Comparative analysis of restoration behavior of *milo* (104A, 401A) and *maldandi* (M31-2A) based male sterile lines in sorghum [*Sorghum bicolor* (L.) Moench]

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**Abstract**  In sorghum, *milo* source of male sterility has been used for developing all the hybrids so far and it created the narrow cytoplasmic base. In addition, it also narrows down the nuclear diversity which may be the invitation for the outbreak of pests and diseases in the near future. To handle this hazard new diverse sources like A₂, A₃, A₄, *maldandi*, VZM and G₁ have been discovered. The availability of restorers on these sources is very difficult hence their utilization is also a challenging task. The present study was, therefore, carried out to test different sorghum lines for restoration behavior on two *milo* lines (104A and 401A) and one *maldandi* (M31-2A) with more emphasis on *maldnadi* source because of its added advantage of enhancing grain size and pest tolerance. In rabi-2017, 125 genotypes were tested for the restoration behavior on these sources, and five restorers viz., IS 19389, IS 995, IS 28389, IS 26046 (BRJ 67-8) and DSMR-8 restored fertility on 104A, two lines viz., IS 29335 and IS 26046 restored on 401A, while on M31-2A six lines viz., IS 19975, BRJ-67-4 (DSMR-4), BRJ 67-8 (DSMR-8), BRJ 67-16, BRJ 67-19, BRJ 67-21 restored the fertility. only two lines DSMR-8 and DSMR-4 exhibited stable, consistent and strong restoration (> 90% seed set) across the seasons (rabi-2017 and kharif-2017) and years (2017 and rabi-2018). All the used MS lines exhibited the restoration complexity in the following order—104A < 401A < M31-2A.

**Keywords**  *Milo* · *Maldnadi* · 104A · 401A · M31-2A · Fertility restoration

**Introduction**

Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth major cereal crop of the world following wheat, rice, maize, and barley in terms of production and utilization. Sorghum grain is a dietary staple for millions of people in semi-arid areas of Asia and Africa where drought stress causes frequent failures of other crops. In Africa and Asia, sorghum grain is mainly used as food, while in the United States and Australia it is used to feed cattle (Reddy et al. 2013). Due to its versatile use as a source of food, feed, fodder and fuel, it is under cultivation in tropical, subtropical and even in temperate regions of the world as great millet. The world’s sorghum production of 57.50 million tonnes comes from the area of 40.28 m ha with the productivity of 1.43 tonnes per hectare during 2019–2020 (FAOSTAT 2020).

Cytoplasmic male sterility is a maternally inherited trait and shows impaired pollen development or abnormal anther dehiscence (Pring et al. 1995). The
exploitation of heterosis in the form of hybrids is a major component of the strategy used by grain sorghum breeding programmes. Despite the identification of other CMS sources, all the hybrids released commercially to date share the same sterile cytoplasm of milo, discovered by Stephens and Holland (1954). This situation can be an invitation for huge damage in the near future as evidenced by the repeated use of Texas cytoplasm in maize (Levings 1990).

Many researchers have reported that most of the lines show the fertile reaction on milo (A1) male sterile source, hence is easy compared to others for hybrid production (Reddy et al. 2007; Praveen et al. 2015; Sandeep and Biradar 2020). The new diverse sterile cytoplasmic sources viz., A2, A3, A4, maldandi, VZM and G1 were identified to overcome the threat of narrow cytoplasmic base. Due to the complex mechanism of restoration on non-milo cytoplasms, the restoration is difficult and research is also lacking in this area. Kishan and Borikar (1989) concluded that most of the genotypes from the Indian programme give a restorer reaction against milo cytoplasm thus; identification of suitable restorer for milo (A1) cytoplasm is quite easy. However, the milo shows poor grain quality, susceptibility to shoot fly, poor fertility restoration in hybrids under rabi environment. The A2, A3 and A4 cytoplasm are the available sources but for this, restoration appeared difficult. Because of these limitations, A2, A3, A4 and other cytoplasmic male sterile lines have not been used for commercial exploitation. Use of indigenous maldandi source of male sterility, instead of exotic milo appears to be the best option. But there are no stable and consistent fertility restorers on this cytoplasm. Hence the present study was undertaken to identify the strong and stable restorers across the seasons and years.

Material and methods

A total of 125 genotypes, comprising 68 (Set-I) and 57 (Set-II) were used as the pollen parents (Table 1 and 2). The Set-I is a part of minicore and the Set-II is comprised of mutant lines of BRJ-67 and BRJ-198. The fertility restoration of both sets was assessed on two MS lines of milo (A1) viz., 104A & 401A and one maldandi (A1m) viz., M31-2A. A set of 204 crosses [(68 + 57) × 3 CMS lines] were developed during summer and kharif season of 2017.

The experiment was conducted at Botany Garden, Agriculture College, UAS, Dharwad during rabi-2017, kharif-2018 and rabi-2018. Each hybrid was evaluated in a single row of 3 m with an intra-row spacing of 15 cm and inter row spacing of 45 cm. The hybrid plants were covered with brown paper bags to avoid cross pollination at physiological maturity. Selected panicles were harvested, observed physically for seed set and per cent seed set was calculated using the following formula (Kishan and Borikar 1989):

\[
\text{Seed set per cent} = \frac{\text{Total number of seeds/panicle}}{\text{Total number of spikelets/panicle}} \times 100
\]

Based on the seed set per cent the genotypes were grouped into different categories of restoration as described by Biradar (1996).

Results

Set-I: fertility restoration behavior of selected sorghum minicore

The sixty eight 68 hybrids based on milo CMS line (104A), fifteen exhibited satisfactory (> 60%) seed setting, while 20 were lacking in seed setting and characterized as perfect maintainers (Table 3). Four genotypes viz., IS 19389, IS 995, IS 28389 and IS 26046 were found as strong restorers as they exhibited 97.99% mean seed set. Nearly 35 per cent of lines were found to be partial restorers with an average seed set per cent of 23.82. The highest proportion of the lines (31.34%) was found to be partial restorers with an average of 24.28% seed set. A total of 11.94% (8) of the total lines were moderate restorers and revealed 97.99% seeds set. Thirteen lines exhibited low restoration with a mean seed set of 8.18%. On the other hand, two hybrids out of 68, exhibited more than 123
Table 1  Restoration status of the minicore genotypes on *milo* and *maldandi* cytoplasm sources of male sterility in *rabi*-2017

| S. No | Genotypes | Sources of CMS | S. No | Genotypes | Sources of CMS | S. No | Genotypes | Sources of CMS |
|-------|------------|----------------|-------|------------|----------------|-------|------------|----------------|
|       |            | *Milo* | *Maldandi* |            | *Milo* | *Maldandi* |            | *Milo* | *Maldandi* |
|       |            | 104A  | 401A     | M31-2A  |            | 104A  | 401A     | M31-2A  |            | 104A  | 401A     | M31-2A  |
| 1     | IS 26617   | 0.00  | 0.00     | 0.00    | 24       | IS 25989 | 14.70 | 5.18     | 0.00    | 47       | IS 12735 | 25.74 | 20.92    | 0.00    |
| 2     | IS 25249   | 66.85 | 88.55    | 0.00    | 25       | IS 29654 | 1.59  | 0.00     | 0.00    | 48       | IS 14290 | 0.00  | 0.00     | 0.00    |
| 3     | IS 28313   | 0.00  | 58.83    | 0.00    | 26       | IS 29914 | 35.72 | 0.00     | 0.00    | 49       | IS 17941 | 0.00  | 0.00     | 0.00    |
| 4     | IS 29335   | 33.65 | 97.91    | 0.00    | 27       | IS 30383 | 26.26 | 21.79    | 0.00    | 50       | IS 19859 | 0.00  | 0.00     | 0.00    |
| 5     | IS 29392   | 20.45 | 17.39    | 0.00    | 28       | IS 30451 | 74.68 | 68.46    | 0.00    | 51       | IS 20195 | 0.00  | 0.00     | 0.00    |
| 6     | IS 30466   | 23.22 | 8.63     | 0.00    | 29       | IS 30536 | 11.26 | 5.76     | 0.00    | 52       | IS 19445 | 0.00  | 0.00     | 2.54    |
| 7     | IS 27912   | 16.56 | 36.37    | 0.00    | 30       | IS 31043 | 36.70 | 28.53    | 0.00    | 53       | IS 27887 | 15.99 | 21.46    | 2.61    |
| 8     | IS 23977   | 4.16  | 8.24     | 0.00    | 31       | IS 31651 | 1.30  | 5.81     | 0.00    | 54       | IS 33353 | 0.00  | 0.00     | 4.30    |
| 9     | IS 8012    | 0.00  | 14.70    | 0.00    | 32       | IS 5667  | 15.52 | 18.62    | 0.00    | 55       | IS 24462 | 0.00  | 0.00     | 5.16    |
| 10    | IS 14861   | 71.22 | 45.93    | 0.00    | 33       | IS 24139 | 4.86  | 6.94     | 0.00    | 56       | IS 24492 | 0.00  | 0.00     | 6.36    |
| 11    | IS 15478   | 27.02 | 80.97    | 0.00    | 34       | IS 4515  | 33.81 | 25.61    | 0.00    | 57       | IS 4060  | 9.86  | 13.97    | 7.44    |
| 12    | IS 19945   | 0.00  | 0.00     | 0.00    | 35       | IS 12937 | 68.72 | 61.73    | 0.00    | 58       | IS 5667  | –    | –        | 10.85   |
| 13    | IS 19389   | 99.35 | 7.21     | 0.00    | 36       | IS 28614 | 15.43 | 9.82     | 0.00    | 59       | IS 25732 | 0.00  | 0.00     | 11.86   |
| 14    | IS 12804   | 14.40 | 71.27    | 10.05   | 37       | IS 995   | 98.27 | 13.29    | 0.00    | 60       | IS 28389 | 98.28 | 86.19    | 12.25   |
| 15    | IS 29468   | 39.28 | 19.12    | 10.54   | 38       | IS 1004  | 9.76  | 11.31    | 0.00    | 61       | IS 27299 | 13.38 | 15.76    | 16.34   |
| 16    | IS 21645   | 0.00  | 12.08    | 45.82   | 39       | IS 2413  | 19.83 | 7.69     | 0.00    | 62       | IS 21512 | 35.17 | 31.46    | 17.09   |
| 17    | IS 29568   | 2.06  | 0.00     | 0.00    | 40       | IS 2872  | 12.79 | 9.72     | 0.00    | 63       | IS 31186 | 0.00  | 0.00     | 23.15   |
| 18    | IS 11473   | 61.61 | 85.21    | 0.00    | 41       | IS 602   | 2.06  | 5.81     | 0.00    | 64       | IS 5919  | 76.90 | 78.16    | 45.97   |
| 19    | IS 7987    | 45.67 | 20.26    | 0.00    | 42       | IS 4581  | 0.00  | 0.00     | 0.00    | 65       | IS 26025 | 15.51 | 10.62    | 46.72   |
| 20    | IS 22616   | 8.32  | 6.49     | 0.00    | 43       | IS 4698  | 0.00  | 0.00     | 0.00    | 66       | IS 26046 | 96.07 | 91.46    | 61.54   |
| 21    | IS 22720   | 0.00  | 1.28     | 0.00    | 44       | IS 9745  | 0.00  | 0.00     | 0.00    | 67       | IS 19975 | 80.00 | 71.51    | 100.00  |
| 22    | IS 24175   | 87.25 | 60.37    | 0.00    | 45       | IS 10302 | 75.52 | 51.82    | 0.00    | 68       | IS 20743 | 65.48 | 68.46    | 0.00    |
| 23    | IS 24348   | 0.00  | 0.00     | 0.00    | 46       | IS 12302 | 85.33 | 75.83    | 0.00    |          |          |       |          |         |
| S. No | Genotypes | Sources of CMS | | | | | Genotypes | Sources of CMS | | | | | | Milo | Maldandi | Milo | Maldandi | Milo | Maldandi | Milo | Maldandi |
|-------|------------|----------------|----------------|----------------|----------------|----------------|------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
|       |            | 104A | 401A | M31-2A | 104A | 401A | M31-2A | 104A | 401A | M31-2A | 104A | 401A | M31-2A |
| 1     | BRJ-67-1   | 56.40 | 60.40 | 42.68 | 20    | BRJ-67-20 | 42.35 | 65.83 | 85.36 | 39    | BRJ-198-5 | 89.65 | 65.20 | 0.00 |
| 2     | BRJ-67-2   | 58.40 | 55.71 | 72.12 | 21    | BRJ-67-21 | 86.30 | 89.62 | 94.62 | 40    | BRJ-198-6 | 85.35 | 78.64 | 5.97 |
| 3     | BRJ-67-3   | 19.58 | 42.92 | 84.92 | 22    | BRJ-67-22 | 75.10 | 56.13 | 81.35 | 41    | BRJ-198-7 | 87.60 | 81.86 | 0.00 |
| 4     | BRJ-67-4   (DSMR-4) | 0.00 | 7.87 | 95.70 | 23    | BRJ-67-23 | 85.10 | 69.48 | 72.65 | 42    | BRJ-198-8 | 87.35 | 50.81 | 0.00 |
| 5     | BRJ-67-5   | 48.65 | 61.25 | 78.95 | 24    | BRJ-67-24 | 67.71 | 56.78 | 68.52 | 43    | BRJ-198-9 | 75.10 | 68.13 | 0.00 |
| 6     | BRJ-67-6   | 76.32 | 68.46 | 81.23 | 25    | BRJ-67-25 | 79.69 | 81.69 | 89.56 | 44    | BRJ-198-10 | 80.25 | 75.62 | 0.00 |
| 7     | BRJ-67-7   | 72.12 | 70.13 | 74.65 | 26    | BRJ-67-26 | 84.30 | 76.50 | 71.25 | 45    | BRJ-198-11 | 82.45 | 72.86 | 4.76 |
| 8     | BRJ-67-8   (DSMR-8) | 91.68 | 42.34 | 99.58 | 27    | BRJ-67-27 | 75.15 | 78.68 | 87.60 | 46    | BRJ-198-12 | 79.15 | 83.49 | 0.00 |
| 9     | BRJ-67-9   | 72.35 | 75.36 | 68.25 | 28    | BRJ-67-28 | 70.10 | 65.89 | 69.38 | 47    | BRJ-198-13 | 88.25 | 85.12 | 0.00 |
| 10    | BRJ-67-10  | 73.65 | 71.42 | 82.33 | 29    | BRJ-67-29 | 75.40 | 70.56 | 85.64 | 48    | BRJ-198-14 | 80.60 | 86.13 | 0.00 |
| 11    | BRJ-67-11  | 74.65 | 69.42 | 72.35 | 30    | BRJ-67-30 | 70.10 | 65.10 | 83.76 | 49    | BRJ-198-15 | 85.50 | 70.82 | 11.68 |
| 12    | BRJ-67-12  | 78.95 | 56.19 | 81.23 | 31    | BRJ-67-31 | 69.23 | 55.90 | 65.31 | 50    | BRJ-198-16 | 88.65 | 72.60 | 0.00 |
| 13    | BRJ-67-13  | 81.23 | 75.62 | 68.24 | 32    | BRJ-67-32 | 53.10 | 75.50 | 61.39 | 51    | BRJ-198-17 | 78.15 | 71.85 | 0.00 |
| 14    | BRJ-67-14  | 72.35 | 61.39 | 79.65 | 33    | BRJ-67-33 | 56.13 | 60.34 | 0.00  | 52    | BRJ-198-18 | 79.80 | 65.42 | 0.00 |
| 15    | BRJ-67-15  | 73.65 | 72.16 | 82.89 | 34    | BRJ-67-34 | 61.38 | 65.39 | 3.25  | 53    | BRJ-198-19 | 72.70 | 60.16 | 0.00 |
| 16    | BRJ-67-16  | 74.65 | 85.45 | 90.18 | 35    | BRJ-198-1 | 75.43 | 78.20 | 0.00  | 54    | BRJ-198-20 | 70.10 | 72.70 | 0.00 |
| 17    | BRJ-67-17  | 78.95 | 65.18 | 76.32 | 36    | BRJ-198-2 | 76.00 | 69.65 | 0.00  | 55    | BRJ-198-21 | 75.55 | 81.64 | 0.00 |
| 18    | BRJ-67-18  | 81.23 | 71.98 | 88.90 | 37    | BRJ-198-3 | 70.65 | 55.89 | 0.00  | 56    | BRJ-67 | 58.40 | 60.40 | 63.70 |
| 19    | BRJ-67-19  | 87.92 | 81.23 | 91.35 | 38    | BRJ-198-4 | 75.71 | 79.05 | 0.00  | 57    | BRJ-198 | 75.71 | 76.00 | 0.00 |

Genotypes in bold letters are strong and stable restorers, identified in this study such as DSMR-8 and DSMR-4.
60 per cent seed setting on selfing on the M31-2A male sterile line and only one line IS 19975 was found to be a strong restorer with 100 per cent seed set. The highest proportion of the lines (72.06%) were turned out to be perfect maintainers and were lacking in seed set. Only one line was recorded as the moderate restorer with 61.54% seed set. Eleven and six genotypes were found to be partial restorers (22.79%) and low restorers (4.74%), respectively. These results revealed that, even on the single source of cytoplasm, the restoration percentage and restoration pattern varies.

Set-II: fertility restoration behavior of mutant lines of BRJ-67 and BRJ-198

Of the 57 hybrids on 104A (milo), a total of 48 lines showed greater than 60 per cent seed set, whereas only one line turned out to be perfect maintainers (Table 4). The mutant, BRJ 67-8 (DSMR-8) exhibited strong restoration (91.68%). Around 54.39% of lines showed moderate restoration with 74.05% seed set. A total of 47 hybrids showed more than 60 per cent seed set on the second milo based CMS line (401A). The strong restorers and perfect maintainers were not observed on 401A. Majority of the lines (38) were noticed as moderate restorers and exhibited 69.82% seed set. Partial restorers (9) possessed 52.52% seed set. Only one line behaved as low restorer with mean seed set per cent of 7.87. Thirty two hybrids out of 57 exhibited greater than 60 per cent seed set on maldandi male sterile line (M31-2A). Out of these, five genotypes viz., BRJ-67-4 (DSMR-4), BRJ 67-8 (DSMR-8), BRJ 67-16, BRJ 67-19, BRJ 67-21 were considered as strong restorers as they restored an average 94.29 per cent fertility. The highest proportion of the lines 35.09% were found to be perfect maintainers with a zero per cent seed set. Fifteen lines were recorded moderate restorers with 70.85 per cent seed set. Two and three lines were turned to be partial and low restorers with 27.18 and 4.66 per cent seed set, respectively.

In all these different categories of strong, high, moderate and partial restorers, identified across the sets, the hybrids revealed the dominant and high level of expression of the fertility restorer gene(s) and similar restoration behavior of hybrids was reported by Elkonin et al. (2005) and Sanjana Reddy et al. (2010). The appearance of partial restorers shows the presence of partial restorer gene(s) in this material on both milo and maldandi sources of male sterility likewise found in studies of Jordan et al. (2010, 2011) and Elkonine et al. (1995).

Further from the two sets, 18 lines (Table 5) were selected and repeated testing was made during kharif-2018 and rabi-2018. Across three seasons two lines

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**Table 3** Classification of restoration based on mean seed set per cent in minicore in rabi-2017

| Restoration class | Seed set per cent | Diverse sources of cytoplasm |
|-------------------|------------------|------------------------------|
|                   |                  | Milo                         | Maldandi                     |
|                   | No. of genotypes | Seed set per cent | Proportion of lines | No. of restorers | Seed set per cent | Proportion of lines | No. of restorers | Seed set per cent | Proportion of lines |
| Strong restoration | > 90%            | 4                           | 97.99                      | 5.97                      | 2                           | 94.69                      | 2.99                      | 1                           | 100                      | 1.47                      |
| High restoration  | 80–90%           | 2                           | 86.29                      | 2.99                      | 4                           | 85.23                      | 5.97                      | 0                           | –                      | 0.00                      |
| Moderate restoration | 60–80%        | 9                           | 71.22                      | 13.43                     | 8                           | 69.47                      | 11.94                     | 1                           | 61.54                    | 1.47                      |
| Partial restoration | 10–60%        | 23                          | 23.83                      | 34.33                     | 21                          | 24.28                      | 31.34                     | 11                          | 22.79                    | 16.18                     |
| Low restoration   | < 10%            | 9                           | 4.89                       | 13.43                     | 13                          | 6.81                       | 19.40                     | 6                           | 4.74                     | 8.82                      |
| No seed set       | 0%                | 20                          | 0.00                       | 29.85                     | 19                          | 0.00                       | 28.36                     | 49                          | 0.00                     | 72.06                      |
Table 4  Classification of restoration based on mean seed set per cent in derived lines of BRJ-67 and BRJ-198 in rabi-2017

| Restoration class               | Seed set per cent | Diverse sources of cytoplasm |
|-------------------------------|-------------------|-----------------------------|
|                               | Milo              | Maldandi                    |
|                               | 104A              | M31-2A                       |
|                               | No. of genotypes  | Seed set per cent | Proportion of lines | No. of restorers | Seed set per cent | Proportion of lines |
| Strong restoration (> 90%)     | 1                 | 91.68                       | 1.75                | 0               | –                 | 0.00                |
| High restoration (80–90%)      | 16                | 85.11                       | 28.07               | 9               | 84.03             | 15.79               |
| Moderate restoration (60–80%)  | 31                | 74.05                       | 54.39               | 38              | 69.82             | 66.67               |
| Partial restoration (10–60%)   | 8                 | 49.13                       | 14.04               | 9               | 52.52             | 15.79               |
| Low restoration (< 10%)        | 0                 | –                           | 0.00                | 1               | 7.87              | 1.75                |
| No seedset                     | 0                 | 0.00                        | 1.75                | 0               | –                 | 0.00                |

Table 5  Selected lines identified as a restorer (> 85%) on M31-2A in rabi-2017 and kharif-2018

| S. No | Genotypes | Per cent restoration |  | S. No | Genotypes | Per cent restoration |  |
|-------|------------|-----------------------|--|-------|------------|-----------------------|--|
|       | Rabi-2017  | Kharif-2018          |  |       | Rabi-2017  | Kharif-2018          |  |
| 1     | IS 19975   | 100.00 78.16         | 7 | BRJ-67-3 | 84.92 58.37 | 13 | BRJ-67-30 | 83.76 82.73 |
| 2     | BRJ-67-8   | 99.58 99.36          | 8 | BRJ-67-25 | 89.56 84.61 | 14 | BRJ-67-15 | 82.89 75.16 |
| 3     | BRJ-67-4   | 95.70 96.81          | 9 | BRJ-67-27 | 87.60 82.08 | 15 | BRJ-67-10 | 82.33 78.62 |
| 4     | BRJ-67-21  | 94.62 86.49          | 10| BRJ-67-18 | 88.90 83.60 | 16 | BRJ-67-22 | 81.35 69.46 |
| 5     | BRJ-67-19  | 91.35 87.15          | 11| BRJ-67-29 | 85.64 81.85 | 17 | BRJ-67-12 | 81.23 52.46 |
| 6     | BRJ-67-16  | 90.18 86.24          | 12| BRJ-67-20 | 85.36 79.59 | 18 | BRJ-67-6  | 81.23 73.12 |

viz., DSMR-8 and DSMR-4 (Table 6) were found very strong and common restorers across two cytoplasm as previously reported by Praveen et al. (2015) and Sanjana Reddy et al. (2010).

Table 6  Consistent lines across the season for fertility restoration behavior against M31-2A in rabi-2018

| S. No | Restorer (DSMR-8) | M31-2A | S. No | Restorer (DSMR-4) | M31-2A |
|-------|-------------------|--------|-------|-------------------|--------|
| 1     | BRJ-67-8          | 98.94  | 2     | BRJ-67-4          | 97.42  |

Genotypes in bold letters are strong and stable restorers, identified in this study such as DSMR-8 and DSMR-4.
Discussion

Unraveling the restorers and maintainers in the given populations enhances the efficiency of selection for good and diversified restorers and maintainers to develop hybrids. In the present study, different ranges of restorers were recorded viz., partial, moderate, high and strong. This range is the result of interaction of fertility restorers gene(s) with modifiers and environment (Maunder and Pickett 1959; Erichsen and Ross 1963). Jorden et al. (2010, 2011) also documented the role of modifier or partial fertility restorer locus in A1 and A2 cytoplasms.

This study has indicated easy availability of restorers on milo compared to maldandi. It is also observed that sorghum lines restoring on maldandi are not restoring on milo. These results showed that DSMR-8 restored the fertility on both milo and maldandi. This indicates that the restorers on maldandi may not always restore the fertility on milo and identification of common restorers on both the sources is a tough task. Pattanashetti et al. (2002) also reported the similar findings. The present study revealed the complex behavior of restoration on maldandi compared to the milo and earlier Sandeep and Biradar (2020) and Sanjana Reddy et al. (2010) also reported this type of complexity. If we compare all the CMS lines used in the order of complexity for the availability of restorers it would be 104A < 401A < M31-2A, whereas the complexity for the availability of perfect maintainers would be M31-2A < 401A < 104A.

Conclusion

In this experiment, a greater number of restorers were recorded for 104A and 401A which had the blood of milo system, revealing the easy availability of restorers for this system compared to maldandi system. All the CMS lines used for this study would be in the order of 104A < 401A < M31-A for the complexity of the availability of restorers and for perfect maintainers the order would be M31-2A < 401A < 104A. This information can be utilized while handling the milo and maldandi sources of male sterility for the identification of restorers and maintainers. The newly identified common restorer on both milo and maldandi can be utilized for hybrid seed production program.

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Declarations

Conflict of interest The authors declare that they have no competing interests.

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