References Cited

- MR Bellon, D Hodson, and J Hellin. Assessing the vulnerability of traditional maize seed systems in mexico to climate change. *Proc Natl Acad Sci U S A*, 108(33):13432–13437, 2011.
- JJ Berg and G Coop. The population genetic signature of polygenic local adaptation. *PLoS Genetics*, In press, 2014.
- MS Bjarnason. The Subtropical, Midaltitude, and Highland Maize Subprogram. CIMMYT, 1994. ISBN 9789686923315. URL http://books.google.com/books?id=sE9rv9Mv7ygC.
- CA Bottoms, S Flint-Garcia, and MD McMullen. Iview: introgression library visualization and query tool.*. *BMC Bioinformatics*, 11 Suppl 6:S28, 2010.
- GS Bradburd, PL Ralph, and GM Coop. Disentangling the effects of geographic and ecological isolation on genetic differentiation.*. *Evolution*, 67(11):3258–3273, 2013.
- Y Brandvain, AM Kenney, L Flagel, G Coop, and A Sweigart. Speciation and introgression between mimulus nasutus and mimulus guttatus. *PLoS Genetics*, In press, 2014.
- KW Broman, H Wu, S Sen, and GA Churchill. R/qtl: Qtl mapping in experimental crosses. *Bioinformatics*, 19(7):889–890, 2003.
- PJ Brown, N Upadyayula, GS Mahone, F Tian, PJ Bradbury, S Myles, JB Holland, S Flint-Garcia, MD McMullen, ES Buckler, and TR Rocheford. Distinct genetic architectures for male and female inflorescence traits of maize.*. *PLoS Genetics*, 7(11):e1002383, 2011.
- ES Buckler, JB Holland, PJ Bradbury, CB Acharya, PJ Brown, C Browne, E Ersoz, S Flint-Garcia, A Garcia, JC Glaubitz, MM Goodman, C Harjes, K Guill, DE Kroon, S Larsson, NK Lepak, H Li, SE Mitchell, G Pressoir, JA Peiffer, MO Rosas, TR Rocheford, MC Romay, S Romero, S Salvo, H Sanchez Villeda, HS da Silva, Q Sun, F Tian, N Upadyayula, D Ware, H Yates, J Yu, Z Zhang, S Kresovich, and MD McMullen. The genetic architecture of maize flowering time.*. Science, 325(5941):714–718, 2009a.
- ES Buckler, JB Holland, PJ Bradbury, CB Acharya, PJ Brown, C Browne, E Ersoz, S Flint-Garcia, A Garcia, JC Glaubitz, MM Goodman, C Harjes, K Guill, DE Kroon, S Larsson, NK Lepak, H Li, SE Mitchell, G Pressoir, JA Peiffer, MO Rosas, TR Rocheford, MC Romay, S Romero, S Salvo, H Sanchez Villeda, HS da Silva, Q Sun, F Tian, N Upadyayula, D Ware, H Yates, J Yu, Z Zhang, S Kresovich, and MD McMullen. The genetic architecture of maize flowering time.*. Science, 325(5941):714–718, 2009b.
- JM Chia, C Song, PJ Bradbury, D Costich, N de Leon, J Doebley, RJ Elshire, B Gaut, L Geller, JC Glaubitz, M Gore, KE Guill, J Holland, MB Hufford, J Lai, M Li, X Liu, Y Lu, R McCombie, R Nelson, J Poland, BM Prasanna, T Pyhajarvi, T Rong, RS Sekhon, Q Sun, MI Tenaillon, F Tian, J Wang, X Xu, Z Zhang, SM Kaeppler, J Ross-Ibarra, MD McMullen, ES Buckler, G Zhang, Y Xu, and D Ware. Maize hapmap2 identifies extant variation from a genome in flux.*. Nat Genet, 44(7):803–807, 2012.

- JP Cook, MD McMullen, JB Holland, F Tian, P Bradbury, J Ross-Ibarra, ES Buckler, and SA Flint-Garcia. Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels.*. *Plant Physiol*, 158(2):824–834, 2012.
- G Coop, D Witonsky, A Di Rienzo, and JK Pritchard. Using environmental correlations to identify loci underlying local adaptation. *Genetics*, 185(4):1411–1423, 2010.
- JF Doebley. Maize introgression into teosinte-a reappraisal. Annals of the Missouri Botanical Garden, pages 1100–1113, 1984.
- PG Dubois, GT Olsefski, S Flint-Garcia, TL Setter, OA Hoekenga, and TP Brutnell. Physiological and genetic characterization of end-of-day far-red light response in maize seedlings.*. *Plant Physiol*, 154(1):173–186, 2010.
- RJ Elshire, JC Glaubitz, Q Sun, JA Poland, K Kawamoto, ES Buckler, and SE Mitchell. A robust, simple genotyping-by-sequencing (gbs) approach for high diversity species. *PLoS One*, 6(5): e19379, 2011.
- Z Fang, T Pyhajarvi, AL Weber, RK Dawe, JC Glaubitz, J Gonzalez Jde, C Ross-Ibarra, J Doebley, PL Morrell, and J Ross-Ibarra. Megabase-scale inversion polymorphism in the wild ancestor of maize.*. Genetics, 191(3):883–894, 2012.
- SA Flint-Garcia, AL Bodnar, and MP Scott. Wide variability in kernel composition, seed characteristics, and zein profiles among diverse maize inbreds, landraces, and teosinte.*. Theor Appl Genet, 119(6):1129–1142, 2009a.
- SA Flint-Garcia, ES Buckler, P Tiffin, E Ersoz, and NM Springer. Heterosis is prevalent for multiple traits in diverse maize germplasm.*. *PLoS One*, 4(10):e7433, 2009b.
- SA Flint-Garcia, KE Dashiell, DA Prischmann, MO Bohn, and BE Hibbard. Conventional screening overlooks resistance sources: rootworm damage of diverse inbred lines and their b73 hybrids is unrelated.*. *J Econ Entomol*, 102(3):1317–1324, 2009c.
- A Fournier-Level, A Korte, MD Cooper, M Nordborg, J Schmitt, and AM Wilczek. A map of local adaptation in arabidopsis thaliana. *Science*, 334(6052):86–89, 2011.
- K Fukunaga, J Hill, Y Vigouroux, Y Matsuoka, J Sanchez, KJ Liu, ES Buckler, and J Doebley. Genetic diversity and population structure of teosinte. *Genetics*, 169(4):2241–2254, 2005.
- AJ Geneva, CA Muirhead, and LAM Lovato. An improved sequence measure used to scan genomes for regions of recent gene flow. arXiv preprint: 1403.1552, 2014.
- Paul Gepts. The contribution of genetic and genomic approaches to plant domestication studies. Current Opinion in Plant Biology, 18(0):51 - 59, 2014. ISSN 1369-5266. doi: http://dx.doi.org/10.1016/j.pbi.2014.02.001. URL http://www.sciencedirect.com/science/article/pii/S136952661400017X. Genome Studies and Molecular Genetics.
- JC Glaubitz, TM Casstevens, F Lu, J Harriman, RJ Elshire, Q Sun, and ES Buckler. Tassel-gbs: a high capacity genotyping by sequencing analysis pipeline. *PLoS One*, 9(2):e90346, 2014.

- MA Gore, JM Chia, RJ Elshire, Q Sun, ES Ersoz, BL Hurwitz, JA Peiffer, MD McMullen, GS Grills, J Ross-Ibarra, DH Ware, and ES Buckler. A first-generation haplotype map of maize.*. *Science*, 326(5956):1115–1117, 2009.
- T Günther and G Coop. Robust identification of local adaptation from allele frequencies. *Genetics*, 195(1):205–220, 2013.
- AM Hancock, B Brachi, N Faure, MW Horton, LB Jarymowycz, FG Sperone, C Toomajian, F Roux, and J Bergelson. Adaptation to climate across the arabidopsis thaliana genome. *Science*, 334 (6052):83–86, 2011.
- Matthew B Hufford, Enrique Martínez-Meyer, Brandon S Gaut, Luis E Eguiarte, and Maud I Tenaillon. Inferences from the historical distribution of wild and domesticated maize provide ecological and evolutionary insight. *PloS one*, 7(11):e47659, 2012a.
- MB Hufford, P Bilinski, T Pyhajarvi, and J Ross-Ibarra. Teosinte as a model system for population and ecological genomics.*. *Trends Genet*, 28(12):606–615, 2012b.
- MB Hufford, X Xu, J van Heerwaarden, T Pyhajarvi, JM Chia, RA Cartwright, RJ Elshire, JC Glaubitz, KE Guill, SM Kaeppler, J Lai, PL Morrell, LM Shannon, C Song, NM Springer, RA Swanson-Wagner, P Tiffin, J Wang, G Zhang, J Doebley, MD McMullen, D Ware, ES Buckler, S Yang, and J Ross-Ibarra. Comparative population genomics of maize domestication and improvement.*. Nat Genet, 44(7):808–811, 2012c.
- MB Hufford, P Lubinksy, T Pyhajarvi, MT Devengenzo, NC Ellstrand, and J Ross-Ibarra. The genomic signature of crop-wild introgression in maize.* *PLoS Genetics*, 9(5):e1003477, 2013.
- HY Hung, C Browne, K Guill, N Coles, M Eller, A Garcia, N Lepak, S Melia-Hancock, M Oropeza-Rosas, S Salvo, N Upadyayula, ES Buckler, S Flint-Garcia, MD McMullen, TR Rocheford, and JB Holland. The relationship between parental genetic or phenotypic divergence and progeny variation in the maize nested association mapping population. *Heredity (Edinb)*, 108(5):490–499, 2012a.
- HY Hung, LM Shannon, F Tian, PJ Bradbury, C Chen, SA Flint-Garcia, MD McMullen, D Ware, ES Buckler, JF Doebley, and JB Holland. Zmcct and the genetic basis of day-length adaptation underlying the postdomestication spread of maize.*. *Proc Natl Acad Sci U S A*, 109(28):E1913–E1921, 2012b.
- HY Hung, LM Shannon, F Tian, PJ Bradbury, C Chen, SA Flint-Garcia, MD McMullen, D Ware, ES Buckler, JF Doebley, and JB Holland. Zmcct and the genetic basis of day-length adaptation underlying the postdomestication spread of maize.*. *Proc Natl Acad Sci U S A*, 109(28):E1913–E1921, 2012c.
- LB Kanizay, T Pyhajarvi, EG Lowry, MB Hufford, DG Peterson, J Ross-Ibarra, and RK Dawe. Diversity and abundance of the abnormal chromosome 10 meiotic drive complex in zea mays.*. *Heredity (Edinb)*, 110(6):570–577, 2013.
- ES Lander, P Green, J Abrahamson, A Barlow, MJ Daly, SE Lincoln, and L Newburg. Mapmaker: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. *Genomics*, 1(2):174–181, 1987.

- N Lauter, C Gustus, A Westerbergh, and J Doebley. The inheritance and evolution of leaf pigmentation and pubescence in teosinte. *Genetics*, 167(4):1949–1959, 2004.
- V Le Corre and A Kremer. The genetic differentiation at quantitative trait loci under local adaptation. *Molecular Ecology*, 21(7):1548–1566, 2012.
- David B. Lobell, Marianne Bnziger, Cosmos Magorokosho, and Bindiganavile Vivek. Nonlinear heat effects on african maize as evidenced by historical yield trials. *Nature Climate change*, 1(1): 42–45, 2011a.
- DB Lobell, W Schlenker, and J Costa-Roberts. Climate trends and global crop production since 1980. Science, 333(6042):616–620, 2011b.
- Y Matsuoka, Y Vigouroux, MM Goodman, G J Sanchez, E Buckler, and J Doebley. A single domestication for maize shown by multilocus microsatellite genotyping. *Proc Natl Acad Sci U S A*, 99(9):6080–6084, 2002.
- MD McMullen, S Kresovich, HS Villeda, P Bradbury, H Li, Q Sun, S Flint-Garcia, J Thornsberry, C Acharya, C Bottoms, P Brown, C Browne, M Eller, K Guill, C Harjes, D Kroon, N Lepak, SE Mitchell, B Peterson, G Pressoir, S Romero, M Oropeza Rosas, S Salvo, H Yates, M Hanson, E Jones, S Smith, JC Glaubitz, M Goodman, D Ware, JB Holland, and ES Buckler. Genetic properties of the maize nested association mapping population.*. *Science*, 325(5941):737–740, 2009.
- DP Melters, KR Bradnam, HA Young, N Telis, MR May, JG Ruby, R Sebra, P Peluso, J Eid, D Rank, JF Garcia, JL Derisi, T Smith, C Tobias, J Ross-Ibarra, I Korf, and SW Chan. Comparative analysis of tandem repeats from hundreds of species reveals unique insights into centromere evolution. *Genome Biol*, 14(1):R10, 2013.
- S Mezmouk and J Ross-Ibarra. The pattern and distribution of deleterious mutations in maize. G3 (Bethesda), 4(1):163–171, 2014.
- C Monfreda, N Ramankutty, and JA Foley. Farming the planet: 2. geographic distribution of crop areas, yields, physiological types, and net primary production in the year 2000. *Global biogeochemical cycles*, 22(1), 2008.
- PL Morrell, ES Buckler, and J Ross-Ibarra. Crop genomics: advances and applications.*. *Nat Rev Genet*, 13(2):85–96, 2011.
- R Nielsen, S Williamson, Y Kim, MJ Hubisz, AG Clark, and C Bustamante. Genomic scans for selective sweeps using snp data. *Genome research*, 15(11):1566–1575, 2005.
- JA Peiffer, SA Flint-Garcia, N De Leon, MD McMullen, SM Kaeppler, and ES Buckler. The genetic architecture of maize stalk strength*. *PloS one*, 8(6):e67066, 2013.
- JA Peiffer, MC Romay, MA Gore, SA Flint-Garcia, Z Zhang, MJ Millard, CA Gardner, MD Mc-Mullen, JB Holland, PJ Bradbury, and ES Buckler. The genetic architecture of maize height.*. Genetics, 2014.

- AL Price, A Tandon, N Patterson, KC Barnes, N Rafaels, I Ruczinski, TH Beaty, R Mathias, D Reich, and S Myers. Sensitive detection of chromosomal segments of distinct ancestry in admixed populations. *PLoS Genetics*, 5(6):e1000519, 2009.
- Michael D Purugganan and Dorian Q Fuller. The nature of selection during plant domestication. *Nature*, 457(7231):843–848, 2009.
- T Pyhajarvi, MB Hufford, S Mezmouk, and J Ross-Ibarra. Complex patterns of local adaptation in teosinte.*. Genome Biol Evol, 5(9):1594–1609, 2013.
- P Ralph and G Coop. Parallel adaptation: one or many waves of advance of an advantageous allele? *Genetics*, 186(2):647–668, 2010.
- RJ Redfield. Why do we have to learn this stuff? Anew genetics for 21st century students. *PLoS Biology*, 10(7):e1001356, 07 2012. doi: 10.1371/journal.pbio.1001356. URL http://dx.doi.org/10.1371%2Fjournal.pbio.1001356.
- JC Reif, ML Warburton, XC Xia, DA Hoisington, J Crossa, S Taba, J Muminović, M Bohn, M Frisch, and AE Melchinger. Grouping of accessions of mexican races of maize revisited with ssr markers. *Theoretical and Applied Genetics*, 113(2):177–185, 2006.
- MD Robinson, DJ McCarthy, and GK Smyth. edgeR: a bioconductor package for differential expression analysis of digital gene expression data. *Bioinformatics*, 26(1):139–140, 2010.
- MC Romay, MJ Millard, JC Glaubitz, JA Peiffer, KL Swarts, TM Casstevens, RJ Elshire, CB Acharya, SE Mitchell, SA Flint-Garcia, MD McMullen, JB Holland, ES Buckler, and CA Gardner. Comprehensive genotyping of the usa national maize inbred seed bank.*. Genome Biol, 14(6):R55, 2013.
- U Rosas, A Cibrian-Jaramillo, D Ristova, JA Banta, ML Gifford, AH Fan, RW Zhou, GJ Kim, G Krouk, KD Birnbaum, MD Purugganan, and GM Coruzzi. Integration of responses within and across arabidopsis natural accessions uncovers loci controlling root systems architecture. *PNAS*, 2013. doi: 10.1073/pnas.1305883110. URL http://www.pnas.org/content/early/2013/08/22/1305883110.abstract.
- J Ross-Ibarra, M Tenaillon, and BS Gaut. Historical divergence and gene flow in the genus zea.*. Genetics, 181(4):1399–1413, 2009.
- O Savolainen, M Lascoux, and J Merilä. Ecological genomics of local adaptation. *Nature Reviews Genetics*, 14(11):807–820, 2013.
- J Shi, SE Wolf, JM Burke, GG Presting, J Ross-Ibarra, and RK Dawe. Widespread gene conversion in centromere cores.*. *PLoS Biol*, 8(3):e1000327, 2010.
- S Sood, S Flint-Garcia, MC Willcox, and JB Holland. Mining natural variation for maize improvement: Selection on phenotypes and genes*. In *Genomics of Plant Genetic Resources*, pages 615–649. Springer, 2014.
- A Studer, Q Zhao, J Ross-Ibarra, and J Doebley. Identification of a functional transposon insertion in the maize domestication gene tb1.*. Nat Genet, 43(11):1160–1163, 2011.

- R Swanson-Wagner, R Briskine, R Schaefer, MB Hufford, J Ross-Ibarra, CL Myers, P Tiffin, and NM Springer. Reshaping of the maize transcriptome by domestication. *PNAS*, 2012. doi: 10.1073/pnas.1201961109. URL http://www.pnas.org/content/early/2012/06/28/1201961109.abstract.
- S Takuno, P Ralph, S Mezmouk, K Swarts, RJ Elshire, JC Glabutiz, ES Buckler, MB Hufford, and J Ross-Ibarra. The molecular basis of parallel adaptation to highland climate in domesticated maize. In Prep.
- MI Tenaillon and A Charcosset. A European perspective on maize history. *Comptes rendus biologies*, 334(3):221–228, 2011.
- F Tian, PJ Bradbury, PJ Brown, H Hung, Q Sun, S Flint-Garcia, TR Rocheford, MD McMullen, JB Holland, and ES Buckler. Genome-wide association study of leaf architecture in the maize nested association mapping population.*. *Nat Genet*, 43(2):159–162, 2011.
- MR Tuinstra, G Ejeta, and PB Goldsbrough. Heterogeneous inbred family (hif) analysis: a method for developing near-isogenic lines that differ at quantitative trait loci. *Theoretical and Applied Genetics*, 95(5-6):1005–1011, 1997.
- J Van Heerwaarden, J Ross-Ibarra, J Doebley, JC Glaubitz, J Gonzalez Jde, BS Gaut, and LE Eguiarte. Fine scale genetic structure in the wild ancestor of maize (*Zea mays* ssp. parviglumis).*. Mol Ecol, 19(6):1162–1173, 2010.
- J van Heerwaarden, FA van Eeuwijk, and J Ross-Ibarra. Genetic diversity in a crop metapopulation. Heredity (Edinb), 104(1):28–39, 2010.
- J van Heerwaarden, J Doebley, WH Briggs, JC Glaubitz, MM Goodman, J de Jesus Sanchez Gonzalez, and J Ross-Ibarra. Genetic signals of origin, spread, and introgression in a large sample of maize landraces.*. *Proc Natl Acad Sci U S A*, 108(3):1088–1092, 2011.
- JP Vielle-Calzada, O Martinez de la Vega, G Hernandez-Guzman, E Ibarra-Laclette, C Alvarez-Mejia, JC Vega-Arreguin, B Jimenez-Moraila, A Fernandez-Cortes, G Corona-Armenta, L Herrera-Estrella, and A Herrera-Estrella. The palomero genome suggests metal effects on domestication. Science, 326(5956):1078, 2009.
- BF Voight, S Kudaravalli, X Wen, and JK Pritchard. A map of recent positive selection in the human genome. *PLoS Biology*, 4(3):e72, 2006.
- HG Wilkes. Teosinte: the closest relative of maize. Teosinte: the closest relative of maize., 1967.
- DM Wills, CJ Whipple, S Takuno, LE Kursel, LM Shannon, J Ross-Ibarra, and JF Doebley. From many, one: Genetic control of prolificacy during maize domestication*. *PLoS Genetics*, 9(6): e1003604, 2013.
- CA Winkler, GW Nelson, and MW Smith. Admixture mapping comes of age. Annual review of genomics and human genetics, 11:65–89, 2010.

- JB Yoder, J Stanton-Geddes, P Zhou, R Briskine, ND Young, and P Tiffin. Genomic signature of adaptation to climate in medicago truncatula. *Genetics*, 2014. doi: 10.1534/genetics.113.159319. URL http://www.genetics.org/content/early/2014/01/15/genetics.113.159319.abstract.
- N Zhang, A Gur, Y Gibon, R Sulpice, S Flint-Garcia, MD McMullen, M Stitt, and ES Buckler. Genetic analysis of central carbon metabolism unveils an amino acid substitution that alters maize nad-dependent isocitrate dehydrogenase activity.* PLoS One, 5(4):e9991, 2010.