

FIGURE 11.27. Estimated locations (*red*) of quantitative trait loci (QTLs) on the maize genetic map that distinguish teosinte from maize. This distribution of QTLs suggests that six chromosomal regions spread over five of the ten chromosomes account for most of the differences between maize and teosinte. The resolution of the mapping data narrows down the search to regions that still contain many genes, and each individual QTL could contain several linked genes that contribute to trait differences. Additional experiments showed that one of the QTLs (near genetic marker M107 on chromosome 1) was due to differences at a single gene—the *tb1* gene.

11.27, modified from Doebley J. et al., Proc. Natl. Acad. Sci. 87: 9888–9892, © 1990 John Doebley

Evolution © 2007 Cold Spring Harbor Laboratory Press