

LEX E. FLAGEL – C.V.

CONTACT INFORMATION

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EMPLOYMENT

Quantitative Genetics Team Lead Monsanto Company	2015 – Present
Computational Geneticist Monsanto Company	2012 – 2015

EDUCATION, TRAINING, AND FACULTY APPOINTMENTS

Adjunct Professor University of Minnesota – Plant & Microbial Biology Dept.	2014 – Present
NIH-NRSA Postdoctoral Fellowship Duke University	2009 – 2012
Graduate Education Iowa State University, PhD, Genetics	2003 – 2009
Undergraduate Education University of Minnesota-Twin Cities, BS, Science in Agriculture	1998 – 2003

PEER REVIEWED PUBLICATIONS (32)

- Khajuria C., S. Ivashuta, E. Wiggins, **L. Flagel**, W. Moar, M. Pleau, K. Miller, Y. Zhang, P. Ramaseshadri, C. Jiang, T. Hodge, P. Jensen, M. Chen, A. Gowda, B. McNulty, C. Vazquez, R. Bolognesi, J. Haas, G. Head, T. Clark. 2018. Development and characterization of the first dsRNA-resistant insect population from western corn rootworm, *Diabrotica virgifera virgifera* LeConte. *PLoS One* 13: e0197059.
- Flagel L.**, Y.W. Lee, H. Wanjugi, S. Swarup, A. Brown, J. Wang, E. Kraft, J. Greenplate, J. Simmons, N. Adams, Y. Wang, S. Martinelli, J.A. Haas, A. Gowda, G. Head. 2018. Mutational disruption of the *ABCC2* gene in fall armyworm, *Spodoptera frugiperda*, confers resistance to the Cry1Fa and Cry1A.105 insecticidal proteins. 2018. *Scientific Reports* 8: 7255.
- Li L., R. Briskine, R. Schaefer, P.S. Schnable, C.L. Myers, **L.E. Flagel**, N.M. Springer, G.J. Muehlbauer. 2016. Co-expression network analysis of duplicate genes in maize (*Zea mays*, L.) reveals no subgenome bias. *BMC Genomics*, 17: 875.
- McGaugh, S.E., A.M. Bronikowski, C.H. Kuo, D.M. Redding, E.A. Addis, **L.E. Flagel**, F.J. Janzen, and T.S. Schwartz. 2015. Rapid molecular evolution across amniotes of the IIS/TOR network. *PNAS*. 112: 7055-7060.
- Sweigart, A.L. and **L.E. Flagel**. 2015. Evidence of natural selection acting on a polymorphic hybrid incompatibility locus in *Mimulus*. *Genetics*. 199: 543-554.
- Flagel L.E.**, S. Swarup, M. Chen, C. Bauer, H. Wanjugi, M. Carroll, P. Hill, M. Tuscan, R. Bansal, R. Flannagan, T. Clark, A.P. Michel, G.P. Head, and B.S. Goldman. 2015. Genetic markers for Western Corn Rootworm resistance to Bt toxin. *G3*. 5: 399-405.

- Brandvain Y., A Kenney, **L. Flagel**, G. Coop, and A. Sweigart. 2014. Speciation and introgression between *Mimulus nasutus* and *Mimulus guttatus*. *PloS Genetics*. 10: e1004410.
- Flagel L.**, J. Willis, T. Vision. 2014. The standing pool of genomic structural variation in a natural population of *Mimulus guttatus*. *Genome Biology and Evolution*. 6: 53-64.
- Flagel L.**, R. Bansal, R. Kerstetter, M. Chen, M. Carroll, R. Flannagan, T. Clark, B. Goldman, and A. Michel. 2014. Western corn rootworm transcriptome assembly and genomic analysis of population structure. *BMC Genomics*. 15: 195.
- Grover C.E, J.P. Gallagher, E.P. Szadkowski, M.J. Yoo, **L.E. Flagel** and J.F. Wendel. 2012. Homoeolog expression bias and expression level dominance in allopolyploids. *New Phytologist*. 196: 966-971.
- Flagel L.**, J. Wendel, and J. Udall. 2012. Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. *BMC Genomics*: 13: 302.
- Bao Y., G. Hu, **L. Flagel**, A. Salmon, M. Bezanilla, A.H. Paterson, Z. Wang, and J.F. Wendel. 2011. Convergent up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (*Gossypium*). *PNAS*. 108: 21152-21157.
- Rapp R.A., Haigler C.H., **Flagel L.**, Hovav R.H., Udall J.A. and J.F. Wendel. 2010. Gene expression in developing fibers of Upland cotton (*Gossypium hirsutum* L.) was massively altered by domestication. *BMC Biology*. 8: 139.
- MacIntosh G.C., M.S. Hillwig, A. Meyer, and **L. Flagel**. 2010. RNase T2 genes from rice and the evolution of secretory ribonucleases in plants. *Molecular Genetics and Genomics*. 283: 381-396.
- Flagel L.E.** and J.F. Wendel. 2010. Evolutionary rate variation, genomic dominance, and duplicate gene expression evolution during allotetraploid cotton speciation. *New Phytologist*. 186: 184-193.
- Salmon A., **L. Flagel**, B. Ying, J.A. Udall, and J.F. Wendel. 2010. Homoeologous non-reciprocal recombination in polyploid cotton. *New Phytologist*. 186: 123-134.
- Chaudhary B., R. Hovav, **L. Flagel**, R. Mittler, and J.F. Wendel. 2009. Parallel expression evolution of oxidative stress-related genes in fiber from wild and domesticated diploid and polyploid cotton (*Gossypium*). *BMC Genomics*. 10: 378.
- Flagel, L.E.** and J. F. Wendel. 2009. Gene duplication and evolutionary novelty in plants. *New Phytologist*. 183: 557-564.
- Chaudhary B.*, **L. Flagel***, R.M. Stupar, J.A. Udall, N.Verma, N.M. Springer, and J.F. Wendel. 2009. Reciprocal silencing, transcriptional bias and functional divergence of homoeologs in polyploid cotton (*Gossypium*). *Genetics*. 182: 503-517.
[*equal contribution]
- Flagel L.E.**, L. Chen, B. Chaudhary, and J.F. Wendel. 2009. Coordinated and fine-scale control of homoeologous gene expression in allotetraploid cotton. *Journal of Heredity*. 100: 487-490.
- Doyle, J.J., **L.E. Flagel**, A.H. Paterson, R. Rapp, D.E. Soltis, P.S. Soltis, and J.F. Wendel. 2008. Evolutionary genetics of genome merger and doubling in plants. *Annual Review of Genetics*. 42: 443-461.

- Hovav R., B. Chaudhary, J.A. Udall, **L. Flagel**, and J.F. Wendel. 2008. Parallel domestication, convergent evolution and duplicated gene recruitment in allopolyploid cotton. *Genetics*. 179: 1725-1733.
- Flagel L.E.**, R.A. Rapp, C.E. Grover, M.P. Widrlechner, J. Hawkins, J.L. Grafenberg, I. Álvarez, G.Y. Chung, and J.F. Wendel. 2008. Phylogenetic, morphological, and chemotaxonomic incongruence in the North American endemic genus *Echinacea*. *American Journal of Botany*. 95: 756-765.
- Hovav R., J.A. Udall, B. Chaudhary, R. Rapp, **L. Flagel**, and J.F. Wendel. 2008. Partitioned expression of duplicated genes during development and evolution of a single cell in a polyploid plant. *PNAS*. 105: 6191-6195.
- Flagel L.**, J. Udall, D. Nettleton, and J. Wendel. 2008. Duplicate gene expression in allopolyploid *Gossypium* reveals two temporally distinct phases of expression evolution. *BMC Biology*. 6: 16.
- Hovav R., J.A. Udall, B. Chaudhary, E. Hovav, **L. Flagel**, G. Hu, and J.F. Wendel. 2008. The evolution of spinnable cotton fiber entailed prolonged development and a novel metabolism. *PLoS Genetics*. 4: e25.
- Hovav R., Udall J.A., E. Hovav, R. Rapp, **L. Flagel**, and J.F. Wendel. 2008. A majority of cotton genes are expressed in single-celled fiber. *Planta*. 227: 319-329.
- Udall J.A., **L.E. Flagel**, F. Cheung, A.W. Woodward, R. Hovav, R.A. Rapp, J.M. Swanson, J.J. Lee, A.R. Gingle, D. Nettleton, C.D. Town, Z.J. Chen, and J.F. Wendel. 2007. Spotted cotton oligonucleotide microarrays for gene expression analysis. *BMC Genomics*. 8: 81.
- Senchina D.S., **L.E. Flagel**, J.F. Wendel, and M.L. Kohut. 2006. Phenetic comparison of seven *Echinacea* species based on immunomodulatory characteristics. *Economic Botany*. 60: 205-211.
- Flagel L.**, J.R. Christensen, C.D. Gustus, K.P. Smith, P.M. Olhoft, D.A. Somers and P.D. Matthews. 2005. Inexpensive, high throughput microplate format for plant nucleic acid extraction. *Crop Science*. 45: 1985-1989.
- Olhoft P.M., **L.E. Flagel**, and D.A. Somers. 2004. T-DNA locus structure in a large population of soybean plants transformed using the *Agrobacterium*-mediated cotyledonary-node method. *Plant Biotechnology Journal*, 2: 289-300.
- Olhoft P.M., **L.E. Flagel**, C.M. Donovan, and D.A. Somers. 2003. Efficient soybean transformation using hygromycin B selection in the cotyledonary-node method. *Planta*. 216: 723-735.

BOOK CHAPTERS (3)

- Flagel L.**, and B. Blackman. 2012. The first ten years of plant genome sequencing and prospects for the next decade. In Wendel J.F. (Ed.). *Plant Genome Diversity (Vol 1: Molecular Biology and Evolution)*, New York, NY, Springer.
- Wendel J.F., **L.E. Flagel**, and K.L. Adams. 2012. Jeans, genes, and genomes: cotton as a model for studying polyploidy. Soltis P. and D. Soltis (Eds.). *Polyploidy and Genome Evolution*, Heidelberg, Springer.
- Adams K.L., **L. Flagel**, and J.F. Wendel. 2009. Responses of the cotton genome to polyploidy. In: Paterson A.H. (Ed.). *Genetics and Genomics of Cotton (Plant Genetics and Genomics: Crops and Models, Vol. 3)*. New York, NY, Springer.

PATENTS (2 PENDING)

Beattie, Crawford, Eads, **Flagel**, Kapoor, Taylor. 2015. Compositions and Methods for Controlling *Leptinotarsa*. US 20150240258

Baum, Bolognesi, **Flagel**, Segers. 2016. Compositions and Methods for Controlling *Diabrotica*. US 20160230185

INVITED LECTURES (15)

St. Olaf University, Biology Department	2015
Plant & Animal Genome, San Diego, CA	2015
SIVB Conference, Savannah, GA	2014
University of Arkansas, Biology	2013
University of Minnesota, Plant Biology	2013
Cal Poly Pomona, Biological Sciences Department	2012
BASF Plant Science, RNA/DNA Technology Group	2012
University of Connecticut, Dept. of Ecology and Evolutionary Biology	2012
West Virginia University, Department of Biology	2012
Monsanto Company, Computational Biology Group	2011
Victorian Dept. of Primary Industries, Australia (Plenary Speaker)	2011
North Carolina State University, Department of Plant Biology	2010
Duke University, Department of Biology	2009
UC Davis, Genome Center	2008
Plant & Animal Genome, San Diego, CA	2008

ABSTRACTS PRESENTED AT CONFERENCES (17)

Flagel L. The genetic architecture of western corn rootworm resistance to the Cry3Bb1 Bt Protein. Plant and Animal Genome. 2015. San Diego, CA.

Flagel L., R. Bansal, R. Kerstetter, M. Chen, M. Carroll, R. Flannagan, T. Clark, B. Goldman, and A. Michel. Western corn rootworm transcriptome assembly and genomic analysis of population structure. International working group on *Ostrinia* and other maize pests 2014. Chicago, IL.

Michael, T.P., **L. Flagel**, S-P. Yang, P. Latreille, Z. Du, R. Bolognesi, M. Chen, N. Juarez-Jimenez, R. Flannagan, B. Goldman, and R. Kerstetter. Building a genomic toolbox for the “billion dollar bug” Western Corn Rootworm. Plant and Animal Genome. 2013. San Diego, CA.

Flagel L. and T. Vision. Genomic structural variation in a natural population of the plant *Mimulus guttatus*. Evolution 2011. Norman, OK.

Flagel L. and J.H. Willis. Leveraging the monkeyflower genome to understand adaptive salt tolerance. Plant and Animal Genome. 2011. San Diego, CA.

Flagel L., B. Chaudhary, J. Udall, and J. Wendel. Evolution of homoeolog expression in allotetraploid cotton. Plant and Animal Genome. 2009. San Diego, CA.

Flagel L., J.A. Udall, D. Nettleton, and J.F. Wendel. Expression evolution in genes duplicated by recent polyploidy in cotton (*Gossypium*). Botany 2008. Vancouver, BC.

- Flagel L.E.**, J.A. Udall, D. Nettleton, and J.F. Wendel. Duplicate gene expression evolution in polyploid cotton. *Evolution* 2008. Minneapolis, MN.
- Flagel L.** Duplicate gene expression evolution in cotton. *Plant and Animal Genome*. 2008. San Diego, CA.
Recording available online: <http://tinyurl.com/6dt5ok>
- McGaugh S. and **L. Flagel**. Amino acid carbon content and usage is negatively correlated and related to essential-nonessential classification. *American Genetic Association Annual Symposium: Mechanisms of Genome Evolution*. 2007. Bloomington, IN.
- Flagel L.**, J.A. Udall, D. Nettleton, and J.F. Wendel. Systematic analysis of duplicate gene expression evolution in cotton. *American Genetic Association Annual Symposium: Mechanisms of Genome Evolution*. 2007. Bloomington, IN.
- Wendel J.F., R. Rapp, **L. Flagel**, and R. Hovav. Polyploidy, domestication, and fiber evolution in *Gossypium*. *The International Conference on Polyploidy, Heterosis, and Epigenetics* 2007. 2007. Beijing, China.
- Flagel L.**, J.A. Udall, D. Nettleton, and J.F. Wendel. Systematic analysis of duplicate gene expression evolution in cotton. *Plant and Animal Genome XV*. 2007. San Diego, CA.
- Flagel L.E.**, P.M. Olhoft, and D.A. Somers. Characterization of T-DNA insertions in transgenic soybean progeny. *Impress the President Day*, University of Minnesota. 2003. Minneapolis, MN.
- Olhoft P.M., **L.E. Flagel**, C.M. Donovan, and D.A. Somers. *Agrobacterium*-mediated transformation of soybean using the cotyledonary-node method. *Ninth Biennial Conference of the Cellular and Molecular Biology of the Soybean*. 2002. Urbana-Champaign, IL.
- Olhoft P.M., **L.E. Flagel**, C.M. Donovan, and D.A. Somers. Improvements in soybean transformation using the *Agrobacterium*-mediated cotyledonary-node method. *Tenth International Association for Plant Tissue Culture & Biotechnology*. 2002. Orlando, FL.
- Flagel L.E.**, P.M. Olhoft, and D.A. Somers. Characterization of T-DNA insertions in T0 and T1 progenies of transgenic soybean. *First International Conference on Legume Genomics and Genetics*. 2002. Minneapolis, MN.
- Christenson J.R, C.D. Gustus, **L.E. Flagel**, P.D. Matthews, and D.A. Somers. Cheap but not dirty! High throughput 96-well format plant genomic DNA extraction -- suitable for restriction digestion, Southern analysis, and PCR. *New York Area Plant Molecular Biology Meeting*. 2002. Rutgers University, New Brunswick, NJ.

GRANTS, FELLOWSHIPS, AND AWARDS

Monsanto Science Fellow	2016 – Present
Iowa State University CALS Young Alum of the Month	July – 2014
National Research Service Award Postdoctoral Fellowship US National Institutes of Health	2010 – 2013
Graduate Thesis Research Excellence Award (top 10%) Iowa State University	2009
Plant Sciences Institute Graduate Fellowship Iowa State University	2003 – 2007
Eloise Van Slyke Scholarship University of Minnesota	2000 – 2001

SERVICE AND OUTREACH

Chaired the Society for the Study of Evolution Diverse Careers Workshop 2016-2017

Wrote a proposal to acquire funding and then led a group that hosted a careers workshop for 60 graduate students and postdocs attending the Evolution conference.

Participated in the filming of *Secrets of Plant Genomes Revealed!*

A movie produced by NSF to get middle and high school students interested in plant genomics.