

# Correlations and Path Coefficient Analysis of Yield and Yield Associated Traits in Bread Wheat Genotypes

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## Abstract

Forty bread wheat genotypes were tested in Randomized complete block design at the experimental farm of the Faculty of Agriculture, Fayoum University, in 2013/2014 and 2014/2015 seasons. The study objective was to estimate the extent of association between trait pairs in genotypic and phenotypic levels and thereby compare the direct and indirect effects of the traits. The data revealed that grain yield had positive and highly significant phenotypic and genotypic correlation with NT, SPL, NGSP, WGSP, SI, NSPM, SYF and HI. On the other hand, grain yield had negative and significant correlation at genotypic and phenotypic level with SPD and with HD at phenotypic level. Path analysis revealed that NSPM (0.618) exerted maximum positive direct effect on grain yield followed by SI (0.448) and NGSP (0.276). However, NSPM indirect effect through NT (0.230) followed by Si (0.219) and NGSP (0.192) indirect effect via WGSP exhibited the highest values indirect effect on grain yield.

**Keywords:** *Wheat, Yield, phenotypic, genotypic correlation, path coefficient analysis.*

## 1. Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops which are associated to the development of the major civilizations all over the world. The importance of wheat lays in the physical and chemical properties of its grain, which makes possible production of bread, a primary source of the staple diet for the poor population and rich one alike. Wheat provides over 20% of the calories and protein requirements for human nutrition, and is a staple food for over 41% of the world's population in more than 40 countries. Wheat also is one of the most important local cereal crops in terms of area and production. Egypt's

total wheat production of grains in 2014/2015 season reached about 9,460 million resulted from about 3.24 million feddan (FAO, 2013). Grain yield is a product of an organized interplay of several factors, which are highly susceptible to environmental fluctuations. However, yield can be estimated on the basis of performance of yield components. Yield is a complex trait dependent upon the interaction of environment and genetic makeup of the wheat plant. Apart from direct selection for grain yield, enhancement in most situations is more effectively fulfilled on the basis of performance of yield components, which are closely associated with grain yield. Correlation analysis provides information about association of plant traits and therefore, leads to a directional model for yield prediction. Path coefficient analysis quantifies the interrelationships between different components in their direct and indirect effects on grain yield. Chowdhry *et al* (2000) reported that there was positive but non-significant correlation between spikelets per spike and 1000-grain weight both at genotypic and phenotypic levels. Numbers of grains per spike has direct positive effects and indirect effect via number of spikelets per spike (Baloch *et al*, 2014). According to Mohy-ud-Din (1995) 1000-grain weight had a negative direct effect on grain yield while positive indirect effects was observed via number of grains per spike and grain weight per spike. The objective of this study was to estimate the extent of association between trait pairs in genotypic and phenotypic levels and thereby compare the direct and indirect effects of the traits to help wheat breeders, how to determine the effect of yield components and what yield components could be efficiently used in breeding programs.

## 2. Materials and Methods

This investigation was carried out at the experimental farm (Demo) of the Faculty of

Agriculture, Fayoum University, Egypt, during the two successive growing seasons, 13/2014 and 14/2015. The experimental material consisted of forty genotypes of bread wheat resulted from a prior study (Ghallab, 2006) in Table(1).

Table (1): List and pedigree of the forty bread wheat genotypes including four check parental cultivars.

G*	Pedigree	G	Pedigree
1	Sakha93 / Gimmeiza5 -2	21	Sids1 / Giza168 -8
2	Sakha93 / Gimmeiza5 -3	22	Sids1 / Giza168 -10
3	Sakha93 / Gimmeiza5 -4	23	Sakha93/ Sids1 -1
4	Sakha93 / Gimmeiza5 -5	24	Sakha93/ Sids1- 2
5	Sakha93 / Gimmeiza5 -6	25	Sakha93/ Sids1 – 3
6	Sakha93 / Gimmeiza5 -7	26	Sakha93/ Sids1 – 4
7	Sakha93 / Gimmeiza5 -9	27	Sakha93 /Sids1- 5
8	Gimmeiza5 / Giza168 -1	28	Sakha93/ Sids1 – 7
9	Gimmeiza5 / Giza168 -4	29	Sakha93/ Sids1 – 8
10	Gimmeiza5 / Giza168 -5	30	Sakha93/ Sids1 – 9
11	Gimmeiza5 / Giza168 -7	31	Sakha93/ Giza168 -1
12	Gimmeiza5 / Giza168 -9	32	Sakha93/ Giza168 -4
13	Gimmeiza5 / Giza168 -10	33	Sakha93/ Giza168 -6
14	Sids1 / Gimmeiza5 -7	34	Sakha93/ Giza168 -7
15	Sids1 / Gimmeiza5 -8	35	Sakha93/ Giza168 -8
16	Sids1 / Giza168 -2	36	Sakha93/ Giza168 -10
17	Sids1 / Giza168 – 3	37	<b>HD2172/Pavon"S"//1158.27/Maya74"S"Sd46-4Sd-2Sd-1Sd-0sd</b>
18	Sids1 / Giza168 – 4	38	Sakha92/TR 810328 S 8871-1S-2S-1S-0S
19	Sids1 / Giza168 – 6	39	MIL/BUC//Seri CM93046 - 8M-0Y-0M-2Y-0B
20	Sids1 / Giza168 -7	40	Vee "S"/SWM 6525 CGM 4017-1GM-6GM-3GM-0GM

\*G= Genotype

The genotypes were planted in the field through a randomized complete block design with three replications. Twelve rows per genotypes were planted in each replication. Each row was of 3.5 m long, with a row to row distance of 0.25 m while distance between plants was 0.05 m (plot size equal 10.5m<sup>2</sup>). All recommended agronomic practices were kept uniform. At maturity ten guarded plants from each replication were taken for recording the data on heading date (HD), days to physiological maturity (MD), plant height, cm (PLH), number of tillers plant<sup>-1</sup> (NT), spike length; cm (SPL), spike density (SPD), number of spikelets spike<sup>-1</sup> (NSSP), number of grains spike<sup>-1</sup> (NGSP), grains weight spike<sup>-1</sup> (WGSP),

1000- grain weight (SI), number of spikes m<sup>-2</sup> (NSPM), grain yield plant<sup>-1</sup>, g (GYP), straw yield, t/fed (SYF), grain yield, ardab/fed (GY) and harvest index (HI). The analysis of variance and covariance for all above mentioned traits was performed according to Gomez and Gomez (1984). Phenotypic (rp) and genotypic (rg) correlations between yield and yield related traits were estimated using the method described by Miller *et al.* (1958) and path coefficient analysis was done according to Dewey and Lu (1959).

### 3.Results

Genotypic and phenotypic correlations between all possible the studied trait pairs are present in Table (2). Data showed that 17 out of 105 phenotypic associations were higher than their corresponding genotypic ( $r_g$ ) correlation coefficients. These trait pairs of higher magnitude of  $r_p$  than  $r_g$  were; PLH with GY; NT with each SPL, SPD, NGSP and GYP; SPD with each NSSP and NGSP as well as NSPM; NSSP with GYP; NGSP with each SI, GYP and NSPM with each GYP and GY; GYP with SYF; SYF with each GY and HI (Table 2). Except these seventeen  $r_p$  values, the remainder trait pairs association showed  $r_g$  higher than the corresponding  $r_p$ , revealing that their association were under genetic control and their genetic variance plays the main role in their expression. So, genotypic correlations are more important for breeding procedure and should be threw spot on it. On the genotypic level, heading date (HD) exhibited positive and highly significant  $r_g$  associations with MD, PLH, NT, SPL, NSSP, NSMP and SYF. However, it showed negative highly significant  $r_g$  values with both SI and HI and significant negative  $r_g$  with WGSP. A day to maturity (DTM) was positively highly significant genotypic ( $r_g$ ) association with PLH, NT, SPL, NSSP, NSPM and SYF. Whereas it had negative and highly significant  $r_g$  with SI and HI. This trait behaved the same trend of heading date.

Plant height (PLH) showed positive highly significant  $r_g$  with NT, SPL, NSSP, NSPM and SYF, but negative highly significant  $r_g$  with WGSP and SI. These negative relations may be due to plant height reversed with spike lacking and grain weight. Number of tillers plant<sup>-1</sup> (NT) exhibited positive highly significant  $r_g$  values with SPL, NSPM, SYF and GY and significant value with GYP. However, it showed negative highly significant  $r_g$  with SPD, WGSP and HI and negative significant with SI. The former positive relations reflecting the importance of NT for productive traits, in spite of its negative relations with spikes laxing and their grain weight. Spike length (SPL) showed positive highly significant  $r_g$  with NSSP, NGSP, WGSP, GYP and SYF as well as significant value with GY, reflecting its effective contribution for spike and yield traits. On the other hand, SPL found to be negatively genotypic correlated with SPD, SI and HI. Spike density (SPD) had positive highly significant  $r_g$  with only NSSP, where it showed negative and highly significant  $r_g$  values with the four productive traits, i.e., NSPM, SI, GYP and SYF. Number of spikelets spike<sup>-1</sup> (NSSP) showed positive highly significant  $r_g$  with NGSP and WGSP and significant value with

SYF. While, it was negatively genotypic correlated with SI and NSPM at highly significant level. These results are logic and confirmed those of SPD. Number of grains spike<sup>-1</sup> (NGSP) had highly significant positive  $r_g$  values with WGSP, SI, GYP and HI. Whereas, it showed negative  $r_g$  with only NSPM. These positive associations revealing the NGSP trait as important yield components, but number of grains spike<sup>-1</sup> may be decreased with increasing spikes number m<sup>-2</sup>. Grains weight spike<sup>-1</sup> (WGSP) found to be genotypically correlated, at highly significant level, with SI, GYP, GY and HI, but had negative  $r_g$  with NSPM at the same level of significance. This trend was similar to that of NGSP whose the two traits are important yield components.

Seed index (SI) was positively highly significant genotypic correlated with GYP, GY and HI, but negatively with NSPM at the same level of significance, revealing its effective contribution as yield component. Number of spikes/m<sup>2</sup> (NSPM) was genotypically correlated with SYF and GY at highly significant level, while it showed negative  $r_g$  with HI. Grain yield plant<sup>-1</sup> (GYP) exhibited highly significant positive  $r_g$  with GY and HI. As well as, GY with HI had positive highly significant  $r_g$  value.

Path coefficient analysis was used to determine direct and indirect associations among different attributes. The direct and indirect effects of different traits on grain yield are presented in Table (3). Direct effects of number of spike/m<sup>2</sup>, NSPM (0.618) on grain yield/feddan followed by 1000-grain weight, SI (0.448) and number of grain/spike, NGSP (0.276) were positive and high effect (Table 3 & Fig.1). Number of spike/m<sup>2</sup> had positive indirect effect via number of tillers plant<sup>-1</sup> (0.230 value) followed by SI (0.219) as well as NGSP indirect effect (0.192) via WGSP and NSPM (0.156) indirect effect through PLH. On the other hand, direct effect of MD (-0.077) and NSSP (-0.058) on grain yield was negative. NSPM indirect effect via SI (-0.136) had negative effect followed by NSPM indirect effect via WGSP as well as SI indirect effect via NSPM on grain yield per feddan. The data led to conclude that GY would be increased through its positive relations with NT (0.280\*\*), SPL (0.180\*), NGSP (0.370\*\*), WGSP (0.350\*\*), SI(0.380\*\*), NSPM(0.420\*\*), SYF (0.260\*\*) and HI (0.570\*\*).

#### 4. Discussion

Sixteen selection genotypes, of hybrid origins together with four paternal cultivates, were evaluated during 13/2014 and 14/2015 seasons at the experimental form of the Faculty of Agriculture, Fayoum University. The experiments were executed through RCBD with three replications. The study aimed to estimate the extent of associations between all possible trait pairs genotypically (rg) and phenotypically (rp) and thereby compare the direct and indirect effects of the traits. It is well known that, in any trait pair relation, if rp value was higher than the corresponding rg one, indicating its influence by environmental factors in addition to genetic effect. The data revealed that 17 out of 105 significant rp values were higher than their rg values. However, the remainder trait pairs relations showed the reverse, where rg was higher than rp, indicating that these associations were mainly under genetic control and their genetic variance plays a considerable role in their expression. Therefore, selection should be effective based on these genotypic relations.

Heading data (HD) had positive rg associations with maturity data (MD) and some yield components, and negative associations with SI, HI and WGSP. These results are logical due to the fact that early heading is normally associated with decreased yield and especially grain weight. The results were coincident with those reported by **Khokhar et al. (2010)** and **Abd El-mohsen et al. (2012)** but the present results are in contrast to the findings of **Anwar et al. (2009)**. These relations were confirmed by the negative rg value of MD with both HI and SI. The results were coincident with those reported by **Anwar et al. (2009)** whereas the findings of **Degewione et al. (2013)** were in contrast to our results. PLH exhibited rg with spike features, positively. But it was negatively correlated with WGSP and SI, indicating that plant height reversed with grain weight. These results were in agreement with those reported by **Degewione et al. (2013)**; **Nawez et al. (2013)** but the results are contradicted with the findings of **Baloch et al. (2013)**. Although SPL showed positive rg with GYP, GY and SYP, it showed negative rg with SPD, SI and HI indicating its effective contribution for yield trait but not for grain weight. These results are in close agreement with the findings reported by **Khokhar et al. (2010)**; **Abd El-mohsen et al. (2012)** and **Baloch et al. (2013)** but it is in contrast to the findings of **Kumar et al. (2013)** and **Hussain et al. (2014)**. SPD was found to be genotypically correlated positively with NSSP only, and negatively with productive traits, indicating that it is not favorable irrespective to

grain weight. These results are in close agreement with the findings of **Khaliq et al. (2004)**. rg relations of NSSP with other traits conformed those of SPD. This is in agreement with the results reported by **Abd El-mohsen et al. (2012)**; **Baloch et al. (2014)** and **Hussain et al. (2014)** but it is in contrast to the findings of **Nawaz et al. (2013)**.

NGSP was genotypically correlated with WGSP, SI, GYP and HI, positively, and with NSPM negatively, reflecting its important yield contributor, irrespective to grains spike<sup>-1</sup>. This is in agreement with the results reported by **Nawaz et al. (2013)** and **Baloch et al. (2014)**. WGSP showed similar trend to that of NGSP. Seed index (SI) as well as number of grains spike<sup>-1</sup> (NSPM) showed positive associations with GY and SYF, reflecting its productive importance. These findings are in harmony with those previously obtained by **Khokhar et al. (2010)**; **Kumar et al. (2013)** and **Baloch et al. (2013)**. This result is in contradiction with the result reported by **Degewione et al. (2013)**. Grain yield plant<sup>-1</sup> (GYP) was genotypically correlated with GY and HI which both had positive rg. So, it should be considered that rg relations of GYP with NT, SPL, NGSP, WGSP, SI and HI were important in further selection for improving the current wheat genotypes. These results confirm the finding of **Khokhar et al. (2010)**; **Baloch et al. (2013)** and **Nawez et al. (2013)** but it is in contrast to the findings of **Abd El-mohsen et al. (2012)** and **Kumar et al. (2013)**. Direct and indirect effects were in line with correlation results, where NSPM followed by SI and NGSP had positive and high effects (**Mohy-ud-Din, 1995** and **Baloch et al., 2014**). Also, **Obsa (2014)** and **Zerga et al., (2016)**, reported that days to maturity was a positive direct effect on grain yield, controversial with the present study. Thus, selection on the basis of these traits in this material would likely to be most useful for increasing grain yield in practical wheat breeding programs.

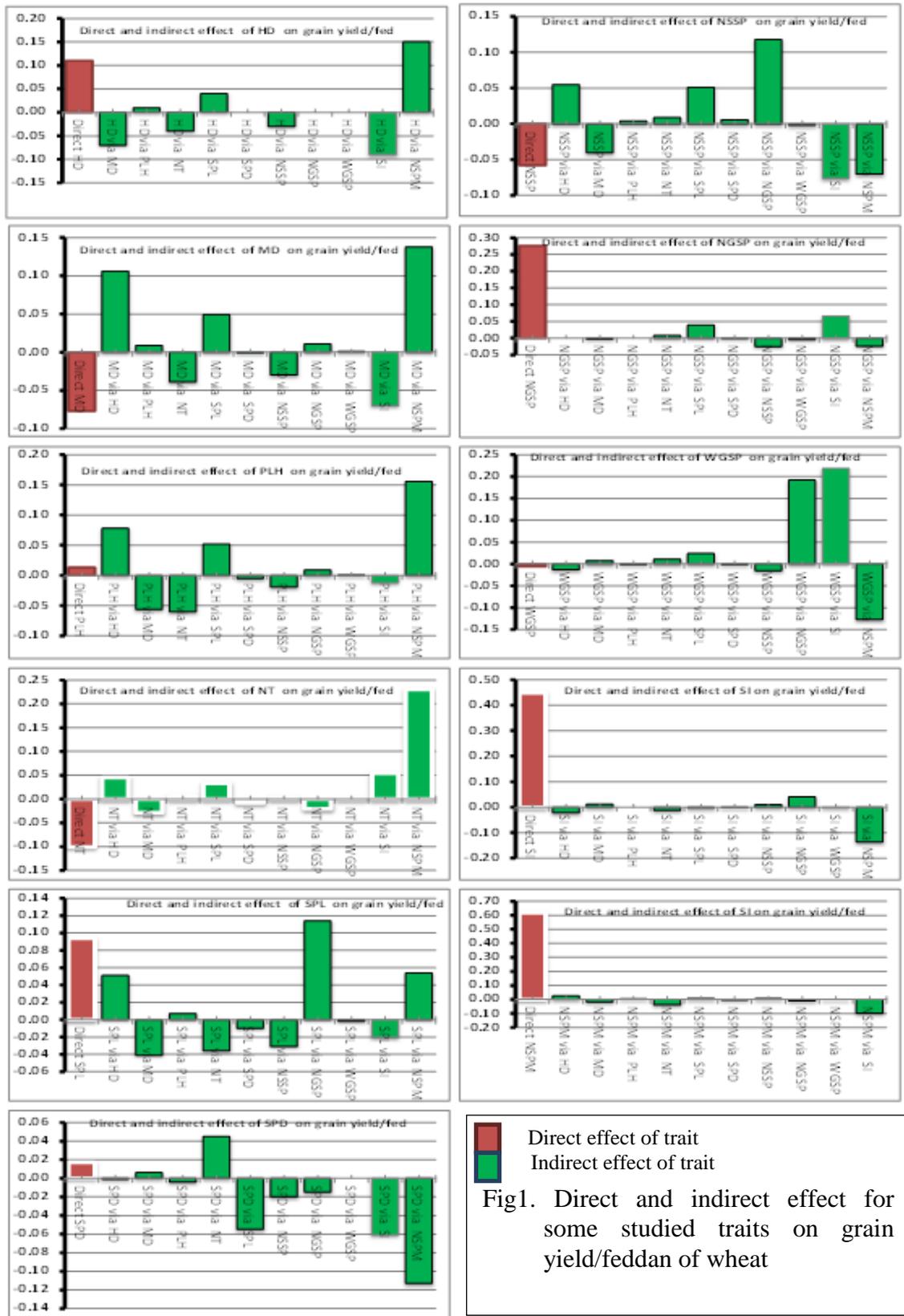
Table (2): Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between grain yield and its contributing traits in bread wheat in 2013/2014 and 2014/2015 (over two seasons).

Trait	HD	MD	PL.H	NT	SPL	SPD	NSSP	NGSP	WGSP	SI	NSPM	GYP	SYF	GY	HI
<b>HD</b>		0.24**	0.76**	0.52**	0.48**	0.017	0.60**	0.018	-0.14*	-0.26**	0.28**	-0.06	0.35**	0.083	-0.21**
<b>MD</b>	0.27**		0.73**	0.50**	0.58**	-0.042	0.64**	0.077	-0.123	-0.22**	0.26**	-0.04	0.33**	0.089	-0.19**
<b>PLH</b>	0.69**	0.66**		0.66**	0.61**	-0.29**	0.46**	0.029	-0.15*	-0.15*	0.29**	0.07	0.52**	0.090	-0.35**
<b>NT</b>	0.32**	0.32**	0.43**		0.34**	-0.33**	0.077	-0.085	-0.25**	-0.15*	0.64**	0.17*	0.47**	0.28**	-0.18**
<b>SPL</b>	0.39**	0.46**	0.50**	0.41**		-0.59**	0.61**	0.39**	0.18**	-0.13*	0.12	0.25**	0.35**	0.18*	-0.15*
<b>SPD</b>	0.04	-0.03	-0.18**	-0.38**	-0.56**		0.28**	-0.017	-0.015	-0.072	-0.27**	-0.24**	-0.29**	-0.26**	0.081
<b>NSSP</b>	0.46**	0.48**	0.37**	0.08	0.55**	0.382**		0.46**	0.72**	-0.19**	-0.67**	0.08	0.15*	-0.053	-0.109
<b>NGSP</b>	0.012	0.049	0.118	0.165*	0.46**	-0.138*	0.39**		0.69**	0.17**	-0.14*	0.53**	0.024	0.37**	0.37**
<b>WGSP</b>	-0.098	-0.080	-0.066	0.052	0.32**	-0.122	0.53**	0.69**		0.63**	-0.339**	0.74**	-0.087	0.35**	0.40**
<b>SI</b>	-0.21**	-0.18**	-0.093	0.045	-0.049	-0.082	-0.114	0.18**	0.44**		-0.31**	0.57**	0.001	0.38**	0.29**
<b>NSPM</b>	0.20**	0.19**	0.22**	0.35**	0.055	-0.137*	-0.16*	0.024	-0.13*	-0.19**		-0.020	0.52**	0.42**	-0.133*
<b>GYP</b>	-0.042	-0.022	0.107	0.38**	0.39**	-0.24**	0.20**	0.61**	0.69**	0.43**	-0.14*		0.055	0.56**	0.46**
<b>SYF</b>	0.20**	0.19**	0.40**	0.158*	0.099	-0.048	0.074	0.103	0.049	-0.029	0.46**	0.15*		0.26**	-0.61**
<b>GY</b>	0.059	0.073	0.15*	0.23**	0.17*	-0.14*	0.048	0.34**	0.27**	0.27**	0.53**	0.49**	0.42**		0.57**
<b>HI</b>	-0.14*	-0.123	-0.28**	0.071	0.070	-0.067	0.006	0.21**	0.19**	0.19**	-0.056	0.29**	-0.64**	0.36**	

\*and \*\*, significant at  $P < 0.05$  and  $P < 0.01$ , respectively

Where, DH= Heading date, DTM = Days to physiological maturity, PLH = Plant height, NT = Number of tillers plant<sup>-1</sup>, SPL= Spike length, SPD = Spike density, NSSP= Number of spikelets spike<sup>-1</sup>, NGSP = Number of grains spike<sup>-1</sup>, WGSP = Grains weight spike<sup>-1</sup>, SI= 1000 – grain weight, NSPM = Number of spikes m<sup>-2</sup>, GYP = Grain yield plant<sup>-1</sup>, SYF = Straw yield, Bio Y= Biological yield , GYF = Grain yield/fed ,HI= Harvest index.

Contribution of traits on grain yield



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