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MEAN-PERFORMANCE, INTERRELATIONSHIPS AND PATH ANALYSIS OF YIELD TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.) CROSSES

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Abstract

Heterosis, heterobeltiosis and inbreeding depression for grain yield and its components were studied through 6 crosses in F_1 and F_2 generations. These crosses were resulted from half diallel mating design between 4 different parents in 2014/2015. In 2017/2018 season, an experiment was conducted in randomized complete block design with three replications at Faculty of Agriculture, Cairo University, Giza, Egypt to evaluate the 16 genotypes (4 parental lines and their 6 crosses in F_1 and 6 crosses in F_2). Moreover, simple phenotypic correlation and path analysis were performed to study the nature of associations between grain yield and its components. The results showed that, for grain yield plant^{-1}, the cross combination (P2 × P3) depicted the highest significant and positive heterosis (88.12%) and heterobeltiosis (81.9%) followed by cross combination (P1 xP2) which exhibited a high positive significant heterosis (83.43%) and high positive significant heterobeltiosis (60.35%). Concerning inbreeding depression, highly significant and positive values of inbreeding depression were detected for total dry matter, spike dry matter, grain yield plant^{-1} and 1000-kernels weight for all crosses. On the other hand, significant and negative values of inbreeding depression were detected in plant height, No. of spikes plant^{-1}, spike length, harvest index and No. of kernels spike^{-1}. Respect to the correlation analysis. The results showed that, highly significant and positive correlation was observed between grain yield plant^{-1} and each of No. of spikes plant^{-1} ($r=0.64^{**}$), biological yield ($r=0.94^{**}$), spike dry matter ($r=0.98^{**}$) and 1000-kernels weight ($r=0.76^{**}$). Concerning path-analysis technique, the spike number plant^{-1} exhibited the highest direct effect value (0.61) towards grain yield plant^{-1} followed by number of kernels spike^{-1} which exhibited a high degree of direct effect (0.547). The greatest indirect effect on grain yield plant^{-1} was achieved by total dry matter *via* number of spikes plant^{-1}. It could be concluded that, plant height, number of spikes plant^{-1}, spike length, No. of kernels spike^{-1} and 1000-kernels weight are major components of wheat yield and could be used as selection criteria in the breeding programs.

Key words : Diallel crosses, heterobeltiosis, inbreeding depression correlation, wheat crosses.

Introduction

Wheat as cereal crop consider the second most important crop that contributes significantly to the global food and food security (Kumar *et al.*, 2013 and Ljubicic, *et al.*, 2014). Through the last 20 years, the global wheat acreage varied between 207 and 227 million hectares with a production and productivity around 728.28 million tons (Ljubicic, *et al.*, 2014).

Increasing wheat grain yield potential by developing new wheat varieties with desirable traits is considered the main objective for wheat breeders, the most tasks in wheat breeding program is crossing the lines having good general combining ability and selecting desirable genotypes within its segregating population. So, Wheat production can be enhanced through the development of new cultivars having wider genetic base and better performance (Erkul *et al.*, 2010 and Ljubicic *et al.*, 2014).

The successful development of hybrid maize in 1930 using principles of heterosis gave great motivation to other crop breeders to develop hybrids. Evidences are now available about the presence of heterotic effects for desirable traits in highly self-pollinated crops like wheat and rice. Heterosis is considered as one of the major achievements of crop breeding endeavors and has been used extensively in cultivars development programs in different crops (Birchler *et al.*, 2003). Recently, according to Rauf *et al., (*2012) manipulation of heterosis is an

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important strategy for increasing the yield potential of wheat. However, wheat hybrids yielded 13.5% more than their parents.

Ilker *et al*., (2010) assessed heterotic effects between three susceptible commercial wheat varieties growing in Turkey and five resistant (powdery mildew) wheat lines procured from CIMMYT. Some F_1 cross combinations were observed the most promising ones to develop new cultivars with shorter stature, longer spikes, high No. of spikelets and kernel spike^{-1}, and higher grain yield coupled with improved powdery mildew resistance.

Khan and Ali (2011) studied heterosis using 10 F_1's obtained through crossing 5 commercial varieties for yield and yield related traits. The highest negative heterotic and heterobeltiotic effects were manifested for plant height (-7.74%). On the other hand, high positive heterobeltiosis (34.85%) was observed for No. of tillers plant^{-1}. Meanwhile, high mid parent (38.40%) and better parent heterosis (31.26%) values were obtained for spike length. The maximum heterosis (45.66%) and heterobeltiosis (42.59%) were detected for spikelets spike^{-1}. Moreover, two cross combinations were recommended for improving yield and enhanced biological production of wheat

Knowledge on the expression levels of the heterosis and inbreeding depression are useful for helping breeders to choose the best hybrid combinations which will serve as the basis for the selection of superior genotypes (Gaur *et al*., 2014 and Kumar *et al.,* 2016). Accordingly, these cross combination may be utilized for improving grain yield as well as production of better transgressive segregates in advanced generations for maintain of specific gene pool of bread wheat through breeding programs in future (Kumar *et al*., 2017)**.**

For future breeding programs, it is important to determine the available genetic variation for plant structure and the nature of associations of yield components. Therefore, the information on association between yield and its components is a prerequisite for breeding program aimed at yield improvement. Yield is a dependable complex inherited trait as a result of interaction of several contributing factors that may be related or unrelated (Subramanian and Subramanian, 1994).

The correlation coefficient which measures the simple linear relationship between two traits does not predict the success of selection (Ali and Shakor, 2012). However, path coefficient analysis is considered an efficiency tool to determine the relative importance of direct and indirect effects of different traits on grain yield (Darvishzadeh, *et al.,* 2011). Moreover, Path coefficient analysis is more informative and useful technique than simple correlation coefficients and widely used in crop breeding to increase the efficiency of selection (Khaliq *et al*., 2004, Sokoto *et al*., 2012 and Janmohammadi *et al*., 2014).

Many researchers mentioned, that grain yield exhibited a positive and significant correlation with the different components *i.e.*, number of grains spike^{-1}, spike length, 1000 grain weight, number of spike plant^{-1} (Aycecik and Yildirim, 2006, Li *et al.,* 2006 and Akram *et al.,* 2008) and plant height (Topal *et al.,* 2004). Therefore, correlation and path analysis technique of yield and yield components are suitable methods to recognize the valuable genotypes (Li *et al.,* 2006).

Thus, the present investigation was carried out to study the heterosis in F_1 over mid-parents and better parent and inbreeding depression in F_2 generations for grain yield and its related traits in bread wheat. Moreover, the present investigation aimed to get information on the nature of association of grain yield and its components *via* simple correlation coefficient analysis and path analysis techniques to increase the effective selection in segregating generations.

Materials and Methods

Plant materials and experimental design

An experiment was conducted at the Agricultural Experiments and Research Station, Faculty of Agriculture, Cairo University, Giza Governorate, Egypt (30º02' N latitude and 31º13' longitude with an altitude of 22.50 meters above sea level) during three successive seasons starting at 2014/2015 season. The study evaluated six crosses in F_1 and F_2 generations and their four parental genotypes of bread wheat namely, L-29, L-41, Sahel1, and Kharchia (Table 1). In the 1st season parental genotypes were sown during 2014/2015 for attempting crossing program in a 4×4 half diallel fashion. In the next season 2015/2016, the experimental material consisted of 10 genotypes (4 parental genotypes and 6 F_1's) was sown in a randomized complete block design with three replications (Shrief *et al.,* 2017).

During the 3rd season 2016/2017 at 21th November 2016 as planting date, an experiment was conducted to evaluate the six crosses in F_1 and F_2 generations and their four parental genotypes. The experimental unit consisted of one row for F_1 and the parental genotypes while for F_2 it consisted of 2 rows, each plot unit replicated three times in a randomized completely block design, each row was 3 m long and 35 cm apart. Plants were spaced 10 cm within each row forming 30 plants row^{-1}. The physical analysis of experimental soil presented that the texture of the soil was clay with the following distribution

Table 1: The name, pedigree of the four genotypes of wheat used as parents in this study.

No.	Genotypes	Pedigree	origin*
P1	L-29	Milan/Kans/Primia/ 3/Bau92	Yemen
P2	L-41	Tacupeto Fzool/Bramb Ling*2/Kach4	Yemen
P3	Sahel1	NS732/PIMA/VEE#5	Egypt
P4	Kharchia	KHLC*5/EG953	India

*Source: Plant Genetic Resources Research Department (Bahteem Gene Bank), FCRI, ARC, Egypt.

39.1% clay, 30.3% silt and 30.6% sand. All cultural practices, including fertilization and irrigation were performed according to the recommendations for wheat production.

Recorded data

Observations were recorded in each replication on eight randomly selected guarded plants in parents and their F_1's and fifteen plants in their F_2's progenies. The following traits were recorded: Plant height in cm (PH), No. of spikes plant^{-1} (S/P), Spike length in cm (SP Length), Total dry matter, (Total DM) in g, Spike dry matter (Spike DM) in g, Harvest index (HI), 1000-kernels weight (KW) in g, No. of grains spike^{-1} (G/S) and grain yield plant^{-1} (GYP) in g.

Biometrical procedures

Statistical analysis

The collected data were checked out for normality distributions in each trait by Wilk Shapiro test (Neter *et al.,* 1996), then the data were subjected to analysis of variance (ANOVA) technique as outlined by Snedecor and Cochran (1989) by using MSTAT-C computer software (Freed *et al.,* 1989) to test the null hypothesis of no significant differences between various F_1's and F_2's and their parental genotypes. Least Significant Difference (LSD) test was applied for means separation and comparison after significance of the ANOVA. Genotypes sum of square and degrees of freedom were partitioned into different components, *i.e.* parents, F_1 crosses, F_2's, parents *vs.* crosses and F_1 *vs.* F_2.

The estimates of simple correlation coefficients and its statistical significance were calculated between grain yield plant^{-1} and its components according to the method described by Steel *et al.,* (1997) and Gomez and Gomez (1984). Correlations were partitioned into path coefficient using the technique outlined by Dewey and Lu (1959). This technique involves partitioning of the correlation coefficient to determine direct (unidirectional pathways 'P') and indirect influence through alternate pathways (pathway (P) × correlation coefficient (r)) of various variables over grain yield plant^{-1}. Grain yield plant^{-1} was considered as the resultant variable and the others as casual variables.

Heterosis

The percent increase or decrease of F_1 crosses over mid parent as well as better parent was calculated to estimate possible heterotic effects for above mentioned traits (Fonseca and Patterson, 1968).

$$Hetrosis = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

$$Hetrobeltiosis = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where: $\overline{F}_1$ = mean of the F_1 cross over replications, $\overline{MP}$ = average of the two parent over replications and $\overline{BP}$ = mean of the better parent over replications.

The significance of the heterosis estimated was tested by the appropriate LSD as follows:

$$\text{LSD for heterosis} = t_{\alpha}\sqrt{\frac{3\,\text{MSe}}{2\text{r}}}$$

$$\text{LSD for heterobeltiosis} = t_{\alpha}\sqrt{\frac{2\,\text{MSe}}{\text{r}}}$$

Where: t is the tabulated t value at 5% and 1% probability for a stated level of probability for degrees of freedom for the error mean square (MSe) and r is the number of replications.

Inbreeding depression (ID%)

$$ID\,\% = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

Where: = mean of the F_1 cross over replications and= mean of the F_2 progenies over replications. The significance of inbreeding depression was tested by the same equation of LSD as used for testing of heterobeltiosis.

Results and Discussion

Analysis of variance

Analysis of variance for studied traits of 16 genotypes (4 parents + 6 F_1 crosses + 6 F_2's) is presented in (Table 2). Results indicated, except harvest index (HI), the mean squares due to genotypes were highly significant for all studied traits. These results indicated the presence of considerable amount of genetic variability in the present sets of material and further genetic analysis would be meaningful. Genotypic differences for these traits were previously recorded by many researches (Singh *et al.,*

Table 2: Pertinent analysis of variance for studied traits of 16 bread wheat genotypes.

S.O.V	df	PH	S/P	SP Length	Total DM	
Replicate	2	22.67	4.43 **	1.10 **	52.99 *	
Genotypes	15	246.12**	5.58 **	2.09 **	234.46 **	
Parents	3	558.37 **	2.02	2.71 **	107.71 **	
F_1's	5	190.15 **	3.14 **	0.83 **	112.93 **	
F_2's	5	143.57 **	9.89 **	2.85 **	60.89 **	
Parent *vs.* F_1's	1	325.36 **	11.76 **	3.73 **	2267.30 **	
F_1's *vs.* F_2's	1	22.77	0.71	1.03 **	57.38 *	
S.O.V	**df**	**Spike DM**	**GYP**	**HI**	**KW**	**K/S**
Replicate	2	32.11 **	25.06 **	134	1.14	3.05
Genotypes	15	75.66 **	36.18 **	58.79	18.85 **	157.53 **
Parents	3	18.90 *	8.70 *	131.65	6.02 *	32.19
F_1's	5	37.36 **	22.66 **	39.29	10.40 **	54.97 *
F_2's	5	8.79	3.3	13.5	8.21 **	242.37 **
Parent *vs.* F_1's	1	837.34 **	386.66 **	101	171.70 **	670.75 **
F_1's *vs.* F_2's	1	10.08	0.18	121.88	0.00	108.95 *

*,** = significant at 0.05 and 0.01, probability levels, respectively. PH =plant height, S/P = number of spikes plant^{-1}, SP Length = Spike length, Total DM= Total dry matter, Spike DM= Spike dry matter, GYP = grain yield plant^{-1}, HI= Harvest index, KW=1000-kernels weight, and K/S=No. of kernels per spike.

2012, Singh *et al.,* 2013, Meena *et al.*, 2014 and Kumar *et al.,* 2016).

Partitioning genotypes mean squares for parents (P), F_1 crosses, F_2's, parents *vs.* F_1 crosses (P vs F_1) and (F_1 vs F_2) table 2 indicted that they were significant (*$P\leq 0.05$*) or highly significant (*$P\leq 0.01$*) for all studied traits, except mean squares of (HI) for (P, F_1, F_2, P vs F_1 and F_1 vs F_2), spike dry matter and grain yield/plant for (F_2), spikes/plant and grain spike^{-1} for (P) which exhibited insignificant mean squares. The significant mean squares due to parents *vs.* F_1's indicated significant heterosis. On the other hand, mean squares due to F_1 *vs.* F_2 were not significant for all studied traits except for spike length, biological yield (TDM) and grain spike^{-1} (G/S).

Mean performance

The performance of the four parental lines, the six F_1 and the six F_2's are presented in (Table 3). In respect plant height for the parental mean performance, it ranged between 67.7 cm (P2) to 99.7cm (P4), for No. of spikes plant^{-1} it ranged between 7.07 (P1) to 8.88 (P2) for spike length it ranged between 7.92 cm (P4) to 10.02 cm (P1), for total dry matter/plant, it ranged between 23.3 to 37.98 g for P1 and P3, respectively. Concerning spikes dry matter it ranged between 13.47g (P1) to 19.06 g (P3). Grain yield plant^{-1} ranged from 9.15 to 13.12 g for P1 and P3, respectively. Harvest index ranged between 35.24 (P3) to 41.14 (P1), concerning 1000-kernels weight P3 exhibited the highest value (38.27g) while (P2) showed the lowest one (35.53 g), with respect to No. of kernels spike^{-1} it ranged between 34.64 (P1) to 42.46 (P3). From the above mentioned results it could be concluded that, out of 9 studied traits, P3 exhibited the highest value in 5 traits, while P1 showed the lowest values for 5 traits.

The general mean of F_1 and F_2 table 3 exhibited a greater values than the general mean of parents meanwhile, the general mean of F_1 is greater than the general mean of F_2 indicating that hybrid vigor is manifested in the all studied traits. For plant height, results indicating that the parent; P4 and its crosses; (P1×P4), (P2×P4) and (P3×P4) gave the highest values in both generations. On the other hand, P1 and P2 as well as the cross combinations; (P1×P2) and (P1×P3) recorded the lowest values for the same trait in both generations (F_1 and F_2). For number of spikes plant^{-1}, the highest mean values were detected by the cross combinations (P1×P2) and (P2×P3) in F_1 while in F_2 the cross combinations (P1×P2), (P2×P4) and (P3×P4) showed the highest mean values. For spike length, data showed that the two crosses (P2×P3) and (P2×P4) exhibited longer spike than the other crosses in F_1, while in F_2, the crosses (P1×P3) and (P2×P3) gave the highest values for spike length. Concerning the biological yield and spike dry matter, the two cross combinations (P2×P3) and (P1×P2) exhibited the highest values in F_1, while in F_2, the cross combinations (P1×P2) and (P2×P4) showed the highest performance.

Grain yield is the final and essential wheat production and the contribution of many components makes the nature of grain yield more complicated. The cross P2×P3,

Table 3: Mean performance of studied traits in bread wheat parents and their F_1 and F_2's.

Genotypes	PH (cm)	S/P	SP Length (cm)	Total DM (g)	Spike DM (g)	GYP (g)	HI (%)	KW (g)	K/S
	Parents								
P1	75.53	7.07	10.02	23.30	13.47	9.15	41.137	37.87	34.64
P2	67.73	8.83	8.52	30.55	18.47	12.23	25.904	35.53	39.02
P3	82.92	8.08	9.48	37.98	19.06	13.12	35.235	38.27	42.46
P4	99.70	8.77	7.91	30.80	16.81	11.66	38.348	35.73	37.34
Parent mean	81.47	8.19	8.98	30.65	16.95	11.54	35.16	36.85	38.36
	F_1 Crosses								
P1×P2	81.03	10.08	9.42	51.79	29.08	19.62	38.683	44.53	43.67
P1×P3	80.13	8.13	9.75	40.41	23.03	16.20	39.791	40.97	48.95
P1×P4	86.75	9.50	9.60	43.45	25.39	17.46	40.394	40.20	45.52
P2×P3	85.42	11.08	10.43	57.30	33.30	23.86	41.908	42.43	50.64
P2×P4	98.83	9.00	10.10	50.85	26.86	17.08	31.842	42.77	44.49
P3×P4	97.00	9.00	8.92	46.60	28.76	19.00	40.786	39.50	54.82
F_1's mean	88.19	9.47	9.70	48.40	27.74	18.87	38.90	41.73	48.02
	F_2's								
P1×P2	81.033	10.083	9.424	46.790	25.575	17.617	38.651	42.467	41.093
P1×P3	79.083	7.033	10.120	35.241	21.446	15.033	41.816	39.300	54.667
P1×P4	95.667	8.333	8.833	38.313	20.990	14.878	38.493	38.200	46.741
P2×P3	83.000	6.167	10.225	34.267	21.367	15.100	44.133	39.900	61.421
P2×P4	93.778	10.111	8.022	40.933	23.189	16.288	40.123	40.667	39.569
P3×P4	89.000	10.500	8.050	38.733	22.283	15.955	40.969	38.067	40.112
F_2's mean	86.93	8.70	9.11	39.05	22.48	15.81	40.70	39.77	47.27
General mean	86.09	8.85	9.29	40.37	23.03	15.89	38.65	39.77	45.44
LSD 0.05	6.84	1.47	0.60	6.00	3.69	2.56	11.70	2.02	7.21
LSD 0.01	8.23	1.77	0.72	7.21	4.44	3.08	14.08	2.43	8.67

*,** = significant at 0.05 and 0.01, probability levels, respectively. PH =plant height, S/P = number of spikes plant^{-1}, SP Length = Spike length, Total DM= Total dry matter, Spike DM= Spike dry matter, GYP = grain yield plant^{-1}, HI= Harvest index, KW=1000-kernels weight, and K/S=No. of kernels per spike.

followed by P1×P2 and P3×P4 showed the highest grain yield plant^{-1} in F_1, while in F_2, the cross combination P1×P2 followed by P2×P4 and P3×P4 exhibited the highest values.

For harvest index, it could be concluded from the obtained results that the crosses (P2×P3) followed by (P3×P4) and (P1×P4) recorded the greatest values for harvest index in F_1 while in F_2 the cross combination (P2×P3) followed by (P1×P3) and (P3×P4) recorded the highest values of harvest index.

Concerning 1000-kernels weight, the cross combinations (P1×P2) followed by (P2×P4) and (P2×P3) exhibited the highest grain index in both generations. Respect to No. of kernels spike^{-1} the cross combinations (P3×P4) followed by (P2×P3) and (P1×P3) showed the highest No. of kernels spike^{-1} in F_1, while the highest No. of kernels spike^{-1} was recorded by the cross combinations (P2×P3) followed by (P1×P3) and (P1×P4) in F2's. The high grain yield plant^{-1} of the previous crosses could be attributed to the high values of one or more of yield components. The available variability among the different genotypes is sufficient for making an effective selection and promising breeding programs in wheat for improving grain yield. These results are in accordance with the finding of Ahmad *et al.*, (2013).

Heterosis and inbreeding depression

The main objective of the all breeding programs is developing new superior varieties irrespective of their use as varieties *per se* or as parents of a hybrid. The suitable mechanism to produce hybrid seed at commercial scale for wheat which consider a self-pollinated crop is not yet available. Therefore, at present the heterosis *per se* may not be of economic value in this crop (Yadav *et al.*, 2017).

Furthermore, the current investigation aimed to identify the superior cross combinations, which are promising in conventional breeding program. The nature and magnitude of the heterosis and heterobeltiosis were detected. So the different crosses exhibited positive or negative heterotic effects which varied from trait to another.

Heterosis expressed as, the percentage deviation of F_1 mean performance from the mid parent values and heterobeltiosis expressed as the percentage deviation of F_1 mean performance from better parent were detected for all the studied traits and presented in (Table 4). Results of table 4 showed that, heterosis of plant height ranged between -0.99 (P1×P4) to 19.06% (P2×P4), three cross combinations, (P1×P2), (P2×P3) and (P2×P4) expressed significant and positive heterotic effects relative to mid-parent. In respect heterobeltiosis for PH, it ranged between 6.08% (P1×P3) to 45.92% (P2×P4). Except only one cross (P1×P3) the five remainder crosses exhibited significant and positive heterotic effects relative to better-parent for PH (the shortest one). Previously, Hussain *et al.,* (2007) reported positive heterosis for plant height; on the other hand negative heterosis has been recorded by Ilker *et al.,* (2010) and Bilgin *et al.,* (2011).

For plant height, dwarfness is a desirable trait for wheat crop; hence negative heterosis is favourable for breeding to lodging resistance thus producing stable yield (Thomas, 2017). Moreover, Inamullah *et al.,* (2006) mentioned that taller plants are likely to lodge quite often and require more energy to translocation solutes to the grain weight and also reported that negative heterosis is desirable. On the other hand, some researchers preferred the tallest plant (Chowdhry *et al.*, 2000, Shahid *et al.*, 2002 and Topal *et al.*, 2004) they reported the importance role of positive heterosis for plant height. In respect inbreeding depression table 5 for plant height, it ranged from -10.28 (P1×P4) to 8.25% (P3×P4), only three cross combinations had significant and positive value of inbreeding depression.

Concerning spikes number/plant, table 4 in any breeding program spike number/plant is consider as selection criteria. Increasing spike number/plant, increasing number of spike/unit area which reflect on increasing yield/unit area. A positive heterosis was detected for all cross combinations with different degree table 4, it ranged between 2.27 to 26.83% for cross combinations (P2×P4) and (P1×P2) respectively. Out of the six crosses, only three cross combinations exhibited significant positive heterosis. Respect to heterobeltiosis, it ranged between 0.52 (P1×P3) to 25.47% (P2×P3) only one cross (P2×P3) exhibited heterobeltiosis in positive and significant direction. Regarding to inbreeding depression of spike number/plant table 5 it is varied from -16.66 (P3×P4) to 44.36% (P2×P3). Out of the 6 cross combinations only three cross combinations (P1×P2, P2×P4 and P3×P4) exhibited significant negative values which display desirable amount of inbreeding depression (transgressive segregation). Finally two cross

Table 4: Estimates of heterosis (%) and heterobeltiosis (%) in bread wheat F_1's for all studied traits.

	PH	S/P	SP Length	Total DM	Spike DM	GYP	HI	KW	K/S
	Mid parent heterosis								
P1×P2	13.12 **	26.83 **	1.65 ns	92.36 **	82.10 **	83.48 **	15.41 ns	21.34 **	18.58 *
P1×P3	1.14 ns	7.26 ns	-0.04 ns	31.91 **	41.58 **	45.50 **	4.20 ns	7.62 **	26.98 **
P1×P4	-0.99 ns	20.00 **	7.09 **	60.63 **	67.72 **	67.75 **	1.64 ns	9.24 **	26.50**
P2×P3	13.40 **	31.03 **	15.82 **	67.25 **	77.49 **	88.21 **	11.78 ns	15.00 **	24.29 **
P2×P4	18.06 **	2.27 ns	23.00 **	65.79 **	52.24 **	43.00 **	-18.46 ns	20.02 **	16.54 *
P3×P4	6.23 ns	6.82 ns	2.55 ns	35.52 **	60.37 **	53.35 **	10.86 ns	6.76 **	37.40 **
	Better parent heterosis (heterobeltiosis)								
P1×P2	19.64 **	14.15 ns	-5.98 *	69.54 **	57.45 **	60.35 **	-5.96 ns	17.61 **	11.92 ns
P1×P3	6.08 ns	0.52 ns	-2.73 ns	6.42 ns	20.81 *	23.49 **	-3.27 ns	7.06 **	15.28 ns
P1×P4	14.85 **	8.37 ns	-4.23 ns	41.08 **	51.03 **	49.70 **	-1.81 ns	6.16 *	21.92 *
P2×P3	26.11 **	25.47 **	9.92 **	50.89 **	74.73 **	81.85 **	5.43 ns	10.89 **	19.25 *
P2×P4	45.92 **	1.89 ns	18.57 **	65.11 **	45.43 **	39.65 **	-19.89 ns	19.68 **	14.03 ns
P3×P4	16.99 **	2.66 ns	-5.98 ns	22.71 **	50.92 **	44.82 **	6.36 ns	3.22 ns	29.11 **
$LSD_{0.05}$(MP)	5.92	1.28	0.52	5.19	3.19	2.22	10.13	1.75	6.24
$LSD_{0.01}$ (MP)	7.13	1.54	0.63	6.25	3.84	2.67	12.19	2.11	7.51
$LSD_{0.05}$(BP)	6.84	1.47	0.60	6.00	3.69	2.56	11.70	2.02	7.21
$LSD_{0.01}$ (BP)	8.23	1.77	0.72	7.21	4.44	3.08	14.08	2.43	8.67

*,** = significant at 0.05 and 0.01, probability levels, respectively. PH =plant height, S/P = number of spikes plant^{-1}, SP Length = Spike length, Total DM= Total dry matter, Spike DM= Spike dry matter, GYP = grain yield plant^{-1}, HI= Harvest index, KW=1000-kernels weight, and K/S=No. of kernels per spike.

Table 5: Estimates of inbreeding depression (ID%) for all studied traits.

	PH	S/P	SP Length	Total DM	Spike DM	GYP	HI	KW	K/S
P1×P2	-0.0004	-0.0033**	-0.0017**	9.65**	12.04**	10.20**	0.08	4.64**	5.90
P1×P3	1.30 **	13.44 **	-3.79**	12.80**	6.86**	7.21**	-5.09**	4.07**	-11.67**
P1×P4	-10.28	12.28**	7.99	11.83**	17.34	14.76**	4.71**	4.98**	-2.67**
P2×P3	2.83 **	44.36	1.91**	40.20	35.84	36.71	-5.30**	5.97	-21.29
P2×P4	5.12 **	-12.34**	20.57	19.50	13.65**	4.66**	-26.00**	4.91**	11.07**
P3×P4	8.25	-16.66 **	9.72	16.88	22.53	16.02**	-0.45**	3.63**	26.83
LSD 0.05	6.48	1.32	0.57	5.46	3.22	2.25	12.85	1.90	6.19
LSD 0.01	7.79	1.59	0.68	6.57	3.88	2.71	15.46	2.29	7.44

*,** = significant at 0.05 and 0.01, probability levels, respectively. PH =plant height, S/P = number of spikes plant^{-1}, SP Length = Spike length, Total DM= Total dry matter, Spike DM= Spike dry matter, GYP = grain yield plant^{-1}, HI= Harvest index, KW=1000-kernels weight, and K/S=No. of kernels per spike.

combinations (P1×P2 and P2×P3) depicted the top two crosses expressed super cross in segregating generation, these crosses could be of greater value if exploited in breeding program were also desirable for most traits. The importance roll of spikes number/plant as selection criteria towards high yielding ability was detected by Kashif and Khaliq (2004).

For spike length table 4 it is considered a major yield component and is directly contributed proportionally to kernels spike^{-1} and consequently to the final product of grain yield. The longer the spike length, the higher will be the grain yield. Significant mid-parent heterosis and heterobeltiosis were detected in 3 crosses out of the 6 F$_1$,s. The heterosis values ranged from -0.04 (P1×P3) to 23% (P2×P4), while F1,s heterobeltiosis ranged between -5.98 (P1×P2) and 18.75% (P2×P4), Masood *et al.,* (2005) reported positive heterosis for spike length, whereas the range of inbreeding depression varied from -0.0017% (P1×P2) to 20.57% (P2×P4) for inbreeding depression, table 5 top two cross combinations were P2×P4 and P3×P4 expressed more desirable transgressive segregates.

For total dry matter (biological yield plant^{-1}), table 4 all cross combinations exhibited positive and significant mid-parent heterosis, which ranged from 31.91 (P1×P3) to 92.36% (P1×P2) and the highest biological yield was detected by the cross (P2×P3) in F$_1$, while the cross combination P1×P2 exhibited the highest biological yield in F$_2$. With respect to heterobeltiosis, it ranged from 6.42% (P1×P3) to 69.54% (P1×P2). Inbreeding depression table 5 was detected in all cross combinations and it ranged between 9.65% (P1×P2) and 40.2% (P3×P3). For development of high yielding ability, bread wheat genotypes which have more biological yield should be used further in breeding program (Desale and Mehta, 2013 and Kumar *et al*., 2016).

For spike dry matter, table 4 the same trend of biological yield was detected for spike dry matter, which reflect the importance roll of exchangeable relationships between the both traits on grain yield. The six cross combinations exhibited significant and positive mid-parent heterosis and heterobeltiosis. So, the mid parent-heterosis ranged between 41.58 (P1×P3) and 82.1 (P1×P2), while the heterobeltiosis ranged from 20.81 (P1×P3) to 74.72% (P2×P3). Concerning inbreeding depression (Table 5) it ranged between 6.86 (P1×P3) and 35.84% (P2×P3), three crosses exhibited significant and positive inbreeding depression for spike DM.

For grain yield**,** significant and positive mid-parent (heterosis) was depicted in all cross combinations (Table 4). The cross P2×P3 depicted the highest positive heterosis value (88.21%) followed by hybrids P1×P2 (83.48%), P1×P4 (67.75%), P3×P4 (53.35%), P1×P3 (45.5%) and P2×P4 (43%), Significant and positive heterobeltiosis was shown by the all cross combinations. Cross P2×P3 exhibited the highest positive heterobeltiosis value (81.86%) followed by crosses P1×P2 (60.35%), P1×P4 (49.7%), P3×P4 (44.82%), P1×P4 (39.65%) and P1×P3 (23.49%), Singh *et al.,* (2013) and Garg *et al*., (2015) also reported similar positive and significant heterosis. Concerning inbreeding depression table 5 except the hybrid P2×P3, the remaining five cross combinations exhibited significant and positive inbreeding values, ranging from 7.21% (P1×P3) to 16.02% for cross (P3×P4) the inbreeding depression for grain yield was recorded in wheat hybrids by many researchers (Kumar *et al.,* 2017 and Yadava *et al.,* 2017).

For harvest index, table 4 a significant heterosis was observed and varied from -18.46 (P2×P4) to 15.41% (P1×P2), except cross P2×P4; the all cross combination exhibited positive heterosis values. In respect to heterobeltiosis for HI, it ranged between -19.89 (P2×P4) and 6.36% (P3×P4); only two crosses (P2×P3 and P3×P4) exhibited heterobeltiosis in positive direction. Concerning with inbreeding depression of harvest index

Table 6: Simple correlation coefficients between studied traits.

Traits	PH	S/P	SP Length	Total DM	Spike DM	GYP	HI	KW	K/S
PH	1.00	0.24	-0.33	0.31	0.25	0.23	-0.34	0.08	0.07
S/P		1.00	-0.35	0.68 **	0.64 **	0.64 **	-0.17	0.38	-0.35
SP Length			1.00	0.26	0.28	0.27	0.06	0.51 *	0.51 *
Total DM				1.00	0.97**	0.94 **	-0.25	0.82 **	0.29
Spike DM					1.00	0.99 **	-0.02	0.79 **	0.43
GYP						1.00	0.08	0.76 **	0.49*
HI							1.00	-0.15	0.40
KW								1.00	0.28
K/S									1.00

*,** = significant at 0.05 and 0.01, probability levels, respectively. PH =plant height, S/P = number of spikes plant^{-1}, SP Length = Spike length, Total DM= Total dry matter, Spike DM= Spike dry matter, GYP = grain yield plant^{-1}, HI= Harvest index, KW=1000-kernels weight, and K/S=No. of kernels per spike.

table 5, it is varied from -26.0 (P2×P4) to 4.71% (P1×P4). Four crosses out of 6 cross combinations displayed desirable amount of inbreeding depression. P2×P4 and P2×P3 were the top two crosses expressed super cross in segregating generation, these crosses could be of greater value if exploited in breeding program were also desirable for straw and showed negative and significant value of inbreeding depression in order to merit. Positive heterosis for harvest index was reported by Singh *et al.,* (2013).

For 1000-kernels weight, table 4 it is an important selection criterion in any breeding programs as it has a positive correlation with grain yield in wheat. All crosses showed highly significant mid parent heterosis values table 4; the maximum value (21.34%) was shown by cross P1×P2 followed by the crosses P2×P4 (20.02%), P2×P3 (15%), P1×P4 (7.625), P3×P4 (6.76%). For better parent heterosis (heterobeltiosis), except the hybrid P3×P4 the remaining five cross combinations exhibited significant and positive heterosis values; the maximum value was exhibited by the hybrid P2×P4 (19.68%) followed by the hybrids P1×P2 (17.61%), P2×P4 (10.89%), P1×P3 (7.06%) and P1×P4 (6.16%). Except P2×P3 significant positive inbreeding depression was detected in all hybrids table 5, it ranged between 3.63% (P3×P4) and 5.97% (P2×P3). In the current studies many hybrids tended to have high thousand grain weight, which is considered as one of the important yield components. By exploiting heterosis for this attribute, many researchers found that this trait has direct contribution for increased grain yield in wheat (Dagustu, 2008).

For No. of kernels spike^{-1} table 4, the all six cross combinations displayed significant heterosis which ranged from 16.54 (P2×P4) to 37.4% (P3×P4). Respect to heterobeltiosis, only three cross combinations exhibited significant and positive values it ranged from 11.92 to 29.11% for P1×P2 and P3×P4, respectively. Concerning inbreeding depression, it ranged between -21.9 (P2×P3) and 26.83 (P3×P4). The hybrid P2×P3 exhibited a high degree of heterosis and heterobeltiosis and expressed the highest No. of kernels spike^{-1} in F_1 (50.64) and F_2 (61.42), indicating significant economic heterosis, whereas, the same cross reflected the highest significant and negative value of inbreeding depression for No. of kernels spike^{-1} (Table 5). The range of inbreeding depression varied from -21.23 to 26.83%. Three crosses out of 6 crosses expressed positive or negative significant inbreeding depression. The desirable cross combination P2×P3 showed the highest inbreeding depression for No. of kernels spike^{-1} (-21.29%). No. of kernels spike^{-1} is considered one of the most important yield contributing parameters in wheat. Along with some other yield components, No. of kernels in a single spike adds tremendously to an increase in yield from a constant unit area. Significant variations for kernels spike^{-1} were also reported by Jadoon *et al.,* (2012).

Correlation Studies

Before starting any breeding program it is very important to know some information regarding the nature of association between grain yield and other contributing parameters. Grain yield is a complex quantitative trait which is more influence by environmental fluctuations. So, the selection based on yield *per se* is not efficient to improve yield production, the selection must be towards the yield components like No. of spike plant^{-1}, spike length, No. of kernels spike^{-1} and 1000-kernels weight.

Correlation coefficients among studied traits are presented in Table 6. Grain yield plant^{-1} exhibited significant and positive association with spike dry matter (r=0.99**), biological yield plant^{-1} (r=0.94**), 1000-kernels weight (r=0.76**), No. of spikes plant^{-1} (r=0.64**) and No. of kernels spike^{-1} (r=0.49*). Concerning the relationships between grain yield with No. of spikes plant^{-1} and its associated traits in wheat, Aycecik and Yildirim, 2006 reported that increasing the number of spikes plant^{-1} normally increases spikes per unit area which in turn results in high grain yield. Also, Kashif and Khaliq (2003) mentioned that the grain yield components like No. of spike plant^{-1}, No. of kernels spike^{-1}, 1000-kernels weight and No. of tillers had significantly contributed to grain yield development. In the same context many researchers mentioned that, plant height, spike length, spikelet number spike^{-1}, grain number spike^{-1} and 1000-kernels weight are considered the major components of wheat yield and could be used as selection criteria in breeding programs (Topal *et al.,* 2004, Aycecik and Yildirim, 2006; Li *et al.,* 2006 and Akram *et al.,* 2008).

Biological yield/plant is considered as one of the most important criteria for high grain yield; increasing biological yield normally increases the number of source cells and increased photosynthetic activity which in turn results in high grain yield. The results showed that biological yield plant^{-1} exhibited significant positive correlation with No. of spikes plant^{-1} (r=0.68**), spike dry matter (r=0.97**) and 1000-kernels weight (r=0.82**). The significant and positive effect of biological yield on No. of spike plant^{-1}, spike dry matter, grain yield plant^{-1} and 1000-kernels weight has been previously elaborated by Khaliq *et al*., (2004).

Also, significant and positive correlation was depicted between spike length and each of No. of kernels spike^{-1} and 1000-kernls weight. Spike dry matter exhibited significant positive correlation with 1000-kernls weight and No. of spike plant^{-1}. The results indicated that plant height had a positive relationship with No. of spike plant^{-1}, biological yield plant^{-1}, spike dry matter and grain yield plant^{-1}. These results are in agreement with those obtained by Khaliq *et al*., (2004). On the other hand, a negative relationship was detected between biological yield and harvest index, also negative correlation was found between No. of kernels spike^{-1} and No. of spike plant^{-1}. These results are confirmed with those obtained by (Topal *et al.,* 2004, Aycecik and Yildirim, 2006; Li *et al.,* 2006 Akram *et al.,* 2008)

Path Analysis

Improving the efficiency of trait selection is considered the main objective in any breeding program. Thus, simple correlations may not provide a clear picture of the importance of each grain yield component to identify the valuable genotypes. However, analysis of multi co-linearity indicated a better understanding of the interrelationships among the measured traits and their relative contribution to grain yield. So, Path analysis technique provided an effective method of partitioning correlation coefficient into direct and indirect pathways to study the magnitude and direction of association of yield with various components (Mahmood *et al*., 2006).

In order to compare the relative importance of the primary yield components *i.e*., No. of spikes plant^{-1}, number of kernels spike^{-1}, 1000-kernels weight and biological yield which exhibited significant and positive correlation with grain yield, the direct and indirect effects of each of the four independent traits on grain yield (dependent) were computed and presented in (Table 7).

Table 7: Path coefficient analysis of the direct (diagonal) and indirect (above and below diagonal) effects of yield components on yield of bread wheat genotypes.

Traits	**X_1**	**X_2**	**X_3**	**X_4**	**GYP**
S/P (X_1)	0.611	0.077	-0.190	0.139	0.638 **
KW (X_2)	0.233	0.203	0.155	0.168	0.759 **
K/S (X_3)	-0.212	0.057	0.582	0.060	0.49*
Total DM (X_4)	0.413	0.166	0.159	0.205	0.944 **

Italic and bold figures denotes direct effects while regular numbers denotes indirect effects.

S/P = number of spikes plant^{-1}, KW=1000-kernels weight, K/S=No. of grain spike^{-1},Total DM=Total dry matter and GYP=grain yield plant^{-1}

The results of the current investigation showed that, the No. of spikes plant^{-1} exhibited the highest positive direct effect on grain yield (0.61), while the indirect effect of No of spikes plant^{-1} *via* biological yield showed a relative medium positive effect (0.14), meanwhile, the indirect effects of this trait via grain index was minimum (0.077). On the other hand, the indirect effect *via* No. of kernels spike^{-1} was negative (-0.19), the important role of spike No. plant^{-1} as selection criterion in wheat was reported by many researchers (Aycecik and Yildirim, 2006 and Salih *et al*., 2017)

The direct effect of No. of kernels spike^{-1} on grain yield plant^{-1} showed a high positive value (0.582). The indirect effects of No. of kernels spike^{-1} *via* No. of spike plant^{-1} exhibited negative effects (-0.21). On the other hand the indirect effect of No. of kernels spike^{-1} *via* 1000-kernels weight and biological yield exhibited a small value which reached to about (0.06) for the both traits. The important role of kernels number spike^{-1} was reported by Shahid *et al.,* (2002), Kashif and Khaliq, (2004) and Salih *et al*., (2017).

Respecting the direct effect of 1000-kernels weight towards grain yield the results exhibited a moderate value (0.20). The indirect effects of 1000-kernels weight *via* No. of spikes plant^{-1} were relatively moderate (0.233), meanwhile, the indirect effects of 1000-kernels weight *via* grain spike^{-1} and total dry matter on grain yield plant^{-1} exhibited moderate values (0.155) and (0.168), respectively. These results are in agreement with those obtained by Shahid *et al.,* 2002, Kashif and Khaliq (2004) and Janmohammadi 2014.

The direct effects of biological yield (TDM) on grain yield showed a moderate value (0.205). The indirect effects of biological yield on grain yield via No. of spike plant^{-1} exhibited the maximum indirect effects (0.413). Also, the indirect effects of biological yield via 1000-kernels weight and No of kernels spike^{-1} on grain yield were moderate values which reached to (0.166 and 0.159), respectively. From the above mentioned results, it could be concluded that, although, the biological yield exhibited the greatest correlation coefficient with grain yield (r=0.944), it showed a moderate direct effect towards grain yield that is due to a greatest indirect effects of biological yield *via* some other yield components, like No. of spikes plant^{-1}, 1000-kernels weight and No. of kernels spike^{-1}. Finally, our results indicated that biological yield, No. of spikes plant^{-1}, 1000 kernels weight and No. of kernels spike^{-1} were more related to higher grain yield.

Conclusion

From our results, it could be concluded that, plant height, number of spikes plant^{-1}, spike length, No. of kernels spike^{-1} and 1000-kernels weight are major components of wheat yield and could be used as selection criteria in the breeding programs. The above mentioned traits along with their direct and indirect causal factors should be considered simultaneously as an effective selection criteria evolving high yielding genotype.

Conflict of Interest

The present study was performed in absence of any conflict of interest.

Author Contributions

This work was carried out in collaboration between all authors. Author S. A. Shrief and M. A. Abd EL-Shafi wrote the protocol and wrote the first draft of the manuscript. Authors Sawsan A. El-Ssadi and H. M Abdel-Lattif designed, performed data analyses and managed the literature searches. All authors designed the study, managed the experimental process, read and approved the final manuscript.

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