



The Art and Design of Model Plant: *Arabidopsis thaliana*

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Abstract

The molecular and evolutionary studies depend on easily manipulable and well-characterized organisms. More than two decades ago, *Arabidopsis thaliana* became the go-to model organism for research in the field of plant biology that enables effective analysis of plant function by integrating traditional genetics with the discipline of molecular biology. Although the *Arabidopsis* genome's complete sequence enables the quick identification of the molecular mechanisms of a characterised mutant, effective characterization of its genome still depends on thoughtfully constructed forward genetic screens, which somewhat remain a potent method for locating genes involved in a variety of processes throughout the plant life cycle. The community framework and technologies needed for integrative and biological approaches in plants are now poised to advance plant biology to its next major milestone through the integration of knowledge and simulation of biological processes. The future of plant science will be enhanced by the coordination of excellent basic research (often carried out in *Arabidopsis*) with strategic goals in crop breeding. As more crop plant genomes are sequenced and analysed, this alignment is improved, and novel information on genome evolution and crop domestication is revealed. The evolution in *Arabidopsis* research over the last five years is reviewed in this article, along with prospective developments in the future and their effects on agricultural science.

Keywords: Genetic screens, Characterized mutant, Genome evolution, Domestication

Introduction

Plants were not the preferred experimental organism when molecular biology began to dominate in the 1970s. One issue was the lack of readily accessible shared resources required to advance plants to the same level of sophistication as other model organisms. Gaining approval for giving an "outsider" special study status at the time was especially challenging due to the agricultural underpinning of plant science at the time. Many plants, including some important crops, have large, polyploid genomes that frequently include highly repetitive DNA. These drawbacks impede the exploration and manipulation of these plant genomes and make genetic and molecular studies extremely challenging. Therefore, an organism with an elementary genome that is suitable for both conventional and molecular genetic studies would need to be the optimal experimental model system for the plant community. *Arabidopsis thaliana* is by far the most researched species of flowering plant out of all those that are currently known.

According to The *Arabidopsis* Genome Initiative (2000), *Caenorhabditis elegans* and *Drosophila melanogaster* were the first two multicellular organisms to have their whole genomes sequenced before *Arabidopsis thaliana*. At the time, it was asserted that the *Arabidopsis* genome sequence offers the possibility of quick, direct access to information that

can help researchers better understand how plants develop and respond to their environments as well as the structure and dynamics of their genomes. The most notable traits were rapid seed production through self-pollination, a short generation period, and the compact size that reduced the need for growth facilities. This article compares work on *Arabidopsis* to that done on other reference organisms, taking a broad and inevitably shallow view of research advancements. The analysis implies that a significant portion of the amazing progress made in the last five years has been based on the genome sequence and demonstrates that it has had a catalytic impact on the scientific community and on how plant science is carried out. But if the *Arabidopsis* and plant science community is to effectively travel the route of integrative biology, it must face unanticipated issues brought forth by an upsurge of data.

History of *Arabidopsis* Research

The pioneer of experimental *Arabidopsis* research is Friedrich Laibach. He returned to this species in the 1930s after becoming a renowned botanist and described its appropriate chromosomal number during his PhD studies. Laibach persuasively argued that *Arabidopsis* was a good prospect for genetic research. The utilisation of natural variation for the examination of physiological factors like flowering time and seed dormancy was another point of emphasis for Laibach and his students. Laibach also started experimenting with *Arabidopsis* using X-rays. This made it possible for Erna Reinholz, his PhD student, to come up with the first induced *Arabidopsis* mutants. The person who presumably coined the phrase "botanical *Drosophila*" initially was Franz Josef Kribben. The quest for an appropriate plant model for molecular genetics research sparked a resurgence in interest in *Arabidopsis* in the late 1970s. It received momentum when various teams started to make use of *Arabidopsis*' genetic capability to identify processes unique to plants. The leadership and encouragement given by prominent figures in US funding organisations, most notably Machi Dilworth, DeLill Nasser, and Mary Clutter at the National Science Foundation (NSF), was a third element in the fast rise of *Arabidopsis* research in the mid-1980s. Together, they made a significant contribution to mentoring young researchers, creating shared resources, and bringing the *Arabidopsis* community into the current era of genomics.

Arabidopsis as an experimental system

Before Friedrich Laibach detailed the benefits of utilising the tiny mustard weed *Arabidopsis thaliana* (family *Brassicaceae*) in genetic tests, botanists had at least four centuries' worth of knowledge about it and had been using it in experiments for around 50 years. *Arabidopsis* is suitable for classical experimental genetics due to number of characteristics, including its small size, rapid generation time (5–6 weeks under ideal growth conditions), ability to grow well in controlled environments (either in soil or in defined media), high fecundity (up to 10,000 seeds per plant), and simplicity in maintaining mutant lines (by self-fertilization and out-crossing) as presented in Figure 1. With the shortest known plant genome (125 Mb) and the fewest repetitive sequences than any of the known higher plants, *Arabidopsis* not only possesses all the essential characteristics of a model organism for classical genetics but also considerably facilitates molecular research and map-based cloning. *Agrobacterium*-mediated gene transfer, which is necessary for many molecular genetic experiments, can also quickly alter *Arabidopsis*.

Although *Arabidopsis* had long been utilised in conventional genetic research, it did not play a similar role to *Drosophila* in the systematic study of developmental and metabolic processes. *Arabidopsis* only became the most studied higher plant after it was realised that it has a very small genome and, thus, the ability to combine traditional genetics with molecular analysis. *Arabidopsis*' success as a model organism is largely attributable to its suitability for forward genetic screens, which are used to intentionally create genetic diversity and screen for desirable phenotypes that have undergone mutagenization.

Arabidopsis as classical genetic screens

The early researchers in *Arabidopsis* genetics carried out screenings on wild-collected populations and were very successful in finding mutants that had noticeable phenotypic alterations. The establishment of *Arabidopsis* as a model genetic organism was greatly aided by mutant screens. In those early days, ethyl methane sulphonate (EMS), which is still an efficacious and prevalent mutagen today, was originally used for mutation studies. It was demonstrated that saturation mutagenesis was a possibility in *Arabidopsis* by identifying numerous mutant alleles of the same gene in a sizable population of M2 seeds. Muller's (1961) embryo test, extensive research on thiamine auxotrophs with a seedling deleterious phenotype, and the prevalence of either chlorophyll-deficient seedlings or sterile plants all served to prove *Arabidopsis*' usefulness for biochemical genetics.

The dynamic genome and genetic map of Arabidopsis

The degree of segmental and gene duplications was one of the key characteristics of the *Arabidopsis* genome revealed by the genome sequencing, which was unexpected given the expectation of a functionally compact genome. It was once believed that a single duplication event—possibly of the entire genome—was the source of about 60% of the genome. These studies back up a model of the evolution of the *Arabidopsis* genome that includes cycles of gene loss, gene duplication, and gene divergence.

The wild plant species *Arabidopsis thaliana* has developed the ability to thrive in a spectrum of environments, and it has long served as a paradigm for adaptability. As a result, growth and environmental sensitive traits exhibit a wide range of natural variation, which serves as an unusually rich source of diversity. Numerous quantitative trait loci (QTL)—loci that show variation in complex traits—have been cloned. One example is the detailed mapping of the FLC and FRI loci that affect flowering time using linkage disequilibrium (LD). Polymorphisms in phytochrome light receptors were found to be the cause of the natural variability in hypocotyl reactions to light.

Arabidopsis was chosen for comprehensive sequencing for several reasons, including its relative paucity of repetitive sequences when compared to other scientifically tractable plants. Two rDNA loci were found at the northern extremities of chromosomes 2 and 4 and large tracts of pericentromeric heterochromatin, according to cytogenetic analyses. According to chromosome sequencing, the pericentromeric areas of these organisms featured a complex assemblage of transposons, retroelements, middle-repetitive sequences, and microsatellites. Homopolymeric tracts with distinctive 180-bp and 160-bp repeats were seen in unsequenced regions close to and including centromeres. Interstitial heterochromatic areas, also known as knobs, have been thoroughly sequenced within the context of nearby low-copy sequences, and these regions have offered profound insights into how heterochromatin is generated and maintained as well as how this chromatin state regulates gene expression. The probable sequences and locations of genes along chromosomes are shown by genetic linkage maps. Linkage (recombination) analysis was the primary technique utilised to gain information on gene locations before physical maps based on contigs of cloned DNA segments could be created (Hall *et al.*, 2002).

Individual chromosomes do not display the cytological details that have proved valuable in cytogenetic research with crop plants because of the modest size of the *Arabidopsis* genome. But when sensitive *in situ* hybridization techniques were combined with pachytene chromosomes, which are longer than mitotic chromosomes and have distinct heterochromatic and euchromatic regions, *Arabidopsis* chromosomes finally became amenable to cytogenetic analysis. This resulted in number of advances, including the identification of chromosome inversions in some accessions.

Bioinformatics and Modelling

The TAIR (The *Arabidopsis* Information Resource) hub and a vast array of specialised genomic databases that disseminate *Arabidopsis* data provide assistance to *Arabidopsis* researchers. A dedicated team is currently centrally annotating *Arabidopsis* and other plant proteins (<ftp://ftp.Arabidopsis.org/home/tair/Genes/GeneOntology/>), and these GO words defining gene functions are beginning to replace the *ad hoc* system of gene descriptions that are currently extensively utilised. The *Arabidopsis* community has demonstrated a commendable level of collegiality and cooperation throughout its recent history. Although there have been occasional disagreements and setbacks, they have not characterised the field or prevented advancement. The majority of plant biologists appeared to understand the importance of teamwork in developing *Arabidopsis* as a useful model. Additionally, being a "simple weed" occasionally reduced conflicts of interest about the useful applications of common resources.

Conclusion and Future Prospects

When remarkable developments in molecular genetics radically altered the field of biology thirty years ago, it was not immediately apparent that plant science would play a major role in the revolution that was about to take place. The majority of the preferred genetic models at the time were challenging to modify, and plant genomes were huge and complex with long life cycles. Despite an illustrious past that includes well-known pioneers like Mendel and McClintock, the future of plant genetics as a field was also dubious. In the end, a variety of factors, including the selection of *Arabidopsis* as a plant model, developments in *Agrobacterium*-mediated transformation, the influx of talented and cooperative individuals into plant biology, and increased funding to support experimental breakthroughs, allowed plant biologists to remain at the forefront of modern biology. The focus of *Arabidopsis* study has been genetic variations during this time, combined with advancements in cell and molecular biology techniques. Recent years have seen a rise in the importance of computational techniques, including modelling at numerous levels. The future of *Arabidopsis* research should indeed be promising, with a well-established model organism providing the basis for ongoing advances in our comprehension of how plants function and the possibility that additional developments in controlling plant growth and development may soon make it possible to practise plant breeding by design. We truly anticipate that plant biologists of the next generation will continue to possess the foresight and tools necessary to maintain *Arabidopsis*' status as an elite member of this exclusive group of organisms.

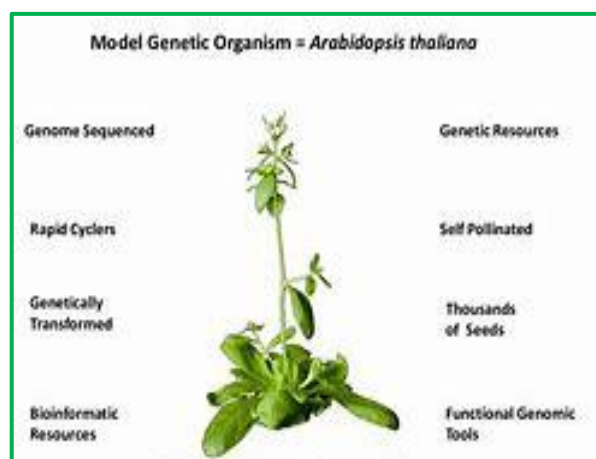


Figure1: Characteristics of model genetic organism (Koorneef and Meinke, 2010)

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