

The Importance of Model Species in Plant Biology: From Arabidopsis Thaliana to Beyond

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Abstract. *Arabidopsis thaliana* has been served as a model species in plant biology for over half a century. Since its earliest adoption in 1980s and the landmark sequencing of its whole genome, *Arabidopsis* has greatly accelerated plant research across multiple domains of plant science. With the help of *Arabidopsis*, plant scientists have been able to study different aspects of land plants, including evolution, epigenetic and plant physiology. These studies also provided insights into working on other plants, especially crops. Flowering time, stress response and growth regulation have been studies on *Arabidopsis*, often in conjunction with other experiment methods such as CRISPR/Cas9 and floral dip. Its role in advancing research into other species and applications in agriculture indicates an irreplaceable contribution to the whole biology field. However, the evolutionary divergence and physiological differences from many crops suggest limitations of this organism. This paper reviews the history and development of *Arabidopsis* as a model organism, as well as the limitations and future implications of model species in plant biology, emphasizing the need for broader representation of plant diversity in research to address global challenges such as climate change, agricultural development, and future plant biology direction.

Keywords: *Arabidopsis thaliana*, plant science, model system, molecular-genetic analysis

1. Introduction

Model species are organisms selected for intensive study due to their experimental advantages, which facilitate the discovery of general biological principles. Familiar model species in biology include fruit flies *Drosophila melanogaster* valued for their small genome and rapid life circle, and mice for medical study because they are mammals and have similar metabolic physiology to humans. In plant biology, an ideal example of model species typically processes relatively short life cycles, self-pollination capability, ease of cultivation and genetic manipulation.

Arabidopsis thaliana, a small flowering plant in Brassicaceae family, stood out from all plants and provided additional advantages that distinguish itself from other plant species. It has the smallest genome among all angiosperms, which was fully sequenced in 2000. This compact and well-annotated genome, combined with highly efficient transformation protocols, makes *Arabidopsis* exceptionally suitable for genetic and genomic analyses. Over the past four decades, it has become a platform for studying plant physiology, gene function, and molecular pathways, enabling researchers to conduct various experiments and apply advanced techniques.

Compared to many agriculturally important crops, which often have large, polyploid, and complex genomes and long generation times, *Arabidopsis* is incredibly experimentally convenient. Its role in plant biology parallels that of *Drosophila melanogaster* in animal research, serving as a versatile and widely adopted testing ground for experimental approaches. The breadth of its utility ranges from classic studies of flowering pathways to cutting-edge research such as testing stress adaptation in extraterrestrial soil analogs [1]. While *Arabidopsis thaliana* is a dominant model species in plant biology, it still has many limitations that need to be overreached by other organisms. Other species, such as *Brachypodium distachyon* and *Nicotiana benthamiana* provide complementary strength for filling the research gap.

This review explores the historical development, key scientific contributions, integration of modern technologies, and cross-species applications of *Arabidopsis*, as well as its limitations and the future directions of plant model species research.

2. History

Somerville & Koornneef (2002) divided the history of *Arabidopsis thaliana* research into two distinct phases: the pre-molecular era and the molecular era. In the pre-molecular era, *Arabidopsis* attracted little attention from botanists, largely because it lacked obvious morphological features of interest and had little direct agricultural value. Most plant scientists instead focused on crops such as maize, tomato, and pea. The first strong advocate for *Arabidopsis* as a genetic model was Friedrich Laibach, who in 1943 drew attention to its value for work in genetics and embryology. He pointed out several advantages of *Arabidopsis*, including high seed yield, short life cycle, ease of growing in limited space, high degree of natural variation, ability to form fertile hybrids, chromosome number, and relative lack of unnecessary seed tissues [2].

By the 1950s and 1960s, *Arabidopsis* was starting to be noticed as a potential model system for mutagenesis and chemical genetics. Because these experiments required large plant populations, *Arabidopsis* was particularly well-suited due to its small space requirements and ease of cultivation. Importantly, embryo-lethal mutations could be readily detected, as they segregated in a characteristic 3:1 ratio, making *Arabidopsis* an ideal system for genetic screening of T1 and T2 seeds [2]. Meanwhile, the *Arabidopsis* community also self-organized, in this case the *Arabidopsis* Information Service (AIS) as a method of information exchange. But by the 1970s, scientists' interest declined. People moved on to more "molecular" systems like *E. coli* for mutagenesis and biochemical genetics.

The molecular era started in the early 1980s when *Arabidopsis* was first widely used as a model plant [2]. A number of important discoveries and breeding innovations made this possible. Perhaps the most important was the discovery that *Agrobacterium tumefaciens* could transfer DNA into the nuclear genome of plants, which greatly accelerated functional studies. An important follow-up discovery that would help transform genetics was a report from the Meyerowitz lab that the *Arabidopsis* nuclear genome was only ~70 Mb, much smaller than most crop genomes. A vibrant research community quickly formed, unified by the recognition that *Arabidopsis* could serve as the "fruit fly of plant biology."

The genomic revolution marked a transformative milestone. In 2000, the *Arabidopsis* Genome Initiative published the complete nuclear genome sequence, making *Arabidopsis* the first plant to have a fully sequenced genome [3]. With this genetic code in hand, genome-wide analyses became a possibility and spurred rapid advances in genomics, transcriptomics, and mutant resource development. Coupled with the preceding milestones, *Arabidopsis* was an outstanding model system for plant biology by this time and remains one of the best today.

3. Scientific impact

3.1. FT: the master regulator of flowering transition

One of the most influential discoveries from *Arabidopsis* research was the identification of the FLOWERING LOCUS T (FT) gene, first described in early observations during the 1960s and later genetically characterized in detail [4]. FT is expressed in the companion cells of the phloem and is transferred to shoot apical meristem and acts as a molecular switch that triggers the transition from vegetative to reproductive growth. Because the FT pathway is conserved across flowering plants, knowledge gained from *Arabidopsis* has been successfully translated to major crops such as rice, wheat, and tomato [5]. This provided plant breeders with molecular tools to manipulate flowering time—an essential trait for optimizing yield and ensuring adaptability to diverse environments.

3.2. FLC – epigenetic control of vernalization

Another landmark case is the role of FLOWERING LOCUS C (FLC), a central floral repressor whose activity is reset by prolonged cold exposure [6]. The study demonstrated that vernalization silences FLC through stable histone methylation, establishing the first clear example of environmentally induced, heritable epigenetic regulation in plants. This finding not only deepened the understanding of flowering control but also provided a model for how external cues can permanently reprogram developmental pathways. Agricultural research has applied these findings to crop breeding, enabling flowering time to align with seasonal conditions and improving adaptation to local environments.

3.3. Hormone regulation of growth: auxin signaling

Arabidopsis has played a significant role in uncovering the molecular basis of auxin perception, a central phytohormone that regulates diverse aspects of plant growth and development. Auxin signaling is primarily regulated by two major gene families: the auxin response factors (ARFs) and the auxin/indole-3-acetic acid (Aux/IAA) proteins. In *Arabidopsis*, ARFs have been shown to regulate organ development, responses to abiotic and biotic stresses, and crosstalk with other phytohormone signaling pathways. A total of 23 ARF members have been identified and characterized in *Arabidopsis*, forming the foundation for comparative studies in other plants such as tomato, rice, wheat, sorghum, and maize [7]. Similarly, 29 Aux/IAA genes have been isolated in *Arabidopsis*, with many candidate regulators of Aux/IAA protein also being identified. The discovery and characterization of these gene families in *Arabidopsis* enabled the recognition of their homologs across various species, including *Eucalyptus grandis*, *Solanum lycopersicum*, *Cucumis sativus*, *Populus trichocarpa*, *Zea mays*, and *Oryza sativa* [8]. Recent study also showed that the auxin co-receptor IAA17/AXR3 regulates the nuclear auxin pathway to control root cell elongation, illustrating how *Arabidopsis* continues to advance hormone biology while guiding crop improvement through synthetic auxin analogs and pathway manipulation [9].

3.4. The phytochrome–PIF pathway: light and temperature sensing

Arabidopsis has also contributed greatly to understanding how plants respond to environmental light and temperature using phytochrome photoreceptors and interacting PIF transcription factors. The PhyB–PIF4 module functions as a thermosensor that integrates red/far-red light signaling with the ambient temperature environment [10] and because this pathway also controls shade avoidance [11],

it represents an ideal model for improving crop productivity traits in response to competition and climate conditions relevant to yield stability under global climate change.

4. Integration with other modern methods

4.1. CRISPR/Cas9 genome editing

Arabidopsis has been widely used to adapt CRISPR/Cas9 tools for plant research. This system enables the generation of targeted loss-of-function mutants and, through promoter engineering or CRISPRa systems, the creation of overexpressor lines, allowing scientists to study protein function at multiple regulatory levels. More recent innovations, such as the viral delivery of RNA-guided genome editors, now enable transgene-free germline editing [12]. This avoids regulatory hurdles and accelerates breeding cycles, positioning Arabidopsis as both a testbed and blueprint for genome-editing applications in crop plants.

4.2. Floral dip transformation – democratizing plant transgenics

The floral dip method revolutionized Arabidopsis research by offering a simple, efficient means of Agrobacterium-mediated transformation [13]. By dipping flowering plants into an Agrobacterium suspension, researchers bypassed the need for labor-intensive tissue culture regeneration. This innovation enabled high-throughput transgenesis and helped establish large-scale mutant collections such as the SALK T-DNA insertion lines, which remain indispensable for functional genomics.

4.3. Systems biology – from gene expression maps to networks

Arabidopsis also spearheaded the integration of systems biology approaches, bridging molecular genetics with large-scale data science. The creation of a gene expression atlas of the shoot apical meristem set a precedent for spatially and temporally resolved transcriptomics [14]. Resources such as The Arabidopsis Information Resource (TAIR) and global network modeling efforts have since expanded into multi-omics platforms, while advanced phenotyping technologies allow quantitative measurements of growth, stress responses, and developmental trajectories. Together, these tools establish Arabidopsis as the reference framework for building the “computable plant.”

5. Beyond Arabidopsis

While *Arabidopsis thaliana* continues to be the most commonly used plant model, the plant research community increasingly adopts other model species to address questions that Arabidopsis alone cannot fully answer. For example, *Brachypodium distachyon*, with its small diploid genome and short life cycle, has become the leading model for grasses. As a monocot, it enables studies of cereal-specific traits such as grain yield, disease resistance, and stress tolerance, complementing Arabidopsis, which as a dicot is less suitable for cereal biology. In evolutionary history of plants, *Marchantia polymorpha* is an interesting example of early land plant evolution. Unlike flowering plants, this simple liverwort has a gametophyte-dominant life cycle and a small, nonduplicated genome, which decodes how plants evolved from aquatic to terrestrial life for elucidating ancestral signaling pathways and plant sex chromosomes [15]. Being the first land plants, its evolutionary position facilitates us to explore the history of origins and generations of land plants.

For more applied examples in agriculture or biotechnology, *Medicago truncatula* is primarily representing legume because of the nitrogen-fixing symbioses with rhizobia, it has been crucial for

sustainable agricultural development by replacing synthetic fertilizers with eco-friendly approaches. In biotechnology, *Nicotiana benthamiana* is another plant model. Unlike *Arabidopsis*, it allows transient protein and gene expression, therefore the florescence can be tested within hours by direct infiltration into *N. benthamiana* leaves, making it highly efficient for determine subcellular expression location. It has become indispensable to study plant-microbe and protein-protein interactions studies, playing an important role in the production of COVID-19 vaccines [16]. Its close relative *Nicotiana tabacum* also remains a classic model, which has been involved in chloroplast genetics and photosynthesis related research. Finally, duckweeds (*Lemnaceae*) have been introduced as an environmental model due to their rapid growth and adaptation to polluted water. They are mainly used as water quality bioindicators and in bioenergy research and. Collectively, these alternative models extend the breath of plant biology, leading to discoveries from evolutionary aspects to practical applications in agriculture, biotechnology, and environment.

6. Utilization and application

The goal of studying model species is to utilize the gained knowledge into daily life. For example, scientists study mice not only to understand mice biology, but also to have a better understanding of their metabolism and to build a preclinical system for drugs testing before utilizing on human. Similarly, as a model species, *Arabidopsis* has potential to produce fundamental biological results that can be applied to things relating to humans, especially in agriculture. Research in *Arabidopsis* has led to many basic findings that have the potential to capture desired traits in our crops. For example, the abscisic acid (ABA) often interacts with other hormones to involve in seedling and fruits developments, therefore studying signaling pathway cascade can increase crops performance such as drought and stress tolerance [17]. In a similar way, studies of root development in *Arabidopsis* have provided valuable models for improving stress tolerance in crops. In addition, research on vernalization and devernization revealed how epigenetic regulations can align flowering with agricultural schedules or environmental conditions. On the molecular level, the CLV–WUS pathway has been applied in tomato to increase fruit size, while *SEPALLATA* (*SEP*) controls floral organ identity, especially carpel numbers, in both *Arabidopsis* and cucumbers (*Cucumis sativus* L.), thus controlling the fruit length and size [18]. These findings provide molecular tools to improve yield, resilience, and productivity in cereals, legumes, and other crops that are important to humans [19]. In this way, *Arabidopsis* functions as a genetic and physiological blueprint that would be much harder to obtain in the complex genomes of crops.

Remarkably, studying *Arabidopsis* has also benefited human biology. Many genes involved in plant and animal immune systems are highly conserved, such as plant NB-LRR proteins in innate immunity, which have functional paralogs in humans involved in inflammatory diseases such as NOD, CARD, and CATERPILLAR genes involved in mammalian innate immunity [20]. Pathogen recognition and immune signaling (PTI/ETI) in *Arabidopsis* have given scientists insight on general principles that apply to human immunity. Similarly, mechanisms of reactive oxygen species (ROS) signaling and programmed cell death, which were first identified in *Arabidopsis*, have provided useful frameworks for cancer and neurodegenerative disease biology. Regarding epigenetics, *Arabidopsis* discoveries in histone modification, chromatin remodeling, and DNA methylation are also guiding human biomedical science. These examples highlight the truly remarkable trans-kingdom implications of doing *Arabidopsis* beyond plants.

7. Discussion

Although *Arabidopsis* is an impressive model species, many limitations remain. One of the limitations relates to the evolutionary differences between *Arabidopsis* and many crop species. *Arabidopsis* has a small, diploid genome and very rapid reproduction, whereas many crops are polyploid, have much larger genomes, and reproduce through special reproductive strategies making it hard to generalize from *Arabidopsis*. Secondly, transformation methods such as floral dip, an essential tool in *Arabidopsis* research, are unsuitable for cannot be used in most crops and hence other less efficient transformation methods must be used. *Arabidopsis*'s trait specific gaps limit its ability to model some biological processes of interest, such as the anatomy of cereal grains, nitrogen-fixing symbioses in legumes, or fleshy fruit in Solanaceae. Most *Arabidopsis* experiments are done under highly controlled conditions which do not reflect the environmental variability and stress combinations that plants face in the real agricultural field. Model crop mismatches highlight the need to move beyond *Arabidopsis* to complementary model systems that allow for representation of diverse plant lines and agricultural traits of interest.

Looking forward, success in plant biology will come from 'going beyond *Arabidopsis*' using multi-model approaches. Related species such as *Brachypodium distachyon*, *Medicago truncatula*, *Marchantia polymorpha* and *Nicotiana benthamiana* offer complementary traits that are missing from *Arabidopsis*, such as cereal architecture, symbiosis and early land plant divergence. Conversely, progress in computational plant biology is driving the need for predictive, computable models that link gene networks, phenotypes and environment. A central thrust will be the integration of multi-functional datasets (genomics, transcriptomics, proteomics, metabolomics and phenomics) into coherent frameworks, enabled by high-throughput phenotyping platforms based on imaging, robotics and artificial intelligence that will link genotype to phenotype at scale. *Arabidopsis* will act as the reference anchor point for translating across species, accelerating gene functional annotation and comparative genomics in crops. In addition, new synthetic biology tools, such as CRISPR, base editors and viral delivery systems, will enable precision editing lines to extend beyond *Arabidopsis* to a broader range of crop species. Finally, the focus on field validation will increase, to ensure that output from the laboratory translates to realistic field conditions for crop improvement [21].

8. Conclusion

Arabidopsis thaliana has served as a cornerstone of plant biology, providing fundamental insights into flowering, growth regulation, stress responses, and hormone signaling. Its compact genome, short life cycle, and extensive research community have made it an indispensable platform for both classical genetics and cutting-edge technologies such as CRISPR/Cas9 and systems biology approaches. However, no single model can capture the full diversity of plant biology. Translating discoveries from *Arabidopsis* to crops and other species requires integrating knowledge from multiple model species, including *Brachypodium*, *Medicago truncatula*, *Marchantia polymorpha*, and *Nicotiana* species. By combining experimental, computational, and cross-species approaches, researchers can achieve a more holistic understanding of plant biology, ultimately improving crop productivity, stress resilience, and biotechnological applications. In summary, *Arabidopsis* remains foundational, but the future of plant biology lies in a multi-model, integrative community resource strategy to take advantage of what *Arabidopsis* has to offer and beyond.

References

- [1] Buckner, A., Lang, S., & Loureiro, R. (2025). Physiological and Transcriptional Responses of *Arabidopsis thaliana* to Simulated Lunar and Martian Regolith Substrates (No. arXiv: 2505.13583). arXiv. <https://doi.org/10.48550/arXiv.2505.13583>
- [2] Somerville, C., & Koornneef, M. (2002). A fortunate choice: The history of *Arabidopsis* as a model plant. *Nature Reviews Genetics*, 3(11), 883–889. <https://doi.org/10.1038/nrg927>
- [3] The Arabidopsis Genome Initiative. (2000). Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature*, 408(6814), 796–815. <https://doi.org/10.1038/35048692>
- [4] Koornneef, M., Hanhart, C. J., & van der Veen, J. H. (1991). A genetic and physiological analysis of late flowering mutants in *Arabidopsis thaliana*. *Molecular & General Genetics: MGG*, 229(1), 57–66. <https://doi.org/10.1007/BF00264213>
- [5] Higuchi, Y. (2018). Florigen and anti-florigen: Flowering regulation in horticultural crops. *Breeding Science*, 68(1), 109–118. <https://doi.org/10.1270/jsbbs.17084>
- [6] Bastow, R., Mylne, J. S., Lister, C., Lippman, Z., Martienssen, R. A., & Dean, C. (2004). Vernalization requires epigenetic silencing of FLC by histone methylation. *Nature*, 427(6970), 164–167. <https://doi.org/10.1038/nature02269>
- [7] Li, Y., Han, S., & Qi, Y. (2023). Advances in structure and function of auxin response factor in plants. *Journal of Integrative Plant Biology*, 65(3), 617–632. <https://doi.org/10.1111/jipb.13392>
- [8] Luo, J., Zhou, J.-J., & Zhang, J.-Z. (2018). Aux/IAA Gene Family in Plants: Molecular Structure, Regulation, and Function. *International Journal of Molecular Sciences*, 19(1), 259. <https://doi.org/10.3390/ijms19010259>
- [9] Kubalová, M., Müller, K., Dobrev, P. I., Rizza, A., Jones, A. M., & Fendrych, M. (2024). Auxin co-receptor IAA17/AXR3 controls cell elongation in *Arabidopsis thaliana* root solely by modulation of nuclear auxin pathway. *New Phytologist*, 241(6), 2448–2463. <https://doi.org/10.1111/nph.19557>
- [10] Legris, M., Klose, C., Burgie, E. S., Rojas, C. C. R., Neme, M., Hiltbrunner, A., Wigge, P. A., Schäfer, E., Vierstra, R. D., & Casal, J. J. (2016). Phytochrome B integrates light and temperature signals in *Arabidopsis*. *Science*, 354(6314), 897–900. <https://doi.org/10.1126/science.aaf5656>
- [11] Gautrat, P., Matton, S. E. A., Oskam, L., Shetty, S. S., van der Velde, K. J., & Pierik, R. (2025). Lights, location, action: Shade avoidance signalling over spatial scales. *Journal of Experimental Botany*, 76(3), 695–711. <https://doi.org/10.1093/jxb/erae217>
- [12] Weiss, T., Kamalu, M., Shi, H., Li, Z., Amerasekera, J., Zhong, Z., Adler, B. A., Song, M. M., Vohra, K., Wirnowski, G., Chitkara, S., Ambrose, C., Steinmetz, N., Sridharan, A., Sahagun, D., Banfield, J. F., Doudna, J. A., & Jacobsen, S. E. (2025). Viral delivery of an RNA-guided genome editor for transgene-free germline editing in *Arabidopsis*. *Nature Plants*, 11(5), 967–976. <https://doi.org/10.1038/s41477-025-01989-9>
- [13] Clough, S. J., & Bent, A. F. (1998). Floral dip: A simplified method for *Agrobacterium* -mediated transformation of *Arabidopsis thaliana*. *The Plant Journal*, 16(6), 735–743. <https://doi.org/10.1046/j.1365-313x.1998.00343.x>
- [14] Yadav, R. K., Girke, T., Pasala, S., Xie, M., & Reddy, G. V. (2009). Gene expression map of the *Arabidopsis* shoot apical meristem stem cell niche. *Proceedings of the National Academy of Sciences of the United States of America*, 106(12), 4941–4946. <https://doi.org/10.1073/pnas.0900843106>
- [15] Berger, F., Bowman, J. L., & Kohchi, T. (2016). *Marchantia*. *Current Biology*, 26(5), R186–R187. <https://doi.org/10.1016/j.cub.2015.12.013>
- [16] Bally, J., Jung, H., Mortimer, C., Naim, F., Philips, J. G., Hellens, R., Bombarely, A., Goodin, M. M., & Waterhouse, P. M. (2018). The Rise and Rise of *Nicotiana benthamiana*: A Plant for All Reasons. *Annual Review of Phytopathology*, 56(Volume 56, 2018), 405–426. <https://doi.org/10.1146/annurev-phyto-080417-050141>
- [17] Ben-Ari, G. (2012). The ABA signal transduction mechanism in commercial crops: Learning from *Arabidopsis*. *Plant Cell Reports*, 31(8), 1357–1369. <https://doi.org/10.1007/s00299-012-1292-2>
- [18] Bennett, M. J., Bhosale, R., Boden, S. A., Chen, S.-Y., Colombi, T., Ito, T., Li, H.-J., Mehra, P., Østergaard, L., Li, M., Liu, L., Otsuka, N., Pandey, B. K., Poethig, S., Prasad, K., Qu, Y., Shirakawa, M., Su, Y. H., Xu, C., ... Wu, S. (2025). Developmental pathways in plants: Lessons from *Arabidopsis* for crop innovation. *The Plant Cell*, 37(7), koaf136. <https://doi.org/10.1093/plcell/koaf136>
- [19] Inzé, D., & Nelissen, H. (2022). The translatability of genetic networks from model to crop species: Lessons from the past and perspectives for the future. *New Phytologist*, 236(1), 43–48. <https://doi.org/10.1111/nph.18364>
- [20] Jones, A. M., Chory, J., Dangel, J. L., Estelle, M., Jacobsen, S. E., Meyerowitz, E. M., Nordborg, M., & Weigel, D. (2008). The Impact of *Arabidopsis* on Human Health: Diversifying Our Portfolio. *Cell*, 133(6), 939–943. <https://doi.org/10.1016/j.cell.2008.05.040>

- [21] Brady, S., Auge, G., Ayalew, M., Balasubramanian, S., Hamann, T., Inze, D., Saito, K., Brychkova, G., Berardini, T. Z., Friesner, J., Ho, C.-H., Hauser, M.-T., Kobayashi, M., Lepiniec, L., Mähönen, A. P., Mutwil, M., May, S., Parry, G., Rigas, S., ... Provart, N. J. (2025). Arabidopsis research in 2030: Translating the computable plant. *The Plant Journal*, 121(5), e70047. <https://doi.org/10.1111/tpj.70047>