CALIFORNIA

Karban, R., 2015. Plant sensing and communication. University of Chicago Press.

Orrock, J.L., Sih, A., Ferrari, M.C., Karban, R., Preisser, E.L., Sheriff, M.J. and Thaler, J.S., 2015. Error management in plant allocation to herbivore defense. Trends in ecology & evolution, 30(8):441-44

Shiojiri, K., Ishizaki, S., Ozawa, R. and Karban, R., 2015. Airborne Signals of Communication in Sagebrush: A Pharmacological Approach. Plant signaling & behavior.

KANSAS

Aiken, R., Baltensperger, D., Krall, J., Pavlista, A., Johnson, J. 2015. Planting methods affect emergence, flowering and yield of spring oilseed crops in the US central High Plains. Industrial Crops and Products. 69:273-277

Stamm, M., Cramer, G., Dooley, S.J., Holman, J.D., Phillips, D., Rife, C.L., Santra, D.K. 2015. Registration of ‘Griffin’ Winter Canola. J. Plant. Reg. 9(2):144-148

ILLINOIS

# Clark, L.V., Stewart, J.R., Nishiwaki, A., Toma, Y., Kjeldsen, J.B., Jorgensen, U., Zhao, H., Peng, J., Yoo, J.H., Heo, K., Yu, C.Y., Yamada, T., Sacks, E.J. 2015. Genetic structure of Miscanthus sinensis and Miscanthus sacchariflorus in Japan indicates a gradient of bidirectional but asymmetric introgression*.* JExp. Bot. 66(14):4213-4225. DOI: 10.1093/jxb/eru511

Głowacka, K., Jørgensen, U., Kjeldsen, J.B., Kørup, K., Spitz, I., Sacks, E.J., Long, S.P. 2015. Can the exceptional chilling tolerance of C4 photosynthesis found in Miscanthus× giganteus be exceeded? Screening of a novel Miscanthus Japanese germplasm collection. Annals of Botany. 115(6):981-990

Nagano, H., Clark, L.V., Zhao, H., Peng, J., Yoo, J.H., Heo, K., Yu, C.Y., Anzoua, K.G., Matsuo, T., Sacks, E.J., Yamada, T. 2015. Contrasting allelic distribution of CO/Hd1 homologues in Miscanthus sinensis from the East Asian mainland and the Japanese archipelago. J Exp Botany. p.292

Tamura, K.I., Sanada, Y., Shoji, A., Okumura, K., Uwatoko, N., Anzoua, K.G., Sacks, E.J., Yamada, T. 2015. DNA markers for identifying interspecific hybrids between Miscanthus sacchariflorus and Miscanthus sinensis. Grassland Science. 61(3):160-166

Yamada, T., Nagano, H., Dwiyanti, M.S., Clark, L.V., Sacks, E.J. 2015. Candidate Gene Approach in Miscanthus spp. for Biorefinery. In Molecular Breeding of Forage and Turf: Springer International Publishing. p. 85-92

INDIANA

Janick, J. 2015. Luther Burbank: Plant breeding artist, horticulturist, and legend. HortScience. 50(2):153-156

Janick, J. 2015. Nikolai Ivanovich Vavilov: Plant geographer, geneticist, martyr of science. HortScience, 50(6):772-776

Whipkey, A., Kalbaugh, K., Franz, A., Janick, J. 2014. A Database for Three Dioscoridean Illustrated Herbals. HortScience. 49(7):977-979

IOWA

Aleliūnas, A., Jonavičienė, K., Statkevičiūtė, G., Vaitiekūnaitė, D., Kemešytė, V., Lübberstedt, T., Brazauskas, G. 2014. Association of single nucleotide polymorphisms in *LpIRI1* gene with freezing tolerance traits in perennial ryegrass. Euphytica. 204(3):523-534

Ding, H., Qin, C., Luo, X., Li, L., Chen, Z., Liu, H., Gao,J., Lin, H., Shen, Y., Zhao, M., Lübberstedt, T., Zhang, Z., Pan, G. 2014. Heterosis in Early Maize Ear Inflorescence Development: A Genome-Wide Transcription Analysis for Two Maize Inbred Lines and Their Hybrid. Int. J. Mol. Sci. 15(8):13892-13915. DOI: 10.3390/ijms150813892

Jeffrey, B., Nettleton, D., Kuzhiyil, N., Rover, M., Brown, R.C., Lamkey, K. and Lübberstedt, T., 2014. Significant variation for bio-oil compounds after pyrolysis/gas chromatography–mass spectrometry of cobs and stover among five near-isogenic brown midrib hybrids in maize. *BioEnergy Research. 7*(2): 693-701

Li L., Hur, M., Lee, J., Zhou, W., Song, Z., Ransom, N., Demirkale, C.Y., Nettleton, D., Westgate, M., Arendsee, Z., Iyer, V., Shanks, J., Nikolau, B., Wurtele, E.S. 2015. A systems biology approach toward understanding seed composition in soybean. BMC Genomics. 201516(Suppl 3):S9. DOI:10.1186/1471-2164-16-S3-S9

Lübberstedt, T. 2014. Significant Variation for Bio-oil Compounds After Pyrolysis/Gas Chromatography-Mass Spectrometry of Cobs and Stover Among Five Near-Isogenic Brown Midrib Hybrids in Maize. BioEnergy Research. 7(2):693-701

Kumar, B., Abdel-Ghani, A.H., Pace, J., Reyes-Matamoros, J., Hochholdinger, F., Lübberstedt, T. 2014. Association analysis of single nucleotide polymorphisms in candidate genes with root traits in maize (Zea mays L.) seedlings. Plant Sci. 224:9-19. ISSN 0168-9452. http://dx.doi.org/10.1016/j.plantsci.2014.03.019

Mantilla Perez, M., Zhao, J., Yin, Y., Hu, J., Salas Fernandez, M.G. 2014. Association mapping of brassinosteroid candidate genes and plant architecture in a diverse panel of *Sorghum bicolor*. Theor and Appl Gen. 127(12):2645-2662

Pace, J., Gardner, C., Romay, C., Ganapathysubramanian, B. and Lübberstedt, T., 2015. Genome-wide association analysis of seedling root development in maize (Zea mays L.) BMC Genomics. 16(1):1 **DOI:** 10.1186/s12864-015-1226-9

Pace J., Lee, N., Naik, H.S., Ganapathysubramanian, B., Lübberstedt, T. 2014. Analysis of Maize (Zea mays L.) Analysis of maize (Zea mays L.) seedling roots with the high-throughput image analysis tool ARIA (Automatic Root Image Analysis). PLoS ONE. 9(9):e108255. DOI: 10.1371/journal.pone.0108255

Poeta, F.B., Rotundo, J. L., Borrás, L., Westgate, M.E. 2014. Seed Water Concentration and Accumulation of Protein and Oil in Soybean Seeds. Crop Sci. 54:2752-2759. DOI: 10.2135/cropsci2014.03.0204

Salas Fernandez, M.G., Okeno, J.A., Mutegi, E., Fessehaie, A., Chalfant, S. 2014. Assessment of genetic diversity among sorghum landraces and their wild/weedy relatives in western Kenya using simple sequence repeat (SSR) markers. Conservation Genetics. 15(6):1269-1280

Salas Fernandez,M.G., Strand, K., Hamblin, M.T., Westgate, M, Heaton, E., Kresovich, S. 2014. Genetic analysis and phenotypic characterization of leaf photosynthetic capacity in a sorghum (*Sorghum* spp.) diversity panel. Genetic Resources and Crop Evolution. 62(6):939-950

## Sebuwufu, G., Mazur, R., Ugen, M., and Westgate, M. 2015. Using improved varieties and fertility enhancements for increasing yield of common beans (Phaseolus vulgaris L.) grown by small-landholder farmers in Uganda. J of African Agri Res. 10(52):4795-4805. DOI: 10.5897/AJAR2015.9638. ISSN: 1991-637X

MICHIGAN

Akond, M., Liu, S., Kantartzi, S.K, Meksem, K., Bellaloui, N., Lightfoot, D.A., Yuan J, Wang, D., Anderson, J., Kassem, M.A. 2015. A SNP genetic linkage map based on the ‘Hamilton’ by ‘Spenser’ recombinant inbred line population identified QTL for seed isoflavone contents in soybean. Plant Breeding DOI: 10.1111/pbr.12298.

Akond, M., Liu, S., Kantartzi, S.K., Meksem, K., Bellaloui, M., Lightfoot, D.A., Yuan, J., Wang, D., Kassem, M.A. 2015. Quantitative trait loci underlying seed sugars content in “MD96-7522” by “Spencer” recombinant inbred line population of soybean. Food and Nutrition Sciences. DOI: 10.4236/fns.2015.611100.

Ando, K., Carr, K.M., Colle, M., Mansfeld, B.N., Grumet, R. 2015. Exocarp properties and transcriptomic analysis of cucumber (*Cucumis sativus)* fruit expressing age-related resistance to *Phytophthora capsici*. PloS One 10: e0142133, doi:10.1371/journal.pone.0142133.

Bamberg, J., del Rio, A., Coombs, J., & Douches, D. (2015). Assessing SNPs Versus RAPDs for Predicting Heterogeneity and Screening Efficiency in Wild Potato (Solanum) Species. Amer. J. Potato Res. 92: 276-283.

Bedewitz, M.A., Góngora-Castillo, E.,  Uebler, J.B., Gonzales-Vigil, E., Wiegert-Rininger, K.E., Childs, K.L., Hamilton, J.P., Vaillancourt, B., Yeo, Y.S., Chappell, J., DellaPenna, D., Jones, A.D., Buell, C.R., Barry, C.S. 2014 A root-expressed L-phenylalanine:4-hydroxyphenylpyruvate aminotransferase is required for tropane alkaloid biosynthesis in *Atropa belladonna*. Plant Cell 26: 3745-3762.

Chavoshi, M., Watkins, C., Oraguzie, B., Zhao, Y., Iezzoni, A., Oraguzie, N. 2014. Phenotyping Protocol for Sweet Cherry (*Prunus avium* L.) to Facilitate an Understanding of Trait Inheritance. Am Pomological Soc. 68(3):125-34

Cichy, K.A., A. Fernandez,  A. Kilian, J.D. Kelly, C.H. Galeano, S. Shaw, M. Brick, D. Hodkinson and E. Troxtell. 2014. QTL analysis of canning quality and color retention in black beans (Phaseolus vulgaris L.). Molecular Breeding 33:139-154.

Guo, Y.,  Wiegert-Rininger, K.E., Vallejo, V.A., Barry, C.S., Warner, R.M. 2015 Transcriptome-enabled marker discovery and mapping of plastochron-related genes in *Petunia* spp. BMC Genomics 16: 726

Hardigan, M.A., Bamberg, J., Buell, C.R., Douches, D.S. 2015. Taxonomy and genetic differentiation among wild and cultivated germplasm of *Solanum* sect. *Petota*. The Plant Genome 8:1-16

King, Z.R., Harris, D.K., Pedley, K.F., Song, Q., Wang, D, Wen Z., Buck JW, Li Z, Boerma, R.H. A novel *Phakopsora pachyrhizi* resistance allee (Rpp) contributed by PI 567068A. Theor Appl GenetiDOI 10.1007/s00122-015-2645-3

Massa, A. N., Manrique-Carpintero, N. C., Coombs, J. J., Zarka, D. G., Boone, A. E., Kirk, W. W., Hackeyy, C.A., Bryan, G.J, Douches, D. S. (2015). Genetic linkage mapping of economically important traits in cultivated tetraploid potato (*Solanum tuberosum* L.). [G3: Genes| Genomes| Genetics 5(11): 2357-2364](http://potatobg.css.msu.edu/Publications/Journal%20Publications/GeneticLinkageMappingofEcon_2015.pdf).

Naegele, R.P., Tomlinson, A.J., and Hausbeck, M.K.  2015.  Evaluation of a diverse, worldwide collection of wild, cultivated and landrace peppers (*Capsicum annuum*) for resistance to *Phytophthora* fruit rot, genetic diversity and population structure. Phytopathology 105: 110-118.

Rosyara, U.R., Sebolt, A.M., Peace, C., Iezzoni, A.F. 2014. Identification of the Paternal Parent of ‘Bing’ Sweet Cherry and Confirmation of Descendants Using Single Nucleotide Polymorphism Markers. J Am Soc Hort Sci. 139(2):148-156

Rubinstein, M., Katzenellenbogen, M., Eshed, R., Rozen, A., Katzir, N., Colle, M., Yang, L., Grumet, R., Weng, Y., Sherman, A., Ophir, R.. 2015. Ultra high-density linkage map for cultivated cucumber using a single nucleotide polymorphism genotyping array. PLoS One 10:e0124101.

Stegmeir, T., Cai, L., Basundari, F.R., Sebolt, A.M., Iezzoni, A.F. 2015. A DNA test for fruit flesh color in tetraploid sour cherry (*Prunus cerasus* L.). Molecular Breeding. 35(7):1-10

Stegmeir, T., Sebolt, A., Iezzoni, A. 2014. Phenotyping Protocol for Sour Cherry (Prunus cerasus L.) to Enable a Better Understanding of Trait Inheritance. J Am Pomological Soc. 68(1):40-47

Vallejo, V.A/, Tychonievich, J., Lin, W.-K., Wangchu, L., Barry, C.S., Warner, R.M. 2015 Identification of QTL for crop timing and quality traits in an interspecific Petunia population. Molecular Breeding 35: 2 DOI 10.1007/s11032-015-0218-4.

Wen, Z., Boyse, J.F., Song, Q., Cregan, P.B., and Wang, D., 2015. Genomic consequences of selection and genome-wide associate mapping in soybean. BMC Genomics DOI: 10.1186/s12864-015-1872-y

Weng Y, Colle M, Wang YH, Yang LM, Rubinstein M, Sherman A, Ophir R, Grumet R. 2015. QTL mapping in multiple populations and development stages reveals dynamic quantitative trait loci for fruit size in cucumbers of different market classes. Theor Applied Genetics 128:1747-1763.

MINNESOTA

Bao, Y., Vuong, T., Meinhardt, C., Tiffin, P., Denny, R., Chen, S., Nguyen, H.T., Orf, J.H., Young, N.D. 2014. Potential of association mapping and genomic selection to explore PI 88788 derived soybean cyst nematode resistance. The Plant Genome. *7*(3)

Bolon, Y.T., Stec, A.O., Michno, J.M., Roessler, J., Bhaskar, P.B., Ries, L., Dobbels, A.A., Campbell, B.W., Young, N.P., Anderson, J.E., Grant, D.M. 2014. Genome resilience and prevalence of segmental duplications following fast neutron irradiation of soybean. Genetics. 198(3):967-981

Campbell, B.W., Mani, D., Curtin, S.J., Slattery, R.A., Michno, J.M., Ort, D.R., Schaus, P.J., Palmer, R.G., Orf, J.H., Stupar, R.M. 2015. Identical Substitutions in Magnesium Chelatase Paralogs Result in Chlorophyll-Deficient Soybean Mutants. G3: Genes| Genomes| Genetics. 5(1):123-131

Lian, L., Wang, F., Denny, R.L., Orf, J.H., Young, N.D., Chen, S. 2014. Soybean Cyst Nematode Resistance in PI 567516C SOYBEAN: A Promising New Source of Resistance. J of Nematology. Marceline, MO Soc Nematologists. 46(2):193

Lin, R., Glazebrook, J., Katagiri, F., Orf, J.H., Gibson, S.I. 2015. Identification of differentially expressed genes between developing seeds of different soybean cultivars. Genomics data. 6:92-98

MISSOURI

Hirsch, C.N., Flint-Garcia, S.A., Beissinger, T.M., Eichten, W.R., Deshpande, S., Barry, K., McMullen, M.D., Holland, J.B., Buckler, E.S., Springer, N., Buell, C.R., de Leon, N., Kaeppler, S.M. 2014. Insights into the Effects of Long-Term Artificial Selection on Seed Size in Maize. Genetics. 198(1):409-421. DOI: 10.1534/genetics.114.167155

# [Venkatesh](http://pubs.acs.org/author/Venkatesh%2C%2BTyamagondlu%2BV), T.V., Harrigan, G.G., [Perez](http://pubs.acs.org/author/Perez%2C%2BTim), T., [Flint-Garcia](http://pubs.acs.org/author/Flint-Garcia%2C%2BSherry),S. 2015.Compositional Assessments of Key Maize Populations: B73 Hybrids of the Nested Association Mapping Founder Lines and Diverse Landrace Inbred Lines. J. Agric. Food Chem. 63(21):5282-5295. DOI: 10.1021/acs.jafc.5b00208

NEBRASKA

Santra, D.K., Heyduck, R.F., Baltensperger, D.D., Graybosch, R.A., Nelson, L.A., Frickel, G., Nielsen, E. 2015. Registration of ‘Plateau’ waxy (amylose-free) proso millet. J. Plant. Reg. 9(1):41-43. DOI: 10.3198/jpr2013.11.0067crc

Vogel, K.P., Mitchell, R.B., Waldron, B.L., Haferkamp, M.R., Berdahl, J.D., Baltensperger, D.D., Erickson, G., Klopfenstein, T.J. 2015. Registration of ‘Newell’ Smooth Bromegrass. J. Plant. Reg. 9(1):35-40

Pavlista, A.D., Baltensperger,D.D., Santra, D.K., Hergert, G.W., Knox, S. 2014. Gibberellic Acid Promotes Early Growth of Winter Wheat and Rye. 2014. Am J of Plant Sci. 5(20):2984 DOI:10.4236/ajps.2014.520315

NEBRASKA, KANSAS, COLORADO, WYOMING

Aiken, R., Baltensperger, D., Krall, J., Pavlista, A., Johnson, J. 2015. Planting methods affect emergence, flowering and yield of spring oilseed crops in the US central High Plains. Industrial Crops and Products. 69:273-277

NORTH DAKOTA

Baasandorj, T., J.B. Ohm, S. Simsek. 2015. Effect of dark, hard, and vitreous kernel content on protein molecular weight distribution and on milling and breadmaking quality characteristics for hard spring wheat samples from diverse growing regions. Cereal Chemistry. 92:570-577.

Bari, M.A.A., and M.J. Carena. 2015. Can Expired Proprietary Maize (Zea mays L.) Industry Lines be Useful for Short-Season Breeding Programs? II. Agronomic Traits. Euphytica 207:69-77.

Elias E.M., F.A. Manthey, and W. AbuHammad. 2015. Registration of ‘Carpio’ Durum Wheat. J. Plant Reg. 9:78–82.

Gilbertson, P.K., Berti, M.T., Johnson, B.L. 2014. Borage cardinal germination temperatures and seed development. Industrial Crops and Products. 59:202-209

Gesch, R.W., Archer, D.W., Berti, M.T. 2014. Dual cropping winter camelina with soybean in the Northern Corn Belt. Agronomy J. 106(5):1735-1745

Helms, T.C., B.D. Nelson, and K.C. Chang. 2015. Registration of ‘ND1406HP’ soybean. J. Plant Reg. 9:315-317.

Johnson, B.L., B.K. Hanson, A. Hermann, M.T. Berti, and P.J. Petersen. 2015. Screening industrial hemp varieties for adaptation in North Dakota. In Proc. 27th Annual Meeting of AAIC. Oct. 18-22, 2015 Overton Hotel and Conference Center Lubbock, TX.

Johnson, B.L., M.T. Berti, S. Dash, P.K. Gilbertson, K. Sahu, and P.J. Petersen. 2015. Screening new crops for adaptation promotes agricultural sustainability. 2015. In Proc. 2nd Intl. Conf. on Sustainable Agriculture and Environment. Sept. 30-Oct. 3, Selcuk University, Konya, Turkey.

Kuruc, J. A., P. Schwarz, and C. Wolf-Hall. Ochratoxin A in stored US barley and wheat. J. Food Protection. 78(3): 597-601, 2015.

Samarappuli, D.P., Johnson, B.L., Kandel, H., Berti, M.T. 2014. Biomass yield and nitrogen content of annual energy/forage crops preceded by cover crops. Field Crops Research. 167:31-39

NEW YORK

Sen, S., M.E. Smith, and T.L. Setter.  2015.  Effect of low nitrogen stress on various shoot traits of maize (*Zea mays* L.).  International Journal of Modern Botany 5(1):18-22

Kear, P., G. Zeigler, O. Hoekenga, M.E. Smith, and I. Baxter. 2014. Identification of maize grain Fe and Zn homeostasis-associated QTL in two mapping populations. Poster No. 757. ASA/CSSA/SSSA International Annual Meeting, 2-5 November 2014, Long Beach CA. <https://scisoc.confex.com/scisoc/2014am/webprogram/Paper87818.html>

Palanichamy, D., M.Smith. J. Yang, and L. Ericson.  2014.  Inheritance of gray leaf spot resistance in a multiple disease resistant maize inbred.  Poster No. 532.  ASA/CSSA/SSSA International Annual Meeting, 2-5 November 2014, Long Beach CA. CA.  <https://scisoc.confex.com/scisoc/2014am/webprogram/Paper88493.html>

Smith, M.E. 2014. Genetically engineered organisms (AKA GMOs): Issues and the science. pp. 48-57. Proceedings 2014 Cornell Nutrition Conference for Feed Manufacturers. 76th Meeting. October 22, 2014. Cornell University Department of Animal Science of the New York State College of Agriculture and Life Sciences. Ithaca NY.

Smith, M.E. 2014. Who put those genes in my food? Facts and myths about genetically engineered crops. pp. 15-17. Proceedings Field Crop Dealer Meetings, November 12, 2014. Soil and Crop Sciences Section, School of Integrative Plant Science, Extension Series No. E14-1

Smith, Margaret.  2015.  What’s your 30 second elevator speech on GMOs?  pp. 17-20.  In:  Proceedings Corn Congress 2015.  Northwest New York Dairy, Livestock, and Field Crops Team, Cornell Cooperative Extension.

OHIO

# Barboza da Silva, C., Marcos-Filho, J., Jourdan, P., Bennett, M.A. 2015. Performance of Bell Pepper Seeds in Response to Drum Priming with Addition of 24-Epibrassinolide. HortScience. 50(6):873-878

Blanca, J., Montero-Pau, J., Sauvage, C., Bauchet, G., Illa, E., Díez, M.J., Francis, D., Causse, M., van der Knaap, E., Cañizares, J. 2015. Genomic variation in tomato, from wild ancestors to contemporary breeding accessions. BMC Genomics. 16(1):1

Cooperstone, J.L., Ralston, R.A., Riedl, K.M., Haufe, T.C., Schweiggert, R.M., King, S.A., Timmers, C.D., Francis, D.M., Lesinski, G.B., Clinton, S.K., Schwartz, S.J. 2015. Enhanced bioavailability of lycopene when consumed as cis‐isomers from tangerine compared to red tomato juice, a randomized, cross‐over clinical trial. Molecular Nutrition & Food Research. 59(4):658-669

Jourdan, P., Zale, P., Stieve, S. 2015. Germplasm characterization for Phlox, Rudbeckia and Coreopsis: determination of genome size by flow cytometry. Acta Hortic. 1104:349-356. DOI: 10.17660/ActaHortic.2015.1104.52. http://dx.doi.org/10.17660/ActaHortic.2015.1104.52

Zale, P.J., Jourdan, P. 2015. Genome Size and Ploidy of Phlox paniculata and Related Germplasm in Subsections Paniculatae and Phlox*.* JASHS. 140(5):436-448

TEXAS

Santra, D.K., Heyduck, R.F., Baltensperger, D.D., Graybosch, R.A., Nelson, L.A., Frickel, G., Nielsen, E. 2015. Registration of ‘Plateau’waxy (amylose-free) proso millet. J of Plant Registrations. 9(1):41-43. DOI: 10.3198/jpr2013.11.0067crc

WISCONSIN

Dodson-Swenson, H.G. and Tracy, W.F., 2015. Endosperm Carbohydrate Composition and Kernel Characteristics of shrunken2-intermediate (sh2-i/sh2-i Su1/Su1) and shrunken2-intermediate-sugary1-reference (sh2-i/sh2 su1-r/su1-r) in Sweet Corn. Crop Science, 55(6):2647-2656

Shelton, A.C. and Tracy, W.F., 2015. Recurrent Selection and Participatory Plant Breeding for Improvement of Two Organic Open-Pollinated Sweet Corn (Zea mays L.) Populations. Sustainability, 7(5):5139-5152

De Vries, B.D., Peters, T.E., Glaza, B.J., Viesselmann, L.M. and Tracy, W.F., 2015. Estimating the Genetic Effects Modifying Endosperm Composition in Maize. Crop Science, 55(2):578-588

Spooner, D.M., Ghislain, M., Simon, R., Jansky, S.H. and Gavrilenko, T., 2014. Systematics, diversity, genetics, and evolution of wild and cultivated potatoes. The Botanical Review, 80(4):283-383