Microcolinearity in sh2-homologous regions of the maize, rice, and sorghum genomes
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Abstract
Large regions of genomic colinearity have been demonstrated among grass species by recombinational mapping, but the degree of chromosomal conservation at the sub-centimorgan level has not been extensively investigated. We cloned the rice and sorghum genes homologous to the sh2 locus of maize on bacterial artificial chromosomes (BACs), and observed that a homologue of the maize a1 gene was also present on each of these BACs. In sorghum, we found a direct duplication of a1 homologues separated by about 10 kb. In maize, sh2 and a1 are approximately 140 kb apart and transcribed in the same direction, with sh2 upstream of a1. In rice and sorghum, this arrangement is fully conserved. However, the sh2 and a1 homologues are separated by about 19 kb in both rice and sorghum. We found low-copy-number and repetitive DNAs between the sh2 and a1 homologues of sorghum and rice. The sh2 and a1 homologues cross-hybridized, but the repetitive DNA and most low-copy-number sequences between these genes did not. These results indicate that maize, sorghum, and rice have conserved gene order and composition in the sh2-a1 region, but have acquired extensive qualitative and quantitative differences in the sequences between these genes.