

## Biographical Sketch — Jeffrey Ross-Ibarra

### (a) Professional Preparation

Institution	Area	Degree / Training	Dates
University of California Irvine	Genetics	Postdoctoral Research	2008
University of Georgia	Genetics	PhD	2006
University of California Riverside	Botany	BA, MS	1998, 2000

### (b) Professional Appointments

Position	Institution	Dates
Professor	University of California Davis	2016-present
Associate Professor	University of California Davis	2012-2016
Assistant Professor	University of California Davis	2009-2012
Profesor de Asignatura	Universidad Nacional Autónoma de México	2001

### (c) Awards

- Fellow, AAAS 2021
- 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

### (d) Mentoring

I have mentored to date 25 postdoctoral scholars, 13 of whom have continued on in academia (9 as professors) and 10 of whom have found careers in industry. Similarly, among the 6 PhD students I have mentored, 5 remain in academia as postdocs, professors, or research scientists, and 1 has a successful career in industry. I have also mentored a large number of undergraduates, many of whom have continued on to careers in science.

### Contributions to Diversity

- Trainer, NSF REU program for research opportunities for diverse undergraduates in evolution and ecology 2022-2023
- Member, IDEA Cmte, Society for Molecular Biology and Evolution 2022-present
- Member, pilot program, graduate student mentor training 2021
- Mentor, Graduate Student Mentoring Initiative, Cientifico Latino (2) 2021
- Advisor, graduate student of color mentoring program (2) 2020-2022
- EVE Diversity cmte (organized 2 workshops) 2020-2021
- Faculty host, HBCU summer research internship program 2020

#### (e) Publications (past 4 years)

- 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. *MOL. BIO. EVOL.* *In Press* 40: msad170
- Flint-Garcia S, Hannes Dempewolf H, Feldmann MJ, Morrell PL, **Ross-Ibarra J** (2023). Diamonds in the Not-So-Rough: Wild Relative Diversity Hidden in Crop Genomes. *PLOS BIOLOGY* 21(7): e3002235
- Phillips AR, Seetharam AR, AuBuchon-Elder T, Birchler J, Buckler ES, 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
- 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. Allele-specific expression reveals multiple paths to highland adaptation in maize. *MOL. BIO. EVOL.* 39: msac239
- **Rushworth CA**, Wardlaw AM, **Ross-Ibarra J**, Brandvain Y (2022). Conflict over fertilization underlies the transient evolution of reinforcement. *PLOS BIOLOGY* 20: e3001814
- 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). Portrait of a genus: genome sequencing reveals evidence of adaptive variation in *Zea*. *NATURE GENETICS* 54: 1736-1745
- 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
- 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
- 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
- **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
- **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
- 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
- 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

- **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
- Calfee E<sup>§</sup>, **Gates DJ, Lorant A, Perkins MT**, Coop GM<sup>§</sup>, **Ross-Ibarra J**<sup>§</sup> (2021). Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. *PLOS GENETICS* 17: e1009810
- **Stitzer MC**<sup>§</sup>, Anderson SN, Springer NM, **Ross-Ibarra J** (2021). The Genomic Ecosystem of Transposable Elements in Maize. *PLOS GENETICS* 17: e1009768
- 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
- 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
- **Wang L**, Josephs EB, Lee KM, Roberts LM, Rellán-Álvarez R, **Ross-Ibarra J**<sup>§</sup>, Hufford MB<sup>§</sup> (2021). Molecular parallelism underlies convergent highland adaptation of maize landraces. *MOL. BIOL. EVOL.* msab119
- Muyle A, **Ross-Ibarra J**, Seymour DK, Gaut BS (2021). Gene body methylation is under selection in *Arabidopsis thaliana*. *GENETICS* 218(2):iyab061
- 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>§</sup>, Gore M<sup>§</sup> (2021). Comparative evolutionary analysis and prediction of deleterious mutation patterns between sorghum and maize. *NATURE PLANTS* 7: 17-24
- 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
- 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.
- **Zeitler L, Ross-Ibarra J**<sup>§</sup>, **Stetter MGS**<sup>§</sup> (2020). Selective loss of diversity in doubled-haploid lines from European maize landraces. *G3* 10: 2497-2506
- 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
- 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
- **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
- 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

- 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
- 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
- **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
- Gonzalez-Segovia E, Pérez-Limon S, Cántora-Martínez C, Guerrero-Zavala A, Jansen G, Hufford MB, **Ross-Ibarra J**, Sawers RJH (2019). Characterization of introgression from the teosinte *Zea mays* ssp. *mexicana* to Mexican highland maize. *PEERJ* 7: e6815.
- **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.