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 rainy semi-arid tropics. The discovery of A1 (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 (A1) system. In addition to the A1, several other cytoplasmic sources like A2, A3, A5, Indian A6 (A7, maldandi, A7, VZM, A6, G1) (Rao et al., 1984), A2, A3 and KS cytoplasts differing from each other and from the A1 (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 14RA 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 A1 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 A1 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 Afzafur local x SPV 488.

The inheritance pattern of fertility restoration was studied in the F2 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 c2 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 F2 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 [c2(variance) =0.07; c2 (05 & 01 df=1)= 3.84 and 6.63] gave a good chi-square (c2) fit to the expected digenic ratio of 15 F : 1 S in F2. In the second cross CSV 14RA x BRJ 62, the F2 population was segregated into 714 fertile plants and 49 completely sterile plants, that corresponds to the digenic ratio of 15:1(c2(variance)=0.01); (c2 (05 & 01 df=1) = 3.84 and 6.63) pattern of segregation which is exactly the expected chi-square (c2) ratio. The F2 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 ((c2(variance) =0.11); (c2 (05 & 01 df=1) = 3.84 and 6.63 pattern.

The present study on F2 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 epistasis gene interaction for the restoration on maldandi cytoplasm. Surprisingly, the F2 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 F2 populations derived from three crosses involving maldandi cytoplasm based MS lines and stable restorer

<table>
<thead>
<tr>
<th>Crosses</th>
<th>Generation</th>
<th>Total No. of plants</th>
<th>Fertile plants (F)</th>
<th>Sterile plants (S)</th>
<th>Expected ratios</th>
<th>Calculated χ2</th>
<th>Table χ2 at 1 df</th>
</tr>
</thead>
<tbody>
<tr>
<td>CS 3541A x BRJ 62</td>
<td>F2</td>
<td>857</td>
<td>801</td>
<td>56</td>
<td>15:1</td>
<td>0.07</td>
<td>0.05 0.01</td>
</tr>
<tr>
<td>M 31-2A x BRJ62</td>
<td>F2</td>
<td>739</td>
<td>554</td>
<td>185</td>
<td>3:1</td>
<td>0.11</td>
<td>3.84 6.63</td>
</tr>
<tr>
<td>CSV 14RA</td>
<td>F2</td>
<td>763</td>
<td>714</td>
<td>49</td>
<td>15:1</td>
<td>0.01</td>
<td>3.84 6.63</td>
</tr>
</tbody>
</table>

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