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Research Article

Trait association and morphological diversity in wheat (*Triticum aestivum* L.) genotypes

Manisha Kumari, Mukesh Kumar*, Vikram Singh, S. Vijay Kumar and Meenakshi Rathi
Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar (Haryana) India- 125004
E-mail: mukeshhau@yahoo.com

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Abstract

Efforts were made to analyze the genetic variability, correlation and path coefficient analysis of yield and its contributing traits in 49 wheat genotypes. The study revealed highly significant differences among the genotypes for yield and its contributing components except grain length and grain breadth. The higher magnitudes of phenotypic coefficient of variation (PCV) were observed than genotypic coefficient of variation (GCV). The estimates of GCV and PCV were high for plant height, number of tillers per meter, spike weight, spike length, number of grains per spike ,number of spikelets per spike, flag leaf area, 1000-grain weight, grain yield. High heritability coupled with high genetic advance in per cent of mean was observed for flag leaf area, biological yield/meter, and number of grains/spike indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. The magnitude of correlation coefficients at genotypic level was higher than phenotypic correlation coefficients. Path analysis showed that harvest index had highest direct positive effect on grain yield followed by biological yield, number of tillers per meter, spike weight and number of grain per spike thereby indicated that these were main contributors to the grain yield. The Mahalanobis D^2 analysis showed the 49 germplasm clustered into 7 clusters. This shows the germplasm to become moderately divergent. Cluster pattern revealed that, cluster 2 was the largest group consisting of 16 genotypes which was followed by cluster 4 (11 genotypes), Maximum difference among the genotypes within the same cluster was shown by cluster 7 (4.95). So, these characters should be taken into consideration in selection for yield improvement.

Key words
GCV, PCV, heritability, yield, cluster, diversity

Introduction

Wheat (*Triticum aestivum L.* em. Thell.) is a self-pollinated crop of the member of *Poaceae* family and one of the most leading cereal of many countries of the world including India. It is the most important food crop of India and is a main source of protein and energy. It is grown in temperate, irrigated to dry and high-rain-fall areas and in warm, humid to dry, cold environments. In India, wheat is the second most important food crop after rice both in terms of area, production and consuming country in the world. After the Green Revolution, the production of wheat has shown a huge increase. The major states involved Uttar Pradesh, Punjab and Haryana. They account for nearly 70 per cent of the total wheat produced in the country. Punjab and Haryana yield the highest amount of wheat because of the availability of better irrigation facilities and congenial weather condition. Haryana state on the whole has achieved a productivity level of 4.55 tons/ha on 2.5 million hectares (Anonymous, 2015). It has been described as the ‘King of cereals’ because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. However, the demand for wheat is expected to grow and therefore productivity increase is needed.

Grain yield is a complex trait made up of the interaction between different yield components and environmental effects. Because of this, it is difficult to improve yield through direct selection (especially in the early generations). The component traits should also be used as selection criteria for yield improvement. This is the reason why it is necessary to know the genetic architecture of yield components. The nature and magnitude of gene effect governing the inheritance of quantitative characters could play a vital role for the plant breeder in formulating the appropriate breeding procedure. The genotypic and phenotypic coefficient of variation are helpful in understanding the clear picture of existing variability in the populations, where as the estimates of heritability and genetic advance provide the indices of transmissibility of characters. Thus, estimates of variability parameters like coefficients of variation, heritability and genetic advance are very useful for devising suitable selection strategy for evolving high yielding genotypes in wheat crop. The most simple and convenient methods for working out the genetic diversity among the genotype are available in the form of D^2 analysis (Mahalanobis, 1936) for grouping or clustering of wheat genotypes. The knowledge about genetic variability, heritability, correlation coefficients and its other parameters help in further improving the grain yield through directed selection of component traits and their interrelationship with yield. The present study was therefore conducted to estimate variability, heritability in wheat for utilization in selection programmes aimed at productivity increase of future genotypes.

Materials and methods

The experimental materials consist of 49 genotypes (Table 1) including released varieties and advanced lines of wheat were grown in the randomized block design (RBD) with three replications. The five plants were evaluated from each replication of each genotype. Recommended packages and practice were followed to raise the crop. The observations were recorded on various quantitative characters *viz.,* Plant height (cm), Number of tillers per meter, Spike length (cm), Spike weight (g), Number of spikelets per spike, Flag leaf area (cm^2), Number of grains per spike, Grain length and breadth (mm), Awn length (cm), 1000 grain weight (g), Harvest Index (%), Biological yield per meter (g), Grain yield per meter (g) Further, the value of harvest index was also calculated. The mean performance of individual genotypes was embayed for statistical analysis. Mean, range and coefficient of variation were also estimated. Analysis of variance to test the significance for each character was carried out as per methodology given by Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV), heritability in broad sense (h^2), genetic advance, correlation coefficient and path coefficient was worked out. Mahalanobis's D^2 statistics was used to calculate the genetic divergence in the present population. The genotypes were grouped into different clusters according to the method described by Tocher's (Rao, 1952).

Results and discussion

Estimation of genetic variability, broad sense heritability and genetic advance: The magnitude of phenotypic coefficient of variance was higher than genotypic coefficient of variance for all the characters which indicated the influence of environmental factors over the seasons under field conditions. High GCV and PCV were observed for number of tillers per meter (17.05, 17.32), spike weight (18.31, 18.59), spike length (17.83, 18.70) number of grains per spike (17.43, 17.69), number of spikelets per spike (17.39, 18.22) flag leaf area (18.57, 18.64) harvest index (11.19, 11.40) and biological yield per meter (7.69, 7.80) (Table 2) Similar findings were reported by Shoran (1995) for grain yield, biological yield, no. of tillers and Pawar *et al.* (1988) for number of tillers and grain yield. High amount of GCV and PCV suggested greater slope of selection of superior genotypes for this traits.

Heritability indicated the effectiveness with which selection of genotypes could be based on phenotypic performance. Broad sense heritability was found helpful in providing idea about the relative improvement of genetic effects, which the selected parents would pass on to their progenies.

In the present study, high heritability was observed for the characters like flag leaf area (99.30%) followed by grain yield (98.10%), biological yield per meter (97.20%), spike weight (97.10%), no of grains per spike (97.00%) and numbers of tillers per meter (96.90%) (Table 2). Shankarrao *et al.* (2010) observed similar reports for grain weight per plant, number of grains per spike and also similar results were reported by Kumar and Mishra (2004). Johnson *et al*. (1955) stated that heritability estimated coupled with genetic advance were more helpful than heritability alone in predicting the progress from the selected better individuals. However, there are limitations of using broad sense heritability as it includes both additive and non-additive gene effects. In the present study highest genetic advance as *per cent* mean was observed for grain yield/ meter (36.06) and biological yield/plant (48.24) (Table 2). Similar findings were reported by Shankarrao *et al.* (2010) for genetic advance as per cent mean for grain yield/meter and Yadawad *et al.* (2015) for grain yield/plant. GCV together with heritability and genetic advance was considered as good estimates of genetic gain to be expected from selection on phenotypic basis.

Correlations and path analysis: Correlation studies were done to find out association at phenotypic and genotypic level among different traits. The magnitude of correlation coefficients at genotypic level was higher than phenotypic correlation coefficients. This revealed a strong inherent association between different traits. Correlation among wheat genotypes showed at both phenotypic and genotypic level of grain yield per meter had significant and positive correlation with number of tillers per meter (0.834, 0.851), spike weight (0.720, 0.738), number of grains/spike (0.790, 0.799), number of spikelet/spike (0.734, 0.763), 1000 grain weight (0.732, 0.767) biological yield/plant (0.532, 0.541), harvest index(0.849, 0.852) and plant height (0.405, 0.422) (Table 3). These results were supported by many other works as of Pirdashti *et al.* (2012) which asserted that biological yield, harvest index had significant and positive correlations with grain yield, Kumar and Hunshal (1998) recorded grain yield had significant positive correlation with all the characters studied except spike length. The same results were supported by the study of Fellahi *et al*. (2013).

The path coefficient analysis takes into account the cause and effect relationship between the variables which is unique in partitioning the associations into direct and indirect effects through other dependent variables. Low residual effect (0.047) in path coefficient analysis indicated a high contribution of independent traits to the dependent trait (grain yield/meter) as shown in (Table 4) Among the traits studied, Harvest index (0.8557), biological yield (0.5489), number of tillers per meter (0.0845), spike weight (0.0591), and number of grains per spike (0.0343) exhibited positive direct effect on grain yield/meter. So, direct selection of genotypes for grain yield through these traits may be effective. Similar results were also reported by Pirdashti *et al*. (2012) for number of grain per spike, 1000 grain weight and biological yield had the most direct and positive effect on grain yield and thus should be considered as important selection criteria for improving yield, Suryakant *et al*. (2011). The path coefficient analysis revealed that number of tillers per meter and biological yield per meter were the major contributor towards the grain yield per plant.

Genetic diversity: D^2 statistic has been a promising tool for estimating the genetic divergence in plant breeding experiments and is the basis of variability and helps to craft the designed genotypes as per the requirement. These 49 genotypes were grouped in 7 (Table 5) clusters revealed variable number of genotypes falling into different clusters on the basis of morpho-agronomic characters which has indicated the presence of considerable amount of genetic diversity in present material. Maximum difference among the genotypes within the same cluster was shown by cluster 7 (4.95). This was followed by cluster 2 (3.19), cluster 1 (3.14), cluster 3 (2.78), cluster 4 (2.50), cluster 5 (1.82), cluster 6 (0.00). Cluster 3 and 6 showed maximum inter cluster distance of 12.92(Figure 1) followed by clusters 1 and 6 (10.92). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants and genotypes with better mean values can be selected among all the genotypes to suit the breeding programme. Our results are in collaboration with many such studies conducted in wheat.

Conclusion

The present study showed that existence of wide range of variation for most of the character among the wheat genotypes. Correlation studies concluded that most prominent for selection because of appeared high significant genotypic and phenotypic correlation with grain yield. The high genetic advance accompanied with high estimate of heritability observed for flag leaf area, spike weight and number of grain per spike indicates that heritability is mainly due to additive gene effect and selection may be effective to improve the traits. The magnitude of correlation coefficients at genotypic level was higher than phenotypic correlation coefficients. This revealed a strong inherent association between different traits. Parents may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations.

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Table 1. List of 49 wheat genotypes used in present study

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	C -306	18	WH 1166	35	WH 1193
2	WH-542	19	WH 1164	36	WH 1194
3	WH 711	20	WH 1157	37	WH 1197
4	WH 730	21	WH 1156	38	RAJ 3765
5	WH 1021	22	WH 1154	39	PBW 698
6	WH 1025	23	WH 1142	40	PBW 550
7	WH 1080	24	WH 1182	41	PBW 373
8	WH 1097	25	WH 1183	42	PBW 343
9	WH 1105	26	WH 1184	43	PBW 175
10	WH 1124	27	WH 1185	44	HD 3086
11	WH 1181	28	WH 1186	45	HD 2967
12	WH 1180	29	WH 1187	46	DPW 621-50
13	WH 1173	30	WH 1188	47	DBW 88
14	WH 1172	31	WH 1189	48	DBW 17
15	WH 1171	32	WH 1190	49	WH 1195
16	WH 1169	33	WH 1191		
17	WH 1167	34	WH 1192		

Table 2. Estimates of mean performance, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) in different genotypes of wheat

Characters	Mean ± S.E(m)	Range	PCV (%)	GCV (%)	h^2(bs) (%)	GA	GA as 5 % of mean
Plant Height (cm)	98.68±1.52	86.33-113.66	8.96	8.55	91.10	16.60	16.82
No. of Tillers / m	76.03±1.34	41.00-100.33	17.32	17.05	96.90	26.29	34.57
Spike length (cm)	8.53±0.28	6.83-11.93	18.70	17.83	90.90	2.99	35.02
Spike Weight (g)	4.42±0.08	2.83-6.10	18.59	18.31	97.10	1.64	37.17
No. of Grains /Spike	68.71±1.21	36.33-95.67	17.69	17.43	97.00	24.30	35.37
No. of Spikelets/Spike	22.49±0.71	12.67-32.67	18.22	17.39	91.00	7.68	34.16
Awn Length (cm)	5.22±0.32	4.00-8.50	19.02	15.79	68.90	1.41	27.01
Flag Leaf Area (cm^2)	37.40±0.33	32.00-67.21	18.64	18.57	99.30	14.26	38.14
Grain Length (mm)	6.74±0.04	6.00-7.20	4.65	4.54	95.30	0.62	9.13
Grain Breadth (mm)	3.90±0.01	3.77-4.00	2.34	2.24	91.50	0.17	4.41
1000 Grain Weight (g)	34.50±0.28	30.07-41.00	5.41	5.22	93.40	0.36	10.40
Harvest Index (%)	40.85±0.51	20.06-48.86	11.40	11.19	96.30	0.92	22.63
Biological Yield/meter (g)	308.89±2.31	260.67-364.67	7.80	7.69	97.20	48.24	15.62
Grain Yield/meter (g)	126.20±1.41	66.67-157.67	14.14	14.00	98.10	36.06	28.57

Table 3. Phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients among various traits of wheat genotypes

Traits	PH	NOT	SL	SW	NOG	NOS/S	AL	FLA	GL	GB	GW	HI	BY	GY
PH	1.000	0.473**	0.387**	0.491**	0.517**	0.548**	0.098	0.027	0.048	-0.239**	0.426**	0.096	0.615**	0.405**
NOT	0.489**	1.000	0.553**	0.827**	0.821**	0.780**	-0.011	0.196*	-0.181*	-0.529**	0.795**	0.660**	0.533**	0.834**
SL	0.414**	0.579**	1.000	0.515**	0.340**	0.349**	0.370**	0.402**	0.181*	-0.263**	0.703**	0.303**	0.384**	0.440**
SW	0.511**	0.871**	0.564**	1.000	0.743**	0.663**	-0.088	0.099	-0.202*	-0.508**	0.795**	0.554**	0.464**	0.720**
NOG	0.530**	0.834**	0.352**	0.765**	1.000	0.898**	-0.086	-0.098	-0.200*	-0.520**	0.638**	0.708**	0.344**	0.790**
NOS/S	0.553**	0.801**	0.361**	0.700**	0.928**	1.000	-0.025	-0.122	-0.118	-0.484**	0.588**	0.631**	0.367**	0.734**
AL	0.121	-0.017	0.409**	-0.066	-0.090	-0.030	1.000	0.392**	0.368**	0.060	0.197*	0.104	0.125	0.133
FLA	0.026	0.200*	0.424**	0.100	-0.098	-0.128	0.476**	1.000	0.288**	0.110	0.328**	0.217**	0.063	0.191*
GL	0.050	-0.188*	0.195*	-0.211**	-0.208*	-0.125	0.459**	0.295**	1.000	0.184*	0.019	-0.095	-0.142	-0.168*
GB	-0.252**	-0.561**	-0.287**	-0.543**	-0.551**	-0.528**	0.093	0.113	0.204*	1.000	-0.377**	-0.359**	-0.389**	-0.520**
GW	0.458**	0.839**	0.759**	0.832**	0.668**	0.641**	0.239**	0.338**	0.024	-0.414**	1.000	0.590**	0.466**	0.732**
HI	0.094	0.684**	0.324**	0.573**	0.722**	0.669**	0.129	0.224**	-0.105	-0.379**	0.625**	1.000	0.009	0.849**
BY	0.654**	0.541**	0.402**	0.480**	0.350**	0.372**	0.142	0.064	-0.148	-0.415**	0.490**	0.025	1.000	0.532**
GY	0.422**	0.851**	0.462**	0.738**	0.799**	0.763**	0.158	0.196*	-0.179*	-0.549**	0.767**	0.852**	0.541**	1.000

* Significant at p= 0.05, ** Significant at p= 0.01

PH- Plant height (cm)
SL- Spike length (cm)
NOS/S- Number of spikelets/spike
GL- Grain length (mm)
GW- 1000 Grain weight (g)
GY- Grain yield per meter (g)
SW- Spike weight (g)
GB- Grain breadth (mm)
NOT- Number of tillers per meter
NOG- Number of grains per spike
AL- Awn length (cm)
BY- Biological yield per meter (g)
HI - Harvest index
FLA- Flag leaf area (cm^2)

Table 4. Direct (diagonal) & Indirect (off-diagonal) effects of traits of wheat on Grain yield per meter

Traits	PH	NOT	SL	SW	NOG	NOS/S	AL	FLA	GL	GB	GW	HI	BY
PH	**0.0011**	0.006	0.0051	0.0063	0.0065	0.0068	-0.0015	0.0003	-0.0006	0.0031	-0.0057	0.0012	0.0081
NOT	0.0413	**0.0845**	0.0489	0.0735	0.0705	0.0677	0.0015	-0.0169	0.0159	0.0474	-0.0708	0.0577	0.0457
SL	0.0008	0.0011	**0.002**	0.0011	0.0007	0.0007	0.0008	0.0008	0.0004	-0.0006	0.0015	0.0006	0.0008
SW	0.0302	0.0515	0.0334	**0.0591**	0.0452	0.0414	-0.0039	0.0059	-0.0125	-0.0321	0.0492	0.0338	0.0284
NOG	0.0182	0.0286	0.0121	0.0262	**0.0343**	0.0318	-0.0031	-0.0034	-0.0071	-0.0189	0.0229	0.0247	0.012
NOS/S	0.0049	0.0071	0.0032	0.0062	0.0083	**0.0089**	0.0003	0.0011	-0.0011	-0.0047	0.0057	0.006	0.0033
AL	-0.0024	0.0003	-0.0079	0.0013	0.0017	0.0006	**0.0194**	0.0092	-0.0089	-0.0018	-0.0046	0.0025	0.0028
FLA	0.0001	0.0011	0.0024	0.0006	-0.0006	-0.0007	0.0027	**0.0057**	0.0017	0.0006	0.0019	0.0013	0.0004
GL	0.0004	-0.0013	0.0014	-0.0015	-0.0015	-0.0009	0.0033	0.0021	**0.0071**	0.0015	0.0002	-0.0007	-0.0011
GB	0.002	0.0045	0.0023	0.0044	0.0044	0.0042	-0.0007	-0.0009	-0.0016	**-0.008**	0.0033	0.003	0.0033
GW	0.0183	0.0335	-0.0304	-0.0333	-0.0267	-0.0257	-0.0096	-0.0135	-0.0009	0.0165	**0.04**	-0.025	-0.0196
HI	0.0807	0.5851	0.2774	0.49	0.6174	0.5726	0.11	0.192	-0.0901	-0.3242	0.5348	**0.8557**	0.021
BY	0.3588	0.2969	0.2207	0.2633	0.1924	0.2042	0.0781	0.0349	-0.0814	-0.228	0.2691	0.0135	**0.5489**
GY	**0.4218**	**0.8511**	**0.4625**	**0.7376**	**0.7987**	**0.7627**	**0.1578**	**0.1961**	**-0.1793**	**-0.5492**	**0.7675**	**0.8516**	**0.5409**

Residual effect = 0.0473

PH- Plant height (cm)
SL- Spike length (cm)
NOS/S- Number of spikelets/spike
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GW- 1000 Grain weight (g)
GY- Grain yield per meter (g)
SW- Spike weight (g)
GB- Grain breadth (mm)
NOT- Number of tillers per meter
NOG- Number of grains per spike
AL- Awn length (cm)
BY- Biological yield per meter (g)
HI - Harvest index
FLA- Flag leaf area (cm^2)

Table 5. Distribution of forty nine wheat genotypes in different clusters

Clusters	Genotypes	No. of genotypes
Cluster 1	WH542, RAJ3765, PBW550, PBW343, WH1184, DBW621-50	6
Cluster 2	WH711, WH1187, WH1188, WH1197, WH1025, WH1124, WH1183, WH1154, PBW698,WH1169, PBW175, WH1167, DBW88, DBW1195, PBW343, WH1080, DBW17	16
Cluster 3	HD3086, HD2967, WH1105	3
Cluster 4	WH1097,WH1166,WH1182,WH730, WH1172, WH1164, WH1171, WH1186, WH1157, WH1142, WH1021	11
Cluster 5	WH1180, WH1156, WH1181,WH1173, WH1185, WH1195	6
Cluster 6	C306	1
Cluster 7	WH1189, WH1190,WH1191,WH1192,WH 1193, WH1194	6

Fig. 1. Intra- and inter- cluster distance for the 7 groups of 49 genotypes of wheat