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Yield Evaluation and Genetic Variability Assessment in Sesame (*Sesamum Indicum L.*) Mutant Population Using Morphological Characters and Simple Sequence Repeat (SSR) Markers

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Abstract

The assessment of genetic variability is of utmost importance in crop improvement and the conservation of genetic resources. In the current study, two high-yielding sesame cultivars, namely SI 10 and SI 04, were subjected to treatment

were applied to both cultivars. In this study we aimed to evaluate the genetic variability in a mutant population of sesame (*Sesamum indicum L.*) by employing morphological characters and Simple Sequence Repeat (SSR) markers.

per plant and seeds per capsule, indirectly indicating their potential as superior yielders. Furthermore, molecular genetic variation was assessed using twenty-eight SSR markers that were widely distributed across the sesame genome to

Euclidean similarity test and a complete link clustering method, were performed to construct a dendrogram based on the morphological data. The mutants were clustered into two major groups and two minor groups. In contrast, the SSR marker-based dendrogram clustering resulted in the discovery of two major clusters, A and B, with a similarity

markers provided a more accurate representation of the true variability in the mutants compared to morphological

importance of assessing genetic variability in sesame mutants using both morphological and molecular approaches.

utilization of SSR markers for accurate characterization of genetic diversity.

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1 . F 1 , 690 2 , B 2021.

1 . F 2 , 10 . . A (A D, 2017).

50% ( ): 50%

50% ( ): 50%

et al. (2018).

A B , A -C , G , H , (GB), 200 D A 12 . CAB CAB C 70% . D A E (1) . A A, D A D A E (1) 0.8% D A 2000 .

. F

( ): 28 25 . 28 13 . 28 , 17 . H , 17 A C .

. F , 20 . 0.75 D A, 2.5 10 C , 1.25 C 2, 2.5 , 0.75 (A , C , G ,), 9.55 , 0.2 14 .

. F 4.2.2 . A , 4.2.2.

: A , 11 .

(1000):

( ): A , . :

Seed yield plot (kg)

F 3.25 (, 2005) . (H), (IC), (HE). 15 .

(A DA)
. , 2,
(< 0.05)
,
.
(2).
A ,
(/) 50%
(D).
, (/), (H),
(B),
(C), 50% (DF),
(C), ( ).
16 .
F
.
C1 18 I10 C1 02 I10
, 130.6 90.3, . ,
C1 10 I04 C4 13 I04 ,
96.5 89.9, . I ,
I10 I04 ,
54.3 54.6, .
I , 240.4 /
C1 18 I10 , C3 06 I10
222.0 / ,
. C , 84.5 /
C1 02 I10 ,
. I10 I04
145.5 / 133.3 / , 17 .
. I ,
, .
. ,
I 04 , C4 13 I04
C1 10 I04,
.
I ( ),
- 0.05. H ,
C1 18 I10 1.7 ,
18 .
, ,
.
,
. F
(3).
(=0.05)
, . 75.2
132.3 .
C4 13 I04, C1 14 I10.
I , E (0.2%)
19 .
, C2 16
I10 C1 18 I10 ,
9 8, .
. I ,
,
. , C2 18 I10
, 3,
.
50% ,
C3 12 I04, 48 ,
I04 (47). ,
C2 15 I10,
32 ,
(I04). , 50%
C1 18 I10,
C3 04 I10,
20 .
I 2 ,
E . H , ,
.
E
.
D
(I10 I04)
.
,
.
(4)
21 .
I ,
C A .

Table 2:

Source of variation	df	Y (kg/ha)	DF	PH	NBPP	NCPP	DM	NSPC	TSW (gm)	CC
Replication	1								0	0
Accession	24									
Residual										

, F 1. B, , C D C C, 22 .

. C B ,

, 14 . I C B

, 38% 90%. , 5 I 04

, C A C 9 I 10. ,

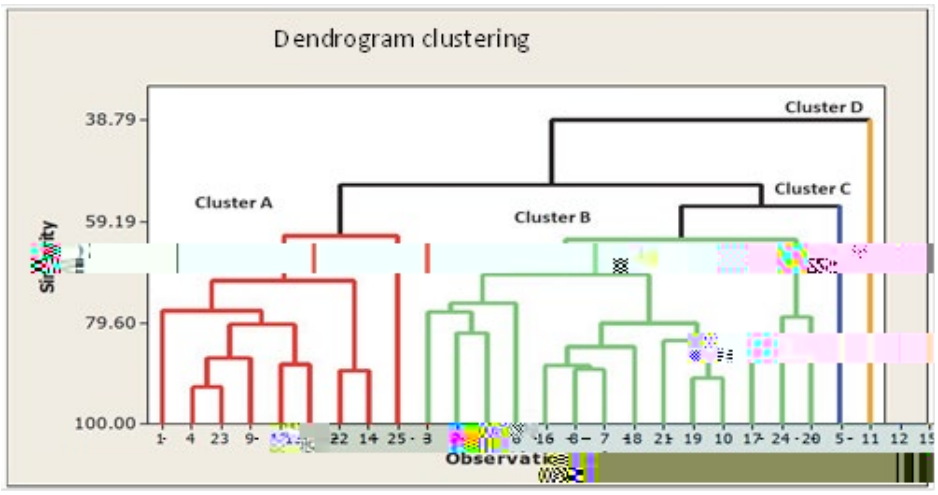

Figure 2:

, C A, E
C B, 58.0%. C A . I ,
. F ,
I 10 , .
.
A 325 ,
I 10 (F 2) 23 . 19.12 . AC558318
,
. I , AC557375
G . , , ,

(IC). 0.07 0.21,
0.16 24 .

0.95,
IC.
0.75 0.94,
.
,
.

H
. I
, 0.04 1.00,
0.53.
,
(7 5) 25 .

, 10% 20%,
. H ,
, , A
B, 79%.

C A, ,
(I, II, III, IX).
I I 04 (C1 31 I04, C3 12 I04,

. H ,
F . (2015).
,
29 .
, , C2 14 I10,
5
. I
.
7 ,
, .
10% 51.2% .
,
.
. (2015),
30 .
, ,
(H ., 2002; ↖ ., 2004; ., 2015;
., 2015).
.
I ,
.
(D ., 2005; .,
2015), .
(IC)
, IC 0.90
17 .
. (2015),
31 .
A ,
, 0.52,
. (2015).
,
32 .
.
, 10% 23%,
10% 51.2% .
,
. ,
,
(., 1996) 33 .
7 - , D ,
. A , C1 18 I10, C3 06 I10,
C4 10 I04 .
, C4 13 I04, C1 10 I04,
C1 18 I10, C2 02 I10 . I
E
,
.
-
,
- . B
,
C4 13 I04 . A , C1 18
I10,
, - , . , C4 13
I04, - ,
. , C1 10 I04, -
,
34 .
,
. B
,
.
, ,
, . F
35 .

C

I ,
.
10-20% ,
10% 51.2%.
, ,
.
A , ,
C1 18 I 10, C3 06 I 10, C4 10 I 04, C4 13 I 04, C1 10
I 04, C1 18 I 10,
.
. I
, , ,
.
B ,
. F ,
.
,
- .
,
,
, .
.
, E (0.5%)

. F