# 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: 6 (25) postdoc, 4 (9) graduate, 3 (30) 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 |
| Campus-wide High-Performance Computing Task Force | 2019 |
| Executive Cmte, Plant Biology Graduate Group | 2019-2021 |
| Ecology Graduate Group admissions committee | 2018 |
| Graduate advisor in ecological genomics, Ecology Graduate Group | 2018-2021 |
| CPB review | |
| Hatch/AES review, Plant Sciences (2018), EVE (2019) | |
| appointment, tenure, full professor, and distinguished professor letters (8) | |
| Campus Disciplinary Peer Review Committee on sexual violence and sexual harassment | 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*

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|---|---|
| Chair, PEQG Conference (2022) | 2022 |
| Advisory board, FOREVER project | 2021 |
| Organizing Committee, PEQG 2020 Conference | 2020 |
| Abstract review, SACNAS | 2020 |
| 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-present | |

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: eLife, Cell, Nature, Nature Communications, Nature Reviews Genetics, Science, PLoS Genetics, Genetics, New Phytologist, The Plant Journal, Plant Cell, Molecular Ecology, G3

### *Contributions to Diversity*

Member, pilot program, graduate student mentor training 2021

EVE Diversity cmte (oragnized 2 workshops) 2020-2021

Spanish translation, Evolution conf. 2021

Advisor, graduate student of color mentoring program (2 students, $\sim$ 45min per week during academic year) 2020-2021

Faculty host, HBCU summer research internship program 2020

## Current Funding

NSF: "Uncovering the role of transposons in maize variation" $800,000 of $4.5M total (Co-PI), 2019-2022

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), 2018-2021

NSF: "The genetics of highland adaptation in maize", $4.2M (PI), 2016-2021

## Invited Seminars, previous 3 years

Advances in Genome Biology and Technology keynote, April 2022

U. British Columbia, Oct 2021

U. Zurich, April 2021

Gates Foundation, April 2021

U. Vienna, Mar. 2021

Fresno State U, Jan. 2021

Carnegie Institution for Science, Stanford, Dec. 2020

Calvin Sperling 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

Keynote Speaker, Seed Central, U. California, Davis, Feb 2019

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

National Science Foundation, Washington DC, Sept 2018

U. Georgia, Athens, Aug 2018

Science and Society public lecture, Woodland, Aug 2018

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

### *Preprints*

**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]

**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. doi: 10.1101/2021.07.14.452335 [0]

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

Chen L*, Luo J*, Minliang Jin*, **Yang N***§, 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**§, Yan J§. Portrait of a genus: the genetic diversity of *Zea*. doi: 10.1101/2021.04.07.438828 [0]

Calfee E§, **Gates DJ**, **Lorant A**, **Perkins MT**, Coop GM§, **Ross-Ibarra J**§. Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. doi: 10.1101/2021.03.05.434040 [0]

Guerra-Garcia A, Rojas-Barrera IC, **Ross-Ibarra J**, Papa R, Piñero D. The genomic signature of wild-to-crop introgression during the domestiation of scarlet runner bean (*Phaseolus coccineus L.*). doi: 10.1101/2021.02.03.429668v1 [0]

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 [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**§, Runcie D, Janzen GM, Romero Navarro A, Willcox M, Sonder K, Snodgrass SJ, Rodríguez-Zapata F, Sawers RJH, Rubén Rellín-Álvarez, Buckler ES, Hearne S, Hufford MB, **Ross-Ibarra J**§. Single-gene resolution of locally adaptive genetic variation in Mexican maize. doi: 10.1101/706739 [11]

**Stitzer MC**§, Anderson SN, Springer NM, **Ross-Ibarra J**. The Genomic Ecosystem of Transposable Elements in Maize. doi: 10.1101/559922 [29]

## *In press or in print*

H-Index 46 (10999 citations as of Wed Jul 28 21:33:51 2021)

97. 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. De novo assembly, annotation, and comparative analysis of 26 diverse maize genomes. Science *Accepted* [11]

96. 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. Constrained non-coding sequence provides insights into regulatory elements and loss of gene expression in maize. Genome Research *Accepted* [0]

95. **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. MBE *Accepted* [9]

94. Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. Genetics *Accepted* [4]

93. 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 [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 [15]

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. [8]

90. **Zeitler L**, **Ross-Ibarra J**[§], **Stetter MGS**[§] (2020). Selective loss of diversity in doubled-haploid lines from European maize landraces. G3 10: 2497-2506 [1]

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 [32]

88. Torres R*, **Stetter MG***, Hernandez R[§], **Ross-Ibarra J**[§] (2020). The temporal dynamics of background selection in non-equilibrium populations. Genetics 214: 1019-1030 [12]

87. **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 [12]

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 [22]

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 [47]

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 [4]

83. **O'Brien AM**§, Sawers RJH, Strauss SY, **Ross-Ibarra J**§ (2019). Adaptive phenotypic divergence in teosinte differs across biotic contexts. Evolution 73: 2230-2246 [9]

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. [10]

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. [29]

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. [28]

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. [21]

78. **Stitzer MC**§, **Ross-Ibarra J** (2018) Maize domestication and gene interaction. New Phytologist 220:395-408 [40]

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* [3]

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. [58]

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 *In Press*. [8]

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 [0]

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 [34]

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 [158]

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 [104]

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 [80]

68. **Lorant A**, Pedersen S, Holst I, Hufford MB, Winter K, Piperno D, **Ross-Ibarra J**§ (2017) The potential role of genetic assimilation during maize domestication. PLoS ONE 12:e0184202 [15]

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 [13]

66. **Stetter MG**§, **Gates DJ**, **Mei W**, **Ross-Ibarra J**§ (2017) How to make a domesticate. Current Biology 27:R896-R900 [31]

65. Swarts K, Gutaker RM, Schuenemann V, Benz B, Blake M, Bukowski R, Holland J, Kruse-Peeples 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 [103]

64. **Bilinski P**§, Han Y, **Hufford MB**, **Lorant A**, Zhang P, Jiang J, **Ross-Ibarra J**§ (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 [646]

62. **Renny-Byfield S**§, Rodgers-Melnick E, **Ross-Ibarra J**§ (2017) Gene fractionation and function in the ancient subgenomes of maize. MBE 34:1825-1832 [39]

61. **Velasco D**, Aradhya M, and and **Ross-Ibarra J**§ (2016) Evolutionary genomics of peach and almond domestication. G3 6:3985-3993 [22]

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 [22]

59. **Durvasula A**‡*, Hoffman PJ*, **Kent TV**‡, Liu C, Kono TJY, Morrell PL§, **Ross-Ibarra J**§ (2016) ANGSD-wrapper. Molecular Ecology Resources 16:1449-1454 [12]

58. **Beissinger TM**§, Wang L, **Crosby K**, **Durvasula A**‡, Hufford MB, **Ross-Ibarra J**§ (2016) Recent demography drives changes in linked selection across the maize genome. Nature Plants 2:16084 [90]

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 [22]

56. Orozco-Ramìrez 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. [42]

55. Gerke JP§, Edwards JW, Guill KE, **Ross-Ibarra J**§, McMullen MD. The genomic impacts of drift and selection for hybrid performance in maize (2015). Genetics 201: 1201-1211 [35]

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 [202]

53. **Takuno S**, Ralph P, Swarts K, Elshire RJ, Glaubitz JC, Buckler ES, **Hufford MB**, **Ross-Ibarra J**§ (2015) Independent molecular basis of convergent highland adaptation in maize. Genetics 200:1297-1312 [59]

52. **Vann LE**, **Kono T**, **Pyhäjärvi T**, **Hufford MB**§, **Ross-Ibarra J**§ (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 [60]

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 [125]

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). [8]

48. Makarevitch I, Waters M, West P, **Stitzer M**, **Ross-Ibarra, J**, Springer NM (2015) Mobile elements contribute to activation of genes in response to abiotic stress. PLoS Genetics 11 (1): e1004915. [302]

47. Tiffin P, **Ross-Ibarra J** (2014) Advances and limits of using population genetics to understand local adaptation. Trends in Ecology and Evolution 29:673-680 [266]

46. **Bilinski P**, **Distor KD**, **Gutierez-Lopez J**, **Mendoza Mendoza G**, Shi J, Dawe RK, **Ross-Ibarra J**[§] (2014) Diversity and evolution of centromere repeats in the maize genome. Chromosoma 0009-5915 [17]

45. **Mezmouk S**, **Ross-Ibarra J**[§] (2014) The pattern and distribution of deleterious mutations in maize. G3 4:163-171 [69]

44. Waters AJ, **Bilinski P**, Eichten SR, Vaughn MW, **Ross-Ibarra J**, Gehring M, Springer NM (2013) Comprehensive analysis of imprinted genes in maize reveals allelic variation for imprinting and limited conservation with other species. PNAS 110:19639-19644 [101]

43. **Pyhäjärvi T**, **Hufford MB**, **Mezmouk S**, **Ross-Ibarra J**[§] (2013) Complex patterns of local adaptation in teosinte. Genome Biology and Evolution 5: 1594-1609 [128]

42. Wills DM, Whipple C, **Takuno S**, Kursel LE, Shannon LM, **Ross-Ibarra J**, Doebley JF (2013) From many, one: genetic control of prolificacy during maize domestication. PLoS Genetics 9(6): e1003604. [96]

41. McCouch S, Baute GJ, Bradeen J, Bramel P, Bretting PK, Buckler E, Burke JM, Charest D, Cloutier S, Cole G, Dempewolf H, Dingkuhn M, Feuillet C, Gepts, P, Grattapaglia D, Guarino L, Jackson S, Knapp S, Langridge P, Lawton-Rauh A, Lijua Q, Lusty C, Michael T, Myles S, Naito K, Nelson RL, Pontarollo R, Richards CM, Rieseberg L, **Ross-Ibarra J**, Rounsley S, Hamilton RS, Schurr U, Stein N, Tomooka N, van der Knaap E, van Tassel D, Toll J, Valls J, Varshney RK, Ward J, Waugh R, Wenzl P, Zamir. (2013) Agriculture: Feeding the future. Nature 499:23-24 [427]

40. **Hufford MB**, Lubinsky P, **Pyhäjärvi T**, **Devengenzo MT**[‡], Ellstrand NC, **Ross-Ibarra J**[§] (2013) The genomic signature of crop-wild introgression in maize. PLoS Genetics 9(5): e1003477. [272]

39. **Provance MC**[§], Garcia Ruiz I, **Thommes C**[‡], **Ross-Ibarra J** (2013) Population genetics and ethnobotany of cultivated *Diospyros riojae* Gómez Pompa (Ebenaceae), an endangered fruit crop from Mexico. Genetic Resources and Crop Evolution 60: 2171-2182. [7]

38. Melters DP[*], Bradnam KR[*], Young HA, Telis N, May MR, Ruby JG, Sebra R, Peluso P, Eid J, Rank D, Fernando Garcia J, DeRisi J, Smith T, Tobias C, **Ross-Ibarra J**[§], Korf IF[§], Chan SW-L. (2013) Patterns of centromere tandem repeat evolution in 282 animal and plant genomes. Genome Biology 14:R10 [288]

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