

VARIABILITY ANALYSIS AND MULTIVARIATE ANALYSIS IN BREAD WHEAT [*TRITICUM AESTIVUM* L.]

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ABSTRACT

Genetic variability and diversity was done with 52 genotypes for fourteen quantitative characters in bread wheat (*Triticum aestivum* L.). The analysis of variance indicated the sufficient genetic variation among the genotypes for all the traits. High genotypic coefficient of variation (GCV) coupled with high heritability and high genetic advance as per cent of mean (GA %) were observed for days to 50% flowering (9.13%, 78.97%, 16.71%), days to maturity (5.45%, 87.73%, 10.52%) plant height (7.60%, 73.32%, 13.41%), number of grains per main spike (9.89%, 78.31%, 18.02%), grain yield per plant (10.12%, 50.18%, 14.76%) and biological yield per plant (7.03%, 59.50%, 11.16%) which might be attributed to additive gene action and phenotypic selection could be effective for these traits. On the basis of Multivariate analysis, 52 genotypes grouped in seven clusters using the Tocher's method. Cluster I topped with maximum (38) genotypes followed by cluster II (5) and cluster III (4), while cluster V to VII were solitary clusters. Maximum genetic distance (D) was found between cluster II and III (15.23). Days to maturity, days to 50% flowering and 100-grain weight also contributed more than 55% of towards total genetic divergence

INTRODUCTION

Wheat (*Triticum spp.*) is usually accorded a premier place among the cereals because of the vast acreage devoted to its cultivation, its high nutritive value and its association with some of the earliest and most important civilization of the world. Wheat is the second most important staple food next to rice, consumed by nearly 35% of the world population and providing 20% of the total food calories. Wheat occupies about 32% of the total acreage under cereals in the world. India accounts an area, production and productivity of 31.34 million ha, 95.91 million metric tonnes and 3061 kg/ha, respectively. In Gujarat, wheat is grown in about 13.51 lakh ha with total production of 36.50 lakh metric tonnes and a productivity of 2702 kg/ha (Anonymous, 2014). Globally, demand for wheat by the year 2020 is forecast at around 950 million tonnes per year. This target will be achieved only, if global wheat production is increased by 2.5% per annum.

The presence of genetic variability and diversity among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Kahrizi *et al.*, 2010). The more genetic diverse parents, the greater chances of obtaining higher heterotic expression in F₁'s and broad spectrum of variability in segregating population as already reported by earlier workers (Shekhawat *et al.*, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin, 1985). Several genetic diversity studies have been conducted on different crop species

based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat *et al.*, 2001; Arega *et al.*, 2007; Daniel *et al.*, 2011 and Kumar *et al.*, 2014a). Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. In views of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme. In views of these facts, fifty-two wheat genotypes were evaluated in this study to determine the magnitude of variability among the germplasm and grouping pattern of genotypes in different cluster. To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

MATERIALS AND METHODS

Fifty-two genotypes of bread wheat collected from the Wheat Research Station, Junagadh Agriculture University, Junagadh were grown in Randomized Block Design with three replications during *rabi* 2013-14 at the Wheat Research Station, Junagadh Agricultural University, Junagadh, Gujarat. Each replication consisted of a single row of 4 m for each entry with row to row and plant to plant spacing being 22.5 cm and 10 cm, respectively. Recommended agronomic practices and plant protection measures were followed to raise a good crop.

Five competitive plants were randomly selected in each entry for recording observations on plant height (cm), number of

effective tillers per plant, number of grains per main spike, number of spike lets per main spike, peduncle length of main spike (cm), length of main spike (cm), 100-grain weight (g), biological yield per plant and harvest index (%). While days to 50% flowering, grain filling period and days to maturity were recorded on plot basis. The genotypic and phenotypic coefficient of variation was estimated as per Burton (1952), while heritability in broad sense and expected genetic advance were estimated as per Allard (1960). Genetic diversity was calculated using Mahalanobis (1936) D^2 statistic and genotypes were grouped into clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

Analysis of variance revealed that variance due to genotypes was highly significant for all the fourteen characters indicating the presence of sufficient variability in the genotypes used in the study and the genotypes selected were developed in different breeding programmes representing different agro-climatic conditions of the country. The experimental material showed wide range of phenotypic variation for number of spike lets per main spike, grain yield per plant and length of main spike as revealed by high values of coefficient of range.

Variability analysis

The values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV), in most of the cases, indicating influence of environmental factors (Table 1). However, low differences were also observed between PCV and GCV for days to 50% flowering, days to maturity, plant height, number of grains per main spike and biological yield per plant which revealed that these five traits were comparatively less influenced by the environments by Sharma *et al.* (2006) and Kumar *et al.* (2014b). High PCV and GCV were observed by Demelash *et al.*, (2013) and Singh *et al.*, (2013) for number of effective tillers per plant, length of main spike, number of spikelets per main spike, number of grains per main spike, 100-grain weight, grain yield per plant and harvest index indicating the presence of wide variation

for these traits to allow selection for individual traits. Moderate estimates of GCV and PCV were observed for days to 50% flowering; plant height and biological yield per plant, while low estimates of GCV were observed for grain filling period, days to maturity, peduncle length of main spike and grain weight per main spike indicated narrow genetic variability for these characters.

The efficacy of selection not only depends on the magnitude of variability present in a trait but also on the extent of heritability of the desirable character. To obtain the heritable portion of variability, it was essential to know the heritability estimates for different traits (Burton, 1952). Johnson *et al.* (1955) suggested that the heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection. In the present study, the estimates of high heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, days to maturity, plant height, number of grains per main spike, grain yield per plant and biological yield per plant indicated preponderance of additive gene action and selection pressure could profitably be applied on these characters for improving the grain yield (Panse, 1957). Arya *et al.* (2013) observed high heritability coupled with high genetic advance for plant height, biological yield per plant, number of grains per spike. Binod kumar *et al.* (2013) also reported high heritability estimates for grain yield per plant, number of seeds per spike, plant height, 1000 seed weight and number of tillers per plant, which support the present findings. On the other hand, moderate heritability along with low GCV and low genetic gain were observed for grain filling period, peduncle length of main spike, grain weight per main spike and harvest index which could be due to preponderance of non-additive (dominant and epistatic) gene action and/or less genetic variability for these three traits in the materials.

Multivariate analysis

Multivariate analysis using Wilk's criterion was carried out to test the differences among 52 genotypes for aggregate of 14 characters. The value of V-statistic (2552.173) which follows

Table 1: Phenotypic range, coefficient of range, phenotypic and genotypic coefficient of variation, heritability, genetic advance and genetic advance expressed as per cent of mean for various characters inbred wheat

Characters	Phenotypic range	Coefficient of range (%)	Mean \pm S.E	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability in broad sense (%)	Genetic advance (GA)	GA (as per cent of mean)
Days to 50% flowering	50.00-73.67	18.50	58.00 \pm 1.57	10.26	9.13	78.97	9.69	16.71
Grain filling period	30.67-39.67	12.79	35.25 \pm 1.72	9.39	4.07	18.76	1.28	3.63
Days to maturity	91.33-117.00	12.32	106.44 \pm 1.25	5.82	5.45	87.73	11.20	10.52
Plant height (cm)	52.13-84.06	23.44	72.85 \pm 1.92	8.87	7.60	73.32	9.77	13.41
No. of effective tillers per plant	8.33-13.00	21.89	10.10 \pm 0.92	17.13	6.53	14.54	0.52	5.13
Length of main spike (cm)	6.83-22.13	52.83	9.48 \pm 0.68	14.07	6.32	20.20	0.55	5.85
Peduncle length of main spike (cm)	25.00-31.33	11.24	28.76 \pm 1.13	8.30	4.68	31.87	1.57	5.44
No. of spikelets per main spike	9.67-18.33	30.93	14.45 \pm 1.16	17.68	9.82	33.33	1.68	11.68
No. of grains per main spike	27.67-44.00	22.78	31.34 \pm 0.94	11.17	9.89	78.31	5.64	18.02
Grain weight per main spike (g)	1.35-1.86	15.89	1.65 \pm 0.07	8.78	4.83	30.21	0.09	5.47
100- grain weight (g)	3.77-5.97	22.59	4.87 \pm 0.30	13.87	8.75	39.78	0.55	11.37
Grain yield per plant (g)	12.53-23.80	31.02	19.17 \pm 1.11	14.28	10.12	50.18	2.83	14.76
Biological yield per plant (g)	35.37-55.32	22.00	46.93 \pm 1.57	9.11	7.03	59.50	5.24	11.16
Harvest index (%)	32.96-50.86	21.36	40.91 \pm 2.92	13.95	6.43	21.26	2.49	6.10

Table 2: Grouping of 52 genotypes of bread wheat in various clusters on the basis of D² statistic

Cluster	No. of genotypes	Name of genotypes	Place of origin			
I	38	9	GW-496, GW-503, GW-11, GW-120, J-24, J-18, GW-450, J-40, LOK-1	WRS, Vijapur (Gujarat)		
		4	HD-3002, HD-2982, HD-2932, DL-788-2	IARI (New Delhi)		
		4	HPW-338, HPW-635, HPW-289	HPAU, Palampur (Himachal Pradesh)		
			HS-522	IARI, Simala (Himachal Pradesh)		
		4	DBW-62, DBW-61, KRL-250, HI-1569	DWR, Karnal (Haryana)		
		4	HUW-638, HUW-635, HUW-629	BHU, Varansi, (Uttar Pradesh)		
			NW-4091	NDUAQT, Faizabad (Uttar Pradesh)		
		3	UP-2672, KALYANSONA	PUA & T, Pantnagar, (Uttarakhand)		
			VL-931	VPKAS, Almora (Uttarakhand)		
		2	SONALIKA, HI-977	IARI, Willington (Tamil Nadu)		
		2	PBW-640, PBW-635	PAU, Ludhiana, (Punjab)		
		2	UAS-327, UAS-324	UAS, Dharwad, (Karnataka)		
		1	AKAW-4498,	Akola, (Maharashtra)		
		1	MP-3288	JNKV, Jabalpur, (Madhya Pradesh)		
		1	RSP-566	SKUAST, (Jammu and Kashmir)		
II	5	2	RAJ-4201	RAU (Rajasthan)		
		2	DBW-60	DWR, Karnal (Haryana)		
			WH-1094	CCSHAU, Hissar (Haryana)		
		1	VL-930	VPKAS, Almora, (Uttarakhand)		
		1	HS-533	IARI, Simala, (Himachal Pradesh)		
III	4	4	NW-4081	NDUAQT, Faizabad, (Uttar Pradesh)		
		4	GW-366, GW-322, GW-273, GW-190	WRS, Vijapur (Gujarat)		
		IV	2	2	VL-943, VL-944	VPKAS, Almora, (Uttarakhand)
				1	PBW-617	PAU (Punjab)
		1	PBW-628	PAU (Punjab)		
		VII	1	1	GW-173	WRS, Vijapur (Gujarat)

Table 3: Average inter and intra-cluster distance ($D = \sqrt{D^2}$) values in bread wheat

	I	II	III	IV	V	VI	VII
I	5.77	9.07	10.75	9.81	7.71	8.08	8.41
II		7.94	15.23	13.55	9.18	8.98	8.66
III			7.40	10.24	13.27	8.11	12.30
IV				3.95	14.10	10.14	11.24
V					0.00	11.73	11.57
VI						0.00	9.72
VII							0.00

χ^2 distribution for 714 degrees of freedom showed highly significant differences among the genotypes for aggregate of 14 characters. Thus, one can proceed for further diversity analysis. The D²-values computed for 1326 pairs ranged from 4.71 (between RSP-566 and VL-931) to 316.22 (between HS-533 and GW-322) indicated the presence of high genetic diversity among the genotypes for all the traits.

All the fifty-two genotypes were grouped into seven clusters, using the Tocher's method, in such a way that the genotypes within the cluster had smaller D² values among themselves than those belonging to different clusters (Table 2). The cluster I was the largest having thirty-eight genotypes from different geographical regions comprising nine from Gujarat, four from New Delhi, Haryana, Himachal Pradesh and Uttar Pradesh each; three from Uttaranchal; two from Punjab, Tamil Nadu, Karnataka each and one from Rajasthan, M.P., Maharashtra, and Jammu and Kashmir each. Likewise, cluster II comprised of 5 genotypes from different locations of India. While cluster III possessed four and VI possessed two genotypes each. The clusters from V to VII had only single genotype in each

cluster. The clustering pattern of genotypes showed that genetic origin was totally independent of their geographical origin. Murty and Arunachalam (1966) also stated that genetic drift and selection in varied environments could cause greater diversity than geographic distance. Further, free exchange of seed materials among the different regions consequently causes characters constellations because of the human interference and material may lose its individuality. Sutariya *et al.* (2011) also reported that there was no parallelism between geographic distribution and genetic diversity in bread wheat.

In general, intra-cluster distances were lower than the inter cluster distances (Table 3). Thus, the genotypes included within a cluster tended to diverse less from one another. Intra cluster distance (D) ranged from 3.95 in cluster IV to 7.94 in cluster III. The analysis of data revealed that the maximum inter cluster distance (D = 15.23) was observed between clusters II and III followed by that between cluster II and IV (D = 13.55) and minimum inter cluster distance (D = 7.71) was observed between cluster I and V. The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, genotypes from cluster II (HS-533, DBW-60, VL-930, WH-1094, NW-4081), cluster III (GW-366, GW-322, GW-273, GW-190) and cluster IV (VL-943, VL-944) could be selected as parents in hybridization programme. Similar findings have been reported by Tsegaye *et al.* (2012) and Binod *et al.* (2013) reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme.

The clustering pattern could be utilized in selection of parents

Table 4: Cluster means for different characters in bread wheat

Clusters	Days to 50% flowering	Grain filling period	Days to maturity	Plant height (cm)	No. of effective tillers per plant	Length of main spike (cm)	Peduncle Length of main spike	No. of spikelets per main spike	No. of grain per main spike	Grain weight per main spike	100-grain weight (g)	Grain yield per plant (g)	Biological yield per plant	Harvest index (%)
I	56.73	35.18	106.55	73.28	10.05	9.35	28.46	14.44	30.58	1.64	4.90	19.25	47.21	40.91
II	58.67	35.00	98.80	61.69	9.47	9.65	27.94	13.40	29.77	1.61	4.88	15.48	41.64	37.05
III	59.83	35.92	111.67	79.87	11.08	9.53	30.23	17.00	41.50	1.78	4.90	21.83	50.99	42.86
IV	73.50	36.00	116.17	73.83	11.17	10.05	28.43	16.00	31.33	1.61	4.27	20.93	49.22	42.52
V	53.00	36.33	95.00	76.20	9.67	10.47	30.33	13.67	30.00	1.76	5.21	21.33	49.82	42.87
VI	69.67	36.67	101.33	81.20	11.33	9.73	32.33	12.33	29.33	1.75	4.86	18.87	47.85	40.60
VII	58.00	32.67	116.33	70.70	8.67	11.07	34.00	9.67	30.67	1.70	4.67	18.40	38.44	47.70
Mean	58.00	35.25	106.44	72.85	10.10	9.48	28.76	14.45	31.34	1.65	4.87	19.17	46.93	40.91
S.Em	1.57	1.72	1.25	1.92	0.92	0.68	1.13	1.16	0.94	0.07	0.30	1.11	1.57	2.92
Percent	17.35	1.28	34.39	9.28	0.60	1.66	0.90	3.17	13.65	1.81	3.32	3.17	7.54	1.89
Contribution towards total genetic divergence														

for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. In the present study, the cluster VII differed from other clusters (Table 4) in respect of length of main spike, peduncle length of main spike and harvest index, while cluster III was the best for number of spikelets per main spike, number of grains per main spike, grain yield per plant and biological yield per plant. The cluster V had desirable rating for days to 50% flowering, days to maturity with maximum 100-grain weight. The cluster II, cluster VI and cluster IX was the best for dwarf plant height and longest grain filling period, respectively.

Contribution of different characters towards total genetic divergence (Table 4) revealed the highest contribution of days to maturity (34.39 %). Three traits contributed more than 55 % of diversity *viz.* days to maturity, followed by days to 50% flowering and number of grains per main spike. Hence, selection of divergent parents based on these three traits would be useful for hybridization programme followed by isolation of desirable transgressive segregants in bread wheat. Similar findings of higher genetic diversity were also reported by Singhal and Upadhyay (1977), Jagadev (1993), Shoran and Tandon (1995).

Overall, it can be concluded that high heritability along with high GCV and high genetic gain were observed for days to 50% flowering, days to maturity, plant height, number of grains per main spike, grain yield per plant and biological yield per plant which might be attributed to additive gene action in their inheritance and phenotypic selection could be effective. Maximum contribution of days to maturity, followed by days to 50% flowering and number of grains per main spike were observed on total genetic divergence. Hence due consideration should be given to these traits while imposing selection for amenability in grain yield per plant in bread wheat.

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