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Phenotyping of wheat cultivar (*Triticum aestivum* L.) using dus characters to work out genetic variability

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Abstract

Genetic variability assess in a core collection is key to find out ways to efficient utilization of genetic resource. Nearly hundred Indian bread wheat cultivars spanning over a century is procured form from the Indian Institute of Wheat & Barely Research (IIWBR), Karnal, used made up of a core collection. A characterization of DUS descriptors like waxiness on plant parts, foliage colour, flag leaf attitude and seed size considerable amount of variability. Quantitative characteristics were recorded to record variation in genotypes at agro-morphological level and analysis of core collection by variations, PCV, GCV, heritability and genetic advance was carried out. Analysis of variance revealed that the mean value due to genotypes showed significant variability for all the traits. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The estimates of GCV were high for yield per plant, number of grains per spike and the remaining traits recorded moderate to low GCV. The heritability and genetic advance were high for plant height, number of days to 50% flowering, number of spikelets per spike, number of grains per spike and average yield per plant. These characters have huge amount of genetic variation, high GCV and PCV value, highly heritable and GAM of all eight characters. It also exhibited high heritability coupled with high genetic advance as percent of mean, might be utilized in hybridization- selection breeding for wheat genotypes.

Keywords: Wheat, Phenotyping, DUS characters, genetic variability, heritability, genetic advance

1. Introduction

Wheat is prominent position in staple food crops. In which 150-200 species have been cultivated and among these ~30 species provide ~90% of world's energy to growing population. Hybridization is one of the methods of collection of desirable genes in a single population using different genetic source. High genetic variability among genotypes is a prerequisite for hybridization. One of the main objective is to assessment of genetic variability. Phenotyping is one most popular method from ancient time to assessment genetic variability through traditional methods. Genetic variability is either heritable or non-heritable having some parameter viz. variance, coefficient of variance, heritability, genetic advance. High heritability with high genetic advance is essential for effective selection. Genetic advance perform better in additive gene action. It is a base of efficient way to improving characters through selection. Genetic yield is a complex trait which interacts with an environment. It is revealed that direct selection could not a efficient way to improving such complex traits. It could be misleading by environment variation. Information based on genetic variability & association of morphological and agronomic with grain yield. High heritability with high genetic advance for plant height, number of spikelet per panicle and 1000 grain weight ^[1]. Among all exiting methods genetic diversity analysis and relationship between existing genotyping are given opportunity to traits in promising genotypes and improving plant progeny for yield. Among molecular markers, micro satellite is important because of codominance, coverage genome, ease to detection, polymorphisms ^[2-4]. In genetic diversity analysis using SSR markers genotyping serves as a selection of outstanding diverse parents.

2. Materials and Methods

Out at the Research Farm, Division of Plant Breeding and Genetics, FOA, Sher-e-Kashmir University of Agricultural Sciences and Technology, Chatha, Jammu. The material for the experiment consisted of a set of 230 elite Indian bread wheat cultivars released during 1910-2006 for commercial cultivation in different agro-climatic regions of the country. The details of the material used during the course of this study are listed in Table 1. These genotypes were procured from the then Directorate of Wheat Research [DWR], now Indian Institute of Wheat and Barley Research (IIWBR), Karnal ^[5].

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There were a total of 35 cultivars developed during the pre-1965 period (the pre-green revolution period), and 195 cultivars developed during the post-1965 period (the post-green revolution period). Based on their SSR profiling,

genetic variability and relatedness among 230 genotypes was assessed to make a core collection of 94 diverse genotypes. Thereafter,

Table 1: Mean, range, standard error, coefficient of variance and critical difference, analysis of variance, Phenotypic coefficient of variance, genotypic coefficient of variance, heritability, genetic advance and genetic advance as a percentage of mean, correlation coefficient among eight quantitative traits for grain yield and other traits

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1	PBC TYPE 11	26	SONORA 64	51	WL 711	76	DL 788-2 (VIDISHA)
2	A 115	27	NP 884	52	DL 153-2 (KUNDAN)	77	HP 1633 (SONALI)
3	A 90	28	HD 1949 (MOTI)	53	HD 2285 (GOBIND)	78	HP 1761 (JAGDISH)
4	8A	29	HD 1982 (JANAK)	54	HD 2385	79	HPW 147
5	NP 111	30	HD 2177	55	HI 784 (SWATI)	80	HS 295
6	NP 165	31	HD 2189	56	HUW 206	81	HS 365
7	C 518	32	HS 1138-6-4	57	J 405	82	K 9644 (ATAL)
8	NP 710	33	HW 657	58	K 8020 (TRIVENI)	83	NIAW 34
9	NP 721	34	HYB 65	59	K 8027 (MAGHAR)	84	PBW 396
10	C 591	35	IWP 72	60	PBN 142 (KAILASH)	85	HPW 89 (SURABHI)
11	HYB 11	36	J 1-7	61	PBW 226	86	HD 2864 (URJA)
12	NP 809	37	K 78	62	RAJ 1482	87	HS 347 (HIMGIRI)
13	NP 832	38	LAL BAHADUR	63	RW 3016	88	HS 420 (SHIVALIK)
14	NI 179	39	NARMADA 4	64	GW 120	89	K 7903 (HALNA)
15	NP 890	40	NARMADA 195	65	DWR 39 (PRAGATI)	90	K 8434 (PRASAD)
16	NP 770	41	UP 215	66	HS 86	91	K 9162
17	HY 5	42	UP 262	67	PBN 51	92	K 9533 (NAINA)
18	C 286	43	UP 368	68	SAGARIKA	93	RAJ 3777
19	HYB 633	44	WG 357	69	NARMADA 112	94	RAJ 4037
20	NP 825	45	GW 40	70	UTKALIKA		
21	NP 852	46	J 24	71	HP 1493	S. No.	Checks
22	SAFED LERMA	47	HD 2329	72	HUW 37	1.	HD2967
23	KHARCHIA 65	48	HD 2135	73	HUW 213	2.	PBW 644
24	C 306	49	HUW 12	74	UP 1109	3.	WH1021
25	NP 824	50	WL 410	75	AKW1071 (PUNA)	4.	RSP 561

this diverse set of 94 elite Indian bread wheat genotypes was used in the present study. The experimental material was evaluated in Augmented Randomized Block Design [6]. The experiment for recording of observations was carried out in Randomized Augmented Design with five blocks. The 98 genotypes (94 core set genotypes and four check varieties) were sown with a row to row distance of 20 cm and 0.5 m distance in between blocks. Each genotype was sown in 3 lines of 2 m length. Check varieties were repeated in each block. All the recommended package of practices for wheat was followed to raise a healthy crop. DUS descriptors were used to discriminate genotypes during germplasm evaluation. Qualitative DUS characters like anthocyanin pigment, auricle pubescence, waxiness of leaf sheath and peduncle, waxiness in leaf blade, waxiness of spike, leaf attitude, foliage colour, spike colour, pith, density of spike, colour of grains, grain shape, size grain were recorded. Quantitative data were recorded on five randomly and competitive plants of each genotype from each replication for eight quantitative characters viz. plant height (cm), days to 50% flowering, days to maturity, number of spikelets per spike, spike length (cm), number of seeds per spike, test weight (gm) and yield per plant (gm) was performed. Both qualitative and quantitative characteristics were recorded to measure variation in genotypes at agro-morphological level. Mean values were subjected to analysis of variance to test the significance for each character as per methodology. GCV and PCV were calculated by the formula given by [7] heritability in broad sense (h^2) by [8] and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by [9].

3. Results and discussion

The present investigation was carried out with a view to know the degree of genetic variability of yield attributing characters

in bread wheat (*Triticum aestivum* L.) at agromorphological level. The experimental material consisted of 94 genotypes which were evaluated in an Augmented Randomized Block Design. Both qualitative and quantitative characteristics were recorded to record variation in genotypes at agro-morphological level. The data were subjected to appropriate statistical analysis for estimation of mean, range, variance, heritability, genetic advance as percentage of mean. The results obtained have been summarized below.

A. Variability of Qualitative DUS characters

Qualitative characteristics studied. It was showed that significant variation among genotypes and efficiently grouped them at agro-morphological level (Table 2; Table 3; Figure 1).

Table 2: Percentage distribution (%) for the discontinuously variable descriptors measured on the bread wheat accessions under study.

Agro-Morphological Descriptors					
Score	1	3	5	7	9
Auricle pigmentation	81.63	-	18.37	-	-
Auricle pubescence	69.39	-	30.61	-	-
Foliage colour	1.01	-	82.83	16.16	-
Spike colour	-	46.94	37.76	15.31	-
Spike density	12.37	3.09	-	46.39	38.14
Waxiness spike	28.41	48.86	18.18	3.41	1.14
Flag Leaf attitude	12.24	37.76	-	42.86	7.14
Waxiness leaf sheath	15.31	21.43	29.59	30.61	3.06
Waxiness leaf blade	-	95.77	2.82	1.41	-
Waxiness of peduncle	22.22	34.57	28.40	14.81	-
Pith	82.47	-	17.53	-	-
Grain shape	44.90	40.82	-	12.24	2.04
Grain. Size (mm)	10.20	41.84	-	47.96	-
Grain colour	-	28.57	67.35	4.08	-

Most of varieties showed green anthocyanin pigment, absence in auricle pubescence, medium to strong waxiness of leaf sheath and peduncle, weak waxiness in leaf blade, absent to weak in waxiness of spike, semi erect to semi drooping leaf attitude, green foliage colour, dull white to brown spike

colour, hollow in pith, dense to very dense in density of spike, dull white to amber colour of grains, round to ovate of grain shape, medium to bold size grain (Table 2; Table 3; Figure 1). Almost similar patterns of DUS descriptors were observed for varieties [10].

Table 3: Frequency distribution (%) for the discontinuously variable descriptors measured on the bread wheat accessions under study'

Agro-Morphological Character	Descriptor state and number of varieties in parenthesis				
	1	3	5	7	9
Auricle pigmentation	Green (80)	-	Purple (18)	-	Dark purple (0)
Auricle pubescence	Absent (68)		Moderate (30)		Strong (0)
Foliage colour	Pale green (1)	-	Green (82)	-	Dark green (16)
Spike colour		Dull white (46)	Brown (37)	Dark brown (15)	
Spike density	lax (12)	Medium (3)		dense (45)	Very dense (37)
Pith	hollow (80)		Medium (17)		Solid (0)
Flag Leaf attitude	Erect (12)	Semi-erect (37)		Semi-drooping (42)	Drooping (7)
Waxiness spike	Absent (25)	Weak (43)	Medium (16)	Strong (3)	Very strong (1)
Waxiness leaf sheath	Absent (15)	Weak (21)	Medium (29)	Strong (30)	Very strong (3)
Waxiness leaf blade	Absent (0)	Weak (68)	Medium (2)	Strong (1)	Very strong (0)
Waxiness of peduncle	Absent (0)	Weak (18)	Medium (28)	Strong (23)	Very strong (12)
Grain shape	Round (44)	Ovate (40)		oblong (12)	Elliptical (2)
Grain. Size (mm)	Small <35 (10)	Medium: 35-40 (41)		Large: 40-45 (47)	Very large (0)
Grain colour	-	Dull white (28)	Amber (66)	Red (4)	

This indicated that irrespective of demography or climate, selection criteria for high yielding genotypes led to selection of similar DUS descriptors. Descriptors like waxiness on

plant parts, foliage colour, flag leaf and seed size were found important in contributing genetic variability in Indian wheat [10].

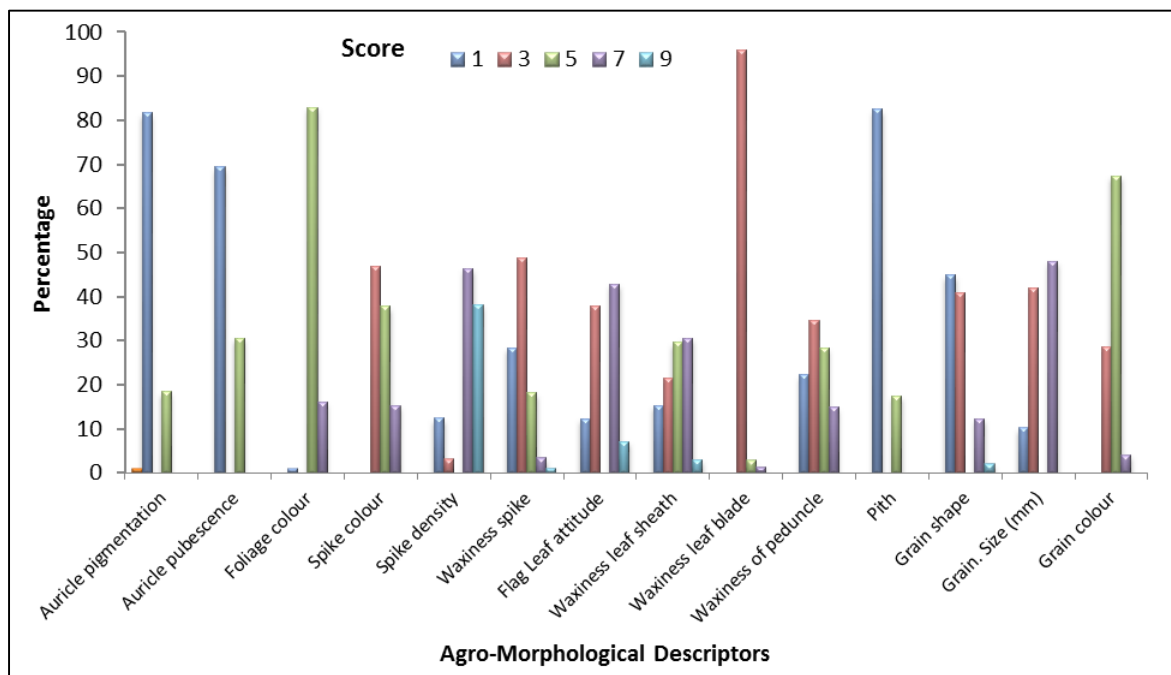


Fig 1: Percentage distribution (%) for the discontinuously variable descriptors measured on the bread wheat accessions under study.

B. Genetic Variability

Ninety four genotypes of bread wheat were critically evaluated for quantitative characters plant height, days to 50

per cent flowering, days to maturity, number of spikelets per spike, spike length, number of seeds per spike,

Table 4: Analysis of variance for grain yield and other traits

Source	d.f.	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of spikelets per ear	Spike length (cm)	No. of grains per spike	TGW (gm)	Avg. yield per plant (gm)
Block (Adj.)	4	17.26	4.425	3.57	1.30	0.94	24.6	38.99	5.73
Genotypes (Adj.)	97	140.38**	22.42**	17.53**	12.60**	1.69**	97.75**	54.93**	109.68**
Among-checks	3	74.30	2.93	5.73	7.80	6.04**	110.53**	122.10**	192.57**
Among-genotypes	93	142.12**	23.12**	17.98**	11.75**	1.39*	86.88**	51.36*	96.37**
Check-vs-Genotypes	1	184.20*	15.69*	10.35	107.50**	16.07**	1077.29**	181.49**	1037.37**
Error	12	26.00	1.89	4.27	2.40	0.59	7.65	25.17	8.63

*, **: Significant at 5 and 1 percent levels respectively

TGW (gm) and average yield per plant (gm). The analysis of variance showed significant variability among all genotypes (Table 4) for all the traits. The mean sum of squares due to genotypes showed significant variability for all the traits while check varieties exhibited non-significant variability for all the traits except spike length, number of grain per spike, test weights and average yield per plants. The blocks exhibited non-significant variability for all traits. The genetic variability of the various traits was also estimated. The largest variation was observed in the test weight (gm) (CV = 16.71)

followed by the Avg. yield per plant (gm), spike length (cm) and plant height (CV = 13.73, 6.96, 5.58%, respectively). Days to maturity showed lowest variation (CV= 1.38%). The minimum to maximum values for yield (gm), days to flowering, days to maturity, plant height (cm), spike length (cm) and test weight (gm) were 4.25-38.50, 56.00-82.00, 145.00-159.00, 67.73- 128.27, 7.67-13.83 and 12.70-45.57 respectively (Table 5). The considerable amount of genetic variability for majority of the traits was studied by ^[11] and ^[12].

Table 5: Mean, range, standard error, coefficient of variance and critical difference for grain yield and other traits

Source	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of spikelets per ear	Spike length (cm)	No. of grains per spike	TGW (gm)	Avg. yield per plant (gm)
Mean	91.35	65.41	153.74	42.28	11.09	57.27	30.03	21.39
S.E.	7.21	1.94	2.92	8.22	1.10	3.91	7.09	4.15
Min	67.73	56.00	145.00	32.00	7.67	30.00	12.70	4.25
Max	128.27	82.00	159.00	48.00	13.83	88.00	45.57	38.50
CV	5.58	2.10	1.34	3.66	6.96	4.83	16.71	13.73
CD	15.71	4.24	6.37	17.90	2.38	8.52	15.46	9.05

The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The estimates of GCV were high for yield per plant (31.10), number of grains per spike (17.17) and the remaining traits recorded moderate to low GCV estimates. The heritability and GAM were high for plant height (81.70, 22.18), number of days to 50% flowering (91.81, 13.79) number of spikelets per spike (79.58, 14.34) number of grains per spike (91.18, 33.77), average yield per plant (91.04, 61.13) (Table 6) Similarly, ^[13] suggested that high heritability

coupled with high genetic advance was observed for grain yield plant ^[14] reported that GCV and PCV were moderate for yield per plant, high heritability and high genetic advance were recorded for all the traits. It had been reported high heritability coupled with high genetic advance for plant height, number of spikelets per spike, and number of days to 50% flowering in wheat ^[15] also reported high heritability estimates for grain yield, number of spikelets per spike, number of seeds per.

Table 6: Phenotypic coefficient of variance, genotypic coefficient of variance, heritability, genetic advance and genetic advance as a percentage of mean for grain yield and other traits

Genetic Analysis	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of spikelets per spike	Spike length (cm)	No. of grains per spike	Test weight (gm)	Avg. yield per plant (gm)
PCV	12.97	7.37	2.76	8.20	11.72	17.98	23.80	32.59
GCV	11.91	6.99	2.43	7.81	8.86	17.17	16.99	31.10
Heritability	81.70	91.81	76.22	79.58	57.23	91.18	51.00	91.04
GA	20.07	9.09	6.66	5.62	1.39	17.51	7.53	18.41
GAM	22.18	13.79	4.37	14.34	13.81	33.77	25.00	61.13

Spike, plant height, which support the present findings. High heritability accompanied with high genetic advance in case of plant height, spike length, number of grains per spike, test weight and yield per plant indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Similar findings have been reported earlier also ^[16, 17, 18]. High

heritability for days to maturity coupled with low genetic advance indicates non-additive gene effects. Therefore, there seems a limited scope for improvement in this trait.

Summary and Conclusion

This study has shown the existence of considerable genetic variation among the genotypes. Among genotypes HPW 89

followed by HS 295, PBC TYPE 11, K 9162, RAJ 3777, PBW 396, DL 788-2 (VIDISHA), DL 153-2 (KUNDAN), PBN 142 (KAILASH), WL 410 and UTKALIKA were found superior in average yield per plant. These genotypes considered with may help for further selection and breeding. However, these genotypes should also be tested in multi-location trials to confirm their superiority and may then be used as parents in hybridization programme to develop high yielding varieties along with desirable character. Parents may be selected from those which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations. In addition to these characters have considerable amount of genetic variation, high GCA value, highly heritable, GAM and positive significant correlation with yield. However further study across location and years needs to be done in order to corroborate the results obtained in the present investigation.

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