

JEFFREY B. ENDELMAN
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<http://potatobreeding.cals.wisc.edu>

APPOINTMENTS

2013–Present Assistant Professor, Potato Breeding & Genetics
 Department of Horticulture
 Plant Breeding and Plant Genetics Graduate Program
 University of Wisconsin, Madison

2011–2013 Postdoctoral Researcher, Cornell University & USDA-ARS, Ithaca, NY

EDUCATION

PhD Crop Science, 2011. Washington State University, Pullman, WA.
 Thesis: Advances in barley genomics: Association analysis, breeding values, and consensus mapping

MS Plant Science, 2009. Utah State University, Logan, UT.
 Thesis: Optimal compost rates for organic crop production based on a decay series

PhD Bioengineering, 2005. California Institute of Technology, Pasadena, CA.
 Thesis: Design and analysis of combinatorial protein libraries created by site-directed recombination

MA Physics, 2002. University of California, Santa Barbara, CA.

BS Chemical Engineering & Applied Math, 2000. Northwestern University, Evanston, IL.

AWARDS

2017 Researcher of the Year, Wisconsin Potato and Vegetable Growers Association
2014 Elton and Carrie Aberle Faculty Fellow Award
2005 Caltech Demetriades-Tsafka Prize for Best Thesis in Bioengineering

TEACHING

Hort/Agron 360 Genetically Modified Crops: Science, Regulation & Controversy (Spring)
Hort/Agron 875 Genetic Analysis with R (Spring, Odd Years)
Hort/Agron 875 Polyploid Genetics (Spring, Even Years)
Agron/Hort 812 Selection Theory for Quantitative Traits in Plants (Spring, Even Years)
Served on 13 graduate student committees, including 3 as major professor

GRANTS

PD/co-PD on extramural grants totaling \$3.3 million since 2013

INVITED TALKS

Dept. Soil and Crop Sciences, Colorado State University. March 30, 2017. *Improving selection in potato breeding with genome-wide markers.*

International Conference on Selection Theory and Breeding Methodology, Freising, Germany. March 24, 2017. *Improving selection in potato breeding.*

Dept. Plant Breeding, Wageningen University, The Netherlands. Nov 16, 2016. *Automated tetraploid genotype calling and its application to pedigree reconstruction in potato.*

100th Annual Meeting of the Potato Association of America, Grand Rapids, MI. Aug. 1, 2016. *Genome-wide prediction of complex traits in tetraploid potato: Empirical results and implications for breeding.*

Plant Breeding Symposium, Texas A&M University. Sept. 3, 2015. *Genomic selection: Using pedigrees and genome-wide markers to maximize genetic gain.*

Plant Breeding and Genetics Symposium, University of Nebraska-Lincoln. April 1, 2014. *Genome-wide selection with the realized relationship matrix.*

4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement, ICRISAT, Hyderabad, India. Feb. 21, 2014. *LPmerge: an R package for merging genetic maps by linear programming.*

SOFTWARE (available at <http://potatobreeding.cals.wisc.edu/software>)

rrBLUP: Ridge regression and other kernels for genomic selection.

GWASpoly: Genome-wide association studies for autopolyploids.

LPmerge: Merging linkage maps by linear programming.

ClusterCall: Genotype assignment for autotetraploids.

VARIETY DEVELOPMENT

Co-inventor for 9 potato varieties that have been licensed for commercial development

Foundation seed of 5 potato varieties released since 2013, with 176 acres of certified seed in 2016

SERVICE

Editorial Board Member for *Crop Science* (2016 –), *Theoretical and Applied Genetics* (2016 –)

Reviewer for *Plant Genome*, *Genetics*, *G3*, *Am. J. Potato Research*, *PLOS ONE*

Chair of the Breeding & Genetics Section, Potato Association of America, 2015–16

REFEREED PUBLICATIONS (last four years)

- Braun SR, Endelman JB, Haynes K, Jansky S (2017) Quantitative trait loci for resistance to common scab and cold-induced sweetening in diploid potato. *Plant Genome*. doi: 10.3835/plantgenome2016.10.0110
- Wang Y, Snodgrass LB, Bethke PC, Bussan AJ, Holm DG, Novy RG, Pavek MJ, Porter GA, Rosen CJ, Sathuvalli V, Thompson AL, Thornton MT, Endelman JB (2017) Reliability of measurement and genotype x environment interaction for potato specific gravity. *Crop Science* 57:1–7. doi:10.2135/cropsci2016.12.0976
- Schmitz Carley CA, Coombs JJ, Douches DS, Bethke PC, Palta JP, Novy RG, Endelman JB (2017) Automated tetraploid genotype calling by hierarchical clustering. *Theoretical & Applied Genetics* 130:717–726.
- Endelman JB, Schmitz Carley CA, Douches DS, Coombs JJ, Bizimungu B, De Jong WS, Haynes KG, Holm DG, Miller JC, Novy RG, Palta JP, Parish DL, Porter DA, Sathuvalli VR, Thompson AL, Yencho GC (2017) Pedigree reconstruction with genome-wide markers in potato. *American Journal of Potato Research* 94:184–190.
- Endelman JB, Jansky SH (2016) Genetic mapping with an inbred line-derived F2 population in potato. *Theoretical & Applied Genetics* 129:935–943.
- Rosyara UR, De Jong WS, Douches DS, Endelman JB (2016) Software for genome-wide association studies in autopolyploids and its application to potato. *Plant Genome* 9, doi:10.3835/plantgenome2015.08.0073
- Wang Y, Bethke PC, Bussan AJ, Glynn MT, Holm DG, Navarro FM, Novy RG, Palta JP, Pavek MJ, Porter GA, Sathuvalli VR, Thompson AL, Voglewede PJ, Whitworth JL, Parish DL, Endelman JB (2016) Acrylamide-forming potential and agronomic properties of elite U.S. potato germplasm from the National Fry Processing Trial. *Crop Science* 56:30–39.
- Olsen DJR, Endelman JB, Jacobson AR, Reeve JR (2015) Compost carryover: Nitrogen, phosphorus and FT-IR analysis of soil organic matter. *Nutrient Cycling in Agroecosystems* 101:317–331.
- Sallam AH, Endelman JB, Jannink J-L, Smith KP (2015) Assessing genomic selection prediction accuracy in a dynamic barley breeding program. *Plant Genome* 8, doi:10.3835/plantgenome2014.05.0020.
- Mohammadi M, Endelman J, Nair S, Chao S, Jones SS, Muehlbauer GJ, Ullrich SE, Baik B-K, Wise ML, Smith KP (2014) Association mapping of grain hardness, polyphenol oxidase, total phenolics, amylose content, and beta-glucan in US barley breeding germplasm. *Molecular Breeding* 34:1229–1243.
- Muñoz-Amatriaín M, Cuesta-Marcos A, Endelman JB, Comadran J, Bonman M, Bockelman H, Chao S, Russell J, Waugh R, Hayes PM, Muehlbauer GJ (2014) The USDA barley core collection: Genetic diversity, population structure, and potential for genome-wide association studies. *PLoS ONE* 9(4):e94688.
- Plomion C, Chancerel E, Endelman J, Lamy J-B, Mandrou E, Lesur I, Ehrenmann F, Isik F, Bink M, van heerwaarden J, Bouffier L (2014) Genome-wide distribution of genetic diversity and linkage disequilibrium in a mass-selected population of maritime pine. *BMC Genomics* 15:171.

Endelman JB, Plomion C (2014) LPmerge: an R package for merging genetic maps by linear programming. *Bioinformatics* 30:1623–1624.

Endelman JB, Atlin GN, Beyene Y, Semagn K, Zhang X, Sorrells ME, Jannink J-L (2014) Optimal design of preliminary yield trials with genome-wide markers. *Crop Science* 54:48–59.

Dawson JC, Endelman JB, Heslot N, Crossa J, Poland J, Dreisigacker S, Manes Y, Sorrells ME, Jannink J-L (2013) The use of unbalanced historical data for genomic selection in an international wheat breeding program. *Field Crops Research* 154:12-22.

Riedelsheimer C, Endelman JB, Stange M, Sorrells ME, Jannink J-L, Melchinger AE (2013) Genomic predictability of interconnected biparental maize populations. *Genetics* 194:493–503.