PCP
PLANT & CELL PHYSIOLOGY

Commentary

Community-building resources for Marchantia—an accessible model plant system

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Received 24 December 2025; Accepted 9 February 2026

Keywords: Marchantia genome • database • commentary

This is a commentary to: Tanizawa, Y., Mochizuki, T., Yagura, M., Sakamoto, M., Fujisawa, T., Kawamura, S., et al. (2026) MarpolBase: genome database for *Marchantia polymorpha* featuring high quality reference genome sequences. *Plant Cell Physiol*. https://doi.org/10.1093/pcp/pcaf159.

Marchantia polymorpha has emerged as an important model system for the study of key aspects of plant biology. As a liverwort, it represents one of the three core groups within the bryophytes, the earliest diverging clade of land plants, which in turn enables the investigation of fundamental evolutionary questions (Kohchi et al. 2021). Low genetic redundancy and the haploid nature of the genome, along with the availability of a range of molecular tools, provide a powerful platform for genetic engineering (Bowman et al. 2017, Sauret-Güeto et al. 2020) alongside efficient transformation methods for the nuclear and chloroplast genomes. The planar mode of growth and easy access to both asexual propagules and spores (Fig. 1) facilitate imaging and tracking of important developmental processes in single cells and more complex three-dimensional tissues (Romani et al. 2024). Despite the advantages of Marchantia and its increasing popularity, the most up-to-date reference genome assemblies remained incomplete (Montgomery et al. 2020).

In this issue, Tanizawa et al. (2025) present near complete telomere-to-telomere assemblies of the *M. polymorpha* subsp. *ruderalis* Tak-1 and Tak-2 genomes. The authors generated PacBio HiFi long reads with a depth of coverage of 106× and 108× for the two accessions, respectively, which were assembled against the v6.1 genomes as reference sequences, and subsequently polished using both Illumina short reads and additional PacBio HiFi reads. The final genome assemblies, labelled v7.1, at ∼240 Mb were ∼10% larger than the previous v6.1 assemblies, primarily due to the incorporation of previously excluded repeat content. Each assembly contained only one gap due to lengthy unresolved tandem duplications, while all the previously unplaced scaffolds were resolved, and previous mis-assemblies on the sex chromosomes were identified and corrected. After lifting over the annotations from the v6.1 genome, improvements were made through manual curation, and with all previously unplaced scaffolds now anchored to chromosomes, all the gene models now have an assigned chromosome position. In addition, functional assignments have been added to gene models, which can be found when searching for individual gene IDs on MarpolBase (https://marchantia.info/).

Alongside the revised genome assemblies, the authors present an up-to-date summary of the analysis tools available on MarpolBase. Originally established as a tool for streamlined gene name registration (Bowman et al. 2016), it now also serves as the central repository for Marchantia genome information and as a platform from which further analysis can be performed on these data. The key functions include the ability to browse and perform homology-based searches against current and past versions of the Tak genomes along with other available accessions (Linde et al. 2020). Users also have access to an extensive gene expression database that provides a range of options for visualization and analysis of genes of interest (Kawamura et al. 2022), along with tools to explore the Marchantia pangenome dataset (Beaulieu et al. 2025). The authors highlight the importance of gene name registration through MarpolBase to avoid naming conflicts or redundancy, and also outline the development of the Marchantia gene identifier system, which is based upon the identifier system used for *Arabidopsis thaliana* and makes use of the chromosome number and gene order (e.g. Mp3g17150), for which tools are provided to convert between old and new versions of gene IDs. One of the main strengths of the MarpolBase platform is the gene-based search function, which provides extensive information about individual genes of interest using either a registered gene name or its unique identifier as the search term.

Through the generation of near-complete Marchantia genome assemblies and the integration of many valuable tools in one location, Tanizawa et al. (2025) have created a versatile platform which will facilitate further high-quality research in Marchantia. The authors include several of the key contributors involved in propagating an open approach

Plant and Cell Physiology, 2026, 67(3),225–227. https://doi.org/10.1093/pcp/pcag024, Advance Access publication on 3 April 2026, available online at https://academic.oup.com/pcp

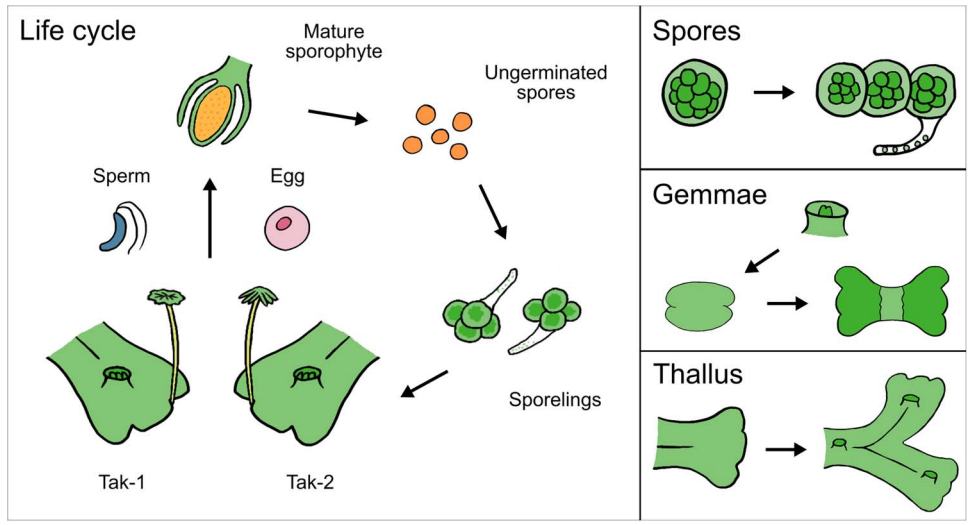

Figure 1. The life cycle of *M. polymorpha* and features of the model system. *M. polymorpha* is dioecious, with separate male (Tak-1) and female (Tak-2) plants. Motile sperm from an antheridiophore fertilizes an egg cell on an archegoniophore, leading to the formation of a mature diploid sporophyte, which produces haploid spores via meiosis. Scientific questions can be interrogated at the single cell level in spores, in the asexual propagules known as 'gemmae', or in the mature thallus.

to the sharing of methods, tools, and information across the developing field. Increasingly, researchers pursuing studies of gene systems characterized in model flowering plants are turning to Marchantia to study homologous pathways and by doing so benefit from the lack of gene redundancy, haploid genetics, spontaneous clonal propagation, fast generation times, and general simplicity and experimental ease offered by the system. The integration of many important bioinformatic workflows within MarpolBase will help to alleviate some of the hurdles involved in genome- and gene-level analysis which can serve as daunting barriers for newcomers to Marchantia.

As Marchantia becomes increasingly popular and further genome assemblies are added to MarpolBase, the ability to easily visualize gene-level differences across multiple accessions, rather than just the main reference sequence, will become increasingly important. These types of future developments will provide new opportunities for both comparative studies and engineering approaches. For example, the repository will be a useful resource for the preparation of Marchantia DNA sequences for molecular cloning toolkits such as MoClo (Weber et al. 2011) and will also facilitate the establishment of an open and accessible registry for Marchantia-specific functional DNA sequences and other tools.

Conflict of Interest

None declared.

Funding

None declared.

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Plant and Cell Physiology, 2026, 67(3),225–227. https://doi.org/10.1093/pcp/pcag024, Advance Access publication on 3 April 2026, available online at https://academic.oup.com/pcp
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