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Genetic Analysis for Grain Yield and Morphological Traits and Their Implication for Improvement in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT

Genetic analysis was carried out in 104 genotypes (24 parents and 80 F_1s) through line ×tester (20 Line×4 Tester) mating design in bread wheat. Analysis of variance (ANOVA) showed revealed the considerable amount of genetic variability among the breeding materials for all the traits under study. The highest value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for flag leaf area (PCV= 14.71& GCV= 13.99), biological yield (PCV= 13.97& GCV= 12.69), grain yield (PCV= 14.96 & GCV= 12.84) and ash content (PCV= 21.30 & GCV= 20.64). Highest heritability coupled with highest genetic advance was recorded for grain yield (h^2=38.63 & GA=22.72), biological yield (h^2=38.47 & GA=23.76), productive tillers (h^2=54.57 & GA=12.52) and harvest index (h^2=38.47 & GA=10.50 indicated the effectiveness of selection for these traits. The traits namely 1000 grain weight (gr = 0.23 & pr = 0.14*), harvest index (gr = 0.24** & Pr = 0.36**), biological yield (gr = 0.87** & Pr = 0.82**), productive tillers (gr = 0.72** & pr = 0.65**) and grains per spike (gr = 0.14* & pr = 0.12*) were found positively correlated (at <5% level of significance) with grain yield. Similarly, harvest index, grains per spike and biological yield showed highest positive direct effects on grain yield therefore indirect selection for these traits would be effective for improving the grain yield in bread wheat.*

Key words: *Genetic variability, Correlation, Path analysis, Yield traits, Bread wheat.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the staple food for a large part of the world population. In India, the crop ranks second in terms of total production next to rice with the production amounting to 93.50 million tons from an area of 30.23 million hectares^2. The major wheat producing countries are China, India, USA, France, Russia, Canada, Australia, Pakistan, Turkey, UK, Argentina, Iran and Italy. These countries contribute about 76 % of the total world wheat production. India holds second position in terms of both in area and production after china. At global level, India`s share in world wheat area is about 12.5%,

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Whereas it occupies 12 % in total world wheat production[2]. Grain yield is a complex trait and determined by many component traits. These component traits affect grain yield directly or indirectly. Yield increases may be effectively tackled on the basis of performance of yield components and other closely related traits[11]. The traits for which variability present should be highly heritable as the progress through selection depend on heritability, selection intensity and genetic advance of the trait. An estimates of high heritability coupled with high genetic advance of a character are more effective for making selection due to the fact that expression of these traits is controlled by additive gene action. The traits with high heritability exhibiting positive association with yield can be used for indirect selection for yield and will serve as an alternate mode of selection for yield improvement. When the indirect associations become complex, path coefficient analysis is the most effective mean to find out direct and indirect causes of association among the different variables. Hence, the knowledge of direct and indirect effects of different components on yield is of prime importance in selection of high yielding genotypes. Thus in order to determine contribution of various characters towards yield, it is necessary that the relationship between yield and its component characters undergoes partitioning into a series of direct and indirect effects revealing specific forces which are acting to build up a given correlation. Hence, in the context of yield improvement, when selecting desirable genotypes it is very important to know the nature and extent of variation present within a set of breeding material as well as the interrelationship between each yield component and grain yield and the exact contribution of each component to yield *via* direct and indirect effects. It is known that the improvement of the genetic architecture of yield must be based on a more intensive study of individual yield components. Keeping this in view, the present study was undertaken to assess the extent of genetic variability, heritability, genetic advance and inter-relationship of yield components and their implication in the selection of better genotypes of wheat through line x tester mating design.

MATERIAL AND METHODS

Twenty genetically divers lines (UP 2338, PBW 550, HD 2967, PBW 502, WCW 98-4, WCW 98-48, WCW 98-19, UP 2425, PBW 373, HUW 213, K 9162, K 712, K 8962, HUW 516, Selection 1, HUW 635, HUW 234, HD 2733, RAJ 3765, PBW 435 and four testers (PBW 343, PBW 226, PBW 590 and DBW 17) were sown during 2010-2011 for attempting crossing programme in a line x tester mating design. In the next crop season *rabi* 2011-2012 experimental materials consisted of 104 genotypes (24 parents and 80 F_1s) was sown in a randomized block design with three replications. The experiment was conducted at crop research center, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Each of the parental lines and crosses were sown by dibbling of seeds in single row plot of 5 m length at spacing of 10 cm between plant to plant within a row and keeping row to row spacing at 23 cm. Observation were recorded on five randomly selected plants in each replications for days to ear emergence, days to maturity, number of productive tillers per plant, plant height (cm), flag leaf area (cm^2), spike length (cm), grains per spike, biological yield per plant (g), harvest index (%), grain yield per plant (g), 1000 grain weight (g) and ash content (%). The analysis of variance (ANOVA), genotypic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) was calculated based on the methods suggested by Panse and Sukhatme[9]. Estimates of heritability in narrow sense were calculated as proposed the method by Kempthorne & Curnow[4] and genetic advance by the formula suggested by Johnson *et al*[3]. The genotypic and phenotypic correlation coefficient was calculated by the formula as suggested by Al-Jibouri *et al*[1]. All the analysis work was done in Microsoft Excel as per the procedure given by Singh and Chaudhary[13].

RESULTS AND DISCUSSION

The presence of appreciable amount of genetic variability is essential among the parental line for planning a successful breeding programme. The analysis of variance (ANOVA) showed highly significant differences among all the 104 treatments for all the 12 characters namely, days to ear emergence, days to maturity, productive tillers, plant height, flag leaf area, spike length, grains per spike, biological yield, harvest index, 1000 grain weight, grain yield and ash content (Table 1) revealing the existence of sufficient genetic variability in the present set of breeding materials for all the traits under study.

Range and mean performance of all 104 genotypes (Table 2) revealed that a wide range of variation was recorded for almost all the morphological traits under study. It is worthful to mention here that the parent HD 2967 took minimum days for ear emergence and days to maturity, PBW 590 good for maximum number of productive tillers, UP 2425 found to be good for plant height, K 712 parent found maximum mean value for flag leaf area, WCW 98-48 found maximum mean value for spike length, PBW 550 found maximum average value for grain per spike, PBW435 had highest mean value for biological yield and HUW234 showed highest value for harvest index and grain yield. Among 80 F_1s only four crosses namely WCW 98-4 x PBW 343, WCW 98-19 x DBW 17, K 712 x PBW 343 and Selection 1 x PBW 590 were found early maturity type. The cross HUW 234 x PBW 343 was observed as highest grain yielder with high harvest Index. Other crosses showed highest mean values for different traits were K 712 x PBW 590 for productive tillers and spike length, UP 2338 x DBW 17 for flag leaf area, PBW 435 x PBW 226 for grains per spike, PBW 502 x DBW 17 for biological yield, HUW 635 x PBW 590 for 1000 grain weight and HD 2733 x PBW 226 for ash content. These better genotypes (crosses/parents) could be utilized in multiple cross breeding programme which may lead to provide a better population after selection or may be utilized as donor parent for specific trait in wheat improvement programme.

Phenotypic coefficient of variation (PCV) for all the characters was higher than the genotypic coefficient of variation (PCV) (Table 2) which reflect the influence of environment on the expression of these traits. Both phenotypic and genotypic coefficient of variation were found to be moderate (10 to 25%) for flag leaf area, biological yield, grain yield and ash content which indicated that these traits would not be influenced by environment. However, remaining traits namely, days to ear emergence, days to maturity, plant height, harvest index and 1000 grain weight showed low values (<10%) of phenotypic and genotypic coefficient of variation which indicated that these traits might be influenced by environment. High genotypic and phenotypic coefficient of variation for grain yield and other morphological traits was reported by Kumar *et al.*[5], Kumar *et al.*[6], Meena *et al.*[7], Singh *et al.*[9], Singh *et al.*[11], Sneha *et al.*[13] and Verma *et al.*[14] in wheat crop. The results revealed the presence of high amount of genetic variability in the evaluated genotypes for the major yield contributing components including grain yield indicating that further improvement for these traits is possible in wheat crop.

Both heritability and genetic advance are two important direct selection parameters independently but estimates of high heritability coupled with high genetic advance of a character are more effective for making selection due to the fact that expression of these traits is controlled by additive gene action. In the present study, high heritability (narrow sense) coupled with high genetic advance as per cent of mean were recorded for biological yield and grain yield (Table 2) which indicates the presence of additive gene action and offer the possibility for improvement of these traits by various selection methods. While the estimates of high heritability coupled with moderate GA as % of mean was recorded for productive tiller and harvest index, indicates the presence of both additive and non additive gene action for these traits. High heritability along with high to moderate genetic advance for grain yield and productive tillers were also reported by Singh *et al.*[9] and Sneha *et al.*[13]; harvest index, biological yield, grain yield, productive tillers by Verma *et al.*[14] and Kumar *et al.*[5]; harvest index and biological yield by Kumar *et al.*[6]. These findings clearly support the results of present investigations. The traits which exhibited high heritability along with high genetic advance indicates the presence of additive and additive x additive type of gene action in the expression of these traits. This also means that for improvement of these traits any type of selection scheme aimed at exploiting additive genetic variance would be helpful.

The improvement of yield components and the knowledge of their association with its main component are beneficial in formulating the effective breeding programme. In the present study, all possible genotypic and phenotypic correlation coefficients were estimated to know the degree of association component traits with grain yield and also among themselves. The results of correlation coefficient between grain yield and other component traits revealed that grain yield showed positive and highly significant correlation with 1000 grain weight, harvest index, biological yield, productive tillers and days to maturity at both genotypic as well as phenotypic level (Table 3). The positive and significant association of 1000 grain weight, productive tillers and days to maturity with grain yield also reported by Singh *et al.*[9] whereas positive association of grain yield with 1000 grain weight, harvest index, biological yield, productive tillers were reported by Kumar *et al.*[6] in wheat crop. Hence selection for these traits would help in improving grain yield in this crop. Positive and significant correlation of different components with grain yield was also reported by Meena *et al.*[7] and Sneha *et al*[13]. Based on the estimates of genotypic and phenotypic correlation, the breeder would also be able to decide the method of breeding to be followed so that the useful correlation could be exploited and the undesirable ones may be modified by generating fresh variability to obtain new recombination. The results of path coefficient analysis indicated that biological yield, harvest index, spike length, grain per spike and flag leaf area exhibited positive phenotypic and genotypic direct effect on grain yield (Table 4). These results are similar to the earlier findings of Kumar *et al.*[6] for biological yield, harvest index, spike length, grain per spike and flag leaf area in wheat. Positive direct effect of different yield components on grain yield also reported by Meena *et al.*[7] and Sneha *et al.*[13] wheat crop. Significant positive association of biological yield and harvest index with grain yield was mainly due to their high positive direct effects. Productive tillers, days to maturity, flag leaf area, 1000 grain weight, spike length and grain per spike via; biological yield contributed to grain yield. This indirect effect may be because of their positive correlation with grain yield. The traits which showed higher direct and indirect positive contribution towards grain yield, indirect selection for those traits would be effective in improving the grain yield in wheat crop. The value of residual effects was low at both genotypic and phenotypic levels indicated that the characters included in the present investigation were sufficient to account for the variability in the dependent character *i.e*. grain yield.

Table 1: Analysis of variance for grain yield and different agromorphological traits in bread wheat

Source of variation	DF	Days to ear emergence	Days to maturity	productive tillers	Plant height	Flag leaf area	Spike length	Grains per spike	Biological yield	Harvest Index	Grain yield	1000 grain weight	Ash content
Replication	2	0.43	2.91	1.27	7.07	3.76	0.72	2.38	3.73	5.42	3.88	1.89	0.00
Treatments	103	19.11**	40.83**	2.87**	132.85**	46.00**	2.39**	51.50**	124.08**	34.62**	27.44**	5.27**	0.50**
Error	206	1.69	1.25	0.54	1.90	1.56	0.60	1.50	8.17	6.73	2.92	2.01	0.01
Total	311	7.45	14.37	1.32	45.30	16.29	1.19	18.07	46.53	15.96	11.05	3.09	0.17

*,** Significant at 5% and 1% probability level respectively

Table 2: Estimates of genetic parameters for grain yield and different agromorphological traits in bread wheat

Character	Mean	Range	PCV	GCV	Heritability narrow sense	G A as % of mean
Days to ear emergence	78.11	73.00 - 84.00	3.51	3.08	24.075	5.59
Days to maturity	135.43	128.00 - 142.33	2.81	2.68	23.156	5.28
Productive tillers	11.13	8.67 - 12.48	10.31	7.92	54.573	12.52
Plant height	93.18	72.96 - 105.72	7.24	7.09	19.523	14.30
Flag leaf area	27.51	20.73 - 36.85	14.71	13.99	12.499	27.40
Spike length	10.26	8.31 - 12.02	10.67	7.52	16.532	10.91
Grains per spike	47.45	38.89 - 55.50	8.98	8.60	15.820	16.97
Biological yield	48.96	31.13 - 61.89	13.97	12.69	38.472	23.76
Harvest Index	45.58	40.12 - 59.98	8.78	6.69	38.472	10.50
Grain yield	22.26	15.84 - 29.04	14.96	12.84	38.638	22.72
1000 grain weight	41.30	37.85 - 43.85	4.26	2.52	5.892	3.07
Ash content	1.96	1.15 - 2.91	21.30	20.64	10.021	41.18

Table 3: Estimates of phenotypic and genotypic correlation among grain yield and different agromorphological traits in bread wheat

Characters	r	Days to ear emergence	Days to maturity	productive tillers	Plant height	Flag leaf area	Spike length	Grains per spike	Biological yield	Harvest Index	1000 grain weight	Ash content	Grain yield
Days to ear emergence	P	1.00	0.38**	0.10	0.16**	0.05	-0.10	-0.09	0.04	-0.02	0.01	-0.06	0.02
	G	1.00	0.43	0.15	0.19	0.05	-0.24	-0.11	0.05	-0.02	0.02	-0.06	0.02
Days to maturity	P		1.00	0.15**	0.10	-0.03	-0.19**	0.03	0.22**	-0.11*	0.11	0.06	0.14*
	G		1.00	0.20	0.12	-0.03	-0.27	0.03	0.25	-0.16	0.19	0.06	0.16
Productive tillers	P			1.00	-0.10	0.21**	0.03	-0.11*	0.67**	0.02	0.00	0.01	0.65**
	G			1.00	-0.14	0.26	0.01	-0.15	0.77	-0.11	0.02	0.03	0.72
Plant height	P				1.00	-0.01	0.19**	0.08	-0.12*	0.01	-0.07	-0.06	-0.11
	G				1.00	-0.02	0.27	0.08	-0.14	-0.01	-0.13	-0.07	-0.15
Flag leaf area	P					1.00	0.01	-0.07	0.11*	-0.09	0.12*	0.10	0.05
	G					1.00	0.06	-0.08	0.11	-0.12	0.19	0.11	0.05
Spike length	P						1.00	0.23**	0.06	0.01	-0.09	-0.09	0.08
	G						1.00	0.34	0.07	-0.03	-0.22	-0.11	0.06
Grains per spike	P							1.00	0.06	0.10	-0.01	-0.06	0.12*
	G							1.00	0.07	0.14	-0.05	-0.07	0.14
Biological yield	P								1.00	-0.21**	0.13*	0.00	0.82**
	G								1.00	-0.25	0.20	0.00	0.87
Harvest Index	P									1.00	0.02	-0.00	0.36**
	G									1.00	0.06	-0.03	0.24
1000 grain weight	P										1.00	0.09	0.14*
	G										1.00	0.12	0.23
Ash content	P											1.00	-0.00
	G											1.00	-0.01

*,** Significant at 5% and 1% probability level respectively

Table 4: Estimates of direct and indirect effect of different agromorphological traits on grain yield at both phenotypic and genotypic level in bread wheat

Character	r	Days to ear emergence	Days to maturity	Productive tillers	Plant height	Flag leaf area	Spike length	Grains per spike	Biological yield	Harvest Index	1000 grain weight	Ash content	Grain yield
Days to ear emergence	P	**-0.0076**	-0.0029	-0.0008	-0.0012	-0.0004	0.0008	0.0007	-0.0004	0.0002	-0.0001	0.0005	**0.0238**
	G	**-0.0136**	-0.0059	-0.0021	-0.0027	-0.0007	0.0033	0.0016	-0.0007	0.0004	-0.0003	0.0009	**0.0240**
Days to maturity	P	0.0032	**0.0083**	0.0013	0.0009	-0.0003	-0.0016	0.0003	0.0018	-0.0010	0.0009	0.0006	**0.1449**
	G	0.0048	**0.0109**	0.0023	0.0013	-0.0004	-0.0030	0.0003	0.0028	-0.0018	0.0021	0.0007	**0.1696**
Productive tillers	P	-0.0007	-0.0010	**-0.0064**	0.0007	-0.0014	-0.0002	0.0007	-0.0043	-0.0001	-0.0001	-0.0001	**0.6511**
	G	-0.0002	-0.0003	**-0.0014**	0.0002	-0.0004	0.0000	0.0002	-0.0011	0.0002	0.0000	0.0000	**0.7213**
Plant height	P	-0.0013	-0.0009	0.0009	**-0.0082**	0.0002	-0.0016	-0.0007	0.0010	-0.0001	0.0006	0.0005	**-0.1110**
	G	-0.0017	-0.0011	0.0013	**-0.0089**	0.0002	-0.0025	-0.0008	0.0013	0.0001	0.0012	0.0006	**-0.1547**
Flag leaf area	P	0.0001	0.0000	0.0003	0.0000	**0.0014**	0.0000	-0.0001	0.0002	-0.0001	0.0002	0.0001	**0.0567**
	G	0.0001	-0.0001	0.0007	-0.0001	**0.0026**	0.0002	-0.0002	0.0003	-0.0003	0.0005	0.0003	**0.0546**
Spike length	P	-0.0012	-0.0021	0.0004	0.0021	0.0001	**0.0106**	0.0025	0.0007	0.0002	-0.0011	-0.0010	**0.0861**
	G	-0.0019	-0.0021	0.0001	0.0022	0.0005	**0.0078**	0.0027	0.0006	-0.0003	-0.0017	-0.0009	**0.0664**
Grains per spike	P	-0.0002	0.0001	-0.0002	0.0002	-0.0002	0.0005	**0.0021**	0.0001	0.0002	0.0000	-0.0001	**0.1288**
	G	-0.0001	0.0000	-0.0002	0.0001	-0.0001	0.0004	**0.0010**	0.0001	0.0001	-0.0001	-0.0001	**0.1488**
Biological yield	P	0.0469	0.2119	0.6427	-0.1153	0.1099	0.0663	0.0640	**0.9501**	-0.2007	0.1299	0.0022	**0.8292**
	G	0.0513	0.2529	0.7764	-0.1405	0.1158	0.0793	0.0707	**0.9987**	-0.2594	0.2033	0.0029	**0.8714**
Harvest Index	P	-0.0158	-0.0679	0.0132	0.0094	-0.0519	0.0107	0.0589	-0.1199	**0.5675**	0.0156	-0.0032	**0.3660**
	G	-0.0150	-0.0851	-0.0557	-0.0062	-0.0631	-0.0188	0.0730	-0.1312	**0.5050**	0.0322	-0.0180	**0.2443**
1000 grain weight	P	0.0000	-0.0002	0.0000	0.0001	-0.0002	0.0001	0.0000	-0.0002	0.0000	**-0.0015**	-0.0001	**0.1441**
	G	0.0001	0.0006	0.0001	-0.0004	0.0006	-0.0007	-0.0002	0.0007	0.0002	**0.0033**	0.0004	**0.2399**
Ash content	P	0.0003	-0.0003	-0.0001	0.0003	-0.0005	0.0004	0.0003	0.0000	0.0000	-0.0004	**-0.0047**	**-0.0053**
	G	0.0003	-0.0003	-0.0001	0.0003	-0.0005	0.0005	0.0003	0.0000	0.0002	-0.0005	**-0.0044**	**-0.0176**

Phenotypic-Residual effects = 0.0752; Genotypic- Residual effects = 0.053

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