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
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

Graduate Population Genomics Workshop (HZAU, UCD)	2024-present
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	2019-2025
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

Co-Chair, International Forum on Maize Biology	2025
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), Associate (2014-2024), Guest (2025-present) Editor, New Phytologist Associate Editor (2021-2022), Peer Review in Evolutionary Bio (2025-present) bioRxiv affiliate (2021-present) eLife Reviewing Editor (2021-2024)

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 Biolgoy, *ad hoc* code of conduct committe	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 Epsil∞n Magazine, Financial History Magazine, National Geographic, Science&Vie, Folha de S.Paulo, South China Post	2022-2025

Invited Seminars, previous 3 years

PEQG Conference (keynote), June 2026

U. Southern California, Jan 2026

UC Davis, Jan 2026

BGI Wuhan, October 2025

Zhejiang University, October 2025

International Forum on Maize Biology (keynote), Wuhan, October 2025

Ecol. & Evol. Genomics Gordon Conference (keynote), Florence, July 2025

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

BAPG Conference (keynote), Nov. 2024

Huazhong Agricultural University, Aug. 2024

Shenzhen Agricultural Genomics Institue, 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

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

Preprints

Xu G, Yang X, Zhang M, Kang C, Tian Z, Qi Y, Luo M, Liu P, **Ross-Ibarra J**, Yang J, Liu H. The dominance of gene expression controlled by trans-eQTL hotspots contributes to phenotypic heterosis in maize
doi: 10.1101/2025.11.03.686376

Liu B, **Fairbanks RA**, Hirsch CN, Munasinghe M, Pope NS, **Ross-Ibarra J**§. Genome-wide selection on transposable elements in maize.
doi: 10.1101/2025.09.16.676665

O'Donnell1 DA, **Yang J**, Zamora P, Lorant A, Miao C, Van Deynze A, Bennett A, **Ross-Ibarra J**§. Heritability and QTL mapping of aerial roots and other yield component traits with implications for N2 fication in *Zea mays*.
doi: 10.1101/2025.09.10.675198v1

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 [10]

In press or in print

126. **Cao Y**, Yan J, **Ross-Ibarra J**§, Yang N§ (2025). Plant Domestication Revisited: Genomic Insights into Origins, Mechanisms, and Convergent Evolution. iScience *Accepted* [0]

125. **Fairbanks R**§, **Ross-Ibarra J**§ (2025). An ancient origin of the naked grains of maize. PNAS 122: e2503748122 [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, Rodrígues-Zapata F, Romero Navarro JA, Sawers RJH, **Snodgrass SJ**, SonderK, Willcox MC, Hearne SJ, **Ross-Ibarra J**§, Runcie DE (2025)§. Environmental data provide marginal benefit for predicting climate adaptation. PLoS Genetics 21: e1011714. [0]

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-Rodriguez 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 [5]

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 [3]

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 [13]

118. **Tittes S**[§], **Lorant A**, **McGinty S**[‡], Doebley JF, Holland JBH, Sànchez-Gonzàlez JdJ, Seetharam A, Tenaillon M, **Ross-Ibarra J**[§] (2023). Not so local: the population genetics of convergent adaptation in maize and teosinte. eLife12:RP92405 [15]

117. **Yang N**[*], Wang Y[*], Liu X, Jin M, Vallebueno-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. [109]

116. Khaipho-Burch M, Cooper M, Corrsa 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. [86]

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 [17]

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 [9]

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:jkad073 [7]

112. Hu H, Crow T, Nojoomi S, Schulz, AJ, Hufford MB, Flint-Garcia SF, Sawers RJ, Rellàn-Àlvarez R, Estèvez-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 [8]

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 [87]

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 [77]

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 [14]

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 [49]

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 [8]

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 [27]

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-Limòn S, Li M, Cintora-Martinez GC, Aguilar-Range MR, Salazar-Vidal MN, Gonzàlez-Segovia E, Blocher-Juàrez K, Guerrero-Zavala A, Barrales-Gamez B, Carcano-Macias J, Nieto-Sotelo J, Martinez de la Vega O, Simpson J, Hufford MB, **Ross-Ibarra J**, Flint-Garcia S, Diaz-Garcia L, Rellàn-Àlvarez R, Sawers RJH (2022). A B73 x Palomero Toluqueño mapping population reveals local adaptation in 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 [14]

101. Calfee E[§], **Gates DJ**, **Lorant A**, **Perkins MT**, Coop GM[§], **Ross-Ibarra J**[§] (2021). Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics 17: e1009810 [77]

100. **Stitzer MC**[§], Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. PLoS Genetics 17: e1009768 [136]

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, 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 [534]

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 [52]

97. **Wang L**, Josephs EB, Lee KM, Roberts LM, Rellán-Álvarez R, **Ross-Ibarra J**§, Hufford MB§ (2021). Molecular parallelism underlies convergent highland adaptation of maize landraces. Molecular Biology and Evolution msab119 [66]

96. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. Genetics 218(2):iyab061 [33]

95. 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**§, Gore M§ (2021). Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. Nature Plants 7: 17-24 [80]

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 [106]

92. 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. [43]

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 [13]

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 [248]

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 [36]

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 [60]

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 [44]

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 [116]

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 [11]

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, 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. [33]

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**§, 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**§, Thornton K, **Ross-Ibarra J**§ (2018) Genetic architecture and selective sweeps after polygenic adaptation to distant trait optima. PLoS Genetics 14(11): e1007794. [56]

79. **O'Brien A**§, Sawers R, **Ross-Ibarra J**, Strauss SY§ (2018) Evolutionary responses to conditionality in species interactions across environmental gradients. American Naturalist 192(6): 715-730. [37]

78. **Stitzer MC**§, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. New Phytologist 220:395-408 [132]

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 [16]

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. [128]

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, Montaño-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**§, Albert P, Berg JJ, Birchler JA, Grote M, **Lorant A**, **Quezada J**‡, Swarts, K, **Yang J**, **Ross-Ibarra J**§ (2018) Parallel altitudinal clines reveal adaptive evolution of genome size in *Zea mays*. PLoS Genetics 14: e1007162 [140]

72. **Mei W**, **Stetter MG**, **Gates DJ**, **Stitzer MC**, **Ross-Ibarra J**§ (2018) Adaptation in plant genomes: bigger is different. American Journal of Botany 105: 16-19 [71]

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 [332]

70. Wang L, **Beissinger TM**, **Lorant A**, **Ross-Ibarra C**, **Ross-Ibarra J**§, Hufford MB§ (2017) The interplay of demography and selection during maize domestication and diffusion. Genome Biology 18:215 [215]

69. **Yang J***§, **Mezmouk S***, Baumgarten A, Buckler ES, Guill KE, McMullen MD, Mumm RH, **Ross-Ibarra J**§ (2017) Incomplete dominance of deleterious alleles contribute substantially to trait variation and heterosis in maize. PLoS Genetics 13:e1007019 [167]

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