Jeffrey Ross-Ibarra

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Education

PhD Genetics, University of Georgia 2006
MS Botany, University of California Riverside 2000
BA Botany, University of California Riverside 1998

Academic Employment

Professor, Dept. Evolution and Ecology, University of California Davis 2019-present
Professor, Dept. Plant Sciences, University of California Davis 2016-2019
Associate Professor, Dept. Plant Sciences, University of California Davis 2012-2016
Assistant Professor, Dept. Plant Sciences, University of California Davis 2009-2012
Postdoctoral Researcher, University of California Irvine 2006-2008
Profesor de Asignatura, Universidad Nacional Autónoma de México 2001

Selected Fellowships and Awards

Corn Pun Trophy, Genetics Society of America 2017
Stadler Mid-Career Excellence in Maize Genetics Award 2016
Faculty Development Award in recognition of university service 2015
DuPont Young Professor Award 2012
Presidential Early Career Award for Scientists and Engineers 2009
Dean's Award for Postdoctoral Excellence, UC Irvine 2008

Instruction and Advising

Current (total) advisees: 4 (22) postdoc, 5 (9) graduate, 3 (30) undergraduate
Plant Biology (UC Davis, PLB200A, graduate), 2018-present
Genetics (UC Davis, BIS 101, undergraduate), 2013-present
Ecological Genomics (UC Davis, ECL 243, graduate), 2014-present
Faculty advisor, Pioneer Hi-Bred/CAES graduate student symposium in plant breeding, 2012-present
Faculty advisor, US-Mexico graduate student exchange program, 2011-2015
Population and Quantitative Genetics (GGG 201D, graduate), 2010-2013
Plant Genetics (PLS 152, undergraduate), 2010-2011
Biología de Plantas I (undergraduate), UNAM, 2001

Service: selected from last 2 years

University

Campus-wide High-Performance Computing Task Force 2019

Executive Cmte, Plant Biology Graduate Group 2019-present

Ecology Graduate Group admissions committee 2018

Campus Disciplinary Peer Review Committee on sexual violence and sexual harassment, 2017-present

Campus Task Force on Bioinformatics, 2017-2018

Section Chair for Agricultural Plant Biology, 2014-2019

Plant Sciences executive committee, 2014-2019

Search committees: Climate Adaptation (2017-2019)

Dept. of Plant Sciences academic planning committee, 2010-2016, 2018-2019

Professional

Organizing Committee, PEQG Conference 2020

LEAD21 Leadership in Land Grant Institutions, Class 14, 2018-2019

Skype-a-Scientist K-12 Outreach: 2018: Espiciencia, Spain; Valleyview Middle School, NJ

Maize Genetics conference steering committee, 2018-present

Maize Genetics Awards Committee, 2017,2019,2020

Editorial Boards: Genes, Genomes, and Genetics (AE 2014-2019, SE 2017-2019), Genetics (Guest, 2018), PLoS Genetics (2018-2019), PeerJ (2013-present, SE 2018-2019), PNAS (Guest, 2018)

Journal peer review: eLife (3), Cell, Nature Communications (3), Nature Reviews Genetics, PNAS (3), Science, PLoS Genetics, New Phytologist (2), Molecular Ecology, G3 (many), Plant Journal, Agriculture, Ecosystems and Environment

Proposal review: NSF (2017)

Invited Seminars: last 12 months

NCSU, Raleigh, Nov 2020

U. Oulu, Finland, April 2020

NYU Abu Dhabi, UAE, Feb. 2020

U. Oregon, Eugene, Feb 2020

U. Massachusetts, Nov 2019

CAAS, Beijing, China, June 2019

U. of Science and Technology, Beijing, China, June 2019

International Forum on Crop Science, Wuhan, China, June 2019

U. California, Riverside, May 2019

U. Vermont, Burlington, Apr 2019

U. Washington, Seattle, Mar 2019

Keynote Speaker, Seed Central, U. California, Davis, Feb 2019

# Publications (lab members bold, *equal contribution, ‡undergraduate, §corresponding, [citations])

Preprints

Lozano R, Gazave E, dos Santos JPR, Stetter MG, Valluru R, Vandliio N, Fernandes SB, Brown PJ, Shakoor N, Mockler T, **Ross-Ibarra J**, Buckler ES, Gore M. Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. doi: 10.1101/777623

Gates DJ§, Runcie D, Janzen GM, Romero Navarro A, Willcox M, Sonder K, Snodgrass SJ, Rodríguez-Zapata F, Sawers RJH, Rubén Rellín-Álvarez, Buckler ES, Hearne S, Hufford MB, **Ross-Ibarra J**§. Single-gene resolution of locally adaptive genetic variation in Mexican maize. doi: 10.1101/706739

Stitzer MC§, Anderson SN, Springer NM, **Ross-Ibarra J**. The Genomic Ecosystem of Transposable Elements in Maize. doi: 10.1101/559922

In press or in print

H-Index 21 (1549 citations as of Wed Jan 29 11:08:44 2014)

91. Chen Q, Samayo LF, Yang CJ, Bradbury PJ, Olukolu BA, Neumeyer MA, Romay, MC, Sun Q, **Lorant A**, Buckler ES, **Ross-Ibarra J**, Holland JB, Doebley JF. The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication PLoS Genetics *Accepted*
90. **Zeitler L**, **Ross-Ibarra J**§, **Stetter MGS**§ (2020). Loss of diversity and accumulation of genetic load in doubled-haploid lines from European maize landraces. G3 *Accepted*
89. Wang B, Lin Z, Li X, Zhao Y, Zhao B, Wu G, Ma X, Wang H, Xie Y, Li Q, Song G, Kong D, Zheng Z, Wei H, Shen R, Chen C, Meng Z, Wang T, Li X, Chen Y, Lai J, Hufford MB, **Ross-Ibarra J**, He H, Wang H (2020). Genome-wide selection and genetic improvement during modern maize breeding. Nature Genetics *In Press*
88. Torres R*, **Stetter MG***, Hernandez R§, **Ross-Ibarra J**§ (2020). The temporal dynamics of background selection in non-equilibrium populations. Genetics 214: 1019-1030
87. **Turner-Hissong SD**§, Mabrey ME, Beissinger TM, **Ross-Ibarra J**, Pires JC (2020). Evolutionary insights into plant breeding. Current Opinion in Plant Biology 54: 93-100
86. Anderson SN, **Stitzer MC**, Zhou P, **Ross-Ibarra J**, Hirsch CD, Springer NM (2019) Dynamic patterns of transcript abundance of transposable element families in maize. G3 9: 3673-3682
85. Anderson SN*, **Stitzer MC***, Brohammer A*, Zhou P, Noshay JM, O'Connor CH, Hirsch CD, **Ross-Ibarra J**, Hirsch CN, Springer NM (2019). Transposable elements contribute to dynamic genome content in maize. The Plant Journal 100: 1052-1065
84. Wei X, Anderson SN, Wang X, Yang L, Crisp PA, Li Q, Noshay J, Albert PS, Birchler JA, **Bilinski MC**, **Stitzer MC**, **Ross-Ibarra J**, Flint-Garcia S, Chen X, Springer NM, Doebley JF (2019). Hybrid decay: a transgenerational epigenetic decline in vigor and viability triggered in backcross populations of teosinte with maize. Genetics 213: 143-160
83. **O'Brien AM**§, Sawers RJH, Strauss SY, **Ross-Ibarra J**§ (2019). Adaptive phenotypic divergence in teosinte differs across biotic contexts. Evolution 73: 2230-2246
82. Gonzalez-Segovia E, Pérez-Limon S, Cíntora-Martínez C, Guerrero-Zavala A, Jansen G, Hufford MB, **Ross-Ibarra J**, Sawers RJH (2019). Characterization of introgression from the teosinte *Zea mays* ssp. *mexicana* to Mexican highland maize. PeerJ 7: e6815.
81. **Josephs EM**§, Berg JJ, **Ross-Ibarra J**, Coop G (2019) Detecting adaptive differentiation in structured populations with genomic data and common gardens. Genetics 211: 989-1004.
80. **Stetter MG**§, Thornton K, **Ross-Ibarra J**§ (2018) Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. PLoS Genetics 14(11): e1007794.
79. **O'Brien A**§, Sawers R, **Ross-Ibarra J**, Strauss SY§ (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. American Naturalist 192(6): 715-730.

78. **Stitzer MC**[§], **Ross-Ibarra J** (2018) Maize domestication and gene interaction. New Phytologist 220:395-408

77. Manchanda N, Snodgrass SJ, **Ross-Ibarra J**, Hufford MB (2018) Evolution and adaptation in the maize genome. *In* The Zea mays Genome, Bennetzen, Flint-Garcia, Hirsch, Tuberosa (Eds.), Springer Nature Publishing *In Press*

76. **Lorant A**, **Ross-Ibarra J**, Maud Tenaillon (2018) Genomics of long- and short- term adaptation in maize and teosinte. *In* Statistical Population Genomics, Dutheil (Ed.), Springer Nature Publishing *In Press*

75. Dawe RK, Lowry EG, Gent J, **Stitzer MC**, Higgins DM, **Ross-Ibarra J**, Wallace JG, Kanizay L, Alabady M, Wang N, Gao Z, Birchler J, Harkess AE, Hodges AL, Hiatt EN (2018) A novel maize kinesin causes neocentromere activity and meiotic drive, altering inheritance patterns across the genome. Cell 173: 839-850.

74. Aburto-Oropeza O, Johnson A, Agha M, Allen E, Allen M, González JA, Arenas-Moreno DM, Beas R, Butterfield H, Caetano G, Caselle J, Casteñada Gaytán G, Castorani MCN, Anh Cat L, Cavanaugh K, Chambers JQ, Cooper RD, Arafeh-Dalmau N, Dawson T, Diaz de la Vega A, DiMento JFC, Domínguez S, Edwards M, Ennen J, Estrada-Medina H, Fierro N, Gadsden H, Galina-Tessaro P, Gibbons P, Goode EV, Gorris ME, Harmon T, Hecht SB, Heredia Fragoso MA, Hernández-Solano A, Hernández-Cortés D, Hernández-Carmona G, Hillard S, Huey RB, Hufford MB, Pàramo Figueroa VH, Jenerette D, Jiménez-Osornio J, López-Nava KJ, Lara R, Leslie H, Lopez-Feldman A, Luja V, Martínez-Méndez N, Mautz W, Medellin-Azuara J, Meléndez-Torres C, de la Cruz FRM, Micheli F, Miles D, Montagner G, Montaño-Moctezuma G, Müller J, Oliva P, Ortinez A, Ortiz Partida JP, Palleiro-Nayar J, Parnell PE, Raimondi P, Ramirez A, Randerson JT, Reed DC, Riquelme M, Torres TR, Rosen PC, **Ross-Ibarra J**, Sanchez-Cordero V, Sandoval-Solis S, Santos J, Sawers R, Sinervo B, Sites J, Sosa-Nishizaki O, Stanton T, Stapp J, Stewart J, Torre J, Torres-Moye G, Treseder KK, Valdez-Villavicencio JH, Jiménez FIV, Vaughn M, Welton L, Westphal MF, Woolrich-Piña G, Yunez-Naude A, Zertuche-González JA, Taylor JE (2018) Harnessing Cross-border Resources to Confront Climate Change. Environmental Science and Policy *In Press*.

73. **Bilinski P**[§], Albert P, Berg JJ, Birchler JA, Grote M, **Lorant A**, **Quezada J**[‡], Swarts, K, **Yang J**, **Ross-Ibarra J**[§] (2018) Parallel altitudinal clines reveal adaptive evolution of genome size in *Zea mays*. PLoS Genetics 14: e1007162

72. **Mei W**, **Stetter MG**, **Gates DJ**, **Stitzer MC**, **Ross-Ibarra J**[§] (2018) Adaptation in plant genomes: bigger is different. American Journal of Botany 105: 16-19

71. Bukowski R, Guo X, Lu Y, Zou C, He B, Rong Z, Wang B, Xu D, Yang B, Xie C, Fan L, Gao S, Xu X, Zhang G, Li Y, Jiao Y, Doebley J, **Ross-Ibarra J**, **Lorant A**, **Buffalo V**, Romay MC, Buckler ES, Ware D, Lai J, Sun Q , Xu Y (2017) Construction of the third generation *Zea mays* haplotype map. GigaScience gix134

70. Wang L, **Beissinger TM**, **Lorant A**, **Ross-Ibarra C**, **Ross-Ibarra J**[§], Hufford MB[§] (2017) The interplay of demography and selection during maize domestication and diffusion. Genome Biology 18:215

69. **Yang J**[*§], **Mezmouk S**[*], Baumgarten A, Buckler ES, Guill KE, McMullen MD, Mumm RH, **Ross-Ibarra J**[§] (2017) Incomplete dominance of deleterious alleles contribute substantially to trait variation and heterosis in maize. PLoS Genetics 13:e1007019

68. **Lorant A**, Pedersen S, Holst I, Hufford MB, Winter K, Piperno D, **Ross-Ibarra J**[§] (2017) The potential role of genetic assimilation during maize domestication. PLoS ONE 12:e0184202

67. Aguilar-Rangel MR, Chàvez Montes RA, Gonzalez-Segovia E, **Ross-Ibarra J**, Simpson JK, Sawers RJH (2017) Allele specific expression analysis identifies regulatory variation associated with stress-related genes in the Mexican highland maize landrace Palomero Toluqueño. PeerJ 5:e3737

66. **Stetter MG**[§], **Gates DJ**, **Mei W**, **Ross-Ibarra J**[§] (2017) How to make a domesticate. Current Biology 27:R896-R900

65. Swarts K, Gutaker RM, Schuenemann V, Benz B, Blake M, Bukowski R, Holland J, Kruse-Peeples M, Lepak N, Matson RG, Prim L, Romay C, **Ross-Ibarra J**, Sanchez J, Schmidt C, Sofro E, Krause

J, Weigel D, Buckler ES, Burbano HA (2017) Genomic estimation of complex traits reveals ancient maize adaptation to temperate North America. Science 357:512-515

64. **Bilinski P**[§], Han Y, **Hufford MB**, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J**[§] (2017) Genomic abundance is not predictive of tandem repeat localization in grass genomes. PLoS ONE 12:e0177896
63. Jiao Y, Peluso P, Shi J, Liang T, **Stitzer MC**, Wang B, Campbell M, Stein JC, Wei X, Chin C-S, Guill K, Regulski M, Kumari S, Olson A, Gent J, Schneider KL, Wolfgruber TK, May MR, Springer N, Antoniou E, McCombie R, Presting GG, McMullen M, **Ross-Ibarra J**, Dawe RK, Hastie A, Rank DR, Ware D (2017) Improved maize reference genome with single-molecule technologies. Nature 546:524-527
62. **Renny-Byfield S**[§], Rodgers-Melnick E, **Ross-Ibarra J**[§] (2017) Gene fractionation and function in the ancient subgenomes of maize. MBE 34:1825-1832
61. **Velasco D**, Aradhya M, and and **Ross-Ibarra J**[§] (2016) Evolutionary genomics of peach and almond domestication. G3 6:3985-3993
60. Ramos-Madrigal J, Smith BD, Moreno-Mayar JV, Gopalakrishnan S, **Ross-Ibarra J**, Gilbert MTP, Wales N (2016) Genome sequence of a 5310-year-old maize cob provides insights into the early stages of maize domestication. Current Biology 26:3195-3201
59. **Durvasula A**[‡*], Hoffman PJ[*], **Kent TV**[‡], Liu C, Kono TJY, Morrell PL[§], **Ross-Ibarra J**[§] (2016) ANGSD-wrapper. Molecular Ecology Resources 16:1449-1454
58. **Beissinger TM**[§], Wang L, **Crosby K**, **Durvasula A**[‡], Hufford MB, **Ross-Ibarra J**[§] (2016) Recent demography drives changes in linked selection across the maize genome. Nature Plants 2:16084
57. Wolfgruber TK, Nakashima MM, Schneider KL, Sharma A, Xie Z, Albert PS, Xu R, **Bilinski P**, Dawe RK, **Ross-Ibarra J**, Birchler JA, Presting G (2016) High quality maize centromere 10 sequence reveals evidence of frequent recombination events. Frontiers In Plant Science 7
56. Orozco-Ramìrez Q, Santacruz-Varela A, **Ross-Ibarra J**, Brush B (2016) Maize diversity associated with social origin and environmental variation in southern Mexico. Heredity 116:477-484.
55. Gerke JP[§], Edwards JW, Guill KE, **Ross-Ibarra J**[§], McMullen MD. The genomic impacts of drift and selection for hybrid performance in maize (2015). Genetics 201: 1201-1211
54. Sosso D, Luo D, Li Q-B, Sassse J, **Yang J**, Gendrot G, Suzuki M, Koch KE, McCarty DR, Chourey PS, Rogoswky PM, **Ross-Ibarra J**, Yang B, Frommer WB (2015) Seed filling in domesticated maize and rice depends on SWEET-mediated hexose transport. Nature Genetics 47:1489-1493
53. **Takuno S**, Ralph P, Swarts K, Elshire RJ, Glaubitz JC, Buckler ES, **Hufford MB**, **Ross-Ibarra J**[§] (2015) Independent molecular basis of convergent highland adaptation in maize. Genetics 200:1297-1312
52. **Vann LE**, **Kono T**, **Pyhäjärvi T**, **Hufford MB**[§], **Ross-Ibarra J**[§] (2015) Natural variation in teosinte at the domestication locus teosinte branched1 (tb1). PeerJ 3:e900
51. Hake S, **Ross-Ibarra J** (2015) Genetic, evolutionary and plant breeding insights from the domestication of maize. eLife 2015;4:e05861
50. Fonseca RR, Smith B, Wales N, Cappellini E, Skoglund P, Fumagalli M, Samaniego JA, Caroe C, Avila-Arcos MC, Hufnagel D, Korneliussen TS, Vieira FG, Jakobsson M, Arriaza B, Willerslev E, Nielsen R, Hufford MB, Albrechtsen A, **Ross-Ibarra J**, Gilbert MT (2015) The origin and evolution of maize in the American Southwest. Nature Plants 1:14003
49. Dyer GA, López-Feldman A, Yúnez-Naude A, Taylor JE, **Ross-Ibarra J** (2015) Reply to Brush *et al.*: A wake up call for crop conservation science. PNAS 112 (1), E2-E2 (letter).
48. Makarevitch I, Waters M, West P, **Stitzer M**, **Ross-Ibarra, J**, Springer NM (2015) Mobile elements contribute to activation of genes in response to abiotic stress. PLoS Genetics 11 (1): e1004915.
47. Tiffin P, **Ross-Ibarra J** (2014) Advances and limits of using population genetics to understand local adaptation. Trends in Ecology and Evolution 29:673-680
46. **Bilinski P**, **Distor KD**, **Gutierez-Lopez J**, **Mendoza Mendoza G**, Shi J, Dawe RK, **Ross-Ibarra J**[§] (2014) Diversity and evolution of centromere repeats in the maize genome. Chromosoma 0009-5915

45. **Mezmouk S**, **Ross-Ibarra J**[§] (2014) The pattern and distribution of deleterious mutations in maize. (2014). G3 4:163-171
44. Waters AJ, **Bilinski P**, Eichten SR, Vaughn MW, **Ross-Ibarra J**, Gehring M, Springer NM (2013) Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. PNAS 110:19639-19644
43. **Pyhäjärvi T**, **Hufford MB**, **Mezmouk S**, **Ross-Ibarra J**[§] (2013) Complex patterns of local adaptation in teosinte. Genome Biology and Evolution 5: 1594-1609
42. Wills DM, Whipple C, **Takuno S**, Kursel LE, Shannon LM, **Ross-Ibarra J**, Doebley JF (2013) From many, one: genetic control of prolificacy during maize domestication. PLoS Genetics 9(6): e1003604.
41. McCouch S, Baute GJ, Bradeen J, Bramel P, Bretting PK, Buckler E, Burke JM, Charest D, Cloutier S, Cole G, Dempewolf H, Dingkuhn M, Feuillet C, Gepts, P, Grattapaglia D, Guarino L, Jackson S, Knapp S, Langridge P, Lawton-Rauh A, Lijua Q, Lusty C, Michael T, Myles S, Naito K, Nelson RL, Pontarollo R, Richards CM, Rieseberg L, **Ross-Ibarra J**, Rounsley S, Hamilton RS, Schurr U, Stein N, Tomooka N, van der Knaap E, van Tassel D, Toll J, Valls J, Varshney RK, Ward J, Waugh R, Wenzl P, Zamir. (2013) Agriculture: Feeding the future. Nature 499:23-24
40. **Hufford MB**, Lubinsky P, **Pyhäjärvi T**, **Devengenzo MT**[‡], Ellstrand NC, **Ross-Ibarra J**[§] (2013) The genomic signature of crop-wild introgression in maize. PLoS Genetics 9(5): e1003477.
39. **Provance MC**[§], Garcia Ruiz I, **Thommes C**[‡], **Ross-Ibarra J** (2013) Population genetics and ethnobotany of cultivated *Diospyros riojae* Gómez Pompa (Ebenaceae), an endangered fruit crop from Mexico. Genetic Resources and Crop Evolution 60: 2171-2182.
38. Melters DP[*], Bradnam KR[*], Young HA, Telis N, May MR, Ruby JG, Sebra R, Peluso P, Eid J, Rank D, Fernando Garcia J, DeRisi J, Smith T, Tobias C, **Ross-Ibarra J**[§], Korf IF[§], Chan SW-L. (2013) Patterns of centromere tandem repeat evolution in 282 animal and plant genomes. Genome Biology 14:R10
37. Kanizay LB, **Pyhäjärvi T**, Lowry E, **Hufford MB**, Peterson DG, **Ross-Ibarra J**, Dawe RK (2013) Diversity and abundance of the Abnormal chromosome 10 meiotic drive complex in *Zea mays*. Heredity 110: 570-577.
36. **Hufford MB**, **Bilinski P**, **Pyhäjärvi T**, **Ross-Ibarra J**[§] (2012) Teosinte as a model system for population and ecological genomics. Trends in Genetics 12:606-615
35. Muñoz Diez C, Vitte C, **Ross-Ibarra J**, Gaut BS, Tenaillon MI (2012) Using nextgen sequencing to investigate genome size variation and transposable element content. *In* Grandbastien M-A, Casacuberta JM, editors. Topics in Current Genetics v24: Plant Transposable Elements - Impact on Genome Structure & Function. pp. 41-58
34. **van Heerwaarden J**[§], **Hufford MB**, **Ross-Ibarra J**[§] (2012) Historical genomics of North American maize. PNAS 109: 12420-12425
33. Swanson-Wagner R, Briskine R, Schaefer R, **Hufford MB**, **Ross-Ibarra J**, Myers CL, Tiffin P, Springer NM. Reshaping of the maize transcriptome by domestication. (2012). PNAS 109: 11878-11883
32. **Hufford MB**[*], Xun X[*], **van Heerwaarden J**[*], **Pyhäjärvi T**[*], Chia J-M, Cartwright RA, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler S, Lai J, Morrell PL, Shannon LM, Song C, Spinger NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES[§], Yang S[§], **Ross-Ibarra J**[§] (2012) Comparative population genomics of maize domestication and improvement. Nature Genetics 44:808-811
31. Chia J-M[*], Song C[*], Bradbury P, Costich D, de Leon N, Doebley JC, Elshire RJ, Gaut BS, Geller L, Glaubitz JC, Gore M, Guill KE, Holland J, **Hufford MB**, Lai J, Li M, Liu X, Lu Y, McCombie R, Nelson R, Poland J, Prasanna BM, **Pyhäjärvi T**, Rong T, Sekhon RS, Sun Q, Tenaillon M, Tian F, Wang J, Xu X, Zhang Z, Kaeppler S, **Ross-Ibarra J**, McMullen M, Buckler ES, Zhang G, Xu Y, Ware, D (2012) Maize HapMap2 identifies extant variation from a genome in flux. Nature Genetics 44:803-807
30. Fang Z, **Pyhäjärvi T**, Weber AL, Dawe RK, Glaubitz JC, Sánchez González J, **Ross-Ibarra C**, Doebley J, Morrell PL[§], **Ross-Ibarra J**[§] (2012) Megabase-scale inversion polymorphism in the wild ancestor of maize. Genetics 191:883-894

29. Cook JP, McMullen MD, Holland JB, Tian F, Bradbury P, **Ross-Ibarra J**, Buckler ES, Flint-Garcia SA (2012) Genetic architecture of maize kernel composition in the Nested Association Mapping and Inbred Association panels. Plant Physiology 158: 824-834
28. Morrell PL, Buckler ES, **Ross-Ibarra J**§ (2012) Crop genomics: advances and applications. Nature Reviews Genetics 13:85-96
27. Studer A, Zhao Q, **Ross-Ibarra J**, Doebley J (2011) Identification of a functional transposon insertion in the maize domestication gene *tb1*. Nature Genetics 43:1160-1163.
26. **van Heerwaarden J**§, Doebley J, Briggs WH, Glaubitz JC, Goodman MM, Sánchez González JJ, **Ross-Ibarra J**§ (2011) Genetic signals of origin, spread and introgression in a large sample of maize landraces. PNAS 108: 1088-1092
25. **Hufford MB**§, Gepts P, **Ross-Ibarra J** (2011) Influence of cryptic population structure on observed mating patterns in the wild progenitor of maize (*Zea mays* ssp. *parviglumis*). Molecular Ecology 20: 46-55
24. Tenaillon MI, **Hufford MB**, Gaut BS, **Ross-Ibarra J**§ (2011) Genome size and TE content as determined by high-throughput sequencing in maize and *Zea luxurians*. Genome Biology and Evolution 3: 219-229
23. Eckert AJ, **van Heerwaarden J**, Wegrzyn JL, Nelson CD, **Ross-Ibarra J**, González-Martínez SC, and Neale DB (2010) Patterns of population structure and environmental associations to aridity across the range of loblolly pine (*Pinus taeda* L, Pinaceae). Genetics 185: 969-982
22. Fuchs EJ, **Ross-Ibarra J**§, Barrantes G (2010) Reproductive biology of *Macleania rupestris*: a pollen-limited Neotropical cloud-forest species in Costa Rica. Journal of Tropical Ecology 26: 351-354
21. Whitney KD, Baack EJ, Hamrick JL, Godt MJW, Barringer BC, Bennett MD, Eckert CG, Goodwillie C, Kalisz S, Leitch I, **Ross-Ibarra J** (2010) A role for nonadaptive processes in plant genome size evolution? . Evolution 64: 2097-2109
20. **van Heerwaarden J**, **Ross-Ibarra J**§, Doebley J, Glaubitz JC, Sánchez González J, Gaut BS, Eguiarte LE (2010) Fine scale genetic structure in the wild ancestor of maize (*Zea mays* ssp. *parviglumis*). Molecular Ecology 19: 1162-1173
19. Shi J, Wolf S, Burke J, Presting G, **Ross-Ibarra J**, Dawe RK (2010) High frequency gene conversion in centromere cores. PLoS Biology 8: e1000327
18. Hollister JD, **Ross-Ibarra J**, Gaut BS (2010) Indel-associated mutation rate varies with mating system in flowering plants. Molecular Biology and Evolution 27: 409-416.
17. **van Heerwaarden J**, van Eeuwijk FA, **Ross-Ibarra J** (2010) Genetic diversity in a crop metapopulation. Heredity 104: 28-39
16. Gore MA*, Chia JM*, Elshire RJ, Sun Q, Ersoz ES, Hurwitz BL, Peiffer JA, McMullen MD, Grills GS, **Ross-Ibarra J**, Ware D, Buckler ES (2009) A first-generation haplotype map of maize. Science 326: 1115-1117.
15. **May MR**‡, **Provance MC**, Sanders AC, Ellstrand NC, **Ross-Ibarra J**§ (2009) A pleistocene clone of Palmer's Oak persisting in Southern California. PLoS ONE 4: e8346.
14. Zhang LB, Zhu Q, Wu ZQ, **Ross-Ibarra J**, Gaut BS, Ge S, Sang T (2009) Selection on grain shattering genes and rates of rice domestication. New Phytologist 184: 708-720.
13. **Ross-Ibarra J**, Tenaillon M, Gaut BS (2009) Historical divergence and gene flow in the genus Zea. Genetics 181: 1399-1413.
12. **Ross-Ibarra J***, Wright SI*, Foxe JP, Kawabe A, DeRose-Wilson L, Gos G, Charlesworth D, Gaut BS (2008) Patterns of polymorphism and demographic history in natural populations of *Arabidopsis lyrata*. PLoS ONE 3: e2411.
11. Lockton S, **Ross-Ibarra J**, Gaut BS (2008) Demography and weak selection drive patterns of transposable element diversity in natural populations of *Arabidopsis lyrata*. PNAS 105: 13965-13970.

10. **Ross-Ibarra J**[§], Gaut BS (2008) Multiple domestications do not appear monophyletic. PNAS 105: E105 (letter).
9. Gaut BS, **Ross-Ibarra J** (2008) Selection on major components of angiosperm genomes. Science 320: 484-486.
8. **Ross-Ibarra J**, Morrell PL, Gaut BS (2007) Plant domestication, a unique opportunity to identify the genetic basis of adaptation. PNAS 104 Suppl 1: 8641-8648.
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