Frontiers in Bioscience Landmark

Front. Biosci. (Landmark Ed) **2025**; 30(4): 37380
https://doi.org/10.31083/FBL37380

Editorial

Brown Algae: Uncovering the Secrets of Evolutionary Genomics and Multicellularity

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Academic Editor: Graham Pawelec
Submitted: 24 January 2025 Revised: 16 March 2025 Accepted: 19 March 2025 Published: 22 April 2025

Brown algae are a tribute to the inventiveness of nature because of their unique evolutionary history and crucial function in marine ecosystems. Their usefulness as a unique model for researching complex independently developed multicellularity, and evolutionary genomics is further shown by their capacity to flourish in dynamic coastal habitats, as recently demonstrated by detailed studies published in *Cell* [1] and *Nature* [2] and commentary [3]. These species are prime examples of the developmental hourglass model, which offers profound insights into the conservation of developmental processes throughout multicellular life forms, in addition to undergoing substantial genomic and transcriptome modifications for adaptation.

An interesting idea in evolutionary biology is the Developmental Hourglass Model [4], which shows how many organisms often go through similar developmental phases while having distinct looks and ways of living (see explanation in [3]). This theory obtained strong molecular transcriptomic support [5–9]. An hourglass example can be used to illustrate this idea. Imagine an hourglass with three sections: top, narrow center, and bottom, which can represent the growth of the organism. The early phases of development, when organisms may differ greatly, are represented by top of the hourglass. In these early stages, for instance, the development of frog embryos might vary significantly from that of chicken embryos. But as growth goes on, these many routes come together to produce a more homogeneous stage, which is symbolized by the hourglass's tight center. Organisms have similar developmental plan throughout this critical and widely preserved intermediate stage. For example, at this stage, the neural tube, the crucial predecessor to the central nervous system, forms in both frog and chicken embryos. The hourglass model identifies this mid-developmental phase similarity across species as a universal developmental stage, indicating common evolutionary ancestry. As growth proceeds, species start to develop their own characteristics. For example, feathers in chickens and particular skin textures in frogs, before diverging again in the broad bottom portion. This model highlights features of biological development where life's complexity is united at a point in the center, demonstrating a profound evolutionary relationship, even if it begins and ends in a variety of forms. In addition to helping scientists comprehend and forecast developmental processes, the Developmental Hourglass Model highlights deep similarities among various living things, showing that all of them go through stages in their development that tie them to common biological heritage.

Adaptation and evolutionary genomics. Genetic foundations that have enabled brown algae to be established as essential elements of coastal ecosystems are examined in research published in *Cell* [1]. Significant horizontal gene transfers, especially from bacterial origins, and gene family amplifications are hallmarks of brown algae's evolutionary history. Brown algae now have distinct metabolic pathways vital to their survival and ecological success as a result of these genetic exchanges. Gene gains that are mostly the result of horizontal gene transfers and domain innovations have defined this genomic evolution, allowing for the creation of complex features including sophisticated cell wall structures and a variety of reproductive methods. Their capacity to flourish in intertidal zones, where environmental conditions are most changeable, depends on these adaptations.

Hourglass Model of Development. The *Nature* paper [2] adds to our knowledge by demonstrating a unique transcriptome hourglass pattern that complex brown algae, including those in the *Fucales* and *Laminariales* orders, display throughout development. This pattern highlights a stable developmental phase that includes times of greater transcriptome variation and during which key body designs are formed. According to the hourglass model, there is notable conservation of gene expression linked to fundamental developmental processes at crucial mid-embryonic periods, even while there is divergence at early and late developmental stages (Fig. 1, Ref. [2]). This points to a common pattern in multicellular animals, where important structural and functional characteristics are maintained during the mid-embryonic period, which serves as a stabilizing force.

Through the use of genomic and transcriptomic data, findings published in *Cell* [1] and *Nature* [2] both illustrate the adaptive methods of brown algae. A species that exhibits extraordinary conservation of developmental processes at crucial periods of embryogenesis is shown by the synthesis of results from these papers while experiencing

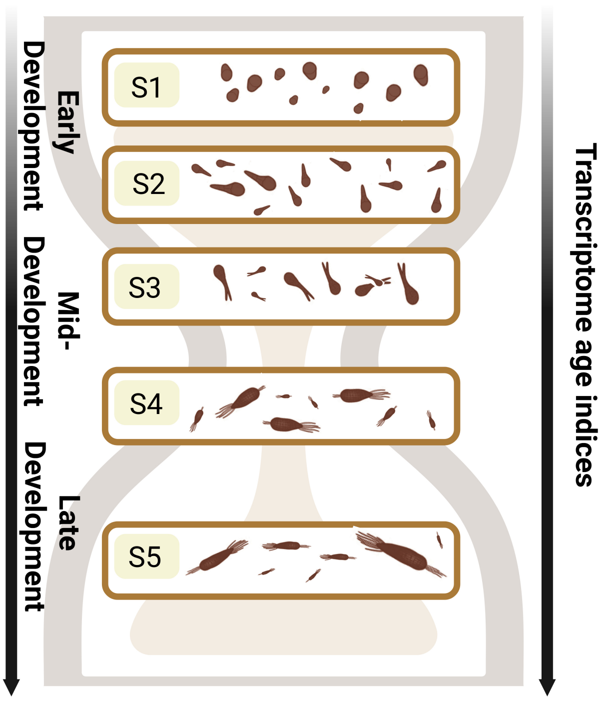

Fig. 1. Schematic of an "hourglass" model depicting five successive developmental stages (S1–S5) from early (top) to late (bottom) development and in parallel a transcriptome age. Each boxed stage (S1–S5) shows representative morphologies in brown, illustrating how cellular brown algae form changes as development proceeds. The hourglass shape behind the stages underscores the concept that mid-development (S4) represents a narrow "bottleneck", whereas early (S1–S3) and late (S5) stages are more divergent. Based on [2]. Created with BioRender.com.

substantial genetic diversification to adapt to varied environmental constraints. A unique window into evolutionary mechanisms that mold living forms in response to environmental stresses is provided by the dual nature of developmental conservation and genetic flexibility. Beyond the realm of marine biology, developmental techniques and the evolutionary history of brown algae provide deep insights. Scientists learn more about principles of development and evolution that apply to the whole tree of life by examining these creatures. Particularly, the hourglass model is consistent with findings in other complex multicellular animals, indicating that mid-developmental conservation may be a crucial stabilizing characteristic that promotes the variety required for species to evolve and adapt.

Building on the evolutionary model of brown algae presented in [1], we can potentially uncover new mechanisms, critical theories, and hidden "secrets" of this lineage. First, expanding genome resources and comparative genomics will be key. Although the paper [1] highlights new genomic assemblies spanning many brown algal families, there is a need to incorporate more taxa, especially those in minor or understudied orders, to sharpen resolution on how genetic innovations appear or disappear across evolutionary branches. Some genomes remain partial; generating chromosome-level assemblies and phasing haplotypes would allow more robust structural comparisons—useful, for instance, in clarifying patterns of viral insertions or gene-family expansions. A second potential approach is integrative omics studies. Although a large fraction of genes lack assigned function, transcriptome, proteome, and metabolome data could link genes to biological processes. Combining multi-omics datasets—for example, across life cycle stages or under different environmental conditions—would clarify how key gene families (e.g., haloperoxidases, cell wall biosynthesis genes, phlorotannin-related polyketide synthases) contribute to adaptation and development. Developmental transcriptomics focusing on sporophytic, gametophytic, and transitional phases in species with distinct life cycles would reveal gene expression shifts throughout development. Proteomic and metabolomic profiling, especially for defense compounds and cell wall polysaccharides, could more precisely track biosynthetic pathways. Third, the widespread presence of integrated *Phaeovirus* sequences in brown algal genomes indicates intriguing virus–host co-evolution. Studies tracking insertions over generations, screening for viral-derived histidine kinases, or experimentally manipulating viral integrases in the lab could illuminate how viruses mediate adaptation.

Brown algae will surely continue to be an important model for studying developmental and genomic evolution in relation to environmental adaptability and survival. In addition to enhancing our knowledge of marine biology, brown algae provide important insights into developmental genetics and evolutionary biology. We can expect to apply this knowledge to a wider range of biological and ecological studies by analyzing how these organisms navigate their constantly changing environment. This could result in understanding conservation tactics that are motivated by the same ideas that have allowed brown algae to thrive for millions of years. To summarize, continuous investigation of genetic and developmental complexities of brown algae is a quest to discover the very blueprint of life's flexibility and tenacity, not only to gain information.

Author Contributions

GŽ has participated sufficiently in the work and agreed to be accountable for all aspects of the work.

Ethics Approval and Consent to Participate

Not applicable.

Acknowledgment

Not applicable.

Funding

The research was supported by the Slovak Research and Development Agency under the Contract no. APVV-23-0212. GŽ is partly funded by the European Union's NextGenerationEU through the Recovery and Resilience Plan for Slovakia under the project No. 09I03-03-V03-00008.

Conflict of Interest

The author declares no conflict of interest.

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