapeutic progress.

The distinction is critical: treating an ancient chemical specialist with broad-spectrum metabolic disruptors may transform a relatively stable biochemical refugee into an actively distressed organism producing inflammatory compounds as stress metabolites.

The marine origins hypothesis transforms *T. schoenleinii* from a puzzling medical curiosity into a molecular window onto early eukaryotic evolution—a living system that preserves biochemical capabilities from marine environments that preceded complex terrestrial life.

Beyond Anthropocentric Classification

The Fundamental Problem of Human-Centered Biology

Current taxonomic frameworks suffer from a systematic bias that prioritizes human-relevant observations over fundamental biological relationships. This anthropocentric approach has created widespread misclassification of ancient organisms, obscuring their true evolutionary significance and preventing recognition of deep biological principles.

The case of *T. schoenleinii* exemplifies this problem perfectly. Because humans encounter this organism on scalp tissue, it was automatically classified as a "human pathogen" and studied exclusively within medical frameworks. This human-centric interpretive lens prevented recognition of its ancient marine heritage for over 150 years, despite clear molecular and biochemical evidence.

The Stinkhorn Precedent: Centuries of Hidden Marine Architecture

This pattern of anthropocentric misclassification extends far beyond microscopic organisms. Stinkhorn fungi provide a striking macroscopic example of how profoundly human bias distorts biological understanding. These organisms were formally classified as terrestrial fungi by Linnaeus in 1753, based entirely on where humans found them and their superficial resemblance to human anatomy. The very name *"Phallus"* reflects this anthropomorphic bias, immediately constraining scientific interpretation within frameworks of terrestrial organisms and human sexuality.

Yet recent molecular analysis reveals that organisms like *Pseudocolus fusiformis* are actually basal, marine demosponges (*Tribrachia fusiformis*), not terrestrial fungi. Their complex three-dimensional architecture represents ancient marine scaffold engineering that has been hiding in plain sight for centuries. Stinkhorns have appeared on the cover of mycological publications for decades—a marine organism masquerading as the archetypal fungus because we classified them based on human observations rather than biological reality.

The historical irony reaches profound depths when we consider that Stinkhorns represent surviving Ediacaran biota—among Earth's most ancient complex multicellular organisms—yet Darwin's own family was destroying these specimens under cover of darkness due to perceived morphological resemblance to human reproductive anatomy (Raverat, G., 1952).

This remarkable case illustrates how anthropocentric interpretive frameworks have led to the systematic destruction and scientific neglect of our planet's most significant evolutionary heritage based on superficial anatomical associations. These weren't sexual aberrations requiring destruction—they were ancient marine engineers, and we failed to recognize their sophisticated biological architecture for centuries.

From Pathogen to Chemical Refugee

The *T. schoenleinii* case study demonstrates how this bias operates at the molecular level, revealing the philosophical poverty of pathogen-based classification. The traditional approach follows a simple anthropocentric logic: organisms found on humans must be human pathogens, and human pathogens must be modern parasitic specialists. This framework immediately constrains interpretation within medical rather than evolutionary contexts.

A chemistry-based approach asks fundamentally different

questions that prioritize biological processes over human associations. Rather than assuming parasitic specialization, this perspective examines what specific substrates the organism metabolizes, which biochemical pathways it utilizes, what other organisms employ identical metabolic strategies, and what chemical environments support its growth. This reframing reveals that *T. schoenleinii's* apparent "pathogenicity" reflects its ability to process biochemical substrates that happen to be available in human tissues—not evolutionary adaptation to human hosts.

The profound realization emerges that human bodies provide environments remarkably similar to ancient marine conditions: rich in sulfur compounds, salt, and complex structural proteins. Rather than a pathogen in the classical sense, *T. schoenleinii* appears to be a chemical refugee—an ancient marine organism whose biochemical niche happens to overlap with human biology. Its ancient genomic signature indicates it was processing similar chemical substrates long before humans existed, making humans the recent arrival in this biochemical relationship, not the evolutionary target.

The Philosophical Revolution: Chemistry Over Ecology

Moving beyond anthropocentric classification requires a fundamental philosophical shift from ecological associations to molecular capabilities. This chemistry-first framework prioritizes genomic architecture and phylogenetic placement alongside biochemical pathway characterization, metabolic substrate specificity, and chemical environment requirements. Morphological features become interpreted through chemical constraints rather than superficial similarities, while ecological associations must demonstrate genuine chemical compatibility rather than mere spatial coincidence.

This philosophical reorientation transforms supposed anomalies into windows into ancient biological processes. Many organisms currently classified as "human-associated" may represent preserved archives of pre-genetic chemical organization that operated long before complex multicellular life existed. Rather than viewing human-associated organisms as necessarily modern or parasitic, chemistry-based analysis reveals ancient biochemical capabilities preserved in organisms that find compatible substrates in human biological systems.

These discoveries suggest that many supposed "pathogens" actually represent ancient chemical systems preserving pre-genetic metabolic pathways, environmental refugees from marine or subsurface environments that opportunistically colonize chemically familiar human habitats, or metabolic fossils retaining ancient biochemical capabilities lost in most modern organisms. The human body becomes not a target for parasitic specialization, but a chemical sanctuary for ancient life seeking familiar biochemical conditions.

Breaking Free from Observational Constraints

The systematic misclassification of both macroscopic Stinkhorns and microscopic *T. schoenleinii* reflects fundamental limitations in observation-based taxonomy developed before molecular tools became available. These anthropocentric frameworks create conceptual barriers that prevent recognition of deep evolutionary relationships and ancient biochemical capabilities, forcing ancient organisms into modern taxonomic categories that obscure their true biological significance.

The philosophical shift from "how does this relate to humans?" to "what fundamental chemistry does this organism perform, and who else performs the same chemistry?" transforms our understanding of life's diversity. This perspective reveals that many organisms classified as modern human-associated species actually represent preserved windows into ancient biological organization, challenging our basic assumptions about the relationship between evolutionary age and ecological niche.

The evidence demonstrates that systematic application of chemistry-based classification criteria reveals chemical fossils systematically misclassified throughout existing taxonomic frameworks. The fundamental reorganization of early life understanding will emerge not from novel discoveries, but from recognizing that ancient biological complexity has persisted within established taxonomic systems while remaining obscured by human-centered observational biases.

This realization carries profound implications for our understanding of life's continuity. The ancestral forms have maintained continuous presence within our scientific purview, hidden not by rarity or extinction, but by the philosophical limitations of anthropocentric classification. The revolution in evolutionary biology may come from recognizing what has been with us all along, awaiting liberation from the conceptual constraints of human-centered taxonomy.

Future Directions

The identification of *T. schoenleinii* as a chemical fossil necessitates fundamental changes in research approach and opens multiple critical research avenues that could transform our understanding of early eukaryotic evolution and biological classification.

Immediate Validation and Characterization

The most pressing research priority involves biochemical validation of the marine origins hypothesis through comparative enzyme analysis. If *T. schoenleinii* genuinely preserves ancient marine biochemistry, its keratinases should exhibit greater similarity to marine extracellular matrix-degrading enzymes than to terrestrial fungal keratinases, revealing conserved active sites and substrate recognition domains. Functional validation through growth assays on marine ECM analogs—including sponge collagen, cnidarian mesoglea components, and synthetic disulfide-rich marine peptides—could provide direct evidence for retained marine biochemical capabilities.

Detailed characterization of the CDO1-SSU1 sulfur-handling pathway, including enzyme kinetics and regulatory networks, would reveal whether this represents optimized marine chemistry rather than derived terrestrial adaptation. Comparison with sulfur-cycling marine extremophiles could illuminate the deep evolutionary origins of these sophisticated metabolic systems.

Environmental ecology investigation represents another critical priority. The assumption that *T. schoenleinii* is "human-specific" likely reflects observational bias rather than biological reality. Comprehensive environmental sampling, particularly in marine and transitional environments, could reveal natural reservoirs and illuminate the full scope of ecological relationships that medical frameworks have obscured.

Methodological Revolution

The discovery of chemical fossils demands fundamental innovations in biological methodology. Chemistry-first classification databases must prioritize biochemical pathway analysis, metabolic substrate specificity, and chemical environment requirements over observational characteristics. This framework would integrate proteomics, metabolomics, and environmental chemistry data to reveal functional relationships that traditional morphology-based approaches systematically miss.

Provenance-Aware Database Architecture

A critical infrastructure challenge revealed by this study involves the systematic exclusion of host and environmental metadata from sequence search results. Current approaches treat sequence identity and taxonomic classification as discrete, authoritative labels when they should be understood as endpoints of complex provenance chains that carry essential biological context.

A robust solution would implement hierarchical provenance tracking where every sequence entry maintains complete derivation history: the target organism, the host or environment from which it was isolated, the isolation method, the degree of purification achieved, and any known co-contaminants or symbionts. Rather than single taxonomic assignments, sequences would carry structured metadata indicating both their attributed identity and their biological context—distinguishing, for example, between a "pure culture of Organism X" and "Organism X isolated from Host Y with Method Z."

Search interfaces must surface this provenance data as a first-class result component, not buried in optional metadata fields. BLAST results should prominently display not only "85% identity to *Emydomyces testavorans*" but "85% identity to *Emydomyces testavorans* [isolated from *Actinemys marmorata*, culture-based, 2016]." This contextual information is as scientifically relevant as the sequence similarity itself and should be equally visible to researchers making interpretive decisions.

Furthermore, similarity scoring algorithms should incorporate provenance-weighted relevance metrics. Matches between sequences with similar ecological or host contexts could receive adjusted confidence scores, while matches between sequences from vastly different biological contexts (e.g., marine environmental samples vs. vertebrate-associated cultures) could be flagged for additional scrutiny rather than treated as straightforward taxonomic assignments. This approach would help distinguish between genuine sequence conservation across environments and potential cross-contamination or misattribution artifacts.

Such a framework would transform sequence databases from static repositories of decontextualized molecular data into dynamic resources that preserve and propagate the biological relationships underlying genomic diversity. This shift is essential for advancing fields that depend on accurate host-microbe, environment-organism, and cross-kingdom relationship inference, and represents a critical foundation for trustworthy comparative genomics across complex, mixed-source, and under-characterized datasets.

Advanced molecular archeology tools could identify ancient molecular signatures within modern genomes, distinguishing preserved ancestral features from recent evolutionary changes. These computational approaches might reveal cryptic chemical fossil components within apparently derived organisms, expanding our understanding of how ancient biological organization persists across evolutionary time.

Systematic Chemical Fossil Discovery

The identification of chemical fossils at both macroscopic

(*Pseudocolus/Tribrachia*) and microscopic (*T. schoenleinii*) scales suggests this phenomenon occurs across multiple biological levels. Systematic application of diagnostic criteria—morphological anomalies, ecological incompatibilities, ancient marine genomic signatures, and provenance analysis—could reveal the true scope of chemical fossil preservation throughout existing taxonomic systems.

Comparative analysis of other putative "dermatophytes" using similar molecular approaches may uncover additional taxonomic misclassifications within this medically-defined group. Given the fundamental biological importance of these discoveries, research should expand beyond dermatological frameworks to engage the broader scientific community in systematic chemical fossil characterization.

The pattern suggests that many organisms currently classified as "human pathogens" may represent ancient lineages whose biochemical capabilities happen to be compatible with human biological systems. Systematic screening of human-associated microorganisms could reveal an extensive archive of pre-genetic chemical organization preserved in taxonomically problematic species.

Broader Evolutionary Implications

Chemical fossils provide unprecedented windows into pre-kingdom evolutionary states that could revolutionize our understanding of early life. Systematic characterization might enable reconstruction of early eukaryotic biochemistry, cellular organization, and developmental capabilities that preceded modern biological modularity. This research could illuminate the transition from chemical to biological complexity during life's earliest evolution.

Investigation of chemical fossils may reveal previously unknown aspects of the marine-to-terrestrial evolutionary transition. Organisms preserving ancient marine biochemistry while exhibiting terrestrial associations could illuminate transitional evolutionary states and environmental adaptation mechanisms that conventional fossils cannot preserve.

The biotechnological potential deserves serious consideration. Ancient biochemical systems preserved in chemical fossils may harbor novel enzymatic capabilities, metabolic pathways, and regulatory mechanisms with significant applications in bioremediation, materials science, and sustainable chemistry. These ancient systems might possess capabilities that modern organisms have lost through evolutionary specialization.

Revolutionary Research Programs

Several revolutionary research directions emerge from this work. Chemical fossil distribution analysis could reveal global patterns of ancient life preservation, potentially identifying biogeographic refugia where pre-genetic biological organization persists. This could transform our understanding of life's continuity and the mechanisms that preserve ancient biological complexity.

Deep time biochemistry reconstruction represents another frontier. If chemical fossils genuinely preserve ancient metabolic systems, comparative analysis across multiple species could enable reconstruction of primordial biochemical networks that operated before modern cellular organization evolved. This could bridge the gap between prebiotic chemistry and cellular biology.

The implications extend to astrobiology and origin of life research. If ancient chemical systems can persist for hundreds of millions of years within modern biological contexts, similar preservation mechanisms might operate on other worlds or in extreme terrestrial environments. Chemical fossils could provide models for how life might persist across cosmic timescales.

Clinical and Therapeutic Reframing

The taxonomic reclassification demands reconceptualization of human-organism interactions. Rather than viewing *T. schoenleinii* as a "pathogen" requiring elimination, the evidence suggests managing an ancient symbiotic relationship that has persisted across evolutionary timescales. Treatment strategies should focus on modulating sulfur metabolism, rebalancing local chemistry, or providing alternative biochemical substrates rather than attempting to eliminate an organism with hundreds of millions of years of evolutionary persistence.

This reframing has broader implications for medical microbiology. Many supposed "pathogens" may represent ancient chemical refugees seeking biochemically familiar environments rather than evolved parasites. Understanding these relationships could transform approaches to human-microorganism interactions from antagonistic to ecological.

The Paradigm Shift

The systematic discovery and characterization of chemical fossils promises to transform evolutionary biology from a discipline focused on genomic relationships to one encompassing the full spectrum of biological organizational strategies. This research program requires expertise from multiple disciplines including evolutionary biology, biochemistry, marine biology, environmental microbiology,

and computational biology.

The fundamental insight that revolutionary biological discoveries can emerge from careful reexamination of familiar organisms using novel theoretical frameworks suggests that many other "well-known" species may conceal fundamental insights into life's deepest history. The systematic application of chemistry-first analytical approaches could reveal that ancient biological complexity remains accessible not only through geological records, but through living systems that never abandoned their chemical heritage.

This work demonstrates that the transition from chemical to biological complexity may be preserved in the genomes of organisms that never fully completed the evolutionary transition from ancient chemical systems to modern biological modularity. The ancestors, in a very real sense, remain among us—not as fossils in rocks, but as living archives of life's deepest organizational principles, awaiting recognition through frameworks sophisticated enough to see beyond anthropocentric observational constraints.

Conclusion

This study demonstrates that *Trichophyton schoenleinii* represents a fundamentally misclassified organism whose true evolutionary relationships have been obscured by decades of anthropocentric taxonomic interpretation. Rather than a derived human pathogen, molecular evidence indicates *T. schoenleinii* preserves genomic architecture from early eukaryotic evolution, exhibiting systematic affinities with ancient lineage representatives across multiple kingdoms while showing poor integration within modern fungal groups.

The organism's systematic matches to slime molds, tardigrades, choanoflagellates, basal metazoans, and ancient protists (corroborated by both nuclear and mitochondrial DNA similarity) reveal a pattern of genomic stasis inconsistent with recent evolutionary origin. These findings, combined with *T. schoenleinii*'s unique morphological features and sophisticated sulfur metabolism, position it as a prime example of a "chemical fossil": an organism that has retained ancient biological organization while most lineages underwent genomic compilation and specialization.

The discovery validates core predictions of the Chemical-Genetic Integration Model and establishes *T. schoenleinii* as the second confirmed example of this molecular pattern, following the recent reclassification of *Pseudocolus fusiformis* as the basal, marine demosponge *Tribrachia fusiformis*. This growing evidence base suggests that systematic application of CGIM diagnostic criteria can identify additional chemical fossils, revealing a previously unrecognized archive of early biological complexity preserved in taxonomically problematic organisms.

Beyond its specific implications for dermatophyte evolution, this research illustrates fundamental limitations in observation-based taxonomic frameworks that prioritize human-relevant characteristics over deep biological relationships. The systematic misclassification of *T. schoenleinii* as a "human pathogen" exemplifies how anthropocentric bias can obscure ancient evolutionary relationships and prevent recognition of organisms' true biological significance.

The study's broader implications extend to taxonomic methodology itself. The consistent recovery of environmental samples and contaminated isolates among supposed fungal relatives indicates widespread misattribution in sequence databases, highlighting the urgent need for provenance-aware database architecture that preserves biological context alongside molecular data. Current approaches that treat sequence identity as discrete taxonomic assignment ignore the complex derivation histories underlying genomic diversity.

Moving forward, chemistry-based taxonomic frameworks that prioritize biochemical capabilities, metabolic pathways, and genomic architecture over ecological associations represent a promising alternative to traditional morphology-driven approaches. Such methods could reveal additional ancient lineages currently classified based on superficial similarities or human interactions rather than fundamental biological relationships.

The identification of *T. schoenleinii* as a chemical fossil also opens new avenues for understanding early eukaryotic evolution. If this organism genuinely preserves ancient biological organization, it represents a molecular window into pre-kingdom evolutionary states, potentially informing reconstruction of early eukaryotic biochemistry, cellular organization, and developmental capabilities.

Finally, this research demonstrates that revolutionary biological discoveries can emerge from careful reexamination of familiar organisms using novel theoretical frameworks. *T. schoenleinii* has been studied for over a century as a medical curiosity, yet its true evolutionary significance remained hidden until approached through the lens of chemical-genetic integration theory. This suggests that many other "well-known" organisms may similarly conceal fundamental insights into life's deepest history, awaiting recognition through chemistry-first analytical approaches that transcend the observational constraints of traditional biological classification.

The systematic discovery and characterization of chemical fossils promises to revolutionize our understanding of early

life, revealing that the transition from chemical to biological complexity may be preserved not only in geological records, but in the genomes of living organisms that never fully completed the evolutionary transition from ancient chemical systems to modern biological modularity.

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.

Note: the author intentionally did not include medical images in this paper due lack of relevance, but also because these images are disturbing to view and they deter non-physicians from reading articles on these topics.

This author cautions dermatologists to consider ceasing their unnecessary practice of including graphic images of human infections directly in their articles about this organism. The author further encourages dermatologists to attempt to gather and publish more photos of the organism itself, and to attempt to create these images with high resolution so their scientist colleagues are able to review in detail. Currently, most published photos of the organism are from dermatologists and are poorly lit, blurry, and out of focus. This is not helpful to scientists.

Acknowledgements

The author conceptualized the study, developed the theoretical framework, and conducted all analyses. This research received no external funding and was conducted using personally acquired resources.

The author acknowledges Molecular Biologist GPT, Scholar GPT, and Claude AI for their assistance with manuscript preparation, data interpretation discussions, and research development over the course of this investigation.

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Appendix A: Summary of BLAST Results

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Emydomyces testavorans (full genome – env. sample)	Fungi - Onygenales, Eurotiomycetes, Ascomycota	CP120628.1	1705	2841	96.774	0
Aspergillus citrinoterreus (full genome – env. sample)	Fungi - Aspergillaceae, Eurotiomycetes, Ascomycota	CP155514.1	1703	2815	96.536	0
Talaromyces rugulosus (full genome – env. sample)	Fungi - Trichocomaceae, Eurotiomycetes, Ascomycota	CP055901.1	1703	2789	96.242	0
Ascosphaera apis	Fungi - Onygenales, Eurotiomycetes, Ascomycota	GQ867785.1	1636	2754	97.127	0
Penicillium roqueforti (full genome – env. sample)	Fungi - Aspergillaceae, Eurotiomycetes, Ascomycota	CP130313.1	1703	2730	95.713	0
Monascus purpureus	Fungi - Aspergillaceae, Eurotiomycetes, Ascomycota	AP025353.1	1706	2721	95.545	0
Xanthoria parietina	Fungi – Lecanoromycetes, Ascomycota	OZ210035.1	1725	2673	94.667	0
Bulgaria inquinans	Fungi - Leotiomycetes, Ascomycota	EU107260.1	1694	2643	94.864	0
Encoelia furfuracea	Fungi – Helotiales, Ascomycota	MT508552.1	1704	2628	94.542	0
Cyttaria darwinii	Fungi - Leotiomycetes, Ascomycota	EU107180.1	1694	2571	94.097	0
Trichia scabra	Slime Mold - Myxogastria, Amoebozoa | RNA	AY187084.1	1340	2163	95.821	0
Tunicaraptor unikontum	Holozoa | RNA	MT611055.1	1717	1997	86.43	0
Salpingoeca kvevrii	Choanoflagellate | RNA	EU011930.1	1723	1976	86.361	0
Leucettidae sp.	Sponge - Clathrinida, Calcarea, Porifera | RNA	KY670632.1	1718	1955	85.856	0
Diaphanoeca grandis	Choanoflagellate | RNA	AF084234.1	1716	1947	85.956	0
Pericharax heteroraphis	Sponge - Clathrinida, Calcarea, Porifera	AM180967.1	1702	1939	85.958	0
Leucetta sp.	Sponge - Clathrinida, Calcarea, Porifera	AF182190.1	1709	1934	85.723	0
Leucetta villosa	Sponge - Clathrinida, Calcarea, Porifera	AM180966.1	1702	1930	85.781	0
Salpingoeca kvevrii	Choanoflagellate	KT757494.1	1694	1925	86.187	0
Salpingoeca aroma	Choanoflagellate	MW843498.1	1683	1925	86.215	0
Parahigginsia sp.	Sponge - Axinellida, Demospongiae, Porifera	PP266643.1	1731	1924	85.384	0
Samsoniella hepiali	Cordycipitaceae, Hypocreales, Sordariomycetes | mtDNA (highest bit for mtDNA)	OM117588.1	2255	1924	79.29	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Axinella polypoides	Sponge - Demospongiae, Porifera	OZ178451.1	1726	1923	85.284	0
Beroe ovata	Comb Jellyfish - Beroida, Nuda, Ctenophora	OR921247.1	1726	1923	85.284	0
Soleneiscus stolonifer	Sponge - Clathrinida, Calcarea, Porifera	AM180955.1	1706	1921	85.639	0
Monosiga ovata	Choanoflagellate | RNA	AF084230.1	1724	1921	85.557	0
Axinella polypoides	Sponge - Demospongiae, Porifera	OZ178462 .1	1725	1920	85.159	0
Clathrina cerebrum	Sponge - Clathrinida, Calcarea, Porifera	U42452.1	1712	1920	85.631	0
Clathrina luteoculcitella	Sponge - Clathrinida, Calcarea, Porifera	AM180959.1	1703	1920	85.672	0
Axinella polypoides	Sponge - Demospongiae, Porifera	OZ178451.1	1726	1919	85.226	0
Pompholyxophrys	Opisthokonta	MK547175.1	1694	1917	85.596	0
Axinella damicornis	Sponge - Axinellida, Demospongiae, Porifera	OZ007506.1	1734	1911	85.006	0
Metridium senile	Sea Anemone - Actiniaria, Hexacorallia, Anthozoa, Cnidaria	OX459095.1	1728	1911	85.243	0
Sandalolitha robusta	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631174.1	1720	1909	85.349	0
Podabacia crustacea	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631170.1	1720	1909	85.349	0
Lobactis scutaria	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631164.1	1720	1909	85.349	0
Herpolitha limax	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631156.1	1720	1909	85.349	0
Halomitra pileus	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631155.1	1720	1909	85.349	0
Fungia fungites	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631154.1	1720	1909	85.349	0
Danafungia horrida	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631153.1	1720	1909	85.349	0
Diaphanoeca undulata	Choanoflagellate	KU587848.1	1690	1909	85.68	0
Cycloseris explanulata	Fungiidae Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631152.1	1721	1908	85.474	0
Salpingoeca prava	Choanoflagellates	MH490946.2	1683	1907	85.977	0
Geodia barretti	Sponge - Tetractinellida, Demospongiae, Porifera	CASHTH 010003473.1	1733	1906	85.228	0
Axinella damicornis	Sponge - Demospongiae, Porifera	OZ007509.1	1735	1905	84.957	0
Salpingoeca urceolata	Choanoflagellate	EU011931.1	1718	1904	85.623	0
Salpingoeca prava	Choanoflagellate	MH490946.2	1718	1904	85.623	0
Eurypon cf. clavatum	Sponge - Axinellida,	AJ621547.1	1733	1903	84.882	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
	Demospongiae, Porifera					
Phyllospongia foliascens	Sponge - Keratosa, Demospongiae, Porifera	OZ156448.1	1727	1901	85.292	0
Corallochytrium limacisporum	Choanoflagellate	L42528.1	1711	1900	85.622	0
Salpingoeca urceolata	Choanoflagellate	EU011931.1	1711	1900	85.622	0
Madrepora sp.	Stony Coral - Scleractinia, Hexacorallia, Anthozoa, Cnidaria	LT631286.1	1719	1896	85.224	0
Tunicaraptor unikontum	Holozoa	MT611055.1	1723	1895	86.941	0
Tethya californiana	Sponge - Demospongiae, Porifera	OZ123596.1	1730	1894	84.971	0
Leiopathes expansa	Black Coral - Antipathidae, Hexacorallia, Anthozoa, Cnidaria	MT318871.1	1730	1893	84.971	0
Leiopathes glaberrima	Black Coral - Antipathidae, Hexacorallia, Anthozoa, Cnidaria	MT318870.1	1730	1893	84.971	0
Tethya sp.	Sponge - Demospongiae, Porifera	EF654532.1	1724	1893	85.035	0
Axinella polypoides	Sponge - Demospongiae, Porifera	EF092266.1	1717	1893	85.032	0
Leiopathes glaberrima	Black Coral - Antipathidae, Hexacorallia, Anthozoa, Cnidaria	PP411001.1	1727	1892	85.003	0
Stichopathes sp.	Black Coral - Antipathidae, Hexacorallia, Anthozoa, Cnidaria	PP410995.1	1727	1892	85.003	0
Calliacantha sp.	Choanoflaggellate	AF272000.1	1715	1889	85.248	0
Tethya californiana	Sponge - Demospongiae, Porifera	OZ123596.1	1730	1886	84.913	0
Pseudoperkinsus (Sphaeroforma) tapetis	Ichthyosporea, Holozoa	AF192386.1	1712	1878	84.93	0
Acanthocoepsis unguiculata	Choanoflagellate	L10823.1	1710	1876	85.029	0
Syssomonas multiformis	Unicellular Flagellated Protist - Holozoa	MF190551.1	1691	1875	85.275	0
Savillea micropora	Choanoflagellate	EU011928.1	1712	1872	85.105	0
Calliacantha natans	Choanoflagellate	KU587842.1	1699	1872	85.168	0
Salpingoeca kvevrii	Choanoflagellate	EU011930.1	1729	1871	86.698	0
Halcurias hiroomii	Sea Anemone - Hexacorallia, Anthozoa, Cnidaria	LC768583.1	1711	1860	84.921	0
Synhalcurias elegans	Sea Anemone - Hexacorallia, Anthozoa, Cnidaria	LC768574.1	1710	1857	84.971	0
Stephanoeca diplocostata	Choanoflagellate	AY149899.1	1722	1856	84.669	0
Pigoraptor chileana	Holozoa	MF190553.1	1714	1855	86.523	0
Urnula craterium	Sarcosomataceae, Pezizomycetes | mtDNA	NC_067992.1	2229	1855	81.92	0
Salpingoeca helianthica	Choanoflagellate	EU011929.1	1715	1854	85.015	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Leucettidae	Sponge - Clathrinida, Calcarea, Porifera	KY670632.1	1727	1853	86.508	0
Isohalcurias carlgreni	Sea Anemone - Hexacorallia, Anthozoa, Cnidaria	LC768589.1	1712	1853	84.871	0
Pseudostephanoeca paucicostata	Choanoflagellate	OP038903.1	1595	1852	86.332	0
Turritopsis sp.	Jellyfish - Oceaniidae, Hydrozoa, Cnidaria	IAAF01053955.1	1739	1851	84.301	0
Chrysaora pacifica	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	KY212123.1	1733	1850	84.478	0
Salpingoeca urceolata	Choanoflagellate	KT757514.1	1689	1848	85.376	0
Atolla vanhoeffeni	Jellyfish - Coronatae, Scyphozoa, Cnidaria	AF100942.1	1732	1834	84.527	0
Clathrina helveola	Sponge - Clathrinida, Calcarea, Porifera	AM180958.1	1713	1834	86.457	0
Capsaspora owczarzaki	Filasterea	AY363957.1	1719	1834	84.351	0
Leucetta sp.	Sponge - Clathrinida, Calcarea, Porifera	AF182190.1	1718	1831	86.321	0
Hydractinia symbiolongicarpus	Hydrozoan - Hydrozoa, Cnidaria	NW_026633886.1	1733	1830	84.189	0
Hydra magnipapillata	Hydrozoan - Hydrozoa, Cnidaria	GL030695.1	1738	1829	84.12	0
Aurelia sp.	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	EU276014.1	1737	1829	84.226	0
Leucetta villosa	Sponge - Leucettidae, Clathrinida, Calcarea, Porifera	AM180966.1	1711	1829	86.382	0
Hydractinia symbiolongicarpus	Hydrozoan - Hydrozoa, Cnidaria	NW_026633886.1	1733	1826	84.132	0
Aurelia solida	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	MZ788653.1	1737	1825	84.168	0
Aurelia sp.	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	IADZ01000102.1	1737	1825	84.053	0
Bebryce sp.	Coral - Octocorallia, Anthozoa, Cnidaria	PP410839.1	1741	1823	84.262	0
Soleneiscus stolonifer	Sponge - Clathrinida, Calcarea, Porifera	AM180955.1	1714	1821	86.289	0
Salpingoeca kvevrii	Choanoflagellate	KT757494.1	1700	1821	86.529	0
Pigoraptor vietnamica	Holozoa	MF190552.1	1720	1818	86.163	0
Pseudogymnoascus pannorum	Ascomycota incertae sedis | mtDNA	KR055655.1	2182	1818	81.943	0
Diaphanoeca grandis	Choanoflagellate	DQ059033.1	1717	1814	86.08	0
Clathrina cerebrum	Sponge - Clathrinida, Calcarea, Porifera	U42452.1	1719	1810	86.097	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Vallicula multiformis	Comb Jelly - Ctenophora	PQ362855.1	1733	1809	83.728	0
Anthothela nuttingi	Soft Coral - Octocorallia, Anthozoa, Cnidaria	AF052922.1	1740	1808	84.023	0
Hydra viridissima	Hydrozoan - Hydrozoa, Cnidaria	OZ173726.1	1736	1808	83.986	0
Pukia falcata	Comb Jelly - Ctenophora	PQ362460.1	1733	1808	83.958	0
Salpingoeca prava	Choanoflagellate	MH490946.2	1685	1808	86.35	0
Cephea cephea	Jellyfish - Rhizostomeae, Scyphozoa, Cnidaria	PQ647263.1	1744	1806	83.773	0
Salpingoeca punica	Choanoflagellate	KT757460.1	1686	1806	84.816	0
Mastigias albipunctata	Jellyfish - Rhizostomeae, Scyphozoa, Cnidaria	PQ647264.1	1751	1805	83.724	0
Hydra viridissima	Hydrozoan - Hydrozoa, Cnidaria	OZ173726.1	1737	1805	83.938	0
Cyanea nozakii	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	MT813455.1	1745	1802	83.782	0
Hydra viridissima	Hydrozoan - Hydrozoa, Cnidaria	OZ173726.1	1740	1801	83.793	0
Coeloplana meteoris	Comb Jelly - Ctenophora	PQ573581.1	1733	1800	83.612	0
Favia fragum	Stony Coral - Scleractinia, Hexacorallia	LT631269.1	1758	1788	83.333	0
Nanomia septata	Siphonophore - Siphonophorae, Hydrozoa, Cnidaria	CM107577.1	1736	1773	83.583	0
Ptychogastria polaris	Jellyfish - Trachymedusae, Hydrozoa, Cnidaria	KY077283.1	1737	1757	83.189	0
Stephanoeca diplocostata	Choanoflagellate	AY149899.1	1733	1744	85.459	0
Sycon ciliatum	Sponge - Leucosolenida, Calcarea, Porifera	NC_088643.1	1733	1738	85.228	0
Protoptilum carpenteri	Coral - Octocorallia, Anthozoa, Cnidaria	OL741701.1	1732	1735	85.277	0
Sycon ciliatum	Sponge - Leucosolenida, Calcarea, Porifera	NC_088643.1	1733	1731	85.17	0
Chrysaora pacifica	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	KY249594.1	1736	1724	85.138	0
Chrysaora pacifica	Jellyfish - Semaeostomeae, Scyphozoa, Cnidaria	KY212123.1	1736	1724	85.138	0
Nanomia septata	Siphonophore - Siphonophorae, Hydrozoa, Cnidaria	CM107577.1	1767	1717	82.456	0
Ptilella inflata	Sea Pen - Octocorallia, Anthozoa, Cnidaria	OL741703.1	1736	1705	84.965	0
Colpophyllia natans	Stony Coral - Scleractinia, Hexacorallia	LT631261.1	1792	1688	81.25	0
Paulinella micropora	Amoeba - Euglyphida, Cercozoa, Rhizaria	BJOX01003760.1	1753	1673	82	0

Species	Tax.	Seq. Id.	Length	Bit Score	Id.	E-Value
Euglypha tuberculata	Euglyphida, Cercozoa, Rhizaria	AJ418787.2	1737	1657	82.038	0
Lycogala flavofuscum	Slime Mold - Myxogastria, Amoebozoa	AY187083.1	1357	1648	87.767	0
Samsoniella hepiali	Cordycipitaceae, Hypocreales, Sordariomycetes | mtDNA	OM117588.1	2179	1615	80.358	0
Phaeodactylum tricornutum	Diatom, Stramenopiles	NC_011681.1	1723	1587	81.602	0
Lycogala flavofuscum	Slime Mold - Myxogastria, Amoebozoa	AY145525.1	1055	1541	92.607	0
Fonticula alba	Slime Mold - Cristidiscoidea, Opisthokonta	FJ816018.1	1744	1549	80.677	0
Heterophryidae	Heliozoan protists	OP101620.1	1764	1507	79.422	0
Ramazzottius varieornatus	Water Bear - Tardigrada	BDGG01000017.1	1744	1457	79.8	0
Phaeodactylum tricornutum	Diatom, Stramenopiles	NC_011681.1	1735	1421	82.133	0
Acutuncus antarcticus	Water Bear - Tardigrada	AB753790.1	1735	1420	79.4	0
Trimastix marina	flagellate amitochondriate microscopic eukaryotes	KT380017.1	1753	1416	79.122	0
Lycogala flavofuscum	Slime Mold - Myxogastria, Amoebozoa	JQ277925.1	1012	1405	91.7	0
Oxnerella micra	Heliozoan protists	JQ245079.1	1754	1375	81.528	0
Lenisia limosa	Breviate amoebae	KT023596.1	1804	1305	77.106	0
Milnesium tardigradum	Water Bear - Tardigrada	U49909.1	1760	1291	77.2	0
Trimastix marina	flagellate amitochondriate microscopic eukaryotes	AF244905.1	1773	1284	76.819	0
Ramazzottius varieornatus	Water Bear - Tardigrada	BDGG01000017.1	1750	1279	80.5	0
Jakoba libera	Jakobid eukaryotes	AY117418.1	1766	1244	76.954	0
Jakoba libera	Jakobid eukaryotes	AF411288.1	1766	1232	76.954	0
Acutuncus antarcticus	Water Bear - Tardigrada	AB753790.1	1740	1227	80	0
Chaetomium globosum	Chaetomiaceae, Sordariomycetes	CH408037.1	2298	1190	72.498	0
Acutuncus antarcticus	Water Bear - Tardigrada	EU266943.1	1625	1158	80.1	0
Reclinomonas americana	Jakobid eukaryotes	AY117417.1	1797	1056	74.124	0
Fonticula alba	Slime Mold - Cristidiscoidea, Opisthokonta	FJ816018.1	1075	1048	84.651	0
Blastocystis	Stramenopiles	JBBPEB010000010.1	1878	565	67.945	2.36E-158
Reclinomonas americana	Jakobid eukaryotes	KC353357.1	1839	409	65.144	8.74E-111
Malawimonas	heterotrophic flagellates	KP165391.1	1907	379	65.915	1.48E-101

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Trichophyton schoenleinii strain ATCC 22775 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1 and 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

GenBank: EF631620.1

GenBank FASTA

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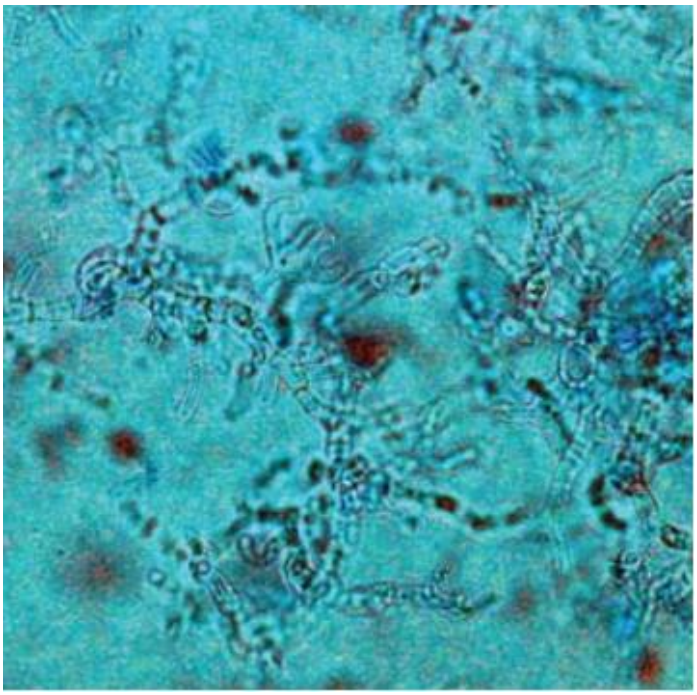
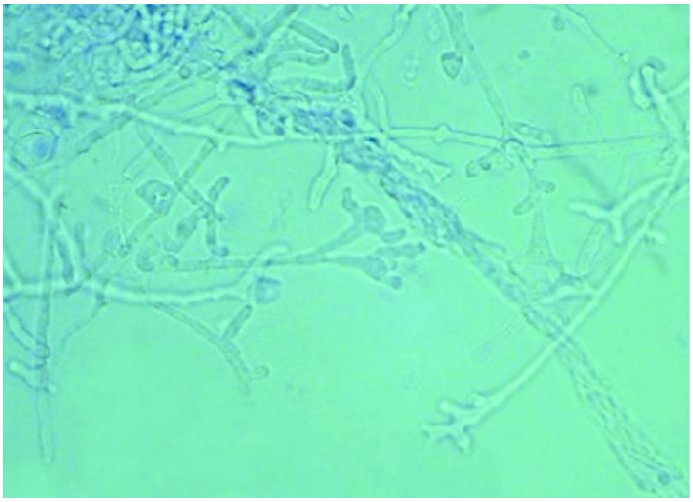
Appendix B: Morphological Images

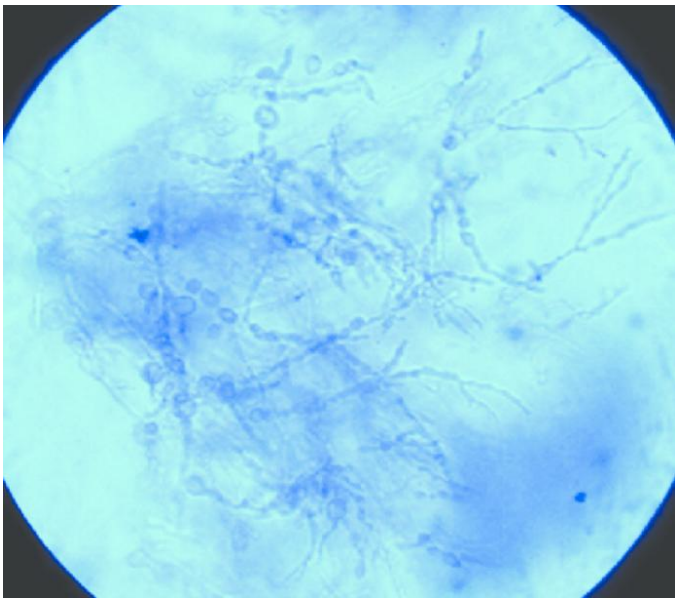
Trichophyton schoenleinii, colony. Sabouraud dextrose agar, 25°C, 62 days. Copyright Chiba University Research Center for Pathogenic Fungi and Microbial Toxicoses, 1999, Japan.



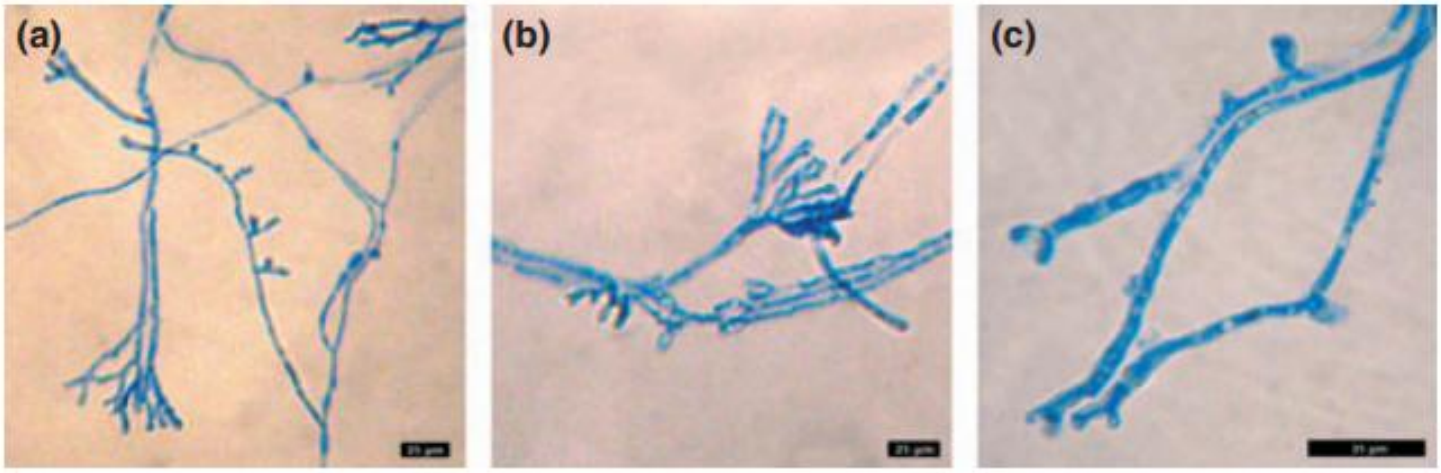
Trichophyton schoenleinii, (Khaled, et al, 2007).



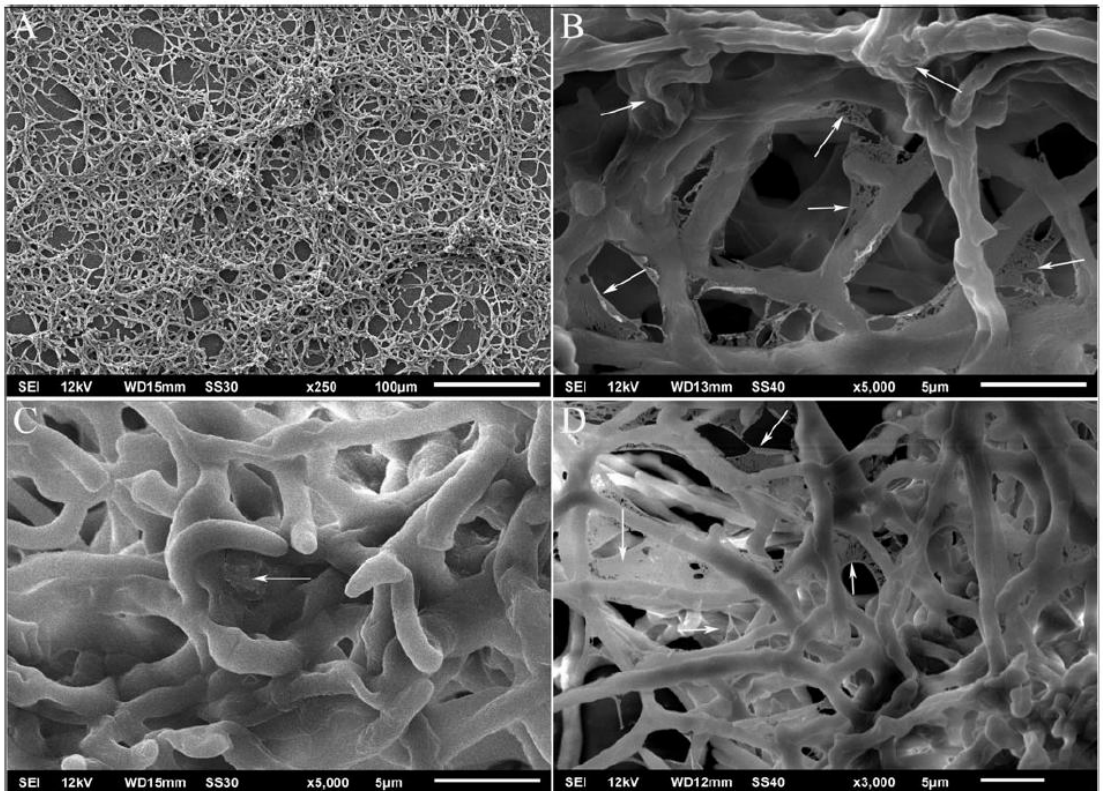
Trichophyton schoenleinii, (Mareş, M. et al 2012).



Trichophyton schoenleinii, (Ghadgepatil, S.S, et al 2015).



Trichophyton schoenleinii, Macura, A., et al, 2011).



SEM images of mature *T. mentagrophytes* biofilm with exopolymeric matrix (Costa-Orlandi, C. B., 2014).

[Note this is *T. mentagrophytes* not *T. schoenleinii*].