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PERSPECTIVE

Arabidopsis research in 2030: Translating the computable plant

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SUMMARY

Plants are essential for human survival. Over the past three decades, work with the reference plant *Arabidopsis thaliana* has significantly advanced plant biology research. One key event was the sequencing of its genome 25 years ago, which fostered many subsequent research technologies and datasets. Arabidopsis has been instrumental in elucidating plant-specific aspects of biology, developing research tools, and translating findings to crop improvement. It not only serves as a model for understanding plant biology and but also biology in other fields, with discoveries in Arabidopsis also having led to applications in human health, including insights into immunity, protein degradation, and circadian rhythms. Arabidopsis research has also fostered the development of tools useful for the wider biological research community, such as optogenetic systems and auxin-based degrons. This 4th Multinational Arabidopsis Steering Committee Roadmap outlines future directions, with emphasis on computational approaches, research support, translation to crops,

conference accessibility, coordinated research efforts, climate change mitigation, sustainable production, and fundamental research. Arabidopsis will remain a nexus for discovery, innovation, and application, driving advances in both plant and human biology to the year 2030, and beyond.

Keywords: *Arabidopsis thaliana*, model system, genomics, translational research, AI, gene regulatory networks.

INTRODUCTION

Plants are absolutely required for humans to survive and thrive. Plants provide us with food, medicine, fuel, natural fibers, oxygen, carbon capture, and a functioning ecosystem.

A better understanding of plants will help us face the challenges of our future, as articulated by the UN's Sustainable Development Goals (SDGs).[1] For example, understanding and manipulating crop biology may address malnutrition and hunger, toward SDG 2: Zero Hunger.[2] The discovery of new plant-based medicines could address human health and well-being, which is SDG 3: Good Health and Well-Being.[3] Improved agricultural practices and genetically modified plants could help reduce run-off, contributing to SDG 6: Clean Water and Sanitation,[4] while the development of new plant materials and sustainable materials/processes would contribute to SDG 12: Responsible Consumption and Production.[5] There is a new awareness that plants may be key to carbon capture as we try to address climate change, encompassed by SDG 13: Climate Action.[6] Finally, documenting and mitigating the loss of plant/animal diversity through ecosystem loss, degradation or disruption addresses the need to preserve and protect life, covered by SDG 15: Life on Land.[7]

ARABIDOPSIS THALIANA

The model flowering plant species *Arabidopsis thaliana* has been a key contributor to plant biology research. It emerged as a research organism more than 60 years ago and the number of laboratories using it has increased steadily since then (Koornneef & Meinke, 2010; Provart et al., 2016; Somerville & Koornneef, 2002).

A key step in the adoption of Arabidopsis as a model organism was the sequencing of its genome almost 25 years ago (Arabidopsis Genome Initiative, 2000). As emphasized in a review by Provart et al. (2020) spanning 20 years of Arabidopsis genomics, the genome sequence—coupled with the huge drop in the price of DNA sequencing—has served as a platform for the development of a vast ecosystem of research technologies, fields, datasets and databases, including insertion mutants (Alonso et al., 2003), 'omics data for the genomes and epigenomes of 1001 Arabidopsis accessions (1001 Genomes Consortium, 2016; Kawakatsu et al., 2016), DAP-seq for determining transcription factor binding specificities and targets (O'Malley et al., 2016), single cell RNA-seq (Denyer et al., 2019; Efroni et al., 2016; Ryu et al., 2019; Shahan et al., 2022; Shulse et al., 2019; Turco et al., 2019), and many others.

Now the Arabidopsis research community is reaching maturity. The number of publications a year has leveled off.[8] As befits a mature field, five researchers from North America were honored for their lifetime contributions to the field of Arabidopsis research at the 34th International Conference on Arabidopsis Research (ICAR): Joanne Chory, Jeff Dangl, Joseph Ecker, Elliott Meyerowitz and Chris Somerville.[9] So many major discoveries and advances have been made in Arabidopsis that it is impossible to document them all here. However, it is worth listing the many ways in which 'basic' research in a model (or 'reference') system can serve both fundamental and applied biology:

1. One area where Arabidopsis serves as an excellent model system is in making new discoveries about plants themselves. For example, the genetic and molecular tests of the ABCE model of flower development, the molecular glue model for hormone action, the concept of basal defense, and the identification of multiple light receptors were first discovered in Arabidopsis (see Provart et al., 2016, figure 3, for a summary).
2. Similarly, many tools for genomic, cell biological, biochemical, and genetic approaches have been developed in Arabidopsis. For example, the first plant genome sequence, the first T-DNA insertion collections, live cell imaging of cellulose synthesis, optical detection of hormones and metabolites, and cell-type specific transcriptomics were developed in Arabidopsis (again, see Provart et al., 2016, figure 3, for a summary). As the community of Arabidopsis researchers has grown, and new discoveries were made, more tools and resources have been developed, creating iterative positive feedback loops between discovery and technical advances. These tools were then applied to other species: an impressive 88% of Arabidopsis papers from 1989 were referenced by non-Arabidopsis papers 26 years after they were published (Provart et al., 2016).
3. Many discoveries made in Arabidopsis have been translated into better breeding and engineering of crops and other useful plants. In fact, Arabidopsis studies form a 'nexus for discovery, innovation, application, and impact'—indeed this was the ICAR 2024 tagline. Arabidopsis research is often where mechanistic discovery

happens, which is then translated to crop plants (Yaschenko et al., 2024). For instance, viral infection causes changes in volatile compound production in both tomato and Arabidopsis (Groen et al., 2016), with implications for bumblebee foraging behavior. Digging deeper, the authors found a microRNA pathway in Arabidopsis that regulates the emission of olfactory signals that are perceived by bees, providing a mechanistic link.

4 Furthermore, Arabidopsis itself can serve as a tool. Discoveries made in other systems can be further dissected and deployed in Arabidopsis. One example is the investigation of strigolactone receptors (a group of α/β hydrolases designated HYPOSENSITIVE TO LIGHT, HTL), which were discovered in model systems, then found by homology in the parasitic plant *Striga hermonthica*. The 11 *Striga HTL* homologs were then studied in an Arabidopsis *htl* knock-out mutant. In this way, the *ShHTL7* receptor, which is responsive to picomolar concentrations of strigolactone released by host roots and triggers germination of nearby *Striga* seeds, was identified. By ' *Striga*-izing' Arabidopsis, the cognate receptor for triggering Striga germination was able to be identified in a way that would not have been possible if working just with Striga itself. In addition, the authors point out that such an Arabidopsis line can act as 'a bioassay that can be used to identify chemicals and crops with altered strigolactone levels' (Toh et al., 2015).

5 While plant research can help solve the major human issues of malnutrition and starvation, it has also led to new understanding of human biology and disease. Many discoveries relevant to human health have been made in plants and in Arabidopsis in particular. Research in Arabidopsis has contributed to, and in some cases made possible our understanding of multiple aspects of human health, including innate immunity, protein degradation, the circadian clock, the ubiquitin cycle, RNA silencing, epigenetics, multiple receptor signaling pathways, and natural variation (Jones et al., 2008).

6 Several tools for animal biology have been generated from plant proteins. Examples include light-regulated optogenetic systems for controlling ion flux and transcriptional regulation (Chernov et al., 2017; Idstein et al., 2023; Tischer & Weiner, 2014) and an auxin-based degron used to rapidly attenuate protein expression (Yesbolatova et al., 2020).

There are admittedly a few areas where Arabidopsis is not a good model system. For example, Arabidopsis lacks some aspects of tree biology, such as extensive wood formation—although it does make wood and possess secondary growth (Chaffey et al., 2002) and, in fact, its inflorescences can be used to make tiny wooden chairs!—and especially deciduousness. There are other examples, such as C4 photosynthesis, self-incompatibility, specialized cell types and metabolites etc. However, even in these cases, methods and resources developed in Arabidopsis, such as genome sequence resources or various '-seq'-based methods, can then be applied to other species to elucidate their biological systems.

MASC

The Multinational Arabidopsis Steering Committee (MASC) was constituted in the 1990s when scientists from the Europe, the United States, Australia and Japan formed an *ad hoc* organization to promote large-scale studies in *A. thaliana*, starting with the sequencing of the Arabidopsis genome. Stock centres and informatic resources were also part of the original vision. Today, MASC operates through three groups that receive continuous input from the wider Arabidopsis and plant communities: MASC Subcommittees, Arabidopsis Community Projects & Resources (e.g., TAIR, ABRC, Gramene, and others), and MASC Country/Region Representatives. The MASC subcommittees, proposed in 2002, were established to help track the progress and advances made by the international Arabidopsis community, and to coordinate efforts. The MASC subcommittees currently provide input on annual progress within the fields of Bioinformatics, Clone-based Functional Genomics, Epigenetics and Epigenomics, Metabolomics, Natural Variation and Comparative Genomics, Proteomics, Phenomics, Plant Immunity, Proteomics, and Systems & Synthetic Biology. Newer topic areas are proposed by the community itself and refined at our annual meetings. The wider Arabidopsis community supports MASC by nominating individual country representatives, who are nationally and internationally well-connected Arabidopsis researchers. To date, 34 countries have supported MASC and the international Arabidopsis community, with 24 country reports being included in the 2023–2024 MASC report.

DECADAL ROADMAPS

In addition to the above, over the past 30 years MASC has led the preparation of a series of decadal Roadmap documents that have promoted and inspired the future activities of the community. These Roadmaps were published in 1990 as 'A Long-range plan for the Genome Research project',[10] in 2002 as 'Beyond the Whole Genome Sequence'[11] and in 2012 as 'From Bench to Bountiful Harvests' (Lavagi et al., 2012). These roadmaps are 'meant to serve scientists, policymakers, and funding agencies on the future foci of Arabidopsis research within the wider plant science landscape'. These decadal plans led to the establishment of many Arabidopsis Community Projects & Resources:

- The first decadal plan foresaw the creation of stock centres to distribute biological material, and during this time two out of three stock/resource centres—the ABRC (Arabidopsis Biological Resource Center, US) and NASC

(Nottingham Arabidopsis Stock Centre, UK)—were founded. The first Arabidopsis database was also created, AtDB (Flanders et al., 1998).

- The second decadal plan saw the roll-out of The Multinational Coordinated *A. thaliana* Functional Genomics Project (2002–2011), which led to the functional annotation of most Arabidopsis genes, at least at the level of their transcript abundance in difference tissues and under different conditions. AtDB became The Arabidopsis Information Resource (TAIR) at the start of this period (Huala et al., 2001).
- The third decadal vision, 'From Bench to Bountiful Harvests' (2012–2022; Lavagi et al., 2012), aimed to 'obtain in-depth knowledge of how the genome is translated into a continuum of processes, from the single molecule to cells and tissues, the whole plant, plant populations, and fields of plants, to be able to build a predictive model of an Arabidopsis plant'. During this time and in response to funding cuts to TAIR, the International Arabidopsis Informatics Consortium (IAIC) was created and helped to set up the Arabidopsis Information Portal, also called Araport, in 2013 (IAIC, 2012; Krishnakumar et al., 2015).

Since 2014, general plant projects and resources have also been included in the yearly MASC reports, reflecting the growing connections between researchers focusing on different plant species. The third decadal roadmap published in 2012 by Lavagi et al. (2012) included the following overarching recommendations:

a Build a predictive model of Arabidopsis
b Build infrastructure to support the International Arabidopsis Informatics Consortium, namely Araport.org
c Exploit natural variation
d Build an effective pipeline from lab to field and back
e Deepen international cooperation and coordination

As Parry et al. pointed out in an Arabidopsis research update by MASC in 2020 (Parry et al., 2020), progress has been made in the above areas, but much work still remains to be done. We now understand much more about the molecular and biochemical events that control how a plant grows and senses its environment. One of the big gaps then, and still now, is how at the cellular level each part of the genome is interconnected to produce an environmentally responsive plant—we are quite a long way from being able to build a fully predictive model. Hopefully efforts like the Plant Cell Atlas project (especially the 'Computation, Modeling, & AI Committee') will help to address this (Rhee et al., 2019). Fortunately, there is awareness that bioinformatics training and the development of digital infrastructures are key for the future in depth analysis of Arabidopsis-derived datasets.

In the 12 years since the publication of the 3rd Roadmap in 2012, the Arabidopsis research community has faced numerous challenges, embraced opportunities, and made many advances. The challenges include dealing with the effect of the COVID-19 pandemic on scientific projects and on the mental health of scientists at many career levels. Public and government support for and confidence in scientific researchers has been declining. Climate change has accelerated and worsened. In terms of opportunities, the advent of artificial intelligence (AI) and large language models (LLMs) are very likely to create new opportunities, not only for streamlining work (thanks to tools like ChatGPT) but in very meaningful ways for biology by helping to understand the grammar of genomic regulation—*cis*-regulatory and other non-coding elements, and gene regulatory networks—with programs like DNABERT or DeepLIFT (Ji et al., 2021; Peleke et al., 2024), to predict perturbation responses and gene networks based on single cell 'omics data with programs like scGPT (Cui et al., 2024), and to extract knowledge from the vast volume of literature with LLMs (PlantConnectome; Fo et al., 2023).

However, despite the challenges encountered, many exciting discoveries were made in the past 13 years, highlighting the continued relevance of Arabidopsis research to the wider plant community. In addition to papers mentioned earlier in this article, a smattering of examples in the area of biological discovery include a novel mechanism for auxin signaling via an ARF3/ETTIN module (Simonini et al., 2016), distinct sensing of limiting blue light by PIF4 and PIF5 that is different from their involvement during the red/far red light response (Pedmale et al., 2016), new mitochondrial components from a mitochondrial 'complexome' study (Senkler et al., 2017), determining the blueprint for immunity pan-NLRomes (van de Weyer et al., 2019), and the identification of FLL2 as a regulator for liquid–liquid phase separations of polyadenylation complexes (Fang et al., 2019). Techniques developed in Arabidopsis useful to the wider community include, among many others, a CRISPR-Cas9 system capable of creating nulliplex mutants even in tetraploid plants (Ryder et al., 2017), an AraGWAS catalog (Togninalli et al., 2018), a sequencing-based method called CrY2H-seq for determining protein–protein interactions (Trigg et al., 2017), and a cutting-edge synthetic biology paper where the light-gated K+ channel BLINK1 was introduced into guard cells to enhance kinetics and water use efficiency (Papanatsiou et al., 2019). AlphaFold2 was also used to generate around 26 000 structures for Arabidopsis proteins (Varadi et al., 2022), and neural networks were used to predict combinations of sequence features that identify transcriptional activation domains (Morffy et al., 2024). The quality of these kinds of predictions will surely improve in future versions of these AI-powered approaches.

VISION FOR 2030

The global Arabidopsis research community has come together over several years to formulate our goals for the fourth decadal roadmap with the intent of looking toward 2030 and the future of Arabidopsis research.

We gathered suggestions and inspiration for the kinds of projects/efforts that would advance scientific findings using Arabidopsis in the next decade including a workshop held at ICAR2023 in Chiba, Japan, and a MASC member survey. We were also inspired by the UN SDGs report mentioned above, by the 'one hundred important questions for plant science' posed in Larson et al. (2023), as well as the 'Plant science decadal vision 2020–2030' by Henkhaus et al. (2020).

MASC workshop at ICAR2023 This workshop consisted of 5 panelists with broad geographic and demographic representation, with moderation by Nicholas Provart, the then MASC president, and an introduction by Masatomo Kobayashi, the MASC Director from RIKEN BRC. The panelists were Dirk Inze from the VIB at the University of Gent Center for Plant Systems Biology in Belgium; Gabriela Auge from the Institute for Agrobiotechnology and Molecular Biology, INTA-CONICET, University of Buenos Aires, Argentina; Mentewab Ayalew, Department of Biology, Spelman College/NAASC representative; Kazuki Saito, RIKEN Center for Sustainable Resource Science in Japan; and Sureshkumar Balasubramanian, Biological Sciences at Monash University in Australia. Approximately 25 people were in attendance and participated in these discussions.

MASC survey After the ICAR2023 workshop, a survey was sent to all MASC members, asking for their input into the 4th decadal vision. Among other questions, members were asked to identify which of the 100 important questions for plant biology from Larson et al. (2023) Arabidopsis researchers should focus on; and on how MASC might enable better opportunities for collaboration, continue to encourage cyberinfrastructure, and take on initiatives related to increasing equity, diversity and inclusion in Arabidopsis research.

Below we present the 4th MASC Roadmap, which covers 8 broad areas—increasing computational approaches; supporting research and training; translating from Arabidopsis to crops—or 'back-translating' into Arabidopsis to elucidate mechanisms in other plants; promoting accessibility and diversity at conferences; coordinating research efforts; understanding/mitigating climate change and plant stress; sustainably producing food, materials, and fuel; and emphasizing the importance of fundamental research.

Increasing computational approaches

The main areas for more computational efforts are the following:

A Integrating, identifying and understanding linkages between different 'omic datasets.
B Identifying all cis/trans epigenetic regulatory elements and chromosomal interactions.
C Modeling which combinations of multiplex gene modifications might be beneficial, for example to increase yield
D Improve on collection and standardization of imaging data.
E Improved techniques for quantitative proteomics and targeted analysis.
F Cyberinfrastructure.
G Understanding the plasticity of the epigenome and using this in a predictive way.
H After the soon-to-be released Arabidopsis Col-0 Community Consensus/TAIR 12 (CC12/TAIR12) genome and updated annotation, creating a Arabidopsis pan-genome using all sequence data from the 1001 Genomes Project. Some effort is being made in this area—first across 69 Arabidopsis accessions (Lian et al., 2024)—but these data need to be readily accessible through TAIR (Reiser et al., 2017) or other online tools, such as Genome Context Viewer (Cleary & Farmer, 2017).

In order to achieve these goals, a competition is proposed—similar to those supported by the XPRIZE Foundation[12]—to build a computational model of Arabidopsis growth, development and metabolism by incorporating phenomics and 'omics data, thereby fostering interdisciplinary collaboration and innovation. This will build unprecedented value for all of plant science. In the past decade or so, the Arabidopsis community has evolved to embrace quantitative and computational approaches, opening opportunities for interdisciplinary competitions and hackathons. Another suggestion was to develop a ChatGPT for Arabidopsis data, and, in fact, the Mutwil Lab has done just that by feeding more than 100 000 Arabidopsis abstracts and articles into OpenAI's GPT-3.5 to identify more than 400 000 functional relationships between genes, metabolites, tissues and other entities (Fo et al., 2023). It is expected that rapid advances in AI and machine learning will lead to a better understanding of the 'grammar' of plant genomes with tools like DNABERT (Ji et al., 2021) or convolutional neural networks to generate four species reference (MSR) models that are highly predictive for expression patterns (Peleke et al., 2024). Making use of structure predictions provided by AlphaFold2 and its successors will also help to accelerate our understanding of plant biology (Varadi et al., 2022).

The cyberinfrastructure upon which Arabidopsis research depends should be consciously and deliberately supported. Dedicated resources like BAR (https://bar.utoronto.ca/) and TAIR (https://arabidopsis.org/) are indispensable in today's research environment and need funding to be maintained. While the mechanism of funding varies, the service provided by such resources is essential.

Supporting research and training

The importance of supporting Arabidopsis research and training for the 21st century to bolster research efforts was discussed. Furthermore, advancing equity and diversity in training, teaching, and dissemination of research were seen as helpful to the wider plant science effort. Increased networking opportunities will help early career researchers interact with more established researchers. Efforts like the Gordon Research Seminars (GRSs), held prior to the main Gordon Research Conference meetings exclusively for graduate students and post-doctoral fellows, really help with creating new connections between up-and-coming researchers and in fostering a sense of identity as part of a research community. Events that precipitated the rescheduling of the 13th International Congress of Plant Molecular Biology revealed that there are diverse needs for promotion of equity and diversity that differ depending on the country and these should be recognized with the intent of creating an international Arabidopsis community where all are welcome. The most recent ICAR in San Diego saw support provided for 86 early career researchers (ECRs) and 9 inclusivity scholars. 47% of mini-symposia speakers at the 2024 ICAR were ECRs, while 44% were women. Following the North American Arabidopsis Steering Committee's (NAASC's) lead (described in a white paper by Friesner et al., 2021), MASC will continue to promote a diversity of speakers at upcoming ICARs.

Studying genes in Arabidopsis and translating research to crops

While the value of studying genes unique to Arabidopsis was debated at the 2023 MASC workshop, it was agreed that Arabidopsis plays an essential role in understanding basic mechanisms and in helping these to be applied in other species. Suggestions from the audience were to have agronomists and crop scientists (e.g., those part of DSSAT.net) participate in Arabidopsis publications and conferences, who might help address real-world applications and challenges more effectively—invitations to such individuals to attend ICARs could well lead to productive insights. It might also be worthwhile to create a MASC 'Arabidopsis Translation' subcommittee to identify opportunities for translation and dissemination of Arabidopsis research results—or at least to highlight interesting examples of translational research each year. This has been done on an *ad hoc* basis in past MASC annual reports, but formalizing an Arabidopsis Translation subcommittee would be a good first step.

Accessibility and diversity in conferences/other equity issues

ICAR 2023 workshop attendees thought that rotating annual Arabidopsis conferences to different regions of the world (including the 'Global South') and encouraging top scientists to attend them would foster greater collaboration and the exchange of ideas. Diversity in speakers (early career vs. late career, gender, ethnicity, organization type including research-intensive universities as well as mostly undergraduate universities, geographic location) was seen as a positive by most workshop members. Conference scientific and organizing committees should also be diverse, begetting speaker diversity. Increased selection of speakers from the Global South should be encouraged, along with recognizing the uneven impact the effects of the COVID-19 pandemic have had on research productivity across the world. Perhaps the usual metrics for evaluating whether or not a speaker should be selected to give a talk at an Arabidopsis conference could be expanded to take into account such unevenness. Several survey responses also mentioned the importance of teaching and, while some recent ICARs have had outreach sessions, these could be a regular feature at all ICARs. It might be useful to reactivate The Arabidopsis Book, or to continue this effort as a wiki on the MASC website, where teaching material—videos, courses, and the like—could be easily shared.

Coordinating research efforts

The ICAR 2023 workshop panelists highlighted the need for better coordination in Arabidopsis research, perhaps by promoting TAIR's database of researchers working on similar topics. Logically and based on past successful coordination efforts, MASC should play a role in coordinating research efforts and planning experiments, drawing further inspiration from successful initiatives like GreeNet,[13] which brings together various stakeholders for ecological preservation. Similar to the previous focus point, efforts should be made to involve researchers from the Global South and to foster collaborations and training opportunities. One suggestion was to transform MASC reports into active opportunities for collaboration, facilitating connections among researchers seeking partners, perhaps by using the MASC website or a similar platform to facilitate real-time connections among researchers seeking collaborations, thereby making the process more dynamic and efficient. Linkages to other supranational groups, such as the Global Plant Council, could also be strengthened.

Understanding and dealing with climate change and plant stress for sustainable food production and preserving species diversity

One of the key issues facing humanity is how plants (and people) will adapt to climate change. Changes to weather patterns, soil physicochemical parameters, and ecosystem balance[14] will require rapid changes to agricultural varieties. Methods developed in Arabidopsis for high-throughput phenotyping, gene modification via CRISPR-Cas9, exploring natural variation and others will be important to help plant breeders develop new varieties. Plant-pathogen dynamics are likely to change too, so understanding eco-evolutionary dynamics and pathogenesis will be increasingly important. Many strides in this area have already been made (e.g., Laflamme et al., 2020; Smakowska-Luzan et al., 2018; van de Weyer et al., 2019), but we also need to prepare for new diseases on the horizon. Furthermore, can we develop ways to improve stress tolerance by identifying cocktails of beneficial microbes for particular climates (Ali et al., 2023) or through priming methods (e.g., Turhan & Asgher, 2024)? Engaging with agronomists (perhaps through an 'Arabidopsis Translation' subcommittee as previously mentioned) will have mutual benefits. Agronomists will better understand the potential of innovative agriculture tools developed and prototyped in Arabidopsis to create climate-resilient crops. Arabidopsis researchers in turn will understand emerging issues relevant to agriculture like evolving herbicide resistance and agricultural run-off and where the development and deployment of new methods would be applicable to mitigate the effects of climate change.

Sustainable production of materials and fuel

Investing in natural, biodegradable materials for sustainability was deemed to be an important area of future focus. Arabidopsis has been used to show the feasibility of using plants for phytoremediation—but also as a happy side product, for 'phytomining' valuable compounds, such as cesium and palladium. In the case of cesium, Adams et al. (2017) undertook a chemical biology screen to identify several compounds that led to the phytoaccumulation of cesium in Arabidopsis tissues. Equally intriguingly, Harumain et al. (2017) followed up on reports that Arabidopsis can concentrate palladium—valuable as a catalyst—in nanoparticles in cells in liquid culture (Parker et al., 2014). The authors were able to extract 18 g kg^{-1} palladium from dried Arabidopsis material. Further experiments investigated the use of mustard, *Miscanthus* and willow plants grown on synthetic tailings containing palladium. With the right treatment (unfortunately involving cyanide), levels of 0.5–0.8 g kg^{-1} palladium could be extracted from dried leaf material, depending on the species. A lifecycle analysis showed a clear benefit of dramatically reduced costs for resources, ecosystems, and human health impacts for an Arabidopsis-based process versus the 'conventional' palladium catalyst generation process of 0.97 points versus 2.95 points (lower is better; Harumain et al., 2017), suggesting that such approaches could lead to more sustainable mining and catalyst generation methods.

Fundamental research

It should be emphasized that in 37 of 50 years covered in a review of 54 033 Arabidopsis papers (Provart et al., 2016) >50% of the cited Arabidopsis papers published each year have been referenced by papers where Arabidopsis was *not* the focus of the research (this was determined by the absence of 'Arabidopsis' in the taxonomic data available for each paper in the BIOSIS database that the authors used). This means that other (plant) researchers are widely referencing discoveries made in Arabidopsis, and that Arabidopsis serves as the knowledgebase for plant biology. Thus, there is considerable rationale for continuing to support Arabidopsis for fundamental research—the results end up percolating into the wider plant research community. It is important also to keep in mind that just over 30% of Arabidopsis genes have had their Gene Ontology Molecular Function or Biological Process determined experimentally—25 years after the Arabidopsis genome was published (Reiser et al., 2024)! So our last recommendation as we look to 2030 is to continue to take advantage of Arabidopsis, using all the tools available to us including natural variation and ecophysiology, cell biological methods, and single cell approaches in order to study cell–cell, organ-organ, plant–plant, plant-environment communication/signaling, perhaps with a focus on the 'unknowns' of the genome, looking for novelty, as often researchers tends to follow up on the known. The Human Frontier Science Program (https://www.hfsp.org/) and ERC Synergy Grants (https://erc.europa.eu/apply-grant/synergy-grant) provide funding opportunities for 'international collaboration in basic research' and for research efforts with 'intrinsic synergetic effect', respectively. We need to encourage additional funding agencies to participate in or initiate similar transnational funding calls to bring together global teams to solve the problems facing all of Earth's inhabitants. Communication with private foundations across the world to emphasize the relevance and importance of this kind of work could also benefit Arabidopsis research by unlocking additional funding sources.

Last, synthetic biology as a research tool for plants, coupled with genome editing approaches and AI is very likely to happen first in Arabidopsis (such methods are already appearing for humans, for example, Gosai et al., 2024; Sanabria et al., 2024). This kind of research would benefit many areas of plant science and could be spearheaded by Arabidopsis researchers, as have many other methods that are now commonly used in plants.

CONCLUSION

In the coming decade, plant science will face numerous hurdles, particularly in achieving sustainable food production, especially in the context of a changing climate. By following this roadmap's objectives, we can leverage the many past research successes in Arabidopsis and advance rapidly toward overcoming these hurdles. A comprehensive grasp of how plant processes interact, traditionally studied in isolation, is within reach, given the mind-blowing advances in AI. Powerful predictive

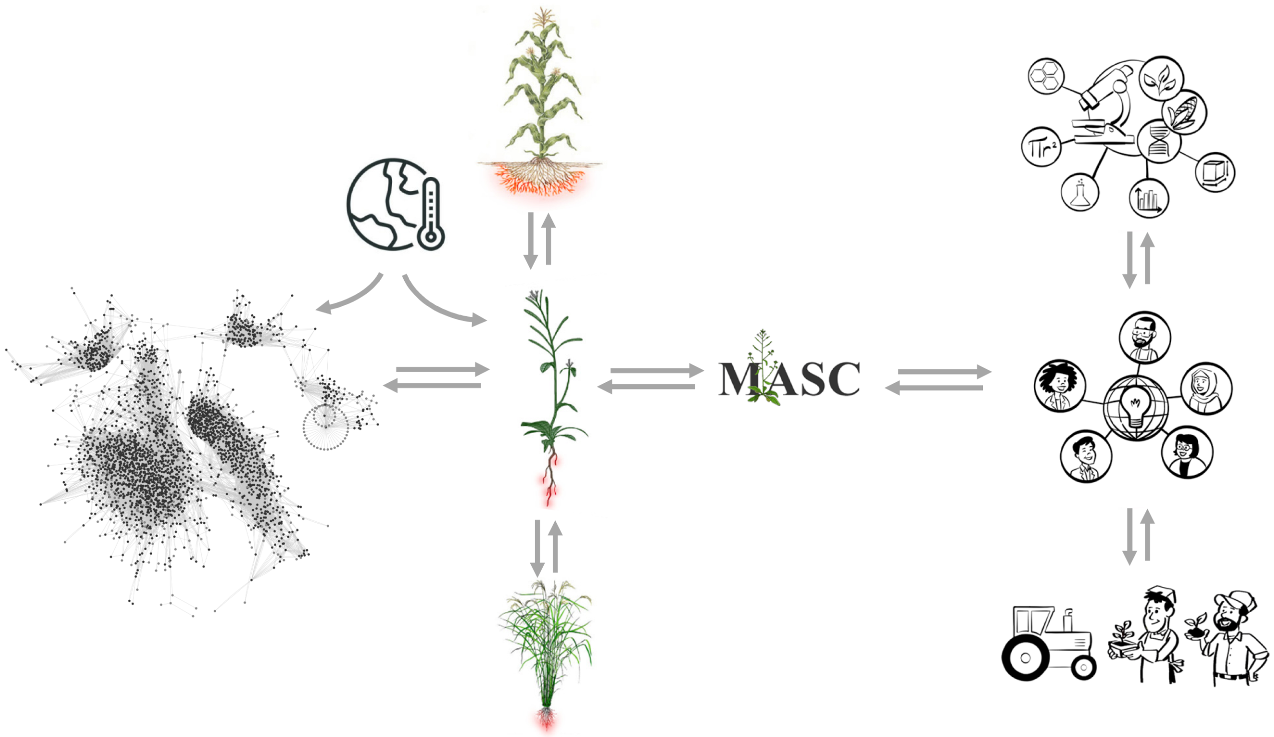

Figure 1. A vision for Arabidopsis research in 2030. Computational models created by integrating large 'omics data using AI would inform experiments in Arabidopsis that could be translated to crop species, especially in the context of climate change. Mechanisms unique to crop species (or coopted by pathogens or parasitic plants) could be elucidated with the help of Arabidopsis. MASC would support accessibility and diversity in conferences and other equity issues, and would help to coordinate research efforts between Arabidopsis and crop researchers/agronomists from around the world. Images on the right from Filament LLC, used with permission.

computational models will likely be developed in the next decade. Integration of climate and environmental data with experimental findings in a holistic manner will deepen our insight into plant-environment interactions, facilitating predictive model development. As shown in Figure 1, our roadmap aims to unify and bolster a cohesive, robust, and productive Arabidopsis research community by setting forth a clear vision and objectives for the next decade. This approach will ensure that the Arabidopsis community continues to spearhead essential advances in our understanding of plant biology, crucial for meeting the looming global challenges ahead.

CONFLICT OF INTEREST

The authors have not declared a conflict of interest.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

ENDNOTES

[1] https://www.undp.org/sustainable-development-goals.

[2] https://www.undp.org/sustainable-development-goals/zero-hunger.

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