Demography and selection during the maize domestication bottleneck

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Discussion

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Discussion 2. This is the second part of the discussion section.

Significance

This work is insignificant ;-)

Reserved for Publication Footnotes

Materials and Methods

Plant materials. Accessions studied were selected from the Maize HapMap2 panel [2] . Principal component analysis was employed to ensure that closely related individuals were not included due to their potential to bias results. Ultimately, 23 maize inbreds derived from a diverse assortment of landraces were selected for inclusion. Thirteen teosinte inbred lines, all members of the subspecies Z. $mays$ ssp. $parviglumis$, were utilized. Sequences were mapped to the maize B73 version 3 reference genome [3] (ftp://ftp.ensemblgenomes.org/pub/plants/release-22/fasta/zea_mays/dna/).

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1. R. Gutenkunst, R. Hernandez,S. Williamson, and C. Bustamante, Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data, PLoS Genetics., 5:10 (2009), e1000695.

2. J. Chia, C. Song, P. Bradbury, D. Costich, N. de Leon, and others, Maize HapMap2 identifies extant variation from a genome in flux, Nature Genetics., 44 (2012), 803-807.

3. P. Schnable, D. Ware, R. Fulton, J. Stein, F. Wei, The B73 maize genome:complexity, diversity, and dynamics, Science., 326:5956 (2009), 1112-1115.