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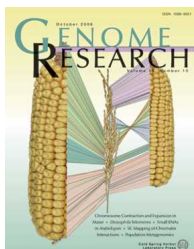
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Cover An alignment illustrating how two large duplicated chromosomal regions of the maize genome, in contrast to the orthologous region in rice, underwent both expansion and contraction following allotetraploidization. Recent construction of a physical map of maize has facilitated the sequencing of two large duplicated chromosomal regions by a BAC-based tiling path. Comparison to the orthologous region of the rice genome has resulted in the identification of syntenic blocks, which demonstrate an unevenness of insertions and deletions of genes and transposable elements following the whole-genome duplication that formed today's maize chromosomes. Furthermore, it appears that maize genes are on average larger than rice genes due to the expansion of introns by transposable elements. (Cover illustration by Arvind Bharti, Remy Bruggmann, and Joachim Messing. [For details, see Bruggman et al., 1241–1251.])