High-Confidence Genetic Alignment Between *Sphaerobolus* (the "Cannonball" Fungi) & *Turritopsis* (the "Immortal Jellyfish")

Cross-Domain Genetic Overlap Discovery Report

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Abstract:

Modern bioinformatics pipelines prioritize speed, statistical confidence, and taxonomic consistency. These design choices enable large-scale annotation but systematically suppress evolutionary anomalies. Classification-optimized workflows treat cross-taxonomic matches and long, moderate-identity alignments as errors requiring filtration rather than signals demanding investigation.

This article reports a high-confidence genomic alignment between *Sphaerobolus* and *Turritopsis*, organisms that current taxonomy separates by kingdoms. Long Alignment BLAST using the REBLAST framework surfaced this relationship by prioritizing structurally conserved sequences across distant taxa.

This analysis of NIH and ENA data identified a 1,359 bp alignment with 70% sequence identity and E-value = 0. Focused single-species database analysis revealed 399 additional alignments. This scale and statistical confidence indicates conserved genomic architecture that contradicts standard phylogenetic expectations.

These findings challenge current placement of *Oceaniidae* and *Geastrales* while revealing systematic underestimation of deep evolutionary relationships. The extensive conservation supports close evolutionary relationship under standard interpretation, contradicting the separation across kingdoms. Multiple explanations warrant investigation: closer phylogenetic affinity, ancient horizontal transfer, or shared multicellular prototype ancestry.

This discovery extends the growing pattern of unexpected long-range homologies across taxonomically distant organisms, demonstrating the utility of discovery-oriented sequence analysis for revealing cryptic evolutionary relationships invisible to conventional approaches. Complete datasets are provided for independent analysis, supporting modular publication of statistically significant homologies that allows early-stage insights to circulate without awaiting comprehensive phylogenetic synthesis.

Keywords:

long-range homology; long alignment BLAST; REBLAST; extended sequence alignment; *Sphaerobolus*; *Turritopsis*; *Oceaniidae*; *Geastrales*; cross-taxonomic analysis; phylogenetic revision; deep homology; evolutionary genomics; sequence conservation; multicellular evolution; discovery methodology; modular architecture; evolutionary bioinformatics; comparative genomics; MCP framework; E-value zero alignments; vertical inheritance; custom databases; taxonomic incongruence; cryptic homology; alignment significance.

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Introduction

This article presents a high-confidence alignment between *Sphaerobolus* and *Turritopsis*, surfaced using discovery-oriented sequence analysis optimized for structural conservation across taxonomic boundaries. The alignment spans 1359 base pairs with 70% identity and an E-value of 0. There were also more than 399 unique matches including several 37-46bp alignments with 100% identity.

This result is shared here as an individual, interpretable lead (one among many discovered in current REBLAST investigations) to accelerate evolutionary insight and allow immediate, independent exploration. This result is selected from a broader discovery effort using custom databases optimized to surface long, structurally significant alignments across distant taxa. While this match ranks among the top hits in this analysis, it is not necessarily the longest or most conserved possible alignment across all databases or in nature.

Many species remain unsequenced or underrepresented, and sequence fragmentation continues to obscure deeper conservation patterns. Thus, each surfaced match is best understood as a lead, not a definitive endpoint. This brief is part of a modular publishing strategy intended to make meaningful signals accessible as they emerge, accelerating both analysis and interdisciplinary interpretation.

This analysis represents one component of a broader methodological framework detailed across companion publications: the REBLAST discovery methodology (Gjøvik, 2025c), the Multiple Multicellular Prototype theoretical framework (Gjøvik, 2025b), and extensive human-siphonophore genetic overlap findings (Gjøvik, 2025a). Readers unfamiliar with these foundational papers may find the current analysis benefits from this broader context.

This paper provides comprehensive methodological detail because it serves as a white paper. Future publications employing these methods will reference this work and present findings more concisely. All additional results from this dataset are archived at Zenodo, with database metadata and related materials indexed at OSF.

Sphaerobolus

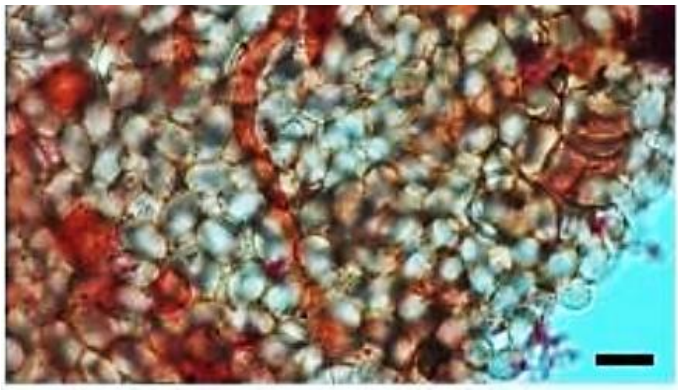
Sphaerobolus, commonly referred to as the artillery fungus, is recognized for its unique ability to forcibly eject peridioles (an assumed spore-containing structure) several meters away from the fruiting body. These peridioles are expelled with significant velocity and adhere to nearby surfaces, a feature that has attracted both scientific attention and horticultural frustration. Morphologically, the fruiting body is small, globose to shallowly cupulate, and typically embedded in decaying plant matter. Upon maturation, the outer peridium splits to reveal a single black glebal mass, which is ejected via turgor-driven rupture of the inner peridium (Geml et al., 2005).

Sphaerobolus stellatus (Michael Wood, MykoWeb).

Ecologically, *Sphaerobolus* is a saprotroph that colonizes decaying wood, leaf litter, and especially high-cellulose substrates such as bark mulch, wood chips, and decomposing straw. It is frequently encountered in landscaped environments and moist temperate forests. The peridiole's sticky coating and phototropic orientation enhance adhesion to vertical or elevated surfaces, an adaptation interpreted to increase dispersal success (Money, 2016). Observations suggest a strong preference for environments with high organic turnover, particularly where lignin degradation is actively occurring (Rosendahl & Kjøller, 2014).

Molecular phylogenetic analyses based on rDNA ITS and LSU sequences have shown *Sphaerobolus* to be a deeply divergent lineage among gasteroid Basidiomycota. While traditionally placed within *Geastrales* or *Phallales*, their phylogenetic relationships remain ambiguous, and some lineages show substantial genetic distance from other gasteroid fungi (Geml et al., 2005; Hibbett et al., 2007). Taxonomic placement is further complicated by morphological reduction and convergence in fruiting body form, with some studies suggesting the genus's current classification may reflect functional traits more than deep evolutionary lineage (Reijnders, 2000; Hibbett & Thorn, 2001).

Geographically, *Sphaerobolus* species have been reported in mulched garden beds, lowland forests, moist disturbed edges, and coastal nutrient-enriched soils. Its frequent occurrence in urban landscapes, compost piles, and regenerating riparian margins has positioned it as a generalist decomposer adapted to substrate-rich, disturbed environments (Ovaskainen et al., 2024; Islam et al., 2020).



Sphaerobolus stellatus "peridiole composed of globular gemmae, hyphae and basidiospores." (Oliveira et al, 2022).

Discovery

Sphaerobolus and *Turritopsis* share 1,359bp sequence identity (70.79%) with E-value = 0. At least 399 unique genetic matches were identified between the species. *Sphaerobolus* and *Turritopsis* are currently taxonomically separated by kingdoms.

Primary Alignment Details

Parameter	Value
Query Organism	*Sphaerobolus stellatus* KN837078.1
Target Organism	*Turritopsis sp.* IAAF01069512.1, IAAF01068133.1
Alignment Length	1359
Bit_score	653
Sequence Identity	70.79%
E-value	0
BLAST Tool(s)	BLASTN; DC-MegaBLAST

This alignment exceeds conventional thresholds for biological relevance, with sequence length, identity, and statistical strength that challenge assumptions about taxonomic distance. This approach foregrounds them as signals of shared molecular architecture, potentially inherited from ancient or parallel developmental systems.

Extended alignments with E=0 and >70% identity across 1,359 bp are statistically incompatible with random convergence or noise. Under standard phylogenetic interpretation, such a result implies either recent common ancestry, ancient vertical inheritance, or non-random horizontal transfer. To dismiss such alignments as spurious is to reject the foundational principles of homology inference in comparative genomics.

While full phylogenetic interpretation is beyond the scope of this brief, frameworks such as REBLAST (Gjøvik, 2025c) and the Multiple Multicellular Prototype model (Gjøvik, 2025b) provide additional interpretive pathways. These offer structured alternatives to standard linear descent models for understanding conserved genomic structures across divergent organisms.

Turritopsis rubra medusa, Peter Devonport, New Zealand; WoRMS, © 2009 Peter Schuchert.

Focused Relationship Analysis

This report presents a brief discovery approach: (1) broad custom database analysis identifying unexpected relationships, followed by (2) focused single-species database analysis quantifying relationship extent.

To better characterize the genomic context of the match, the query sequence was aligned against a refined database containing only sequences from *Turritopsis*. This 1:1 mapping yielded a total of 399 matches.

This result suggests that the conserved architecture is not isolated but may occur multiple times within the *Sphaerobolus* and *Turritopsis* genome. Additional outputs and mapping details are included in the supplemental data.

Additional Matches: A Coherent Biological Pattern

Beyond *Turritopsis*, REBLAST identified extensive sequence conservation with multiple marine organisms sharing a striking common feature: extreme regeneration and

longevity strategies. This pattern reveals systematic relationships invisible to standard bioinformatics approaches.

The strongest matches included *Hydra vulgaris* (the classical model of animal regeneration), *Clytia hemisphaerica* (another evolutionary biology model organism), *Aurelia aurita* (long-lived "moon jellyfish"), and *Henneguya salminicola* (a multicellular animal that has no mitochondrial DNA). Each of these organisms represents a different solution to the fundamental challenge of cellular persistence and renewal.

Additional matches included the tunicate *Clavelina lepadiformis* (1165 bp), an extremophile diatom within *Bacillariaceae* (1202 bp), the stress-tolerant endosymbiotic dinoflagellate *Durusdinium trenchii* (1158 bp), and the submarine cave-dwelling glass sponge *Oopsacas minuta* (1020 bp—notable for its minimal genome lacking key metazoan genes).

Subject Title	Align. Len.	% Id.	Bit Score	E Value
Henneguya salminicola	1513	67.019	440	1.13E-117
Hydra vulgaris	1490	68.322	541	4.50E-148
Clytia hemisphaerica	1465	69.829	641	1.79E-178
Orciraptor agilis	1449	65.839	344	5.76E-90
Aurelia aurita	1366	70.425	630	3.24E-175
Turritopsis sp.	1359	70.787	653	0
Turritopsis sp.	1359	70.787	653	0
Bacillariaceae sp.	1202	65.058	386	4.95E-102
Clavelina lepadiformis	1165	72.189	628	1.36E-175
Durusdinium trenchii	1158	68.739	448	4.20E-121
Oopsacas minuta	1020	70.882	494	3.55E-135

Standard phylogenetic approaches would predict these organisms—spanning cnidarians, protists, and sponges—to share minimal sequence similarity. Classification-based tools like NIH BLAST would route these sequences to their respective taxonomic databases, never detecting cross-kingdom conservation. The pattern REBLAST reveals suggests these organisms share ancient molecular toolkits for cellular persistence, regeneration, and stress resistance—strategies that current taxonomy treats as unrelated convergences.

This demonstrates a fundamental limitation of classification-optimized bioinformatics. Standard approaches are architected to confirm existing taxonomic relationships, not discover unexpected ones. When molecular evidence contradicts phylogenetic expectations, it is systematically filtered out as "noise" rather than investigated as potential signal. REBLAST bypasses these assumptions, revealing conservation patterns that suggest biology operates under different organizational principles than current frameworks recognize.

The functional convergence across these organisms (neural-like signaling without neurons, syncytial organization, electrical coordination, and regenerative capacity) represents either impossible independent evolution of complex molecular systems, or shared inheritance from ancient strategies that current models fail to detect.

Protocol Validation

Quality Assurance: Basic validation confirmed the *Turritopsis* sequences originated from the PRJDB4516 ENA project, representing de novo sequencing with contigs "c60504_g1_i2" and "c60792_g1_i1" from the 2016 study "De Novo Assembly of the Transcriptome of Turritopsis, a Jellyfish that Repeatedly Rejuvenates" (Hasegawa et al., 2016). Additionally, the top matching *Sphaerobolus stellatus* sample originated from a U.S. DOE Joint Genome Institute initiative (Project ID 403670) and the 2015 study "Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists" (Kohler, A., Kuo, A., Nagy, L. *et al,* 2015).

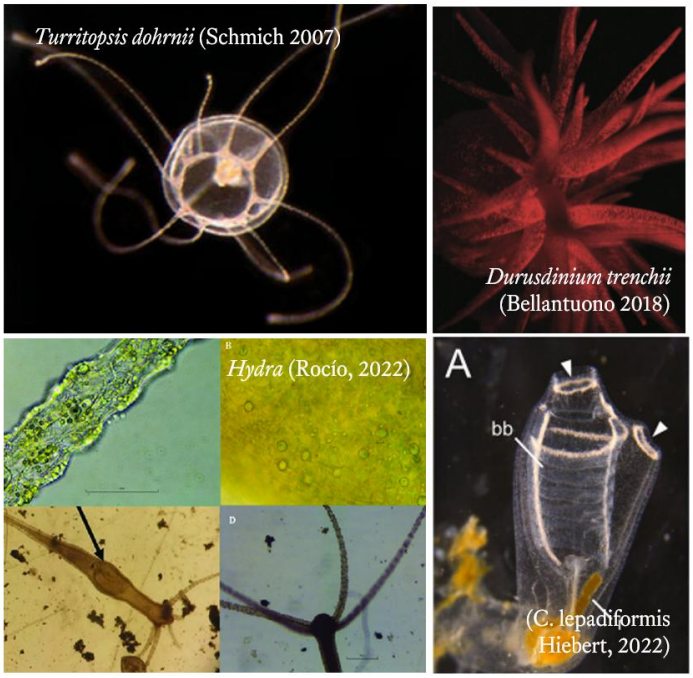
Standard BLAST: To test whether standard bioinformatics approaches could detect the relationships REBLAST identified, the matching *Sphaerobolus* and *Turritopsis* sequence segments were submitted to NIH Web BLAST across all standard databases (core_nt, nt_euk, nt_prok, nt_viruses, and nt_others).

Results demonstrate fundamental tool limitations:

- **For *Sphaerobolus*** (a "fungus"): NIH BLAST returned both Basidiomycete mushrooms (*Agrocybe praecox, Suillus discolor*) and arthropods, including wasps (*Apaeleticus inimicus*) and moths (*Saragossa porosa, Calymma communicmacula*). However, the same sequence producing both fungal and arthropod matches, and not surfacing cnidarian matches, raises questions about classification accuracy.
- **For *Turritopsis*** (a cnidarian jellyfish): NIH BLAST returned wasps (*Microctonus brassicae*), bee-flies (*Bombylius major*), and craneflies (*Pedicia rivosa*)—classifying an aquatic cnidarian as terrestrial arthropods.

Images of NIH Web BLAST Matches:

Images of Long Alignment and REBLAST Matches:



Tool Architecture Prevents Discovery: Standard BLAST workflows are optimized for taxonomic confirmation within expected phylogenetic boundaries. When sequences exhibit conservation across kingdoms, the system routes them to separate databases, preventing cross-taxonomic detection. The algorithm preferentially reports high-identity matches to phylogenetically "appropriate" organisms rather than biologically meaningful conservation with "inappropriate" ones.

Systematic Data Gaps: Despite ten independent runs across the same alignment regions between *Sphaerobolus* and *Turritopsis*, standard approaches never detected their shared genetic architecture. This demonstrates that substantial discovery gaps exist in default bioinformatics workflows, where statistically significant biological relationships remain invisible due to methodological assumptions rather than absence of signal.

Discovery vs. Classification: While NIH tools confidently assigned arthropod identities to both organisms, REBLAST revealed their actual shared molecular architecture: 1359bp of conserved sequence underlying sophisticated transformation mechanisms. This demonstrates that classification-optimized tools systematically obscure the very relationships most informative for evolutionary biology.

Turritopsis (The Immortal Jellyfish)

Turritopsis species are uniquely capable of reverting from adult medusae to juvenile polyps: a process known as life cycle reversal. This ability, most prominently studied in *Turritopsis dohrnii*, involves transdifferentiation—a reprogramming of mature somatic cells into earlier developmental states (Lisenkova et al., 2017). The phenomenon is considered unique among known metazoans and has generated interest as a model for regenerative biology and aging studies (Mas-Bargues, 2025; Murshid, 2024). The process appears to be triggered by physiological stress, injury, or starvation, initiating cellular dedifferentiation and transformation back into a colonial form.

Turritopsis species are pelagic hydrozoans typically found in coastal zones, harbors, and subsurface marine layers, where they feed on plankton and small invertebrates. Their life cycle includes both sessile polyp colonies and free-swimming medusae. Under environmental stress, *T. dohrnii* has been observed to abandon the terminal medusa form and regenerate into a new polyp colony through a reversal of ontogeny (Miglietta & Lessios, 2009). This capacity is not universal across Hydrozoa and is thought to be specific to certain *Turritopsis* lineages, especially those isolated in subtropical and warm-temperate waters (Miglietta et al., 2019).

Phylogenetically, *Turritopsis* is placed within the family *Oceaniidae* and the order *Anthoathecata*. Genetic studies based on mitochondrial and ribosomal sequences suggest substantial cryptic diversity within the genus, prompting taxonomic redefinitions that now distinguish *T. dohrnii* from the formerly broader *T. nutricula* complex (Miglietta et al., 2019; De Vito et al., 2006). Although firmly situated within Cnidaria, the mechanisms underlying its regenerative capacity remain poorly understood, and much of the genomic architecture related to transdifferentiation is only beginning to be mapped (Lisenkova et al., 2017; Mendelsohn

& Lei, 2022).

Turritopsis species have been reported in tropical and subtropical harbors, island reef margins, floating debris zones, and artificial substrates such as pilings and buoys. Their presence in ballast water and aquaculture zones has been widely documented, suggesting anthropogenic dispersal routes (Bayha & Graham, 2014). Ecologically, they tend to persist in areas with stable salinity, moderate currents, and periodic nutrient input, and their reversion capabilities appear linked to environmental variability and stress exposure (Miglietta et al., 2009; Mas-Bargues, 2025). The genus is often described as opportunistic, with a high degree of developmental plasticity relative to other hydrozoans.

Turritopsis and Sphaerobolus

Both species employ sophisticated transformation mechanisms with remarkable precision, suggesting shared evolutionary strategies rather than independent innovation.

Hierarchical Control Systems: Both organisms use multi-stage transformation cascades with specific molecular markers. *Sphaerobolus* employs a six-layer peridium forming two distinct "cups," with glebal discharge occurring with temporal precision 5-6 hours after the apex has split following enzymatic conversion of glycogen to glucose (Walker 1927; Geml et al. 2005). *Turritopsis* proceeds through four morphologically distinct stages: healthy medusa, unhealthy medusa, four-leaf clover and cyst, with specific tissue reorganization occurring at each phase (Carla et al. 2003).

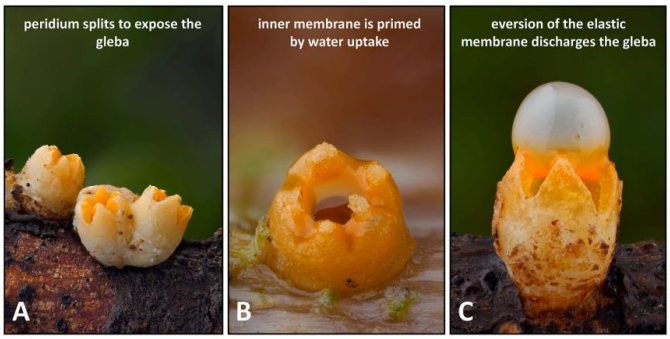
Pressure-Driven Mechanisms: Both systems employ sophisticated osmotic control fundamental to their transformation capabilities. *Sphaerobolus* creates precisely controlled gradients through enzymatic conversion of glycogen to glucose that increases internal osmotic pressure and turgidity of palisade cells (Fletcher and Cooke 1984). *Turritopsis* cnidarians similarly employ pressurized capsules for explosive discharge mechanisms operating on timescales comparable to other ultra-fast projectile systems found in nature such as fungal spore discharge (Weiss et al. 2022).

Adhesion-Dependent Success: Both species exhibit obligate dependence on adhesion for lifecycle completion. *Sphaerobolus* produces discharged spores that strongly adhere to whatever surface they encounter, maintaining viability for up to 11 years while attached (Geml et al. 2005). *Turritopsis* transformation requires medusae to settle onto the substrate before metamorphosis can proceed, making adhesion both a developmental trigger and survival necessity (Matsumoto et al. 2019).

Energy Investment Strategies: Both demonstrate remarkable energy allocation prioritizing transformation capability over conventional efficiency. *Sphaerobolus* consumes 80 times more energy than an individual gilled mushroom to release the same number of "spores" using the fastest and most powerful mechanism of fungal spore discharge (Sakes et al. 2023).

While comparable quantitative analysis of *Turritopsis* remains lacking, complete cellular reprogramming for life cycle reversal necessarily involves massive energetic investment, supported by upregulation of genes associated with "aging/lifespan, DNA repair and damage response" (Matsumoto and Miglietta 2021).

The convergent evolution of such sophisticated transformation mechanisms across phylogenetically distant lineages suggests either fundamental constraints channeling evolution toward specific solutions, or shared inheritance from ancient multicellular prototypes (exactly what the MCP framework predicts).



Sphaerobolus (© Timothy Boomer; Money et al, 2024).

Discovery Origins: Human-Sphaerobolus Conservation

This investigation began during broader research into Stinkhorn and Bird's Nest fungi, with particular focus on *Sphaerobolus stellatus* due to its unusual physiology for a taxon classified as a terrestrial mushroom. Early analysis revealed unexpected sequence conservation between human genetic material and *Sphaerobolus.* This includes 2,825 unique matches, including alignment lengths up to 445 bp and many short sequences showing 90–100% identity.

While individual matches were generally moderate in strength (bit-scores up to 236), the systematic nature of the pattern demanded further investigation. Notably, many of the human-*Sphaerobolus* conserved regions also aligned with cnidarian sequences, suggesting that these relationships reflect deeply shared genomic architecture rather than direct human–fungal affinity.

REBLAST analysis of the human–*Sphaerobolus* alignments revealed deeper conservation patterns extending across bacteria and archaea—including *Thermoplasmata*,

Ferroplasma, *Acidiplasma*, *Heimdallarchaeota*, *Azospirillum*, and *Pseudomonas*. This broad taxonomic range indicates a core genomic substrate shared across distant domains of life. This trajectory eventually led to the human–siphonophore findings detailed in a companion publication (Gjøvik, 2025a).

The evidence suggests that the *Sphaerobolus*–human alignments primarily reflect genomic regions shared between humans and ancient aquatic lineages—particularly Cnidaria, Ctenophora, Porifera, and Rhizaria. The repeated appearance of cnidarian-like sequences in both human and *Sphaerobolus* genomic regions implies non-random, organized conservation.

Importantly, humans rarely exhibit this level of sequence conservation with most eukaryotic lineages — especially not with terrestrial fungi. The pattern observed here (e.g., 2,825 reproducible alignments, including matches with significant identity) is not consistent with noise and cannot be accounted for by current phylogenetic models.

While the origin and significance of these matches remain unresolved, their statistical strength and biological coherence strongly suggest a shared genomic architecture that predates, or bypasses, modern taxonomic boundaries. These findings will be expanded in forthcoming analyses, including significantly longer alignments with additional 'terrestrial fungi.' The pattern is real, systematic, and far from isolated. Its recurrence across multiple 'fungal' genera suggests an overlooked continuity that may reshape our understanding of terrestrial-marine genomic relationships.

The *Sphaerobolus–Turritopsis* relationship reported here serves as a direct confirmation of this broader trend, demonstrating how investigation into anomalous human–fungal conservation can reveal cryptic genomic continuity across deep biological divides.

Conclusion

Extended sequence alignments of this length (1359bp) with perfect statistical significance (E-value = 0) and moderate identity (>70%) indicate close evolutionary relationship between *Sphaerobolus* and *Turritopsis*. The identification of 399 additional extended alignments strengthens this conclusion, demonstrating systematic rather than isolated conservation.

These conservation patterns call into question current taxonomic frameworks and reveal a consistent underestimation of deep evolutionary relationships. Multiple explanations warrant investigation: closer phylogenetic relationship than currently recognized, ancient horizontal gene transfer events, shared membership in early multicellular lineages, or revision of current phylogenetic frameworks.

Similar long-range homologies across other taxonomically distant groups suggest this may represent a broader pattern requiring methodological innovation in sequence analysis. The functional similarities—sophisticated transformation cascades, pressure-driven mechanisms, adhesion-dependent lifecycles—support biological coherence rather than chance conservation.

These findings demonstrate the utility of discovery-oriented sequence analysis for revealing cryptic evolutionary relationships invisible to conventional approaches. Standard BLAST protocols systematically exclude precisely the evidence most informative for deep evolutionary relationships, while length-prioritized analysis recovers biologically meaningful patterns.

Given the constraints of fragmentary sequence databases and classification-optimized tools, evolutionary biology may benefit from a lead-based discovery approach where individual high-confidence relationships are reported as identified, rather than awaiting comprehensive phylogenetic reconstruction. Each statistically impossible alignment represents a discrete evolutionary puzzle warranting immediate attention.

The broader implication is clear: our current understanding of evolutionary relationships may be fundamentally constrained by methodological assumptions rather than biological reality. These findings suggest that many "well-established" taxonomic boundaries may reflect analytical limitations rather than evolutionary truth.

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.

This *Sphaerobolus-Turritopsis* relationship represents one component of systematic investigation into misclassified terrestrial fungi. Forthcoming publications will detail comprehensive profiles of Stinkhorn and Bird's Nest species using extended sequence analysis, revealing significant long alignments with marine organisms. At least one species, *Pseudocolus*, is currently classified as a terrestrial fungus, but appears to be a mis-classified ancient marine proto-animal.

Overall, the broader implication is clear: our current understanding of evolutionary relationships may be fundamentally constrained by methodological assumptions

rather than biological reality. The forthcoming Stinkhorn and Bird's Nest analyses will provide additional test cases for these methods.

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Appendix

Appendix A: REBLAST & Long Alignment Review

Subject Title	Accession No.	Alignment Length	%_Identity	Bit_Score	E_Value
Henneguya salminicola	SGJC01000940.1	1513	67.019	440	1.13E-117
Hydra magnipapillata (vulgaris)	GAOL01025214.1	1490	68.322	541	4.50E-148
Clytia hemisphaerica	HAMV01004864.1	1465	69.829	641	1.79E-178
Orciraptor agilis	HBWU01002015.1	1449	65.839	344	5.76E-90
Aurelia aurita	GBRG01184965.1	1366	70.425	630	3.24E-175
Turritopsis sp.	IAAF01068133.1	1359	70.787	653	0
Turritopsis sp.	IAAF01069512.1	1359	70.787	653	0
Bacillariaceae sp.	JBKBDC010000635.1	1202	65.058	386	4.95E-102
Clavelina lepadiformis	HCDF01024642.1	1165	72.189	628	1.36E-175
Durusdinium trenchii	CAXAMM010043494.1	1158	68.739	448	4.20E-121
Trichoplax adhaerens	XM_002114871.1	1157	67.502	405	3.60E-108
Trichoplax adhaerens	XM_002110202.1	1143	69.029	457	6.50E-124
Oopsacas minuta	JAKMXF010000071.1	1020	70.882	494	3.55E-135
Hormiphora californensis	PQ367784.1	443	80.135	383	9.01E-106
Pukia falcata	PQ367781.1	443	80.361	388	7.39E-107
Ctenophora sp.	PP905525.1	442	80.543	393	1.74E-108
Lampea lactea	PP905522.1	442	80.09	379	1.10E-104
Callianira antarctica	PQ357472.1	442	80.317	389	2.12E-107
Dryodora glandiformis	PP905538.1	441	80.272	389	2.12E-107
Cladococcus viminalis	KT390043.1	434	80.184	384	5.51E-107
Salpingoeca macrocollata	KT757483.1	166	96.386	274	1.05E-71
Cryptodendrum adhaesivum	KC812216.1	165	96.364	272	1.60E-70
Triactis producta	KC841875.1	165	96.364	272	1.60E-70
Heterodactyla hemprichii	KC812218.1	165	96.364	272	1.60E-70
Thalassianthus aster	KC812220.1	165	96.364	272	1.60E-70
Phyllodiscus semoni	KC812205.1	165	96.364	272	1.60E-70
Turritopsis nutricula	KT757169.1	163	95.092	255	1.72E-65
Turritopsis dohrnii	EU272596.1	163	95.092	255	1.72E-65
Turritopsis sp.	EU305538.1	163	95.092	255	1.72E-65

Appendix B: NIH Web Blast Alignment Data

RID: 4HMW986M114 (June 10 2025).

Job Title:gb|KN837078.1|Program: BLASTN

Query: ***Sphaerobolus stellatus*** SS14 unplaced genomic scaffold SPHSTscaffold_3 ID: KN837078.1(DNA) Length: 1358

Subject: TSA: ***Turritopsis*** **sp**. SK-2016 mRNA, contig: c60792_g1_i1. ID: IAAF01069512.1(rna) Length: 1354

Sequences producing significant alignments:

Description	Max Score	Total Score	Query cover	E value	Per. Ident	Acc. Len	Accession
TSA: Turritopsis sp. SK-2016 mRNA, contig: c60792_g1_i1	653	653	100%	0	70.79	5047	IAAF01069512.1

Alignments:

>TSA: Turritopsis sp. SK-2016 mRNA, contig: c60792_g1_i1, transcribed RNA sequence

Sequence ID: IAAF01069512.1 Length: 5047

Range 1: 1362 to 2716

Score:653 bits (723), Expect:0.0,

Identities:962/1359(71%), Gaps:5/1359(0%), Strand: Plus/Minus

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Query 448235  TAAAGATCAAAAATGGTACACCGCCAGTACGTAAGACTGCACTTCGTCAAATCACTGATA  448294
              ||||||| ||||| || ||||| ||| | | ||| |||| ||||| ||| | |||||||
Sbjct 2716    TAAAGATTAAAAACGGAACACCACCAATGAGAAAGGCTGCTCTTCGACAAGTTACTGATA  2657

Query 448295  AGGCACGCGAATTTGGTGCTGGTCCTCTATTCGACAAAATCCTTCCCTTGCTTATGGAGC  448354
              | || || ||||||||| || |||| | |||| | |||| | || |||||| |||  |
Sbjct 2656    AAGCTCGGGAATTTGGAGCAGGTTCATTATTTAATCAAATATTGCCATTGCTCATGTCTC  2597

Query 448355  GGACACTGGAGGATCAAGAACGTCATTTGCTGGTCAAGGTTATTGACCGTGTCTTGTATA  448414
               || || || |||||||||||||||||| ||||| || |||||| || ||| |||||||| |
Sbjct 2596    CAACCCTTGAAGATCAAGAACGTCATTTATTGGTAAAAGTTATCGATCGTATCTTGTACA  2537

Query 448415  AGTTGGATGACCTTGTTCGTCCATACGTCCACAAGATTCTTGTCGTTATTGAGCCTCTTT  448474
              | | |||||| || || || ||||| || |||||||||||| || || |||||||| | |
Sbjct 2536    AACTTGATGATCTGGTACGACCATATGTTCACAAGATTCTGGTGGTCATTGAGCCCTTGT  2477

Query 448475  TGATCGACGAGGACTATTACGCTCGCGTCGAAGGTCGTGAAATCATCTCTAACTTGGCCA  448534
              |||| || ||||| ||||| ||||| || |||||| || || ||||| || || ||||| |
Sbjct 2476    TGATTGATGAGGATTATTATGCTCGTGTTGAAGGCCGAGAGATCATTTCAAATTTAGCAA  2417

Query 448535  AGGCAGCTGGTTTGGCACACATGATCTCCACAATGCGGCCAGATATCGACCACGCCGATG  448594
```

Query 449434 CAAGAACAGACGACTGAGGATCAAGTGATGTTGGATGGTTTCGGTACCGTTGTTAACGCA 449493
Sbjct 1520 CAGGAACAGACGAATGAGGATGTGGTCATGCTGAATGGGTTTGGTACGGTTATAAATGCA 1461

Query 449494 CTTGGCATCCGTGTCAAGCCATACCTTACTCAAATCGTTTCGACGGTCCTATGGCGACTG 449553
Sbjct 1460 TTTGGGGCACGAACTAAACCATACTTACCACAGATCTGTGGTACCATTTTATGGCGTTTA 1401

Query 449554 AACAACAAGAGTGCAAAGGTCCGACAACAAGCTGCCGAT 449592
Sbjct 1400 AACAATAAGTCTGCAAAAGTTCGTCAACAGGCTGCCGAT 1362

RID: 4HNK0E3H114 (June 10 2025)
Job Title:gb|KN837078.1| Program: BLASTN

Query: Sphaerobolus stellatus SS14 unplaced genomic scaffold SPHSTscaffold_3 ID: KN837078.1(DNA) Length: 1358

Subject: TSA: Turritopsis sp. SK-2016 mRNA, contig: c60504_g1_i2. ID: IAAF01068133.1(rna) Length: 1354

Sequences producing significant alignments:

Description	Max Score	Total Score	Query cover	E value	Per. Ident	Acc. Len	Accession
TSA: Turritopsis sp. SK-2016 mRNA, contig: c60504_g1_i2	653	653	100%	0	70.79	5045	IAAF01068133.1

Alignments:

>TSA: Turritopsis sp. SK-2016 mRNA, contig: c60504_g1_i2, transcribed RNA sequence

Sequence ID: IAAF01068133.1 Length: 5045

Range 1: 2330 to 3684

Score:653 bits (723), Expect:0.0,
Identities:962/1359(71%), Gaps:5/1359(0%), Strand: Plus/Plus

Query 448235 TAAAGATCAAAAATGGTACACCGCCAGTACGTAAGACTGCACTTCGTCAAATCACTGATA 448294
Sbjct 2330 TAAAGATTAAAAACGGAACACCACCAATGAGAAAGGCTGCTCTTCGACAAGTTACTGATA 2389

Query 448295 AGGCACGCGAATTTGGTGCTGGTCCTCTATTCGACAAAATCCTTCCCTTGCTTATGGAGC 448354
Sbjct 2390 AAGCTCGGGAATTTGGAGCAGGTTCATTATTTAATCAAATATTGCCATTGCTCATGTCTC 2449

Query 448355 GGACACTGGAGGATCAAGAACGTCATTTGCTGGTCAAGGTTATTGACCGTGTCTTGTATA 448414
Sbjct 2450 CAACCCTTGAAGATCAAGAACGTCATTTATTGGTAAAAGTTATCGATCGTATCTTGTACA 2509

Query 448415 AGTTGGATGACCTTGTTCGTCCATACGTCCACAAGATTCTTGTCGTTATTGAGCCTCTTT 448474

Sbjct 2510 AACTTGATGATCTGGTACGACCATATGTTCACAAGATTCTGGTGGTCATTGAGCCCTTGT 2569

Query 448475 TGATCGACGAGGACTATTACGCTCGCGTCGAAGGTCGTGAAATCATCTCTAACTTGGCCA 448534
Sbjct 2570 TGATTGATGAGGATTATTATGCTCGTGTTGAAGGCCGAGAGATCATTTCAAATTTAGCAA 2629

Query 448535 AGGCAGCTGGTTTGGCACACATGATCTCCACAATGCGGCCAGATATCGACCACGCCGATG 448594
Sbjct 2630 AAGCGGCAGGCTTAGCCACCATGATTTCCACTATGAGACCAGATATTGATAATATTGATG 2689

Query 448595 AGTATGTACGAAATACCACTGCCCGTGCTTTCTCAGTCGTTGCATCCGCACTTGGTATCC 448654
Sbjct 2690 AATATGTGAGAAACACAACTGCCAGAGCATTTGCAGTTGTTGCATCTGCACTAGGAATAC 2749

Query 448655 CTTCACTTCTTCCTTTCCTCAAGGCCGTATGTCGCTCGAAAAAGTCGTGGCAGGCTCGTC 448714
Sbjct 2750 CTTCATTGTTACCCTTCTTAAAAGCTGTGTGTAAAAGTAAAAAATCTTGGCAAGCTCGTC 2809

Query 448715 ATACTGGTATCCGTATTGTCCAGCAGATCGCCATTATGATGGGTTGTGCTATCCTTCCCC 448774
Sbjct 2810 ACACTGGAATTAAAATTGTGCAACAAATTGCCATTTTGATGGGATGTGCTATCTTGCCAC 2869

Query 448775 ATCTTCGCAATCTCGTTGATTGTATCGCTCATGGTTTGGAGGATGAGCAGCAGAAGGTCC 448834
Sbjct 2870 ATCTGAGAAATCTTGTTGAAATTATTGAACATGGTCTTGTTGATGAGCAGCAGAAAGTTC 2929

Query 448835 GCACGATGACTGCCCTAGCATTGGCAGCGTTGGCCGAAGCTGCGGCACCGTACGGTATCG 448894
Sbjct 2930 GTACCATTACAGCTCTTGCCATTGCTGCTTTGGCTGAAGCTGCTACGCCCTATGGTATTG 2989

Query 448895 AATCATTCGATAACGTCTTGAAGCCTTTATGGAGCGGTATCCGACTGCATCGCGGAAAGG 448954
Sbjct 2990 AGTCATTTGACAGTGTCTTAAAACCGTTATGGAAAGGTATCAAACAACATCGTGGAAAGG 3049

Query 448955 GTTTGGCGGCATTCTTGAAGGCAATCGGCTTCATTATCCCTCTTATGGACCCTGAATATG 449014
Sbjct 3050 GCTTGGCTGCATTCTTAAAAGCGATTGGCTATTTGATCCCACTTATGGATGCTGACTATG 3109

Query 449015 CAAATTACTATACAAAGGGTGGCGTTACAGACACACTGATTCGTGAATTCCAATCCTCGG 449074
Sbjct 3110 CTTACCACTACACAA---GAGAAGTGATGATTATTCTAATTCGTGAGTTTCAATCTCCTG 3166

Query 449075 ATGAAGAAATGAAGAAGATCGTTCTCAAGGTCGTCAAACA-AGTTGCCGCGACCGAAGGA 449133
Sbjct 3167 ATGAAGAAATGAAGAAAATTGTATTGAAGGTTGTTAAGCAGTGTTG-TGCAACTGATGGT 3225

Query 449134 GTCACGCCTCAGTATATCAAGGAGGCCCTCTTACCCGACTTCTTCAAATCTTTCTGGGTA 449193
Sbjct 3226 GTAGAAGCTAATTATATTAAAGAGGAAATTTTACCAGAGTTTTTTAAACATTTCTGGACT 3285

Query 449194 CGTCGCATGGCATTAGATAGACGGAACTATCGCCAGGTCGTCGAAACTACTGTCGAATTA 449253
Sbjct 3286 CATCGAATGGCATTAGATAGACGTAACTACAGACAGTTGGTAGACACTACTGTAGAAGTG 3345

Query 449254 GCCCAAAAAGCAGGTGTTGCTGAGATTGTCGGAAAAATTGTTGATGGTCTGAAGGATGAT 449313
Sbjct 3346 GCAAACAAAGTGGGAGCAGCACACATCATTGGCCGTGTTGTTGATGATTTGAAAGATGAA 3405

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Query 449314  GCCGAGCCCTATCGAAAGATGGTTATGGAGACAATTACCAAGGTCATAGCCTCTCTTGGT  449373
              || | |||||||| ||||| | || || |||  ||||| || ||  |||||
Sbjct 3406    AATGAACAATATCGAAAAATGGTATTAGAAACTATTGAAAAGGTGATGGCAAACCTTGGA  3465

Query 449374  GCTGCAGATATTGATGAGCGTCTGGAGGTTCGTCTTGTGGACGGTATCATTTATTCCTTC  449433
              ||| |||| |||||||  | |||| | | || | || ||||| | ||| | |||
Sbjct 3466    GCTTCAGAGATTGATTCAAGATTGGAAGAACAACTGATTGATGGTATATTGTATGCATTC  3525

Query 449434  CAAGAACAGACGACTGAGGATCAAGTGATGTTGGATGGTTTCGGTACCGTTGTTAACGCA  449493
              || |||||||||| ||||||  || ||| || |||| || |||||||||| | || |||
Sbjct 3526    CAGGAACAGACGAACGAGGATGTGGTCATGCTGAATGGATTTGGTACCGTTATAAATGCA  3585

Query 449494  CTTGGCATCCGTGTCAAGCCATACCTTACTCAAATCGTTTCGACGGTCCTATGGCGACTG  449553
              ||||  ||  || ||||||| | ||| ||| |  || | ||||||| |
Sbjct 3586    TTTGGTGCACGAACTAAACCATACTTACCACAGATCTGTGGTACCATTTTATGGCGTTTA  3645

Query 449554  AACAACAAGAGTGCAAAGGTCCGACAACAAGCTGCCGAT  449592
              ||||| ||| |||||| || || ||||| |||||||||
Sbjct 3646    AACAATAAGTCTGCAAAAGTTCGTCAACAGGCTGCCGAT  3684
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