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Genetic Component and Character Association for Yield and Yield Component Traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract

The current research involves the implementation of half diallel crosses between ten genotypes of bread wheat in 2018-2019. The parents and their F1 generation, excluding reciprocals, were then cultivated in the 2019-2020 growing season at the agriculture research farm, School of Agricultural Sciences and Engineering, IFTM University, Lodhipur Rajput, Moradabad (U.P.) and R.B. (PG) College, Mudi, Agra, using a randomized complete block design with three replications. Knowledge of type of gene action controlling target traits and genetic behaviour is a basic principle for designing an appropriate breeding procedure for the purpose of genetic improvement. Hence, the success of any selection or hybridization breeding program for developing varieties depends on precise estimates of genetic variation components for traits of interest which may be additive, dominant and non-allelic interaction effects. Significant genotype means squares and its components (parents and crosses) were obtained for all traits in both locations. Genetic components analysis found that additive (D) and Dominance (H1) was significant in all the traits. The value of mean degree of dominance was greater than additive, indicating availability of over dominance for all the traits. The present investigation revealed that grain yield was positively correlated with days to maturity, plant height, number of effective tillers per plant spike length, number of spikelets per spike, days to 50% heading and yield (q ha-1). Hence, more importance should be given to these traits while exercising selection. Based on the correlation and path studies it was reported that days to ear head emergence, days to maturity, plant height, number of effective tillers per plant, number of spikelets per spike, number of grains per spike, grain yield per plant and 1000 grain weight could be used as important selection traits in order of merit to improve productivity during designing a suitable breeding programme in wheat.

Keywords: *Genetic Component, Diallel analysis, Correlation coefficient, Path Coefficient, Bread wheat*

1. Introduction

Wheat (*Triticum aestivum* L.) is second important staple food crop in India next to rice. It is widely cultivated due to its remarkable adaptation to a wide range of environment. India is one of the major producers of wheat and occupies second position after China. Much of the emphasis on wheat breeding has been placed on increasing productivity of the crop. The choice of suitable parents for evolving better varieties/hybrids is a matter of concern to the plant breeders. In plant breeding programs, diallel crosses are mostly used to provide information on genetic effects for a number of parental varieties or estimates of general and specific combining ability variance components and heritability for plant population from randomly chosen parental varieties. Diallel mating design has been extensively used to identify parents with better potential to transmit desirable characteristics to its progenies and to identify the best specific crosses for yield and various quality parameters. The yield ceiling in the wheat can be brokenly developing high yielding varieties/hybrids through hybridization, which reshuffles the genes from suitable diverse parents (Monpara and Kamani, 2007). The increase in yield potential has always been of fundamental importance in wheat breeding programmes. Genetic analysis of wheat yield improvement had shown that grain yield is determined by component traits, and is a highly complex character (Adams, 1967; Blum, 1988). The analysis showed that genes for yield per se do not exist (Grafius, 1959). Knowledge about combining ability is important in selecting suitable parents for hybridization, understanding of inheritance of quantitative traits and also in identifying the promising crosses, further use in breeding programmes. For the wheat improvement programme, the knowledge of gene action controlling the desired traits to be improved helps to develop an effective breeding program, Analysis of quantitative variation to estimate additive, dominance and additive × additive epitasis in most of self – pollinated crops is proposed (Kamara *et al*., 2021). Half diallel crossing pattern among the genotype is to determine the nature and magnitude of genotypes. Gene actions not only helps breeder in selecting desirable parental genotypes and their crosses but also gives an opportunity to select most effective techniques among the hybrid populations for separation o superior genotypes in a symmetric way. However, it remains unutilized in the wheat crop. The future scope of hybrid technology in wheat depends on the male sterility system, floral biology, level of combining ability, heterosis and its exploitation at commercial level that may be useful in breaking yield barriers and enhancing the productivity in major wheat belt of the country (Gunasekaran *et al*., 2020)

Many of the crop improvement programmes aimed, in improvement of other characters in addition to yield, which were further related among themselves and to yield. As a result, studying the correlation between traits that affect yield can aid in the selection of traits that are linked to yield. As an example, the numbers of independent factors influencing a specific dependent variable such as yield. Correlation studies along with path analysis give a better understanding of the interaction of different characters with grain yield. Breeders should concentrate on producing productive wheat types by crossing high-yielding combination lines and choosing transgressive sergeants from the resulting hybrids. Investigation of the correlation coefficient and the path coefficient analysis may enhance the reproductive efficacy of the programme with the use of adequate measures for selection. Correlation coefficient analysis evaluates the combination of varieties of plant characters. We also identify the element traits on which form base of genetic selection and further improved production strategy. To find the level and direction of performance, association with traits contributes to performance and interactions between traits were identified. As a result, the current research was conducted to investigate the correlation and path coefficient analysis between yield attributing variables and quality traits in bread wheat. In this experiment, we have studied the correlation or mutual association among different yield contributing characters and their direct and indirect effects were also estimated through path coefficient analysis. The inter-relationship between the yield components will be helpful to a breeder for assessing the nature, extent and direction of selection pressure on characters. In the present investigation, efforts have also been made to understand the nature and estimate the genetic component of yield and its contribution in wheat.

2. Materials And Methods

In this investigation, Ten diverse genotypes viz. HD – 2967, PBW – 343, DPW -621-50, PBW -154, K -9107, SUPER 111, RAJ -3765, UP -2338, K -7903, PBW -502 these selected genotypes were planted for hybridization in half diallel fashion excluding reciprocals crosses to produce 45 F1,s. Ten parents and their 45

F_1, s was grown in a Randomized Block Design with three replications. Each parent and their F1,s were grown in single row of 5 m length with row to row and plant to plant distance of 22.5×10 cm respectively, during Rabi season at the agriculture research farm, School of Agricultural Sciences and Engineering, IFTM University, Lodhipur Rajput, Moradabad (U.P.) and R.B. (PG) College, Mudi, Agra, in the year of 2018-19 to 2019-20. Recommended cultural practices were adopted in order to raise a healthy crop. Observation were recorded on twenty randomly selected competitive plants of each parent and their F1's in every replication for following traits viz., days to ear head emergence, days to blooming, days to maturity, plant height (cm), number of effective tillers per plant, spike length (cm), number of spikelet's per spike, number of grains per spike, grain yield per plant, 1000 grain weight (gm), days to 50% heading and yield (q ha-1). The mean of each plot used for statistical analysis. The data were first subjected to the design for individual environment s suggested by Panse and Sukhantme, (1985). The data were subjected to genetic analysis of following Hayman (1954 a, b) and Jinks (1954).

3. Results and Discussion

In any crop improvement programme, genotypic value of the lines used as parent as well as those that are selected as promising lines for a defined trait is very crucial. The relative contribution of additive, dominant and epistatic effects in governing a trait provides information on genotypic values of the individuals and, consequently, mean genotypic values of families and generations. In this research investigation, generation mean analysis was done to determine the prevalence as well as the relative contribution of different gene In any crop improvement programme, genotypic value of the lines used as parent as well as those that are selected as promising lines for a defined trait is very crucial. The relative contribution of additive, dominant and epistatic effects in governing a trait provides information on genotypic values of the individuals and, consequently, mean genotypic values of families and generations. In this research investigation, generation mean analysis was done to determine the prevalence as well as the relative contribution of different gene. In any crop improvement programme, genotypic value of the lines used as parent as well as those that are selected as promising lines for a defined trait is very crucial. The relative contribution of additive, dominant and epistatic effects in governing a trait provides information on genotypic values of the individuals and, consequently, mean genotypic values of families and generations. In this research investigation, generation mean analysis was done to determine the prevalence as well as the relative contribution of different gene. In any crop improvement programmed, genotypic value of the lines used as parent as well as those that are selected as promising lines for a defined trait is very crucial. The relative contribution of additive, dominant and epistatic effects in governing a trait provides information on genotypic values of the individuals and, consequently, means genotypic values of families and generations.

Per se **performance of parents and F_1,s**

The highest performing genotypes for days to ear head emergence is UP -2338 × PBW -502 (77.57). For days to blooming was in PBW -154 (96.57) and for days to maturity HD – 2967 (157.00). Number of effective tillers per plant showed highest value in DPW -621-50 × K -9107 (23.01). For spike length (cm), HD – 2967

× UP -2338 (17.60cm) showed highest value of mean performance. In number of spikelets per spike, the genotype HD – 2967 (22.55) showed highest value. The highest mean value was observed by PBW -154 × UP -2338 (83.62) for the number of grains per spike. In the character, grain yield per plant (gm), HD – 2967

× UP -2338 (848.16gm) was recorded highest value. For 1000 grain weight (gm), the genotype K -7903× PBW -502 (43.58gm) showed highest mean value. For days to 50 per cent heading, the genotype K -9107 × K -7903 (117.79) showed highest mean performance. The yield (q ha-1) of wheat genotype is an important aspect for which the genotype HD – 2967 (48.97q ha-1) showed highest mean value. The figure 1 showed highest value for different characters of wheat genotype.

Table 1.1: Highest and lowest mean performance of different genotypes for different

Characters	Genotypes	Highest mean value
Days to ear head emergence	UP -2338 × PBW -502	77.57
Days to blooming	PBW -154	96.57
Days to maturity	HD – 2967	157.00
Plant height at maturity (cm)	K -9107	116.03
No. of effective tillers per plant	DPW -621-50 × K -9107	23.01
Spike length (cm)	HD – 2967 × UP -2338	17.60
No. of spikelet’s per spike	HD – 2967	22.55
Number of grains per spike	PBW -154 × UP -2338	83.62
Grain yield per plant (gm)	HD – 2967 × UP -2338	848.16
1000 grain weight (gm)	K -7903 × PBW -502	43.58
Days to 50 per cent heading	K -9107 × K -7903	117.79
yield (q ha-1)	HD – 2967	48.97

Figure 1: Highest mean performance of the genotypes of wheat for different characters

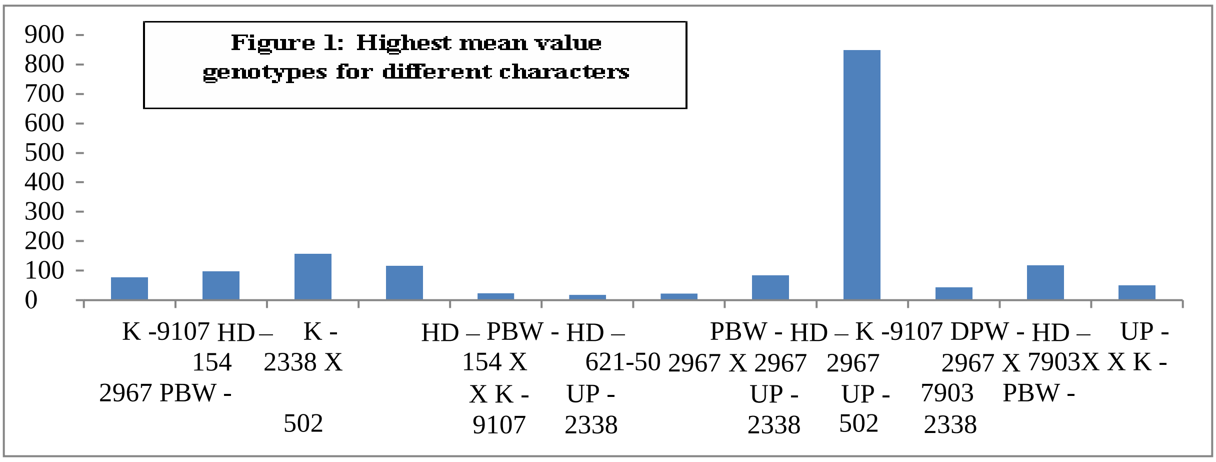

Figure 1: Highest mean value genotypes for different characters

Correlation Coefficient

Analysis of Variance indicated highly significant differences among the genotypes for all the characters (Table 1.2). The variance due to hybrids was also significant for all the characters studied suggesting the generation of good amount of variability among the hybrids and also the possibilities of identifying the superior hybrids from the study. The variation among these traits can be utilized in further breeding programme for improvement and selection of traits. Therefore, genes for such traits may be utilized from other source such as from germplasm and other diverse genotypes. Similar finding was reported by Nagar *et al.*, (2018). Correlation is a method for deterring the relationship between various traits and determining which component characters might to be used in breeding programme to boost yield (Bhushan *et al.*, 2013)

Character association analysis gives us an estimate of degree of association among two or more variable or characters. The dependence of yield on different yield attributing characters can be known by correlation coefficients. The correlation coefficients were estimated between all possible pairs of characters involving 10 parents and their F1s generation was computed. Correlation studies aid in the selection process and give a better understanding of the yield components. Table 1.3 displays the correlation coefficient correlations between positive and negative characters.

With the exception of days to blooming (-0.0406), all of the characters had a highly significant positive link with the character days to ear head emergence. Days to Blooming for each character exhibited a highly significant negative correlation with each character except 100 grain weight and days to 50% heading. Except for 1000 grain weight, there was a positive and significant correlation between days to maturity and all other characteristics. Plant height at maturity was highly correlated in positive direction with all of the characteristics except grain production per plant. Except for 1000 grain weight, the number of effective tillers per plant showed extremely significant values for all of the characters. Spike length showed a highly positive significant association with all of the characters except for 1000 grain weight and days to 50% heading. Except for days to 50% heading, the number of spikelet's/spikes exhibited a positive association with all of the other characteristics. Except for thousand grain weight, the number of grains per spike had a significant association in positive direction with all of the other variables. These results were in agreement with those of Ojha *et al.*, (2018), Oinam and Mehta (2020); Khanal *et al*., (2020); Barman *et al.*, (2020); Ayer *et al.*, (2017); Sharma *et al.*, (2017); Pooja *et al.*, (2018); Tarkeshwar *et al.*, (2020) and Kumar *et al.*, (2018).

The character grain yield per plant had positive and significant association with all the characters except days to blooming and plant height at maturity. 1000 grain weight showed highly significant correlation with plant height at maturity (0.2018**), days to blooming (0.1278*) and number of spikelets per spike (0.1202*). The character days to 50% heading showed highly significant correlation with days to ear head emergence (0.5868**), days to blooming (0.2155**), days to maturity (0.3076**), number of grains per spike (0.1633**) and plant height at maturity (0.3531**). The character yield showed highly significant correlation with days to ear head emergence (0.1737**), plant height (0.2122**), number of effective tillers per plant (0.1864**), spike length (0.1864**), number of spikelets per spike (0.1667**), and number of grains per spike (0.1857**) are the most important traits for boosting of yield. These results were also similar finding of Mecha *et al.*, (2017); Sakuma and Schnurbusch (2020) for the number of grains per spike; Wolde *et al*., (2019); Khanal *et al*. (2020); Tabassum *et al*., (2018) and Kumar *et al.*, (2022). A positive correlation between desirable characters is favorable to the plant breeder because it helps in simultaneous improvement of both the characters. A negative correlation, on the other hand, will hinder the simultaneous expression of both the characters with high values.

Path Coefficient Analysis

Path coefficient analysis, on the other hand, is better for dividing direct and indirect reasons o correlation, as well as allowing breeders to compare component elements based on their proportional importance. The direct and indirect impacts of independent variables on dependent variables are shown via path analysis Upadhyay, (2020). The result of the present investigation for path coefficient analysis are presented in table (1.4). The days to blooming character (0.578) was found having highest positive direct effects with yield (0.123), and also showed the positive indirect effect with days to maturity (0.1.34), number of spikelets per spike (0.410) and number of grains per spike (0.377) towards yield. The character days to ear head emergence (0.347) was found to be positive direct effect with yield (0.013) and also showed the positive indirect effect with all the characters. The plant height (0.416) showed high positive direct effect with yield (0.235) and the plant height showed positive indirect effects with all the characters except days to blooming (-0.190). This was confirmatory with the findings of Baye *et al.*, (2020). The character number of grains per spike (0.553) almost near to highest direct effects with yield (0.264) observed and also showed positive and indirect effects with all the character except number of effective tillers per plant (-0.338). These results agreed with the findings of Tabassum *et al*., (2018); Mecha *et al*., (2017); Kumar *et al.*, (2018); Hamid *et al.*, (2017); Khanal *et al.* (2020); Ozukum *et al.,* (2019) and Kumar *et al.*, (2022).

Gene action

Genetic component analysis was observed on diallel crosses and its parents using yield and yield components. The estimates of genetic components of variance presented in (Table 1.5). This approach was applied the allelic content of the parent used in the diallel with respect to quantitative traits. Genetic components analysis found that additive (D) and Dominance (H1) was significant in all the traits. The value of mean degree of dominance was greater than additive, indicating availability of over dominance for all the traits. Genetic component was indicated that both additive and dominance gene actions were involved in the expression of all the traits under study. In all the traits were showed (H2) genetic variance was highly significant which indicated symmetrically distribution of alleles. In these studies, all traits, additive and dominance (D, H1 and H2) was showed highly significant, which explained that both types of gene actions i.e. additive and dominance were involved in the expression gene. Environmental components (E) were positive and significant or all the under study, suggesting environmental influence in the modification of these traits Ahmad *et al*., (2017). Positive values of Fr indicated that the proportion of dominance allele was in excess than the recessive allele or all the traits. The values of mean degree o dominance were greater than one, which indicated availability o over dominance for all the traits. The values of (H2/4H1) was less than 0.25 which indicated asymmetrical distribution of dominant and recessive allele for all the traits except to number of effective tillers per plant for these traits among the parents. Over dominance effect of heterozygous loci (h2) was found to be significant in all the traits. Degree of dominance [(H1/D) 1/2] ranged from over dominance for all the characters to partial dominance in case of spike length. The values of (4DH1)1/2 + F/(4DH1)1/2 – F was more than one which indicated, excess of dominant genes present among the parents than recessive genes for all the traits. Narrow sense heritability lower for the traits including grain yield per plant and 1000 grain weight indicated that dominance variance was more than the additive variance. Similar results were obtained by Kutlu and Othun, (2015); Hosary and Deen, (2015); Ahmad *et al.*, (2016); Omar *et al.*, (2020) and These results were in conformity with the earlier results in which both additive and dominance effects were important in controlling various metric characters studied with preponderance for dominance gene actions.

4. Conclusion

In general, the half Diallel analysis of this study revealed that dominance gene effects were the dominating component and accounted for the majority of the total variance in yield and its features. We conclude through the values of the genetic correlation that the yield character showed highly significant correlation with days to ear head emergence, plant height, numbers of effective tillers per plant, spike length, number of spikelet's per spike and number of grains per spike means these characters can be selected for the character association which helps in selection of the genotypes for specific character. The characters based on path analysis such as days to blooming and number of grains per spike showed highest positive direct effects and almost near to highest direct effects respectively with yield. Therefore, we can select these two characters for the enhancement of yield in wheat. Through such kind of informative research we can improve the genotypes for the specific character in breeding programme.

Table 1.2: Analysis of variance (ANOVA) for the different characters of wheat genotypes

Source of variation	**d. f.**	**Mean Sum of Square**											
		DEE	**DB**	**DM**	**PH**	**NETP**	**SL**	**SPS**	**NGPS**	**GYPP**	**TGW**	**DFH**	**YD**
Replication	2	53.90	434	233.89	303	92.79	24.63	23.65	332.64	21367.13	18.23	634.42	152.46
Treatment	54	39.44**	89.30**	88.20**	148.58**	12.63**	6.02**	7.33**	193.76**	16709.93	12.35**	33.21**	58.99**
Error	108	5.98	0.008	1.90	1.53	0.24	0.67	1.41	3.92	12182.16	8.08	5.80	4.76
GM		72.16	78.58	144.67	103.79	18.85	15.10	19.13	76.29	702.52	39.95	111.68	39.01
Sem		1.41	0.05	0.80	0.71	0.28	0.47	0.69	1.14	63.72	1.64	1.39	1.26
CD5%		3.96	0.14	2.23	1.99	0.79	1.32	1.92	3.20	178.63	4.60	3.90	3.53
CD1%		5.24	0.19	2.95	2.65	1.04	1.76	2.54	4.24	236.31	6.09	5.12	4.67
CV		3.39	0.11	0.95	1.19	2.58	5.43	6.21	2.59	15.71	7.12	2.16	5.59

Table 1.3: Correlation coefficients of yield and component characters in wheat

Character	**DEE**	**DB**	**DM**	**PH**	**NETP**	**SL**	**SPS**	**NGPS**	**GYPP**	**TGW**	**DFH**	**YD**
DEE	**1.0000**	-.0406	.4896 **	.4603**	.2773**	.2839**	.2647**	.2920**	.1021*	.0239	.5868**	.1737**
DB		**1.0000**	-.4974 **	-	-	-	-	-	-.0127	.1278*	.2155**	-.0036
DM			**1.0000**	.6877**	.4359**	.4657**	.4933**	.6991**	.1622**	.0651	.3076**	.0575*
PH				**1.0000**	.5016**	.4792**	.3922**	.6380**	.0969	.2018**	.3531**	.2122**
NETP					**1.0000**	.5918**	.3918**	.6115**	.1915*	-.0337	.1888*	.1864**
SL						**1.0000**	.4595**	.5981**	.2272**	-.0284	.0412	.1807**
SPS							**1.0000**	.6380**	.2651**	.1202*	.0214	.1667**
NGPS								**1.0000**	.1831*	.0327	.1633**	.1857**
GYPP									**1.0000**	.0501	.0674	.1090*
TGW										**1.0000**	.0097	.0080
DFH											**1.0000**	-.1190*
YD												**1.0000**

*<0.05 and **P<0.01

DEE: Days to ear head emergence; DB: Days to blooming, DM: Days to maturity, PH: Plant height (cm), NETP: Number of effective tillers per plant, SL: Spike Length (cm), SPS: Number of spikelet's/spike, NGPS: Number of grains per spike; GYPP: Grain yield per plant (gm), TGW: 1000 grain weight (gm), DFH: Days to 50% heading, YD: Yield (q ha-1).

Table 1.4: Direct and indirect effects of morphological traits on grain yield in wheat

Character	**DEE**	**DB**	**DM**	**PH**	**NETP**	**SL**	**SPS**	**NGPS**	**GYPP**	**TGW**	**DFH**	**YD**
DEE	**0.347**	-0.023	-0.123	0.191	-0.010	0.212	-0.034	0.16	0.005	-0.003	-0.350	0.013
DB	0.014	**0.578**	0.134	-0.190	0.013	-0.039	0.410	0.377	-0.001	-0.018	-0.128	0.123
DM	0.170	-0.287	**-0.269**	0.286	-0.016	-0.035	-0.063	0.387	0.009	-0.009	-0.184	0.019
PH	0.156	-0.264	-0.185	**0.416**	-0.019	0.036	-0.050	0.352	0.005	-0.028	-0.184	0.235
NETP	0.096	-0.264	-0.117	0.208	**-0.037**	0.044	-0.500	-0.338	0.010	0.005	-0.211	0.096
SL	0.098	-0.308	-0.125	0.199	-0.022	**0.075**	-0.059	0.330	0.012	0.004	-0.113	0.135
SPS	0.091	-0.184	-0.132	0.163	0.014	0.034	**-0.128**	0.035	0.014	-0.016	-0.024	0.258
NGPS	0.101	-0.393	-0.188	0.265	-0.023	0.045	-0.082	**0.553**	0.009	--0.005	-0.013	0.264
GYPP	0.035	-0.007	-0.143	0.040	-0.007	-0.170	-0.034	0.101	**0.054**	-0.006	-0.097	-0.161
TGW	0.008	0.073	-0.017	0.083	0.001	-0.002	-0.015	0.018	0.003	**-0.139**	-0.040	0.246
DFH	0.203	0.124	-0.083	0.146	-0.007	0.003	-0.003	0.090	0.004	0.006	**-0.601**	0.313
YD	0.103	0.236	0.103	0.253	-0.009	0.013	0.321	0.362	0.023	0.012	0.086	**0.359**

Residual factor 0 .7052

DEE: Days to ear head emergence; DB: Days to blooming, DM: Days to maturity, PH: Plant height (cm), NETP: Number of effective tillers per plant, SL: Spike Length (cm), SPS: Number of spikelet's/spikes, NGPS: Number of grains per spike; GYPP: Grain yield per plant (gm), TGW: 1000 grain weight (gm), DFH: Days to 50% heading, YD: Yield (q ha-1)

Table1.5: Genetic Components analysis of Wheat

Parameters	DEE	DB	DM	PH	NETP	SL	SPS	NGPS	GYPP	TGW	DFH	YD

D	12.45**	10.86**	562.57**	22.78**	3.58**	2.78**	1.86**	4.64**	14.77**	6.52**	11.92**	16.42**
SE±	4.29	3.50	67.84	6.78	1.24	1.56	1.11	1.48	5.79	2.87	5.23	6.48
F	21.74**	18.37**	426.58**	27.19**	9.18**	5.26**	3.49**	11.27**	34.16**	17.26**	28.34**	39.14**
SE±	7.52	8.64	128.15	13.22	4.72	2.69	1.28	6.34	10.21	5.87	8.37	11.89
H1	46.23**	38.21**	798.35**	59.21**	23.15**	17.28**	10.28**	29.18**	79.24**	42.38**	61.13**	78.25**
SE±	12.31	9.24	241.12	18.34	11.28	9.74	3.46	12.38	32.85	21.36	26.86	31.78
H2	31.58**	27.35**	628.18**	44.38**	19.58**	12.30**	9.35**	14.43**	28.75**	31.29**	36.58**	39.52**
SE±	8.69	15.23	86.34	13.48	6.48	6.24	3.13	4.58	12.25	3.28	7.65	9.28
h2	17.26**	14.12	348.26**	26.18**	11.23**	7.26	5.17	8.67**	16.49**	18.29**	20.38**	21.87**
SE±	9.28	17.29	75.26	16.27	6.28	12.58	12.38	2.38	6.87	14.25	12.23	16.28
E	3.29	8.26	2.59	6.98	2.58	23.35	5.68	2.89	16.58	21.35	5.29	7.58
SE±	1.28	2.19	32.35	2.85	13.26	3.28	1.89	32.12	5.98	9.27	11.28	2.58
Sqrt(h1/d)	1.18	1.23	6.28	1.12	3.28	1.26	3.15	16.28	1.28	12.58	2.89	1.25
H2/4hl	0.88	0.65	0.46	0.28	0.16	0.89	0.87	0.79	0.87	0.86	0.94	0.49
[(4DH1)^.5+F)]/[(4DH1))^.5-F)]	1.18	2.38	2.56	1.23	1.26	1.28	2.19	2.87	1.59	3.98	2.56	1.48
h^2/H2	0.78	0.58	0.89	0.29	0.28	0.42	0.85	0.78	0.67	0.56	0.48	0.42
R Value	-0.46**	-0.03	-0.74**	-0.65**	-0.85**	-0.54**	-0.65**	-0.48**	-0.51**	-0.68**	-0.72**	-0.61**
Heritability (narrow sense)	84.84	99.99	97.85	98.97	98.10	88.87	80.76	97.98	27.10	34.57	82.54	91.93

DEE: Days to ear head emergence; DB: Days to blooming, DM: Days to maturity, PH: Plant height (cm), NETP: Number of effective tillers per plant, SL: Spike Length (cm), SPS: Number of spikelet's/spike, NGPS: Number of grains per spike; GYPP: Grain yield per plant (gm), TGW: 1000 grain weight (gm), DFH: Days to 50% heading, YD: Yield (q/ha).

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