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Genetic variability and character association in late sown wheat genotypes

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Abstract

Bread wheat (*Triticum aestivum* L.) is considered as one of the most important cereal crop in the World and fundamental to human cultivation. Development of high yielding genotypes is the focal objective of any wheat breeding programme. Identification of superior genotypes with desirable traits and their consequent use in breeding program and establishment of successful selection criteria can be helpful for successful varietal improvement. The experiment was carried out with 24 wheat genotypes to estimate the genetic variability and association of characters among different genotypes of wheat. Findings indicated that narrow difference was present in respect to GCV and PCV among all the traits which suggested little environmental influence for the expression of different traits in wheat. All the traits showed high heritability. The characters namely plant height, tillers per sq.m, spike length, grains per spike, total chlorophyll content total biomass and harvest index were likely to be governed by additive gene action and early generation of selection would be helpful for improvement of such traits. Out of ten yield attributed components, only harvest index was correlated positively and significantly with grain yield/plant ($r_P = 0.526$; $r_G = 0.530$). Path coefficient analysis revealed that the magnitude of positive direct effect on grain yield per plant was highest through harvest index (1.496 for phenotypic path & 1.50 for genotypic path) and biomass content (1.29 for both genotypic and phenotypic path) on grain yield per plant. The present analyses confirmed that harvest index and biomass content emerged as the most important selection indices for enhancing grain yield of wheat.

Keywords: Genetic variability, character association, heritability

Introduction

Bread wheat (*Triticum aestivum* L) is considered as one of the most important cereal crops and its cultivation has been linked to the development of major civilizations all over the world. 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. The overall production of wheat in the country has gone up tremendously from 12.26 million tonnes in 1964-65 to 93.5 million tonnes in 2015-16. Recently, an estimate of wheat production by Ministry of Agriculture, Govt. of India states that India is expected to touch the new level of wheat production about 100.0 million tonnes in 2018-19.

However, raising temperature, unexpected hailstorms, erratic and unusual precipitation during February-March is hampering wheat production almost every year. West Bengal is not categorized as traditional wheat-growing state of the country because of its mild and short winter, humid climate and late sowing due to delay in harvesting of kharif rice and sometimes excessive soil moisture after rice harvest. However, at present, wheat has become a staple food crop next to rice and its consumption is gradually increasing because of change in food habit. It occupies about 0.335 million hectares areas and contributes about 0.950 million tons wheat grain productions in the state. The average yield of wheat is about 2.836 t/ha which is less than the national average of 2.989 t/ha suggesting ample scope for improving yield of wheat in West Bengal condition. Short span of winter leading to incidence of high temperature during flowering and grain filling, lack of available short duration and terminal thermal stress in genotypes are the major bottlenecks to enhance area and productivity of wheat in West Bengal. The study was thus aimed at the evaluation of wheat genotypes under late sown condition with the following objective-

- To estimate the genetic variability association of characters among different genotypes of wheat.

Materials and Methods

The present investigation was carried out at AB Block Farm, Bidhan Chandra Krishi Viswavidyalaya, Kalyani, situated at 21.5°N latitude and 85°E longitude and 11.7m above the

Mean Sea Level. The research farm is located at the Gangetic New Alluvial plain of India. The experimental site belongs to typical sub-tropical climate with regular South -Western monsoon generally between June to October.

Plant materials

Twenty four genotypes viz., K1614, UBW14, JKW234, HD3267, HUW820, HD3265, PBW771, DBW240, PBW772, DBW90, DBW237, UP2987, WH1227, NW7010, WH1227, KI612, RAJ4503, K1613, WH1228, DBW239, NW7007, HD3059, UP2984 and HUW819 assembled from All India Co-ordinated Wheat and Barley Improvement Project, Bidhan Chandra Krishi Viswavidyalaya constituted the plant material for the present study. These genotypes were evaluated during Rabi season of 2016-17 and 2017-18 under late sown condition (sowing on 25th December) following Randomized Block Design (RBD) with three replications in 2.5m x 0.36m plot, maintaining a spacing of 18 cm since the crop was planted under late sown condition.

Observations recorded

The crop was grown on two consecutive years i.e., Rabi 2016 and Rabi 2017, and the average data from the two consecutive years was generated for further analysis to determine the genetic variability and character association among the 24 wheat genotypes. Ten random plants per replication were sampled to record the characters viz., plant height (cm), days to heading, spike length (cm), days to maturity, number of grains per spike, grain weight per spike (g), test weight (g), total biomass, harvest index and grain yield per plant (g). Number of tillers was recorded per square meter basis. Total chlorophyll content of the flag leaf was estimated as per Sadasivam and Manickam (1996) [22].

Statistical and biometrical analyses

The mean data were subjected to analysis of variance to test the level of significance among the genotypes for different characters. The coefficient of variation (CV) was measured as it is the basis for comparing the extent of variation between different characters. Considering that all the genotypes tested here, were genetically uniform, the expected mean sum of square for error (EMS), i.e. σ^2_e would be purely a random environmental variance. The mean squares between genotypes will consist of variances.

- i) Attributing to varietal differences (i.e., genotypic differences) and
- ii) Due to environmental variation among individual of each genotypes.

The genotypic (GCV) and phenotypic (PCV) coefficients of variations were calculated as per Burton (1952) and Burton and De Vane (1953) [4, 5]. Heritability in broad sense (h^2) was estimated by the formula suggested by Hanson *et al.* (1956) [11]. Genetic advance as percentage of mean (GA %) was estimated as per Johnson *et al.* (1955) [13]. Correlation between two variables includes both genotypic and environmental effects. Phenotypic and genotypic correlation coefficients were calculated as per Al-Jiboari *et al.* (1958) [2]. Path co-efficient analysis is simply standardized partial regression coefficient, which splits this correlation coefficient into measures of direct and indirect effects of a set of independent variables on the dependent variable. Path co-efficient analysis was carried out at the genotypic and phenotypic level as suggested by Wright (1921) and discussed by Dewey and Lu (1959) [9]. Residual effect measures the

contribution of the characters not considered in the scheme was obtained as residual effect.

Results and Discussion

Estimation of genetic parameters:

Mean performances different yield attributing traits of 24 wheat genotypes for are given below (table no. 1). The present study was initiated to examine the nature and magnitude of variability for 11 different characters of 24 wheat genotypes. Analysis of variance revealed that highly significant variation was present for thirteen different component characters among the different genotypes. Most of the characters showed coefficient of variation below 10% except total Chlorophyll content suggesting less genotype X environment interaction. The coefficient of variation observed for total biomass was 10.34 indicating that there was a considerable amount of environmental influence for expression of the character.

The genotypic coefficient of variation (GCV) also helps to determine the magnitude of genetic variability in the traits at genotypic level. The range of GCV varied from 1.16% to 15.99% whereas, PCV varied from 1.34% to 19.04% (table no. 2). The estimates of Phenotypic coefficient of variance (PCV) is the sum total of GCV and ECV. The values of PCV were always higher than the corresponding GCV indicating that environmental influence was present among the different characters. The GCV and PCV results indicated that narrow difference was present among all the traits, concluding that environmental influence was very little for the expression of different traits in wheat. Similar results were also reported by Singh *et al.* (2014) [25], Kaddem *et al.* (2014) [14], Kyosev *et al.* (2015) [16] and Deoraj *et al.* (2016) [8]. High value of GCV suggested better improvement for selection of different traits but GCV is not alone sufficient for the estimation of degree of variation that disseminate for one generation to next. As a consequence, GCV together with heritability and genetic advance might give a clear-cut idea that can be utilized during selection. A character with high heritability and high genetic advance may positively due to the action of additive genes (Panse, 1957) [21]. The characters without such combinations appear due to non additive genes (Liang and Walter, 1968) [17].

The coefficient of variation indicated only the extent of variability present in the characters and does not indicate the heritable portion. This could be estimated from heritability estimates, which in broad sense include both additive and non-additive gene effects and in narrow sense include the proportion of heritable variation which is due to additive component (Lush, 1949) [18]. Heritability (broad sense) values of traits are of vital significance because it determines response to selection (Yao *et al.*, 2014) [28]. In the present investigation all the traits (plant height, days to heading, tillers per square meter, days to maturity, test weight, length of spike, total chlorophyll, total biomass, harvest index and yield) showed high range of heritability. High heritability coupled with high genetic advance was observed in tillers per sq meter, total chlorophyll content and harvest index. Whereas high heritability accompanied by moderate genetic advance was recorded for the traits like plant height, spike length, grains per spike, total biomass content and yield per plant. Hanson (1963) [12] stated that heritability and genetic advance are two complementary concepts. Rest of the traits although showed high heritability but magnitude of GA was somehow little or less amount. The characters showed high heritability and moderate to high amount of genetic advance

indicated preponderance of additive gene action and selection will be rewarding for such traits. Differential heritability for different genotypes in wheat had earlier been reported by Majumder *et al.* (2008) ^[19], Singh *et al.* (2009) ^[24], Ullah *et al.* (2011) ^[27] and Kyosev *et al.* (2015) ^[16].

Character association for grain yield components of wheat

Yield component concept in breeding has got much importance in improving yield potential. Selection on the basis of performance of yield alone, a polygenic complex trait is usually not very efficient. Therefore, selection based on yield components was suggested to be more effective rather than yield alone.

Correlation coefficients

Understanding about the nature and magnitude of correlations between traits of interest is of utmost importance because selection for a particular trait may either increase or reduce the expression of another trait, depending on the genetic correlation between them. Correlation studies provide important information to identify and determine the proportion of the phenotypic correlation that is associated with genetic causes, to verify whether the selection for a certain trait influences another one, to quantify indirect gains due to selection of correlated traits, and to evaluate the complexity of the traits (Cruz *et al.*, 1988; Tiwari and Upadhyay, 2011) ^[6, 26]. In fact, knowledge of genotypic interrelationship between characters is also of theoretical interest because genotypic correlation may be derived from genetic linkage, pleiotropy or developmentally induced relationship between components, which are only indirectly the consequence of gene action (Adams, 1967) ^[1]. The intensity and direction of association among the characters can conveniently be measured by genotypic and phenotypic correlation coefficient.

Genotypic correlations were slightly higher in magnitude than the corresponding phenotypic ones, thereby establishing strong relationship among the traits studied which agreed well to some earlier reports (Tiwari and Upadhyay, 2011; De Souza *et al.*, 2012) ^[26, 7]. Statistical significance of the phenotypic correlation coefficients between pair of characters has been utilized to study the character association.

Yield is a complex trait associated with a number of plant characters and is the prime concern of the plant breeder, hence all the changes in yield must be accompanied by changes in one or more characters (Graffius, 1964) ^[10]. It appeared from the present investigation that of the 10 yield components, only harvest index was correlated positively and significantly with grain yield/plant ($r_P = 0.526$; $r_G = 0.530$) (table no. 3). Kumar and Hunshal (1998) ^[15] also observed in wheat that harvest index was one of the most important components of grain yield which agreed well to the present findings. In the present investigation, biomass content registered positive but non-significant correlation with grain yield ($r_P = 0.142$; $r_G = 0.146$). Earlier report of Okuyama *et al.* (2004) ^[20] and Sapi *et al.* (2017) ^[23] also indicated that

biomass content or biological yield was significantly related to higher grain yield which supported the present findings. Correlation between two characters may not be established due to their mutual cancellation in the plant itself. For this reason, apparently important grain yield components viz., spike length, grain per spike and test weight of grain did not register any significant correlation with grain yield/plant. Chlorophyll content of leaf generally gives a general indication of photosynthetic efficiency but partitioning of photosynthates for the grain yield depends on many other physiological factors. However, somewhat unexpectedly, grain yield / plant registered significantly negative correlation with total chlorophyll content ($r_P = -0.457$; $r_G = -0.552$) contents of leaf which did not find support from the earlier findings of Sapi *et al.* (2017) ^[23]. Plant height also showed significant negative correlation with grain yield/plant which was also supported by the works of Ayer *et al.* (2017) ^[3]. No other pair of characters registered marked correlations between them which clearly indicated that balancing and mutual cancellation of the characters was operative during character expression.

Path coefficient analysis

Linear correlation between any two characters may present a confusing picture because any character may exert simultaneous influence on many characters of the plant. On the other hand, path coefficient analysis gives more specific information on the direct and indirect influence of each of the component characters upon grain yield. In the path coefficient analysis, grain yield represented the dependent variable and plant height, days to heading, tiller number /plant, days to maturity, spike length, grain number / spike, total chlorophyll contents of leaf, biomass content and harvest index were the independent ones.

The path coefficient analysis using phenotypic and genotypic correlation coefficients among pair of characters depicting direct and indirect effect on grain yield/ has been presented in (table no. 4). Mean residual effect was negligible 0.00056 for genotypic path and 0.02060 for phenotypic path, suggesting the inclusion of almost all the grain yield contributing characters in this study. Path coefficient analysis revealed that the magnitude of positive direct effect on grain yield per plant was highest through harvest index (1.496 for phenotypic path & 1.50 for genotypic path) followed by biomass content (1.29 for both genotypic and phenotypic path). This result was also supported by the findings of Sapi *et al.* (2017) ^[23].

Important plant characters influencing grain yield per plant

Important plant characters for enhancing grain yield/plant in wheat have been identified from the studies of correlation and path coefficient analysis utilizing 24 genotypes which were evaluated for 11 characters. The present analyses confirmed that harvest index and biomass content emerged as the most important selection indices for enhancing grain yield of wheat.

Table 1: Mean performance of different yield attributing traits of 24 wheat genotypes

Traits	Plant height	Days to heading	Tillers/ sqm	Days to maturity	Test weight	Spike length	Grains/ spike	Total chl	Biomass	Harvest index	Economic Yield
K1614	93.90	66.17	62.33	99.33	9.63	26.50	42.25	1.38	808.83	35.44	31.78
UBW14	93.33	63.00	59.67	98.83	10.42	26.00	37.30	1.90	811.00	31.57	28.08
JKW234	98.13	66.50	70.33	100.00	10.83	30.33	36.53	1.30	810.00	32.76	29.60
HD3267	91.08	62.17	74.00	98.17	10.88	29.83	35.85	2.17	827.33	31.75	29.32
HUW820	91.25	63.67	57.33	99.67	9.60	25.83	43.97	2.23	768.50	33.72	28.75
HD3265	90.23	66.67	69.00	102.50	10.30	32.50	37.25	1.97	721.17	38.64	30.99
PBW771	93.10	65.33	79.33	99.33	10.27	30.33	34.28	1.27	859.83	32.27	31.28
DBW240	92.36	65.67	53.33	98.67	10.57	25.17	44.05	1.63	685.67	39.80	30.48
PBW772	98.03	67.33	63.67	97.83	10.83	31.00	39.47	1.97	674.83	42.52	32.00
DBW90	82.97	68.33	60.00	98.50	10.13	27.17	42.88	1.70	704.17	41.78	32.82
DBW237	83.27	58.67	70.33	98.00	10.42	28.33	38.35	1.73	660.33	43.09	31.69
UP2987	87.08	65.67	67.33	98.00	10.47	29.50	34.55	1.80	635.83	43.70	30.78
WH1227	96.23	64.17	57.33	99.17	10.57	31.00	40.52	1.43	843.50	33.42	31.45
NW7010	95.18	64.67	57.00	99.17	10.68	28.17	39.33	1.90	813.67	34.14	30.99
WH1227	95.72	69.17	50.00	99.33	9.95	29.67	35.18	2.10	806.33	31.61	28.63
K1612	94.51	68.67	78.67	99.50	10.28	27.83	41.17	2.07	791.33	36.31	32.02
RAJ4503	85.60	65.33	55.00	97.67	9.50	26.17	35.15	1.57	745.17	39.16	32.59
K1613	94.13	65.67	60.00	96.33	8.90	29.83	34.77	1.80	702.00	38.46	29.93
WH1228	95.38	63.17	68.33	98.50	11.07	28.17	36.47	1.53	819.00	34.29	31.32
DBW239	98.53	66.33	72.67	100.33	10.10	30.17	38.97	1.83	829.67	38.31	35.22
NW7007	96.16	64.67	53.00	98.45	10.52	29.00	33.90	1.63	718.17	42.00	33.21
HD 3059	92.10	67.33	58.00	100.33	10.73	29.17	38.70	1.80	693.67	38.99	29.58
UP2984	82.77	67.83	67.67	98.50	10.30	29.17	38.48	1.43	787.00	40.49	35.43
HUW819	89.03	64.33	70.33	98.97	10.20	28.00	41.32	1.17	850.67	40.44	37.78
G. Mean	92.09	65.44	63.94	98.96	10.30	28.70	38.36	1.72	765.32	37.28	31.49
S.E.	0.37	0.49	0.80	0.38	0.16	0.37	0.32	0.10	3.72	0.20	0.19
C.D (5%)	1.06	1.40	2.27	1.09	0.45	1.06	0.91	0.29	10.57	0.58	0.55
C.V (%)	0.70	1.31	2.17	0.67	2.66	2.25	1.44	10.34	0.84	0.95	1.07

Table 2: Anova of different yield attributing characters studied

Traits	G.M	G.C.V	P.C.V	Heritability	G.A	G.A% Mean	C.D	C.V (%)
Plant height	92.09	5.18	5.23	98.20	9.74	10.57	1.06	0.70
Days to heading	65.44	3.48	3.71	87.61	4.39	6.70	1.40	1.31
Tillers/sqm	63.94	12.79	12.97	97.21	16.61	25.98	2.27	2.17
Days to maturity	98.96	1.16	1.34	74.33	2.03	2.06	1.09	0.67
Test weight	10.30	4.63	5.34	75.24	0.85	8.28	0.45	2.66
Spike length	28.70	6.40	6.78	89.01	3.57	12.43	1.06	2.25
Grains/spike	38.36	8.08	8.21	96.93	6.29	16.39	0.91	1.44
Total chlorophyll	1.72	15.99	19.04	70.50	0.48	27.66	0.29	10.34
Biomass	765.32	8.78	8.82	99.09	137.89	18.01	10.57	0.84
Harvest index	37.28	10.80	10.85	99.24	8.27	22.17	0.58	0.95
Economic yield	31.49	7.21	7.29	97.86	4.63	14.70	0.55	1.07

Table 3: Genotypic and phenotypic correlation study between different yield attributing characters

Traits		Plant height	Days to heading	Tillers/ Sq. m	Days to maturity	Test weight	Spike length	Grains /spike	Total chl	Biomass	Harvest index	Economic Yield
Plant Height	G	1	0.166	-0.059	0.192	0.209	0.297*	-0.097	0.1	0.368**	-0.478**	-0.258*
	P	1	0.156	-0.053	0.169	0.171	0.268*	-0.099	0.102	0.365**	-0.473**	-0.250*
Days to heading	G		1	-0.125	0.222	-0.199	0.189	0.099	0.033	-0.029	0.07	0.114
	P		1	-0.101	0.183	-0.108	0.169	0.086	0.051	-0.031	0.065	0.099
Tillers/ sq. m	G			1	0.196	0.244*	0.364**	-0.113	-0.164	0.287*	-0.047	0.288*
	P			1	0.181	0.209	0.337**	-0.105	-0.146	0.277*	-0.04	0.286*
Days to maturity	G				1	0.264*	0.354**	0.158	-0.008	0.271*	-0.243*	-0.008
	P				1	0.213	0.294*	0.127	-0.019	0.223	-0.196	-0.008
Spike length	G					1	0.265*	-0.033	-0.059	0.067	-0.056	-0.046
	P					1	0.228	-0.041	-0.034	0.049	-0.043	-0.037
Test weight	G						1	-0.492**	0.029	0.043	0.008	0.062
	P						1	-0.455**	-0.028	0.039	0.011	0.051
No of Grains per spike	G							1	0.041	0.013	0.087	0.176
	P							1	0.017	0.011	0.087	0.174
Total chlorophyll	G								1	-0.294*	-0.116	-0.552**
	P								1	-0.241*	-0.105	-0.457**
Biomass	G									1	-0.760**	0.146
	P									1	-0.761**	0.142

Harvest index	G										1	0.530**
	P										1	0.526**
Yield	G											1
	P											1

Table 4: Genotypic and Phenotypic path studies of different yield attributing characters

Genotypic Path											
Traits	Plant height	Days to heading	Tillers/sq. m	Days to maturity	Test weight	Spike length	Grains/spike	Total chl	Biomass	Harvest index	Economic Yield
Plant height	-0.02	0.01	0.00	0.00	-0.01	0.01	0.00	0.00	0.48	-0.72	-0.258*
Days to heading	0.00	0.04	0.00	0.00	0.01	0.00	0.00	0.00	-0.04	0.10	0.114
Tillers/sq. m	0.00	0.00	0.00	0.00	-0.01	0.01	0.00	0.00	0.37	-0.07	0.288*
Days to maturity	0.00	0.01	0.00	0.00	-0.01	0.01	0.01	0.00	0.35	-0.36	-0.008
Test weight	0.00	-0.01	0.00	0.00	-0.04	0.01	0.00	0.00	0.09	-0.08	-0.046
Spike length	-0.01	0.01	0.00	0.00	-0.01	0.02	-0.02	0.00	0.06	0.01	0.062
Grains/spike	0.00	0.00	0.00	0.00	0.00	-0.01	0.03	0.00	0.02	0.13	0.176
Total chl	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.38	-0.17	-0.552**
Biomass	-0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.29	-1.14	0.146
Harvest index	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.98	1.50	0.530**

Residual = 0.00056

Pehnotypic Path											
Traits	Plant height	Days to heading	Tillers/sq. m	Days to maturity	Test weight	Spike length	Grains/spike	Total chl	Biomass	Harvest index	Economic yield
Plant height	-0.014	0.006	0.000	-0.001	-0.005	0.000	-0.003	0.001	0.472	-0.707	-0.250*
Days to heading	-0.002	0.040	0.000	-0.001	0.003	0.000	0.002	0.000	-0.040	0.098	0.099
Tillers/sq. m	0.001	-0.004	0.003	-0.001	-0.006	0.000	-0.003	-0.001	0.357	-0.060	0.286*
Days to maturity	-0.002	0.007	0.001	-0.006	-0.006	0.000	0.003	0.000	0.288	-0.293	-0.008
Test weight	-0.002	-0.004	0.001	-0.001	-0.028	0.000	-0.001	0.000	0.063	-0.064	-0.037
Spike length	-0.004	0.007	0.001	-0.002	-0.006	0.001	-0.011	0.000	0.050	0.016	0.051
Grains/spike	0.001	0.003	0.000	-0.001	0.001	0.000	0.025	0.000	0.015	0.130	0.174
Total chl	-0.001	0.002	0.000	0.000	0.001	0.000	0.000	0.009	-0.311	-0.157	-0.457**
Biomass	-0.005	-0.001	0.001	-0.001	-0.001	0.000	0.000	-0.002	1.291	-1.139	0.142
Harvest index	0.006	0.003	0.000	0.001	0.001	0.000	0.002	-0.001	-0.982	1.496	0.526**

Residual = 0.02060

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