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Genetic variability, selection parameters and their association analysis for yield and its component traits in bread wheat (*Triticum aestivum* L.)

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Abstract
In order to estimate genetic variability, selection parameters and their association analysis for nine traits of wheat, 15 hybrids were synthesized in a 6×6 diallel fashion excluding reciprocals. Analysis of variation established significant relationship for most of the traits that reveals existence of genetic variability for these traits. The PCV values were greater than GCV indicating little influence of environment in expression of traits. High value of heritability along with genetic advance was observed for days to maturity. Genotypic correlations found to be greater than phenotypic correlations for all the traits. Days to maturity (0.63), number of productive tillers per plants (0.202), number of spikelets per spike (0.732) and number of grains per main spike (0.410) exhibited the positive direct effect on grain yield. Therefore, selection for grain yield via these traits will be effective.

Keywords: genetic variability, heritability, genetic advance, correlation, direct and indirect effects, yield

Introduction
Wheat (*Triticum aestivum* L.emend Fiori & Paol.) is one of the most important cereal crop of the world. Manifestation of wheat yield fluctuates widely as a result of its interaction with environment because grain yield is a complex inherited character and is the product of several contributing factors affecting yield directly or indirectly (Akram *et al.*, 2008) [1]. World population has experienced continuous growth rate. Hence producing more wheat is becoming an urgent task for Indian agricultural sector. To produce more cereals, the prevailing environmental constraints must be mastered and adequate producing technologies put forward. Use of varieties with better yield potential and wide range of adaptability is of prime importance for increasing wheat production. Thus development of high yielding wheat cultivars has always been a major objective of wheat breeding programs throughout the world (Bhutta, 2006) [6].
Variability in genotypes for grain yield and yield components traits play a vital role for crop improvement while making selection. Heritability and genetic advance are other important selection parameters. The estimates of heritability and genetic advance as per cent of mean help the plant breeder in determining the character for which selection would be rewarding.
The knowledge about the extent and nature of inter relationship among yield components provide a better understanding in improving yield through selection. Grain yield, being a complex character, is highly influenced by environment; therefore, direct selection for yield would not give better results. Indirect selection in such a situation is more effective. The path coefficient analysis facilitates the partitioning of the correlation coefficients into different components of direct and indirect effects. Thus, study on association among different character is very essential for developing effective selection criteria (Singh *et al.*, 2009) [20]. Keeping this view, the present study was conducted to study genetic variability, heritability, and association studies for yield and its component traits in bread wheat (*Triticum aestivum* L.).

Material and Methods
The present investigation was undertaken to estimate statistical genetic parameters for yield for yield and its component traits in diallel fashion (excluding reciprocals) in bread wheat. The experimental work was conducted at Crop Research Farm of CSAUA&T, Kanpur (26 °46'N and 80 °33'E and 126msl), Uttar Pradesh, India. In 2014-2015 Rabi season for attempting the crosses in 6×6 diallel fashion and in 2015-2016 following season for comprising total 21 genotypes (6 parental and 15 F$_1$'s). The parents (PBW 343, K 1006, K9107, K607, K424 and K9423) were chosen on the basis of wide variability existing between them for yield

contributing traits for this study. Resulting 15 hybrids along with their parents were planted in a randomized block design with three replication. Each of the parental lines and crosses were sown by hand dibbling method in 3 rows plot (3m length keeping 23cm spacing between row and 10cm within plants). The recommended package of practices and cultural operations were followed to raise good crop and for proper expression of material. Observations were collected from 5 randomly selected competitive plants in each of three replications for nine traits namely: days to 75% flowering, days to maturity, plant height (cm), number of productive tillers per plant, spike length (cm), number of spikeletes per spike, number of grain per main spike, 1000-grain weight (g) and grain yield per plant (g). The pedigree details and other pass port data showing diversity among these genotypes are given below in Table 1.

Statistical analysis was done on the mean values of 5 competitive plants per treatment in each of three replications for 9 characters. The statistical software (WINDOSTAT version 8.0) was used to work out analysis of variance, gene action, heritability, genetic advance, correlation, direct and indirect effects. The data after compilation for each character was subjected to standard statistical method of analysis of variance following Panse and Sukhatme (1967) [15], genotypic coefficient of variation (GCV %) and phenotypic coefficient of variation (PCV %) were estimated by the formula as suggested by Burton (1952) [7], heritability in narrow sense in percent (h^2) and genetic advance as percent of mean were estimated by the formula as proposed by Crumpacker and Allard (1962) [8] and Robinson et al. (1949) [17]. The estimate of GCV and PCV were classified as suggested by Sivasubramanian and Madhavamenon (1973) [22]. The heritability was categorized as suggested by Robinson et al. (1965) [18]. Again, genetic advance was classified by adopting the method of Johnson et al. (1955a) [12]. The genotypic and phenotypic correlation coefficients were calculated as suggested by Al-Jibouri et al. (1958) [3]. Path coefficient analysis was performed according to the method of Dewey and Lu (1959) [9] by solving simultaneous equations using genotypic correlations.

Table 1: Pedigree and other passport data of parental lines used for study

S. No	Parents	Parentage	Release year	Source/ Origin
1.	PBW343	ND/VG 1944/KAL/BB/3/YAC 'O' 5 /4/ VEE≠ 5 "S"	1996	PAU, Ludhiana
2.	K1006	PBW34 /HP1731	2014	CSAUAT, Kanpur
3.	K9107	K8107/K68	1996	CSAUAT, Kanpur
4.	K607	HUW468/HD2402/2/K9162	2011	CSAUAT, Kanpur
5.	K424	K8962/K8020	2010	CSAUAT, Kanpur
6.	K9423	HP1633/KSona/UP262	2004	CSAUAT, Kanpur

Results and Discussion

The result of variance analysis of nine yield related traits for the twenty one genotypes (six parents and fifteen F1s) showed significant differences between genotypes for all studied traits, indicating that there is variability between studied genotypes to measured traits (Table 2). Parents and crosses showed highly significant effects for all traits also reported earlier by Hassani et al. (2005) [11]. This result implied that this population of wheat cultivars would respond positively to selection.

The genotypic and phenotypic coefficients of variation which are free from the unit of measurement, can be conveniently employed for making comparison between populations and for different metric traits of population. The genotypic coefficient of variation (GCV) ranged from 4.67% to 21.75% and phenotypic coefficient of variation (PCV) from 4.81% to 23.09% (Table 3). Number of productive tillers per plant exhibited highest genotypic coefficient of variation (21.75%) followed by grain yield per plant (18.55%) and spike length (14.72%) which indicated moderate % of GCV. The highest phenotypic coefficient of variation was found for number of productive tillers per plant (23.09%) followed by grain yield per plant (19.44%) and spike length (15.38%) which indicated moderate % of PCV. Moderate grain yield per plant for GCV and PCV were also reported by Kumar and Kerkhi (2015) [13]. For rest of traits, GCV and PCV were less than 10. PCVs were slightly higher than GCVs for all selection parameters indicating presence of environmental influence on the expression of characters (table 3) as earlier reported by Fellahi et al. (2013) [10].

The values of heritability, genetic advance and genetic advance as percent of mean (5%) were given in table 3. Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of a trait (Allard, 1960) [4]. Effective selection can be achieved only when additive effects are substantial and environmental effects are small. High estimates of narrow sense heritability were observed for days to maturity (92.24%), number of productive tillers per plant (80.36%), plant height (63.40%), days to 75% flowering (57.20%), spike length (53.51%), number of grains per main spike (53.37%), grain yield per plant (51.10%) and number of spikelets per spike (48.26%) (Table 4.). High heritability were also reported by Singh et al. (2012) [21] for days to maturity, Ali et al. (2008) and Kumar and Kerkhi et al. (2015) [13] for number of productive tillers per plant, plant height, spike length, number of grains per main spike, grain yield per plant and number of spikelets per spike.

Johnson et al. (1955) [12] have reported that heritability estimates along with genetic advance will be more useful than heritability value alone in selecting best individuals. Hanson (1963) stated that heritability and genetic advance are two complementary concept. The genetic advance as % of mean is more advantageous for observing the genetic gain. Based on this consideration, high heritability accompanied by high genetic advance as percent of mean was observed for number of productive tillers per plant, grain yield per plant and spike length suggesting predominance of additive gene action in the expression of these traits. Hence selection may be effective for these traits. High heritability along with moderate genetic advance was noticed for days to maturity, plant height, number of spikelets per spike and number of grain per main spike suggesting predominance of additive and non-additive gene action in the expression of this trait. Therefore, this trait can be improved by mass selection. High heritability coupled with low genetic advance for days to 75% flowering is indicative of predominance of non-additive gene actions which could be exploited through heterosis breeding, also suggested by Kumar and Kerkhi et al. (2015) [13].

The knowledge of association and relationship between grain yield and its components is of paramount importance to the breeder for making improvement in complex quantitative trait

like grain yield for which direct selection is not much effective. Therefore, association analysis was undertaken to determine the direction of selection and number of traits to be considered in improving grain yield. The results of phenotypic and genotypic correlations among different attributes are presented in Table 4. Genotypic correlation coefficients were generally higher than phenotypic correlation coefficient for most of the character (Rahman *et al.*, 2015) [16]. The positive and significant correlation of grain yield were observed with days to 75% flowering (0.631), days to maturity (0.761), plant height (0.494), number of productive tillers per plant (0.603), spike length (0.629), number of spikelets per spike (0.639), number of grains per main spike (0.727) and1000-grain weight (0.808) at phenotypic level. A strong correlation of these traits with grain yield indicated that, simultaneous improvement of all the traits is possible. Several researchers also reported significant positive association of grain yield per plant with different attributes

like days to maturity, number of productive tillers per spike, spike length and number of grain per main spike (Bhutto *et al.*, 2006), plant height (Sultan and Malik, 2006) [23], number of spikelets per spike (Kumar *et al.*, 2013) [14] and 1000-grain weight (Sherif *et al.*, 2005) [19].

Path-coefficient analysis using grain yield as dependent variable and other traits as independent variables is presented in Table 5. The highest positive direct effects on yield were exhibited by days to maturity (0.673), followed by number of grains per main spike (0.732), number of grains per main spike (0.410) and number of productive tillers per plant (0.202). Anwar *et al.* (2009) [5] also reported highest direct positive effect of days to maturity on grain yield in wheat under normal conditions. Positive direct effects of these traits on grain yield indicated their importance in determining this complex trait and therefore, should be kept in mind while practicing selection for improvement of grain yield in wheat.

Table 2: Analysis of variance of parents and F$_1$s for nine traits in diallel cross of bread wheat

Source of variation	d.f.	Days to 75 % flowering	Days to maturity	Plant height	Number of productive tillers per plant	Spike length	Number of spikelets per spike	Number of grains per main spike	1000-grain weight	Grain yield per plant
Replications	2	2.59	0.30	0.58	0.26	0.48	0.49	5.13*	0.06	0.40
Treatments	20	42.54**	323.16**	120.20*	6.02**	7.35**	5.53	47.57**	20.82**	8.21**
Parents	5	66.36**	656.19**	211.97*	11.54**	10.39**	8.92**	67.73**	18.53**	11.53**
F$_1$s	14	36.88**	214.74**	93.03**	4.47**	6.64**	4.68**	43.58**	21.49**	7.49**
P vs F$_1$s	1	2.79*	176.02**	41.61**	0.27	2.09**	0.53	2.56	22.81**	1.58**
Error	40	0.82	0.83	4.81	0.23	0.21	0.43	1.36	0.19	0.28

*Significant at 5% level; ** Significant at 1% level

Table 3: Grand Mean, heritability (narrow sense), genetic advance & genetic advance in % over mean in nine traits bread wheat

Traits	Grand mean	Range	PCV %	GCV %	Narrow sense heritability[(h2) %]	Genetic advance	Genetic advance over % mean
Days to 75 % flowering	79.78	73.67-85.67	4.81	4.67	57.20	7.47	9.36
Days to maturity	110.41	93.67-125.33	9.42	9.39	92.24	21.27	19.26
Plant height	81.91	74.20-94.67	8.03	7.57	63.40	12.04	14.70
Number of productive tillers per plant	6.36	3.63-9.22	23.11	21.83	80.36	2.70	42.45
Spike length	10.48	8.40-14.13	15.35	14.72	53.51	3.05	29.10
Number of spikelets per spike	17.60	16.06-20.96	8.29	7.41	48.26	2.40	13.64
Number of grains per main spike	44.48	39.14-49.44	9.29	8.82	53.37	7.75	17.42
1000-grain weight	38.95	35.15-44.28	6.82	6.73	28.78	5.33	13.68
Grain yield per plant	9.07	6.68-12.63	18.85	17.92	51.10	3.19	35.17

Table 4: Phenotypic and Genotypic correlation for nine traits in a set of diallel crosses

Traits	Days to 75 % flowering	Days to maturity	Plant height	Number of productive tillers per plant	Spike length	Number of spikelets per spike	Number of grains per main spike	1000-grain weight	Grain yield per plant
Days to 75 % flowering	1.000	0.833** (0.862)	0.445* (0.508)	0.656** (0.737)	0.390 (0.411)	0.497* (0.604)	0.720** (0.781)	0.629** (0.661)	0.631** (0.681)
Days to maturity		1.000	0.688** (0.736)	0.812** (0.870)	0.323 (0.339)	0.413 (0.470)	0.764** (0.804)	0.764** (0.781)	0.761** (0.799)
Plant height			1.000	0.479* (0.548)	0.127 (0.518)	0.195 (0.245)	0.478* (0.532)	0.422 (0.464)	0.494* (0.543)
Number of productive tillers per plant				1.000	0.273 (0.312)	0.290 (0.292)	0.727** (0.785)	0.623** (0.654)	0.603** (0.708)
Spike length					1.000	0.630** (0.753)	0.584** (0.627)	0.467* (0.495)	0.629** (0.686)
Number of spikelets per spike						1.000	0.465* (0.487)	0.663** (0.720)	0.639** (0.765)
Number of grains per main spike							1.000	0.663** (0.648)	0.727** (0.792)
1000-grain weight								1.000	0.808** (0.868)

Genotypic correlation is given under parenthesis. *Significant at 5% level, ** Significant at 1% level

Table 5: Direct (bold) and indirect effects of nine traits on seed yield of bread wheat as independent variable at genotypic level

Traits	Days to 75 % flowering	Days to maturity	Plant height	Number of productive tillers per plant	Spike length	Number of spikelets per spike	Number of grains per main spike	1000-grain weight	Grain yield per plant
Days to 75 % flowering	-0.718	0.580	-0.034	0.149	-0.038	0.442	0.321	-0.020	0.681
Days to maturity	-0.619	0.673	-0.049	0.175	-0.031	0.344	0.330	-0.024	0.799
Plant height	-0.364	0.495	-0.067	0.111	-0.015	0.180	0.218	-0.014	0.543
Number of productive tillers per plant	-0.529	0.585	-0.037	0.202	-0.029	0.214	0.322	-0.020	0.708
Spike length	-0.295	0.228	-0.011	0.063	-0.093	0.551	0.257	-0.015	0.686
Number of spikelets per spike	-0.434	0.316	-0.016	0.059	-0.070	0.732	0.200	-0.022	0.765
Number of grains per main spike	-0.561	0.541	-0.036	0.158	-0.058	0.356	0.410	-0.020	0.792
1000-grain weight	-0.475	0.526	-0.031	0.132	-0.046	0.527	0.266	-0.031	0.868

Note: Residual effect =0.0513, Bold values = Direct effect

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