Physical and genetic structure of the maize genome reflects its complex evolutionary history

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Wei F, Coe E, Nelson W, Bharti AK, Engler F, Butler E, Kim H, Goicoechea JL, Chen M, Lee S, Fuks G, Sanchez-Villeda H, Schroeder S, Fang Z, McMullen M, Davis G, Bowers JE, Paterson AH, Schaeffer M, Gardiner J, Cone K, Messing J, Soderlund C, Wing RA.

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Abstract
Maize (Zea mays L.) is one of the most important cereal crops and a model for the study of genetics, evolution, and domestication. To better understand maize genome organization and to build a framework for genome sequencing, we constructed a sequence-ready fingerprinted contig-based physical map that covers 93.5% of the genome, of which 86.1% is aligned to the genetic map. The fingerprinted contig map contains 25,908 genic markers that enabled us to align nearly 73% of the anchored maize genome to the rice genome. The distribution pattern of expressed sequence tags correlates to that of recombination. In collinear regions, 1 kb in rice corresponds to an average of 3.2 kb in maize, yet maize has a 6-fold genome size expansion. This can be explained by the fact that most rice regions correspond to two regions in maize as a result of its recent polyploid origin. Inversions account for the majority of chromosome structural variations during subsequent maize diploidization. We also find clear evidence of ancient genome duplication predating the divergence of the progenitors of maize and rice. Reconstructing the paleoethnobotany of the maize genome indicates that the progenitors of modern maize contained ten chromosomes.