

# 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  |                 |
| Founder and 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 (2), Trends in Genetics (2), Current Biology, Molecular Ecology (2), PNAS (2), Scientific Reports, Genetics, Nature Reviews Genetics, G3 (many), The Plant Journal, New Phytologist, eLife (2) |                 |

*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 |
|-------------------------------|------|

**Invited Seminars, previous 3 years**

Society of American Archaeology, April 2023  
 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  
 U. Vienna, Mar. 2021  
 Fresno State U, Jan. 2021  
 Carnegie Institution for Science, Dec. 2020  
 Calvin Sperling Memorial Biodiversity Lectureship, CSSA meeting, Nov 2020  
 NC State, Nov 2020  
 Stony Brook U, Sept. 2020  
 U. Oulu, 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, June 2019  
 International Forum on Crop Science, Wuhan, June 2019

**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 [1]

**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]

**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 48 (12423 citations as of Mon Jun 6 20:15:19 2022)

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 Accepted*
107. 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.). *EVOLUTION LETTERS Accepted* [3]
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, Stuttsa WL, Chiu Y-C, Jackson D, Fiehn O, Runcie D, Buckler ES, **Ross-Ibarra J**, Hufford M, Sawers RJH, Rellán-Álvarez R (2022). Teosinte introgression modulates phosphatidylcholine levels and induces early maize flowering. *PNAS Accepted* [9]
105. **Horvath R**<sup>§</sup>, **Menon M**, Stitzer M, **Ross-Ibarra J**<sup>§</sup> (2022). An age-adjusted site frequency spectrum identifies selection on transposable elements while controlling for demography and variable transposition rate. *GENOME BIOLOGY AND EVOLUTION Accepted* [0]
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 In Press* [2]
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 (2022). A B73 x Palomero Toluqueño mapping population reveals local

adaptation in 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>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 In Press* [15]
99. **Stitzer MC**<sup>S</sup>, Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. *PLOS GENETICS In Press* [41]
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 [63]
97. Song CB, Wang H, Wu, Y, Rees E, **Gates DJ**, Burch M, Bradbury PJ, **Ross-Ibarra J**, Kellogg EA, Hufford MB, Romy 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 [12]
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. *MBE* msab119 [17]
95. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. *GENETICS* 218(2):iyab061 [6]
94. Lozano R, Gazave E, dos Santos JPR, Stetter MG, Valluru R, Bandillo N, Fernandes SB, Brown PJ, Shakoore 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 [24]
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 [33]
91. Chen Q, Samayo LF, Yang CJ, Bradbury PJ, Olukolu BA, Neumeyer MA, Romy, 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. [20]
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 [60]
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 [19]
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 [18]
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 [69]
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 [8]
83. **O'Brien AM**<sup>§</sup>, Sawers RJH, Strauss SY, **Ross-Ibarra J**<sup>§</sup> (2019). Adaptive phenotypic divergence in teosinte differs across biotic contexts. *EVOLUTION* 73: 2230-2246 [14]
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. [16]
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. [36]
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. [36]
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. [0]
78. **Stitzer MC**<sup>§</sup>, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. *NEW PHYTOLOGIST* 220:395-408 [48]
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. [74]
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, Palheiro-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*. [13]
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 [0]
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 [40]
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 [189]
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 [124]
69. **Yang J<sup>§</sup>**, **Mezmouk S<sup>\*</sup>**, 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 [95]
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 [19]
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 [16]
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 [46]

65. Swarts K, Gutaker RM, Schuenemann V, Benz B, Blake M, Bukowski R, Holland J, Kruse-Peoples 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 [123]
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 [7]
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 [791]
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. *MBE* 34:1825-1832 [45]
61. **Velasco D**, Aradhya M, and **Ross-Ibarra J<sup>S</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>S</sup>, **Ross-Ibarra J<sup>S</sup>** (2016) ANGSD-wrappier. *MOLECULAR ECOLOGY RESOURCES* 16:1449-1454 [0]
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 [97]
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. [46]
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 [39]
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 [270]
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 [63]
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