

Jeffrey Ross-Ibarra

Department of Plant Sciences
Center for Population Biology
Genome Center
University of California Davis

Phone: (530) 752-1152
Fax: (530) 752-4604
Email: rossibarra@ucdavis.edu
Web: www.rilab.org, [@jrossibarra](https://twitter.com/jrossibarra)

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. Plant Sciences, University of California Davis 2016-present
Associate Professor, Dept. Plant Sciences, University of California Davis 2012-2016
Assistant Professor, Dept. Plant Sciences, University of California Davis 2009-2012
Postdoctoral Researcher (with BS Gaut), University of California Irvine 2006-2008
Profesor de Asignatura, Universidad Nacional Autónoma de México 2001

Selected Fellowships and Awards

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: 7 (19) postdoc, 4 (7) graduate, 3 (28) undergraduate
Instructor, Frontiers and Techniques in Plant Science, CSHL, July 2015
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

College review, NSF limited submission, 2018

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

Campus Task Force on Bioinformatics, 2017-present

Campus High Performance Computing Advisory Committee, 2016-present

Section Chair for Agricultural Plant Biology, 2014-present

Plant Sciences executive committee, 2014-present

Search committees: Dept. Chair of Plant Sciences (Chair, 2016), Climate Adaptation (2017-2018)

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

Professional

Skype-a-Scientist K-12 Outreach: 2017: Korematsu Elementary, CA; Shelburne Middle School, VA; Summit Hill Elementary, IL; 2018: Espiciencia, Spain; Valleyview Middle School, NJ

Maize Genetics Awards Committee, 2017

External search committee, Dept. Plant Biology, Swedish University of Agricultural Sciences (2016)

Editorial Boards: Genes, Genomes, and Genetics (AE 2014-present, SE 2017-present), Genetics (AE, 2018), PLoS Genetics (2018-Present), PeerJ (2013-present, SE 2018-present), Axios Reviews (2013-2017), PNAS (Guest, 2018), eLife (Guest, 2016)

Journal peer review: Nature (3), eLife, Cell, Nature Communications, PNAS (3), The Plant Cell, Genome Research, New Phytologist, Genome Biology & Evolution, Molecular Ecology (3), G3 (many), BMC Genomics (2), Plant Journal, Scientific Reports, Agriculture, Ecosystems and Environment

Proposal review: NSF (2016, 2017 (2)), Swiss National Science Foundation (2016), GWIS (2016), Israeli Science Foundation (2016)

Current Funding

NSF: "Harnessing convergence and constraint to predict adaptations to abiotic stress for maize and sorghum" \$740,000 of \$5.4M total (Co-PI), 2018-2022

NSF: "The evolutionary genetics of pollen-pistil incompatibility and reproductive isolation in *Zea mays*" \$320,000 of \$1M total (Co-PI), 2018-2021

NSF: "The genetics of highland adaptation in maize", \$4.2M (PI), 2016-2021

NSF: "Biology of rare alleles in maize and its wild relatives" \$3.2M of \$14M total (Co-PI), 2013-2019

Invited Seminars: last 12 months

National Science Foundation, Washington DC, Sept 2018

U. Georgia, Athens, Aug 2018

Science and Society public lecture, Woodland, Aug 2018

Fisher Biosciences, July 2018

Corteva Agriscience, Johnston, July 2018

Plenary Speaker, Maize Genetics Conference, Saint-Malo, France, Mar 2018

University of Paris-Saclay, Gif-sur-Yvette, France, Mar 2018

U. California, Davis, Mar 2018

Plant And Animal Genome Conference (two workshops), San Diego, Jan 2018

U. Nebraska, Lincoln, Nov 2017

U. Colorado, Boulder, Oct 2017

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

Preprints

O'Brien AM§, Sawers RJH, Strauss SY, Ross-Ibarra J§. Adaptive phenotypic divergence in teosinte differs across biotic contexts. doi: 10.1101/382770 [o]

Josephs EM§, Berg JJ, **Ross-Ibarra J**, Coop G. Detecting adaptive differentiation in structured populations with genomic data and common gardens. doi: 10.1101/368506 [o]

Stetter MG§, Thornton K, **Ross-Ibarra J**§. Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. doi: 10.1101/313247 [o]

In press or in print

H-Index 35 (6014 citations as of Tue Sep 18 15:42:03 2018)

79. **O'Brien A**§, Sawers R, **Ross-Ibarra J**, Strauss SY§ (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. *AMERICAN NATURALIST* *Accepted* [2]
78. **Stitzer MC**, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. *NEW PHYTOLOGIST* *In Press* [1]
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* [o]
76. **Anne Lorant**, **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* [o]
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. [3]
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, Medellín-Azuara J, Meléndez-Torres C, de la Cruz FRM, Micheli F, Miles D, Montagner G, Montaña-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 ME, 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*. [0]
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 [9]
 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 [6]
 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 [20]
 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 [15]
 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 [10]
 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 [1]
 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 [2]
 66. **Stetter MG[§]**, **Gates DJ**, **Mei W**, **Ross-Ibarra J[§]** (2017) How to make a domesticate. *CURRENT BIOLOGY* 27:R896-R900 [3]
 65. Swarts K, Gutaker RM, Schuenemann V, Benz B, Blake M, Bukowski R, Holland J, Kruse-Peebles 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 [18]
 64. **Bilinski P[§]**, Han Y, **Hufford MB**, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J[§]** (2017) Diverse origins of high copy tandem repeats in grass genomes. *PLoS ONE* 12:e0177896 [0]
 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 [107]
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 [11]
 61. **Velasco D**, Aradhya M, and **Ross-Ibarra J[§]** (2016) Evolutionary genomics of peach and almond domestication. *G3* 6:3985-3993 [13]
 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 [13]
 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 [3]
 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 [33]
 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 [13]
 56. Orozco-Ramírez 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. [14]
 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 [16]
 54. Sosso D, Luo D, Li Q-B, Sasse J, **Yang J**, Gendrot G, Suzuki M, Koch KE, McCarty DR, Chourey PS, Rogoswsky 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]
 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 [32]
 52. **Vann LE**, **Kono T**, **Pyhäjärvi T**, **Hufford MB[§]**, **Ross-Ibarra J[§]** (2015) Natural variation in teosinte at the domestication locus *tb1*. *PEERJ* 3:e900 [6]
 51. Hake S, **Ross-Ibarra J** (2015) Genetic, evolutionary and plant breeding insights from the domestication of maize. *ELIFE* 2015;4:e05861 [21]
 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 [57]

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). [4]
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. [131]
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 [141]
46. **Bilinski P**, **Distor KD**, **Gutierrez-Lopez J**, **Mendoza Mendoza G**, Shi J, Dawe RK, **Ross-Ibarra J**^S (2014) Diversity and evolution of centromere repeats in the maize genome. *CHROMOSOMA* 0009-5915 [14]
45. **Mezmouk S**, **Ross-Ibarra J**^S (2014) The pattern and distribution of deleterious mutations in maize. (2014). *G3* 4:163-171 [37]
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 [55]
43. **Pyhäjärvi T**, **Hufford MB**, **Mezmouk S**, **Ross-Ibarra J**^S (2013) Complex patterns of local adaptation in teosinte. *GENOME BIOLOGY AND EVOLUTION* 5: 1594-1609.[73]
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. [46]
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 [238]
40. **Hufford MB**, Lubinsky P, **Pyhäjärvi T**, **Devenganzo MT**[†], Ellstrand NC, **Ross-Ibarra J**^S (2013) The genomic signature of crop-wild introgression in maize. *PLOS GENETICS* 9(5): e1003477. [144]
39. **Provance MC**^S, 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. [3]
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**^S, Korf IF^S, Chan SW-L. (2013) Patterns of centromere tandem repeat evolution in 282 animal and plant genomes. *GENOME BIOLOGY* 14:R10 [160]
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. [11]

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[37]
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 [13]
34. **van Heerwaarden J[§], Hufford MB, Ross-Ibarra J[§]** (2012) Historical genomics of North American maize. *PNAS* 109: 12420-12425 [85]
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 [74]
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[430]
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[396]
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 [43]
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 [209]
28. Morrell PL, Buckler ES, **Ross-Ibarra J[§]** (2012) Crop genomics: advances and applications. . *NATURE REVIEWS GENETICS* 13:85-96[316]
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. [289]
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 [234]
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 [14]
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 EVOLU-*

TION 3: 219-229 [128]

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 [269]
22. Fuchs EJ, **Ross-Ibarra J^S**, 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 [5]
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 [62]
20. **van Heerwaarden J**, **Ross-Ibarra J^S**, 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 [32]
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 [82]
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. [33]
17. **van Heerwaarden J**, van Eeuwijk FA, **Ross-Ibarra J** (2010) Genetic diversity in a crop metapopulation. . HEREDITY 104: 28-39 [234]
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. [590]
15. **May MR[†]**, **Provance MC**, Sanders AC, Ellstrand NC, **Ross-Ibarra J^S** (2009) A pleistocene clone of Palmer's Oak persisting in Southern California. . PLoS ONE 4: e8346. [22]
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. [109]
13. **Ross-Ibarra J**, Tenaillon M, Gaut BS (2009) Historical divergence and gene flow in the genus *Zea*. . GENETICS 181: 1399-1413. [119]
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. [145]
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. [65]
10. **Ross-Ibarra J^S**, Gaut BS (2008) Multiple domestications do not appear monophyletic. PNAS 105: E105 (letter). [20]

9. Gaut BS, **Ross-Ibarra J** (2008) Selection on major components of angiosperm genomes. . SCIENCE 320: 484-486. [65]
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. [267]
7. **Ross-Ibarra J**^S (2007) Genome size and recombination in angiosperms: a second look. . JOURNAL OF EVOLUTIONARY BIOLOGY 20: 800-806. [29]
6. Wares JP, Barber PH, **Ross-Ibarra J**, Sotka EE, Toonen RJ (2006) Mitochondrial DNA and population size. . SCIENCE 314: 1388-90 (letter). [30]
5. **Ross-Ibarra J**^S (2005) QTL and the study of plant domestication. . GENETICA 123: 197-204. [27]
4. **Ross-Ibarra J**^S (2004) The evolution of recombination under domestication: a test of two hypotheses. . AMERICAN NATURALIST 163: 105-112. [69]
3. **Ross-Ibarra J** (2003) Origin and domestication of chaya (*Cnidoscolus aconitifolius* Mill I. M. Johnst): Mayan spinach. . MEXICAN STUDIES 19: 287-302. [10]
2. **Ross-Ibarra J**^S, Molina-Cruz A (2002) The ethnobotany of Chaya (*Cnidoscolus aconitifolius* ssp. *aconitifolius* Breckon): A nutritious Maya vegetable. . ECONOMIC BOTANY 56: 350-365. [67]
1. Neel MC, **Ross-Ibarra J**, Ellstrand NC (2001) Implications of mating patterns for conservation of the endangered plant *Eriogonum ovalifolium* var. *vineum*. . AMERICAN JOURNAL OF BOTANY 88: 1214-1222. [33]