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Genetic divergence and molecular characterization of sorghum hybrids and their parents for reaction to *Atherigona soccata* (Rondani)

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Summary

Simple sequence repeat (SSR) markers linked to quantitative trait loci (QTL) associated with resistance to sorghum shoot fly, *Atherigona soccata* were used to characterize the genetic and phenotypic diversity of 12 cytoplasmic male-sterile (CMS) and maintainers, 12 restorer lines, and 144 F_1 hybrids. The genetic diversity was quite high among the shoot fly-susceptible parents and the hybrids based on them, as indicated by high polymorphic information content (PIC) values, while limited genetic diversity was observed among shoot fly-resistant lines. The phenotypic and genotypic dissimilarity analysis indicated that the shoot fly-resistant and -susceptible parents were 73.2 and 38.5% distinct from each other, and the morphological and genetic distances of certain resistant and susceptible cross combinations was more than their resistant or susceptible parents. Genetic variability among the groups was low (10.8%), but high within groups (89.2%). The genetic and morphological distances suggested that the F_1 hybrids were closer to CMS (5 to 12% dissimilar) than the restorer (11 to 87% dissimilar), suggesting that CMS influences the expression of resistance to sorghum shoot fly. The SSR markers can be used to characterize the homologous traits in sorghum germplasm.

Introduction

Sorghum [*Sorghum bicolor* (L.) Moench] is one of the most important cereal crops in Africa, Asia, USA, Australia, and Latin America. Several biotic and abiotic constraints limit the production and productivity of this crop. Amongst the biotic constraints, insect-pests are predominant, causing nearly US$1 billion loss to the actual produce in semi-arid tropics (ICRISAT, 1992). More than 150 species of insects have been recorded as pests of sorghum, of which sorghum shoot fly, *Atherigona soccata* (Rondani) (Muscidae: Diptera) is an important pest in Asia, Africa, and the Mediterranean Europe (Jotwani et al., 1980; Sharma, 1993). Host plant resistance is one of the most effective means of keeping shoot fly populations below economic threshold levels. A number of genotypes with resistance to shoot fly have been identified, but the levels of resistance are low to moderate (Sharma et al., 2003). Since, most of the area under improved cultivars is planted to high-yielding hybrids, the future breeding efforts should focus on developing high yielding shoot fly-resistant hybrids. The discovery of usable sources of cytoplasmic male-sterility (CMS) (Stephens & Holland, 1954) has made it easier to incorporate the desired traits into hybrid parents (House, 1985). However, large-scale cultivation of hybrids based on a single source of CMS may be a potential danger to the stability of crop production due to their vulnerability to insect pests and diseases (Yang et al., 1989; Sharma et al., 2004). Therefore, it is important to identify shoot fly-resistant cytoplasmic male-sterile (A-lines), maintainer (B-lines), and restorer (R-lines) lines with different mechanisms of resistance, understand the nature of gene action, and transfer genes conferring resistance to shoot fly into high yielding genetic cultivars (Dhillon, 2004).