STUDIES ON ESTIMATION OF GENETIC DIVERSITY IN HYBRID SORGHUM PARENTAL LINES USING RAPD MARKERS

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ABSTRACT

The development of multicut sorghum hybrid using CMS system between Sorghum (*S.bicolor*) and Sudan grass (*S.sudanense*) is an important area of research to achieve quantum jump in fodder yield. An accurate classification of parental lines in to heterotic group is essential to facilitate selection of parents and predicting the performance of F1 hybrids. In recent years, attention has focused on molecular genetic markers for assessing genetic variability and relationship among genotypes for their application in crop improvement. Therefore, the present study aimed to investigate genetic divergence among hybrid parental lines by employing RAPD markers. This will aid the long –term objectives of predicting the level of heterosis in F1 hybrid.

The genetic diversity of 15 forage sorghum parental lines comprised of five male sterile lines and ten restorer lines were estimated employing RAPD markers. Genetic distance was determined by Jaccard's similarity coefficients. Cluster dendrogram generated nine sub clusters for assessing molecular genetic diversity among the genotypes. Genetic variability among restorer lines was much higher than among cytoplasmic male sterile lines (CMS). PCR analysis based on 15 RAPD primers detected sufficient polymorphism for germplasm characterization and genetic distance. The cluster analysis based on these markers revealed that SDSL92140 (restorer line) and 2219A (cytoplasmic male sterile line) were most distant to each other and could be used in hybrid breeding programme.

Keywords- Sorghum bicolor, RAPD, Genetic Divergence, Molecular marker, Male sterile line

INTRODUCTION

The development of multicut sorghum hybrids using CMS system between sorghum(*S.bicolor*) and Sudan grass (*S.sudanense*) is an important area of research to achieve quantum jump in fodder yield(Paroda *et al* 1975). Considerable progress in this direction had already been made in the U.S.A., Australia and Russia. Where forage sorghum hybrids with nearly 40% increase over standard variety have been identified (House, L.R.1985) An accurate classification of parental lines in to heterotic group is essential to facilitate selection of parents and predicting the performance of F1 hybrids(Murty *et al.*1967). In recent years, attention has focused on molecular genetic

Table2: The number of RAPD loci of fifteen genotypes of sorghum detected using fifteen primers.

S.N.	Operon	Sequence	Total No.	Polymorphic Loci	
	Code		of loci	Number	%
1.	OPH-02	TCGGACGTGA	17	14	82.00
2.	OPE-18	GGACTGCAGA	16	16	100.00
3.	OPH-03	AGACGTCCAC	16	13	81.25
4.	OPH-04	GGAAGTCCCC	14	13	92.85
5.	OPH-05	AGTCGTCCCC	08	07	87.50
6.	OPT-02	GGAGAGACTC	13	12	92.30
7.	OPH-08	GAAACACCCC	09	05	55.55
8.	OPH-07	CTGCATCGTG	11	09	81.81
9.	OPH-09	TGTAGCTGGG	04	04	100.00
10.	OPH-14	ACCAGGTTGG	08	06	75.00
11.	OPA-04	AATCGGGCTG	10	08	80.00
12.	NO.2	TGAGTCACCCG	08	05	62.50
13.	OPH-11	CTTCCGCAGT	18	15	83.33
14.	OPH-12	ACGCGCATGT	15	14	93.33
15.	OPA-17	GACCGCTTGT	03	03	100.00
		TOTAL	170	144	84.70

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