

Patterns of interspecific hybridization among crop and wild sorghum in open-pollinated fields

Abstract

Background and Objective: Spontaneous temporal and spatial interspecific hybridization between crops and their weedy progenitors may have potential environmental risks and implications in the adoption of genetically modified crops. This study determined the pattern of gene flow from *S. bicolor* to *S. halepense*, *S. sudanense* and *S. bicolor* ssp. *verticilliflorum* in open-pollinated field plots. **Materials and Methods:** Concentric field designs were planted to evaluate the pattern of gene flow from crops to weedy sorghums. *Sorghum halepense*, *Sorghum sudanense* and *Sorghum verticilliflorum* seed were sampled. Crop alleles in the weedy backgrounds were analysed using PCR analysis of SSR loci. A regression model with log transformation on geneflow was evaluated. **Results:** Results show the presence of spontaneous interspecific hybridization in unlimited flow design (UFD) plots. Up to 61% hybridization was observed at 5 m, 30% at 70 m and 45% at 90-100 m. A regression model $\log_{10}Y = \log_{10}A+Bx$ was determined to best fit and explain the short distance and long-distance gene flow. Species variations were seen in the flow of genes from crop to weedy sorghums in UFD plots. More interspecific hybridization events were observed above 100 m from pollen source in *S. halepense* (14.7%) and *S. sudanense* (18.8%) than in *S. verticilliflorum* (1.4%). **Conclusion:** There exist species differences in the flow of genes from crop to weedy sorghums. Therefore, isolation distances of more than 200 m and early detection of interspecific hybridization events using effective sampling and detection approaches are necessary to mitigate the potential risks.

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