

Bart, Rebecca 2018

CURRICULUM VITAE

Rebecca Bart

Assistant Member and Principal Investigator
Danforth Plant Science Center
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EDUCATION

2004-2009	PhD Plant Pathology	Advisor: Pamela Ronald	UC Davis
1999-2003	B.A. Biology	Advisor: Jay Mellies	Reed College, Portland OR

PROFESSIONAL EXPERIENCE

2013-present	Assistant Member and P.I.		DDPSC, St. Louis MO
2010-2013	Postdoctoral Research	Advisor: Brian Staskawicz	UC Berkeley
2003-2004	Research Assistant	Advisor: Sarah Hake	PGEC, Albany CA

PROFESSIONAL SOCIETIES

American Phytopathological Society
American Society of Plant Biologists
The American Association for the Advancement of Science
IS-Molecular Plant Microbe Interactions

HONORS, AWARDS and APPOINTMENTS

ASPB Science Policy Committee (2016 – present)
NIFA postdoctoral fellow (2011-2013)
Mentor-initiated Sponsored Projects for Undergraduate Research (2010-2011)
William G. and Kathleen Golden International Agriculture Fellowship (2007-2008)
Consortium for Women in Research Fellowship (2007)
D. Marlin Brandon Fellowship (2006)
Henry A. Jastro and Peter J. Shields Graduate Research Scholarship (2005-2006)
William G. and Kathleen Golden International Agriculture Fellowship (2005-2006)

INVITED PRESENTATIONS

Invited Speaker, Phenomics Symposium, WSU, 2018
Invited Speaker, One Health Research Symposium, 2018
Selected Speaker, Cassava Global Partnership, Benin, 2018
Invited Speaker, Iowa State University, Dept. of Plant Pathology and Microbiology, 2017
Invited Speaker, Annual Plant Sciences Symposium, University of Wisconsin-Madison, 2017
Invited Speaker, St. Louis University, Biology Department, 2017
Invited Speaker, Genomics-enabled Accelerated Crop Breeding, Banbury Conference, 2016
Selected Speaker, ICM PMI, Portland, OR, 2016
Selected Speaker, PAG, San Diego, CA, 2016
Selected Speaker, ASPB, Minneapolis, MN, 2015
Selected Speaker, 5th Xanthomonas Genomics Conference – XGC 2015, Colombia, 2015

Invited Speaker, Plant Breeding and Genetics seminar, Cornell University, 2015
Invited Speaker, AgBiome, Durham, North Carolina, 2014
Invited Speaker, Donald Danforth Plant Science Center 16th Annual Fall Symposium, 2014
Invited Speaker, University of Illinois, Department of Plant Biology, IL, 2014
Invited Speaker, University of Missouri-St. Louis, Department of Biology, 2014
Invited Speaker, Washington University Medical School, 2014
Invited Speaker, Plant and Animal Genome Conference, San Diego, CA 2014

PUBLICATIONS

RESEARCH PUBLICATIONS (*DENOTES BART AS CORRESPONDING AUTHOR)

2018

Berry, J., Fahlgren, N., **Bart, R.**, Veley, K. A statistical method for image set standardization including measurement of variation. *PeerJ*. [10.7717/peerj.5727](https://doi.org/10.7717/peerj.5727)

Gomez, M.A., Lin, Z.D., Moll T., Luebbert, C., Chauhan, R.D., Vijayaraghavan, A., Renninger, K., Beyene, G., Taylor, N.J., Carrington, J.C., Staskawicz, B.J., **Bart, R.*** (2018) Simultaneous CRISPR/Cas9-mediated editing of cassava *eIF4E* isoforms *nCBP-1* and *nCBP-2* confers elevated resistance to cassava brown streak disease. *Plant Biotechnology Journal*. Accepted. doi.org/10.1101/209874

Phillips, A.Z., Wheeler, T., Woodward, J., **Bart, R.*** (2018). *Pseudomonas syringae* pathogen causes foliar disease of Upland Cotton in Texas. *Plant Disease*. <https://doi.org/10.1094/PDIS-11-17-1700-PDN>

Hummel, A. W., Chauhan, R. D., Cermak, T., Mutka, A. M., Vijayaraghavan, A., Boyher, A., Starker, C. G., **Bart, R.**, Voytas, D. F. and Taylor, N. J. (2018), Allele exchange at the EPSPS locus confers glyphosate tolerance in cassava. *Plant Biotechnol J*. doi:10.1111/pbi.12868

2017

Odipio, J., Alicai, T., Ingelbrecht, I., Nusinow D.A., **Bart, R.**, Taylor, N.J. (2017) Efficient CRISPR/Cas9 Genome Editing of Phytoene desaturase in Cassava. *Frontiers in Plant Science* 8:1780. doi: 10.3389/fpls.2017.01780

Veley, K.M., Berry, J.C., Fentress, S.J., Schachtman, D.P., Baxter, I., **Bart, R.*** (2017) High-throughput profiling identifies resource use efficient and abiotic stress tolerant sorghum varieties. *Plant Direct*, 2017;00:1–13. <https://doi.org/10.1002/pld3.23>

Phillips, A.Z., Berry, J.C., Wilson, M.C., Vijayaraghavan, A., Burke, J., Bunn, I., Allen, T.W., Wheeler, T., **Bart, R.*** (2017). Genomics-enabled analysis of the emergent disease cotton bacterial blight. *PLoS Genetics* 13(9): e1007003. <https://doi.org/10.1371/journal.pgen.1007003>

Wilson, M.C., Mutka, A.M., Hummel, A.W., Berry, J., Chauhan, R.D., Vijayaraghavan, A., Taylor, N.J., Voytas, D.F., Chitwood, D.H., **Bart, R.S.*** (2017) Gene expression analysis provides insight into the physiology of the important staple food crop cassava. *New Phytologist*, 213, no.4:1632-1641. doi:10.1111/nph.14443

Ramu, P., Esuma W., Kawuki R., Rabbi I.Y., Egesi, C., Bredeson J.V., **Bart, R.S.**, Verma J., Buckler, E.S., Lu F. (2017) Cassava haplotype map highlights fixation of deleterious mutations during clonal propagation. *Nature Genetics*, 49: 959-963. doi:10.1038/ng.3845

2016

Mutka, A.M., Fentress, S.J., Sher, J.W., Berry, J.C., Pretz, C., Nusinow, D.A., **Bart, R.S.*** (2016) Quantitative, image-based phenotyping methods provide insight into spatial and temporal dimensions of plant disease. *Plant Physiology*, 172, no. 2: 650-660. [dx.doi.org/10.1104/pp.16.00984](https://doi.org/10.1104/pp.16.00984)

Bredeson, J.V., Lyons, J.B., Prochnik, S.E., Wu, G.A., Ha, C.M., Edsinger-Gonzales, E., Grimwood, J., Schmutz, J., Rabbi, I.Y., Egesi, C., Nauluvula, P., Lebot, V., Ndunguru, J., Mkamilo, G., **Bart, R. S.**, Setter, T.L., Gleadow, R.M., Kulakow, P., Ferguson, M.E., Rounsley, S., Rokhsar, D. S. (2016). Sequencing Wild and Cultivated Cassava and Related Species Reveals Extensive Interspecific Hybridization and Genetic Diversity. *Nat. Biotechnol.*, 34, no. 5: 562–570. [doi:10.1038/nbt.3535](https://doi.org/10.1038/nbt.3535)

Chern, M., Xu Q, **Bart, R.S.**, Bai, W., Ruan, D., Sze-To, W.H., Canlas, P.E., Jain, R., Chen, X., Ronald, P.C. (2016) A Genetic Screen Identifies a Requirement for Cysteine-Rich–Receptor-Like Kinases in Rice NH1 (OsNPR1)-Mediated Immunity. *PLoS Genet.*, 12(5): e1006049. [doi: 10.1371/journal.pgen.1006049](https://doi.org/10.1371/journal.pgen.1006049)

2015

Wang, H., Beyene, G., Zhai, J., Feng, S., Fahlgren, N., Taylor, N., **Bart, R.**, Carrington, J.C., Jacobsen, S.E., Ausin, I. (2015). CG gene body DNA methylation changes and evolution of duplicated genes in cassava. *PNAS*, 112 (44) 13729–13734; published ahead of print October 19, 2015, [doi:10.1073/pnas.1519067112](https://doi.org/10.1073/pnas.1519067112)
13. Schwartz, A.R., Potnis, N., Timilsina, S., Wilson, M., Patane, J., Martins, J., Minsavage, G.V., Dahlbeck, D., Akhunova, A., Almeida, N., Vallad, G.E., Barak, J.D., White, F.F., Miller, S.A., Ritchie, D., Goss, E., **Bart, R.S.**, Setubal, J.C., Jones, J.B., Staskawicz, B.J. (2015). Phylogenomics of *Xanthomonas* field strains infecting pepper and tomato reveals diversity in effector repertoires and identifies determinants of host specificity. *Front. Microbiol.*, 6:535. [doi: 10.3389/fmicb.2015.00535](https://doi.org/10.3389/fmicb.2015.00535)

2014

Timilsina, S., Jibrin, M., Potnis, N., Minsavage, G., Kebede, M., Schwartz, A., **Bart, R.**, Staskawicz, B., Boyer, C., Vallad, G., Pruvost, O., Jones, J.B., Goss, E.M. (2014). Multilocus sequence analysis of xanthomonads causing bacterial spot of tomato and pepper reveals strains generated by recombination among species and recent global spread of *Xanthomonas gardneri*. *Appl. Environ. Microbiol.*, 81:1520-1529. [doi: 10.1128/AEM.03000-14](https://doi.org/10.1128/AEM.03000-14).

Cohn, M.¹, **Bart, R.**¹, Shybut, M., Dahlbeck, D., Gomez, M., Morbitzer, R., Hou, B. H., Frommer, W. B., Lahaye, T., Staskawicz, B. J. (2014). *Xanthomonas axonopodis* virulence is promoted by a transcription activator like (TAL) effector mediated induction of a SWEET sugar transporter in cassava. *Mol. Plant Microbe Interact.*, 27: 1186-1198. <http://dx.doi.org/10.1094/MPMI-06-14-0161-R>. ¹**Equal contribution.**

PRIOR TO 2014

Arrieta-Ortiz, M. L., Rodriguez-R, L. M., Perez-Quintero, A. L., Poulin, L., Díaz, A. C., Arias Rojas, N., Trujillo, C., Restrepo Benavides, M. **Bart, R.**, et al. (2013). Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen *Xanthomonas axonopodis* pv. *manihotis* Strain CIO151. *PLoS One*, 8(11), e79704. [doi:10.1371/journal.pone.0079704](https://doi.org/10.1371/journal.pone.0079704)

Bart, R., Cohn, M., Kassen, A., McCallum, E. J., Shybut, M., Petriello, A., Krasileva, K., Dahlbeck, D., Medina, C., Alicai, T., Kumar, L., Moreira, L.M., Rodrigues Neto, J., Verdier, V., Santana, M.A., Kositcharoenkul, N., Vanderschuren, H., Grisseem, W., Bernal, A. & Staskawicz, B. (2012). High-throughput genomic sequencing of

cassava bacterial blight strains identifies conserved effectors to target for durable resistance. *PNAS*, 109(28), E1972–E1979. doi:10.1073/pnas.1208003109

Bart, R. S., Chern, M., Vega-Sánchez, M. E., Canlas, P., & Ronald, P. C. (2010). Rice Snl6, a cinnamoyl-CoA reductase-like gene family member, is required for NH1-mediated immunity to *Xanthomonas oryzae* pv. *oryzae*. *PLoS Genetics*, 6(9), e1001123. doi:10.1371/journal.pgen.1001123

Park, C.-J., **Bart, R.**, Chern, M., Canlas, P. E., Bai, W., & Ronald, P. C. (2010). Overexpression of the endoplasmic reticulum chaperone BiP3 regulates XA21-mediated innate immunity in rice. *PLoS One*, 5(2), e9262. doi:10.1371/journal.pone.0009262

Ding, X., Richter, T., Chen, M., Fujii, H., Seo, Y. S., Xie, M., et al. (2009). A rice kinase-protein interaction map. *Plant Physiol.*, 149(3), 1478–1492. doi:10.1104/pp.108.128298

Park, C.-J., Peng, Y., Chen, X., Dardick, C., Ruan, D., **Bart, R.**, et al. (2008). Rice XB15, a protein phosphatase 2C, negatively regulates cell death and XA21-mediated innate immunity. *PLoS Biol.*, 6(9), e231. doi:10.1371/journal.pbio.0060231

Bart, R., Chern, M., Park, C.-J., Bartley, L., & Ronald, P. C. (2006a). A novel system for gene silencing using siRNAs in rice leaf and stem-derived protoplasts. *Plant Methods*, 2(1), 13. doi:10.1186/1746-4811-2-13

PATENTS

a. SUBMITTED

Meyers, B., **Bart, R.**, Veley, K., Okwuomu, I. (2017) “SureFire Homologous Recombination” U.S. Provisional Application No. 62/598,831

Bart, R., Phillips, AZ. (2017) “Methods for increasing resistance to cotton bacterial blight and plants produced thereby.” U.S. Provisional Application No. 62/483,174

Hummel, A., Voytas, D., **Bart, R.**, Taylor, N. (2016) “Glyphosate tolerant plants having modified 5-enolpyruvylshikimate-3-phosphate synthase gene regulation” Application No. 62277734

b. GRANTED

Bart, R. Chern, M., Ronald, Pamela C.; Vega-Sanchez, Miguel E. (2018) “Inhibition of Snl6 expression for biofuel production.” Patent No.: 9932601

PERSPECTIVES & REVIEWS

Michelmore, R., Coaker, G., **Bart, R.**, et.al. (2017) Foundational and translational research opportunities to improve plant health. *Molecular Plant-Microbe Interactions*, 30, no.7: 515-516. doi.org/10.1094/MPMI-01-17-0010-CR

Bart, R.S.*, Taylor, N.J. (2017) New opportunities and challenges to engineer disease resistance in cassava, a staple food of African small-holder farmers. *PLOS Pathogens*. 13, no.5. https://doi.org/10.1371/journal.ppat.1006287

Pauli, D., Chapman, S.C., **Bart, R.**, Topp, C.N., Lawrence-Dill, C.J., Poland, J., Gore, M.A. (2016) The quest for understanding phenotypic variation via integrated approaches in the field environment. *Plant Physiology*, 172, no.2: 622-634. https://doi.org/10.1104/pp.16.00592

Fahlgren N, **Bart R**, Herrera-Estrella L, Rellan-Alvarez R, Chitwood DH, Dinneny JR. Plant scientists: GM technology is safe. *Science*. 2016;351(6275):824-824. doi:10.1126/science.351.6275.824-a.

Mutka, A. & **Bart. R.*** (2015). Image-based phenotyping of plant disease symptoms. *Front. Plant Sci.*, 5:734. doi: 10.3389/fpls.2014.00734

Schwessinger, B., **Bart, R.**, Krasileva, K., Coaker, G. (2015). Focus issue on plant immunity: from model systems to crop species. *Front. Plant Sci.*, 6:195. doi: 10.3389/fpls.2015.00195

Bart, R., Ronald, P., & Hake, S. (2006b). Fertility versus disease resistance, a hard choice. *Genes & Develop.*, 20(10), 1215–1217. doi:10.1101/gad.1437706