

GENETIC VARIABILITY AND CORRELATION IN RICE UNDER NORMAL AND WATER STRESS CONDITIONS

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ABSTRACT

This experiment (genetic variability for irrigated and water stress rice) was conducted at the new experimental Farm, The University of Agriculture Peshawar Pakistan during 2020 rice growing season. The experiment consisted of thirty genotypes and was laid out in randomized complete block design Row length was 5m with row to row distance of 30cm and plant to plant distance of 10 cm. The objective of this experiment was to study the genetic variability. Analysis of variance showed highly significant differences ($P \leq 0.01$) among genotypes for all the studied traits. Genotype PK-386/ DR-82 took minimum (177.33) days to 50% flowering, Minimum days to 50% maturity (174.33 days) were observed for genotype Basmati 385/ PK-386. Among all the genotypes the lowest (80.67 cm) plant height was recorded for Basmati 385/ PK-386 while maximum plant height was recorded for DR-82/ PK-386 (117.80 cm). Minimum flag leaf area (17.28 cm²) was measured for genotype JP-5/ KS-282 while maximum flag leaf area (38.34 cm²) was observed for KS-282/ Swat-2. Minimum panicle length (19.27 cm) was noticed for genotype KS-282/ JP-5 while maximum panicle length (29.07 cm) was measured for DR-82/ PK-386. Minimum tillers per plant (9.23) was counted for genotype JP-5/ Basmati 385 while maximum (16.90) were recorded for Basmati 385/ PK-386. Minimum biological yield (6082.73g) was recorded for genotype JP-5/ Basmati 385 while the maximum biological yield (19708.03 g) was weighed for genotype KS-282/ Basmati 385. Minimum grain yield (734.79 g) was weighed for genotype KS-282/ PK-386 while maximum grain yield (4542.58 g) was recorded for genotype KS-282/ Basmati 385. Genotypes DR-82/ PK-386, KS-282/ PK-386, PK-386/ DR-82, Basmati 385/ PK-386 performed well and showed early flowering, Early maturity, maximum tillers plant⁻¹, high biological yield and higher grain yield hence, these genotypes can be recommended for future breeding programs.

Key points. Rice genotypes. water stress conditions. Correlation.

I. INTRODUCTION

Rice is a self-pollinated cereal crop belonging to the family Gramineae under the order Cyperales and class monocotyledon having chromosome number $2n=24$. The genus *Oryza* is known to consist of two cultivated species i.e., Asian rice (*O. sativa*, $2n=24=AA$) and African rice (*O. glaberrima*, $2n=24=AA$) and 22 wild species ($2n=24$, 48) [2]. The river valleys of Yangtze, Mekon River area in China could be the primary center of origin of *Oryza sativa*. *Oryza glaberrima* is indigenous to the upper valley of the Niger River and it is cultivated only in western tropical Africa (Maclean et al., 2002)

Before placing strong emphasis on breeding for yield improvement trait, the knowledge on the association between yield and yield attributes will enable the breeder in the improvement of yield. The correlation coefficient may also help to identify characters that have little or no importance in the selection program. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in their combination (Oad et al., 2002).

It is one of the most important staple food in the world (Munir et al., 2006). On the nutritional basis, cultivated rice provides 35-60% of their total calorie intake to about 3.3 billion people in Asia. Based on Kernel color, rice is classified into two classes i.e. brown rice and white rice. The nutritional value of brown rice is more as compared to that of white rice, because their outer brown layer contains protein and minerals. The white part of rice is mainly carbohydrates. . Grain size of Pakistani rice is especially longer than that of the rice cultivars of other countries. In Pakistan, the study reveals that the longest fine rice cultivars are found in Khyber Pakhtunkhwa but the area under cultivation is smaller (Siddiqui et al., 2007).

Grain yield is dependent on many yield contributing characters as well as on the environmental influence. Association of different characters is essential to determine their contribution towards yield. The knowledge about genetic variability of yield contributing characters, interrelationship among them and their relationship with yield are necessary for a successful breeding program. Moreover, knowledge of heritability is essential for selection-based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan et al., 2009).

Rice is cultivated in 117 countries across all the habitable continents and is planted on area of about 163 million hectare with the global production of about 740 millions tons with an average yield of about 4,539 kg/ha (FAOSTAT,2014).The Asian contents ranks first with over 90.1% of world production, followed by the American continent (5.1%), African continent (4.2%), Europe (0.5%) and Oceania (0.1%) respectively. The major producing countries are China (206.5 million tons), India (157.2 million tons), Indonesia (70.8 million tons), Bangladesh (52.2 million tons) and Vietnam with 44.9 million tons (FAOSTAT, 2014)

Rice (*Oryza sativa L.*) is one of the major staple food crops for more than 3.5 billion global population. The production and consumption of global rice accounted for almost 90% by Asian countries; mainly China and India contribute about 55% of the total (Kong et al., 2015).

The presence of genetic variation for the desired traits is the basis of crop breeding and provides a great array of genotypes that can be selected to develop new varieties or breeding material. Variability in terms of genetic divergence for agronomic trait is the key component of breeding programs for broadening the gene pool of rice and requires reliable estimates of heritability helps plant breeders to predict the nature of the succeeding generation , to make an appropriate selection and to assess the magnitude of genetic improvement through selection (Khatun et al., 2015)

According to recent report of United Nation, it is predicted that the world population is going to cross 8 billion mark by 2030 and 9.6 billion by the year 2050 and rice production must be increased by 50% in order to meet the growing demand (Konate et al., 2016). To ensure the future requisites resulting from population growth, development of new high yielding rice genotypes is therefore a necessity. Thus, to ensure these requisites and obtain rice self-sufficiency, plant breeders must evolve high yielding cultivars with desirable agronomic trait for vast ecosystems.

Among the cereals, rice provides up to 20% of their regular calorie intake for millions of global populations. In order to ensure nutritional food security, the projected rice production must be increased to 852 million tons by 2035 (Brar et al., 2018) With the intensifications of diverse food demands and living standards of global populations, rice grain appearance and quality have become a primary concern for rice breeders.

Therefore, there is an urgent need to increase the grain yield along with desirable grain nutritional quality (GQ) traits in rice (Sreenivasulu et al., 2015 and Sun et al., 2018)

The genetic variability components like GV, PV along with heritability are used to determine the heritable potential of the concerned genes as well as the effect of environment over them. The GCV and PCV are categorized into Low (0-10), moderate (10-20), High (≥ 20) (Johnson et al. 1995) which suggests the possibility of improving the traits through selection. So keeping in view the above traits, the present experiment has been conducted to study the effect of genetic variability and heritability for various morphological and yield attributed traits in RIL population of basmati Rice.

The success of breeding program depends upon the quantum of genetic variability available for exploitation and the extent to which the desirable characters are heritable (TIWARI ET AL., 2001). Variability refers to the presence of differences among the individuals of plant population. Variation results due to difference either in genetic constitution of the individual of the plant population or in environment, they have grown. The existence of variability is essential for improvement of genetic material. Selection is also effective when there is significant amount of genetic variability among the individuals in breeding materials.

Several field crop varieties have been released possessing resistance against drought stress conditions. (Salekdeh et al. 2016) introduced drought stress response mechanism in rice. It indicated the yield enhancement in rice under drought stress by optimizing physiological process and mechanisms for avoiding water stress in plants. Fukai and Cooper classified the important mechanisms of rice function into three groups considering drought stress and its predictability i.e. yield potential, phenology (drought escape) and drought tolerance. Zhou et al. have reported that drought resistant genotypes can be determined by measuring some characteristics such as yield potential, delayed flowering, reduced plant height or drought response index (DRI) under both normal and drought stress conditions.

Knowledge on the nature and magnitude of genetic variation governing the inheritance of quantitative and qualitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability is the prerequisite for initiating any crop improvement program and for adaption of appropriate selection techniques.

III. MATERIALS AND METHODS

This experiment was conducted at New Experimental Farm, The University of Agriculture Peshawar, Pakistan during 2019 rice crop growing season. Five rice genotypes provided by University of Agriculture Peshawar were evaluated in randomized complete block design with three replications. Rice genotypes used in study were Basmati 385, PK-386, DR-82, KS-282 and Swat-2. Nursery was raised in the first week of May while transplantation of seedlings was done to the paddy field in 3rd week of June. After transplantation, the experimental field will be irrigated on daily basis for twenty days. At this stage water stress will be imposed for fifteen days through non-supply of irrigation water. After imposing the above-mentioned water stress the field will be irrigated only once in a week till crop maturity.

Each rice genotype was planted in three rows with row length of three meters and row to row distance of 30 cm.

IV. RESULTS AND DISCUSSION

Plant Height

Plant height is an important breeding trait of rice that directly affects the yield of the crop. It has been one of the primary targets for improving resistance against lodging.

Analysis of variance for plant height shows significant differences among genotypes ($P \leq 0.05$) presented in (Table 2). The mean value of plant height ranged from 80.67 cm to 117.80 cm. Minimum plant height (80.67 cm) was recorded for Basmati 385/ PK-386 while maximum plant height was recorded for DR-82/ PK-386 (117.80 cm) (Table 3). Results are in agreement with Jamal et al (2009) who observed the similar trend of plant height in their study. They recorded minimum and maximum plant height for genotypes YUNLEN2 82.2 and 124.9 for JP-5 respectively.

The analysis of association showed that, plant height revealed strong and positive correlation with grain yield, and biological yield and showed non-significant correlation with days to flowering, days to maturity, and harvest index. While the correlation was negative with flag leaf area (Table 8).

Flag Leaf Area

The uppermost leaf below the panicle is flag leaf area that provides the source of photosynthetic energy during reproduction and grain filling, thereby has greater impact in panicle development and grain yield in rice.

The genotypes displayed highly significant ($P \leq 0.01$) differences for flag leaf area as shown in (Table 2). Data ranged from 17.28 cm to 38.34 cm. Minimum flag leaf area (17.28 cm²) was measured for genotype JP-5/ KS-282 while maximum flag leaf area (38.34 cm²) was observed for KS-282/ Swat-2 (Table 3). Jamal et al (2009) for yield and yield contributing traits the evaluated five exotic genotypes along with a check variety. Minimum and maximum flag leaf area was shown by the genotypes PR26881-JP16-4B-78-5-1 (10cm²) and IRI384 (13cm²) respectively.

Flag leaf area was observed having significant and negative association with grain yield, biological yield, days to flowering, and days to maturity. (Table 8).

Panicle length

Panicle length is an important yield contributing trait that is measured at maturity stage.

Highly significant differences ($P \leq 0.01$) were observed among all tested genotypes for panicle length (Table 2). Mean values ranged from 19.27 cm to 29.07 cm. Minimum panicle length (19.27 cm) was manifested by genotype KS-282/ JP-5 while maximum panicle length (29.07 cm) was measured for DR-82/ PK-386 (Table 3). Rao et al (2014) assessed 49 rice genotypes to evaluate genetic variability, character association and path analysis between yield and yield related traits. Analysis of variance showed the presence of significant differences among genotypes for all traits studied. Also grain yield was significantly and positively correlated with number of grains per panicle, panicle length and test weight.

Analysis of correlation revealed that there is significant and negative association of panicle length with grain yield, biological yield, days to flowering, flag leaf area, and harvest index and manifested non-significant correlation with days to maturity and plant height. (Table 8).

Tillers plant⁻¹

Rice tillers are specialized grain bearing branches that are formed on elongated basal internodes and gives the crop necessary number of stalks required for a good production.

All the genotypes manifested non-significant differences for number of tillers plant⁻¹ (Table 4). The mean value for tillers plant⁻¹ varied from 9.23 to 16.90. Minimum tillers plant⁻¹ (9.23) was counted for genotype JP-5/ Basmati 385 while maximum (16.90) were recorded for Basmati 385/ PK-386 (Table 5). Jamal et al (2009) for yield and yield contributing traits the evaluated five exotic genotypes along with a check variety. Minimum number of tillers plant⁻¹ of 10.7 were taken by the rice genotype IRI384. While the maximum data were recorded for genotype PR26881-JP16-4B-78-5-1 that was 15.3 tillers plant⁻¹.

The analysis of correlation showed that tillers per plant revealed significant and negative correlation with days to flowering, days to maturity, flag leaf area, harvest index, and plant height. While demonstrated non-significant correlation with grain yield and biological yield. (Table 8).

Days to maturity

Days to maturity is an important trait that indices for harvesting of rice.

Significant differences ($P \leq 0.05$) were observed among rice genotypes for days to maturity (Table 4). The mean values ranged from 174.33 to 181 days. Minimum days to 50% maturity (174.33 days) were observed for genotype Basmati 385/ PK-386 while maximum days to 50% maturity (181 days) were counted for genotype KS-282/ DR-82 (Table 5). Fatherlrahman et al (2015) investigated genetic variability of rice in yield and yield contributing components. For all the traits studied showed that the phenotypic coefficient of variance was high than that of genotypic coefficient for the same traits which indicate that the characters was highly influenced by the environmental factors. Highly significant differences were observed in both seasons for plat height, days 50% maturity, and days to 50% flowering.

Association explores that there is significant and positive relationship of days to maturity with days to flowering and exhibited negative strong association with grain yield, while showed non-significant relation with biological yield. (Table 8).

Days to 50% Flowering

Days to flowering is an important phenological trait and may vary a little depending on growing conditions especially water availability and solar radiation.

Non-significant differences were observed among rice genotypes for days to flowering 50% (Table 4). The data distributed around the mean from 127.33 to 134. The minimum days to flowering (127.33) was measured for genotype PK-386/ DR-82 while the maximum days to flowering (134) were recorded for genotype Swat-2/ DR-82 (Table 5). Rehman et al. (2015) observed high significantly differences for days to emergence in their study but the present result for grain yield panicle may be due to genetic makeup or environmental factors.

Analysis of correlation explores that there is strong non-significant relation with grain yield biological yield. (Table 8).

Biological yield

Biological yield refers to the total dry matter accumulation of a plant system and have significant impact on economic yield.

Analysis of data regarding biological yield showed significant differences ($P \leq 0.05$) among the tested genotypes (Table 6). Biological yield plant⁻¹ ranged from 6082.73 g to 19708.03 g. The minimum biological yield (6082.73g) was recorded for genotype JP-5/ Basmati 385 while the maximum biological yield (19708.03 g) was weighed for genotype KS-282/ Basmati 385 (Table 7). Pandey et al (2012) studied the various quantitative traits and their inter relationship with each other. They evaluated 52 rice genotypes for all the traits, they observed high genetic variation which showed sufficient possibility of selection. The value of heritability was high for biological yield, spikelets per panicle, flag leaf area, 1000-grain weight and harvest index.

The analysis or association revealed that there is significant and negative association of biological yield with grain yield. (Table 8).

Grain yield

Highly significant differences ($P \leq 0.01$) were observed among all tested genotypes for grain yield (Table 6). The mean value scattered from 734.79 g to 4542.58 g. Minimum grains yield (734.79 g) were weighed for genotype KS-282/ PK-386 while maximum grain yield (4542.58 g) were recorded for genotype KS-282/ Basmati 385 (Table 7). Idris et al (2012) conducted an experiment to study the genetic variability and correlation among rice genotypes for yield and yield related traits. The results showed that there was highly significant difference between most of the traits under study except for percentage of fulfilled grains per panicle. For yield kg/ha they recorded the highest value of phenotypic and genotypic variance.

The analysis of correlation explored that grain yield is having positive significant association with plant height, while days to maturity, flag leaf area, panicle length and biological yield showed significant and negative association and days to flowering, tillers per plant and harvest index exhibiting significant relation with grain yield. (Table 8).

Harvest Index

Harvest index is used to measure a productive efficiency in any field crop.

Analysis Of variance revealed significant differences ($P \leq 0.05$) among rice genotype for harvest index (Table 6). The mean value ranged from 4.82% to 53.11%. The minimum harvest index (4.82%) was computed for genotype KS-282/ PK-386 while maximum harvest index (53.11 %) was calculated for genotype Basmati 385/ Swat-2 (Table 7). Bitew et al (2016) studied genetic variability for yield and yield related traits using 22 rainfed upland rice varieties. The analysis of variance showed significant differences between the genotypes for all traits except harvest index, indicating presence of a considerable amount of variability among genotypes.

Harvest index was found having significant and negative association with biological yield, days to maturity, and flag leaf area. While revealed non-significant relation with grain yield and days to flowering. (Table 8).

Table 2. Mean squares values for plant height, flag leaf area, and penical length of rice genotypes at The University of Agriculture Peshawar during 2020.

SOV	DF	PH	FLA	PNCL LNTH
REP				
	2	181.39	26.43	4.25
GENO				
	29	275.48*	93.08**	20.00**
ERROR				
	58	158.40	9.74	6.31
CV (%)				
		12.66	11.62	9.88

* = Sig. at 5% ** = Sig. at 1% NS = Non-Significant

Table 3. Mean values for plant height, flag leaf area, and penical length of rice genotypes at The University of Agriculture Peshawar during 2020.

GENO	PLNT HT	FLA	PNCL LNTH
Basmati 385/ PK-386	80.67	22.80	24.76
Basmati 385/ DR-82	91.87	26.14	21.92
Basmati 385/ KS-282	104.10	34.45	21.18
Basmati 385/ Swat-2	108.80	29.05	24.77
Basmati 385/ JP-5	103.60	31.27	26.17
PK-386/ Basmati 385	91.67	30.59	25.87
PK-386/ DR-82	91.40	33.24	26.52
PK-386/ KS-282	88.57	18.31	28.74
PK-386/ Swat-2	96.27	30.79	24.90
PK-386/ JP-5	105.90	33.42	26.19
DR-82/ Basmati 385	89.87	30.46	23.45
DR-82/ PK-386	117.80	24.81	29.07
DR-82/ KS-282	94.40	38.12	27.81
DR-82/ Swat-2	85.34	24.15	24.89
DR-82/ JP-5	93.07	25.44	27.82
KS-282/ Basmati 385	109.77	19.04	24.30
KS-282/ PK-386	111.93	30.76	28.09
KS-282/ DR-82	90.35	22.56	27.31
KS-282/ Swat-2	96.20	38.34	22.45
KS-282/ JP-5	92.47	25.65	19.27
Swat-2/ Basmati 385	113.87	18.70	23.83
Swat-2/ PK-386	101.67	22.78	23.29
Swat-2/ DR-82	96.93	25.19	21.32
Swat-2/ KS-282	102.73	23.08	23.39
Swat-2/ JP-5	107.27	25.60	28.72
JP-5/ Basmati 385	114.37	30.62	27.42
JP-5/ PK-386	91.40	22.92	28.77
JP-5/ DR-82	105.60	26.68	25.65
JP-5/ KS-282	109.67	17.28	27.50
JP-5/ Swat-2	96.00	23.66	26.96
LSD(0.05)		5.09695	
	20.55		4.10

Table 4. Mean squares values for tillers plant⁻¹, days to maturity, and days to 50% emergence of rice genotypes at The University of Agriculture Peshawar during 2020.

SOV	DF	TP⁻¹	DTM	DTF 50%
REP				
	2	1.52	3.1	84.23
GENO				
	29	7.31NS	12.49*	15.03NS
ERROR				
	58	4.43	5.93	30.42
CV (%)				
		16.78	1.37	4.23

* = Sig. at 5% ** = Sig. at 1% NS = Non-Significant

Table 5. Mean values for tillers plant⁻¹, days to maturity, and days to 50% emergence of rice genotypes at The University of Agriculture Peshawar during 2020.

GENO	TLR PLNT	DTM	DTF 50%
Basmati 385/ PK-386	16.90	174.33	130.00
Basmati 385/ DR-82	13.04	176.00	128.33
Basmati 385/ KS-282	13.60	179.00	128.33
Basmati 385/ Swat-2	12.33	175.33	132.00
Basmati 385/ JP-5	14.00	178.67	128.67
PK-386/ Basmati 385	13.87	175.67	128.00
PK-386/ DR-82	10.67	174.33	127.33
PK-386/ KS-282	9.67	175.00	131.67
PK-386/ Swat-2	12.43	176.00	131.33
PK-386/ JP-5	11.67	179.67	132.00
DR-82/ Basmati 385	11.93	174.00	130.67
DR-82/ PK-386	11.87	180.00	128.33
DR-82/ KS-282	11.70	177.67	130.67
DR-82/ Swat-2	14.00	176.67	126.00
DR-82/ JP-5	11.33	177.67	126.67
KS-282/ Basmati 385	12.87	178.00	134.00
KS-282/ PK-386	11.83	178.00	133.33
KS-282/ DR-82	12.53	181.00	133.00
KS-282/ Swat-2	14.13	176.33	130.33
KS-282/ JP-5	12.13	177.33	131.33
Swat-2/ Basmati 385	11.87	179.33	131.33
Swat-2/ PK-386	12.47	178.33	133.33
Swat-2/ DR-82	14.03	175.67	134.00
Swat-2/ KS-282	13.73	175.00	133.67
Swat-2/ JP-5	10.30	176.67	129.67
JP-5/ Basmati 385	9.23	180.00	130.00
JP-5/ PK-386	12.07	178.33	132.00
JP-5/ DR-82	12.03	180.33	130.33
JP-5/ KS-282	13.33	180.00	127.67
JP-5/ Swat-2	14.60	179.67	130.00
LSD(0.05)	3.44	3.98	9.01

Table 6. Mean squares values for biological yield, grain yield, and harvest index of rice genotypes at The University of Agriculture Peshawar during 2020.

SOV	DF	BY	GY	HI
REP				
	2	11313350.6	1073849	152.09
GENO				
	29	39370975.6*	3411778**	349.06*
ERROR				
	58	20904520.5	1506041	171.89
CV (%)				
		32.92	54.35	69.51

* = Sig. at 5% ** = Sig. at 1% NS = Non-Significant

Table 7. Mean values for biological yield, grain yield, and harvest index of rice genotypes at The University of Agriculture Peshawar during 2020.

GENO	BIO. YLD	GRN. YLD	HARVST INDX
Basmati 385/ PK-386	13576.64	3452.55	27.15
Basmati 385/ DR-82	10535.28	1823.60	17.71
Basmati 385/ KS-282	10340.63	1572.99	15.10
Basmati 385/ Swat-2	7299.27	3886.86	53.11
Basmati 385/ JP-5	11435.52	1155.72	10.64
PK-386/ Basmati 385	16666.67	885.64	5.37
PK-386/ DR-82	17761.56	1503.65	8.69
PK-386/ KS-282	12652.07	4143.55	35.59
PK-386/ Swat-2	10839.42	2541.36	24.59
PK-386/ JP-5	14233.58	2459.85	19.39
DR-82/ Basmati 385	13138.69	2354.01	18.06
DR-82/ PK-386	13868.61	2405.11	17.27
DR-82/ KS-282	11800.49	2635.04	27.12
DR-82/ Swat-2	12895.38	1201.95	10.18
DR-82/ JP-5	10583.94	2008.52	19.30
KS-282/ Basmati 385	19708.03	4542.58	25.34
KS-282/ PK-386	17396.59	734.79	4.82
KS-282/ DR-82	16301.70	1527.98	9.36
KS-282/ Swat-2	18856.45	1173.97	6.76
KS-282/ JP-5	17274.94	2465.94	17.17
Swat-2/ Basmati 385	18978.10	1695.86	9.98
Swat-2/ PK-386	9610.71	2671.53	26.68
Swat-2/ DR-82	14476.89	4262.77	31.79
Swat-2/ KS-282	12165.45	2057.18	18.15
Swat-2/ JP-5	13503.65	1102.19	8.85
JP-5/ Basmati 385	6082.73	1812.65	29.20
JP-5/ PK-386	12652.07	964.72	7.40
JP-5/ DR-82	17396.59	3751.82	29.91
JP-5/ KS-282	20681.27	2169.10	11.34
JP-5/ Swat-2	13990.27	2772.51	19.96
LSD(0.05)	7466.28	2004.02	21.41

Table 8. Correlation among yield and yield contributing traits in ricegenotypes atThe University of Agriculture Peshawar during 2020.

	GRN	BIO	DTF	DTM	FLA	HARVST	PLNT
BIO	-0.0424						
DTF	0.4134 ^{NS}	0.0564 ^{NS}					
DTM	-0.1387	0.1319 ^{NS}	0.0039 ^{**}				
FLA	-0.3272	-0.2207	-0.1762	-0.1385			
HARVST	0.8358 ^{NS}	-0.4943	0.3264 ^{NS}	-0.1780	-0.0890		
PLNT	0.0099 ^{**}	0.0477 [*]	0.1867 ^{NS}	0.5397 ^{NS}	-0.0324	0.0691 ^{NS}	
PNCL	-0.1774	-0.0380	-0.1771	0.2906 ^{NS}	-0.1092	-0.1110	0.1666 ^{NS}
TLR	0.0538 ^{NS}	0.1739 ^{NS}	-0.0499	-0.1491	-0.0585	-0.1075	-0.3312

GRN= grain yield, BIO= biological yield, DTF= days to flowering, DTM= days to maturity, FLA= flag leaf area, HI= harvest index, PNCL= panicle length, PH= plant height, TLR= tillers per plant.

*,** means significance at 1% and 5% probability respectively

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