ISSN: 3049-0677 (Online)

PhytoTalks
April 2025; Volume 2: Issue 1: 292-296
https://doi.org/10.21276/pt.2025.v2.i1.8

Review Article

OPEN ACCESS

Bioinformatics' usefulness in relation to the Bryophytes

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Article History
Received: 27.03.2025
Revised: 15.04.2025
Accepted: 21.04.2025
Availabale online
Version: 1

Additional Information
Peer review: The publisher expresses gratitude to the anonymous reviewers and sectional editors for their invaluable contributions during the peer review process.
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Publisher's note: Regarding jurisdictional claims in published maps and institutional affiliations, PhytoTalks maintains its objectivity.
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Cite this article: Khushbu A, Alam A. Bioinformatics' usefulness in relation to the Bryophytes. *PhytoTalks*. 2025; 2(1): 292-296.

Abstract

Bryophytes, such as mosses, liverworts, and hornworts, are vital species for studying plant evolution because they serve as a bridge between aquatic algae and terrestrial vascular plants. Their haploid-dominant life cycle, basic shape, and absence of intricate vascular systems offer special insights into the evolution of plants. By making it possible to analyze massive genomic, transcriptomic, and proteomic datasets, the development of bioinformatics has significantly advanced the study of bryophytes. This study examines the use of bioinformatics techniques and tools, with a particular emphasis on transcriptome analysis, comparative genomics, genome sequencing, and molecular clock research, to comprehend the evolution of bryophytes. Important new information about the evolution of bryophytes, the dynamics of gene families, and adaptations to terrestrial life has been made possible by these methods. We also discuss the challenges in bryophyte research and outline future directions, emphasizing the need for expanding genomic datasets, integrating multi-omics approaches, and leveraging advanced computational tools.

Keywords: Bryophytes, bioinformatics, plant evolution, genomic analysis, transcriptomics, comparative genomics, adaptation.

1. Introduction

Because of their distinct biological characteristics and evolutionary status as early land plants, bryophytes—which include mosses, liverworts, and hornworts—are becoming more and more important in the field of bioinformatics. Utilizing computational tools to examine their genomic, transcriptomic, and metabolomic data, their application in bioinformatics encompasses multiple important domains. They offer crucial details regarding the transition from aquatic algae to terrestrial plants. These tiny plants differ from vascular plants in that they have a haploid-dominant gametophytic phase, a basic shape, and no vascular supply. Their ability to maintain ancestral characteristics while displaying notable alterations that made the shift to land easier explains their evolutionary relevance. Our knowledge of bryophyte evolution has been completely transformed by bioinformatics, especially in the fields of transcriptomics, comparative genomics, and genome sequencing. By making it possible to analyze large biological datasets, these techniques have assisted scientists in understanding the molecular mechanisms behind their evolutionary history and adaptations. Species like *Physcomitrium patens* (moss) and *Marchantia polymorpha* (thalloid liverwort) are used as model systems for the study of plant evolution, development, and stress responses. Functional genomics is made simpler by their prominent haploid gametophytic phase, which allows simple genome editing through homologous recombination or CRISPR[1].

The expansion of bryophyte genome and transcriptome databases has led to the emergence of specialized bioinformatics resources. MarpolBase provides tools like BLAST and JBrowse to examine transcripts, proteins, and genomes across a variety of bryophyte species, including Arabidopsis comparisons. PEATmoss offers a gene expression atlas for bryophytes, which makes transcriptomic research easier[2,3].

2. Methodology

This paper's appraisal uses a qualitative methodology and secondary data sources, primarily academic literature. Using academic databases that are available to the public, such as NCBI, Google Scholar, PubMed, Scopus, and Web of Science, a thorough analysis of pertinent papers was carried out. In order to investigate important concepts, synthesize data, and interpret outcomes, the process comprised a methodical study, extensive reading, and in-depth analysis of the chosen sources. The main focus of this paper is a textual documentary analysis that provides a thorough assessment of the body of knowledge already available on the topic.

3.1. Bryophytes as Evolutionary Models

Using bioinformatics methods, phylogenomic time trees are generated to identify evolutionary connections and gene incongruences among bryophytes over a 500 million-year period. These studies make use of programs like Newick tools for phylogenetic tree processing and AliView for sequence alignment. In the plant kingdom, bryophytes play a vital evolutionary role by bridging the gap between vascular plants and green algae. The persistence of essential traits including a haploid-dominant life cycle, unbranched sporophytes, and adaptations for terrestrial living such resistance to desiccation4 underscores their evolutionary relevance[4].

Because of their small size, scant fossil record, and phenotypic flexibility, bryophytes provide special difficulties for conventional taxonomic and evolutionary research, despite their crucial importance in comprehending plant evolution. By enabling the sequencing and comparison of genomes, transcriptomes, and proteomes, bioinformatics has emerged as a crucial tool for overcoming these obstacles and obtaining insights that would be challenging to obtain from morphology alone[5].

3.2. Bioinformatics Tools and Techniques in Bryophyte Research

Large-scale transcriptome and genome datasets for bryophytes have been made possible by next-generation sequencing (NGS) and other high-throughput sequencing methods. The moss *Physcomitrium patens*, the liverwort Marchantia polymorpha, and a number of hornwort species are among the significant bryophyte species that have been employed as model organisms for genomic studies. Bioinformatics tools such as DESeq2, OrthoFinder, and BLAST have facilitated comparative genomics, gene family analysis, and differential expression studies.

3.2.1. *Coevolution Detection Using CoMap:*

Coevolutionary analysis (amino acid residue) were conducted in CoMap v1.5.2, which employs compensation and clustering approaches. Parameters included aligned sequences, a phylogenetic tree, a substitution model, and discrete rate distribution. Coevolving residues were assessed for statistical significance ($p\text{-value} \leq 0.05$) using R, with bootstrap replicates ($n = 1000$) and false discovery rate (FDR) evaluation[6]. Ground-breaking findings about the genomic traits of bryophytes have been made possible by these methods, including the identification of significant regulatory networks, the loss of genes associated with vascular development, and a deeper understanding of adaptations to terrestrial environments. The availability of many bryophyte genomes facilitates comparative studies to understand gene family evolution, whole-genome duplications, and gene loss events, particularly when mosses are compared to liverworts and hornworts[5].

3.3. Phylogenomics and Comparative Genomics

By using large datasets of orthologous genes to construct phylogenetic trees, phylogenomics has shed light on the evolutionary connections between bryophytes and vascular plants. Bioinformatics has resolved long-standing disputes over bryophyte monophyly and their relationship to vascular plants. For example, recent analyses have altered our understanding of early plant diversification by showing that hornworts belong to a clade that also contains mosses and liverworts. Comparative genomics has provided valuable new insights into the genetic advances and reductions that have occurred in bryophytes. For example, because bryophytes lack genes involved in the creation of lignin and other processes necessary for vascular growth, they have a simpler morphology than vascular plants. However, *Physcomitrium patens* and other bryophyte gene duplication occurrences suggest a history of genomic innovation that may have been crucial for adaption to terrestrial environments.

3.4. Key Insights from Bioinformatics in Bryophyte Evolution

Bioinformatics has uncovered several key insights into bryophyte evolution:

3.4.1. ***Genomic Innovation and Reduction:*** Early land plant gene duplication events served as the foundation for later terrestrial adaptations. Gene loss in bryophytes is indicative of a more simplified evolutionary path than the vascular plant's elaboration of characteristics.

3.4.2. ***Regulatory Networks:*** Although bryophyte-specific regulatory modules imply distinct adaptations, the conservation of transcription factors and non-coding RNAs between bryophytes and vascular plants suggests common developmental processes.

3.4.3. ***Adaptation to Terrestrial Life:*** The molecular mechanisms behind bryophytes' ability to withstand desiccation, a crucial adaptation for colonizing terrestrial ecosystems, have been clarified by transcriptome investigations.

3.4.4. ***Molecular Clock Studies:*** Bioinformatics has revised the chronology of the divergence of vascular plants and bryophytes by combining genetic data with fossil calibrations, placing this event in the Cambrian epoch (515–494 million years ago).

3.5. Metabolomics and Ecometabolomics:

Analysis of Secondary Metabolite: Bryophytes generate a variety of secondary metabolites that include cytotoxic, antifungal, and antibacterial qualities. ClassyFire and ChemOnt ontology are two examples of bioinformatics pipelines that automate compound classification. These pipelines use ultra-performance liquid chromatography coupled with mass spectrometry (UPLC/ESI-QTOF-MS). These techniques aid in determining the ecological functions of substances, such as sesquiterpenoids for pathogen defense or flavonoids for light protection[7, 8].

3.5.1. ***Data Processing Tools:*** To overcome obstacles such the absence of reference spectra for new chemicals, software such as xcms, metAlign, and MzMine analyzes huge metabolomic datasets from bryophytes are utilized in forensic bioinformatics to track down plant pieces. In educational labs, students learn techniques like as DNA isolation, PCR, gel electrophoresis, and genotyping (e.g., RAPD-PCR). They also sequence plastid introns and utilize bioinformatics to identify species. These techniques take advantage of bryophytes' capacity to adhere to surfaces and preserve DNA[9,10].

3.5.2. ***Educational Resources***: By combining bryophyte forensics with bioinformatics, open-inquiry laboratories let students learn how to identify species by analyzing sequence data, improving their molecular biology and computational analysis abilities[11].

3.6. Environmental and Ecological Studies:

Bioindicators: Because bryophytes are sensitive to changes in their surroundings, they are perfect for biomonitoring. In order to associate species composition with environmental variables, bioinformatics examines their distribution and life-form patterns across land cover types using techniques such as variance partitioning and canonical correspondence analysis[12].

3.6.1. ***eDNA Metabarcoding***: By processing sequencing data through computational pipelines, hybridization capture and PCR-based environmental DNA (eDNA) metabarcoding track the variety of bryophytes in environments such as rivers.

3.7. Phenotypic analysis and bioimaging:

Image processing: For bioinformatics applications, high-quality macroscopic and microscopic photographs of bryophytes—like those in the Scapaniaceae family—are annotated with machine-actionable metadata. In computational ecology, these datasets aid in picture segmentation and machine learning while evaluating phenotypic diversity[13].

4. Challenges and Future Directions

There are still a number of issues in bryophyte genomics despite tremendous progress. Studies of the molecular clock are challenging due to the poor fossil record of bryophytes. Furthermore, the haploid-dominant genomes of bryophytes necessitate specific computational algorithms since they differ from the diploid-dominant genomes of vascular plants. Because just a small portion of the estimated 20,000 bryophyte species have been sequenced, there is also a lack of taxon sampling[5].

Data Gaps: Comprehensive bioinformatics investigations are hampered by scant fossil records and the absence of constitutive reference spectra for bryophyte metabolites.

Future studies should focus on expanding genomic datasets to include more bryophyte species, particularly underrepresented hornworts and liverworts. Multi-omics approaches may provide a more complete understanding of evolutionary processes by integrating transcriptomics, metabolomics, and genomes. Additionally, advancements in machine learning and artificial intelligence may enhance our ability to spot subtle evolutionary patterns in massive datasets[14].

Emerging Technologies: New developments like as single-cell RNA sequencing, long-read transcriptome sequencing, and nanopore protein sequencing could improve bryophyte bioinformatics and provide more profound understanding of proteomics and gene regulation[15].

Multidisciplinary Methods: By combining ecological, metabolomic, and genomic data using bioinformatics, bryophyte adaptations and their ecological roles will be better understood, promoting conservation and biotechnology uses[16].

5. Discussion and Conclusion

Bryophytes are crucial for studying plant evolution, ecological adaptations, and bioactive compounds in bioinformatics. Databases, metabolomic pipelines, and sequence alignment tools are examples of computational resources that enable researchers to use bryophyte data for environmental monitoring, forensics, and evolutionary biology. As genomic and transcriptome datasets expand, bioinformatics will continue to uncover bryophytes' promise for both scientific and commercial applications other than *Physcomitrella patens*[17, 18, 19], and *Marchantia polymorpha*[20, 21]. Bioinformatics has revolutionized our understanding of bryophyte evolution by providing us with essential information about the genetic innovations and adaptations that enabled the transition from aquatic to terrestrial life. By using genomic and transcriptome data, bioinformatics has identified key regulatory networks, clarified adaptations like desiccation tolerance, and identified the evolutionary connections between bryophytes and other plant lineages. With the development of sequencing technologies and computational tools, bryophytes can be used as a model to better understand the deep evolutionary history of terrestrial plants.

Acknowledgements

The authors express gratitude to Prof. Ina Aditya Shastri, Vice Chancellor, Banasthali Vidyapith (Rajasthan) for her assistance in providing facilities for this research work. We also thank the Bioinformatics Center, which is financed by DST, for providing all the facilities needed for this effort.

Authors Contributions

AA conceptualized the manuscript and decided the various aspects to be covered. KA collected and compiled the data and wrote the first draft of the manuscript. Both the authors have finalized the manuscript.

Conflicts of Interest

Authors declare no conflict of interest.

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