

# 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  
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

Fellow, AAAS 2021  
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: 3 (26) postdoc, 5 (10) graduate, 2 (32) 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, 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*

Chair, CBS High Performance Computing Advisory Cmte	2021
Chair and Co-Chair, Ecology & Evolution Seminar Series	2020-2022
EVE representative, Faculty Executive Cmte, College of Biological Sciences	2020-2021
Advisory cmte, controlled environment facility	2020-2021
Executive Cmte, Plant Biology Graduate Group	2019-2021
Graduate advisor: Ecology Graduate Group (2018-2021), Plant Biology (2021)	
Campus-wide High-Performance Computing Task Force	2019
Hatch/AES review, Plant Sciences (2018), EVE (2019)	
Ecology Graduate Group admissions committee	2018
appointment, tenure, full professor, and distinguished professor letters (8)	
Confidential committee for the Office of the Vice Provost — Academic Affairs	2017-2021
Section Chair for Agricultural Plant Biology	2014-2019
Plant Sciences executive committee	2014-2019
Faculty advisor, Corteva graduate student symposium in plant science	2012-2021
Search committees: Climate Adaptation (PLS)	2017-2019
Dept. of Plant Sciences academic planning committee	2010-2016, 2018-2019

### *Professional*

Chair, PEQG Conference (2022)	2022
Advisory board, FOREVER project	2021
Organizing Committee, PEQG 2020 Conference	2020
Abstract review, SACNAS	2020
LEAD21 Leadership in Land Grant Institutions, Class 14	
Organizer, Zeavolution webinar series	2019-2020
Maize Genetics conference steering committee	2018-2021
Maize Genetics Awards Committee	2017,2019-2020
Advisory Board, PeerJ Preprints	2016-2019
Editorial Boards: Genes, Genomes, and Genetics Senior (2017-2021) and Associate (2014-2021) Editor, New Phytologist Associate Editor (2021), eLife Reviewing Editor (2021) PLoS Genetics Associate Editor (2018-2019), PeerJ Senior (2018-2019) and Associate (2013-2021) Editor	
Grant peer review: NSF	
Journal peer review: Cell, Nature, Nature Communications (2), Science, PLoS Genetics, Plant Cell, Trends in Genetics (2) , Current Biology , Molecular Ecology (2) , PNAS (3) , Scientific Reports , Genetics , Nature Reviews Genetics, G3, The Plant Journal, New Phytologist, eLife (3)	

*Contributions to Diversity*

Member, pilot program, graduate student mentor training	2021
Spanish translation, Evolution conf.	2021
Mentor, Graduate Student Mentoring Initiative, Cientifico Latino (2)	2021
Advisor, graduate student of color mentoring program (2)	2020-2021
EVE Diversity cmte (organized 2 workshops)	2020-2021
Faculty host, HBCU summer research internship program	2020

*Outreach*

Radiolab episode "body count"	2020
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**Current Funding**

NSF: "Uncovering the role of transposons in maize variation" \$800,000 of \$4.5M total (Co-PI), 2019-2023

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), 2018-2022

USDA: "Mapping the genetic loci controlling highland adaptation in maize", \$29,000 (PI) 2021-2023

NSF: "The genetics of highland adaptation in maize", \$4.2M (PI), 2016-2022

**Invited Seminars, previous 3 years**

U. British Columbia, Oct 2021

U. Zurich, April 2021

Gates Foundation (plenary), April 2021

U. Vienna, Mar. 2021

Fresno State U, Jan. 2021

Carnegie Institution for Science, Stanford, Dec. 2020

Calvin Spering Memorial Biodiversity Lectureship, CSSA meeting, Nov 2020

NC State, Nov 2020

Stony Brook U, Sept. 2020

U. Oulu, Finland, April 2020

NYU Abu Dhabi, Feb. 2020

U. Oregon, Feb 2020

U. Massachusetts, Nov 2019

Chinese Academy of Agricultural Sciences, June 2019

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

International Forum on Crop Science, Wuhan, June 2019

UC Riverside, May 2019

U. Vermont, Apr 2019

U. Washington, Mar 2019

Seed Central (keynote), Davis, Feb 2019

James Brewbaker Lecture on Genetics & Plant Breeding, U. Hawaii, Manoa Dec. 2018

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

### Preprints

**Tittes S**<sup>§</sup>, **Lorant A**, **McGinty S**<sup>†</sup>, Doebley JF, Holland JBH, Sánchez-González JdJ, Seetharam A, Tenailon M, **Ross-Ibarra J**<sup>§</sup>. Not so local: the population genetics of convergent adaptation in maize and teosinte. doi: 10.1101/2021.09.09.459637 [0]

**Horvath R**<sup>§</sup>, **Menon M**, Stitzer M, **Ross-Ibarra J**<sup>§</sup>. An age-adjusted site frequency spectrum identifies selection on transposable elements while controlling for demography and variable transposition rate. doi: 10.1101/2021.08.16.456262 [0]

**Hudson AI**, **Odell SG**, Dubreuil P, Tixier M-H, Praud S, Runcie DE, **Ross-Ibarra J**. Analysis of genotype by environment interactions in a maize mapping population. doi: 10.1101/2021.07.21.453280 [0]

**O'Brien AM**, Sawers RJH, Gasca-Pineda J, Baxter I, Eguiarte LE, **Ross-Ibarra J**, Strauss SY. Strengthened mutualistic adaptation between teosinte and its rhizosphere biota in cold climates. doi: 10.1101/2021.04.20.440703 [0]

Chen L\*, Luo J\*, Minliang Jin\*, **Yang N**<sup>§</sup>, Liu X, Peng Y, Li W, Liu Q, Yin Y, Ye X, Yan J, Zhang Q, Zhang X, Gui S, Wu S, 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**<sup>§</sup>, Yan J<sup>§</sup>. Portrait of a genus: the genetic diversity of *Zea*. doi: 10.1101/2021.04.07.438828 [0]

Guerra-Garcia A, Rojas-Barrera IC, **Ross-Ibarra J**, Papa R, Piñero D. The genomic signature of wild-to-crop introgression during the domestication of scarlet runner bean (*Phaseolus coccineus* L.). doi: 10.1101/2021.02.03.429668v1 [2]

Rodríguez-Zapata F, Barnes AC, 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. Teosinte introgression modulates phosphatidylcholine levels and induces early maize flowering. doi: 10.1101/2021.01.25.426574 [7]

**Rushworth CA**, Wardlaw AM, **Ross-Ibarra J**, Brandvain Y. Conflict over fertilization underlies the transient evolution of reinforcement. doi: 10.1101/2020.11.10.377481v1 [0]

**Gates DJ**<sup>§</sup>, Runcie D, Janzen GM, Romero Navarro A, Willcox M, Sonder K, Snodgrass SJ, Rodríguez-Zapata F, Sawers RJH, Rubén Rellán-Álvarez, Buckler ES, Hearne S, Hufford MB, **Ross-Ibarra J**<sup>§</sup>. Single-gene resolution of locally adaptive genetic variation in Mexican maize. doi: 10.1101/706739 [12]

*In press or in print*

H-Index 47 (11624 citations as of Fri Dec 3 06:16:12 2021)

103. 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 Accepted* [0]
102. 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. A B73 × Palomero Toluqueño mapping population reveals local adaptation in Mexican highland maize. *G3 In Press* [0]
101. **Odell SG, Hudson AI**, Praud S, Dubreuil P, Tixier M-H, **Ross-Ibarra J**, Runcie DE. Modeling allelic diversity of multi-parent mapping populations affects detection of quantitative trait loci (2022). *G3 In Press* [1]
100. Calfee E<sup>§</sup>, **Gates DJ, Lorant A, Perkins MT**, Coop GM<sup>§</sup>, **Ross-Ibarra J**<sup>§</sup> (2021). Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. *PLOS GENETICS In Press* [5]
99. **Stitzer MC**<sup>§</sup>, Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. *PLOS GENETICS In Press* [31]
98. 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, Llaca V, Fengler K, Schmitz RJ, **Ross-Ibarra J**, Yu J, Gent JI, Hirsch CN, Ware D, Dawe RK (2021). De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. *SCIENCE* 373:655-662 [27]
97. 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 [0]
96. **Wang L**, Josephs EB, Lee KM, Roberts LM, Rellán-Álvarez R, **Ross-Ibarra J**<sup>§</sup>, Hufford MB<sup>§</sup> (2021). Molecular parallelism underlies convergent highland adaptation of maize landraces. *MBE* msab119 [12]
95. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. *GENETICS* 218(2):iyab061 [5]
94. 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**<sup>§</sup>, Gore M<sup>§</sup> (2021). Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. *NATURE PLANTS* 7: 17-24 [13]
93. **Ross-Ibarra J**, Piperno D (2020). Maize moving. Figshare. doi: 10.6084/m9.figshare.12781307.v1 [0]

92. 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 [18]
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 (2020). The genetic architecture of the maize progenitor, teosinte, and how it was altered during maize domestication PLOS GENETICS 16.5:e1008791. [18]
90. **Zeitler L**, **Ross-Ibarra J**<sup>S</sup>, **Stetter MGS**<sup>S</sup> (2020). Selective loss of diversity in doubled-haploid lines from European maize landraces. G3 10: 2497-2506 [0]
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 52: 565-571 [41]
88. Torres R\*, **Stetter MG**\*, Hernandez R<sup>S</sup>, **Ross-Ibarra J**<sup>S</sup> (2020). The temporal dynamics of background selection in non-equilibrium populations. GENETICS 214: 1019-1030 [14]
87. **Turner-Hissong SD**<sup>S</sup>, Mabrey ME, Beissinger TM, **Ross-Ibarra J**, Pires JC (2020). Evolutionary insights into plant breeding. CURRENT OPINION IN PLANT BIOLOGY 54: 93-100 [15]
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 [23]
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 [57]
84. 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 [6]
83. **O'Brien AM**<sup>S</sup>, Sawers RJH, Strauss SY, **Ross-Ibarra J**<sup>S</sup> (2019). Adaptive phenotypic divergence in teosinte differs across biotic contexts. EVOLUTION 73: 2230-2246 [13]
82. 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. [13]
81. **Josephs EM**<sup>S</sup>, Berg JJ, **Ross-Ibarra J**, Coop G (2019) Detecting adaptive differentiation in structured populations with genomic data and common gardens. GENETICS 211: 989-1004. [31]
80. **Stetter MG**<sup>S</sup>, Thornton K, **Ross-Ibarra J**<sup>S</sup> (2018) Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. PLOS GENETICS 14(11): e1007794. [35]
79. **O'Brien A**<sup>S</sup>, Sawers R, **Ross-Ibarra J**, Strauss SY<sup>S</sup> (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. AMERICAN NATURALIST 192(6): 715-730. [23]

78. **Stitzer MC<sup>§</sup>, Ross-Ibarra J** (2018) Maize domestication and gene interaction. *NEW PHYTOLOGIST* 220:395-408 [42]
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* [3]
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* [4]
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. [66]
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 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*. [10]
73. **Bilinski P<sup>§</sup>**, Albert P, Berg JJ, Birchler JA, Grote M, **Lorant A**, **Quezada J<sup>†</sup>**, Swarts, K, **Yang J**, **Ross-Ibarra J<sup>§</sup>** (2018) Parallel altitudinal clines reveal adaptive evolution of genome size in *Zea mays*. *PLOS GENETICS* 14: e1007162 [72]
72. **Mei W**, **Stetter MG**, **Gates DJ**, **Stitzer MC**, **Ross-Ibarra J<sup>§</sup>** (2018) Adaptation in plant genomes: bigger is different. *AMERICAN JOURNAL OF BOTANY* 105: 16-19 [35]
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. *GIGA SCIENCE* gix134 [172]
70. Wang L, **Beissinger TM**, **Lorant A**, **Ross-Ibarra C**, **Ross-Ibarra J<sup>§</sup>**, Hufford MB<sup>§</sup> (2017) The interplay of demography and selection during maize domestication and diffusion. *GENOME BIOLOGY* 18:215 [113]
69. **Yang J<sup>§</sup>**, **Mezmouk S\***, Baumgarten A, Buckler ES, Guill KE, McMullen MD, Mumm RH, **Ross-Ibarra J<sup>§</sup>** (2017) Incomplete dominance of deleterious alleles contribute substantially to trait variation and heterosis in maize. *PLOS GENETICS* 13:e1007019 [85]

68. **Lorant A**, Pedersen S, Holst I, Hufford MB, Winter K, Piperno D, **Ross-Ibarra J<sup>§</sup>** (2017) The potential role of genetic assimilation during maize domestication. *PLoS ONE* 12:e0184202 [16]
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 [15]
66. **Stetter MG<sup>§</sup>**, **Gates DJ**, **Mei W**, **Ross-Ibarra J<sup>§</sup>** (2017) How to make a domesticate. *CURRENT BIOLOGY* 27:R896-R900 [37]
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 [111]
64. **Bilinski P<sup>§</sup>**, Han Y, **Hufford MB**, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J<sup>§</sup>** (2017) Genomic abundance is not predictive of tandem repeat localization in grass genomes. *PLoS ONE* 12:e0177896 [8]
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 [711]
62. **Renny-Byfield S<sup>§</sup>**, Rodgers-Melnick E, **Ross-Ibarra J<sup>§</sup>** (2017) Gene fractionation and function in the ancient subgenomes of maize. *MBE* 34:1825-1832 [41]
61. **Velasco D**, Aradhya M, and **Ross-Ibarra J<sup>§</sup>** (2016) Evolutionary genomics of peach and almond domestication. *G3* 6:3985-3993 [24]
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 [24]
59. **Durvasula A<sup>‡\*</sup>**, Hoffman PJ\*, **Kent TV<sup>‡</sup>**, Liu C, Kono TJY, Morrell PL<sup>§</sup>, **Ross-Ibarra J<sup>§</sup>** (2016) ANGSD-wrapper. *MOLECULAR ECOLOGY RESOURCES* 16:1449-1454 [13]
58. **Beissinger TM<sup>§</sup>**, Wang L, **Crosby K**, **Durvasula A<sup>‡</sup>**, Hufford MB, **Ross-Ibarra J<sup>§</sup>** (2016) Recent demography drives changes in linked selection across the maize genome. *NATURE PLANTS* 2:16084 [91]
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 [24]
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. [43]
55. Gerke JP<sup>§</sup>, Edwards JW, Guill KE, **Ross-Ibarra J<sup>§</sup>**, McMullen MD. The genomic impacts of drift and selection for hybrid performance in maize (2015). *GENETICS* 201: 1201-1211 [38]



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 [227]
53. **Takuno S**, Ralph P, Swarts K, Elshire RJ, Glaubitz JC, Buckler ES, **Hufford MB**, **Ross-Ibarra J**<sup>S</sup> (2015) Independent molecular basis of convergent highland adaptation in maize. *GENETICS* 200:1297-1312 [59]
52. **Vann LE**, **Kono T**, **Pyhäjärvi T**, **Hufford MB**<sup>S</sup>, **Ross-Ibarra J**<sup>S</sup> (2015) Natural variation in teosinte at the domestication locus *teosinte branched1* (*tb1*). *PEERJ* 3:e900 [12]
51. Hake S, **Ross-Ibarra J** (2015) Genetic, evolutionary and plant breeding insights from the domestication of maize. *ELIFE* 2015;4:e05861 [69]
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 [132]
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