Plant Archives Vol. 25, Supplement 1, 2025 pp.1670-1675 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-1.229

ASSESSMENTS OF GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR YIELD AND YIELD ATTRIBUTING TRAITS IN RICE (*ORYZA SATIVA* L.) GENOTYPES FOR GRAIN YIELD UNDER IRRIGATED CONDITION

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(Date of Receiving : 18-09-2024; Date of Acceptance : 12-11-2024)

ABSTRACT

An experiment was carried out, 100 genotypes of rice (*Oryza sativa* L.) during kharif, season at Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh in Randomized Block Design with two replications under irrigated condition to analyse genetic parameter, correlation and path analysis. Biometrical observations were taken by thirteen characters *viz.,* days to flowering, plant height, flag leaf length, flag leaf width, number of tillers, panicle length, biological yield per plant, grain yield per plant, harvest index, total grain weight, number of filled grain, number of unfilled grain and total number of grains. Analysis of variance revealed presence of high significant variability for all the traits. Harvest index, number of filled grain per plant, number of unfilled grains per plant, total number of grain and thousand grain weight exhibited higher variation (*i.e.,* high value of GCV, PCV and high heritability coupled with high genetic advance as percent of mean). Character association of the yield and yield attributing traits revealed significant positive association of grain yield with days to flowering, flag leaf length, panicle length, biological yield, harvest index, number of filled grains and total number of grains both at phenotypic and genotypic level. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that a very high positive direct effect on grain yield was exhibited by number of filled grains and number of unfilled grains at phenotypic level along with biological yield and harvest index. Hence selection for these traits could bring improvement in yield and yield component in rice.

***Keywords* :** Genetic variability, Correlation and path analysis, Yield attributing traits, Rice (*Oryza sativa* L.)

Introduction

Rice is an important part of India's agriculture, and the contribution of rice is 17% of GDP and it provides 43% of the calories, which is the basic requirement of more than 70% of the population of India. Among the 25 species of rice, only two species are cultivated these are *Oryza sativa* and *Oryza glaberrima*. Typically, Rice is grown globally, while *Oryza glaberrima* is grown mostly in Africa. The *Oryza sativa* is divided into three species based on geographic as well as agro-ecological requirements such as *indica*, *japonica* and *javanica*. It should be noted that the difference between the two types of *indica* and *japonica*, related to morphological, physiological and biochemical basis which makes them uncommon. Chhattisgarh is famous as Rice bowl of India, because rice is grown in the maximum land area. The diversity of rice in Chhattisgarh is proof of this statement. In the *Kharif* season the Chhattisgarh state rice covers the maximum and pays significantly to the “national rice production”. The state relies on monsoons with annual rainfall of 1200-1600 millimetres. Therefore, identifying and collecting the characteristics of rice is not only important for the proper use of donors in the breeding program, but it is also important today to protect the unique rice germplasm. The statistical procedure which separates or splits the total variation into different components is known as analysis of variation. Coefficient of variation was calculated at genotypic and phenotypic levels as analysis of variance permits estimation of phenotypic, genotypic and environmental coefficient of variation (Burton, 1952). As usual, phenotypic coefficient of variation was higher in magnitude than genotypic coefficient of variation. Heritability estimates provide the information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. Thus, heritability is the heritable portion of the phenotypic variance. Association analysis is an important approach in a breeding programme. It gives an idea about relationship among the various characters and determines the component characters, on which selection can be based for genetic improvement in the grain yield. Degree of association also affects the effectiveness of selection process. The correlation coefficient analysis is the index of association between two variables. Path coefficient analysis is helpful in partitioning the correlation into the measures of direct and indirect effects. It measures the direct and indirect contribution of independent variables on depended variable. The path coefficient analysis was carried out by using the correlation coefficient between different quantitative characters to obtain direct and indirect effects of different characters on grain yield per plant.

Materials and Methods

100 genotypes of rice were chosen for this research. Nurseries were raised and 21 days old seedlings were eventually transplanted in the field, in RBD with 2 replications and observation were recorded for 13 characters, days to flowering, plant height(cm), flag leaf length(cm), flag leaf width(cm), number of tillers, panicle length(cm), Biological yield per plant(g), 1000 grain weight(g), Grain yield per plant(g), harvest index (%), number of filled grain, number of unfilled grains, total number of grains. R X R and P X P distance of 25 cm X 15 cm and net plot area was 3m X 1.5 m.

The crop was preserved under irrigated condition. Fertilizer dose @ of 50:40:30 kg per hectare (NPK) was applied. All the treatment was similar for agronomical practices. Random 5 plant are selected from each of the lines were taken for collecting data on yield and yield attributing traits. The present research work was regulated at Research cum Instructional farm, Department of Genetics and Plant Breeding, College of agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh, during the *Kharif* season of 2018.

Results and Discussion

Analysis of Variance for Quantitative Characters in Rice (*Oryza sativa* L.)

The analysis of variance of 13 yield and yield attributing traits of rice germplasm accessions presented in Table 1. The results of the analysis of variance indicated that the mean sum of squares due to accession for genotypes were significant for all the characters indicating the presence of substantial amount of variability among the rice genotypes. Among 100 genotypes the highest grain yield (g) was recorded in Baila Aankhi (29.66 g) followed by Sua Pankhi (29.60 g) and Bawati Chudi (29.19 g). Coefficient of variation was calculated at genotypic and phenotypic levels as analysis of variance permits estimation of phenotypic, genotypic and environmental coefficient of variation (Burton, 1952). The highest value of PCV coupled with GCV was recorded for number of unfilled grains (99.51% and 67.93%) followed by number of filled grains (67.47%, 52.39%), total number of grains (60.83%, 48.25%), biological yield per plant (47.53%, 47.40%), harvest index (45.61%, 45.07%), thousand grain weight (38.11%, 37.84%), grain yield (37.42%, 37.06%), number of tillers (35.88%, 34.41%) and flag leaf length (30.23%, 28.58%). The values of PCV are higher than GCV, indicates the apparent variation is not only due to genotypes but also due to the influence of environment.

Heritability

As given by Johnson *et al.* (1955) heritability values are categorised as low (<30%), medium (30 - 60%), and high (>60%). proposed by Hanson *et al.*, 1956.

Highest estimate of heritability was found for biological yield (99.47 %) followed by days to 50 % flowering (98.69%), grain yield (98.09%), thousand grain weight (98.63%), harvest index (97.66%), flag leaf width (95.34%), flag leaf length (89.35%) and total number of grains (62.91%). Rest of the traits was found to have moderate heritability

Genetic Advance as Percent of Mean

The estimation of genetic advance as percent mean is classified as low (<10%), Moderate (10-20%) and high (>20%) proposed by Johnson *et al.* (1955).

The magnitude of genetic advance as percent of mean was recorded high for all the traits *viz* biological yield per plant (97.38), Number of unfilled grain

(95.52), Harvest index (91.75), Number of filled grain (83.80), Total number of grains (78.84), Thousand grain weight (77.43), Grain yield per plant) (75.62), Number of tillers (68.03), Flag leaf length (55.66). Only panicle length (11.60) showed moderate genetic advance.

Table 1: Analysis of variance for thirteen yield and yield attributing traits under irrigated condition during wet season *Kharif* 2018

Source of variation	DF	Mean Sum of Squares (MSS)												
		DTF	PH	FLL	FLW	NT	PL	TGW	NFG	NUFG	TNG	BYP	HI	GYP
Replication	1	0.84	5882.22**	68.07	0.02**	2.15**	130.38**	1.03	1452.92**	4315.48**	10776.441**	5850.80**	0.19	31.85**
Genotypes	99	220.70**	1327.45**	391.46**	0.09**	8.41**	12.38**	143.597**	14543.18**	1640.24**	18419.57**	39375.63**	13.65**	68.06**
Error	99	1.45	466.61	22.02	0.00	0.35	4.35	0.99	1613.00	720.01	2320.77	104.99	0.34	0.66

DTF = Days to flowering; PH =plant height (cm); FLL = Flag leaf Length (cm); FLW = Flag leaf width (cm); NT = Number of tillers; PL = Panicle Length (cm); TGW = Thousand grain weight (g); NFG = Number of filled grains; NUFG = Number of unfilled grains; TNG = Total Number of grains; BYP = Biological yield per plant (g); HI = Harvest index (%); GYP = Grain yield per plant (g)

Table 2: Mean and genetic variability parameters for thirteen yield and yield attributing traits under irrigated condition during wet season *Kharif* 2018

Genetic Parameters	Grand Mean	PCV (%)	GCV (%)	h^2 (%)	GA (%)	SD	CV (%) as mean
DTF	96.15	10.96	10.89	98.69	22.29	10.50	10.92
PH (cm)	130.49	22.95	15.90	47.98	22.69	25.76	19.74
FLL (cm)	47.55	30.23	28.58	89.35	55.66	13.99	29.42
FLW (cm)	1.26	17.00	16.60	95.34	33.40	0.21	16.80
NT	5.83	35.88	34.41	91.98	68.03	2.05	35.15
PL (cm)	24.65	11.73	8.12	47.99	11.60	2.49	10.09
TGW (g)	22.31	38.11	37.84	98.63	77.43	8.47	37.98
NFG	141.18	67.47	52.39	60.29	83.80	85.27	60.40
NUFG	33.61	99.51	67.93	46.60	95.52	28.64	85.20
TNG	174.80	60.83	48.25	62.91	78.84	55.97	32.01
BYP (g)	295.63	47.53	47.40	99.47	97.38	40.31	13.63
HI (%)	6.37	45.61	45.07	97.66	91.75	2.61	43.22
GYP (g)	15.66	37.42	37.06	98.09	75.62	5.83	37.24

Table 3: List of germplasm categorized into early, medium, late and very late days to flowering

Category	Duration	Genotypes
Early	91- 90days	29 (R-RF-75, Bagri, Satha dhan, Nagina-22, Hardi chudi, Koto, R-RF-75, Karhani, Basigal(ii), Kotte (II), Lalmati, Jhitpiti, Karhani, Luchai(A), Bakal, Danteshwari, Unknown, Laloo-14, Bisni-I, Kadam Phool, MTU-1010, IGKV R1, Bhejari, Peelee Luchai, Kohaka, Bhulau, Tulsi Phool, Baisur, Elayachi)
Medium	91-110days	62 (Angur Guchcha, Tebaroo Mundaria,Bodi, Kanak Jira,WR99, Koudi dhull, Silipat, Bylao,E-1702, Elayachi, Muni Bhog, Chapti gurmatia, Bhainsa Punchhi, Bhaniya, IR 42253, Moroberekan, IR64, Farsa Phool, Kating, Mehapal, Sindur senga, Lokti Machhi, Bhanta Phool-1, Paltu, Ama Dhul , Asam Chudi, Jalle, Hunuman Langur, Shyam jira-1, Bawati chudi, Kalajira, Sau pankhi, Ama jhopa, Parmal, Jeera Phool, Raja Bangla, Swarna, Cross 116, Roti, Khatia pati, Farsa Phool, Padari dhan IV, Baila Aankhi, Nariyal Chudi, Hathi panjra, Bokra Mundi, Jal Ponga, Lanji, Budhiya wako, Bhejari, Dokra Dokri, Bhainsa Mundariya, Dokrae mechha, Bhamasur, Kanak, Sonapan, Deshi lal dhan, Ichchawati, BD kankari bija, Lahsun Bhog, Tulsi Mala, Ram Jira)
Late	111-130days	9 (Tulsi manjari, Laxmi Bhog, Banda, Chiko, Jou Phool, Jou Phool-2, CR-1014, Tulsi Mongra, Danwar)
Very Late	(> 131days	-

Correlation Coefficient of Analysis

In this research, grain yield showed positive and significant correlation with biological yield (0.47, 0.48), days to 50% flowering (0.41, 0.42), flag leaf length (0.37, 0.39), panicle length (0.24, 0.35), harvest index (0.30, 0.29), number of filled grains (0.27, 0.31) and total number of grains (0.20, 0.24) both at phenotypic and genotypic level. Plant height (0.17) is positive but non-significant and Number of unfilled grains (-0.15) were the only one character which resulted negative and non- significant association with grain yield at genotypic level only.

In the present investigation grain yield showed positive and significant correlation with days to flowering (Vanishree *et al*., 2013; Madhavilatha *et al*., 2005; Agahi *et al*., 2007), flag leaf length (Chuchert *et al*., 2017), panicle length (Khare *et al*., 2015), biological yield (Girish *et al*. 2006), harvest index (Vanishree *et al.,* 2013 and Chakraborty *et al*., 2010), number of filled grains (Satheeshkumar and Saravanan, 2012; Islam *et al*., 2015; Naseer *et al.,* 2015) and total number of grains (Satheeshkumar and Saravanan, 2012; Naseer *et al*., 2015) both at phenotypic and genotypic level. It indicates strong correlation of these traits with grain yield and selection of these traits will be useful in improving grain yield.

Table 4: Association analysis between grain yield and yield attributing traits under irrigated condition during *Kharif* 2018.

Parameters		DTF	PH	FLL	FLW	NT	PL	BYP	GYP	HI	TGW	NFG	NUFG	TNG
DTF	P	***1.00***												
	G	***1.00***												
PH	P	0.42**	***1.00***											
	G	0.58**	***1.00***											
FLL	P	0.61**	0.45**	***1.00***										
	G	0.65**	0.68**	***1.00***										
FLW	P	-0.46**	-0.31**	-0.37**	***1.00***									
	G	-0.48**	-0.48**	-0.39**	***1.00***									
NT	P	-0.03^{NS}	-0.28**	-0.12^{NS}	-0.23**	***1.00***								
	G	-0.02^{NS}	-0.42**	-0.14*	-0.24**	***1.00***								
PL	P	0.44**	0.40**	0.41**	-0.24**	-0.21**	***1.00***							
	G	0.65**	0.99**	0.66**	-0.37**	-0.32**	***1.00***							
BYP	P	0.29**	0.08^{NS}	0.26**	0.01^{NS}	0.18**	0.21**	***1.00***						
	G	0.30**	0.12^{NS}	0.27**	0.01^{NS}	0.19**	0.30**	***1.00***						
GYP	P	**0.41****	0.11^{NS}	**0.37****	-0.03^{NS}	0.08^{NS}	**0.24****	**0.47****	***1.00***					
	G	**0.42****	**0.17***	**0.39****	-0.03^{NS}	0.08^{NS}	**0.35****	**0.48****	***1.00***					
HI	P	-0.01^{NS}	0.02^{NS}	0.03^{NS}	0.01^{NS}	-0.18**	-0.04^{NS}	-0.59**	**0.30****	***1.00***				
	G	-0.01^{NS}	0.04^{NS}	0.03^{NS}	0.07^{NS}	-0.19**	-0.01^{NS}	-0.60**	**0.29****	***1.00***				
TGW	P	-0.09^{NS}	0.03^{NS}	0.17*	0.40**	-0.26**	0.03^{NS}	0.02^{NS}	0.11^{NS}	0.06^{NS}	***1.00***			
	G	-0.09^{NS}	0.06^{NS}	0.19**	0.41**	-0.28**	0.04^{NS}	0.02^{NS}	0.11^{NS}	0.06^{NS}	***1.00***			
NFG	P	0.41**	0.08^{NS}	0.19**	-0.36**	0.32**	0.12^{NS}	0.18**	**0.27****	-0.02^{NS}	-0.53**	***1.00***		
	G	0.47**	0.13^{NS}	0.22**	-0.41**	0.39**	0.23**	0.20**	**0.31****	-0.02^{NS}	-0.60**	***1.00***		
NUFG	P	0.17*	0.08^{NS}	0.07^{NS}	-0.22**	0.08^{NS}	0.13^{NS}	-0.08^{NS}	-0.10^{NS}	-0.09^{NS}	-0.28**	0.18*	***1.00***	
	G	0.26**	-0.04^{NS}	0.13^{NS}	-0.35**	0.12^{NS}	0.43**	-0.01^{NS}	**-0.15***	-0.14*	-0.44**	0.32**	***1.00***	
TNG	P	0.42**	0.10^{NS}	0.19**	-0.39**	0.31**	0.15*	0.14*	**0.20****	-0.05^{NS}	-0.56**	0.94**	0.49**	***1.00***
	G	0.48**	0.10^{NS}	0.23**	-0.45**	0.38**	0.31**	0.16*	**0.24****	-0.05^{NS}	-0.64**	0.97**	0.53**	***1.00***

***, ** significant at 5% and 1% probability level**

DTF = Days to flowering; PH = plant height (cm); FLL = Leaf Length (cm); FLW = Leaf width (cm); NT = Number of tillers; PL = Panicle Length (cm); TGW = Thousand grain weight (g); NFG = Number of filled grains; NUFG = Number of unfilled grains; TNG = Total Number of grains; BYP = Biological yield per plant (g); HI = Harvest index (%); GYP = Grain yield per plant (g)

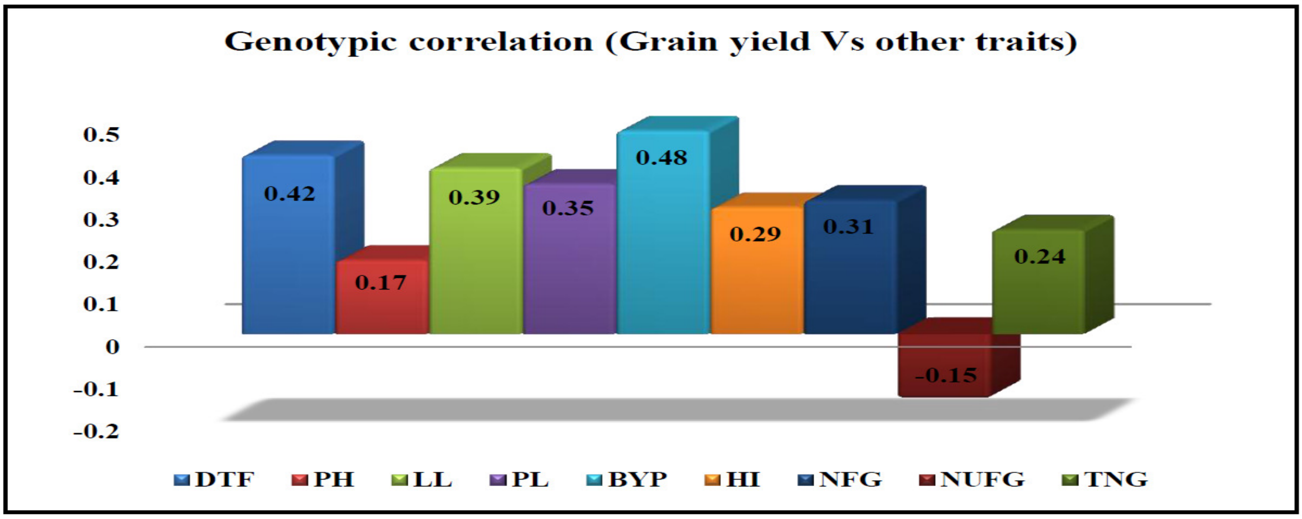

Fig. 1: Graph representing significant correlation between grain yield and other traits

Path coefficient analysis

In these studies, direct effect is recorded for the traits under present investigation, it was observed that the very high positive direct effect and significant on grain yield was exhibited by number of filled grains (16.38) and number of unfilled grains (6.25) at phenotypic level. Biological yield (0.91, 0.97) and harvest index (0.86, 0.89) exhibited high positive direct effect and significant with grain yield at phenotypic and genotypic level and Total number of grains (-18.50) shows highest negative and significant at phenotypic level. Low residual value (P= 0.23, G= 0.04) was observed, it indicates that the characters taken for study is sufficient to explain the variability.

The high positive direct effect of number of filled grains on grain yield was in accordance with Sawant *et al.*, 1995; Sarawgi *et al.*, 1997; Bhagat *et al.*, 2007. For biological yield and harvest index, Jayasudha and Sharma (2010); Bhagat *et al.* (2007) also reported that selection of these traits would help to achieve high grain yield. This trait primarily contributed to yield and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Association and path coefficient analysis was performed between 13 yield characters among 100 rice germplasm accessions. The summarized data representing the direct effect on grain yield along with its correlation values at phenotypic and genotypic level. The results revealed that the correlation between grain yield and other traits is due to direct effects as depicted in a foresaid table clearly indicates a true relationship between them and direct selection of these traits will be rewarding for yield improvement. Highest correlation value of (0.47 and 0.48) was recorded by biological yield followed by harvest index (0.30 and 0.29). The information obtained by this technique helps in direct selection for genetic improvement of grain yield.

Table 5: Summarized data representing the direct effects of different traits on grain yield along with its correlations at phenotypic level

Traits		**Direct effects**	**Correlation**
		Grain yield	
Number of filled grains	P	16.38	0.27*
	G	-	0.31*
Number of unfilled grains	P	6.25	-
	G	-	-0.15*
Total number of grains	P	-18.50	0.20*
	G	-	0.24*
Biological yield per plant	P	0.91	0.47*
	G	0.97	0.48*
Harvest index	P	0.86	0.30*
	G	0.89	0.29*

Table 6: Direct and indirect path coefficient analysis of yield attributing traits under irrigated condition during *Kharif* 2018

Characters		**DTF**	**PH**	**FLL**	**FLW**	**NT**	**PL**	**BYP**	**HI**	**TGW**	**NFG**	**NUFG**	**TNG**
P	**DTF**	***0.13***	-0.01	0.00	-0.01	0.00	0.00	**0.27**	-0.01	-0.01	**6.72**	**1.07**	**-7.77**
G		***0.10***	-0.01	-0.01	0.01	0.00	-0.04	**0.29**	-0.01	-0.02	-0.01	0.00	0.11
P	**PH**	0.05	***-0.03***	0.00	0.00	-0.02	0.00	0.08	0.02	0.00	**1.34**	0.56	**-1.89**
G		0.06	***-0.02***	-0.01	0.01	0.00	-0.06	0.12	0.04	0.01	0.00	0.00	0.02
P	**FLL**	0.08	-0.02	***0.00***	0.00	-0.01	0.00	**0.24**	0.03	0.02	**3.13**	0.48	**-3.61**
G		0.07	-0.01	***-0.02***	0.01	0.00	-0.04	**0.27**	0.03	0.04	-0.01	0.00	0.05
P	**FLW**	-0.06	0.01	0.00	***0.01***	-0.01	0.00	0.01	0.01	0.05	**-5.89**	**-1.41**	**7.28**
G		-0.05	0.01	0.01	***-0.01***	0.00	0.02	0.01	0.01	0.08	0.01	0.00	-0.11
P	**NT**	0.00	0.01	0.00	0.00	***0.06***	0.00	0.17	-0.16	-0.03	**5.37**	**0.55**	**-5.91**
G		0.00	0.01	0.00	0.00	***0.01***	0.02	0.19	-0.17	-0.05	-0.01	0.00	0.09
P	**PL**	0.06	-0.01	0.00	0.00	-0.01	***0.01***	**0.19**	0.00	0.00	**2.01**	**0.85**	**-2.86**
G		0.07	-0.02	-0.01	0.01	0.00	***-0.06***	**0.29**	-0.01	0.01	-0.01	0.01	0.07
P	**BYP**	0.04	0.00	0.00	0.00	0.01	0.00	***0.91***	-0.51	0.00	**3.03**	**-0.36**	**-2.66**
G		0.03	0.00	0.00	0.00	0.00	-0.02	***0.97***	-0.54	0.01	0.00	0.00	0.04
P	**HI**	0.00	0.00	0.00	0.00	-0.01	0.00	**-0.55**	***0.86***	0.01	-0.37	**-0.56**	**0.93**
G		0.00	0.00	0.00	0.00	0.00	0.00	**-0.59**	***0.89***	0.01	0.00	0.00	-0.01
P	**TGW**	-0.01	0.00	0.00	0.00	-0.02	0.00	0.03	0.06	***0.12***	**-8.76**	**-1.76**	**10.49**
G		-0.01	0.00	0.00	-0.01	0.00	0.00	0.03	0.06	***0.19***	0.01	-0.01	-0.15
P	**NFG**	0.05	0.00	0.00	0.00	0.02	0.00	0.17	-0.02	-0.07	***16.38***	**1.13**	**-17.45**
G		0.05	0.00	0.00	0.01	0.00	-0.01	0.20	-0.02	-0.12	***-0.02***	0.00	0.23
P	**NUFG**	0.02	0.00	0.00	0.00	0.00	0.00	-0.05	-0.08	-0.03	**2.95**	***6.25***	**-9.18**
G		0.03	0.00	0.00	0.00	0.00	-0.03	-0.08	-0.13	-0.09	-0.01	***0.01***	0.12
P	**TNG**	0.05	0.00	0.00	0.00	0.02	0.00	0.13	-0.04	-0.07	**15.45**	**3.10**	***-18.50***
G		0.05	0.00	0.00	0.01	0.00	-0.02	0.16	-0.05	-0.13	-0.02	0.01	***0.23***

P	**Residual are 0.23**
G	**Residual are 0.04**

DTF = Days to 50% flowering; PH = plant height (cm); FLL = Leaf Length (cm); FLW = Leaf width (cm); NT = Number of tillers; PL = Panicle Length (cm); TGW = Thousand grain weight (g); NFG = Number of filled grains; NUFG = Number of unfilled grains; TNG = Total Number of grains; BYP = Biological yield per plant (g); HI = Harvest index(%); GYP=Grain yield per plant(g)

Conclusion

All the 13 and its component traits showed significant variation. The high value of PCV along with GCV as well as with high heritability was recorded for total number of grains, biological yield per plant, harvest index, thousand grain weight, grain yield and flag leaf length. Grain yield showed positive and significant correlation with days to 50% flowering, flag leaf length, panicle length, biological yield, harvest index, number of filled grains and total number of grains both at phenotypic and genotypic level. Path analysis showed that the very high direct and positive effect on grain yield was exhibited by "number of filled grains and number of unfilled grains at phenotypic level along with biological yield and harvest index. According to the results obtained from the studies, it was concluded that traits like Grain yield exhibited positive and significant correlation with biological yield, harvest index, number of filled grains and also exhibited positive direct effect.

Conflict of interest

The authors declare no conflicts of interest.

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