

Blake C. Meyers

Donald Danforth Plant Science Center,
Member & Principal Investigator
University of Missouri, Division of Plant Sciences,
Professor

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Citizenship: U.S. and U.K. (dual)

Professional Preparation.

University of Chicago	Biology	B.A. (honors)	1992
University of California, Davis	Genetics	M.S.	1995
University of California, Davis	Genetics	Ph.D.	1998
DuPont Crop Genetics	Plant Genomics	Post-doc	1998 – 2000
University of California, Davis	Genomics	Post-doc	2000 – 2002

Appointments.

2016 – Member, The Donald Danforth Plant Science Center, St. Louis, MO
Professor, University of Missouri, Division of Plant Science & Technology,
Columbia, MO
Adjunct Professor, Department of Biology, Washington University, St. Louis

2010 – 2015 Edward F. & Elizabeth Goodman Rosenberg Professor

2009 – 2015 Professor, Dept. of Plant and Soil Sciences, University of Delaware.
Secondary Appointments:
Dept. of Computer and Information Sciences, College of Engineering (since 2006)
Dept. of Biological Sciences, College of Arts & Sciences (since 2014)

2009 – 2015 Department Chair, Dept. of Plant and Soil Sciences, University of Delaware.

2002 – 2006 Assistant Professor, 2006 – 2009 Associate Professor
Dept. of Plant and Soil Sciences, University of Delaware.

2001 – 2002 Assistant Research Geneticist (adjunct faculty). University of California, Davis.

Awards and Honors

Elected Member, US National Academy of Sciences, 2022
Editor-in-Chief, *The Plant Cell*. 2020 – 2024.
Elected Fellow, American Society of Plant Biologists (ASPB), 2017
Charles Albert Shull Award, American Society of Plant Biologists (ASPB), 2017
ISI/Clarivate Highly Cited Researcher: 2014, 2015, 2016, 2018 (Top 1% most-cited)
Elected Fellow, American Association for the Advancement of Science (AAAS), 2012
Edward F. and Elizabeth Goodman Rosenberg Professor, 2010 – 2015
Elected member, North American Arabidopsis Steering Committee (NAASC), 2009 – 2013
President of NAASC, 2012 – 2013
National Science Foundation Pre-Doctoral Fellow, 1992 – 1995
Phi Beta Kappa honor society member since 1992

Selected significant publications. (*indicates co-corresponding authors.)

Total refereed publications, 200+

[Google Scholar](#): total citations, 35,800+; h-index, 89; i10-index, 209

ISI Researcher ID, B-6535-2012

ORCID: <http://orcid.org/0000-0003-3436-6097>

Karimi HZ, Baldrich P, Rutter BD, Borniego L, Zajt KK, **Meyers BC**, Innes RW. Arabidopsis apoplastic fluid contains sRNA- and circular RNA-protein complexes that are located outside extracellular vesicles. (2022) *Plant Cell*. 34:1863-1881. doi: 10.1093/plcell/koac043/6529400. *bioRxiv*. doi: 10.1101/2021.10.02.462881

- Hacquard T, Clavel M, Baldrich P, Lechner E, Perez-Salamo I, Schepetilnikov M, Derrien B, Dubois M, Hammann P, Kuhn L, Brun D, Bouteiller N, Vaucheret H, **Meyers BC**, Genschik P. (2022) The Arabidopsis F-box protein FBW2 degrades AGO1 to avoid spurious loading of illegitimate small RNA. *Cell Reports*. 39:110671. doi: 10.1016/j.celrep.2022.110671. *bioRxiv* doi: 10.1101/2021.03.24.436811
- Nan GL, Teng C, Fernandes J, O'Connor L, **Meyers BC**, Walbot V. A Cascade of bHLH-regulated pathways program maize anther development. (2022) *Plant Cell*. 34: 1207–1225. doi: 10.1093/plcell/koac007.
- Pokhrel S, Huang K, **Meyers BC**. (2021) Conserved and non-conserved triggers of 24-nt reproductive phasiRNAs in eudicots. *Plant J*. 107: 1332-1345. doi: 10.1111/tpj.15382. *bioRxiv* doi: 10.1101/2021.01.20.427321
- Pokhrel S, Huang K, Belanger S, Caplan JL, Kramer EM, **Meyers BC**. Pre-meiotic, 21-nucleotide reproductive phasiRNAs emerged in seed plants and diversified in flowering plants. *Nature Communications*, 12: 4941. doi: 10.1038/s41467-021-25128-y. *bioRxiv* doi:10.1101/2020.10.16.341925
- Patel P, Mathioni SM, Hammond R, Harkess AE, Kakrana A, Arikat S, Dusia A, **Meyers BC** (2021) Reproductive phasiRNA loci and DICER-LIKE5, but not microRNA loci, diversified in monocotyledonous plants. *Plant Physiology*. 185:1764-1782. doi: 10.1093/plphys/kiab001. *bioRxiv*, doi: 10.1101/2020.04.25.061721.
- Veley K, Okwuonu I, Jensen G, Yoder M, Taylor N, **Meyers BC**, Bart R. Gene-tagging via CRISPR-mediated homology-directed repair in cassava. *G3*, 11:jkab028. doi: 10.1093/g3journal/jkab028. *bioRxiv*, doi: 10.1101/2020.05.14.090928
- Lee YS, Maple R, Dürr J, Dawson A, Tamim S, del Genio C, Papareddy R, Luo A, Lamb JC, Sylvester AW, Birchler JA, **Meyers BC**, Nodine MD, Rouster J, Gutierrez-Marcos J. A retrotransposon surveillance mechanism that safeguards plant male fertility during heat stress. (2021) *Nature Plants*. 7, 34–41. doi: 10.1038/s41477-020-00818-5.
- Bélanger S, Pokhrel S, Czymmek K, **Meyers BC**. (2020) Pre-meiotic, 24-nt reproductive phasiRNAs are abundant in anthers of wheat and barley but not rice and maize. *Plant Physiology*. 184:1407-1423. doi: 10.1104/pp.20.00816. *bioRxiv*, doi: 10.1101/2020.06.18.160440.
- Huang K, Demirci F, **Meyers BC**, Caplan JL. (2020) Quantitative, super-resolution localization of small RNAs with sRNA-PAINT. *Nucleic Acids Research*. 48:e96. doi: 10.1093/nar/gkaa623. *bioRxiv* doi: 10.1101/716696v1.
- Teng C*, Zhang H*, Hammond R, Kuang H, **Meyers BC**†, Walbot V†. (2020) *Dicer-like 5* deficiency confers temperature-sensitive male sterility in maize. *Nature Communications*, 11: 2912. doi: 10.1038/s41467-020-16634-6 *bioRxiv* doi: 10.1101/498410 *equal contributions †co-corresponding authors
- Nakano M, McCormick K, Demirci C, Demirci F, Gurazada SGR, Ramachandruni D, Dusia A, Rothhaupt JA, **Meyers BC**. (2020) Next-gen sequence databases: RNA and genomic informatics resources for plants. *Plant Physiology*. 182: 136-146. doi: 10.1104/pp.19.00957
- Ji L, Mathioni S, Johnson S, Tucker D, Bewick A, Kim K, Daron J, Slotkin RK, Jackson S, Parrott W, **Meyers BC**†, Schmitz R†. (2019) Genome-wide reinforcement of DNA methylation during somatic embryogenesis. *The Plant Cell*. 31: 2315-2331. doi: 10.1105/tpc.19.00255. †co-corresponding authors
- Trolet A*, Baldrich P*, Criqui, M-C, Dubois M, Clavel M, **Meyers, BC**, Genschik P. (2019) Cell cycle-dependent regulation and function of ARGONAUTE1 in plants. *The Plant Cell*. 31: 1734-1750. doi: 10.1105/tpc.19.00069. *equal contributions

- Huang K, Baldrich P, **Meyers BC**†, Caplan J†. (2019) sRNA-FISH: versatile fluorescent *in situ* detection of small RNAs in plants. *The Plant Journal*, 98: 359-369. doi: 10.1111/tpj.14210 †co-corresponding authors
- Baldrich P, Rutter RD, Zandkarimi H, Podicheti R, **Meyers BC**†, Innes RW†. (2019) Plant extracellular vesicles contain diverse small RNA species and are enriched in 10 to 17 nucleotide “tiny” RNAs. *The Plant Cell*, 31: 315-324. doi: 10.1105/tpc.18.00872. *bioRxiv* doi: 10.1101/472928 †co-corresponding authors
- Xia R†, Chen C, Pokhrel S, Ma W, Huang K, Patel P, Wang F, Liu Z, Li J, **Meyers BC**†. (2019) 24-nt reproductive phasiRNAs are broadly present in angiosperms. *Nature Communications* 10: 627. doi: 10.1038/s41467-019-08543-0. †co-corresponding authors
- Axtell MJ, **Meyers BC**. (2018) Revisiting criteria for plant miRNA annotation in the era of big data. *The Plant Cell*, 30:272-284. doi: 10.1105/tpc.17.00851 *bioRxiv*, DOI:10.1101/213314
- Sidorenko LV*†, Lee TF*, Woosley A, Moskal WA, Bevan SA, Owens Merlo PA, Walsh TA, Wang X, Weaver S, Glancy T, Wang P, Yang X, Sriram S & **Meyers BC**†. (2017) GC-rich coding sequences reduce transposon-like, small RNA-mediated transgene silencing. *Nature Plants*, 3:875-884. DOI: 10.1038/s41477-017-0040-6 *equal contributions †co-corresponding authors
- Huang K, Doyle F, Wurz ZE, Tenenbaum SA, Hammond R, Caplan JL* & **Meyers BC***. (2017) FASTmiR: An RNA-based sensor for *in vitro* and live-cell detection of small RNAs. *Nucleic Acids Research*. 45: e130. DOI: 10.1093/nar/gkx504
- Xia R, Xu J, **Meyers BC**. The emergence, evolution, and diversification of the miR390-TAS3-ARF pathway in land plants. (2017) *The Plant Cell*. 29:1232-1247. DOI: 10.1105/tpc.17.00185
- Fan Y, Yang J, Mathioni S, Yu J, Yang X, Wang L, Zhang Q, Shen J, Cai Z, Xu C, Li X, Xiao J, **Meyers BC** & Zhang Q (2016). PMS1T, producing phased small interfering RNAs, regulates photoperiod-sensitive male sterility in rice. *Proc. Natl. Acad. Sci. USA (PNAS)*, 113(52):15144-49.
- Fei Q, Yang L, Liang W, Zhang D* & **Meyers BC** (2016). Dynamic changes of small RNAs in rice spikelet development reveal specialized reproductive phasiRNA pathways. *J. Exp. Botany*, 67(21): 6037-6049. DOI: 10.1093/jxb/erw361
- Char SN, Neelakandan A, Nahampun H, Frame B, Main M, Spalding M, Becraft P, **Meyers BC**, Walbot V, Wang K, & Yang B (2016). An Agrobacterium-delivered CRISPR/Cas9 system for high-frequency targeted mutagenesis in maize. *Plant Biotechnology Journal*, [epub]. DOI: 10.1111/pbi.12611
- Zhang Y, Xia R, Kuang H, & **Meyers BC** (2016). The diversification of plant NBS-LRR defense genes directs the evolution of microRNAs that target them. *Mol Biol Evol*, 33: 2692-2705. DOI: 10.1093/molbev/msw154
- Wendel JF, Jackson SA, **Meyers BC** & Wing RA (2016). Evolution of plant genome architecture. *Genome Biology*. 17:37. DOI: 10.1186/s13059-016-0908-1
- Zhai, J., Bischof, S., Wang, H., Feng, S., Lee, T.-F., Teng, C., Chen, X., Park, S.Y., Liu, L., Gallego-Bartolome, J., Liu, W., Henderson, I.R., **Meyers, B.C.**, Ausin, I., and S.E. Jacobsen. (2015) A one precursor one siRNA model for Pol IV-dependent siRNA biogenesis. *Cell*. 163:445-455. DOI: 10.1016/j.cell.2015.09.032.
- Xia, R., Xu, J., and **B.C. Meyers**. (2015) Extensive families of miRNAs and PHAS loci in Norway spruce demonstrate the origins of complex phasiRNA networks in seed plants. *Molecular Biology and Evolution*. 32: 2905-2918. DOI: 10.1093/molbev/msv164

- Fei, Q., Li, P., Teng, C., and **B.C. Meyers**. (2015) Secondary siRNAs from *Medicago* NB-LRRs modulated via miRNA-target interactions and their abundances. *The Plant Journal*. 83: 451-465. DOI: 10.1111/tpj.12900
- Zhai, J., H. Zhang, S. Arikiti, K. Huang, G.L. Nan, V. Walbot, and **B.C. Meyers**. (2015). Spatiotemporally dynamic, cell-type dependent premeiotic and meiotic phasiRNAs in maize anthers. *Proc. Natl. Acad. Sci. USA (PNAS)*. 112: 3146-3151. DOI: 10.1073/pnas.1418918112
- Arikiti, S., Xia, R., Kakrana, A., Huang, K., Zhai, J., Yan, Z., Valdés-López, O., Prince, S., Musket, T.A., Nguyen, H.T., Stacey, G., and **B.C. Meyers**. (2014) An atlas of soybean small RNAs demonstrates regulation by phased siRNAs of hundreds of coding genes. *Plant Cell*. 26: 4584-4601. DOI: 10.1105/tpc.114.131847
- Wei, L., Gu, L., Song, X., Cui, X., Lu, Z., Zhou, M., Wang, L., Hu, F., Zhai, J., **Meyers, B.C.**, and X. Cao. (2014) Dicer-like 3 produces MITE-associated heterochromatic-siRNAs that control agricultural traits in rice. *Proc Natl Acad Sci USA*. 111: 3877-82.
- Creasey, K.M., Zhai, J., Borges, F., Van Ex, F., **Meyers, B.C.**, and R.A. Martienssen. (2014) miRNAs trigger widespread epigenetically-activated siRNAs from transposons in *Arabidopsis*. *Nature*. 508: 411-415. DOI: 10.1038/nature13069.
- Zhai, J., Zhao, Y., Simon, S.A., Huang, S., Petsch, K., Arikiti, S., Pillay, M., Ji, L., Xie, M., Cao, X., Yu, B., Timmermans, M., Yang, B., Chen, X., and **B.C. Meyers**. (2013). Plant MicroRNAs display differential 3'- truncation and tailing, modifications which are ARGONAUTE1-dependent and conserved across species. *The Plant Cell*. 25: 2417-2428.
- Stroud, H., Ding, B., Simon, S.A., Feng, S., Pellegrini, M., Wang, G.-L., **Meyers, B.C.**, and S.E. Jacobsen. (2013) Aberrant loss of DNA methylation in transgenic rice. *eLife*. 2: e00354.
- Nobuta, K., Lu, C., Shrivastava, R., Pillay, M., De Paoli, E., Accerbi, M., Arteaga-Vasquez, M., Sidorenko, L., Jeong, D.-H., Yen, Y., Chandler, V. *, Green, P.J., and **B.C. Meyers** *. (2008) A novel size distribution of endogenous siRNAs in maize: evidence from deep sequencing in the *mop1-1* mutant. *Proc Natl Acad Sci USA*. 105:14958-63.
- German, M.A., Pillay, M., Jeong, D.-H., Hetawal, A., Luo, S., Janardhanan, P., Kannan, V., Rymarquis, L., Nobuta, K., German, R., De Paoli, E., Lu, C., Schroth, G., **Meyers, B.C.** *, and P.J. Green *. (2008) Novel microRNA-target RNA pairs revealed by Parallel Analysis of RNA Ends (PARE). *Nature Biotechnology*. 26:941-946. * co-corresponding authors.
- Lu, C., Tej, S.S., Luo, S., Haudenschild, C.D., **Meyers, B.C.***, and P.J. Green.* (2005) Elucidation of the small RNA component of the transcriptome. *Science*. 309: 1576-1569.

A full publication list is available on Google Scholar:

https://scholar.google.com/citations?user=5hd_tmMAAAAJ&hl=en

Synergistic Activities.

1. Active leadership roles in the scientific community:
 - North American *Arabidopsis* Steering Committee (NAASC), 2009-2013, including a term as president.
 - Director since 2011, International Arabidopsis Informatics Consortium (IAIC). Supported by an NSF Research Coordination Network (RCN) award.
 - Steering committee of "Epigenomics of Plants Consortium (EPIC)"
 - Scientific Advisory Board, Institute of Plant and Microbial Biology--IPMB, Academia Sinica, Taipei, Taiwan (2015 – 2019)
 - Organizer of numerous meetings, workshops, minisymposia, etc.

2. Editorial board member for four journals: *The Plant Cell* (since 2008; senior editor 2017-2020; Editor-in-Chief 2020-2024); *Tropical Plant Biology*; *Rice*, *Current Opinion in Plant Biology*.
3. Consultant to numerous agricultural biotechnology companies.
4. Chair of my department for nearly seven years; a department with ~30 faculty, ~20 staff, 140 graduates and undergraduates, and a total portfolio of ~\$28M in sponsored research. Hired six faculty in this time of which three have since been awarded NSF CAREER grants.

Invited seminars.

1. Seminars or presentations within the United States.
 - Over 160 invited talks in the US since 1998.
2. International seminars or presentations.
 - Over 100 invited talks at international meetings or institutions since 1998.

Teaching, mentoring, and advising (from 2002 to the present). (*Univ. of Delaware; Univ. of Missouri; Danforth Center*)

1. >20 postdoctoral scientists supervised.
2. >15 research associates or staff programmers supervised.
3. Graduate Student Major Advisor or Supervisor:
 - a. Plant & Soil Sciences (UD), Div. of Plant Science & Tech. (MU), or Wash U: 10 Ph.D. students.
 - b. Computer & Information Sciences, or Electrical & Computer Engineering (bioinformatics) at UD: 8 Ph.D. students, 27 M.S. students.
 - c. Bioinformatics at UD: 4 Ph.D. students, 3 M.S. students.
 - d. Visiting graduate students: 7 international Ph.D. students.
4. Awards received by lab members include NSF Postdoctoral Fellowships (2), IGERT scholarships (5), HHMI Hanna Gray Fellowship, University of Delaware Fellowships, Thousand Talents Program Finalist – award offered (China) (two lab members), a Life Sciences Research Foundation Post-Doctoral Fellowship, a Ford Foundation Diversity Postdoctoral Fellowship, ASPB Travel Awards, and other awards.
5. Alumni of my lab are employed in a wide variety of positions including faculty appointments, in industry (from plant biotech to computer science, and microchip fabrication to satellites), and in the government.