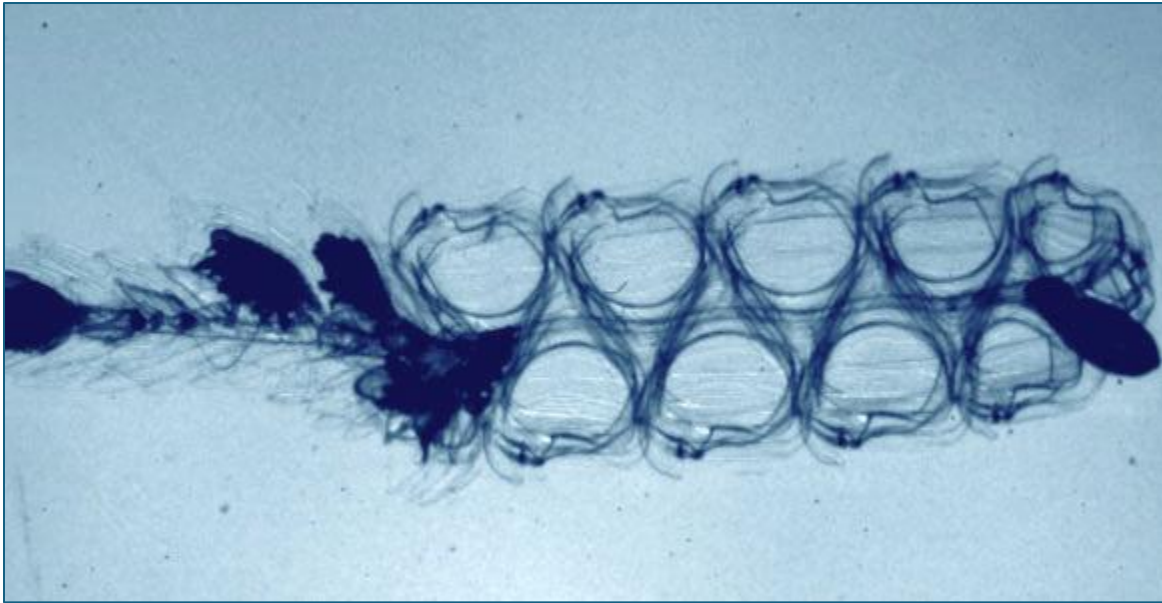


EXTENSIVE HUMAN/SIPHONOPHORE GENETIC SEQUENCE OVERLAP: *A Brief Communication*

Authors: Ashley Gjovik, B.S., J.D. (ashleymgjovik@protonmail.com) | **Date:** June 4 2025



Nanomia (Sci-News.com, 2015, Image credit: Costello, J. et al.).

Abstract:

BLAST analysis using a custom database compiled from NIH and ENA sequences revealed extensive sequence conservation between human genome assemblies and diverse marine invertebrate species. Alignments showed 70-82% identity across 1,762-2,198 base pairs with E-values of 0, indicating extremely high statistical significance indicating non-random alignment. Top matches included cnidarians *Nanomia septata* and *Turritopsis nutricula*, gastropods *Pupa nitidula*, *Bosellia mimetica*, *Tylodina fungina*, *Microhedyle glandulifera*, and *Aplysia punctata*; echinoderm *Cucumaria elongata*; amoebas *Vermamoeba*, *Euglypha*, and *Paraflabellula*; and carnivorous demosponge *Chondrocladia grandis*. The statistical impossibility of such extensive conservation across taxa separated by hundreds of millions of years challenges existing phylogenetic models and demands systemic investigation.

Keywords:

BLAST analysis, sequence homology, marine invertebrates, cnidaria, siphonophore, porifera, comparative genomics, evolutionary biology, genome conservation, E-value, phylogenetic analysis, colonial organisms, systematic genomics

Citation:

Gjøvik, Ashley M.. “Extensive Human/Siphonophore Genetic Sequence Overlap: A Brief Communication”. *The Journal of Decolonized Ecology and Evolution*, 1, no. 1 (June 4, 2025). <https://doi.org/10.5281/zenodo.15596204>.

INTRODUCTION

This communication presents BLAST analysis results revealing extensive sequence conservation between human genome assemblies and diverse marine invertebrate species. The findings emerged from systematic comparative genomics using a custom database compiled from NIH and ENA sequences.

The statistical significance of these alignments—featuring E-values of 0 across sequence lengths exceeding 2,000 base pairs—demands immediate investigation by the genomics community. While the biological implications remain to be determined, the mathematical impossibility of these matches occurring by chance requires mechanistic explanation independent of current taxonomic and bureaucratic frameworks.

This communication represents preliminary findings from a larger investigation currently in preparation. Additional genomic analyses and expanded theoretical frameworks will be presented in forthcoming publications.

FINDINGS

Comparative analysis using a custom BLAST database compiled from NIH and ENA sequences yielded the following representative results, with extensive replication:

Top alignments by length with E-value = 0:

- *Xenoturbella bocki*, Eumetazoa
2,374 bp; 65.4% identity; E-value: 4.91E-120*

*Note: *Xenoturbella* alignment shows the only non-zero E-value in the discussed long length matches.

- *Nanomia septata*, Cnidaria, Siphonophorae
2,198 bp; 70.8% identity; E-value: 0; Bit_Score 1,058
6,484 individual matches with lengths > 2,000 bp
- *Cucumaria elongata*, Echinoderm
1,952 bp; 77.3% identity; E-value: 0; Bit_Score 1,000
- *Pupa nitidula*, Gastropoda
1,941 bp; 80.3% identity; E-value: 0; Bit_Score 1,345
- *Vermamoeba vermiformis*, Amoebozoa
1,941 bp; 72.5% identity; E-value: 0; Bit_Score 897
- *Bosellia mimetica*, Gastropoda
1,931 bp; 79.8% identity; E-value: 0; Bit_Score 1,273
- *Tylodina fungina*, Gastropoda
1,928 bp; 80.0% identity; E-value: 0; Bit_Score 1,310
- *Microhedyle glandulifera*, Gastropoda
1,927 bp; 80.0% identity; E-value: 0; Bit_Score 1,295

- *Aplysia punctata*, Gastropoda
1,927 bp; 79.3% identity; E-value: 0; Bit_Score 1,230
- *Japonacteon nipponensis*, Gastropoda
1,926 bp; 82.0% identity; E-value: 0; Bit_Score 1,557
- *Euglypha acanthophora*, Rhizaria, Cercozoa
1,922 bp; 71.6% identity; E-value: 0; Bit_Score 822
- *Paraflabellula*, Amoebozoa
1,921 bp; 72.5% identity; E-value: 0; Bit_Score 975
- *Turritopsis nutricula*, Cnidaria, Hydrozoa
1908 bp; 76.8% identity; E-value: 0; Bit_Score 1,273
- *Chondrocladia grandis*, Porifera, Cladorhizidae
1,762 bp; 80.7% identity; E-value: 0; Bit_Score 1,288

Systematic patterns include multiple human genome contigs showing consistent matches; alignment lengths up to 2,198 base pairs with statistical confidence (E-value = 0); and Bit scores exceeding 1,000+ across all major alignments except amoeba.

MORPHOLOGICAL OBSERVATIONS

Beyond sequence homology, striking anatomical parallels warrant consideration. *Nanomia septata* colony organization bears remarkable resemblance to human organ systems: branching patterns mirror cardiovascular/respiratory networks, while specialized colonial units (zooids) parallel organ and glandular structures. The siphonophore's coordinated jet propulsion mechanism shows functional similarity to cardiac/pulmonary circulation.

Human physiology exhibits characteristics consistent with marine colonial organization: ~60% water content approximating seawater composition, lymphatic systems resembling colonial circulation networks, and organ systems functioning as specialized units within a coordinated whole.

Gastropod progression patterns: The sequence identity progression correlates with increasing protective structure complexity (shell-less → minimal shell → developed shell), suggesting evolutionary development toward integrated barrier systems.

Aplysia (the sea hare model organism fundamental to neuroscience research), shows remarkable genetic similarity potentially representing early mammalian-like neural architecture in marine form.



Aplysia (Golestani et al, 2019).

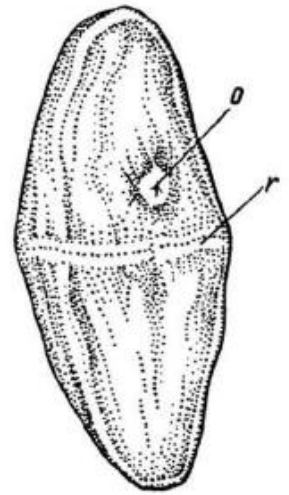
Protective system internalization: *Cucumaria elongata* (77.3% identity, 1,952 bp) exhibits advanced skin-like barrier systems, while gastropod shell development patterns suggest internalization of protective technology. *Chondrocladia grandis* (80.7% identity, 1,762 bp, >50 alignments) represents foundational internal calcium architecture through spicule formation, the original internal skeletal technology. Shell and bone composition show fundamental similarities—calcium-based mineralization with protein matrix scaffolding, identical layered architecture, and shared cytoskeletal construction mechanisms.



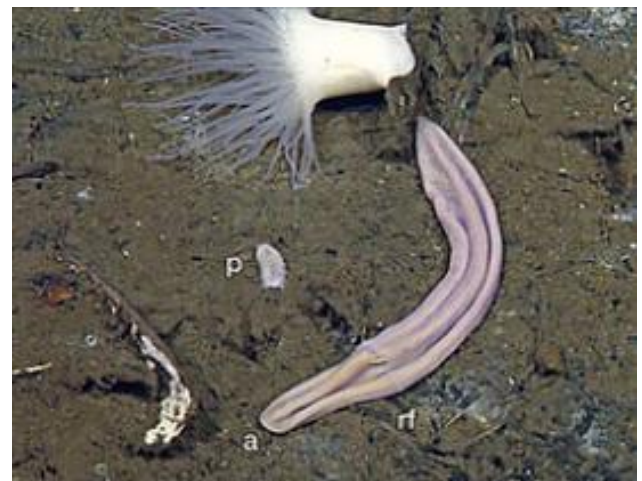
Cucumaria frondosa (Hinz, H., n.d.)

The architectural progression from sponge spicules (internal calcium structures) → gastropod shells (external calcium protection) → mammalian bones (refined internal calcium systems) demonstrates systematic development of calcium-based structural support. The gastropod sequence progression may document the transition from external protective shells to internalized skeletal systems, with high genetic similarity corresponding to advanced shell architecture.

Xenoturbella integration hypothesis: The unique statistical pattern of *Xenoturbella bocki* (long alignment at 2,374 bp but lowest identity at 65.4%, E-value 4.91E-120) may represent evidence of colonial incorporation rather than evolutionary divergence. The marginally weaker statistical significance suggests *Xenoturbella* represents a surviving remnant from experimental phases of colonial development—specifically, early attempts at creating oceanic containment systems for environmental gatekeeping rather than terrestrial adaptation, as evidenced by sophisticated barrier systems in marine mammals.



Xenoturbella bocki
(Raikova, O., 2008)



Xenoturbella profunda (Rouse et al, 2016).

Salinity conservation: Human extracellular fluid—particularly blood plasma—maintains a sodium chloride concentration of approximately 0.9%, a value that closely mirrors the estimated salinity of the Precambrian and early Paleozoic oceans. In contrast, modern seawater has a salinity of ~3.5%. This discrepancy suggests that as ocean chemistry changed over geological time, early metazoans evolved internal homeostatic systems to conserve their ancestral ionic environment.

These include semipermeable membranes, active ion transporters, and renal systems capable of fine-tuned osmoregulation. The constancy of the ionic ratios (e.g., Na^+ , Cl^- , K^+ , Ca^{2+} , and HCO_3^-) in vertebrate extracellular

fluids from marine fishes to humans supports the hypothesis that modern animals retain a "molecular memory" of their marine origins.



Tylodina perversa (Pillon, R., 2012).

This conservation of internal salinity, despite external fluctuation, highlights the evolutionary advantage of maintaining stable intracellular and extracellular environments. It is likely that such conserved salinity profiles were crucial for the emergence of nerve conduction, muscle contraction, and enzyme activity, all of which depend on tightly controlled ionic gradients.

These observations, while preliminary, suggest morphological patterns that complement the genetic findings and merit systematic comparative analysis.

Note: The author holds science and law degrees, with a systems engineering background. This interdisciplinary perspective may reveal patterns less apparent within single disciplines.

METHODS

Custom BLAST databases were constructed from sequences obtained from NIH and ENA databases, organized into generalized taxonomic groups: siphonophores, primordial marine organisms, amoebas, sponges, and euopisthobranchia. Database composition and complete sequence listings are provided as supplementary data.

BLAST analyses were performed using BLASTN with two search strategies: standard BLASTN (E-value threshold $1E-10$) and dc-megablast (E-value threshold $1E-5$). Query sequences consisted of human genome assemblies from Reference_Humans.fasta. All searches used 8 CPU threads and tabular output format including query sequence ID, subject sequence ID, subject title, alignment length, percent identity, bit score, E-value, mismatches, query coverage, query coverage per HSP, gap openings, query length, query start/end positions, subject length, and subject start/end positions.

Self-matches were excluded using PowerShell filtering to remove alignments where query and subject sequence IDs were identical. dc-megablast was used preferentially except when computational constraints required standard BLASTN due to database size limitations.

Database searches were conducted against the following taxonomic groups:

- Siphonophores (both standard BLASTN and dc-megablast)
- Primordial ocean organisms (standard BLASTN)
- Amoebas (both standard BLASTN and dc-megablast)
- Sponges (standard BLASTN)
- Euopisthobranchia (standard BLASTN)

All analyses were performed on 2025-05-31 with results exported to tab-separated value files for downstream analysis. This research was designed for a different investigation, and the results discussed herein were not expected or targeted. This research also appears to point toward long-alignment sequence matching as a novel and fruitful method to uncover deep evolutionary relationships.

DISCUSSION

The statistical impossibility (E-value = 0) of alignments exceeding 2,000 base pairs occurring by chance represents the most significant finding. The longest alignment (*Nanomia septata* at 2,198 bp) with over 6,000 unique matches above 2,000 bp and mathematical confidence of non-random origin fundamentally challenges existing models. Even moderate identity percentages (65-70%) become irrelevant when sustained across such lengths with zero statistical error. The taxonomic breadth—spanning cnidarians, mollusks, echinoderms, and xenoturbellids—suggests systematic rather than isolated conservation.

Current phylogenetic models place these taxa divergences at hundreds of millions of years ago, making this level of conservation unusual in comparative genomics. The consistency across multiple human genome assemblies and diverse marine invertebrate species indicates robust, reproducible findings.

These results represent systematic architectural patterns demanding investigation:

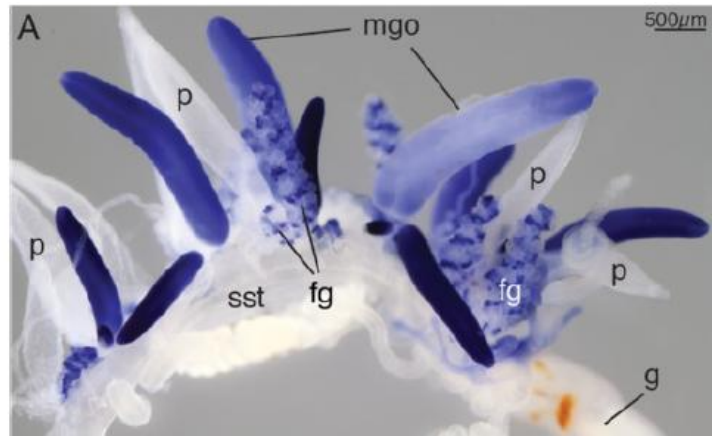
1. **Conservation across impossible statistical thresholds:** E-values of 0 across 2,000+ base pair alignments indicate deterministic rather than stochastic relationships.

2. **Modular organizational systems:** sequence homology correlates with functional complexity progression in protective architecture development.
3. **Integrated multi-component design:** genetic, physiological, and morphological evidence converges on colonial assembly mechanisms.
4. **Historical system requirements preservation:** salinity maintenance demonstrates persistent design specifications across geological timescales.

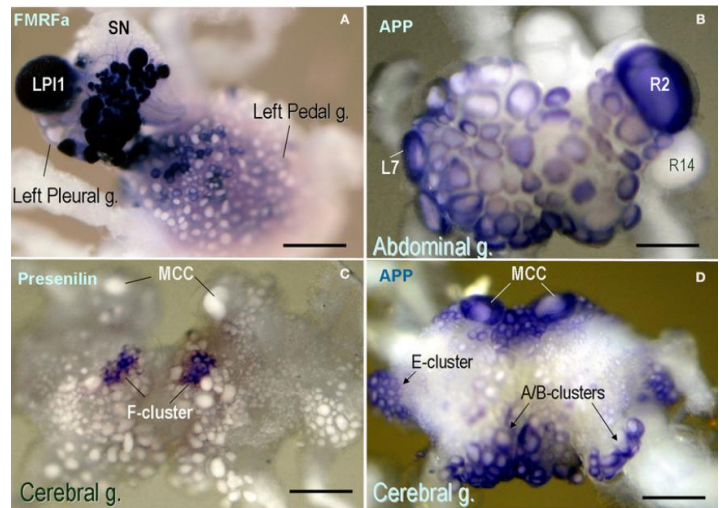
The data patterns suggest biological systems operating under engineering principles rather than traditional evolutionary models. Investigation priorities may focus on:

- Independent validation using expanded sequence databases.
- Systematic analysis of colonial organization across marine invertebrates.
- Comparative physiology of barrier/containment systems.
- Historical ocean chemistry correlates with internal fluid composition.

Current evolutionary models position tunicates (sea squirts) as close invertebrate relatives to vertebrates. However, these BLAST results also demonstrate significantly sequence conservation with cnidarian colonial organisms suggesting revision of animal evolutionary frameworks may be warranted.



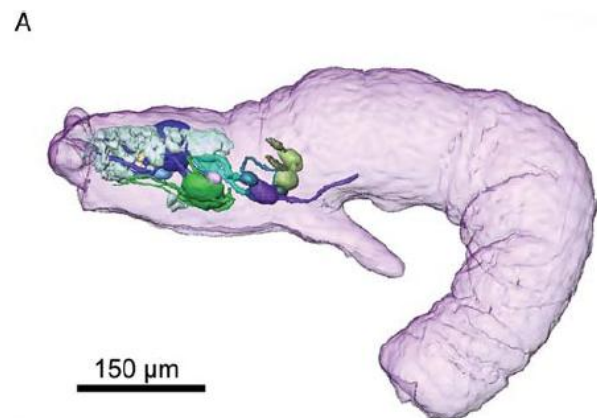
Nanomia bijuga, Siphonophorae (Siebert et al., 2015).



Aplysia californica (Moroz, L. and Kohn, A.B., 2010).



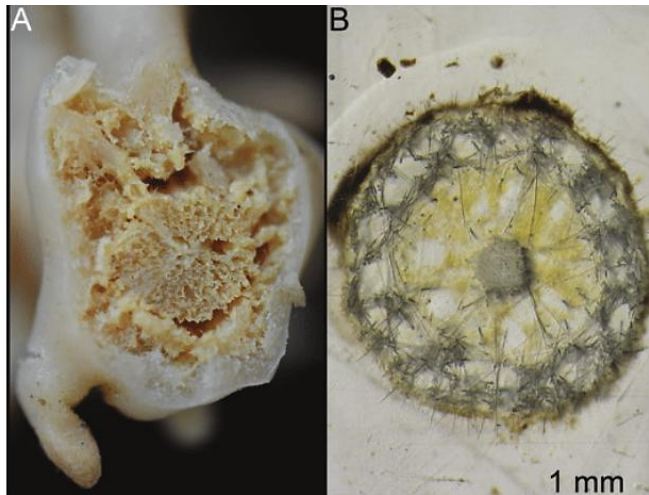
Pupa (Valdés et al, 2023).



Microhedyle glandulifera (Eder, et al, 2011).



Japonacteon (Shellpedia, n.d.)



Chondrocladia grandis, (A) Cross section of upper stem, (B) cross section of process. (Hestetun et al, 2017).



Bosellia mimetica (Vitale, F., 2022).

CONCLUSION

The data presents systematic patterns requiring investigation independent of theoretical frameworks. Statistical impossibilities demand mechanistic explanations. Multiple convergent evidence streams—genetic homology, physiological specifications, morphological organization—indicate integrated biological systems operating under design principles.

Priority investigation areas include expanded genomic validation, colonial organization analysis, and historical specification maintenance mechanisms. The patterns suggest biological architecture following engineering logic rather than traditional evolutionary models.

These findings present testable hypotheses for immediate investigation by specialists equipped with appropriate analytical resources.

DATA AVAILABILITY

All sequences referenced are publicly available through NIH/NCBI and ENA databases. Custom FASTA databases, output files, and sequence listings are provided as supplementary material at <https://osf.io/69whf/>.

Note: This brief communication presents preliminary findings from a larger research program currently under development. Extended analysis and additional theoretical frameworks will be detailed in subsequent publications.

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.

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