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Research Article

Assessment of genetic diversity in rabi sorghum landraces using D^2 statistics

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Abstract

We used D^2 statistics to evaluate the diversity among 91 rabi sorghum landraces including 5 checks. The analysis of variance revealed that except for the number of green leaves at maturity, the genotypic variances for all traits were significant. The 96 lines were grouped into 7 clusters where cluster I was the largest containing 80 genotypes followed by cluster II with 8 genotypes, cluster III with 4 genotypes and the remaining 4 were solitary clusters. Based on the cluster mean values, cluster V was superior for grain yield, panicle width, panicle weight and test weight, while cluster IV was noted the best for early flowering and cluster IV was good for SPAD at boot leaf and maturity stage. Based on the inter cluster distances the genotypes belonging to the clusters separated by high genetic distance genotypes from cluster IV and V (B35 and IC420956) could be used in hybridization programme for obtaining a wide spectrum of variation among the sergeants. Among the 14 characters studied panicle length (25.4%) followed by panicle weight (15.3%) and test weight (11.1%) contributed the most to the genetic divergence of the genotypes.

Keywords: Rabi sorghum landraces, genetic diversity, D^2 statistics, trait contribution.

1. Introduction

Sorghum (*Sorghum bicolor* L. Moench, 2n = 20) is the fifth largest planted crop in the world, after wheat, maize, rice, and barley (http://www.fao.org). It is often seen as a crop cultivated and consumed mostly by the poor and is habitually referred to as the poor man's crop. It is the staple food for millions of poor people in Africa and Asia's semi-arid tropics. Compared to fine cereals, sorghum is a hardy crop that has better adaptation to harsh dry conditions including excellent tolerance to drought and heat stresses.

Across the globe, sorghum is cultivated in more than 100 countries with an annual production of 62.33 million tonnes, with a productivity of 1490 kg per hectare (FAO, 2021-22). India accounts for 8% of the global production and occupies third position in terms of area after Sudan and Nigeria. In India, sorghum is cultivated during both rainy season (kharif) and post-rainy (rabi) seasons. Currently, it is cultivated in 4.00 million hectares in both seasons, with a production of 4.50 million tonnes and a productivity of 0.98 tonnes per ha. (http://www.fao.org). Because of its good grain quality, nutrition, and food value, more than 95% of post-rainy sorghum produce is used for human consumption (Ruth *et al.* 2023). In India post-rainy sorghum is grown in an area of 2.70 million hectares primarily in the states of Maharashtra, Karnataka, Telangana, with an annual production of 2.80 million tonnes and a productivity of 1030 kg ha^{-1}.

Genetic gain in any crop is determined by the amount of genetic diversity present in its base population. Hybridization between genotypes of diverse origins is suggested to uncover novel recombinants with improved genetic potential. In selecting parents to create high yielding progenies, genetic divergence has been widely used as an indirect indicator of modest efficiency. As a quantitative measure of divergence, Mahalanobis (1936) proposed the generalized distance (D^2) statistic. Plant breeders have been employing the D^2 statistic to measure genetic divergence among genotypes based on the measurement of character aggregates of genotypes so that potential parents can be selected for hybridization to achieve better genetic gains.

Landraces are the locally adapted and preferred varieties cultivated by the farmers (Elangovan *et al.*, 2012), and are the best sources of genes/alleles for adaptability, stability, and traits of economic importance and famers acceptance. Rabi sorghum has hundreds of landraces adapted and cultivated by farmers across the states of Maharashtra, Karnataka, and Telangana. The genetic diversity available in the landraces needs to be ascertained to effectively select and employ the genotypes as donors of traits in hybridization. Attempts have previously been made to estimate genetic diversity in sorghum (Doijad, *et al.*, 2015; Kavya, *et al.* (2019); Allan, *et al.* (2020); Harsh, *et al.*, 2020; Navya, *et al.*, (2021); Lokesh, *et al.* (2022); Patroti, *et al.* (2022); Kiran *et al.* (2023). Most of these studies were done with only a limited number of rabi genotypes as well as a smaller number of yield attributing traits. The current study focusses on measuring the genetic diversity among the 91 rabi sorghum landraces collected from major rabi sorghum states by measuring 14 varied quantitative traits.

2. Materials and Methods

The present investigation comprised of 91 rabi sorghum landrace accessions collected from different rabi sorghum growing states like Karnataka, Maharashtra, Telangana, and Andhra Pradesh and were evaluated along with five checks *viz.*, M35-1, CSV-22R, CSV-26R, CSV-29R and B35 (Table 1). This experiment was carried out at ICAR-Indian Institute of Millets Research, Hyderabad, Telangana, during Rabi 2019-2020. The genotypes were planted in Alpha lattice design (Patterson and Williams, 1976) with three replications. A total of 96 entries were fitted in twelve incomplete blocks in a replicate with eight plots per block in each replication according to the design generated by the Breeding Management System software (BMS software provided by the Integrated Breeding Platform), and all recommended package of practices were followed to grow a normal crop.

From each plot, five plants were randomly selected, tagged with colored ribbons in each replication for taking morphological observations on days to 50% flowering (DFF; days), plant height (PH; cm), number of green leaves at boot stage (NGLB; number), number of green leaves at maturity stage (NGLM; number), SPAD meter reading at boot stage (SPADB; reading), SPAD meter reading at maturity stage (SPADM; reading), panicle length (PL; cm), panicle width (PW; cm), number of primary branches per panicle (NPBPP; number), number of secondary branches on central primary branch of the panicle (NSBPP; number), number of seed on secondary branch (NSSB: number) panicle weight per plant (PWPP; g), grain yield per plant (GYPP; g) and 100 grain weight (TW; g).

All the statistical analyses were performed using "*metan*" package (Olivoto, 2020) under R environment. D^2 analysis was performed using "*mahala* ()" function. The data collected on 14 characters was analyzed using 'Mahalanobis' D^2 analysis to determine the genetic divergence among the rabi landraces. Tocher's method (Rao, 1952) was used to group the genotypes into different clusters. Average inter- and intra- cluster distances and the relative percentage contribution of characters towards total genetic divergence were estimated as per the procedure outlined by Singh and Choudhary (1977).

Table 1. List of genotypes used for the characterization.

Sl. No.	Genotype	Collected location	Indian State
1	M35-1	Mohal	Maharashtra
2	CSV-22R	Vijayapura	Karnataka
3	CSV-26R	Solapur	Maharashtra
4	CSV-29R	Vijayapura	Karnataka
5	B35	USA	-

6	Muguti	Akola	Maharashtra
7	Ekarjuna-113	Ekarjuna	Maharashtra
8	Hinganghat Local-17	Hinganghat	Maharashtra
9	IC343556	Beed	Maharashtra
10	IC343562	Aurangabad	Maharashtra
11	IC343564	Aurangabad	Maharashtra
12	IC343570	Dadar	Maharashtra
13	IC343578	Bellary	Karnataka
14	IC343579	Solapur	Maharashtra
15	IC343581	Solapur	Maharashtra
16	IC343590	Sultanpur	Maharashtra
17	IC345186	Raichur	Karnataka
18	IC345188	Kalmala	Karnataka
19	IC345191	Raichur	Karnataka
20	IC345199	Karadigutta	Karnataka
21	IC392141	Medak	Telangana
22	IC420956	Satara	Maharashtra
23	IS 1522	Pollipet	Tamilnadu
24	IS 17774	Alur	Andhra Pradesh
25	IS 17909	Gulberga	Karnataka
26	IS 17913	Bidar	Karnataka
27	IS 18030	Akola	Maharashtra
28	IS 18385	Parbhani	Maharashtra
29	IS 18388	Parbhani	Maharashtra
30	IS 18396	Parbhani	Maharashtra
31	IS 18402	Parbhani	Maharashtra
32	IS 18408	Parbhani	Maharashtra
33	IS 18424	Nagpur	Maharashtra
34	IS 18512	Dharwad	Karnataka
35	IS 2176	Mumbai	Maharashtra
36	IS 22109	Gadag	Karnataka
37	IS 22116	Gadag	Karnataka
38	IS 22117	Gadag	Karnataka
39	IS 22125	Kadampur	Karnataka
40	IS 22127	Annigeri	Karnataka
41	IS 22152	Timmapur	Karnataka
42	IS 22176	Giddangeri	Karnataka
43	IS 24329	Amravati	Maharashtra
44	IS 24331	Akola	Maharashtra
45	IS 24339	Dasarkhed	Maharashtra
46	IS 24342	Thuradkheda	Maharashtra

47	IS 24361	Badewadi Local	Maharashtra
48	IS 24365	Sangli	Maharashtra
49	IS 26977	Darai	Maharashtra
50	IS 26981	Parbhani	Maharashtra
51	IS 4592	Nanded	Maharashtra
52	IS 4948	Dhule	Maharashtra
53	IS 4959	Akola	Maharashtra
54	IS 5010	Amravathi	Maharashtra
55	IS 5031	Wardha	Maharashtra
56	IS 5036	Wadra	Maharashtra
57	IS 5581	Bidar	Karnataka
58	IS 5586	Chittapur	Karnataka
59	IS 5659	Bijapur	Karnataka
60	Malegaon Local	Malegaon	Maharashtra
61	PR3015	Solapur	Maharashtra
62	PR3047	Solapur	Maharashtra
63	PR3074-2	Solapur	Maharashtra
64	PR3090-1	Solapur	Maharashtra
65	PR3116	Solapur	Maharashtra
66	PR3167	Solapur	Maharashtra
67	PVRL16-1	Dagdi	Maharashtra
68	PVRL16-12	Parbhani	Maharashtra
69	PVRL16-4	Beed	Maharashtra
70	PVRL16-6	Sindkheda	Maharashtra
71	RSLG2218	Bhoom	Maharashtra
72	RSLG2238	Ahmednagr	Maharashtra
73	RSLG2241	Ahmednagar	Maharashtra
74	RSLG2276	Beed	Maharashtra
75	RSLG2332	Kharda	Maharashtra
76	RSLG2367	Solapur	Maharashtra
77	RSLG2386	Bramhunath Tanda	Maharashtra
78	RSLG2387	Mantha, Parbhani	Maharashtra
79	RSLG2389	Edsi	Maharashtra
80	RSLG2413	Osmanabad	Maharashtra
81	TSLC-11	Pagidimani	Telangana
82	TSLC-12	Antharam-3	Telangana
83	TSLC-14	Parvathapally	Telangana
84	TSLC-17	Rudraram	Telangana
85	TSLC-22	Ameenpur	Telangana
86	TSLC-23	Goneer-3	Telangana
87	TSLC-25	Navalga-3	Telangana

88	TSLC-26	Bichael	Telangana
89	TSLC-3	Narayanpet	Telangana
90	TSLC-4	Yanagunde	Telangana
91	TSLC-5	Pagidimani	Telangana
92	TSLC-9	Ameenpur	Telangana
93	Washim Local-3	Washim	Maharashtra
94	SPV2217	Dharwad	Karnataka
95	DSV4	Dharwad	Karnataka
96	Kalagunda local	Kalagunda	Karnataka

3. Results and Discussion

Table 2 provides the details of analysis of variance and summary statistics for 14 traits measured during rabi 2019-20 in a set of 96 sorghum rabi genotypes. Except for NGLM (P = 0.10), the genotypic variances for all traits were significant. For grain yield and panicle weight, IC420956 was the best, while for Pwd, SPV2217 was the best. SPAD at maturity was maximum in B35. Washim Local-3 was the best for PL and NPBPP traits. IS 18512 was the earliest to flower, PR3167, TSLC-3 were the tallest, and TSLC-5 was the best for TW. The adequate variability as seen in the range (minimum and maximum) for each trait suggests that improvement in these traits can be achieved by using appropriate breeding and selection strategies. The presence of adequate variability is the basic requirement of any trait improvement program. The good amount of variability is observed in the present set of 96 rabi sorghum genotypes signifies their utility as a base population for crop improvement. Good levels of genetic variability have been reported in sorghum in earlier studies as well (Patroti *et al.*2022, Anisha *et al.*2022, Lokesh *et al.* 2022, Doijad *et al.* 2016).

Table 2. Analysis of variance and summary statistics for 14 traits in sorghum landraces (Rabi 2019)

Trait	**Genotypes**			**Range**		**Mean**	**h^2**
	DFG	**MSG**	**PFG**	**Min.**	**Max.**		
DFF (days)	95	15.25	<0.001	63.00 (IS 18512)	76 (PR3047)	72.00	0.81
PH (cm)	95	1639.5	<0.001	106.00 (B35)	270.00 (PR3167, TSLC-3)	229.00	0.87
NGLB (no.)	95	4.30	<0.001	7.20 (IS 5010)	12.00 (RSLG2367)	9.99	0.93
NGLM (no.)	95	1.10	0.10	1.60 (IS 24342)	5.70 (RSLG2386)	3.46	0.32
SPADB	95	36.09	<0.001	35.24 (TSLC-1	57.14 (IS 22152)	43.95	0.80
SPADM	95	51.59	<0.001	19.97 (IS 1522)	56.02 (B35)	36.83	0.74
NPBPP (no.)	95	464.18	<0.001	46.67 (IS 24342	147.39 (Washim Local-3)	71.29	0.88
NSBPP (no.)	95	0.76	0.01	5.13 (B35)	8.00 (Malegaon Local, TSLC-23)	6.68	0.35
NGCPRB (no.)	95	140.15	<0.001	24.17 (PVRL16-4)	72.39 (IS 22127)	40.06	0.78
PL (cm)	95	39.95	<0.001	10.26 (IS 22116)	24.91 (Washim Local-3)	18.00	0.96
Pwd (cm)	95	0.91	<0.001	4.03 (B35)	6.79 (SPV2217)	5.72	0.79
PW (g)	95	746.78	<0.001	24.56 (B35)	103.89 (IC420956)	62.54	0.95
GYPP (g)	95	625.71	<0.001	15.11 (B35)	86.67 (IC420956)	48.59	0.94
TW (g)	95	0.90	<0.001	1.73 (IS 22116)	4.43 (TSLC-5)	3.11	0.93

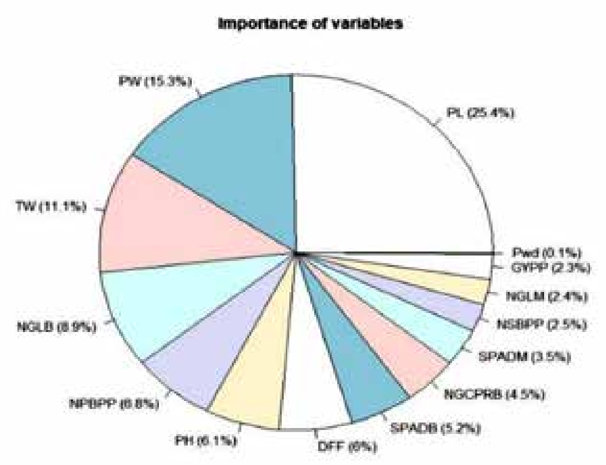
* DFG =The degree of freedom for genotype, MSG = The mean sum of squares for genotype, PFG = P-values for genotypes

DFF=Days to 50% flowering, PH= Plant Height, NGLB = No. of Green Leaves at Boot leaves stage, NGLM =No. of Green Leaves at Maturity stage, SPADB= SPAD at Boot stage, SPADM= SPAD at Maturity, NPBPP= No. of Primary Branches Per Panicle, NSBPP= number of secondary branches on central primary branch of the panicle, NGCPRB =No. of Grains of Central Primary Branch, PL= Panicle Length, Pwd= panicle weight, GYPP=grain yield per plant, TW=100 seed weight

h2=broad-sense heritability

Contribution of individual characters towards divergence

The percentage contribution of 14 characters towards total genetic divergence is depicted in Fig 1. Panicle length contributed maximum (25.4%), followed by panicle weight (15.3%), test weight (11.1%), no. of green leaves at boot stage (8.9%), no. of primary branches per panicle (6.8%), plant height (6.1%), days to 50% flowering (6%), SPAD at boot stage (5.2%), number of grains on central primary branch (4.5%), SPAD at maturity (3.5%,) number of secondary branches on central primary branch of the panicle (2.5%), no. of green leaves at maturity (2.4%), grain yield per plant (2.3%) and panicle width (0.1%). Among all the characters, panicle length, panicle weight, test weight, number of green leaves at boot stage together have contributed 60% to the total divergence. Similar results have been reported earlier by Ashwini and Kajjidoni (2019), Allan *et al.* (2020), Sameera *et al.* (2021) and Deepak *et al.* (2022).



* **DFF**=Days to 50% flowering, **PH**= Plant Height, **NGLB** = No. of Green Leaves at Boot leaves stage, **NGLM** =No. of Green Leaves at Maturity stage, **SPADB**= SPAD at Boot stage, **SPADM**= SPAD at Maturity, **NPBPP**= No. of Primary Branches Per Panicle, **NSBPP**= number of secondary branches on central primary branch of the panicle, **NGCPRB** =No. of Grains of Central Primary Branch, **PL**= Panicle Length, **Pwd**= panicle weight, **GYPP**=grain yield per plant, **TW**=100 seed weight

Fig 1: Percent Contribution of different characters towards genetic diversity of 96 sorghum genotypes

Genetic diversity and Composition of Clusters

The mean values for different quantitative characters studied were utilized for working out genetic distances between pairs of genotypes. Estimation of D^2 values was carried out for 96 genotypes and genetic diversity was calculated. Using Tocher's method (Rao,1952), the genotypes were grouped into seven distinct clusters based on D^2 values.

The 96 genotypes were grouped into seven clusters (Table 3), with I cluster accommodating maximum number of genotypes (80) followed by cluster II having 8 genotypes, cluster III with 4 genotypes and the remaining four clusters being solitary. Cluster I in this study accommodated genotypes from different geographic origins that are grouped into single cluster indicating there is no relation between genetic diversity and place of origin. This is similar to the findings of Swamy *et al.* (2018). Kavya *et al.* (2019), Umakanth *et al.* (2019), Lokesh *et al.* (2022) also documented solitary clusters in their findings. The formation of solitary clusters could be caused by complete isolation, which inhibits gene flow, or by severe natural/human selection for diverse adaptive complexes. As a result, these genotypes may be quite distinctive and advantageous in terms of breeding perspective. Intermating between the genotypes of these solitary and unique genotypes may produce desirable transgressive segregants.

Average intra and inter cluster distances.

The average intra and inter-cluster (D^2 values) distances are provided in Table 4. D^2 values within clusters ranged from zero (clusters IV, V, VI, and VII) to 72.44 (cluster III). Cluster III has the highest intra-cluster distance (72.44), followed by Cluster II (60.70) and Cluster I (57.17). Clusters IV, V, VI, and VII were solitary and had zero intra-cluster distance. Intra-cluster distance of cluster III has the highest D^2 value, indicating that the genotypes in this cluster have a high level of genetic diversity and appear to differ more from one another for the characters measured.

Maximum inter-cluster distance was observed between cluster IV and cluster V (479.97) followed by cluster III and cluster IV (375.17) and cluster IV and cluster VII (360.33), whereas the minimum inter-cluster distance was noticed between cluster I and cluster V (106.7). The larger the diversity among parental genotypes, the greater the likelihood of heterotic crossings (Falconer, 1964). The inter cluster distances were higher than the intra cluster distances between the genotypes, which indicates the presence of sufficient amount of genetic divergence among genotypes under studied. The high inter cluster distance between cluster IV and cluster V indicated that if hybridization is attempted between the genotypes included in those clusters (B35 and IC420956), lot of genetic diversity will be produced in the segregating generations and the selection for desirable genotypes can be produced. Similarly, IS 24361, TSLC-3, IS 22116, RSLG2386 from III cluster and B35 from IV cluster may also produce good segregants upon hybridization. The hybridization between different genotypes included in the most divergent clusters to get desirable segregants for yield and other traits is also advocated earlier by Aruna and Audilakshmi (2008), Sinha and Kumaravadivel (2016), Harsh *et al.*, (2019), Kanbar *et al.*, (2020), Deepak *et al.* (2022).

Table 3. Clustering pattern of 96 sorghum genotypes based on 14 traits byTocher's method

Cluster No.	No. of Entries	Genotypes included
I	80	IS18385, IS18388, IS18396, IS18408, IS18030, IS24331, Kalagunda local, IS4592, IS5659, IS5036, IS18424, IS18402, PVRL16-12, IS 5586, IC343562, M35-1, IC345191, PR3074-2, TSLC-23, RSLG2218, IC343581, IC343578, IC343590, IS 2176, TSLC-25, TSLC-14, HINGANGHAT LOCAL-17, IC343579, IC343570, RSLG2241, RSLG2367, RSLG2413, RSLG2389, IS 17909, IS26977, IC343556, TSLC-26, IS17913, IC345186, RSLG2332, CSV-26R, TSLC-9, IS5581, IS24365, PR3116, TSLC-17, PR3047, TSLC-12, RSLG2238, IC392141, PVRL16-1, IC343564, PVRL16-6, IC345188, PR3090-1, PR3167, IS 24339, Muguti, TSLC-11, MALEGAON LOCAL, RSLG2387, CSV-22R, SPV2217, RSLG2276, IC345199, TSLC-5, IS 26981, TSLC-4, TSLC-22, EKARJUNA-113, DSV4, IS5031, CSV-29R, IS22127,IS22176, IS22109, IS22125, PR3015, IS24342, IS 24329
II	8	IS 22117, IS 22152, IS 4948, IS 5010, IS 18512, PVRL16-4, IS 1522, IS 17774
III	4	IS 24361, TSLC-3, IS 22116, RSLG2386
IV	1	B35
V	1	IC420956
VI	1	IS 4959
VII	1	WASHIM LOCAL-3

Table 4. Average intra- and inter-cluster D^2 values among 7 clusters for 96 sorghum genotypes

Clusters	I	II	III	IV	V	VI	VII
N=	**80**	8	4	1	1	1	1
I	**57.17**	128.80	134.77	247.78	106.70	113.43	188.89
II		**60.70**	142.06	222.18	230.39	176.21	320.94
III			**72.44**	375.17	138.71	211.24	263.30
IV				**0**	479.97	113.98	360.33
V					**0**	254.16	237.73
VI						**0**	133.64
VII							0

* Diagonal bold values indicate intra cluster distances

Cluster means

Table 5 displays the character-wise total score over seven clusters as well as the cluster means for 14 characters. In the current study, there was considerable variation in cluster mean values for all the characteristics. The cluster V (IC 420956) manifested highest mean values for grain yield per plant (82.95 gm), test weight (3.74 gm), panicle width (6.27 cm), plant height (257 cm), no. green leaves at maturity (3.68), panicle weight (100.38 gm) and lowest mean value for SPAD at boot stage (37.01). The cluster IV (B35) showed highest mean values for SPAD at boot stage (52.08), SPAD at maturity stage (44.45) and lowest mean value for days to 50% flowering (68 days) this indicates this group having early flowering genotype, plant height (124 cm), no. of primary branches per panicle (56.51), number of secondary branches on central primary branch of the panicle (6.11), no. of grains of central primary branch of panicle (32.57), panicle width (4.36 cm), panicle weight (26.16), grain yield per plant (16.24 gm).The cluster VII (Washim local-3) showed highest mean value for no. of primary branches per panicle (138.84), panicle length (24.59cm), panicle width (6.27 cm) and days to 50% flowering (74) which depicts this group is having late flowering genotype.

Cluster III (IS 24361, TSLC-3, IS 22116 and RSLG2386) depicted the highest mean value for no. green leaves at boot leaves stage (12.21) and no. of grains of central primary branch (41.57). Cluster I had manifested highest cluster mean value for no. of secondary branches per panicle (6.71). The cluster II showed lowest mean value for no. of green leaves at boot stage (8.21) and panicle length (12.62 cm) while cluster VI depicted lowest mean value for no. of green leaves at maturity stage (3.16), SPAD at maturity (33.14) and test weight (1.87 gm).

The above results showed a broad range of mean values among the clusters, which suggested that the genotypes under study showed significant amounts of variation. Simultaneous improvement of two characters can be done by selecting the genotypes from those clusters having highest values of those characters as parents for hybridization. Similar studies have been reported earlier by Kiran *et al.* (2023), Patroti *et al.* (2022), Lokesh *et al.,* (2022), Navya *et al.*, (2021), Allan, *et al.* (2020) Kavya, *et al.* (2019),

Conclusion

Mahalanobis D^2 statistics was employed in the present study to assess the divergence among the 96 rabi landraces. The analysis of variance revealed that except for the number of green leaves at maturity, the genotypic variances for all traits were significant. The 96 landraces were grouped into 7 clusters where cluster I was largest containing 80 genotypes followed by cluster II with 8 genotypes, cluster III with 4 genotypes and the remaining 4 were solitary clusters. Based on the cluster mean values, cluster V was superior for grain yield, panicle width, panicle weight and test weight, while cluster IV was noted as the best for early flowering and cluster IV was good for SPAD at boot leaf and maturity stage. Among all the characters, panicle length, panicle weight, test weight, number of green leaves at boot stage together have

Table 5. Cluster mean performance for 96 genotypes of seven clusters

Cluster	DFF	PH	NGLB	NGLM	SPADB	SPADM	NPBPP	NSBPP	NGCPRB	PL	Pwd	PW	GYPP	TW
I	72.31	232.61	10.04	3.46	43.89	37.11	70.74	6.71	40.61	18.60	5.81	65.28	51.21	3.26
II	68.38	202.38	8.21	3.42	45.80	34.01	65.06	6.57	36.13	12.62	4.90	38.01	25.89	2.38
III	73.00	248.50	12.21	3.58	42.48	37.21	79.53	6.61	41.57	13.18	5.91	57.02	43.28	2.31
IV	68.00	124.00	8.72	3.26	52.08	44.45	56.51	6.11	32.57	23.70	4.36	26.16	16.24	1.95
V	73.00	257.00	12.11	3.68	37.01	33.48	78.32	6.67	34.97	14.82	6.27	100.38	82.95	3.74
VI	74.00	209.00	9.73	3.16	41.86	33.14	72.17	6.68	33.99	23.52	4.92	42.60	26.61	1.87
VII	74.00	241.00	11.18	3.47	40.58	35.11	138.84	6.68	40.25	24.59	6.27	80.33	62.05	2.47

* **DFF**=Days to 50% flowering, **PH**= Plant Height, **NGLB** = No. of Green Leaves at Boot leaves stage, **NGLM** =No. of Green Leaves at Maturity stage, **SPADB**= SPAD at Boot stage, **SPADM**= SPAD at Maturity, **NPBPP**= No. of Primary Branches Per Panicle, **NSBPP**= number of secondary branches on central primary branch of the panicle, **NGCPRB** =No. of Grains of Central Primary Branch, **PL**= Panicle Length, **Pwd**= panicle weight, **GYPP**=grain yield per plant, **TW**=100 seed weight

contributed 60% to the total divergence. The inter cluster distance was maximum between cluster IV and V followed by cluster III and IV. Based on the inter cluster distance and the performance *per se*, it is advisable to attempt crossing of the genotypes from clusters IV (B35) and V (IC420956), IS 24361, TSLC-3, IS 22116, RSLG2386 from III cluster and B35 from IV which may lead to a wide range of favorable genetic variations and produce good segregants upon hybridization.

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Author contributions

All authors contributed equally for preparing the final version of the manuscript.

Conflict of Interest

Authors declare no conflict of interest.

Ethical Approval

The article doesn't contain any study involving ethical approval.

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