

# 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](mailto:rossibarra@ucdavis.edu)  
Web: [rilab.ucdavis.edu](http://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  
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  
Fellow, AAAS, 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: 3 (29) postdoc, 7 (13) graduate, 2 (40) undergraduate  
Faculty trainer, Evolution and Ecology Scholars program, 2023-present  
NSF REU (EEREC) faculty advisor, 2022-present  
Plant Biology (UC Davis, PLB200A, graduate), 2018-2022  
Ecological Genomics (UC Davis, ECL 243, graduate), 2014-present  
Genetics (UC Davis, BIS 101, undergraduate), 2013-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)	
appointment, tenure, full professor, and distinguished professor letters	
Confidential committee for the Office of the Vice Provost — Academic Affairs	2017-2023
Faculty advisor, Corteva graduate student symposium in plant science	2012-2021

### *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-present
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-present) and Associate (2014-present)	
Editor, New Phytologist Associate Editor (2021-2022), eLife Reviewing Editor (2021-present) PeerJ Senior (2018-2019) and Associate (2013-2021) Editor	
Grant peer review: NSF	
Journal peer review: Cell, Nature, Science, Plant Cell, Trends in Genetics (2), Current Biology, Evolutionary Applications, Molecular Ecology, PNAS (2), Scientific Reports, Genetics, G3 (many), The Plant Journal, eLife	

### *Contributions to Diversity*

Maize Genetics code of conduct committee	2023-present
Faculty representative, Pop Bio graduate student DEI cmte	2023-present
Faculty representative, EEB grad preview workshop	2023
Member, IDEA Cmte, Society for Molecular Biology and Evolution	2022-present
Trainee, EEREC REU program,	2022-2023
Member, pilot program, graduate student mentor training	2021
Spanish translation: Evolution Conf., UC Master Gardeners	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

## Outreach

Eat This podcast “A New Story for Maize Domestication”	2023
Expert interview for National Geographic , KQED , Science&Vie , Folha de S.Paulo , South China Post	
San Francisco Exploratorium panel on crop domestication,	2023
Good Food podcast “Maize is life”	2022

## Current Funding

NSF: “REUSite: Ecology, Evolution, and Equity in Environmental Change (4EC)” \$350,000 (PI) *Recommended for Funding 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: “Uncovering the role of transposons in maize variation” \$800,000 of (Co-PI), 2019-2024

## Invited Seminars, previous 3 years

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

Advances in Genome Biology and Technology (keynote), April 2022

IPK Gatersleben, Feb, 2022

UC Davis Plant Biology, Feb. 2022

U. British Columbia, Oct 2021

U. Zurich, April 2021

Gates Foundation (plenary), April 2021



111. 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 [3]
110. **Rushworth CA**, Wardlaw AM, **Ross-Ibarra J**, Brandvain Y (2022). Conflict over fertilization underlies the transient evolution of reinforcement. *PLoS BIOLOGY* 20: e3001814 [5]
109. Chen L\*, Luo J\*, Minliang Jin\*, **Yang N\***<sup>§</sup>, 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**<sup>§</sup>, Yan J<sup>§</sup> (2022). Genome sequencing reveals evidence of adaptive variation in the genus *Zea*. *NATURE GENETICS* 54: 1736–1745 [37]
108. 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<sup>§</sup>, **Ross-Ibarra J**<sup>§</sup>, Li Y<sup>§</sup>, Wang T<sup>§</sup>, Wang H<sup>§</sup> (2022). Genomic Insights into Historical Improvement of Heterotic Groups during Modern Hybrid Maize Breeding. *NATURE PLANTS* 8: 750-763 [41]
107. 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 [6]
106. 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, Stuttza 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 [37]
105. **Horvath R**<sup>§</sup>, **Menon M**, Stitzer M, **Ross-Ibarra J**<sup>§</sup> (2022). Controlling for Variable Transposition Rate with an Age-Adjusted Site Frequency Spectrum. *GENOME BIOLOGY AND EVOLUTION* 14: evac016 [5]
104. **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 [15]
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* 17: e1009797 [9]
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 (2022). A B73 x Palomero Toluqueño mapping population reveals local adaptation in Mexican highland maize. *G3* 12: jkab447 [11]
101. **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 [5]

100. Calfee E<sup>S</sup>, **Gates DJ**, **Lorant A**, **Perkins MT**, Coop GM<sup>S</sup>, **Ross-Ibarra J**<sup>S</sup> (2021). Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. *PLoS GENETICS* 17: e1009810 [53]
99. **Stitzer MC**<sup>S</sup>, Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. *PLoS GENETICS* 17: e1009768 [95]
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 JJ, Hirsch CN, Ware D, Dawe RK (2021). De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. *SCIENCE* 373:655-662 [300]
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 [33]
96. **Wang L**, Josephs EB, Lee KM, Roberts LM, Rellán-Álvarez R, **Ross-Ibarra J**<sup>S</sup>, Hufford MB<sup>S</sup> (2021). Molecular parallelism underlies convergent highland adaptation of maize landraces. *MOLECULAR BIOLOGY AND EVOLUTION* msab119 [44]
95. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. *GENETICS* 218(2):iyabo61 [15]
94. Lozano R, Gazave E, dos Santos JPR, Stetter MG, Valluru R, Bandillo N, Fernandes SB, Brown PJ, Shakoor N, Mockler T, Cooper EA, **Perkins MT**, Buckler ES, **Ross-Ibarra J**<sup>S</sup>, Gore M<sup>S</sup> (2021). Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. *NATURE PLANTS* 7: 17-24 [52]
93. **Ross-Ibarra J**, Piperno D (2020). Maize moving. Figshare. doi: 10.6084/m9.figshare.12781307.v1 [1]
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 [70]
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. [29]
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 [9]
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 [170]

88. Torres R\*, **Stetter MG\***, Hernandez R<sup>§</sup>, **Ross-Ibarra J<sup>§</sup>** (2020). The temporal dynamics of background selection in non-equilibrium populations. *GENETICS* 214: 1019-1030 [28]
87. **Turner-Hissong SD<sup>§</sup>**, Mabrey ME, Beissinger TM, **Ross-Ibarra J**, Pires JC (2020). Evolutionary insights into plant breeding. *CURRENT OPINION IN PLANT BIOLOGY* 54: 93-100 [41]
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 [38]
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 [99]
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 [9]
83. **O'Brien AM<sup>§</sup>**, Sawers RJH, Strauss SY, **Ross-Ibarra J<sup>§</sup>** (2019). Adaptive phenotypic divergence in an annual grass differs across biotic contexts. *EVOLUTION* 73: 2230-2246 [23]
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. [24]
81. **Josephs EM<sup>§</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. [42]
80. **Stetter MG<sup>§</sup>**, Thornton K, **Ross-Ibarra J<sup>§</sup>** (2018) Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. *PLOS GENETICS* 14(11): e1007794. [53]
79. **O'Brien A<sup>§</sup>**, Sawers R, **Ross-Ibarra J**, Strauss SY<sup>§</sup> (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. *AMERICAN NATURALIST* 192(6): 715-730. [28]
78. **Stitzer MC<sup>§</sup>**, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. *NEW PHYTOLOGIST* 220:395-408 [99]
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* [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 [10]
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. [112]

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, 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*. [21]
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 [119]
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 [52]
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 [270]
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 [176]
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 [137]
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 [25]
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 [20]
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 [64]
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 [174]



64. **Bilinski P<sup>S</sup>**, Han Y, **Hufford MB**, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J<sup>S</sup>** (2017) Genomic abundance is not predictive of tandem repeat localization in grass genomes. *PLoS ONE* 12:e0177896 [119]
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 [1078]
62. **Renny-Byfield S<sup>S</sup>**, Rodgers-Melnick E, **Ross-Ibarra J<sup>S</sup>** (2017) Gene fractionation and function in the ancient subgenomes of maize. *MOL. BIOL. EVOL.* 34:1825-1832 [73]
61. **Velasco D**, Aradhya M, and **Ross-Ibarra J<sup>S</sup>** (2016) Evolutionary genomics of peach and almond domestication. *G3* 6:3985-3993 [32]
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 [32]
59. **Durvasula A<sup>†\*</sup>**, Hoffman PJ\*, **Kent TV<sup>†</sup>**, Liu C, Kono TJY, Morrell PL<sup>S</sup>, **Ross-Ibarra J<sup>S</sup>** (2016) ANGSD-wrapper. *MOLECULAR ECOLOGY RESOURCES* 16:1449-1454 [17]
58. **Beissinger TM<sup>S</sup>**, Wang L, **Crosby K**, **Durvasula A<sup>†</sup>**, Hufford MB, **Ross-Ibarra J<sup>S</sup>** (2016) Recent demography drives changes in linked selection across the maize genome. *NATURE PLANTS* 2:16084 [119]
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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. [66]
55. Gerke JP<sup>S</sup>, Edwards JW, Guill KE, **Ross-Ibarra J<sup>S</sup>**, McMullen MD. The genomic impacts of drift and selection for hybrid performance in maize (2015). *GENETICS* 201: 1201-1211 [53]
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 [396]
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 [72]
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 [16]
51. Hake S, **Ross-Ibarra J** (2015) Genetic, evolutionary and plant breeding insights from the domestication of maize. *eLIFE* 2015;4:e05861 [115]

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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). [11]
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