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Study of genetic diversity and principal component analysis under limited irrigation in durum wheat (*Triticum durum* L.)

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Abstract

Drought is one of the major environmental factors affecting the yield and plant architecture of durum wheat. Days to heading, days to maturity, number of grains per spike, spike length, peduncle length, number of effective tillers per meter, plant height, protein content, sedimentation value, chlorophyll content, canopy temperature after 5 days and 15 days of anthesis like morphological, biochemical, physiological traits were measure in this study. In the current study, ten clusters of forty different durum wheat genotypes were formed, with the highest distance between clusters 6 and 10 (D^2 = 373.85) followed by clusters 9 and 10 (D^2 = 331.09). A total of around 73.82 percent of the overall variation seen across the forty durum wheat genotypes was explained by five main components, each having an eigenvalue ranging from 1.21 to 4.93. Different clusters 6, 9, and 10 include genotypes with particular characteristics. These genotypes may produce desirable genetic recombinants that help breeders create drought-tolerant cultivars. The PC1, PC2, PC3, PC4, and PC5 involve characters of major economic traits *viz*., plant height, number of grains per spike, spike length, peduncle length, 1000 grain weight, chlorophyll content, biological yield per plot, grain yield per plot, canopy temperature after 5 and 15 days of anthesis. The results of the entire experiment showed that the genotypes of durum wheat evaluated under limited irrigation circumstances had a sufficient amount of variability and diversity.

Keywords durum wheat, genetic diversity, principal component analysis, restricted irrigation conditions

Introduction

Durum wheat which is tetraploid (*Triticum durum* L.) is the most important cereal crop after hexaploid wheat (*Triticum aestivum* L.) cultivated in 10 to 11 percent of the world wheat area and accounting for about 8 percent of the total wheat production [1].

Nowadays, certain water deficit conditions were occurred because of uneven rainfall due to global warming effects and the lowering of the groundwater table. So, there is a need to develop varieties that can tolerate this uneven drought or deficit water conditions and give a certain yield. Grain yield is the most paramount character of the wheat crop which is contributed by some complex quantitative characters. Hence, the indirect selection of these yield contributing characters instead of direct selection is to be considered because the direct selection of grain yield character was sometimes misleading due to polygenically controlled. The study of D^2 Analysis and PCA gives information about the presence of genetic diversity and variation by components in the population. Between 1982 and 2017, research activities in Ethiopia resulted in the production of 39 durum wheat varieties; however none of them were specifically released in a moisture-stress environment [2].

Limiting irrigation is the best way to create a drought environment which minimizes the challenges associated with the screening of drought stress breeding in the field. Contemporary drought screening research is attempted by controlling soil moisture, applying limited irrigations, controlling rainfall *etc*, for effective breeding for drought tolerance, information on the extent of variation and diversity from moisture stress would be most useful and is a prerequisite for varietal development of durum wheat through hybridization. Although several investigations are reported for wheat [3] and for durum wheat [3-8] which gave a piece of sparse information about the drought environment.

Methodology

Forty genotypes obtained from the Main Wheat Research Station, Sardarkrushinagar Dantiwada Agricultural University, Vijapur were used in this study. The experiment was conducted at Vanbandhu Polytechnic in Agriculture, S. D. Agricultural University, Khedbrahma. This study was conducted with four replications using a Randomized Block Design (RBD) during *Kharif* 2021. Only three irrigations except germination irrigation were applied given in this present investigation. The genotypes were sown in two rows each with the distance between two rows being 18 cm with 3.0 m row length. Five randomly selected plants are taken and made average for sixteen different morphological, physiological and biochemical observations and averaged worked out *viz*. Plant height, peduncle length, spike length, and the number of grains per spike The diversity analysis was carried out which was described by Rao, 1952 [9]. The multivariate analysis divergence using Mahalonabis's D^2 statics [10]. Simple non-parametric methods such as principal component analysis can be used to draw out important data from data sets that contain confounding variables. This provides a step-by-step guide on how to condense a complex data collection into simple structures that often highlight it with the barest of work. The goal behind the principal component analysis is to rank data based on PC scores and to determine the smallest number of components that may explain the greatest amount of variability out of the overall variability. Using a data reduction strategy under factor analysis, PCA was carried out using the statistical program SPSS 16.0.

Results and Discussion

Genetic divergence

In the current study, forty genotypes of durum wheat were divided into ten clusters using Tocher's approach [9], which is shown in Table 1 and the contribution to divergence is shown in Table 2. The results showed that cluster 1 had the highest number of diversified genotypes (10 genotypes), followed by seven genotypes in each of clusters 2 and 4, and cluster 5 contains six genotypes. It was comparable to the findings of Alam et al., [11] and Santosh et al., [12] that intra-cluster distance was often smaller than inter-cluster distance. As a result, there was a tendency for the genotypes included in the cluster to be less different from one another.

The intra-cluster distance varied from 0.00 (clusters 6, 7, and 10) to 72.45 (cluster 9), and these large intra-cluster distances meant that the genotypes had a wider genetic diversity that could be employed in yield improvement programs for the durum wheat. Cluster 6 and cluster 10 have the greatest inter-cluster distance with a D^2 value of 373.85 followed by cluster 9 and cluster 10 with a D^2 value of 331.09 and cluster 3 and cluster 9 with a D^2 value of 318.69. Clusters 1 and 2 had the lowest inter-cluster distance currently observed (D^2 = 57.70). Table 3 shows that cluster 6, 9, and 10 have the highest genetic divergence.

Table 2 showed that days to heading (32.56 %) contributed the maximum towards genetic divergence followed by the number of grains per spike (29.23 %), day to maturity (20.00 %), peduncle length (9.10 %), chlorophyll content (2.18 %), spike length (1.79 %) and protein content (1.79 %), while the number of tillers per meter, 1000 grain weight, biological yield per plot, sedimentation value, harvest index, canopy temperature after 5 and 15 days of anthesis, plant height and grain yield per plant contributed

Table 1. Different durum wheat clusters' distribution of genotypes that have been assessed for grain yield

Cluster	Number of genotypes	Name of genotypes
1	10	VD 2020-8, 51st IDYN 799, HI 8737, 51st IDYN 798, IDSN 7040, 50th IDYN 737, GW(D)2019-970, NDSN IDYN 744, 51st IDYN 796, 51st IDYN 708, 50th IDYN 721
2	7	51st IDYN 760, 50th IDYN 712, 51st IDYN 740, 51st IDYN 709, 51st IDYN 750, 51st IDYN 743,
3	3	VD -2019-03, 51st IDYN 706, 51st IDYN 752
4	7	50th IDYN 718, VD 2020-4, VD 2020-14, 50th IDYN 722, VD 2020-11, 50th IDYN 706, VD 2020-4
5	6	GDW-1255, VD 2020-6, 50th IDYN 719, GW(D) -2019-975, VD 2019-08, 50th IDYN 7076
6	1	GW (D)2019-973
7	1	VD 2020-2
8	2	VD 2020-3, VD 2020-7
9	2	GM 1357, HI 8498
10	1	51st IDYN 746

Table 2. Various characters' contributions to overall genetic divergence

SN.	Characters	Contribution (%)
1.	Days to heading (N)	32.56
2.	Days to maturity (N)	20.00
3.	Plant height (cm)	0.00
4.	Number of effective tillers per meter (N)	0.51
5.	Number of grains per spike (N)	29.23
6.	Spike length (cm)	1.79
7.	Peduncle length (cm)	9.10
8.	1000 grains weight (gm)	0.51
9.	Biological yield per plot (kg)	0.26
10.	Protein content (%)	1.79
11.	Sedimentation value (ml)	0.64
12.	Harvest index (%)	0.77
13.	Canopy temperature after 5 days of anthesis	0.00
14.	Canopy temperature after 15 days of anthesis	0.13
15.	Chlorophyll content	2.18
16.	Grain yield per plant (g)	0.51

negligibly towards the total genetic divergence. Therefore, selection for divergent parents based on these seven traits might help exploit heterosis breeding in durum wheat, if commercially viable.

Table 3. Forty durum wheat genotypes' average intra and inter cluster D^2 values

Cluster	1	2	3	4	5	6	7	8	9	10
1	**52.26**	57.70	115.49	114.40	121.85	60.87	110.29	224.03	180.99	277.36
	(7.50)	(7.60)	(10.75)	(10.70)	(11.04)	(7.80)	(10.50)	(14.97)	(13.45)	(16.65)
2		**55.76**	137.64	115.88	109.46	65.02	122.87	207.23	133.25	278.69
		(7.47)	(11.73)	(10.76)	(10.46)	8.06	(11.08)	(14.40)	(11.54)	(16.69)
3			**34.12**	140.17	134.37	177.76	82.65	182.15	318.69	143.43
			(5.84)	(11.84)	(11.59)	(13.33)	(9.09)	(13.50)	(17.85)	(11.98)
4				**56.34**	157.01	160.48	73.64	107.17	217.91	258.71
				7.51	(12.53)	(12.67)	(8.58)	(10.35)	(14.76)	(16.08)
5					**43.31**	169.89	130.42	124.34	124.25	102.58
					6.58	(13.03)	(11.42)	(11.15)	(11.15)	(10.13)
6						**0.00**	172.64	286.75	154.99	373.85
						(0.00)	(13.14)	(16.93)	(12.45)	(19.34)
7							**0.00**	96.23	270.69	161.51
							(0.00)	(9.81)	(16.45)	(12.71)
8								**33.85**	220.61	127.22
								(5.82)	(14.85)	(11.28)
9									**72.45**	331.09
									(8.51)	(18.20)
10										**0.00**
										(0.00)

In the current research, high mean values by cluster 3 (14.37) and cluster 4 (8.57) for peduncle length and spike length, respectively. Cluster 6 expressed the highest average values for the number of tillers per meter (76.25), protein content (19.20), and sedimentation value (58.40). Cluster 10 had high means value for 1000 grain weight (41.10), and Cluster 8 had high mean values for the number of grains per spike (58.75), spike length (8.57), and biological yield per plot (1.52). Chlorophyll content (55.64) was recorded highest in cluster 3 while for negative traits cluster 10 had the lowest mean for the days to heading (52.50), days to maturity (98.75), plant height (64.20), and Canopy temperature after 5 days of anthesis in cluster 4 and canopy temperature after 15 days of anthesis in cluster 6 (Table 4). Intercrossing of these genotypes implicated in these clusters would be beneficial for inducing variability in the corresponding traits and rational improvement for enhancing grain yield in durum wheat. The present findings for high cluster mean for various characters were also recorded by different researchers [13-15] in durum wheat.

Principal component analysis

Principal Component Analysis is a useful technique for reducing the variability of many traits to their principal components, with the principal component retaining the maximum variability. Since it does not require the normal distribution assumptions of populations, PCA with a correlation matrix is the best method for identifying the key components [16-17]. High factor loadings and high eigenvalues of any major component were regarded as the best representation of all qualities. Therefore, PCA was used in the current experiment to analyze the yield and the factors that contribute to it in durum wheat. Among the sixteen, five main components have more than one eigenvalue.

Table 4. Cluster mean for 16 different characters in forty genotypes of durum wheat

Cluster	DH	DM	PH	TIL/M	GPS	SL	PL	TGW	BYP	Pro	Sedi	HI	TEMP5	TEMP15	CC	GY
I	62.91	109.02	72.35	73.23	43.89	6.97	11.24	34.24	1.32	16.96	52.85	27.90	20.06	28.81	48.25	362.50
II	61.83	109.67	70.28	70.38	43.71	6.59	11.72	31.86	1.22	16.87	51.73	26.82	20.18	29.13	52.11	328.75
III	61.08	104.00	73.65	68.92	45.17	7.01	14.37	37.62	1.37	16.36	53.68	29.05	21.02	28.69	55.64	394.17
IV	60.29	108.07	71.89	69.57	57.54	8.57	12.48	40.57	1.42	15.85	50.37	32.55	19.83	29.49	50.67	458.57
V	56.08	104.92	69.61	72.13	41.04	7.02	11.11	36.30	1.29	15.91	51.14	31.95	20.34	29.04	48.06	411.67
VI	63.25	111.75	77.71	76.25	41.00	6.29	11.75	30.78	1.42	19.20	58.40	19.97	20.08	27.55	35.35	282.50
VII	60.50	105.50	70.10	65.75	57.25	6.61	11.19	32.40	1.32	16.13	52.20	33.46	20.35	29.23	42.43	440.00
VIII	53.88	104.00	68.42	64.63	58.75	8.57	12.85	38.11	1.52	15.25	50.14	31.59	20.54	28.75	47.40	471.25
IX	56.50	110.38	69.54	60.00	41.38	6.98	10.87	35.73	1.05	16.55	51.94	28.10	24.36	28.99	43.16	291.25
X	52.50	98.75	64.20	74.50	44.00	7.03	12.13	41.10	1.28	15.28	50.20	34.98	20.88	29.50	45.93	447.50

Table 5. Eigenvalues and percent variance explained in various PCs for Sixteen durum wheat traits

Component	Total	% of Variance	Cumulative %
1	4.932	30.823	30.823
2	2.291	14.318	45.141
3	2.093	13.084	58.225
4	1.277	7.984	66.208
5	1.218	7.613	73.821
6	0.955	5.966	79.787
7	0.885	5.529	85.316
8	0.618	3.864	89.180
9	0.514	3.215	92.395
10	0.411	2.570	94.965
11	0.362	2.262	97.227
12	0.176	1.100	98.327
13	0.127	0.795	99.121
14	0.087	0.541	99.663
15	0.049	0.306	99.969
16	0.005	0.031	100.000

Maximum variability was seen among the first five principal components, with PC1 exhibiting the most variability among the four, accounting for 30.82% of the overall variability, followed by PC2, PC3, PC4, and PC5, which displayed 14.32, 13.08, 7.98, and 7.61, respectively (Table 5). The number of grains per spike, peduncle length, 1000 grain weight, biological yield per plot, harvest index, canopy temperature after 5 and 15 days of anthesis, chlorophyll content, and grain yield per plot was the main contributors to the variance depicted in the first principal component. Days to heading, plant height, number of tillers per meter, number of grains per spike, peduncle length, biological yield per plot, chlorophyll content, and grain yield per plot are the main contributors to variances for the second principle component traits. While 3rd principal component had major significant contributors like plant height, spike length, 1000 grain weight, biological yield per plot, sedimentation value, and grain yield per plot induce variations. Plant height, spike length, peduncle length, canopy temperature after 5 days of anthesis, and chlorophyll content all contributed to variation 7.98 of the fourth main component. Days to heading, days to maturity, number of grains per spike, 1000 grain weight, canopy temperature after 15 days of anthesis, and chlorophyll content were all significant contributors to variance in the fifth main component (Table 6).

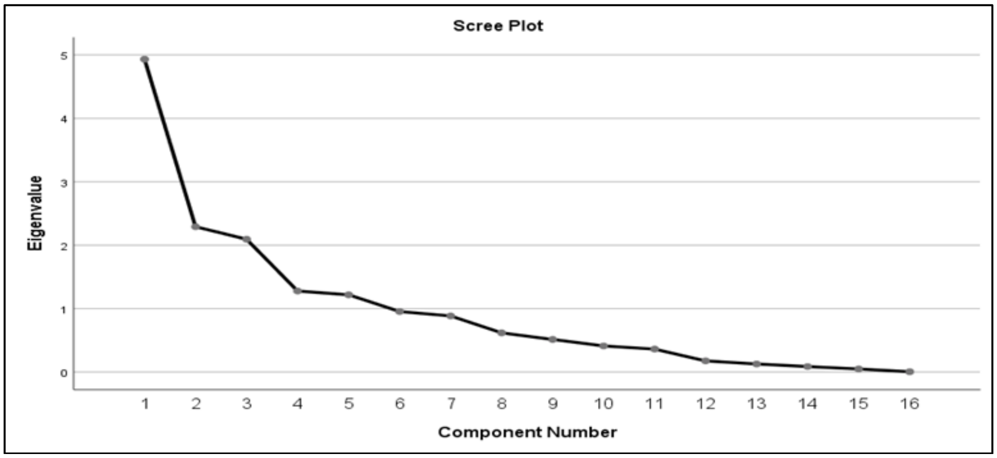

Figure 1. Scree plot showing eigen values and percentage of cumulative variability

Scree plot which showing that the percent of cumulative variability through eigen values with respect to component number. Between component 1 and 2 vast differences are seen in Figure 1, which shows the variation difference is higher in component 1 compared to component 2 as per Table 5. The findings revealed the importance of characteristics (unique to each PC) in determining the genotypes of durum wheat genotypes. When a large number of characters are considered together, PCA primarily contributes to the consideration of multiple traits simultaneously in the selection of materials with the added benefit of selectively rejecting traits due to their duplication, which leads to not only an increase in the number of labour but also loss of precision in the selection process.

Conclusion

Geographic regions did not affect genetic diversity since genotypes from the same area were divided into different clusters and genotypes from different locations were grouped in the same cluster. As a result, a plant breeder must analyze his material for genetic variety rather than just geographical diversity. The clustering pattern might be used in the selection of parents for crossing and finding the optimum cross combinations that will provide superior genotypes for various attributes. The genotypes of clusters 3, 6, 9, and 10 may be intercrossed based on the maximum genetic distance to generate wide-spectrum genetic diversity and isolate transgressive segregants for increased grain production in durum wheat. Inter-crossing of such genotypes associated with these clusters would thus be beneficial for producing diversity in the corresponding traits and rationally improving grain yield in durum wheat.

Table 6. The compound matrix computed in the first five PCs of durum wheat genotypes

Characters	PC 1	PC 2	PC 3	PC 4	PC 5
DH	-0.707	0.443	-0.199	0.057	0.225
DM	-0.736	0.085	-0.161	-0.013	0.206
PH	-0.299	0.681	0.286	0.473	0.002
TIL/M	-0.284	0.422	0.077	-0.392	-0.535
GPS	0.541	0.232	0.176	-0.254	0.480
SL	-0.073	-0.195	0.830	0.100	0.034
PL	0.455	0.406	-0.133	0.419	-0.093
TGW	0.557	-0.412	0.348	0.067	0.220
BYP	0.246	0.623	0.645	-0.069	0.099
PRO	-0.907	-0.043	0.192	-0.120	0.076
SV	-0.664	-0.106	0.345	-0.078	-0.169
HI	0.855	0.085	-0.135	-0.070	-0.228
TEMP5	0.193	-0.452	0.030	0.635	-0.141
TEMP15	0.390	-0.070	-0.313	-0.382	0.107
CC	0.103	0.478	-0.567	0.215	0.124
GY	0.806	0.415	0.265	-0.126	-0.099

PCA can be used to examine the genetic variation existing in the set of genotypes. Although each method has benefits and drawbacks for synthesizing observed data and providing classificatory analysis, all methods were compared to identify the elite genotypes with associated quantitative traits such as the number of grains per spike, peduncle length, biological yield per plot, 1000 grain weight, chlorophyll content, and grain yield per plot and designing a selection strategy for crop improvement in durum wheat.

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