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Genetic Analysis of Grain Yield and Phenological Traits in Bread Wheat (*Triticum aestivum* L.)

Sandeep Kumar, Pradeep Kumar, S. A. Kerkhi

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Abstract Genetic analysis was carried out in 55 genotypes (10 parents and 45 F_1s) through half-diallel mating design in bread wheat. The highest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was found for biological yield (PCV=9.66 and GCV=8.22), flag leaf area (PCV=6.46 and GCV=5.82), productive tillers (PCV=5.99 and GCV=4.61) and grain yield (PCV=9.07 and GCV=8.08). Highest heritability along with highest genetic advance was estimated for flag leaf area (h^2=17.70 and GA=10.81), biological yield (h^2=10.90 and GA=14.42) and grain yield (h^2=10.60 and GA=14.84), therefore selection will be effective based on these traits. Phenological traits mamely productive tillers (gr=0.90** and pr=0.74**), biological yield (gr=1.00** and pr=0.88**) and flag leaf area (gr=0.24* and pr=0.19*) were found significantly correlated (at <1% level of significance) with grain yield. Similarly path coefficient analysis estimates for biological yield, flag leaf area and productive tillers showed high positive direct effects on grain yield, therefore these traits may be used as an index for selection to high yield in bread wheat genotypes.

Keywords Genetic parameters, Diallel analysis, Grain yield, Phenological traits, Wheat.

Introduction

Bread wheat (*Triticum aestivum* L.) is the largest grown cereal crop in the world after rice that contributes to the nutrients supply of the world's populations. India holds second position in both area and production after China and at global level, India's share in world wheat area is about 12.5%, whereas it occupies 12% in total world wheat production (http://directorate of wheat research 2014-2015). The increase in yield potential has always been fundamental importance in wheat breeding program. Genetic analysis of wheat yield improvement had shown that grain yield is determined by component traits and is a highly complex character. For the solution of this problem, the knowledge of selection parameters and eye judgment of the breeder will apply after creation of genetic variability. Exploitation of variability in wheat is regarded as a

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S. Kumar, S. A. Kerkhi
Sardar Vallabhbhai Patel University of
Agriculture and Technology,
Meerut 250110, UP, India

P. Kumar*
Indian Institute of Wheat and Barley Research,
Karnal 132001, Haryana, India
e-mail : pradeeptaliyan231@gmail.com
*Correspondence

Table 1. Pedigree and other available details of the parental lines used in crossing program.

Parents	Species	Parentage/pedigree	Origin/Source
PBW-435	*T. aestivum*	HD 2160/CALIDAD	Ludhiana
HD-2967	*T. aestivum*	ALD/COC/URES/HD2160M/HD2278	New Delhi
MP-3336	*T. aestivum*	HD2402/4W173	Jabalpur
MP-4010	*T. aestivum*	ANGOSTURA88	Jabalpur
DBW-90	*T. aestivum*	HUW468/WH 730	Karnal
HD-2824	*T. aestivum*	PTO-1/CNO79/PRL/GAA/3/HD 1951	New Delhi
HD-3095	*T. aestivum*	CPAN300/WR426//HW2007//HD2851	New Delhi
RAJ 4246	*T. aestivum*	RAJ 3765/WR544	Durgapura
NW-5038	*T. aestivum*	WAXWING*2/VIVITSI	Kumarganj
HD-2733	*T. aestivum*	ATTILA/3/TUI/CARC//CHENICHTO/4/ATTILA	New Delhi

breakthrough in the field of wheat improvement for developing superior genotypes. Hence, the existing variability and selection parameters are equally important in any crop improvement program. Diallel analysis is most effective for ascertaining the systematic genetic architecture of metric traits within short periods. In the present study heritability and genetic advance were considered as direct selection parameters, whereas correlation and path coefficient were regarded as indirect selection parameters. The genotypic and phenotypic coefficient of variation is helpful in understanding the clear cut picture of existing variability in the material. Several researchers have also reported earlier the importance of genetic variability and selection parameters for grain yield and various phenological traits in bread wheat [1—3]. In diallel technique, analysis of genetic variability (mean performance, mean range, PCV and GCV) and selection parameters (heritability, genetic advance, correlation and path coefficient) are of considerable use in gathering precise picture of genetic architecture of metric traits. Therefore the major objective of the present study was genetic analysis of grain yield and phenological traits in bread wheat.

Materials and Methods

Ten genotypes of bread wheat namely PBW 435, HD 2967, MP 3336, MP 4010, DBW 90, HD 2824, HD 3095, RAJ 4246, NW 5038 and HD 2733 (Table 1) were sown during *rabi* of 2012–2013 for attempting crossing program in a 10 × 10 diallel fashion excluding reciprocals. In the next crop season *rabi* of 2013–2014, experimental material consisted 55 genotypes (10 parents and 45 F_1s) was sown in a randomized block design with three replications. Each of the parental lines and crosses were sown by dibbling of seeds in two row plot of 2 meter length at spacing of 10 cm between plants within a row keeping row to row spacing at 23 cm. All the standard agronomical practices (dose of fertilizer, irrigation at all critical stages) were followed to raise normal crop from sowing to till harvest of crop. Observations were recorded on five randomly selected plants in each replication for fourteen characteristics namely days to emergence, days to 50%

Table 2. Analysis of variance for grain yield and phenological traits in bread wheat. DTE-Days to emergence, DTF-Days to 50% flowering, PL-Peduncle length, FLA-Flag leaf area, PT-Productive tillers, SL-Spike length, BY-Biological yield, GY-Grain yield, HI-Harvest index, *, ** Significant at 5% and 1% probability level respectively.

SOV	DF	DTE	DTF	PL	SL	PT	BY	GY	HI	FLA
Replication	02	0.12	0.26	1.44	0.07	0.36	2.13	1.26	1.67	2.37
Treatments	54	4.96**	3.02**	7.96**	0.57**	0.74**	42.10**	9.85**	4.60*	12.00**
Parents	09	11.94**	7.34**	4.36**	1.00**	0.20	20.54**	7.11**	7.62**	25.82**
Hybrids	44	3.55**	21.16**	7.13**	0.49**	0.20	18.78**	3.75**	4.07	8.72**
Parents Vs F_1s	01	3.78**	1.89	77.12**	0.01	29.06**	1262.36**	302.73**	0.44	32.27**
Error	108	0.76	0.57	1.76	0.02	0.14	4.73	0.78	2.75	0.86
Total	164	2.132	1.37	3.8	0.20	0.34	17.0	3.77	3.35	4.55

Table 3. Genotypic and phenotypic correlation coefficients for grain yield and phenological traits in bread wheat. *, ** Significant at 5% and 1% probability level respectively.

Traits	r	DTE	DTF	PL	SL	PT	BY	HI	FLA	GY
DTE	G	1.0000	0.8209	0.3988	-0.1162	0.2374	0.0202	0.2220	0.2164	0.0635
	P	1.0000	0.5288**	0.2543**	-0.1064	0.1027	0.0417	0.0087	0.1595*	0.0379
DTF	G		1.0000	0.2889	0.1903	0.2703	0.1927	0.1441	0.1246	0.2121
	P		1.0000	0.1531*	0.1774*	0.1524	0.0921	0.0922	0.0911	0.1335
PL	G			1.0000	-0.2564	0.4398	0.2373	0.0304	0.1548	0.2532
	P			1.0000	-0.1743*	0.3301**	0.1445	0.1327	0.1185	0.1991*
SL	G				1.0000	0.0505	0.3938	-0.2476	-0.0641	0.3431
	P				1.0000	0.0510	0.3041**	-0.0701	-0.0392	0.2890**
PT	G					1.0000	0.8474	0.2239	0.2365	0.9094
	P					1.0000	0.6880**	0.0974	0.1312	0.7437**
BY	G						1.0000	-0.1791	0.2511	1.0000
	P						1.0000	-0.2948**	0.1525	0.8809**
HI	G							1.0000	-0.0324	0.0255
	P							1.0000	0.0461	0.0682
FLA	G								1.0000	0.2462
	P								1.0000	0.1932*

flowering, number of productive tillers, flag area (cm^2), spike length (cm), peduncle length (cm), biological yield (g), grain yield (g) and harvest index (%). For flag leaf area (cm^2), length and the maximum width of flag leaf was measured and the area was calculated using the following formula suggested by Muller [4] as flag leaf area = leaf length × maximum leaf width × correction factor (0.74). The analysis of variance (ANOVA) was based on the model suggested by Panse and Sukhatme [5]. Heritability (in narrow sense) in F_1s generation based on component analysis was calculated as proposed by Crumpacker and Allard [6]. The genetic advance was worked out by the formula proposed by Robinson et al. [7]. The genotypic and phenotypic correlation coefficients were calculated as suggested by Al-Jibouri et al. [8]. In path analysis; direct, indirect as well as residual effects were calculated.

Results and Discussion

Analysis of variance (ANOVA) among all the 55 treatments (parents and their F_1s crosses) showed highly significant differences (at 1% level of significance) for all the metric traits except productive tillers in parents; productive tillers, harvest index in hybrid and days to 50% flowering, spike length, harvest index in parents vs hybrids, revealing existence of sufficient variability in the present set of material (Table 2) and further genetic analysis would be meaningful.

The understanding of variability and genetic architecture of population is essential for the implementation of systematic breeding program. The general mean of F_1 crosses were greater than their corresponding parents for 9 metric traits namely days to ear emergence, days to 50% flowering, peduncle length,spike length, biological yield, grain yield, flag leaf area whereas, lower for harvest index. The range of mean in F_1s crosses were higher than their corresponding parental line for 5 traits namely days to 50% flowering, peduncle length, grain yield, biological yield and harvest index. Present results indicated that the variability in progenies which was obtained through hybridization could be properly utilized for selection of suitable genotypes on the basis of different genetic parameters. Similar findings were also reported by earlier reporters [1—3, 9, 10] in wheat crop at different locations of India.

Result of GCV and PCV revealed that there was least difference between the GCV value and PCV value for corresponding traits except harvest index and indicated that there was not much influence of environment in the expression of these metric traits. The highest value of PCV and GCV were recorded for biological yield (PCV=9.66 and GCV=8.22), grain yield (PCV=9.07 and GCV=8.08), flag leaf area (PPCV=6.46

Table 4. Direct (diagonal) and indirect effects of phenological traits on grain yield in bread wheat. *, ** Significant at 5% and 1% probability level respectively.

Traits	Path	DTE	DTF	PL	SL	PT	BY	HI	FLA	GY
DTE	G	-0.7406	-0.6080	-0.2954	0.0861	-0.1758	-0.0149	-0.1644	-0.1603	0.0635
	P	0.0106	0.0056	0.0027	-0.0011	0.0011	0.0004	0.0001	0.0017	0.0379
DTF	G	0.2726	0.3321	0.0959	0.0632	0.0898	0.0640	0.0478	0.0414	0.2121
	P	-0.0039	-0.0073	-0.0011	-0.0013	-0.0011	-0.0007	-0.0007	-0.0007	0.1335
PL	G	-0.0528	-0.0382	-0.1324	0.0339	-0.0582	-0.0314	-0.0040	-0.0205	0.2532
	P	0.0009	0.0006	0.0037	-0.0006	0.0012	0.0005	0.0005	0.0004	0.1991*
SL	G	0.0095	-0.0155	0.0209	-0.0813	-0.0041	-0.0320	0.0201	0.0052	0.3431
	P	0.0065	-0.0109	0.0107	-0.0612	-0.0031	-0.0186	0.0043	0.0024	0.2890**
PT	G	0.0547	0.0623	0.1014	0.0116	0.2305	0.1953	0.0516	0.0545	0.9094
	P	0.0155	0.0229	0.0497	0.0077	0.1505	0.1035	0.0146	0.0197	0.7437**
BY	G	0.0170	0.1627	0.2003	0.3324	0.7152	0.8440	-0.1511	0.2120	1.0099
	P	0.0303	0.0670	0.1050	0.2211	0.5002	0.7270	-0.2143	0.1109	0.8809**
HI	G	0.0145	0.0094	0.0020	-0.0161	0.0146	-0.0117	0.0651	-0.0021	0.0255
	P	0.0024	0.0253	0.0364	-0.0192	0.0267	-0.0809	0.2744	0.0127	0.0682
FLA	G	0.0246	0.0142	0.0176	-0.0073	0.0269	0.0285	-0.0037	0.1137	0.2462
	P	0.0026	0.0015	0.0020	-0.0006	0.0022	0.0025	0.0008	0.0165	0.1932*

and GCV=5.82) and productive tillers (PCV=5.99 and GCV=4.61). Similar findings were also reported by Singh et al. [9] and Dhakar et al. [11] for grain yield whereas Kumar et al. [3] for productive tillers in wheat crop in India. Rest of the traits namely days to emergence, days to flowering and harvest index showed low value of PCV and GCV. Similar findings were also reported by earlier reporters [3, 11] for days to flowering in bread wheat. present results indicated that useful variability in progenies may be utilized while making selection of suitable genotypes on the basis of different genetic parameters to improve grain yield in wheat.

Estimates of high narrow sense heritability coupled with high genetic advance of a character are more effective for selection due to the fact that expression of these traits are controlled by additive gene action. Highest heritability along with highest genetic advance was recorded for flag leaf area (h^2=17.7 and GA=10.81), biological yield (h^2=10.9 and GA=14.42) and grain yield (h^2=10.6 and GA=14.84) revealing the presence of additive and additive × additive type of gene effects in the expression of above traits. Similar findings were reported by Singh et al. [1] and Kumar et al. [3] in wheat. Present results indicated that useful variability in progenies develop through hybridization can be properly utilized and selection of suitable genotypes on the basis of genetic parameters can be done to get high yield in bread wheat.

Genotypic correlation coefficients were, in general, slightly higher than the corresponding phenotypic correlation coefficient for almost all the traits under study (Table 3). The phenological traits namely biological yield (0.88), productive tiller (0.74) and spike length (0.29), showed highly significant positive correlation whereas peduncle length (0.20) and flag leaf area (0.19) showed significant positive correlation (at 1% and 5% level of significant respectively) with grain yield,at both genotypic as well as phenotypic level indicating that grain yield and these phenological traits has the same physiological basis for their expression. Similar findings of correlation coefficient between grain yield and different phenological traits in wheat were also earlier reported by Singh et al. [1] and Kumar et al. [3] for biological yield, productive tillers, spike length and Kumar et al. [10] for productive tillers and biological yield in wheat crop at different locations of India. In the present investigation, the traits which showed direct positive correlation with grain yield may be considered as most important traits combination for grain yield improvement in bread wheat through selection.

In path coefficient analysis, selection may be

Table 5. Genetic parameters for grain yield and phenological traits in bread wheat. *, ** Significant at 5% and 1% probability level respectively.

Traits	Grand mean	Range	PCV	GCV	Heritability narrow sense	GA as % of means
Days to ear emergence	76.12	72.00 - 77.67	1.93	1.55	77.9	2.58
Days to 50% flowering	85.46	82.00 - 87.00	1.38	1.06	71.5	1.67
Peduncle length	35.77	32.34 - 39.40	5.47	4.02	41.2	6.08
Spike length	9.86	8.63 - 10.86	4.59	4.33	68.1	8.40
Productive tillers	9.70	8.47 - 10.67	5.99	4.61	-0.1	7.29
Biological yield	42.92	33.66 - 50.16	9.66	8.22	10.9	14.42
Grain yield	21.51	16.64 - 24.23	9.07	8.08	10.6	14.84
Harvest index	50.26	46.52 - 54.53	3.65	1.56	0.6	1.38
Flag leaf area	33.12	28.54 - 38.95	6.46	5.82	17.7	10.81

done on the basis of direct effects of the components traits towards grain yield for improvement of wheat crop. In the present study 5 phenological traits namely biological yield, days to 50% flowering, number of productive tillers, flag leaf area and harvest index showed positive direct effets on grain yield whereas, rest of the traits showed negative direct effect on grain yield (Table 4). Present findings were in accordance to the findings of Singh et al. [1] for biological yield and productive tillers; Kumar et al. [10] for harvest index and biological yield and Kumar et al. [3] for biological yield, days to 50% flowering, productive tillers, flag leaf area and harvest index at different locations of India in wheat. Hence, these traits should be considered while exercising selection procedures for improvement of grain yield. All the traits have direct and indirect effects on grain yield through several other traits. Therefore, the traits which were showing positive indirect effects on grain yield except days to flowering (where negative effects are desirable) should also be used for the improvement of grain yield. It means these are the best traits by which we improved the grain yield by improving these traits, because these traits have positive direct and indirect effect on grain yield with positive and significant correlation coefficient.

Based on the findings of this investigation, it may be concluded that only three yield components namely flag leaf area, biological yield and grain yield showed highest heritability coupled with highest genetic advance and also have highest PCV anf GCV therefore selection well be effective based on these traits due to the maximum contribution of additive gene action (Table 5). Productive tillers, biological yield, flag leat area and peduncle length showed positive significant correlation and also have positive direct effects on grain yield at both genotypic as well as phenotypic level, indicating that we might improve grain yield by improving these traits and thus emphasis should be given on these traits for the selection of elite genotypes from the segregating generations. It is evident that genotypes developed might serve as good source of material for further breeding program. Therefore information generated from this research article on variability (mean, range of mean, PCV and GCV) and selection parameters (narrow sense heritability, genetic advance, correlation coefficient and path coefficient) could helps the breeders to develop superior cultivars within a short time.

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