

STUDIES ON MOLECULAR CHARACTERISATION OF ELITE BC_3F_3 PROGENIES FOR SORGHUM DOWNY MILDEW RESISTANCE IN MAIZE (*ZEA MAYS* L.)

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ABSTRACT

Downy mildews, caused by several species in the genera *Peronosclerospora* and *Sclerophthora*, represent a destructive systemic disease of major economic importance to maize. Sorghum downy mildew caused by *Peronosclerospora sorghi* is considered as the most important biotic constraint limiting maize productivity. Cost concerns and the emerging problem of chemical resistance buildup in the pathogen point to the use of resistant varieties as a cost-effective and environmentally safe alternative for managing the disease. Two maize inbred lines UMI 79 and UMI 936(w) with varied responses to sorghum downy mildew incidence were crossed and the resultant progenies were backcrossed with the recurrent parent, UMI 79 for introgression of sorghum downy mildew resistant genes into the elite inbred. Three BC_3F_1 progenies (7-2-3, 7-7-7 and 7-2-10) carrying the SDM resistant QTL selected based on the heterozygosity produced by the polymorphic SSR markers were selectively selfed to generate the BC_3F_2 population. The three progenies were phenotypically screened for sorghum downy mildew resistance in sick plot condition. Progeny 7-2-10 was found to be highly susceptible to the disease and thus eliminated from further studies. Progeny 7-7-7 and 7-2-3 showed moderate level of resistance with progeny 7-7-7 showing higher resistance to sorghum downy mildew.

In the present study thirty eight phenotypically resistant individuals from 7-2-3 progeny and sixty five phenotypically resistant individuals from progeny no. 7-7-7 were selfed to generate the BC_3F_3 generation. Among these eight superior progenies were selected for genotyping with the SSR markers phi053 (chromosome 3) and nc013 (chromosome 6). One BC_3F_3 progeny (7-7-7-53) was identified homozygous for UMI 936(w) allele for both the markers and two progenies (7-7-7-85 and 7-2-3-8) were identified homozygous for UMI 936(w) allele for marker nc013 alone. These three lines can be designated as NILs (Near Isogenic Lines) resistant to the sorghum downy mildew disease and can be used in further breeding programmes. Four BC_3F_3 progenies (7-7-7-59, 7-7-7-84, 7-7-7-86 and 7-2-3-2) were identified heterozygous for the markers. They are to be selfed and advanced into next generation to identify more NILs differing for the resistance QTL alone.

KEYWORDS: Maize, Sorghum Downy Mildew, Backcross, Genotyping, Molecular Characterization, Resistant

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