

A timeline of discovery and innovation in Arabidopsis

Catherine Freed,^{1,2} Arif Ashraf,^{2,3} Nancy A. Eckardt,⁴ Adrienne H.K. Roeder,^{2,5,*} Joanna D. Friesner^{2,*}

¹Department of Biochemistry, University of Wisconsin-Madison, Madison, WI 53706, USA

²North American Arabidopsis Steering Committee, Corvallis, OR 97330, USA

³Department of Botany, University of British Columbia, Vancouver, BC, Canada V6T 1Z4

⁴American Society of Plant Biologists, USA

⁵School of Integrative Plant Science, Section of Plant Biology and Weill Institute for Cell and Molecular Biology, Cornell University, Ithaca, NY 14853, USA

*Author for correspondence: ahr75@cornell.edu (A.H.K.R.), friesnerconsult@gmail.com (J.F.)

The author responsible for distribution of materials integral to the findings presented in this article in accordance with the policy described in the Instructions for Authors (<https://academic.oup.com/plcell/pages/General-Instructions>) is: Adrienne H.K. Roeder (ahr75@cornell.edu).

To celebrate this Focus Issue on Translational Research from Arabidopsis to Crop Plants and Beyond, we present a timeline highlighting some of the exceptional discoveries, innovations, and community milestones in Arabidopsis research over the past 150+ years (Supplementary Figure S1). This timeline showcases multinational Arabidopsis efforts from as early as 1873 to the present, divided into five categories: technology, community, landmark paper, resource, and application. The technology category encompasses novel discoveries and research that have been particularly critical for advancing plant science into the 21st century. The community category showcases activities that helped to establish the Arabidopsis research community and enabled its evolution. The landmark paper category includes 25 of the top-cited Arabidopsis publications from *The Plant Cell* each year over the last 25 years. The resource category features new tools and resources developed by the Arabidopsis community, such as the creation of the Arabidopsis seed stock centers and online databases that have enabled plant researchers to gain a broader understanding of plant biology in Arabidopsis and other species. The application category highlights key technologies and plant products that have been made possible through fundamental Arabidopsis research efforts. This is not an exhaustive list, but a few examples that have made it to market. See the rest of the focus issue for other applications. Together, this timeline illustrates the rich history of Arabidopsis research and the Arabidopsis community, and the pivotal role Arabidopsis has played in advancing plant biology and developing the critical tools, resources, and technologies that continue to underpin innovations. Looking ahead, how will Arabidopsis-based research and discovery help to advance agriculture and biotechnology 25 years from now?

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1873—Technology—First Arabidopsis mutant published (Braun 1873; Yaschenko et al. 2024).

1935—Technology—N. Titova proposes Arabidopsis as a genetic tool (Titova 1935; Meyerowitz and Pruitt 1985).

1943—Technology—F. Laibach proposes Arabidopsis as a genetic tool (Laibach 1943; Meyerowitz and Pruitt 1985).

1947—Technology—X-Ray mutagenesis of Arabidopsis (Reinholz 1947).

1962—Technology—EMS mutagenesis of Arabidopsis seeds (Röbbelen 1962; McKelvie 1963).

1964—Community—The Arabidopsis Information Service—first community newsletter—founded.

1965—Resource—Early community Arabidopsis seed stock list (Röbbelen 1965).

1965—Community—First Arabidopsis community conference in Gottingen, Germany (Röbbelen 1965).

1975—Technology—G. Rédei proposes Arabidopsis as a genetic tool (Rédei 1975).

1982—Technology—First Arabidopsis plants in space (Merkys and Laurinavicius 1983).

1984—Technology—Arabidopsis has a small genome, good for positional cloning (Leutwiler et al. 1984).

1985—Community—Arabidopsis is recognized as a model system for basic research in plant molecular biology (Meyerowitz and Pruitt 1985).

1986—Technology—T-DNA-mediated transformation of Arabidopsis (An et al. 1986; Lloyd et al. 1986).

1987—Community—First modern era International Conference on Arabidopsis Research (ICAR) at Michigan State University, USA.

1987—Resource—Modern era community Arabidopsis seed stock list (Kranz and Kirchheim 1987).

1989—Technology—T-DNA mutagenesis (Feldmann et al. 1989; Marks and Feldmann 1989).

1990—Community—Multinational Arabidopsis Steering Committee (MASC) founded.

1990—Community—Broad Arabidopsis community email list-serv (Bionet) founded.

1991—Resource—Major Arabidopsis Seed Stock centers (ABRC, USA & NASC, UK) established.

1992—Community—North American Arabidopsis Steering Committee (NAASC) founded.

1992—Resource—Arabidopsis database created (AATDB) (Michael Cherry et al. 1992).

1994—Technology—Cloning of the first NLR innate immune receptors (Bent et al. 1994; Mindrinis et al. 1994 Grant et al. 1995).

1995—Technology—Microarrays to quantify whole Arabidopsis transcriptome (Schena et al. 1995).

1997—Technology—dsRNAi for gene silencing in Arabidopsis (Chuang and Meyerowitz 2000).

1997—Application—Paradigm Genetics and Mendel Biotechnology were both founded on the use of Arabidopsis genetics and genomics to derive function for translational use.

1998—Community—Arabidopsis is declared a model organism (Meinke et al. 1998).

1998—Technology—Arabidopsis floral dip with *Agrobacterium tumefaciens* (Clough and Bent 1998).

2000—Resource—Arabidopsis genome sequence is released. First plant/third eukaryote genome sequenced (The Arabidopsis Genome Initiative 2000).

2000—Community—Workshop Report: “The 2010 Project” Functional Genomics & the Virtual Plant. A Blueprint for Understanding How Plants Are Built & How to Improve Them (Chory et al. 2000).

2000—Landmark Paper—Hd1, a Major Photoperiod Sensitivity Quantitative Trait Locus in Rice, Is Closely Related to the Arabidopsis Flowering Time Gene *CONSTANS* (Yano et al. 2000).

2000—Technology—TILLING developed in Arabidopsis (McCallum et al. 2000).

2001—Landmark Paper—Growth Stage-Based Phenotypic Analysis of Arabidopsis: A Model for High Throughput Functional Genomics in Plants (Boyce et al. 2001).

2001—Resource—The Arabidopsis Information Resource (TAIR) released (Huala et al. 2001).

2002—Landmark Paper—Arabidopsis Transcriptome Profiling Indicates That Multiple Regulatory Pathways Are Activated during Cold Acclimation in Addition to the CBF Cold Response Pathway (Fowler and Thomashow 2002).

2003—Resource—Large-scale Arabidopsis T-DNA insertion line collection with locations sequenced (Alonso et al. 2003).

2003—Landmark Paper—Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) Function as Transcriptional Activators in Absciscic Acid Signaling (Abe et al. 2003).

2004—Landmark Paper—Novel and Stress-Regulated MicroRNAs and Other Small RNAs from Arabidopsis (Sunkar and Zhu 2004).

2005—Technology—Translating Ribosome Affinity Purification (TRAP) was first developed in Arabidopsis and then applied to other organisms (Zanetti et al. 2005).

2005—Landmark Paper—Functional Genomic Analysis of the AUXIN RESPONSE FACTOR Gene Family Members in *Arabidopsis thaliana*: Unique and Overlapping Functions of ARF7 and ARF19 (Okushima et al. 2005).

2006—Landmark Paper—First gene silencing by artificial miRNAs in Arabidopsis. Highly Specific Gene Silencing by Artificial MicroRNAs in Arabidopsis (Schwab et al. 2006).

2007—Technology—Arabidopsis Electronic Fluorescent Pictograph (eFP) Browser released (Winter et al. 2007).

2007—Landmark Paper—MYC2 Differentially Modulates Diverse Jasmonate-Dependent Functions in Arabidopsis (Dombrecht et al. 2007).

2008—Resource—The 1001 Genomes Project was launched to discover detailed whole-genome sequence variation in at least 1001 strains (accessions) of *Arabidopsis thaliana* (Alonso-Blanco et al. 2016).

2008—Landmark Paper—A Battery of Transcription Factors Involved in the Regulation of Secondary Cell Wall Biosynthesis in Arabidopsis (Zhong et al. 2008).

2009—Application—Auxin inducible degron (AID) system based on Arabidopsis auxin signaling, adapted to inducibly

degrade target proteins in yeast & mammalian cells (Nishimura et al. 2009).

2009—Landmark Paper—MYB58 and MYB63 Are Transcriptional Activators of the Lignin Biosynthetic Pathway during Secondary Cell Wall Formation in Arabidopsis (Zhou et al. 2009).

2009—Application—Optogenetics: Light switchable protein interaction based on PHY-PIF system (Levskaya et al. 2009).

2010—Landmark Paper—The bHLH Transcription Factor POPEYE Regulates Response to Iron Deficiency in Arabidopsis Roots (Long et al. 2010).

2011—Technology—INTACT (isolation of nuclei tagged in specific cell types) developed in Arabidopsis (Deal and Henikoff 2011).

2011—Landmark Paper—The Arabidopsis bHLH Transcription Factors MYC3 and MYC4 Are Targets of JAZ Repressors and Act Additively with MYC2 in the Activation of Jasmonate Responses (Fernández-Calvo et al. 2011).

2012—Landmark Paper—Genome-Wide Analysis Uncovers Regulation of Long Intergenic Noncoding RNAs in Arabidopsis (Liu et al. 2012).

2013—Technology—Arabidopsis and *Nicotiana* were the first plants to be edited using CRISPR (Li et al. 2013).

2013—Landmark Paper—Jasmonate Regulates the INDUCER OF CBF EXPRESSION- C-REPEAT BINDING FACTOR/DRE BINDING FACTOR1 Cascade and Freezing Tolerance in Arabidopsis (Hu et al. 2013).

2014—Landmark Paper—Arabidopsis miR156 Regulates Tolerance to Recurring Environmental Stress through SPL Transcription Factors (Stief et al. 2014).

2015—Application—BASF introduced the PodGuard trait to Canola farmers which was developed by Bayer based on discoveries of the Arabidopsis *INDEHISCENT* gene (Liljegren et al. 2004; Liljegren and Yanofsky 2006; Aguilera 2019).

2015—Landmark Paper—A Cascade of Sequentially Expressed Sucrose Transporters in the Seed Coat and Endosperm Provides Nutrition for the Arabidopsis Embryo (Chen et al. 2015).

2015—Technology—Development of the MorphoGraphX image analysis software (Barbier de Reuille et al. 2015).

2016—Landmark Paper—Regulation of Leaf Starch Degradation by Absciscic Acid Is Important for Osmotic Stress Tolerance in Plants (Thalman et al. 2016).

2016—Technology—DAP-seq developed in Arabidopsis (O'Malley et al. 2016).

2017—Landmark Paper—Arabidopsis WRKY46, WRKY54, and WRKY70 Transcription Factors Are Involved in Brassinosteroid-Regulated Plant Growth and Drought Responses (Chen et al. 2017).

2018—Landmark Paper—The m6A Reader ECT2 Controls Trichome Morphology by Affecting mRNA Stability in Arabidopsis (Wei et al. 2018).

2019—Application—First commercial production of CoverCress: field pennycress converted into a winter-annual oil-seed crop based on Arabidopsis information (Phippen et al. 2022; Chopra et al. 2018, 2020).

2019—Landmark Paper—Dynamics of Gene Expression in Single Root Cells of *Arabidopsis thaliana* (Jean-Baptiste et al. 2019).

2019—Technology—Large-scale single cell transcriptomics in plants in Arabidopsis roots (Denyer et al. 2019; Jean-Baptiste et al. 2019; Ryu et al. 2019; Shulze et al. 2019; Zhang et al. 2019).

2020—Landmark Paper—Persulfidation-based Modification of Cysteine Desulfhydrase and the NADPH Oxidase RBOHD Controls Guard Cell Absciscic Acid Signaling (Shen et al. 2020).

2021—Landmark Paper—Distinct identities of leaf phloem cells revealed by single cell transcriptomics (Kim et al. 2021).

2021—Application—During 2000–2018 Corteva field-testing and screening for traits to improve crop tolerance to abiotic stress, over 90% of the 35,000 genes in the prescreening were identified in Arabidopsis. (Simmons et al. 2021).

2022—Landmark Paper—HPCA1 is required for systemic reactive oxygen species and calcium cell-to-cell signaling and plant acclimation to stress (Fichman et al. 2022).

2023—Application—Pairwise developed Conscious Greens, a nutritious and better tasting mustard green, using CRISPR to knock out the myrosinase genes to make them less bitter (Grinstein 2023). This was based on decades of research on glucosinolates and the myrosinase enzymes that break them down in Arabidopsis and other Brassicaceae plants (Halkier and Gershenzon 2006).

2023—Technology—Spatial single cell sequencing in Arabidopsis (Nobori et al. 2023).

2023—Landmark Paper—Auxin contributes to jasmonate-mediated regulation of abscisic acid signaling during seed germination in Arabidopsis (Mei et al. 2023).

2023—Application—Introduction of AtNPR1 into sweet orange trees to increase resistance to Huanglongbing (HLB) citrus greening in 2015 (Dutt et al. 2015). As of 2023, this technology is currently under regulatory status review by USDA APHIS (Silva et al. 2018; USDA APHIS 2023).

2024—Technology—Arabidopsis single cell proteomics (Montes et al. 2024).

2024—Landmark Paper—The m⁶A reader ECT1 drives mRNA sequestration to dampen salicylic acid-dependent stress responses in Arabidopsis (Lee et al. 2024).

2024—Application—Norfolk HP developed The Purple Tomato, bioengineered to have increased antioxidants. Arabidopsis-based gene discovery aided in development of purple tomato as the project started with the extraction of AtMYB12 protein from Arabidopsis and exploration revealed that AtMYB12 increases flavonoid accumulation and phenylpropanoid biosynthesis in tomato (Zhang et al. 2015). The Purple Tomato was released by Norfolk Healthy Produce as an FDA-approved product in 2023 and became available for purchase in 2024 (Martin and Butelli 2025).

2024—Community—First Arabidopsis community awards given (North American Arabidopsis Steering Committee).

Supplementary data

The following materials are available in the online version of this article.

Supplementary Figure S1. Full size timeline pdf.

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Data availability

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References

- Abe H, Urao T, Ito T, Seki M, Shinozaki K, Yamaguchi-Shinozaki K. Arabidopsis AtMYC2 (bHLH) and AtMYB2 (MYB) function as transcriptional activators in abscisic acid signaling. *Plant Cell*. 2003;15(1):63–78. <https://doi.org/10.1105/tpc.006130>
- Aguilera, MC. Shatterproof: the seeds of a blockbuster discovery. UC San Diego Today. 2019. https://today.ucsd.edu/story/shatterproof_the_seeds_of_a_blockbuster_discovery
- Alonso JM, Stepanova AN, Leisse TJ, Kim CJ, Chen H, Shinn P, Stevenson DK, Zimmerman J, Barajas P, Cheuk R, et al. Genome-wide insertional mutagenesis of Arabidopsis thaliana. *Science*. 2003;301(5633):653–657. <https://doi.org/10.1126/science.1086391>
- Alonso-Blanco C, Andrade J, Becker C, Bemm F, Bergelson J, Borgwardt KM, Cao J, Chae E, Dezwaan TM, Ding W, et al. 1,135 genomes reveal the global pattern of polymorphism in Arabidopsis thaliana. *Cell*. 2016;166(2):481–491. <https://doi.org/10.1016/j.cell.2016.05.063>
- An G, Watson BD, Chiang CC. Transformation of tobacco, tomato, potato, and Arabidopsis thaliana using a binary ti vector system 1. *Plant Physiol*. 1986;81(1):301–305. <https://doi.org/10.1104/pp.81.1.301>
- Barbier de Reuille P, Routier-Kierzkowska A-L, Kierzkowski D, Bassel GW, Schüpbach T, Tauriello G, Bajpai N, Strauss S, Weber A, Kiss A, et al. MorphoGraphX: a platform for quantifying morphogenesis in 4D. *Elife*. 2015;4:e05864. <https://doi.org/10.7554/eLife.05864>
- Bent AF, Kunkel BN, Dahlbeck D, Brown KL, Schmidt R, Giraudat J, Leung J, Staskawicz BJ. RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant disease resistance genes. *Science*. 1994;265(5180):1856–1860. <https://doi.org/10.1126/science.8091210>
- Boyes DC, Zayed AM, Ascenzi R, McCaskill AJ, Hoffman NE, Davis KR, Görlach J. Growth stage-based phenotypic analysis of Arabidopsis: a model for high throughput functional genomics in plants. *Plant Cell*. 2001;13(7):1499–1510. <https://doi.org/10.1105/tpc.010011>
- Braun A. *Sitzungsberichte der gesellschaft naturforschender freunde zu Berlin*. Berlin: Gesellschaft Naturforschender Freunde; 1873.
- Chen J, Nolan TM, Ye H, Zhang M, Tong H, Xin P, Chu J, Chu C, Li Z, Yin Y. Arabidopsis WRKY46, WRKY54, and WRKY70 transcription factors are involved in brassinosteroid-regulated plant growth and drought responses. *Plant Cell*. 2017;29(6):1425–1439. <https://doi.org/10.1105/tpc.17.00364>
- Chen L-Q, Lin IW, Qu X-Q, Sosso D, McFarlane HE, Londoño A, Samuels AL, Frommer WB. A cascade of sequentially expressed sucrose transporters in the seed coat and endosperm provides nutrition for the Arabidopsis embryo. *Plant Cell*. 2015;27(3):607–619. <https://doi.org/10.1105/tpc.114.134585>
- Cherry JM, Cartinhour SW, Goodman HM. AAtDB, an Arabidopsis thaliana database. *Plant Mol Biol Rep*. 1992;10(4):308–309. <https://doi.org/10.1007/BF02668902>
- Chopra R, Johnson EB, Daniels E, McGinn M, Dorn KM, Esfahanian M, Folstad N, Amundson K, Altendorf K, Betts K, et al. Translational genomics using Arabidopsis as a model enables the characterization of pennycress genes through forward and reverse genetics. *Plant J*. 2018;96(6):1093–1105. <https://doi.org/10.1111/tbj.14147>
- Chopra R, Johnson EB, Emenecker R, Cahoon EB, Lyons J, Kliebenstein DJ, Daniels E, Dorn KM, Esfahanian M, Folstad N, et al. Identification and stacking of crucial traits required for the domestication of pennycress. *Nat Food*. 2020;1(1):84–91. <https://doi.org/10.1038/s43016-019-0007-z>

- Chory J, Ecker JR, Briggs S, Caboche M, Coruzzi GM, Cook D, Dangel J, Grant S, Gueriot ML, Henikoff S, et al. National Science Foundation-sponsored workshop report: "the 2010 project" functional genomics and the virtual plant. A blueprint for understanding how plants are built and how to improve them. *Plant Physiol.* 2000;123(2):423–426. <https://doi.org/10.1104/pp.123.2.423>
- Chuang C-F, Meyerowitz EM. Specific and heritable genetic interference by double-stranded RNA in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A.* 2000;97(9):4985–4990. <https://doi.org/10.1073/pnas.060034297>
- Clough SJ, Bent AF. Floral dip: a simplified method for -mediated transformation of. *Plant J.* 1998;16(6):735–743. <https://doi.org/10.1046/j.1365-313x.1998.00343.x>
- Deal RB, Henikoff S. The INTACT method for cell type-specific gene expression and chromatin profiling in *Arabidopsis thaliana*. *Nat Protoc.* 2011;6(1):56–68. <https://doi.org/10.1038/nprot.2010.175>
- Denyer T, Ma X, Klesen S, Scacchi E, Nieselt K, Timmermans MCP. Spatiotemporal developmental trajectories in the *Arabidopsis* root revealed using high-throughput single-cell RNA sequencing. *Dev Cell.* 2019;48(6):840–852.e5. <https://doi.org/10.1016/j.devcel.2019.02.022>
- Dombrecht B, Xue GP, Sprague SJ, Kirkegaard JA, Ross JJ, Reid JB, Fitt GP, Sewelam N, Schenk PM, Mannes JM, et al. MYC2 differentially modulates diverse jasmonate-dependent functions in *Arabidopsis*. *Plant Cell.* 2007;19(7):2225–2245. <https://doi.org/10.1105/tpc.106.048017>
- Dutt M, Barthe G, Irey M, Grosser J. Transgenic citrus expressing an *Arabidopsis* NPR1 gene exhibit enhanced resistance against huanglongbing (hlb; citrus greening). *PLoS One.* 2015;10(9):e0137134. <https://doi.org/10.1371/journal.pone.0137134>
- Feldmann KA, Marks MD, Christianson ML, Quatrano RS. A dwarf mutant of *Arabidopsis* generated by T-DNA insertion mutagenesis. *Science.* 1989;243(4896):1351–1354. <https://doi.org/10.1126/science.243.4896.1351>
- Fernández-Calvo P, Chini A, Fernández-Barbero G, Chico J-M, Gimenez-Ibanez S, Geerinck J, Eeckhout D, Schweizer F, Godoy M, Franco-Zorrilla JM, et al. The *Arabidopsis* bHLH transcription factors MYC3 and MYC4 are targets of JAZ repressors and act additively with MYC2 in the activation of jasmonate responses. *Plant Cell.* 2011;23(2):701–715. <https://doi.org/10.1105/tpc.110.080788>
- Fichman Y, Zandalinas SI, Peck S, Luan S, Mittler R. HPCA1 is required for systemic reactive oxygen species and calcium cell-to-cell signaling and plant acclimation to stress. *Plant Cell.* 2022;34(11):4453–4471. <https://doi.org/10.1093/plcell/koac241>
- Fowler S, Thomashow MF. *Arabidopsis* transcriptome profiling indicates that multiple regulatory pathways are activated during cold acclimation in addition to the CBF cold response pathway. *Plant Cell.* 2002;14(8):1675–1690. <https://doi.org/10.1105/tpc.003483>
- Grant MR, Godiard L, Straube E, Ashfield T, Lewald J, Sattler A, Innes RW, Dangel JL. Structure of the *Arabidopsis* RPM1 gene enabling dual specificity disease resistance. *Science.* 1995;269(5225):843–846. <https://doi.org/10.1126/science.7638602>
- Grinstein JD. Salad days: pairwise gene edits food to topple nutrition barriers. *GEN Biotechnol.* 2023;2(1):5–9. <https://doi.org/10.1089/genbio.2023.29078.jdg>
- Halkier BA, Gershenzon J. Biology and biochemistry of glucosinolates. *Annu Rev Plant Biol.* 2006;57(1):303–333. <https://doi.org/10.1146/annurev.arplant.57.032905.105228>
- Hu Y, Jiang L, Wang F, Yu D. Jasmonate regulates the INDUCER OF CBF EXPRESSION–C-REPEAT BINDING FACTOR/DRE BINDING FACTOR1 cascade and freezing tolerance in *Arabidopsis*. *Plant Cell.* 2013;25(8):2907–2924. <https://doi.org/10.1105/tpc.113.112631>
- Huala E, Dickerman AW, Garcia-Hernandez M, Weems D, Reiser L, LaFond F, Hanley D, Kiphart D, Zhuang M, Huang W, et al. The *Arabidopsis* Information Resource (TAIR): a comprehensive database and web-based information retrieval, analysis, and visualization system for a model plant. *Nucleic Acids Res.* 2001;29(1):102–105. <https://doi.org/10.1093/nar/29.1.102>
- Jean-Baptiste K, McFaline-Figueroa JL, Alexandre CM, Dorrity MW, Saunders L, Bubbs KL, Trapnell C, Fields S, Queitsch C, JT C. Dynamics of gene expression in single root cells of *Arabidopsis thaliana*. *Plant Cell.* 2019;31(5):993–1011. <https://doi.org/10.1105/tpc.18.00785>
- Kim J-Y, Symeonidi E, Pang TY, Denyer T, Weidauer D, Bezruczyk M, Miras M, Zöllner N, Hartwig T, Wudick MM, et al. Distinct identities of leaf phloem cells revealed by single cell transcriptomics. *Plant Cell.* 2021;33(3):511–530. <https://doi.org/10.1093/plcell/koaa060>
- Kranz AR, Kirchheim B. *Genetic resources in Arabidopsis: computerized listing of seed bank material.* Vol. 24. Frankfurt: Botanical Institute, J.W. Goethe-University, *Arabidopsis* Information Service; 1987. p. 1–167.
- Laibach F. *Arabidopsis thaliana* (L.) Heynh. als Objekt für genetische und entwicklungsphysiologische Untersuchungen. *Bot Archiv.* 1943;44:439–455.
- Lee KP, Liu K, Kim EY, Medina-Puche L, Dong H, Di M, Singh RM, Li M, Qi S, Meng Z, et al. The m6A reader ECT1 drives mRNA sequestration to dampen salicylic acid-dependent stress responses in *Arabidopsis*. *Plant Cell.* 2024;36(3):746–763. <https://doi.org/10.1093/plcell/koad300>
- Leutwiler LS, Hough-Evans BR, Meyerowitz EM. The DNA of *Arabidopsis thaliana*. *Mol Gen Genet.* 1984;194(1–2):15–23. <https://doi.org/10.1007/BF00383491>
- Levskaia A, Weiner OD, Lim WA, Voigt CA. Spatiotemporal control of cell signalling using a light-switchable protein interaction. *Nature.* 2009;461(7266):997–1001. <https://doi.org/10.1038/nature08446>
- Li J-F, Norville JE, Aach J, McCormack M, Zhang D, Bush J, Church GM, Sheen J. Multiplex and homologous recombination-mediated genome editing in *Arabidopsis* and *Nicotiana benthamiana* using guide RNA and Cas9. *Nat Biotechnol.* 2013;31(8):688–691. <https://doi.org/10.1038/nbt.2654>
- Liljegen S, Yanofsky M. Control of fruit dehiscence in *Arabidopsis* by indehiscent genes. United States Patent. Patent No. 6,998,517. 2006.
- Liljegen SJ, Roeder AHK, Kempin SA, Gremski K, Østergaard L, Guimil S, Reyes DK, MF Y. Control of fruit patterning in *Arabidopsis* by INDEHISCENT. *Cell.* 2004;116(6):843–853. [https://doi.org/10.1016/S0092-8674\(04\)00217-X](https://doi.org/10.1016/S0092-8674(04)00217-X)
- Liu J, Jung C, Xu J, Wang H, Deng S, Bernad L, Arenas-Huertero C, Chua N-H. Genome-wide analysis uncovers regulation of long intergenic noncoding RNAs in *Arabidopsis*. *Plant Cell.* 2012;24(11):4333–4345. <https://doi.org/10.1105/tpc.112.102855>
- Lloyd AM, Barnason AR, Rogers SG, Byrne MC, Fraley RT, Horsch RB. Transformation of *Arabidopsis thaliana* with *Agrobacterium tumefaciens*. *Science.* 1986;234(4775):464–466. <https://doi.org/10.1126/science.234.4775.464>
- Long TA, Tsukagoshi H, Busch W, Lahner B, Salt DE, Benfey PN. The bHLH transcription factor POPEYE regulates response to iron deficiency in *Arabidopsis* roots. *Plant Cell.* 2010;22(7):2219–2236. <https://doi.org/10.1105/tpc.110.074096>

- Marks MD, Feldmann KA. Trichome development in *Arabidopsis thaliana*. I. T-DNA tagging of the GLABROUS1 gene. *Plant Cell*. 1989;1(11):1043–1050. <https://doi.org/10.2307/3869021>
- Martin C, Butelli E. The purple tomato story; from laboratory bench to the consumer. *ACS Food Sci Technol*. 2025;5(1):19–28. <https://doi.org/10.1021/acsfoodscitech.4c00692>
- McCallum CM, Comai L, Greene EA, Henikoff S. Targeted screening for induced mutations. *Nat Biotechnol*. 2000;18(4):455–457. <https://doi.org/10.1038/74542>
- McKelvie AD. Studies in the induction of mutations in *Arabidopsis thaliana* (L.) Heynh. *Radiat Bot*. 1963;3(2):105–123. [https://doi.org/10.1016/S0033-7560\(63\)80032-0](https://doi.org/10.1016/S0033-7560(63)80032-0)
- Mei S, Zhang M, Ye J, Du J, Jiang Y, Hu Y. Auxin contributes to jasmonate-mediated regulation of abscisic acid signaling during seed germination in *Arabidopsis*. *Plant Cell*. 2023;35(3):1110–1133. <https://doi.org/10.1093/plcell/koac362>
- Meinke DW, Cherry JM, Dean C, Rounsley SD, Koornneef M. *Arabidopsis thaliana*: a model plant for genome analysis. *Science*. 1998;282(5389):662–682. <https://doi.org/10.1126/science.282.5389.662>
- Merkys AJ, Laurinavicius RS. Complete cycle of individual development in plants of *Arabidopsis thaliana* (L.) Heynh. aboard the salyut-7 orbital station. *Dokl Bot Sci*. 1983;271–273:68–70.
- Meyerowitz EM, Pruitt RE. *Arabidopsis thaliana* and plant molecular genetics. *Science*. 1985;229(4719):1214–1218. <https://doi.org/10.1126/science.229.4719.1214>
- Mindrinis M, Katagiri F, Yu G-L, Ausubel FM. The *A. thaliana* disease resistance gene RPS2 encodes a protein containing a nucleotide-binding site and leucine-rich repeats. *Cell*. 1994;78(6):1089–1099. [https://doi.org/10.1016/0092-8674\(94\)90282-8](https://doi.org/10.1016/0092-8674(94)90282-8)
- Montes C, Zhang J, Nolan TM, Walley JW. Single-cell proteomics differentiates *Arabidopsis* root cell types. *New Phytol*. 2024;244(5):1750–1759. <https://doi.org/10.1111/nph.19923>
- Nishimura K, Fukagawa T, Takisawa H, Kakimoto T, Kanemaki M. An auxin-based degron system for the rapid depletion of proteins in nonplant cells. *Nat Methods*. 2009;6(12):917–922. <https://doi.org/10.1038/nmeth.1401>
- Nobori T, Oliva M, Lister R, Ecker JR. Multiplexed single-cell 3D spatial gene expression analysis in plant tissue using PHYTOmap. *Nat Plants*. 2023;9(7):1026–1033. <https://doi.org/10.1038/s41477-023-01439-4>
- Okushima Y, Overvoorde PJ, Arima K, Alonso JM, Chan A, Chang C, Ecker JR, Hughes B, Lui A, Nguyen D, et al. Functional genomic analysis of the AUXIN RESPONSE FACTOR gene family members in *Arabidopsis thaliana*: unique and overlapping functions of ARF7 and ARF19. *Plant Cell*. 2005;17(2):444–463. <https://doi.org/10.1105/tpc.104.028316>
- O'Malley RC, Huang SC, Song L, Lewsey MG, Bartlett A, Nery JR, Galli M, Gallavotti A, Ecker JR. Cistrome and epicistrome features shape the regulatory DNA landscape. *Cell*. 2016;165(5):1280–1292. <https://doi.org/10.1016/j.cell.2016.04.038>
- Phippen W, Rhykerd R, Sedbrook J, Cristine H, Csonka S. From farm to flight: covercress as a low carbon intensity cash cover crop for sustainable aviation fuel production. a review of progress towards commercialization. *Frontiers (Boulder)*. 2022;10:793776. <https://doi.org/10.3389/fenrg.2022.793776>
- Rédei GP. *Arabidopsis* as a genetic tool. *Annu Rev Genet*. 1975;9(1):111–127. <https://doi.org/10.1146/annurev.ge.09.120175.000551>
- Reinholz E. Röntgenmutationen bei *Arabidopsis thaliana* (L.) heynh. *Naturwissenschaften*. 1947;34(1):26–28. <https://doi.org/10.1007/BF00633319>
- Röbbelen G. Wirkungsvergleich zwischen Äthylmethansulfonat und Röntgenstrahlen im Mutationsversuch mit *Arabidopsis thaliana*. *Naturwissenschaften*. 1962;49(3):65. <https://doi.org/10.1007/BF00595396>
- Röbbelen G. The laibach standard collection of natural races. *Arabidopsis Information Service*. 1965;2:36–42.
- Ryu KH, Huang L, Kang HM, Schiefelbein J. Single-cell RNA sequencing resolves molecular relationships among individual plant cells. *Plant Physiol*. 2019;179(4):1444–1456. <https://doi.org/10.1104/pp.18.01482>
- Schena M, Shalon D, Davis RW, Brown PO. Quantitative monitoring of gene expression patterns with a complementary DNA microarray. *Science*. 1995;270(5235):467–470. <https://doi.org/10.1126/science.270.5235.467>
- Schwab R, Ossowski S, Riester M, Warthmann N, Weigel D. Highly specific gene silencing by artificial microRNAs in *Arabidopsis*. *Plant Cell*. 2006;18(5):1121–1133. <https://doi.org/10.1105/tpc.105.039834>
- Shen J, Zhang J, Zhou M, Zhou H, Cui B, Gotor C, Romero LC, Fu L, Yang J, Foyer CH, et al. Persulfidation-based modification of cysteine desulfhydrase and the NADPH oxidase RBOHD controls guard cell abscisic acid signaling. *Plant Cell*. 2020;32(4):1000–1017. <https://doi.org/10.1105/tpc.19.00826>
- Shulze CN, Cole BJ, Ciobanu D, Lin J, Yoshinaga Y, Gouran M, Turco GM, Zhu Y, Malley O, Brady RC, et al. High-throughput single-cell transcriptome profiling of plant cell types. *Cell Rep*. 2019;27(7):2241–2247.e4. <https://doi.org/10.1016/j.celrep.2019.04.054>
- Silva KJP, Mahna N, Mou Z, Folta KM. NPR1 as a transgenic crop protection strategy in horticultural species. *Hortic Res*. 2018;5(1):15. <https://doi.org/10.1038/s41438-018-0026-1>
- Simmons CR, Lafitte HR, Reimann KS, Brugière N, Roesler K, Albertsen MC, Greene TW, Habben JE. Successes and insights of an industry biotech program to enhance maize agronomic traits. *Plant Sci*. 2021;307:110899. <https://doi.org/10.1016/j.plantsci.2021.110899>
- Stief A, Altmann S, Hoffmann K, Pant BD, Scheible W-R, Bäurle I. *Arabidopsis* miR156 regulates tolerance to recurring environmental stress through SPL transcription factors. *Plant Cell*. 2014;26(4):1792–1807. <https://doi.org/10.1105/tpc.114.123851>
- Sunkar R, Zhu J-K. Novel and stress-regulated microRNAs and other small RNAs from *Arabidopsis*. *Plant Cell*. 2004;16(8):2001–2019. <https://doi.org/10.1105/tpc.104.022830>
- Thalmann M, Pazmino D, Seung D, Horrer D, Nigro A, Meier T, Kölling K, Pfeifhofer HW, Zeeman SC, Santelia D. Regulation of leaf starch degradation by abscisic acid is important for osmotic stress tolerance in plants. *Plant Cell*. 2016;28(8):1860–1878. <https://doi.org/10.1105/tpc.16.00143>
- The *Arabidopsis* Genome Initiative. Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature*. 2000;408(6814):796–815. <https://doi.org/10.1038/35048692>
- Titova NN. Poiski rastitel'noy drosophily. (search of plant *Drosophila*). *Sovetsk Bot*. 1935;2:61–67.
- USDA APHIS. Citrus x sinensis transgenic lines tolerant to citrus greening disease. 2023 [accessed 2025 March 28]. <https://www.aphis.usda.gov/sites/default/files/23-213-01rsr.pdf>
- Wei L-H, Song P, Wang Y, Lu Z, Tang Q, Yu Q, Xiao Y, Zhang X, Duan H-C, Jia G. The m6A reader ECT2 controls trichome morphology by affecting mRNA stability in *Arabidopsis*. *Plant Cell*. 2018;30(5):968–985. <https://doi.org/10.1105/tpc.17.00934>
- Winter D, Vinegar B, Nahal H, Ammar R, Wilson GV, Provart NJ. An “electronic fluorescent pictograph” browser for exploring and analyzing large-scale biological data sets. *PLoS One*. 2007;2(8):e718. <https://doi.org/10.1371/journal.pone.0000718>
- Yano M, Katayose Y, Ashikari M, Yamanouchi U, Monna L, Fuse T, Baba T, Yamamoto K, Umehara Y, Nagamura Y, et al. Hd1, a

- major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS. *Plant Cell*. 2000;12(12):2473–2483. <https://doi.org/10.1105/tpc.12.12.2473>
- Yaschenko AE, Alonso JM, Stepanova AN. Arabidopsis as a model for translational research. *Plant Cell*. 2024;37(5):koae065. <https://doi.org/10.1093/plcell/koae065>
- Zanetti ME, Chang I-F, Gong F, Galbraith DW, Bailey-Serres J. Immunopurification of polyribosomal complexes of Arabidopsis for global analysis of gene expression. *Plant Physiol*. 2005;138(2):624–635. <https://doi.org/10.1104/pp.105.059477>
- Zhang T-Q, Xu Z-G, Shang G-D, Wang J-W. A single-cell RNA sequencing profiles the developmental landscape of Arabidopsis root. *Mol Plant*. 2019;12(5):648–660. <https://doi.org/10.1016/j.molp.2019.04.004>
- Zhang Y, Butelli E, Alseekh S, Tohge T, Rallapalli G, Luo J, Kwar PG, Hill L, Santino A, Fernie AR, et al. Multi-level engineering facilitates the production of phenylpropanoid compounds in tomato. *Nat Commun*. 2015;6(1):8635. <https://doi.org/10.1038/ncomms9635>
- Zhong R, Lee C, Zhou J, McCarthy RL, Ye Z-H. A battery of transcription factors involved in the regulation of secondary cell wall biosynthesis in Arabidopsis. *Plant Cell*. 2008;20(10):2763–2782. <https://doi.org/10.1105/tpc.108.061325>
- Zhou J, Lee C, Zhong R, Ye Z-H. MYB58 and MYB63 are transcriptional activators of the lignin biosynthetic pathway during secondary cell wall formation in Arabidopsis. *Plant Cell*. 2009;21(1):248–266. <https://doi.org/10.1105/tpc.108.063321>