RFLP mapping of a cross between Sorghum Bicolor and S. propinquum, suitable for high-density mapping, suggests ancestral duplication of Sorghum chromosomes 2001-1988
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Abstract
The first "complete" genetic linkage map of Sorghum section Sorghum is described, comprised of ten linkage groups putatively corresponding to the ten gametic chromosomes of S. bicolor and S. propinquum. The map includes 276 RFLP loci, predominately detected by PstI-digested S. bicolor genomic probes, segregating in 56 F2 progeny of a cross between S. bicolor and S. propinquum. Although prior cytological evidence suggests that the genomes of these species are largely homosequential, a high level of molecular divergence is evidenced by the abundant RFLP and RAPD polymorphisms, the marked deviations from Mendelian segregation in many regions of the genome, and several species-specific DNA probes. The remarkable level of DNA polymorphism between these species will facilitate development of a high-density genetic map. Further, the high level of DNA polymorphism permitted mapping of multiple loci for 21 (8.2%) DNA probes. Linkage relationships among eight (38%) of these probes suggest ancestral duplication of three genomic regions. Mapping of 13 maize genomic clones in this cross was consistent with prior results. Mapping of heterologous cDNAs from rice and oat suggests that it may be feasible to extend comparative mapping to these distantly-related species, and to ultimately generate a detailed description of chromosome rearrangements among cultivated Gramineae. Limited investigation of a small number of RFLPs showed several alleles common to S. bicolor and S. Halepense ("johnson-grass"), but few alleles common to S. propinquum and S. halepense, raising questions about the origin of S. halepense.