

Jeffrey Ross-Ibarra

Department of Evolution and Ecology
Center for Population Biology
Genome Center
University of California Davis

Phone: (530) 752-4565
Email: rossibarra@ucdavis.edu
Web: rilab.ucdavis.edu, [@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. Evolution and Ecology, University of California Davis	2019-present
Scientific Director, UC Davis High Performance Computing Core Facility	2024-present
Chair Professor, College of Plant Sciences, Huazhong Agricultural University	2024
Paternity leave	2017
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

NAS Prize in Food and Agriculture	2024
College of Biological Sciences Award for Research Excellence	2024
Fellow, American Association for the Advancement of Science	2020
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

Instruction and Advising

Current (total) advisees: 4 (30) postdoc, 6 (13) graduate, 1 (40) undergraduate	
Hablemos de Evolución y Ecología (First year seminar)	2025
Graduate Advisor, Plant Biology Graduate Group	2021-present
Faculty trainer, Evolution and Ecology Scholars program	2023-present
NSF REU (EEREC) faculty advisor	2022-present
Plant Biology Graduate Core (PLB200A)	2018-2022

Graduate advisor, Ecology Graduate Group	2018-2021
Ecological Genomics (ECL 243)	2014-present
Genetics (UC Davis, BIS 101, undergraduate)	2013-2022
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 3 years

University

Scientific Director, High Performance Computing Core Facility	2024-present
START taskforce on Research Computing	2024-present
Member, Advanced Computing Committee, UC Davis Health	2025-present
Member, Computer Support Committee, College of Letters & Science,	2024-present
Chair and Co-Chair, Ecology & Evolution Seminar Series	2020-2022
EVE representative, Faculty Executive Cmte, College of Biological Sciences	2020-2022
Advisory cmte, controlled environment facility	2020-2024
Executive Cmte, Plant Biology Graduate Group	2019-present
Confidential committee for the Office of the Vice Provost — Academic Affairs	2017-2024
appointment (1), tenure (4), full professor (2) and distinguished professor letters	2022-2025

Professional

Organizing Committee, Society for Molecular Biology and Evolution Conference	2024
Chair, Genetics Society of America PEQG Conference	2022
Chair, Plant Genomes Online Conference	2022
Board of Directors, Maize Genetics Corporation	2022-present
Maize Genetics Advocacy Cmte,	2022-present
Executive Council, Society of Molecular Biology and Evolution	2022-2024
Scientific Advisory Board, FOREVER project	2021-present
Founder and organizer, Zeavolution webinar series	2019-present
Maize Genetics Awards Committee	2017,2019-2020,2022
Editorial Boards: Genes, Genomes, and Genetics Senior (2017-2024) and Associate (2014-2024) Editor, New Phytologist Associate Editor (2021-2022), eLife Reviewing Editor (2021-2024) PeerJ Senior (2018-2019) and Associate (2013-2021) Editor	
Journal peer review: Molecular Ecology, Science (2), eLife (7), Genetics , Plant Cell, Trends in Genetics , Trends in Ecology , Evolution, Evolutionary Applications, PNAS (5) , Nature Communications , G3 (3) , PLoS Genetics (2), American J Botany (2), Current Biology	

Contributions to Diversity

Maize Genetics code of conduct committee	2023-present
Society of Molecular Biology, <i>ad hoc</i> code of conduct committee	2024-2025
Faculty representative, Pop Bio graduate student DEI cmte	2023-2024
Chair, Maize Genetics review of multi-society DEI initiative	2023
Faculty representative, EEB grad preview workshop	2023
Member, IDEA Cmte, Society for Molecular Biology and Evolution	2022-2024

Outreach

Talking Biotech podcast	2025
Corteva "Breeding Bites" podcast	2024
KQED Documentary "Your Corn Tortilla Sucks... Science Can Fix It"	2024
Eat This podcast "A New Story for Maize Domestication"	2023
San Francisco Exploratorium panel on crop domestication,	2023
Good Food podcast "Maize is life"	2022
Expert interview for National Geographic, Science&Vie, Folha de S.Paulo, South China Post	2022-2025

Current Funding

NSF: "REUSite: Ecology, Evolution, and Equity in Environmental Change (4EC)" \$350,000 (PI) <i>Recommended for Funding</i> 2024-2027
NSF: "DISES: Coevolutionary dynamics of humans and maize in the Americas" \$1.6M (PI), 2023-2026
Gates Foundation: "Study and test approaches for identifying alleles associated with environmental adaptation" \$320,000 (Co-PI), 2022-2026
NSF: "PGRP: Uncovering the role of transposons in maize variation" \$800,000 of (Co-PI), 2019-2025

Invited Seminars, previous 3 years

UC Davis, May 2025
UC Berkeley, May 2025
Gomez-Pompa lecture, UC Riverside, May 2025
Maize Biology Conference of China (keynote), April 2025
Darwin Day lecture, U. Calgary, Feb 2025
Huazhong Agricultural University, Aug. 2024
Shenzhen Agricultural Genomics Institute, Aug. 2024
Yazhouwan National Laboratory, Aug 2024
Sacramento Archeological Society, July 2024
Corteva Agriscience, June 2024
U. Cologne, Mar. 2024
U. Oregon, Feb. 2024
U. Helsinki, Jan. 2024

MexPopGen International Conference (keynote), Oct. 2023

Danforth Center, Aug. 2023

Bayer Crop Science, Aug. 2023

U. Missouri, Aug. 2023

Forest Genetics Conference (keynote), July 2023

Google X, July 2023

Plant and Animal Genome Conference, Jan 2023

Iowa State University, Sep. 2022

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

Preprints

Stitzer MC, Seethara AS, Scheben A, Hsu S-K, Schulz AJ, AuBuchon-Elder T, El-Walid M, Ferebee TH, Hale CO, La T, Liu Z-Y, McMorrow SJ, Minx P, **Phillips AR**, Syring M, Wrightsman T, Zhai J, Pasquet R, McAllister C, Malcomber S, Traiperm P, Layton D, Zhong J, Costich DE, Dawe RK, Fengler K, Harris C, Irelan Z, Llaca V, Parakkal P, Zastrow-Hayes G, Woodhouse MR, Cannon EKS, Portwood J, Andorf CM, Albert PS, Birchler JA, Siepel A, **Ross-Ibarra J**, Romay MC, Kellogg E, Buckler ES, Hufford MB. Extensive genome evolution distinguishes maize within a stable tribe of grasses. doi: 10.1101/2025.01.22.633974 [5]

In press or in print

H-Index 63 (18140 citations as of Tue May 20 23:05:26 2025)

125. **Fairbanks R, Ross-Ibarra J** (2025). An ancient origin of the naked grains of maize. *PNAS Accepted*[0]
124. **Cryan E, Phinney G**, Seetharam AS, Evans MMS, Kellogg EA, Zhan J, Meyers BC, Kliebenstein DE, **Ross-Ibarra J** (2025). Molecular evolution of a reproductive barrier in maize and related species. *GENETICS In Press* [0]
123. **Li F, Gates DJ**, Buckler ES, Hufford MB, Janzen GM, Reallán-Álvarez R, Rodríguez-Zapata F, Romero Navarro JA, Sawers RJH, **Snodgrass SJ**, Sonderk, Willcox MC, Hearne SJ, **Ross-Ibarra J**, Runcie DE (2025). The utility of environmental data from traditional varieties for climate-adaptive maize breeding. *PLoS GENETICS In Press* [2]
122. Engelhorn J, **Snodgrass SJ**, Kok A, Seetharam AS, Schneider M, Kiwit T, Singh A, Banf M, Khaipo-Burch M, Runcie DE, Sánchez Camargo V, Torres-Rodríguez JV, Sun G, Stam M, Fiorani F, Schnable JC, Bass HW, Hufford MB, Stich B, Frommer WB, **Ross-Ibarra J**, Hartwig T (2025). Phenotypic variation in maize can be largely explained by genetic variation at transcription factor binding sites. *NATURE GENETICS In Press* [4]
121. Andorf CM, **Ross-Ibarra J**, Seetharam AS, Hufford MB, Woodhouse MR (2024). A unified VCF data set from nearly 1,500 diverse maize accessions and resources to explore the genomic landscape of maize. *G3 jkae281* [3]
120. **O'Brien AM**, Sawers RJH, Gasca-Pineda J, Baxter I, Eguiarte LE, **Ross-Ibarra J**, Strauss SY (2024). Teosinte populations exhibit weak local adaptation to their rhizosphere biota despite strong effects of biota source on teosinte fitness and traits. *EVOLUTION* 78: 1991-2005 [1]
119. Berube B, Ernst E, Cahn J, Roche B, de Santis Alves C, Lynn J, Scheben A, Siepel A, **Ross-Ibarra J**, Kermicle J, Martienssen RA (2024). Teosinte Pollen Drive guides maize domestication and evolution by RNAi. *NATURE* 633: 380-388 [10]
118. **Tittes S**§, **Lorant A**, **McGinty S**†, Doebley JF, Holland JBH, Sánchez-González JdJ, Seetharam A, Tenaillon M, **Ross-Ibarra J**§ (2023). Not so local: the population genetics of convergent adaptation in maize and teosinte. *eLife*12:RP92405 [15]
117. **Yang N***, Wang Y*, Liu X, Jin M, Vallebuena-Estrada M, Calfee E, Chen L, Dilkes BP, Gui S, Fan X, Harper TK, Kennett DJ, Li W, Lu Y, Luo J, **Mambakkam S**†, **Menon M**, Snodgrass S, Veller C, Wu

- S, Wu S, Xiao Y, Yang X, Stitzer MCS, Runcie DE, Yan J[§], **Ross-Ibarra J[§]** (2023). Two teosintes made modern maize. *SCIENCE* 382: eadg8940. [93]
116. Khaipho-Burch M, Cooper M, Corra J, de Leon N, Holland J, Lewis R, McCouch S, Murray SC, Rabbi I, Ronald P, **Ross-Ibarra J**, Weigel D, Yan J, Buckler ES (2023). Genetic modification can improve crop yields — but stop overselling it. *NATURE* 621:470-473. [79]
 115. Flint-Garcia S, Feldmann MJ, Dempewolf H, Morrell PL, **Ross-Ibarra J** (2023). Diamonds in the Not-So-Rough: Wild Relative Diversity Hidden in Crop Genomes *PLoS BIOLOGY* 21: e3002235 [14]
 114. Sun S, Wang B, Li C, Xu G, Yang J, Hufford MBH, **Ross-Ibarra J**, Wang H, Wang L (2023). Unraveling prevalence and effects of deleterious mutations in maize elite lines across decades of modern breeding *MOLECULAR BIOLOGY AND EVOLUTION* 40: msad170 [6]
 113. **Phillips AR***, Seetharam AR*, Albert PS, AuBuchon-Elder T, Birchler JA, Buckler ESB, Gillespie LJ, Hufford MB, Llaca V, Romay MC, Soreng RJ, Kellogg E, **Ross-Ibarra J** (2023). A happy accident: a novel turfgrass reference genome. *G3* 13:jkado73 [7]
 112. Hu H, Crow T, Nojoomi S, Schulz, AJ, Hufford MB, Flint-Garcia SF, Sawers RJ, Rellán-Álvarez R, Estévez-Palmas JM, **Ross-Ibarra J**, Runcie DE (2023). Allele-specific expression reveals multiple paths to highland adaptation in maize. *MOL. BIO. EVOL.* 39: msac239 [15]
 111. **Rushworth CA**, Wardlaw AM, **Ross-Ibarra J**, Brandvain Y (2022). Conflict over fertilization underlies the transient evolution of reinforcement. *PLoS BIOLOGY* 20: e3001814 [6]
 110. Chen L*, Luo J*, Minliang Jin*, **Yang N*[§]**, Liu X, Peng Y, Li W, **Phillips AR**, **Cameron B**, Bernal J, Rellán-Álvarez R, Saers RJH, Liu Q, Yin Y, Ye X, Yan J, Zhang Q, Zhang X, Wu S, Gui S, Wei W, Wang Y, Luo Y, Jiang C, Deng M, Jin M, Jian L, Yu Y, Zhang M, Yang X, Hufford MB, Fernie AR, Warburton ML, **Ross-Ibarra J[§]**, Yan J[§] (2022). Genome sequencing reveals evidence of adaptive variation in the genus *Zea*. *NATURE GENETICS* 54: 1736–1745 [81]
 109. Li C, Guan H, Jing X, Li Y, Wang B, Li Y-X, Liu X, Zhang D, Liu C, Xie X, Zhao H, Wang Y, Liu J, Zhang P, Hu G, Li G, Li S, Sun D, Wang X, Shi Y, Song Y, Jiao CZ[§], **Ross-Ibarra J[§]**, Li Y[§], Wang T[§], Wang H[§] (2022). Genomic Insights into Historical Improvement of Heterotic Groups during Modern Hybrid Maize Breeding. *NATURE PLANTS* 8: 750-763 [69]
 108. Guerra-Garcia A, Rojas-Barrera IC, **Ross-Ibarra J**, Papa R, Piñero D (2022). The genomic signature of wild-to-crop introgression during the domestication of scarlet runner bean (*Phaseolus coccineus* L.). *EVOLUTION LETTERS* 6: 295-307 [15]
 107. Barnes AC, Rodríguez-Zapata F, Blöcher-Juárez KA, **Gates DJ**, Kur A, Wang L, Janzen GM, Jensen S, Estévez-Palmas JM, Crow T, Taylor Crow, Aguilar-Rangel R, Demesa-Arevalo E, Skopelitis T, Pérez-Limón S, Stuttsa WL, Chiu Y-C, Jackson D, Fiehn O, Runcie D, Buckler ES, **Ross-Ibarra J**, Hufford M, Sawers RJH, Rellán-Álvarez R (2022). An adaptive teosinte mexicana introgression modulates phosphatidylcholine levels and is associated with maize flowering time *PNAS* 119: e2100036119 [47]
 106. **Horvath R[§]**, **Menon M**, Stitzer M, **Ross-Ibarra J[§]** (2022). Controlling for Variable Transposition Rate with an Age-Adjusted Site Frequency Spectrum. *GENOME BIOLOGY AND EVOLUTION* 14: evac016 [7]

105. **Hudson AI, Odell SG**, Dubreuil P, Tixier M-H, Praud S, Runcie DE, **Ross-Ibarra J** (2022). Analysis of genotype by environment interactions in a maize mapping population. *G3* 12: jkac013 [25]
104. Samayoa LF, Olukolu BA, Yang CJ, Chen Q, Stetter MG, York AM, Sanchez-Gonzalez JJ, Glaubitz JC, Bradbury PJ, Romay MC, Sun Q, Yang J, **Ross-Ibarra J**, Buckler ES, Doebley JF, and Holland JB (2022). Domestication reshaped the genetic basis of inbreeding depression in a maize landrace compared to its wild relative, teosinte. *PLOS GENETICS* 17: e1009797 [14]
103. Perez-Limón S, Li M, Cintora-Martinez GC, Aguilar-Range MR, Salazar-Vidal MN, González-Segovia E, Blocher-Juárez K, Guerrero-Zavala A, Barrales-Gamez B, Carcano-Macias J, Nieto-Sotelo J, Martínez de la Vega O, Simpson J, Hufford MB, **Ross-Ibarra J**, Flint-Garcia S, Diaz-Garcia L, Rellán-Álvarez R, Sawers RJH (2022). A B73 x Palomero Toluqueño mapping population reveals local adaptation in Mexican highland maize. *G3* 12: jkab447 [13]
102. **Odell SG, Hudson AI**, Praud S, Dubreuil P, Tixier M-H, **Ross-Ibarra J**, Runcie DE (2022). Modeling allelic diversity of multi-parent mapping populations affects detection of quantitative trait loci. *G3* 12: jkac011 [11]
101. Calfee E^S, **Gates DJ, Lorant A, Perkins MT**, Coop GM^S, **Ross-Ibarra J^S** (2021). Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. *PLOS GENETICS* 17: e1009810 [75]
100. **Stitzer MC^S**, Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. *PLOS GENETICS* 17: e1009768 [127]
99. Hufford MB, Seetharam AS, Woodhouse MR, Chougule KM, Ou S, Liu J, Ricci WA, Guo T, Olson A, Qiu Y Della Coletta R, **Tittes S, Hudson AI**, Marand AP, Wei S Lu Z, Wang B, Tello-Ruiz MK, Piri R, Wang N, Kim D, Zeng Y, O'Connor CH, Li X, Gilbert AM, Baggs E, Krasileva KV, Portwood JL, Cannon EKS, Andorf CM, Manchanda N, Snodgrass SJ, Hufnagel DE, Jiang Q, Pedersen S, Syring ML, Kudrna DA, Llacá V, Fengler K, Schmitz RJ, **Ross-Ibarra J**, Yu J, Gent JL, Hirsch CN, Ware D, Dawe RK (2021). De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. *SCIENCE* 373:655-662 [508]
98. Song CB, Wang H, Wu, Y, Rees E, **Gates DJ**, Burch M, Bradbury PJ, **Ross-Ibarra J**, Kellogg EA, Hufford MB, Romay MC, Buckler ES (2021). Constrained non-coding sequence provides insights into regulatory elements and loss of gene expression in maize. *GENOME RESEARCH* gr.266528.120 [51]
97. **Wang L**, Josephs EB, Lee KM, Roberts LM, Rellán-Álvarez R, **Ross-Ibarra J^S**, Hufford MB^S (2021). Molecular parallelism underlies convergent highland adaptation of maize landraces. *MOLECULAR BIOLOGY AND EVOLUTION* msab119 [63]
96. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. *GENETICS* 218(2):iyab061 [30]
95. Lozano R, Gazave E, dos Santos JPR, Stetter MG, Valluru R, Bandillo N, Fernandes SB, Brown PJ, Shakoob N, Mockler T, Cooper EA, **Perkins MT**, Buckler ES, **Ross-Ibarra J^S**, Gore M^S (2021). Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. *NATURE PLANTS* 7: 17-24 [74]

94. **Ross-Ibarra J**, Piperno D (2020). Maize moving. Figshare. doi: 10.6084/m9.figshare.12781307.v1 [1]
93. Xu G, Lyu J, Li Q, Liu H, Wang D, Zhang M, Springer NM, **Ross-Ibarra J**, Yang J (2020). Adaptive evolution of DNA methylation reshaped gene regulation in maize NATURE COMMUNICATIONS 11: 5539 [103]
92. Chen Q, Samayo LF, Yang CJ, Bradbury PJ, Olukolu BA, Neumeyer MA, Roday MC, Sun Q, **Lorant A**, Buckler ES, **Ross-Ibarra J**, Holland JB, Doebley JF (2020). The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication PLOS GENETICS 16.5:e1008791. [42]
91. **Zeitler L**, **Ross-Ibarra J**[§], **Stetter MGS**[§] (2020). Selective loss of diversity in doubled-haploid lines from European maize landraces. G3 10: 2497-2506 [12]
90. 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 52: 565-571 [244]
89. Torres R*, **Stetter MG***, Hernandez R[§], **Ross-Ibarra J**[§] (2020). The temporal dynamics of background selection in non-equilibrium populations. GENETICS 214: 1019-1030 [35]
88. **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 [53]
87. 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 [43]
86. 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 [115]
85. Wei X, Anderson SN, Wang X, Yang L, Crisp PA, Li Q, Noshay J, Albert PS, Birchler JA, **Bilinski P**, **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 [10]
84. **O'Brien AM**[§], Sawers RJH, Strauss SY, **Ross-Ibarra J**[§] (2019). Adaptive phenotypic divergence in an annual grass differs across biotic contexts. EVOLUTION 73: 2230-2246 [28]
83. Gonzalez-Segovia E, Pérez-Limon S, Cántora-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. [32]
82. **Gates DJ**[§], Runcie D, Janzen GM, Romero Navarro A, Willcox M, Sonder K, Snodgrass SJ, Rodríguez-Zapata F, Sawers RJH, Rellán-Álvarez R, Buckler ES, Hearne S, Hufford MB, **Ross-Ibarra J**[§] (2019). Single-gene resolution of locally adaptive genetic variation in Mexican maize. BIORxiv 706739; doi: 10.1101/706739 [41]

81. **Josephs EM^S**, Berg JJ, **Ross-Ibarra J**, Coop G (2019) Detecting adaptive differentiation in structured populations with genomic data and common gardens. *GENETICS* 211: 989-1004. [52]
80. **Stetter MG^S**, Thornton K, **Ross-Ibarra J^S** (2018) Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. *PLOS GENETICS* 14(11): e1007794. [55]
79. **O'Brien A^S**, Sawers R, **Ross-Ibarra J**, Strauss SY^S (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. *AMERICAN NATURALIST* 192(6): 715-730. [36]
78. **Stitzer MC^S**, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. *NEW PHYTOLOGIST* 220:395-408 [127]
77. Manchanda N, Snodgrass SJ, **Ross-Ibarra J**, Hufford MB (2018) Evolution and adaptation in the maize genome. pages 319-332 *In THE ZEA MAYS GENOME*, Bennetzen, Flint-Garcia, Hirsch, Tuberosa (Eds.), Springer Nature Publishing [7]
76. **Lorant A**, **Ross-Ibarra J**, Maud Tenaillon (2018) Genomics of long- and short- term adaptation in maize and teosinte. Pages 289-311 *In STATISTICAL POPULATION GENOMICS*, Dutheil (Ed.), Springer Nature Publishing [15]
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. [127]
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, Montañño-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* 87: 128-132. [23]
73. **Bilinski P^S**, Albert P, Berg JJ, Birchler JA, Grote M, **Lorant A**, **Quezada J[†]**, Swarts, K, **Yang J**, **Ross-Ibarra J^S** (2018) Parallel altitudinal clines reveal adaptive evolution of genome size in *Zea mays*. *PLOS GENETICS* 14: e1007162 [142]
72. **Mei W**, **Stetter MG**, **Gates DJ**, **Stitzer MC**, **Ross-Ibarra J^S** (2018) Adaptation in plant genomes: bigger is different. *AMERICAN JOURNAL OF BOTANY* 105: 16-19 [68]
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 [328]

70. Wang L, **Beissinger TM**, **Lorant A**, **Ross-Ibarra C**, **Ross-Ibarra J^S**, Hufford MB^S (2017) The interplay of demography and selection during maize domestication and diffusion. *GENOME BIOLOGY* 18:215 [212]
69. **Yang J^S**, **Mezmouk S***, Baumgarten A, Buckler ES, Guill KE, McMullen MD, Mumm RH, **Ross-Ibarra J^S** (2017) Incomplete dominance of deleterious alleles contribute substantially to trait variation and heterosis in maize. *PLoS GENETICS* 13:e1007019 [160]
68. **Lorant A**, Pedersen S, Holst I, Hufford MB, Winter K, Piperno D, **Ross-Ibarra J^S** (2017) The potential role of genetic assimilation during maize domestication. *PLoS ONE* 12:e0184202 [31]
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 [21]
66. **Stetter MG^S**, **Gates DJ**, **Mei W**, **Ross-Ibarra J^S** (2017) How to make a domesticate. *CURRENT BIOLOGY* 27:R896-R900 [79]
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 [204]
64. **Bilinski P^S**, Han Y, Hufford MB, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J^S** (2017) Genomic abundance is not predictive of tandem repeat localization in grass genomes. *PLoS ONE* 12:e0177896 [10]
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 [1224]
62. **Renny-Byfield S^S**, Rodgers-Melnick E, **Ross-Ibarra J^S** (2017) Gene fractionation and function in the ancient subgenomes of maize. *MOL. BIOL. EVOL.* 34:1825-1832 [86]
61. **Velasco D**, Aradhya M, and **Ross-Ibarra J^S** (2016) Evolutionary genomics of peach and almond domestication. *G3* 6:3985-3993 [34]
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 [34]
59. **Durvasula A^{†*}**, Hoffman PJ*, **Kent TV[†]**, Liu C, Kono TJY, Morrell PL^S, **Ross-Ibarra J^S** (2016) ANGSD-wrapper. *MOLECULAR ECOLOGY RESOURCES* 16:1449-1454 [21]
58. **Beissinger TM^S**, Wang L, **Crosby K**, **Durvasula A[†]**, Hufford MB, **Ross-Ibarra J^S** (2016) Recent demography drives changes in linked selection across the maize genome. *NATURE PLANTS* 2:16084 [130]

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 [34]
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. [68]
55. Gerke JP^S, Edwards JW, Guill KE, **Ross-Ibarra J**^S, McMullen MD. The genomic impacts of drift and selection for hybrid performance in maize (2015). *GENETICS* 201: 1201-1211 [57]
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 [455]
53. **Takuno S**, Ralph P, Swarts K, Elshire RJ, Glaubitz JC, Buckler ES, **Hufford MB**, **Ross-Ibarra J**^S (2015) Independent molecular basis of convergent highland adaptation in maize. *GENETICS* 200:1297-1312 [80]
52. **Vann LE**, **Kono T**, **Pyhäjärvi T**, **Hufford MB**^S, **Ross-Ibarra J**^S (2015) Natural variation in teosinte at the domestication locus *teosinte branched1* (*tb1*). *PEERJ* 3:e900 [19]
51. Hake S, **Ross-Ibarra J** (2015) Genetic, evolutionary and plant breeding insights from the domestication of maize. *ELIFE* 2015;4:e05861 [140]
50. Fonseca RR, Smith B, Wales N, Cappellini E, Skoglund P, Fumagalli M, Samaniego JA, Caroe C, Avila-Arcos MC, Huftnagel 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 [0]
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). [13]
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. [469]
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 [395]
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 [21]
45. **Mezmouk S**, **Ross-Ibarra J**^S (2014) The pattern and distribution of deleterious mutations in maize. *G3* 4:163-171 [99]
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 [136]

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 [157]
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. [144]
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 [630]
40. **Hufford MB**, Lubinsky P, **Pyhäjärvi T**, **Devenganzo MT[‡]**, Ellstrand NC, **Ross-Ibarra J[§]** (2013) The genomic signature of crop-wild introgression in maize. *PLOS GENETICS* 9(5): e1003477. [368]
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. [10]
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 [532]
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. [28]
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 [97]
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 [24]
34. **van Heerwaarden J[§]**, **Hufford MB**, **Ross-Ibarra J[§]** (2012) Historical genomics of North American maize. *PNAS* 109: 12420-12425 [190]
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 [176]
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 [959]

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 [680]
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 [123]
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 [420]
28. Morrell PL, Buckler ES, **Ross-Ibarra J**[§] (2012) Crop genomics: advances and applications. *NATURE REVIEWS GENETICS* 13:85-96 [588]
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. [804]
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 [493]
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 [27]
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 [207]
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 [441]
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 [20]
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 [92]
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 [47]

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 [145]
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. [49]
17. **van Heerwaarden J**, van Eeuwijk FA, **Ross-Ibarra J** (2010) Genetic diversity in a crop metapopulation. *HEREDITY* 104: 28-39 [52]
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. [892]
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. [33]
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. [178]
13. **Ross-Ibarra J**, Tenaillon M, Gaut BS (2009) Historical divergence and gene flow in the genus *Zea*. *GENETICS* 181: 1399-1413. [211]
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. [211]
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. [107]
10. **Ross-Ibarra J[§]**, Gaut BS (2008) Multiple domestications do not appear monophyletic. *PNAS* 105: E105 (letter). [23]
9. Gaut BS, **Ross-Ibarra J** (2008) Selection on major components of angiosperm genomes. *SCIENCE* 320: 484-486. [84]
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. [567]
7. **Ross-Ibarra J[§]** (2007) Genome size and recombination in angiosperms: a second look. *JOURNAL OF EVOLUTIONARY BIOLOGY* 20: 800-806. [37]
6. Wares JP, Barber PH, **Ross-Ibarra J**, Sotka EE, Toonen RJ (2006) Mitochondrial DNA and population size. *SCIENCE* 314: 1388-90 (letter). [35]
5. **Ross-Ibarra J[§]** (2005) QTL and the study of plant domestication. *GENETICA* 123: 197-204. [43]
4. **Ross-Ibarra J[§]** (2004) The evolution of recombination under domestication: a test of two hypotheses. *AMERICAN NATURALIST* 163: 105-112. [118]

3. **Ross-Ibarra J** (2003) Origen y domesticación de la chaya (*Cnidoscolus aconitifolius* Mill IM Johnst): La espinaca Maya (*Cnidoscolus aconitifolius* Mill I. M. Johnst): Mayan spinach. MEXICAN STUDIES 19: 287-302. [53]
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. [198]
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. [39]