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Inheritance pattern of fertility restoration on maldandi cytoplasm in *rabi* sorghum (*Sorghum bicolor* (L.) Moench*

Sorghum [*Sorghum bicolor* (L.) Moench], together with maize (*Zea mays* (L.) and pearl millet (*Pennisetum glaucum* (L. R. Br.], constitutes the most important cereal crops in the rainfed semi-arid tropics. The discovery of A$_1$ (*milo*) cytoplasmic nuclear male sterility (CMS) in sorghum and its subsequent exploitation for hybrid production has revolutionized sorghum production world wide. Effective use of CMS has made it easier to incorporate the desired characters into hybrid parents. Hybrid sorghum seed production relies exclusively on CMS systems and almost all hybrid sorghum seed is produced by using the *milo* CMS (A$_1$) system. In addition to the A$_1$, several other cytoplasmic sources like A$_2$, A$_3$, A$_4$, Indian A$_4$ (A$_4$ *maldandi*, A$_4$ VZM, A$_4$ G$_1$) (Rao *et al.,* 1984), A$_5$, A$_6$ and KS cytoplasms differing from each other and from the A$_1$ (*milo*) CMS system were identified. The inheritance of male sterility/fertility is dependent on the genetic make up of cytoplasm and nucleus. Male fertility restoration is controlled by a single gene in some cytoplasm + nuclear background but is polygenic when the combination changes. Intra and interallelic interaction and complementation influence the fertility restoration. Understanding the genetics of male sterility and fertility restoration of these CMS systems can enhance the efficiency of selection of good restorer and maintainer parents to develop high yielding hybrids with yield advantage based on diversified CMS seed parents (Guha *et al.,* 2002). However, inheritance studies involving iso-plasmic and allo-nuclear MS lines with common restorers are limited. This study was planned by utilizing the set of three iso-plasmic and allo-nuclear male sterile lines crossed with a common restorer that restore fertility on all these lines to determine the inheritance pattern of fertility restoration on these combination of cytoplasmic and nuclear factors.

The *maldandi* cytoplasm based MS lines (CS 35-1A, CSV 14R and M 31-2A) with different nuclear background were crossed with a common restorer *viz.,* BR J 62 that restorers fertility on all these three lines, during *rabi* 2010. Two A lines *viz.,* CS 3541A, CSV 14RA used in the study were developed at All India Coordinated Sorghum Improvement Project, Regional Agricultural Research Station, Bijapur and the other A line M 31-2A was evolved from natural mutation in M 35-1 at U.A.S., Raichur. The R line BRJ 62 was derived from the cross Afzalfur local x SPV 488.

The inheritance pattern of fertility restoration was studied in the F$_2$ of the three crosses during *rabi* 2011 and was scored for the segregation ratios (Fertility v/s Sterility) to determine the number of genes involved in the fertility restoration on *maldandi* based cytoplasmic-genic male sterility (CMS) system. The c^2 test for homogeneity of genetic ratios for each cross across the *rabi* season was done.

The results obtained on the segregation pattern in the crosses involving the restorer parent, BRJ 62 and *maldandi* cytoplasm based A lines *viz.,* CS 3541A, M 31-2A and CSV 14R are presented in the Table 1. The F$_2$ population of the cross CS 3541 x BRJ 62 segregated into 801 fertile and 56 sterile plants that correspond to the digenic ratio of 15:1. These results [c^2_{fact}=0.07; c^2 (05 & 01, df=1) = 3.84 and 6.63] gave a good chi-square (c^2) fit to the expected digenic ratio of 15 F : 1 S in F$_2$. In the second cross CSV 14RA x BRJ 62, the F$_2$ population was segregated into 714 fertile plants and 49 completely sterile plants, that corresponds to the digenic ratio of 15:1(c^2_{fact}=0.01); (c^2 (05 & 01 df=1) = 3.84 and 6.63) pattern of segregation which is exactly the expected chi-square (c^2) ratio. The F$_2$ population of the cross M 31-2A x BRJ 62 segregated into 554 fertile plants and 185 completely sterile plants, that corresponds to the monogenic ratio of 3:1 ((c^2_{fact}=0.11); (c^2 (05 & 01 df=1) = 3.84 and 6.63 pattern.

The present study on F$_2$ population revealed that the crosses CS 3541A x BRJ 62 and CSV 14RA x BRJ 62 segregated in the pattern of 15:1 (Table 1), indicating that the restoration pattern on nucleus of CS 3541A and CSV 14RA with *maldandi* cytoplasmic background is governed by two independent major genes *i.e.,* duplicate epistasis. Ahmadikhah *et al.* (2007) and Reddy *et al.* (2010) also observed duplicate epitasis gene interaction for the restoration on *maldandi* cytoplasm. Surprisingly, the F$_2$ of a cross M 31-2A x BRJ 62 showed monogenic ratio of 3:1 pattern. Based on the results obtained on the three crosses it could be concluded that restoration pattern depends both on the type of cytoplasm and nucleus of the parents.

Table 1. Segregation ratios for fertile and sterile plants in F$_2$ populations derived from three crosses involving maldandi cytoplasm based MS lines and stable restorer

Crosses	Generation	Total No. of plants	Fertile plants (F)	Sterile plants (S)	Expected ratios	Calculated χ^2	Table χ^2 at 1 df	
CS 3541A x BRJ 62	F$_2$	857	801	56	15:1	0.07	0.05	0.01
M 31-2A x BRJ62	F$_2$	739	554	185	3:1	0.11	3.84	6.63
CSV 14RA	F$_2$	763	714	49	15:1	0.01	3.84	6.63

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