

**Curriculum Vitae**  
**Richard Michael Clark**

School of Biological Sciences  
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EDUCATION

*Stanford University*, Stanford, CA, USA. **PhD** in Developmental Biology (1994-2001)  
*Kenyon College*, Gambier, OH, USA. **BA** in Biology (1990-1994)

RESEARCH EXPERIENCE & APPOINTMENTS

*Associate Director for Graduate Programs*: School of Biological Sciences, University of Utah, Salt Lake City, Utah. 2020-2021.

*Director of Graduate Studies*: School of Biological Sciences, University of Utah, Salt Lake City, Utah. 2018-2021.

*Professor*: School of Biological Sciences, University of Utah, Salt Lake City, Utah. **Genetics and genomics**. 2018-present.

*Associate Professor*: Department of Biology, University of Utah, Salt Lake City, Utah. **Evolutionary genetics and plant-herbivore interactions**. 2014-2018.

*Assistant Professor*: Department of Biology, University of Utah, Salt Lake City, Utah. **Evolutionary genetics, association mapping, and plant-herbivore interactions**. 2008-2014.

*Postdoctoral Fellow*: Max Planck Institute for Developmental Biology, Tübingen, Germany. **Evolutionary genetics and genomics of *Arabidopsis thaliana* and its congeners**. 2004-2008. (Research advisor: Dr. Detlef Weigel)

*Postdoctoral Fellow*: Laboratory of Genetics, University of Wisconsin, Madison, WI, USA. **Genetics of maize domestication**. 2001-2004. (Research advisor: Dr. John F. Doebley)

*Doctoral Student*: Department of Developmental Biology, Stanford University, Stanford, CA, USA. **Molecular genetics of vertebrate limb formation**. 1994-2001. (Research advisor: Dr. David M. Kingsley)

AWARDS & HONORS

A Showcase of Extraordinary Faculty Achievements, J. Willard Marriott Library & Vice President of Research (2016)

Selected as an AAAS Fellow (November 2013)

Selected to Faculty of 1000 (Plant Genomes & Evolution Section) (2011-2015)

Ruth L. Kirschstein NRSA Postdoctoral Fellowship, NIH (2002-2004)

National Science Foundation Graduate Fellowship (1994-1997)  
Graduated 2<sup>nd</sup> in class with Highest Honors, Kenyon College, Gambier, OH (1994)  
Maxwell Elliot Power Prize for Biology, Kenyon College, Gambier, OH (1994)  
Robert Bowan Brown, Jr. Prize in Biology, Kenyon College, Gambier, OH (1994)  
Barry M. Goldwater Science Scholarship (1993-1994)

## PUBLICATIONS

\* — co-first authorship; \*\* — corresponding or co-corresponding author

### **Published:**

#### **2023**

Ji, M., Vandenhole, M., De Beer, B., De Rouck, S., Villacis-Perez, E., Feyereisen, R., **Clark, R. M.\*\***, and Van Leeuwen, T. 2023. A nuclear receptor HR96-related gene underlies large *trans*-driven differences in detoxification gene expression in a generalist herbivore. *Nature Communications* 14:4990. doi: 10.1038/s41467-023-40778-w. (PMCID: PMC10435515)

Gill, G. S., Bui, H., **Clark, R. M.**, and Ramirez, R. A. 2023. Spider mite resistant maize lines, B75 and B96, maintain resistance under water-stress. *Journal of Pest Science* 96:1117-1132. doi.org/10.1007/s10340-022-01584-3.

#### **2022**

Kurlovs, A. H., De Beer, B., Ji, M., Vandenhole, M., De Meyer, T., Feyereisen, R., **Clark, R. M.\*\***, and Van Leeuwen, T. 2022. *Trans*-driven variation in expression is common among detoxification genes in the extreme generalist herbivore *Tetranychus urticae*. *PLoS Genetics* 18:e1010333. doi: 10.1371/journal.pgen.1010333. (PMCID: PMC9704763)

Ji, M., Bui, H., Ramirez, R. A., and **Clark, R. M.\*\*** 2022. Concerted *cis* and *trans* effects underpin heightened defense gene expression in multi-herbivore-resistant maize lines. *The Plant Journal* 111:508-528. doi: 10.1111/tpj.15812. (PMID: 35575017)

#### **2021**

Fotoukiai, S. M., Wybouw, N., Kurlovs, A. H., Tsakireli, D., Pergantis, S. A., **Clark, R. M.**, Vontas, J., and Van Leeuwen, T. 2021. High-resolution genetic mapping reveals *cis*-regulatory and copy number variation in loci associated with cytochrome P450-mediated detoxification in a generalist arthropod pest. *PLoS Genetics* 17:e1009422. doi: 10.1371/journal.pgen.1009422. (PMCID: PMC8248744)

Bui, H., Greenhalgh, R., Gill, G. S., Ji, M., Kurlovs, A. H., Ronnow, C., Lee, S., Ramirez, R. A., and **Clark, R. M.\*\*** 2021. Maize inbred line B96 is the source of large-effect loci for resistance to generalist but not specialist spider mites. *Frontiers in Plant Science* 12:693088. doi: 10.3389/fpls.2021.693088. (PMCID: PMC8256171)

Villacis-Perez, E., Snoeck, S., Kurlovs, A. H., **Clark, R. M.**, Breeuwer, J. A. J., and Van Leeuwen, T. 2021. Adaptive divergence and post-zygotic barriers to gene flow between sympatric populations of a herbivorous mite. *Communications Biology* 4:853. doi: 10.1038/s42003-021-02380-y. (PMCID: PMC8270941)

## 2020

Greenhalgh, R., Dermauw, W., Glas, J. J., Rombauts, S., Wybouw, N., Thomas, J., Alba, J. M., Pritham, E. J., Legarrea, S., Feyereisen, R., Van de Peer, Y., Van Leeuwen, T., **Clark, R. M.\*\***, and Kant, M. R. 2020. Genome streamlining in a minute herbivore that manipulates its host plant. *Elife* 9:e56689. doi: 10.7554/eLife.56689. (PMID: 33095158)

Gill, G. S., Bui, H., **Clark, R. M.**, and Ramirez, R. A. 2020. Varying responses to combined water-stress and herbivory in maize for spider mite species that differ in host specialization. *Environmental & Experimental Botany* 177:104131. doi: 10.1016/j.envexpbot.2020.104131.

## 2019

**Clark, R. M.\*\*** and Ragland, G. J. 2019. Editorial overview: Tapping arthropod diversity to elaborate the genotype-to-phenotype map. *Curr Opin Insect Sci.* 36:v-viii. doi: 10.1016/j.cois.2019.10.003. (PMID: 31732447)

Kurlovs, A. H., Snoeck, S., Kosterlitz, O., Van Leeuwen, T., and **Clark, R. M.\*\*** 2019. Trait mapping in diverse arthropods by bulked segregant analysis. *Curr Opin Insect Sci.* 36:57-65. doi: 10.1016/j.cois.2019.08.004. (PMID: 31499416)

Wybouw, N., Kurlovs, A. H., Greenhalgh, R., Bryon, A., Kosterlitz, O., Manabe, Y., Osakabe, M., Vontas, J., **Clark, R. M.\*\***, and Van Leeuwen, T. 2019. Convergent evolution of cytochrome P450s underlies independent origins of keto-carotenoid pigmentation in animals. *Proceedings of the Royal Society B* 286:20191039. doi: 10.1098/rspb.2019.1039. (PMCID: PMC6661338)

Snoeck, S., Kurlovs, A. H., Bajda, S., Feyereisen, R., Greenhalgh, R., Villacis-Perez, E., Kosterlitz, O., Dermauw, W., **Clark, R. M.\*\***, and Van Leeuwen, T. 2019. High-resolution QTL mapping in *Tetranychus urticae* reveals acaricide-specific responses and common target-site resistance after selection by different METI-I acaricides. *Insect Biochem Mol Biol.* 110:19-33. doi: 10.1016/j.ibmb.2019.04.011. (PMID: 31022513)

Wybouw, N., Kosterlitz, O., Kurlovs, A. H., Bajda, S., Greenhalgh, R., Snoeck, S., Bui, H., Bryon, A., Dermauw, W., Van Leeuwen, T., and **Clark, R. M.\*\*** 2019. Long-Term Population Studies Uncover the Genome Structure and Genetic Basis of Xenobiotic and Host Plant Adaptation in the Herbivore *Tetranychus urticae*. *GENETICS* 211:1409-1427. doi: 10.1534/genetics.118.301803. (PMCID: PMC6456322)

Simma, E. A., Dermauw, W., Balabanidou, V., Snoeck, S., Bryon, A., **Clark, R. M.**, Yewhalaw, D., Vontas, J., Duchateau, L., and Van Leeuwen, T. 2019. Genome-wide gene expression profiling reveals that cuticle alterations and P450 detoxification are associated with deltamethrin and DDT resistance in *Anopheles arabiensis* populations from Ethiopia. *Pest Management Science* 75:1808-1818. doi: 10.1002/ps.5374. (PMID: 30740870)

## 2018

Bui, H., Greenhalgh, R., Ruckert, A., Gill, G. S., Lee, S., Ramirez, R. A., and **Clark, R. M.\*\*** 2018. Generalist and specialist mite herbivores induce similar defense responses in maize and barley but differ in susceptibility to benzoxazinoids. *Frontiers in Plant Sciences* 9:1222. doi: 10.3389/fpls.2018.01222. (PMCID: PMC6110934)

## 2017

Snoeck, S., Greenhalgh, R., Tirry, L., **Clark, R. M.**, Van Leeuwen, T., and Dermauw, W. 2017. The effect of insecticide synergist treatment on genome-wide gene expression in a polyphagous pest. *Scientific Reports* 7:13440. (PMCID: PMC5647426)

Bryon, A., Kurlovs, A. H., Dermauw, W., Greenhalgh, R., Riga, M., Grbic, M., Tirry, L., Osakabe, M., Vontas, J., **Clark, R. M.\*\***, and Van Leeuwen, T. 2017. Disruption of a horizontally transferred phytoene desaturase abolishes carotenoid accumulation and diapause in *Tetranychus urticae*. *PNAS* 114: E5871-E5880. (PMCID: PMC5530703)

Bryon, A., Kurlovs, A. H., Van Leeuwen, T., and **Clark, R. M.\*\*** 2017. A molecular-genetic understanding of diapause in spider mites: current knowledge and future directions. *Physiological Entomology* 42:211-224. (Special issue on “Photoperiodic Induction of Diapause and Seasonal Morphs”; <http://onlinelibrary.wiley.com/doi/10.1111/phen.12201/full>)

Rabanal, F.A., Mandáková, T., Soto-Jiménez, L. M., Greenhalgh, R., Parrott, D.L., Lutzmayer, S., Steffen, J. G., Nizhynska, V., Mott, R., Lysak, M. A., **Clark, R. M.**, and Nordborg, M. 2017. Epistatic and allelic interactions control expression of ribosomal RNA gene clusters in *Arabidopsis thaliana*. *Genome Biol.* 18:75. (PMCID: PMC5414317)

Imprialou, M., Kahles, A., Steffen, J. G., Osborne, E. J., Gan, X., Lempe, J., Bhomra, A., Belfield, E., Visscher, A., Greenhalgh, R., Harberd, N. P., Goram, R., Hein, J., Robert-Seilaniantz, A., Jones, J., Stegle, O., Kover, P., Tsiantis, M., Nordborg, M., Rättsch, G., **Clark, R. M.**, and Mott R. 2017. Genomic Rearrangements in *Arabidopsis* Considered as Quantitative Traits. *GENETICS* 205: 1425-1441. (PMCID: PMC5378104)

## 2016

Ngoc, P. C., Greenhalgh, R., Dermauw, W., Rombauts, S., Bajda, S., Zhurov, V., Grbić, M., Van de Peer, Y., Van Leeuwen, T., Rouzé, P., and **Clark, R. M.\*\*** 2016. Complex Evolutionary Dynamics of Massively Expanded Chemosensory Receptor Families in an Extreme Generalist Chelicerate Herbivore. *Genome Biology & Evolution* 8:3323-3339. (PMCID: PMC5203786)

Jonckheere, W., Dermauw, W., Zhurov, V., Wybouw, N., Van den Bulcke, J., Villarroel, C. A., Greenhalgh, R., Grbić, M., Schuurink, R. C., Tirry, L., Baggerman, G., **Clark, R. M.**, Kant, M. R., Vanholme, B., Menschaert, G., and Van Leeuwen, T. 2016. The Salivary Protein Repertoire of the Polyphagous Spider Mite *Tetranychus urticae*: A Quest for Effectors. *Molecular & Cellular Proteomics* 15:3594-3613. (PMCID: PMC5141274).

Meng, D., Dubin, M., Zhang, P., Osborne, E. J., Stegle, O., **Clark, R. M.**, and Nordborg, M. 2016. Limited Contribution of DNA Methylation Variation to Expression Regulation in *Arabidopsis thaliana*. *PLoS Genetics* 12:e1006141. (PMCID: PMC4939946)

## 2015

Bajda, S., Dermauw, W., Greenhalgh, R., Nauen, R., Tirry, L., **Clark, R. M.**, and Van Leeuwen T. 2015. Transcriptome profiling of a spirodiclofen susceptible and resistant strain of the European red mite *Panonychus ulmi* using strand-specific RNA-seq. *BMC Genomics* 16:974. (PMCID: PMC4652392)

Dubin, M. J., Zhang, P., Meng, D., Remigereau, M. S., Osborne, E. J., Paolo Casale, F., Drewe, P., Kahles, A., Jean, G., Vilhjálmsson, B., Jagoda, J., Irez, S., Voronin, V., Song, Q., Long, Q., Rättsch, G., Stegle, O., **Clark, R. M.**, and Nordborg, M. 2015. DNA methylation in *Arabidopsis* has a genetic basis and shows evidence of local adaptation. *Elife* 4:e05255. (PMCID: PMC4413256)

## 2014

Thakare, D., Yang, R., Steffen, J.G., Zhan, J., Wang, D., **Clark, R. M.**, Wang, X., and Yadegari, R. 2014. RNA-Seq analysis of laser-capture microdissected cells of the developing central starchy endosperm of maize. *Genomics Data* 2:242-5. (PMCID: PMC4535972)

Demaeght, P., Osborne, E. J., Odman-Naresh, J., Grbić, M., Nauen, R., Merzendorfer, H., **Clark, R. M.\*\***, and Van Leeuwen, T. 2014. High resolution genetic mapping uncovers chitin synthase-1 as the target-site of the structurally diverse mite growth inhibitors clofentezine, hexythiazox and etoxazole in *Tetranychus urticae*. *Insect Biochem Mol Biol.* 51:52-61. (PMCID: PMC4124130)

Jali, S. S., Rosloski, S. M., Janakirama, P., Steffen, J. G., Zhurov, V., Berleth, T., **Clark, R. M.\*\***, and Grbić V. 2014. A plant-specific *HUA2-LIKE* (*HULK*) gene family in *Arabidopsis thaliana* is essential for development. *Plant J.* 80:242-54. (PMCID: PMC4283595)

Zhurov, V., Navarro, M., Bruinsma, K. A., Arbona, V., Santamaria, M. E., Cazaux, M., Wybouw, N., Osborne, E. J., Ens, C., Rioja, C., Vermeirssen, V., Rubio-Somoza, I., Krishna, P., Diaz, I., Schmid, M., Gómez-Cadenas, A., Van de Peer, Y., Grbic, M., **Clark, R. M.**, Van Leeuwen, T., and Grbic, V. 2014. Reciprocal responses in the interaction between *Arabidopsis* and the cell-content-feeding chelicerate herbivore spider mite. *Plant Physiology* 164:384-99. (PMCID: PMC3875816)

## 2013

Slotte, T., Hazzouri, K. M., Agren, J. A., Koenig, D., Maumus, F., Guo, Y. L., Steige, K., Platts, A. E., Escobar, J. S., Newman, L. K., Wang, W., Mandáková, T., Vello, E., Smith, L. M., Henz, S. R., Steffen, J., Takuno, S., Brandvain, Y., Coop, G., Andolfatto, P., Hu, T. T., Blanchette, M., **Clark, R. M.**, Quesneville, H., Nordborg, M., Gaut, B. S., Lysak, M. A., Jenkins, J., Grimwood, J., Chapman, J., Prochnik, S., Shu, S., Rokhsar, D., Schmutz, J., Weigel, D., and Wright, S. I. 2013. The *Capsella rubella* genome and the genomic consequences of rapid mating system evolution. *Nature Genetics* 45:831-835. (PMID: 23749190)

Dermauw, W., Osborne, E. J., **Clark, R. M.**, Grbić, M., Tirry, L., and Van Leeuwen, T. 2013. A burst of ABC genes in the genome of the polyphagous spider mite *Tetranychus urticae*. *BMC Genomics* 14:317. (PMID: 23663308)

Kopischke, M., Westphal, L., Schneeberger, K., **Clark, R. M.**, Ossowski, S., Wewer, V., Fuchs, R., Landtag, J., Hause, G., Dörmann, P., Lipka, V., Weigel, D., Schulze-Lefert, P., Scheel, D., and Rosahl, S. 2013. Impaired sterol ester synthesis alters the response of *Arabidopsis thaliana* to *Phytophthora infestans*. *Plant Journal* 73:456-68. (PMID: 23072470)

Dermauw, W., Wybouw, N., Rombauts, S., Menten, B., Vontas, J., Grbić, M., **Clark, R. M.**, Feyereisen, R., and Van Leeuwen, T. 2013. A link between host plant adaptation and pesticide resistance in the polyphagous spider mite *Tetranychus urticae*. *Proc Natl Acad Sci USA* 110:E113-22. (PMID: 23248300)

## 2012

Van Leeuwen, T., Demaeght, P., Osborne, E. J., Dermauw, W., Gohlkec, S., Nauend, R., Grbić, M., Tirrya, L., Merzendorfer, H., and **Clark, R. M.\*\*** 2012. Population bulk segregant mapping uncovers resistance mutations and the mode of action of a chitin synthesis inhibitor in arthropods. *Proc Natl Acad Sci USA* 109:4407-4412. (PMID: 22393009)

## 2011

Grbić, M.\*, Van Leeuwen, T.\*, **Clark, R. M.\***, Rombauts, S., Rouzé, P., Grbić, V., Osborne, E. J., Dermauw, W., Ngoc, P. C., Ortego, F., Hernández-Crespo, P., Diaz, I., Martinez, M., Navajas, M., Sucena, E., Magalhães, S., Nagy, L., Pace, R. M., Djuranović, S., Smagghe, G., Iga, M., Christiaens, O., Veenstra, J. A., Ewer, J., Villalobos, R. M., Hutter, J. L., Hudson, S. D., Velez, M., Yi, S. V., Zeng, J., Pires-daSilva, A., Roch, F., Cazaux, M., Navarro, M., Zhurov, V., Acevedo, G., Bjelica, A., Fawcett, J. A., Bonnet, E., Martens, C., Baele, G., Wissler, L., Sanchez-Rodriguez, A., Tirry, L., Blais, C., Demeestere, K., Henz, S. R., Gregory, T. R., Mathieu, J., Verdon, L., Farinelli, L., Schmutz, J., Lindquist, E., Feyereisen, R., and Van de Peer, Y. 2011. The genome of *Tetranychus urticae* reveals herbivorous pest adaptations. *Nature* 479:487-492. (PMID: 22113690)

Gan, X., Stegle, O., Behr, J., Steffen, J. G., Drewe, P., Hildebrand, K. L., Lyngsoe, R., Schultheiss, S. J., Osborne, E. J., Sreedharan, V. T., Kahles, A., Bohnert, R., Jean, G., Derwent, P., Kersey, P., Belfield, E., Harberd, N., Kemen, E., Kover, P., Toomajian, C., **Clark, R. M.\*\***, Rätsch, M., and Mott, R. 2011. Multiple reference genomes and transcriptomes for *Arabidopsis thaliana*. *Nature* 477:419-423. (PMID: 21874022)

Hu, T. T., Pattyn, P., Bakker, E. G., Cao, J., Cheng, J. F., **Clark, R. M.**, Fahlgren, N., Fawcett, J. A., Grimwood, J., Gundlach, H., Haberer, G., Hollister, J. D., Ossowski, S., Ottillar, R. P., Salamov, A. A., Schneeberger, K., Spannagl, M., Wang, X., Yang, L., Nasrallah, M. E., Bergelson, J., Carrington, J. C., Gaut, B. S., Schmutz, J., Mayer, K. F., Van de Peer, Y., Grigoriev, I. V., Nordborg, M., Weigel, D., and Guo, Y. L. 2011. The *Arabidopsis lyrata* genome sequence and the basis of rapid genome size change. *Nature Genetics* 43:476-481 (PMID: 21478890)

## 2010

**Clark, R. M.\*\*** 2010. Genome-wide association studies coming of age in rice. *Nature Genetics* 42:926-927. (PMID: 20972439)

Ossowski, S., Schneeberger, K., Lucas-Lledó, J. I., Warthmann, N., **Clark, R. M.**, Shaw, R. G., Weigel, D., and Lynch, M. 2010. The rate and molecular spectrum of spontaneous mutations in *Arabidopsis thaliana*. *Science* 327:92-94. (PMID: 20044577)

## 2009

McNally, K. L., Childs, K. L., Bohnert, R., Davidson, R. M., Zhao, K., Ulat, V. J., Zeller, G., **Clark, R. M.**, Hoen, D. R., Bureau, T. E., Stokowski, R., Ballinger, D. G., Frazer, K. A., Cox, D. R.,

Padhukasahasram, B., Bustamante, C. D., Weigel, D., Mackill, D. J., Bruskiewich, R. M., Ratsch, G., Buell, C. R., Leung, H., and Leach, J. E. 2009. Genomewide SNP variation reveals relationships among landraces and modern varieties of rice. *Proc Natl Acad Sci USA* 106:12273-12278. (PMID: 19597147)

## 2008

Ossowski, S., Schneeberger, K., **Clark, R. M.**, Lanz, C., Warthmann, N., and Weigel, D. 2008. Sequencing of natural strains of *Arabidopsis thaliana* with short reads. *Genome Research* 18:2024-2033 (PMID: 18818371).

Zeller, G., **Clark, R. M.**, Schneeberger, K., Bohlen, A., Weigel, D., and Ratsch, G. 2008. Detecting polymorphic regions in *Arabidopsis thaliana* with resequencing microarrays. *Genome Research* 18:918-29. (PMID: 18323538)

## 2007

Weber, A., **Clark, R. M.**, Vaughn, L., Sanchez-Gonzalez, J. J., Yu, J., Yandell, B. S., Bradbury, P., and Doebley, J. 2007. Major regulatory genes in maize contribute to standing variation in teosinte (*Zea mays* ssp. *parviglumis*). *Genetics* 177:2349-59. (PMID: 17947410)

**Clark, R. M.**, Schweikert, G., Toomajian, C., Ossowski, S., Zeller, G., Shinn, P., Warthmann, N., Hu, T. T., Fu, G., Hinds, D. A., Chen, H., Frazer, K. A., Huson, D. H., Scholkopf, B., Nordborg, M., Ratsch, G., Ecker, J. R., and Weigel, D. 2007. Common sequence polymorphisms shaping genetic diversity in *Arabidopsis thaliana*. *Science* 317:338-342. (PMID: 17641193)

Kim, S., Plagnol, V., Hu, T. T., Toomajian, C., **Clark R. M.**, Ossowski, S., Ecker, J. R., Weigel, D., and Nordborg, M. 2007. Recombination and linkage disequilibrium in *Arabidopsis thaliana*. *Nature Genetics* 3:1151-1155. (PMID: 17676040)

Tang, C., Toomajian, C., Sherman-Broyles, S., Plagnol, V., Guo, Y. L., Hu, T. T., **Clark, R. M.**, Nasrallah, J. B., Weigel, D., and Nordborg, M. 2007. The evolution of selfing in *Arabidopsis thaliana*. *Science* 317:1070-1072. (PMID: 17656687)

## 2006

**Clark, R. M.**, Wagler, T. N., Quijada, P., and Doebley, J. 2006. A distant upstream enhancer at the maize domestication gene *tb1* has pleiotropic effects on plant and inflorescent architecture. *Nature Genetics* 38:594-597. (PMID: 16642024)

Balasubramanian, S., Sureshkumar, S., Agrawal, M., Michael, T. P., Wessinger, C., Maloof, J., **Clark, R.**, Warthmann, N., Chory, J., and Weigel, D. 2006. The *PHYTOCHROME C* photoreceptor gene mediates natural variation in flowering and growth responses of *Arabidopsis thaliana*. *Nature Genetics* 38:711-715. (PMID: 16732287)

## 2005

**Clark, R. M.**, Tavare, S., and Doebley, J. F. 2005. Estimating a nucleotide substitution rate for maize from polymorphism at a major domestication locus. *Molecular Biology & Evolution* 22:2304-2312. (PMID: 16079248)

**2004**

**Clark, R. M.**, Linton, E., Messing, J., and Doebley, J. F. 2004. Pattern of diversity in the genomic region near the maize domestication gene *tb1*. *Proc. Natl. Acad. Sci. USA* 101:700-707. (PMID: 14701910)

**2001**

**Clark, R. M.**, Marker, P.C., Roessler, E., Dutra, A., Schimenti, J.C., Muenke, M., and Kingsley, D.M. 2001. Reciprocal mouse and human limb phenotypes caused by gain- and loss-of-function mutations affecting *Lmbr1*. *Genetics* 159:715-726. (PMID:11606546)

**2000**

**Clark, R. M.\***, Marker, P. C.\*, and Kingsley, D.M. 2000. A novel candidate gene for mouse and human preaxial polydactyly with altered expression in limbs of *Hemimelic extra-toes* mutant mice. *Genomics* 67:19-27. (PMID: 10945466)

ORAL PRESENTATIONS (partial list)

**2023**

**Clark, R. M.**, Ji, M., Vandenhole, M., De Beer, B., De Rouck, S., Villacis-Perez, E., Feyereisen, R., and Van Leeuwen, T. Genetic basis of detoxification gene expression variation in a generalist herbivore. *13<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (September 11-14, 2023)*. (**Invited Speaker**)

**2022**

**Clark, R. M.**, Ji, M., Bui, H., and Ramirez, R. Multi-herbivore resistance and genetic regulation of defense pathways in maize. *Brigham Young University, Provo, Utah (October 27, 2022)*. (**Invited Speaker**)

**Clark, R. M.**, Ji, M., Bui, H., and Ramirez, R. Multi-herbivore resistance and genetic regulation of defense pathways in maize. *12<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (October 17-20, 2022)*. (**Invited Speaker**)

**2021**

**Clark, R. M.** Genic architecture at the lower limits of metazoan genome size: lessons from mite herbivores of varying host breadth. *University College London, London, United Kingdom (April 21, 2021)*. (**Invited Speaker**)

**2020**

**Clark, R. M.**, Bui, H., Greenhalgh, R., Ji, M., Hawks, A., Gross, S., Gill, G. S., and Ramirez, R. A. Molecular-genetic basis of maize resistance to spider mite herbivores. *Plant Biology 2020, American Society of Plant Biologists, Washington DC, USA (July 27-31, 2020)*.

**2018**



Bui, H., Greenhalgh, R., Gill, G. S., Ronnow, C., Lee, S., Kurlovs, A., Ramirez, R. A., and **Clark, R. M.** The genetic architecture of resistance to a generalist spider mite herbivore in maize. *10<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (November 5-8, 2018)*. (**Invited Speaker**)

**Clark, R. M.** Learning from long haplotypes: Selection and genetic diversity in an extreme generalist herbivore. *2018 Arthropod Genomics Symposium, University of Illinois Champaign–Urbana, Illinois, USA (June 7-9, 2018)*. (**Invited Speaker**)

**Clark, R. M.** Genetics of diapause and carotenoid metabolism in spider mites. *Chemical Ecology Symposium of Natural Products, University of Utah, Salt Lake City, Utah, USA (May 17, 2018)*. (**Invited Speaker**)

## 2017

**Clark, R. M.**, Kurlovs, A., Greenhalgh, R., Bui, H., Kosterlitz, O., Dermauw, W., Bryon, A., Bajda, S., Van Leeuwen, T. Genomes of *Tetranychus urticae* strains reveal multiple selective sweeps in a global population sample. *Member Symposium: Genomics of Adaptation: Linking the Next Generation of Genome-Wide Analysis to Understand and Manage Complex Traits, Entomology 2017, Denver, Colorado, USA (November 5-8, 2017)*.

## 2016

**Clark, R. M.**, Kurlovs, A., Greenhalgh, R., Bui, H., Steffen, J., Dermauw, W., Bryon, A., Bajda, S., and Van Leeuwen, T. Microevolutionary patterns in the generalist herbivore *Tetranychus urticae* as revealed by large-scale strain sequencing. *Arthropod Population Genomics Symposium, XXV International Congress of Entomology, Orlando, Florida, USA (September 25-30, 2016)*. (**Invited Speaker**)

**Clark, R. M.**, Huyen, B., Greenhalgh, R., Ruckert, A., Ramirez, R. Cereal Defense Responses to Agriculturally Important Generalist and Specialist Mite Herbivores. *American Society of Plant Biologists – Western Section Meeting, Brigham Young University, Provo, Utah (May 19-20, 2016)*. (**Invited Speaker**)

## 2013

Kurlovs, A., Greenhalgh, R., Osborne, E.J., and **Clark, R. M.** Genes and gene regulatory pathways underlying plant-herbivore interactions. *Evolution 2013, EDEN symposium: The Evolution of Gene Regulatory Networks, Snowbird, Utah (June 21-25, 2013)*. (**Invited Speaker**)

## 2012

**Clark, R. M.** Understanding ecologically and agriculturally relevant traits in *Arabidopsis* and mites. *The Gregor Mendel Institute, Vienna, Austria (April 12, 2012)*. (**Invited Speaker**)

**Clark, R. M.** Understanding ecologically and agriculturally relevant traits in *Arabidopsis* and mites. *The Donald Danforth Plant Sciences Center, St. Louis, Missouri (March 14, 2012)*. (**Invited Speaker**)

**Clark, R. M.** Small pests, large losses: genomic studies reveal why mites can eat so much. *The University of Utah, NAKAMA presentation, Salt Lake City, Utah (February 3, 2012)*. (**Invited Speaker**)

**2011**

**Clark, R. M.** Reference genomes and transcriptomes for functional and evolutionary studies in *Arabidopsis*. *USC Center of Excellence in Genomic Science (CEGS) annual retreat, University of Southern California, Los Angeles, California (March 22, 2011).*

**2010**

**Clark, R. M.** Characterizing genotype to phenotype relationships in plants and mites. *School of Biology, Georgia Tech, Atlanta, Georgia (October 14, 2010).* **(Invited Speaker)**

**Clark, R. M.,** and Osborne, E. J. Genetic polymorphisms in spider mite populations: discovery and patterns. *Second Spider Mite Genome Meeting, Tivat, Montenegro (September 20-23, 2010).*

**2009**

**Clark, R. M.** High-throughput genomic approaches to describe genome evolution and the genotype-phenotype map. *College of Agriculture & Life Sciences, Interdisciplinary Plant Biology Seminar Program, University of Arizona School of Plant Sciences (December 1, 2009).* **(Invited Speaker).**

**Clark, R. M.** Genomic approaches for understanding genome evolution and the genotype-phenotype map. “*Genomics, Evolution, and Association Mapping*” seminar series, *University of Minnesota Microbial and Plant Genomics Institute (MPGI) (November 17, 2009).* **(Invited Speaker).**

**Clark, R. M.** Towards understanding the impact of natural variation on plant development. *25<sup>th</sup> Symposium in Plant Biology: “The Evolution of Development” at the University of California Riverside (January 29-31, 2009).* **(Invited Speaker)**

**2008**

**Clark, R. M.** Massive variation in the *Arabidopsis thaliana* genome revealed by “next-generation” sequencing.” *University of Queensland, Australia (May 26, 2008).* **(Invited Speaker)**

**2006**

**Clark, R. M.,** Ossowski, S., Schweikert, G., Zeller, G., Shinn, P., Rätsch, G., Warthmann, N., Fu, G., Hinds, D., Chen, H.-M., Frazer K., Toomajian, C., Hu, T., Huson, D. H., Schölkopf, B., Nordborg, M., Ecker, J. R., and Weigel, D. Natural variation in *Arabidopsis* and its close relations. *ESF-WellcomeTrust Conference: Crop Genomics, Trait analysis and Breeding (November 8-11, 2006).* **(Invited Speaker)**

**Clark, R. M.,** Ossowski, S., Schweikert, G., Zeller, G., Shinn, P., Rätsch, G., Warthmann, N., Fu, G., Hinds, D., Chen, H.-M., Frazer K., Toomajian, C., Hu, T., Huson, D. H., Schölkopf, B., Nordborg, M., Ecker, J. R., and Weigel, D. The common sequence variation of *Arabidopsis thaliana* as revealed by whole genome resequencing arrays. *Plant Genomics European Meeting, #5 (October 11-14, 2006).*

**Clark, R. M.,** Ossowski, S., Schweikert, G., Zeller, G., Shinn, P., Rätsch, G., Warthmann, N., Fu, G., Hinds, D., Chen, H.-M., Frazer K., Toomajian, C., Hu, T., Huson, D. H., Schölkopf, B., Nordborg, M., Ecker, J. R., and Weigel, D. Genome inventory of sequence polymorphisms in *Arabidopsis thaliana*. *Ludweg-Maximilians-University, Munich, Germany (July 18, 2006).* **(Invited Speaker)**

**2005**

**Clark, R. M.** Long-distance regulatory control of the *tb1* gene and the evolution of plant architecture in maize. *Society for Experimental Biology Annual Main Meeting (July 11-15, 2005)*. (**Invited Speaker**)

**Clark, R. M.**, Warthmann, N., Fu, G., Frazer K., and Weigel, D. Genome inventory of sequence polymorphisms for *Arabidopsis thaliana*. *16<sup>th</sup> International Conference on Arabidopsis Research (June 15-19, 2005)*.

Bergelson, J., Borevitz, J., **Clark, R. M.**, Gaut, B., Hall, A., Langley, C., Neuffer, B., Mayer, K., Nordborg, M., Savolainen, O., Peer, Y. V. D, Weigel, D., and Wright., S. Sequencing the *Arabidopsis lyrata* and *Capsella rubella* genomes: what lessons will *A. thaliana*'s near relatives teach? *16<sup>th</sup> International Conference on Arabidopsis Research, Relatives Workshop (June 15-19, 2005)*.

**2004**

**Clark, R. M.** Morphological adaptation in response to strong selection: lessons from the maize domestication locus, *teosinte branched 1 (tb1)*. *Montana State University, Bozeman, Montana, USA. (November 9, 2004)*. (**Invited Speaker**)

**2003**

**Clark, R. M.**, Doebley, J. Defining sequences at the *teosinte branched1* locus selected during maize domestication. *American Society of Plant Biologists--Plant Genetics 2003: Mechanisms of Genetic Variation (October 22-26, 2003)*. (**Invited Speaker**)

**Clark, R. M.** The complexity of selection at a major effect QTL in maize, *teosinte branched1 (tb1)*. *Regulation of Inflorescence morphology—Insights from Genetics and Genomics, The Banbury Center, Cold Spring Harbor Laboratory (September 21-24, 2003)*. (**Invited Speaker**)

**POSTERS/ABSTRACTS (partial list)**

**2023**

Ji, M., De Beer, B., Vandenhole, M., Feyereisen, R., **Clark, R. M.**, and Van Leeuwen, T. A *trans*-eQTL hotspot underlies large differences in detoxification gene expression in the generalist herbivore *Tetranychus urticae*. *Plant and Animal Genome Conference (PAG) 30, San Diego, California, USA (Jan 13-18, 2023)*

**2022**

Dermauw, W., Van Leeuwen, T., Kant, M., Wybouw, N., **Clark, R. M.**, and Greenhalgh, R. Extreme genome reduction in the minute tomato pest *Aculops lycopersici*. *2022 XXVI International Congress of Entomology (Helsinki, Finland, July 17-22, 2022)*.

Vandenhole, M., Kurlovs, A., Snoeck, S., Dermauw, W., Wybouw, N., **Clark, R. M.**, and Van Leeuwen, T. Mapping of resistance traits in mites by bulked segregant analysis. *2022 XXVI International Congress of Entomology (Helsinki, Finland, July 17-22, 2022)*.

Van Leeuwen, T., Vandenhole, M., Kurlovs, A., De Beer, B., and **Clark, R. M.** The contribution to adaptation of *cis* versus *trans* gene regulation in a polyphagous arthropod, the spider mite *Tetranychus urticae*. *2022 XXVI International Congress of Entomology (Helsinki, Finland, July 17-22, 2022)*.

Ji, M., Bui, H., Greenhalgh, R., Gill, G. S., Ramirez, R. A., and **Clark, R. M.** Molecular-genetic basis of high-level resistance of maize line B96 to the two-spotted spider mite, *Tetranychus urticae*. *Plant and Animal Genome Conference (PAG) XXIX, San Diego, California, USA (Jan 8-12, 2022)*

## 2021

Dermauw, W., Greenhalgh, R., Glas, J., Wybouw, N., Van Leeuwen, T., **Clark, R. M.**, and Kant, M. Extreme gene and intron loss in the miniature genome of the tomato russet mite. *Symposium on Insect-Plant Interactions 2021, session "Genomics of plant-insect interactions," Leiden, Netherlands, held online because of the COVID-19 pandemic (July 25-30, 2021)*

Ji, M., Bui, H., Quist, A. J., Ramirez, R. A., and **Clark, R. M.** Transcriptional underpinnings of high-level resistance to the generalist spider mite *Tetranychus urticae* in maize. *Plant Biology 2021, American Society of Plant Biologists (July 19-23, 2021)*.

## 2019

Kurlovs, A., De Beer, B., Vandenhole, M., Njiru, C., **Clark, R. M.** and Van Leeuwen, T. The molecular genetic mechanisms of extreme adaptation in the spider mite *Tetranychus urticae*. *11<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (November 4-6, 2019)*.

Gill, G., Lu, H., Price, S., Bui, H., **Clark, R. M.** and Ramirez, R. Generalist spider mites behave on resistant maize while specialists do not. *Entomology 2019, St. Louis, Missouri, USA (November 17-20, 2019)*.

Gill, G., Bui, H., **Clark, R. M.** and Ramirez, R. Understanding how water stress affects spider mite resistance in maize. *Entomological Society of America, 2019 Pacific Branch Meeting San Diego, California, USA (March 31 – April 3, 2019)*.

Greenhalgh, R., Bui, H., Kosterlitz, O., Wybouw, N., Kurlovs, A., Bajda, S., Snoeck, S., Bryon, A., Dermauw, W., Van Leeuwen, T. and **Clark, R. M.** An improved *Tetranychus urticae* genome facilitates identification of loci associated with adaptation to agriculture. *The Plant and Animal Genome XXVII Conference (PAG), San Diego, California, USA (January 12-16, 2019)*.

## 2018

Gill, G., Bui, H., **Clark, R. M.**, and Ramirez, R. Understanding how water stress affects spider mite resistance in maize. *Entomology 2018, Vancouver, British Columbia, Canada (November 11-14, 2018)*.

Dermauw, W., Greenhalgh, R., Van Leeuwen, T., **Clark, R. M.**, and Kant, M. R. Extreme genome reduction in the specialist eriophyid mite herbivore *Aculops lycopersici*. *Entomology 2018, Vancouver, British Columbia, Canada (November 11-14, 2018)*.

Van Leeuwen, T., Wybouw, N., Kosterlitz, O., Kurlovs, A., Bajda, S., Greenhalgh, R., Snoeck, S., Bui, H., Bryon, A., Villacis-Pérez, E., Dermauw, W., and **Clark, R. M.** Experimental evolution followed by genome resequencing using a chromosome-level assembly reveals the complex genetic architecture of xenobiotic adaptation in *Tetranychus urticae*. *Entomology 2018, Vancouver, British Columbia, Canada (November 11-14, 2018)*.

Snoeck, S., Kurlovs, A., Bajda, S., Greenhalgh, R., Feyereisen, R., Villacis-Pérez, E., Wybouw, N., Dermauw, W., **Clark, R. M.**, and Van Leeuwen, T. High resolution QTL mapping reveals parallel and divergent selection responses to different METI-I acaricides in *Tetranychus urticae*. *Entomology 2018, Vancouver, British Columbia, Canada (November 11-14, 2018)*.

Wybouw, N., Kurlovs, A., Tsakireli, D., Bryon, A., Osakabe, M., Vontas, J., **Clark, R. M.**, and Van Leeuwen, T. 2018. Convergent evolution within the cytochrome P450 family underlies independent origins of red coloration in animals. *10<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (November 5-8, 2018)*.

Kurlovs, A., Kosterlitz, O., Wybouw, N., Bui, H., Greenhalgh, R., Bajda, S., Snoeck, S., Bryon, A., Damaeght, P., Dermauw, W., Van Leeuwen, T., and **Clark, R. M.** A chromosome-level assembly and strain sequencing data reveal striking patterns of genetic variation in a global *Tetranychus urticae* population sample. *10<sup>th</sup> Spider Mite Genome Meeting, Logrono, La Rioja, Spain (November 5-8, 2018)*.

Kurlovs, A., Kosterlitz, O., Bui, H., Greenhalgh, R., Bryon, A., Bajda, S., Van Leeuwen, T., and **Clark, R. M.** Forces shaping genetic diversity in the globally distributed generalist herbivore, *Tetranychus urticae*. *Society for Molecular Biology and Evolution Satellite Meeting: Molecular Evolution and the Cell, Park City, Utah, USA (May 9-12, 2018)*.

## 2017

Gill, G. S., Bui, H., **Clark, R. M.**, and Ramirez, R. A. Water-stress alters plant defense responses toward generalist and specialist spider mites in maize. *Entomology 2017, Denver, Colorado, USA (November 5-8, 2017)*.

Bui, H., Greenhalgh, R., Ruckert, A., Lee, S., Gill, G. S., Ramirez, R., and **Clark, R. M.** The genetic basis of variation in monocot resistance to spider mite herbivores. *Plant Biology 2017, Annual Meeting of the American Society of Plant Biologists, Honolulu, Hawaii, USA (June 24-28, 2017)*.

Gill, G. S., Ruckert, A., Bui, H., **Clark, R. M.**, and Ramirez, R. A. Plant defense responses to generalist and specialist spider mites in maize. *101st Annual Meeting of the Pacific Branch of the Entomological Society of America, Portland, Oregon, USA (April 2-5, 2017)*.

Bui, H., Greenhalgh, R., Ruckert, A., Lee, S., Gill, G. S., Ramirez, R., and **Clark, R. M.** Differential impact of benzoxazinoids on generalist and grass-specialist spider mite herbivores. *Plant-Herbivore Interaction Gordon Research Conference, Ventura, CA, USA (February 12-17, 2017)*.

## 2016

Bui, H., Greenhalgh, R., Lee, S., Ruckert, A., Ramirez, R. A., and **Clark, R. M.** Defense responses of maize and barley to generalist and specialist spider mite herbivores. *Genetics & Genomics of Crop Improvement, 18<sup>th</sup> Annual Fall Symposium, Donald Danforth Plant Science Center, Saint Louis, Missouri, USA (September 28-30, 2016).*

Dermauw, W., Wybouw, N., Feyereisen, R., **Clark, R. M.**, and Van Leeuwen, T. A link between host plant adaptation and pesticide resistance in the polyphagous spider mite *Tetranychus urticae*. *XXV International Congress of Entomology, Orlando, Florida, USA (September 25-30, 2016).*

Bryon, A., Kurlovs, A., Tirry, L., **Clark, R. M.**, and Van Leeuwen, T. Carotenoids and diapause in the two-spotted spider mite: Lessons from an albino mutant. *XXV International Congress of Entomology, Orlando, Florida, USA (September 25-30, 2016).*

Van Leeuwen, T., and **Clark, R. M.** Mutations in chitin synthase-1 (CHS-1) confer resistance to a range of structurally diverse acaricides and insecticides. *XXV International Congress of Entomology, Orlando, Florida, USA (September 25-30, 2016).*

Greenhalgh, R., Bui, H., Ruckert, A., Ramirez, R., and **Clark, R. M.** Shared and species-specific transcriptional responses of barley (*Hordeum vulgare* L.) to generalist and specialist spider mite herbivores. *The Allied Genetics Conference 2016, Orlando, Florida, USA (July 13-17, 2016).*

Bui, H., Greenhalgh, R., Ruckert, A., Ramirez, R., and **Clark, R. M.** Dynamic yet Correlated Responses of Barley (*Hordeum vulgare* L.) to Generalist and Specialist Spider Mite Herbivores. *Plant Biology 2016, Annual meeting of the American Society of Plant Biologists, Austin, Texas, USA (July 9-13, 2016).*

## 2013

Osborne, E. J., and **Clark, R. M.** Genetic and environmental contributions to gene expression variation in *Arabidopsis thaliana*. *Evolution 2013, Snowbird, Utah (June 21-25, 2013).*

Kurlovs, A., and **Clark, R. M.** *Arabidopsis* intraspecific variation affects fitness of a generalist mite herbivore. *Evolution 2013, Snowbird, Utah (June 21-25, 2013).*

Greenhalgh, R., and **Clark, R. M.** Patterns of gene expression variation in *Arabidopsis thaliana* as revealed by allele-specific transcriptome sequencing. *Evolution 2013, Snowbird, Utah (June 21-25, 2013).*

Stegle, O., Drewe, P., Kahles, A., Zhon, Y., Steffen, J., Greenhalgh, R., Toomajian, C., Gan, X., Mott, R., **Clark, R. M.**, and Rättsch, G. Advanced intercross genetic design reveals extensive genetic control of the transcriptional landscape in *Arabidopsis thaliana*. *The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (May 7-11, 2013).*

Osborne, E. J., Stegle, O., Remigereau, M. S., Vilhjalmsón, B., Zhang, P., Drewe, P., Kahles, A., Korte, A., Rättsch, G., Nordborg, M., and **Clark, R. M.** Genetic and environmental influences on gene expression in *Arabidopsis thaliana*. *The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (May 7-11, 2013).*

## 2012

Osborne, E. J., Remigereau, M. S., Zhang, P., Vilhjalmsón, B., Stegle, O., Drewe, P., Quan, L., Umit, S., Kahles, A., Song, Q., Korte, A., Nordborg, M., Smith, A., Rättsch, G., and **Clark, R. M.** Transcriptome variation across environments in Swedish *Arabidopsis thaliana*. *Plant Biology 2012: The Annual Meeting of the American Society of Plant Biologists, Austin, Texas (July 20-24, 2012)*.

Greenhalgh, R., Steffen, J., Stegel, O., Drewe, P., Gan, X., Imprialou, M., Behr, J., Osborne, E., Toomajian, C., Kover, P., Rättsch, G., Mott, R., and **Clark, R. M.** Pervasive genomic and gene expression variation in the magic population of recombinant inbred lines. *Plant Biology 2012: The Annual Meeting of the American Society of Plant Biologists, Austin, Texas (July 20-24, 2012)*.

## 2011

Steffen, J. J., Osborne, E. J., Stegle, O., Behr, J., Drewe, P., Gan, X., Hildebrand, K. L., Remigereau, M. S., Zhang, P., Long, Q., Vilhjalmsón, B., Greenhalgh, R., Nordborg, M., Toomajian, C., Mott, R., Rättsch, G., and **Clark, R. M.** Genomewide variation in sense and antisense transcription across 19 *Arabidopsis thaliana* strains. *Plant Genomes & Biotechnology: From Genes to Networks, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (Nov 30 – Dec 3, 2011)*.

Remigereau, M. S., Zhang, P., Osborne, E. J., Long, Q., Vilhjalmsón, B., **Clark, R. M.**, and Nordborg, M. Integrating the transcriptome layer to the genotype-phenotype map in *A. thaliana*. *Plant Genomes & Biotechnology: From Genes to Networks, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York (Nov 30 – Dec 3, 2011)*.

Steffen, J., Behr, J., Drewe, P., Hildebrand, K., Kover, P., Lyngsoe, R., Mott, R., Osborne, E. J., Rättsch, G., Schultheiss, S., Sreedharan, V., Stegle, O., Toomajian, C., Xiangchao, G., and **Clark, R. M.** Extensive genomic and transcriptomic variation in the 19 founders of the *Arabidopsis* MAGIC lines. *The 22<sup>nd</sup> International Conference on Arabidopsis Research (ICAR), Madison, Wisconsin (June 22-25, 2011)*.

Gan, X., Behr, J., Steffen, J., Hildebrand, K., Allchin, L., Goodstadt, L., Stegle, O., Drewe, P., Lyngsoe, R., Sreedharan, V., Osborne, E. J., Toomajian, C., Kover, P., Rättsch, G., **Clark, R. M.**, and Mott, R. Accurate sequencing of 18 genomes of *Arabidopsis thaliana* and its use in imputing the genome sequences of over 600 MAGIC recombinant inbred lines. *The 22<sup>nd</sup> International Conference on Arabidopsis Research (ICAR), Madison, Wisconsin (June 22-25, 2011)*.

Cazaux, M., Poo, C., Navarro, M., **Clark, R. M.**, Grbić, M., and Grbić V. Genetic dissection of the plant/pest interaction: mapping of *Arabidopsis* resistance gene to *Tetranychus urticae* (two spotted spider mite) feeding. *The 22<sup>nd</sup> International Conference on Arabidopsis Research (ICAR), Madison, Wisconsin (June 22-25, 2011)*.

Hildebrand, K., Behr, J., Drewe, P., Xiangchao, G., Kahles, A., Lyngsoe, R., Osborne, E. J., Schultheiss, S., Sreedharan, V., Steffen, J., Stegle, O., **Clark, R. M.**, Kover, P., Mott, R., Rättsch, G., and Toomajian, C. Patterns of genome and transcriptome variation in *Arabidopsis thaliana*. *The Evolution Meeting, Norman, Oklahoma (June 17-21, 2011)*.

## 2010

Osborne, E. J. and **Clark R. M.** The spider mite transcriptome: patterns by developmental stage and host species. *Second Spider Mite Genome Meeting, Tivat, Montenegro (September 20-23, 2010)*.

## 2008

Vilhjalmsson, B., Atwell, S., Willems, G., Huang, Y., Jiang, R., Li, Y., Zhang, X., Hu, T., **Clark, R. M.**, Toomajian, C., Aranzana, M. J., Zhao, K., Tarone, A., Lee, R., Jung, C., Meng, D., Platt, A., Lister, C., Horton, M., Bergelson, J., Shindo, C., Dean, C., Ecker, J. R., Weigel, D., Borevitz, J., Marjoram, P., Nordborg, M. Genome-wide association mapping in *Arabidopsis thaliana*. *19<sup>th</sup> International Conference on Arabidopsis Research (July 23-27, 2008)*.

Poo, C., Mathieu, J., **Clark, R. M.**, Schmid, M., Grbić, M., and Grbić, V. Interaction between plant and pest genomes: *Arabidopsis*-two spotted spider mite *Tetranychus urticae*, novel model for plant-herbivore interactions. *19<sup>th</sup> International Conference on Arabidopsis Research (July 23-27, 2008)*.

Toomajian, T., Hu, T., Plagnol, V., **Clark, R. M.**, Li, Y., Pattyn, P., Schmutz, J., Bergelson, J., Borevitz, J., Ecker, J., Gaut, B., Kreitman, M., Marjoram, P., Rokhsar, D., Peer Y. V., Weigel, D., and Nordborg, M. Genome-wide patterns of recombination in *Arabidopsis thaliana* and their impact on the efficacy on natural selection. *Society for Molecular Biology and Evolution (June 5-8, 2008)*.

## 2006

Zeller, G., Schweikert, G., **Clark, R.**, Ossowski, S., Warthmann, N., Shinn, P., Frazer, K., Ecker, J., Huson, D., Weigel, D., Schölkopf, B., and Rätsch, G. Machine Learning Algorithms for Polymorphism Detection. *14<sup>th</sup> Annual International Conference on Intelligent Systems for Molecular Biology (Aug. 6-10, 2006)*.

Hu, T., Kim, S., Plagnol, V., Toomajian, C., **Clark, R.**, Lister, C., Dean, C., Ecker, J., Weigel, D., and Nordborg, M. The genomic pattern of linkage disequilibrium in *Arabidopsis thaliana*. *17<sup>th</sup> International Conference on Arabidopsis Research, Relatives Workshop (June 28 - July 2, 2006)*.

**Clark, R. M.**, Ossowski, S., Schweikert, G., Zeller, G., Shinn, P., Rätsch, G., Warthmann, N., Fu, G., Hinds, D., Chen, H.-M., Frazer K., Toomajian, C., Hu, T., Huson, D. H., Schölkopf, B., Nordborg, M., Ecker, J. R., and Weigel, D. An inventory of common sequence polymorphisms for *Arabidopsis*. *17<sup>th</sup> International Conference on Arabidopsis Research, Relatives Workshop (June 28 - July 2, 2006)*.

Kim, S., Plagnol, V., Hu, T., Toomajian, C., **Clark, R.**, Lister, C., Dean, C., Ecker, J., Weigel, D. and Nordborg, M. Recombination and linkage disequilibrium in *Arabidopsis thaliana*. *Beyond HapMap: 3<sup>rd</sup> Annual International HapMap Project Community Analysis Meeting (May 8-10, 2006)*.

**Clark, R. M.**, Ossowski, S., Schweikert, G., Zeller, G., Shinn, P., Rätsch, G., Warthmann, N., Fu, G., Hinds, D., Chen, H.-M., Frazer K., Toomajian, C., Hu, T., Huson, D. H., Schölkopf, B., Nordborg, M., Ecker, J. R., and Weigel, D. An inventory of sequence polymorphisms for *Arabidopsis*. *The Biology of Genomes, Cold Spring Harbor Laboratory (May 10-14, 2006)*.

**Clark, R. M.**, Guo, Y., Bergelson, J. M., Borevitz, J. O., Gaut, B. S., Hall, A. E., Langley, C. H., Neuffer, B., Mayer, K. F. X., Nordborg, M., Savolainen, O., Peer, Y. V. D., Wright, S., and Weigel, D. Sequencing *Arabidopsis lyrata* and *Capsella rubella*: what we can learn from the genomes of *A. thaliana*'s close relatives. *First Annual DOE Joint Genome Institute User Meeting (March 29 – April 1, 2006)*.

**Clark, R. M.**, Wagler, T. N., Quijada, P., and Doebley, J. A distant upstream enhancer at the maize domestication gene, *tb1*, has pleiotropic effects on plant and inflorescent architecture. *48<sup>th</sup> Annual Maize Genetics Conference (March 9-12, 2006)*.



**2003**

**Clark, R. M.**, Linton, E. W., Messing, J., Doebley, J. A large region upstream to the *teosinte branched1* (*tb1*) locus was selected during maize evolution. *45<sup>th</sup> Annual Maize Genetics Conference (March 13-16, 2003)*.

**2002**

Bomblies, K., **Clark, R. M.**, Doebley, J. Investigation of candidate genes for QTL involved in maize domestication. *FASEB Summer Research Conferences: Mechanisms in Plant Development (August 10-14, 2002)*.

Doebley, J., **Clark, R. M.** The evolution of plant form: An example from maize. *BSDB/Genetics Society Joint Spring Meeting on Evolution and Developmental Mechanisms*. (March 20-23, 2002).

**Clark, R. M.**, Linton, E.W., Messing, J., Doebley, J. Functional and molecular characterization of selection at the maize domestication locus *teosinte branched1* (*tb1*). *44<sup>th</sup> Annual Maize Genetics Conference (March 14-17, 2002)*.