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### Estimation of genetic components, correlation and path coefficient in some bread wheat genotypes (*Triticum aestivum* L.)

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#### ABSTRACT

Six cultivars of bread wheat were used in a half diallel during the three successive seasons of 2020/2021, 2021/2022 and 2022/2023 to study some genetic components, correlations and path coefficients. Results indicated that Misr 3 (P6) cultivar had the earliest plants in heading (DH), the shortest plants (PH) and the highest grain yield/plant (GY/P). The greatest grain yield/plant were recorded by crosses (P4xP6), (P3xP4), (P4xP5), (P1xP4) and (P5xP6) in F<sub>1</sub> and crosses (P1xP2), (P1xP6), (P4xP6), (P2xP4) and (P1xP3) in F<sub>2</sub>. Grain yield per plant exhibited positive significant genotypic and phenotypic correlations with number of spikes/plant (NS/P), biological yield/plant (BY/P), harvest index (HI), number of spikelets/spike (NST/S) and weight of grains/spike (WG/S). Path analysis revealed high and positive direct effects on grain yield/plant via BY/P, HI, WG/S, NS/P, PH, 1000 grain weight (1000-GW) and DH. High positive indirect effects were observed for traits; spike length (SL), NS/P, BY/P, NST/S, weight/spike (WS), number of grains/spike (NG/S) and 1000-GW on grain yield/plant via weight of grains/spike. It is proved the importance of these traits as selection criteria in improving grain yield in wheat.

**Keywords:** wheat, diallel, hayman, association, path analysis.

#### INTRODUCTION

Bread wheat is an important cereal crop all over the world and in Egypt. The main goal of Egyptian is to reduce the gap between wheat production and consumption. In recent years, various approaches have

been undertaken to increase wheat yield capacity. Despite these efforts, annual production has reached only 9.8 million tons, falling significantly short of the 20.6 million tons required to meet local

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consumption needs (USDA, 2023). The development of enhanced wheat cultivars has consistently been a primary focus for wheat breeders worldwide. To achieve this improvement, breeders must depend on the selection of appropriate parents and cross combinations. Consequently, assessing the genetic variances available in the early generations of crosses can prove highly beneficial for plant breeders.

Understanding the heritability of quantitative traits is crucial for any plant improvement program. The diallel cross technique consider a good method for estimating the inheritance and behavior of quantitative traits. The application of models proposed by **Griffing (1956)**, **Hayman (1954 a and b)**, and **Jinks (1954)** in the  $F_1$  generation offers valuable insights into the nature and extent of gene action involved in the inheritance of a given trait. This information aids plant breeders in identifying the types of genetic variation present in traits targeted for selection, as well as in efficiently evaluating yield potential by pinpointing crosses capable of producing superior genotypes. Diallel analysis was the primary method used in earlier research on the inheritance of different wheat characteristics. The most important factor in any breeding program is yield. Therefore, increasing yield is the breeder's ultimate goal. **Kamara *et al.* (2021)** noted that the estimates of dominance component ( $H_1$ ) were higher than the additive component (D) for all studied traits. The additive (D) genetic variance and dominance ( $H_1$ ) and ( $H_2$ ) showed significant estimates for plant height, number of spikes/plant, number of grains/spike, 1000 grain weight and grain yield/plant (**Elgammaal *et al.*, 2023**). However, the parameters of D and  $H_1$  were significant, the significant contribution of variance D indicated that the gene action additive effects played the most crucial role

in the genetic regulation of agronomic traits (**Ahangar and Ghojogh, 2023**). The additive genetic variations (D) were significant ( $P < 0.01$ ) for most traits. The dominance genetic variation  $H_1$  and  $H_2$  were significant ( $P < 0.01$ ) for all traits. Moreover, the estimates of  $H_1$  and  $H_2$  were found greater in magnitude than D estimates for most traits. The ratio of KD / KR found more than unity for all traits, except grain yield/plant. Moderate heritability values were found for DH, PH and SL. For the other traits, low narrow sense heritability was determined (**Dawwam *et al.* 2020**).

The relationship between traits can be assessed through phenotypic correlation coefficients. However, correlation coefficient analysis may not provide an accurate evaluation of the direct and indirect contributions of each yield component to grain yield. A correlation study among various traits can help plant breeders understand how improving one trait could simultaneously influence others (**Sabit *et al.*, 2017 and Kadan *et al.*, 2022**). Conversely, Path coefficient analysis assesses how independent factors affect dependent variables both directly and indirectly. This method helps breeders identify the underlying causes of associations between traits. Furthermore, **Milkessa, 2022** noted that path coefficient analysis partitions the correlation coefficient into effects, both direct and indirect, offering insights into how related traits influence the target trait. The current investigation's goals were to: 1) estimate genetic components and heritability for yield and its related traits in bread wheat  $F_1$  and  $F_2$  generations. 2) determine the relationship between yield and its related traits in  $F_1$  generation by using correlation coefficient and path coefficient.

## MATERIAL AND METHODS

The present study was carried out during three successive seasons 2020/2021, 2021/2022 and 2022/2023 at a private farm

of Bany omran village, Diermawas city, El Minia governorate, Egypt. In this study, six Egyptian bread wheat (*Triticum aestivum* L.

em. Thell) cultivars were employed as parents; their pedigree is listed in Table 1.

**Table 1. Names and pedigrees of the bread wheat cultivars.**

Code no.	Genotypes	Pedigree
P1	Sakha 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1
P2	Giza 168	MRL/BUC//SERI
P3	Giza 171	SAKHA 93/GEMMEIZA 9
P4	Sids 14	BOW "S" / VEE"S" // BOW"S" / TSI/3/ BANI SEWEF 1
P5	Misr 2	SKAUZ/BAV92
P6	Misr 3	ATTILA*2/PBW65*2/KACHU

**2020/2021 season**, the six parental cultivars were sown at various dates (15<sup>th</sup>, 25<sup>th</sup> November and 5<sup>th</sup> December) in order to overcome the differences in time of flowering. Using hand emasculation and pollination, we created a half diallel sequence of fifteen crosses using all feasible combinations among parents, omitting reciprocals.

**2021/2022 season**, the twenty-one entries, consisting of fifteen F<sub>1</sub> crosses and six parents were grown in a randomized complete block design (RCBD) with three replications. The experimental plot was a single row 3 m. long and 30 cm apart, with 10 cm between plants within row.

**2022/2023 season**, fifteen F<sub>2</sub> of single crosses and six parents were grown in a randomized complete block design (RCBD) with three replications using the same cultivation distance.

The following characters were recorded based on plot mean of the parents, and F<sub>1</sub> crosses; days to 50% heading [DH], plant height [PH] in cm, spike length [SL] in cm, number of spikes/plant [NS/P], biological yield/plant [BY/P] in gm, grain yield/plant [GY/P] in gm, harvest index% [HI], weight/spike [WS] in gm, number of spikelets/spike [NST/S] in gm, number of grains/spike [NG/S], weight of grains/spike

[WG/S] in gm, 1000 grains weight [1000-GW] in gm.

The genetic parameters were estimated using the procedure described by **Hayman (1954 a and b)**. Heritability in narrow-sense was estimated according to **Mather and Jinks (1971)** for F<sub>1</sub>'s data, and **Verhalen and Murray (1969)** for the F<sub>2</sub>'s data. The data of F<sub>1</sub> hybrids and parental lines were analyzed according to the method suggested by **Steel and Torrie (1984)**. The method described by **Kown and Torrie (1964)** and **Dewey and Lu (1959)** was followed to calculate phenotypic and genotypic correlation coefficients, and path coefficient, respectively.

## RESULTS AND DISCUSSION

### 1- Mean performance

Mean performance for six parents and their 15 F<sub>1</sub> and F<sub>2</sub> generations of bread wheat are presented in Table 2. The parental variety P6 showed the earliest in days to heading (88.33 days), the shortest plant height (94.54 cm.) and the highest grain yield per plant (23.54 gm.). while P5 was the latest in days to heading by 92.67 days. P2 gave the tallest plant height (107.88 cm.) and the latest parent in NS/P, BY/P, GY/P, HI and NST/S by 4.20, 53.13 gm., 15.03

gm., 28.28 and 18.38, respectively. The highest values for SL (13.02 cm.), NS/P (7.50), BY/P (70.28 gm.), HI (36.15 %), WS (5.56 gm.), NST/S (21.10), NG/S (68.23), WG/S (3.04 gm.) and 1000-GW (52.27 gm.) were recorded for P2, P1, P4, P3, P2, P1, P4, P3 and P3, respectively. While P5 recorded the lowest values for SL (11.03 cm.), WS (4.11 gm.) and 1000-GW (46.47 gm.). Similarly, P6 recorded the lowest values for NG/S (55.76) and WG/S (2.19 gm.).

**In F<sub>1</sub> generation**, the cross P2XP3 was the earliest in DH (81.33 days), the tallest SL (14.63 cm.) and the highest WS (5.89 gm.). Meanwhile, this cross recorded the lowest NS/P (6.10) because of the earliness in DH. By contrast the cross P4XP6 gave the high yielding GY/P (29.06 gm.). The cross P5XP6 recorded the shortest plant height (94.18 cm.). Moreover, the contrary showed with cross P1XP2 that gave the tallest plant height (113.35 cm.) and the highest value for NST/S (24.82). The cross P2XP5 recorded the lowest values for BY/P (52.51 gm.), GY/P (19.64 gm.) and WG/S (2.76 gm.) while, the highest for HI (37.59 %). The highest values for NS/P (9.63), NG/S (79.34), WG/S (4.35 gm.), BY/P (85.10 gm.) and 1000-GW (58.87 gm.) were recorded for crosses P4XP5, P3XP4, P3XP4, P1XP3 and P2XP3, respectively. The lowest values for SL (11.85 cm.), HI (30.02), WS (4.49 gm.), NST/S (20.15), NG/S (58.45) and 1000-GW (50.67 gm.) were recorded for crosses P1XP6, P1XP2,

P1XP3, P2XP4, P3XP6 and P4XP5, respectively.

**In F<sub>2</sub> generation**, the cross P1XP2 recorded the highest values for NS/P (9.27), BY/P (81.57 gm.) and GY/P (28.42), while recorded the tallest plant height (109.85 cm.). The two crosses P1XP5 and P3XP6 showed the earliest in days to heading (85.33 days), while the cross P1XP5 recorded the lowest values for SL (11.34 cm.), HI (31.07 %), WS (3.52 gm.), NG/S (46.09) and WG/S (2.17 gm.). The cross P3XP5 recorded the highest values for SL (14.75 cm.), WS (5.74 gm.), NG/S (78.07) and WG/S (3.77 gm.) while, recorded the lowest value for NS/P (5.14). The highest values for HI (36.25 %), NST/S (21.66) and 1000-GW (59.01 gm.) were recorded for crosses P4XP6, P1XP3 and P4XP6, respectively. The lowest values for BY/P (45.88 gm.), GY/P (14.57 gm.), NST/S (19.16), WG/S (2.17 gm.) and 1000-GW (43.18 gm.) were recorded for crosses P5XP6, P5XP6, P1XP4, P1XP5 and P2XP5, respectively. It's observed that F<sub>1</sub>'s crosses gave high values for all traits compared to F<sub>2</sub> generation. This may be attributed to the genetic segregation that happened in F<sub>2</sub> generation. These results are in harmony with those obtained by **Motawea (2017)**, **Abdel-Khalik *et al.* (2018)**, **El-Gammaal and Yahya (2018)**, **Hammam *et al.* (2021)**, **Fouad *et al.* (2022)**, **Hassan *et al.* (2022)**, **Yassin *et al.* (2022)** and **Darwish *et al.* (2024)**.

**Table 2. Means of parents, F<sub>1</sub> and F<sub>2</sub> generations for all studied traits.**

Genotype	DH	PH; cm.	SL; cm.	NS/P	BY/P; gm.	GY/P; gm.	HI%	WS; gm.	NST/S	NG/S	WG/S; gm.	1000- GW; gm.
<b>P1</b>	91.33	97.21	11.75	7.50	64.71	22.21	34.32	4.18	21.10	64.43	2.54	48.47
<b>P2</b>	89.33	107.88	13.02	4.20	53.13	15.03	28.28	5.56	18.38	61.82	2.72	51.87
<b>P3</b>	89.33	98.50	12.59	6.00	62.16	22.50	36.15	5.44	19.31	63.14	3.04	52.27
<b>P4</b>	91.33	101.94	12.47	6.53	70.28	20.11	29.05	4.28	18.56	68.23	2.79	51.07
<b>P5</b>	92.67	102.76	11.03	7.30	65.18	21.93	33.93	4.11	20.56	58.62	2.39	46.47
<b>P6</b>	88.33	94.54	11.81	7.27	67.08	23.54	35.15	4.13	20.46	55.76	2.19	50.37
<b>Mean</b>	90.39	100.47	12.11	6.47	63.75	20.89	32.82	4.62	19.73	62.00	2.61	50.08
<b>F<sub>1</sub></b>												
<b>P1 x P2</b>	88.67	113.35	13.53	7.00	82.41	24.72	30.02	5.82	24.82	65.64	3.74	56.27
<b>P1 x P3</b>	86.33	98.88	13.28	8.33	85.10	26.26	30.89	4.49	23.25	61.05	3.46	56.07
<b>P1 x P4</b>	91.67	97.96	12.60	8.37	82.74	27.09	32.74	4.59	23.80	65.64	3.67	55.27
<b>P1 x P5</b>	85.33	102.65	11.97	7.70	68.63	23.32	34.08	4.85	22.47	59.08	3.12	52.27
<b>P1 x P6</b>	83.67	102.62	11.85	7.57	74.41	23.03	30.99	4.93	22.95	58.83	3.19	53.97
<b>P2 x P3</b>	81.33	106.66	14.63	6.10	69.00	23.59	34.27	5.89	23.29	76.74	3.55	58.87
<b>P2 x P4</b>	82.67	111.67	14.52	6.67	62.40	20.92	33.60	5.44	20.15	76.77	3.10	55.97
<b>P2 x P5</b>	82.67	107.88	13.59	6.67	52.51	19.64	37.59	4.58	21.37	60.30	2.76	55.77
<b>P2 x P6</b>	86.67	111.86	13.34	6.53	67.33	20.94	32.03	5.14	20.27	70.15	2.78	55.77
<b>P3 x P4</b>	87.67	104.60	13.80	8.10	83.41	28.17	33.86	5.46	22.64	79.34	4.35	54.47
<b>P3 x P5</b>	90.67	105.57	12.86	7.10	71.05	23.16	32.66	4.53	22.01	71.69	3.56	54.77
<b>P3 x P6</b>	84.33	97.38	12.66	7.43	76.21	23.94	31.47	3.64	21.75	58.45	3.14	52.37
<b>P4 x P5</b>	88.67	101.50	12.59	9.63	74.42	27.85	37.44	4.93	21.34	73.61	3.13	50.67
<b>P4 x P6</b>	84.67	105.14	12.70	8.47	77.70	29.06	37.35	4.64	21.82	72.51	3.19	57.77
<b>P5 x P6</b>	84.67	94.18	11.91	9.50	76.91	26.78	34.80	4.72	21.68	67.96	3.40	51.47
<b>Mean</b>	85.98	104.13	13.05	7.68	73.62	24.56	33.59	4.91	22.24	67.85	3.34	54.78
<b>R.L.S.D 5%</b>	4.57	8.99	7.19	1.21	1.34	0.78	1.20	3.67	0.26	0.03	0.95	5.34
<b>R.L.S.D 1%</b>	6.12	11.90	9.62	1.61	1.79	1.04	1.58	4.83	0.34	0.04	1.25	7.98
<b>F<sub>2</sub></b>												
<b>P1 x P2</b>	91.33	109.85	13.16	9.27	81.57	28.42	34.82	4.22	19.65	68.23	2.97	45.14
<b>P1 x P3</b>	90.67	102.53	13.17	8.40	69.13	24.01	35.25	4.88	21.66	62.67	2.86	48.94
<b>P1 x P4</b>	91.67	99.43	12.63	7.21	62.73	21.47	35.95	4.51	19.16	61.38	2.86	49.85
<b>P1 x P5</b>	85.33	107.71	11.34	7.41	58.29	17.62	31.07	3.52	19.83	46.09	2.17	52.35
<b>P1 x P6</b>	85.67	100.28	12.49	8.40	76.17	26.44	35.23	4.40	19.44	58.39	3.14	52.88
<b>P2 x P3</b>	91.00	103.22	14.16	6.71	68.32	23.24	34.16	5.59	21.54	63.34	3.43	55.60
<b>P2 x P4</b>	95.67	108.42	14.20	7.59	68.20	24.22	35.50	4.77	20.28	68.99	3.42	48.93
<b>P2 x P5</b>	91.33	107.37	12.80	7.08	62.58	21.02	33.82	4.27	21.02	69.26	2.65	43.18
<b>P2 x P6</b>	95.67	102.99	12.94	6.42	63.55	20.08	32.26	4.68	20.25	67.67	2.92	46.20
<b>P3 x P4</b>	97.67	96.17	13.80	6.57	71.00	23.29	33.29	5.52	20.61	76.93	3.54	48.07
<b>P3 x P5</b>	94.67	98.69	14.75	5.14	55.86	19.94	35.67	5.74	21.10	78.07	3.77	48.88
<b>P3 x P6</b>	85.33	90.23	11.95	5.17	53.57	17.33	32.66	4.92	20.31	61.34	3.07	53.88
<b>P4 x P5</b>	98.00	101.82	12.94	6.18	57.28	19.44	34.00	4.62	20.24	58.95	3.00	54.58
<b>P4 x P6</b>	96.33	103.26	13.61	7.36	67.88	24.32	36.25	4.99	19.97	61.20	3.32	59.01
<b>P5 x P6</b>	91.00	96.54	11.54	5.33	45.88	14.57	31.54	4.17	19.50	60.83	2.50	46.14
<b>Mean</b>	92.09	101.90	13.03	6.95	64.13	21.69	34.10	4.72	20.30	64.22	3.04	50.24
<b>R.L.S.D 5%</b>	4.81	10.90	7.94	1.13	0.70	0.68	0.92	8.24	0.47	6.96	4.68	16.34
<b>R.L.S.D 1%</b>	6.36	14.42	10.63	1.49	0.92	0.90	1.21	10.91	0.63	9.43	6.26	26.52

## 2- Genetic components and heritability

The estimates of the genetic components of variance in accordance with Hayman analysis for tested traits in F<sub>1</sub> and F<sub>2</sub> generations are presented in Tables (3) and (4). Estimates of the environmental variance (E) were significant (P < 0.05 or 0.01) for

days to 50% heading, spike length, grain yield/plant, harvest index and weight of grains/spike in F<sub>1</sub>, and harvest index in F<sub>2</sub>, indicating that these traits have been affected by environmental factors. Additive components of genetic variability (D) were positive and significant (P < 0.05 or 0.01) for number of grains/spike, grain yield/plant,

harvest index, 1000 grain weight and weight of spike in  $F_1$  and spike length, weight of spike and number of spikelets/spike in  $F_2$ . This indicates the relevance of additive variance and selection for these characters in segregating generations would be effective. The component F was positive but not significant for GY/P, HI, WS and NST/S in  $F_1$  and DH, SL, NS/P, BY/P, GY/P, WS, WG/S, NST/S and 1000-GW in  $F_2$  which exhibited that the alleles distribution in the parents was unknown. While the rest traits exhibited negative F value indicated that recessive alleles were more frequent in the rest traits. SL, HI and NST/S in  $F_2$  and all traits except spike length in  $F_1$  exhibited positive and significant ( $P < 0.05$  or  $0.01$ ) estimates for the dominance component ( $H_1$ ) and greater in magnitude compared to the D estimates. Significant ( $P < 0.05$  or  $0.01$ ) estimates for dominance components related to gene distribution ( $H_2$ ) were exhibited for all tested traits excluding spike length and harvest index in  $F_1$ , while in  $F_2$ , SL and NST/S exhibited positive and significant estimates for the dominance component and greater in magnitude compared to the D estimates, suggesting that the dominant form of gene action was the most prevalent genetic component in how these traits are inherited. The estimates of  $H_1$  were greater than the  $H_2$  estimates for all traits in both generations, suggesting that the parents' allele frequencies were not equal. This observation is consistent with the findings by **Hayman (1954 b)**. Heterozygous loci's overall dominance effects ( $h^2$ ) demonstrated significant ( $P < 0.05$  or  $0.01$ ) for tested traits excluding harvest index and weight of spike in  $F_1$  while negative and insignificant for all tested traits except harvest index in  $F_2$ , suggesting that since homozygosity was the cause of the dominance, the most frequent factor influencing the inheritance of previous traits was additive gene action. These results agree with those mentioned by **EL-Hosary and Gehan Nour El Deen**

**(2015), Afridi *et al.* (2018), El-Gammaal and Yahya (2018), Al-Timimi *et al.* (2020) and Kumar *et al.* (2023)**. For all tested traits in two generations, the dominance average degree  $(H_1/D)^{0.5}$  was found higher than unity, suggesting the existence of certain traits over dominance. Whenever positive and negative alleles are evenly distributed in the parental varieties, the ratio of  $H_2/4H_1$  is expected to be 0.25. The estimates of  $H_2/4H_1$  were found near to this value (0.25) for the most traits; indicating that positive and negative alleles are similarly distributed between the parents for these traits. The dominant ratio to recessive genes (KD/KR) was larger than unity for GY/P, HI, WS and NST/S in  $F_1$  and for SL, WS, NST/S and WG/S in  $F_2$ , furthermore, confirming that the parental cultivars for these traits have more dominant than recessive genes. The estimates of broad sense heritability were high for all traits excluding SL and HI in  $F_1$ , and moderate for SL, WS and NST/S in  $F_2$ . Hence, the genetic system that controls these characters might be explained by the additive effects of genes. Subsequently, pedigree selection program for these traits would be more suitable for other characters; low narrow sense heritability was determined. Consequently, breeding programs towards pure line selections appeared pointless. Thus, the bulk method for these characters might be quite promising. These findings are consistent with **Afridi *et al.* (2018), El-Gammaal and Yahya (2018), Al-Timimi *et al.* (2020), Abd El-Aty *et al.* (2024) and Darwish *et al.* (2024)**.

**Table 3. Haymans analysis for all studied traits in F<sub>1</sub> generation.**

component	DH	PH	SL	NS/P	BY/P	GY/P	HI	WS	NST/S	NG/S	WG/S	1000-GW
E	3.78**±0.82	6.28±2.69	0.63**±0.04	0.22±0.1	15.8±10.08	1.71**±0.29	3.67*±0.9	0.07±0.04	0.34±0.39	10.61±5.47	0.05*±0.01	0.1±0.24
D	-1.09±2.16	16.12±7.11	-0.11±0.1	1.33**±0.27	18.61±26.66	7.77**±0.78	7.29*±2.39	0.40*±0.11	0.95±1.03	8.68±14.47	0.05±0.03	4.84**±0.64
F	-6.17±5.28	-17.98±17.36	-1.40**±0.25	-0.41±0.66	-31.92±65.13	0.45±1.89	16.1±5.85	0.17±0.27	0.31±2.52	-16.2±35.36	-0.1±0.08	-0.66±1.56
H <sub>1</sub>	29.38**±5.49	52.00*±18.04	-0.4±0.25	1.99*±0.68	203.56*±67.68	24.21**±1.97	25.65*±6.08	0.85*±0.28	7.91*±2.62	123.55*±36.74	0.61**±0.08	25.26**±1.62
H <sub>2</sub>	30.19**±4.9	45.88*±16.11	-0.29±0.23	1.89*±0.61	172.59*±60.46	21.35**±1.76	13.78±5.43	0.73*±0.25	6.94*±2.34	96.00*±32.82	0.60**±0.07	24.09**±1.45
h <sup>2</sup>	51.95**±3.3	33.63*±10.85	2.12**±0.15	3.95**±0.41	261.32**±40.69	36.59**±1.18	-0.39±3.65	0.2±0.17	17.34**±1.57	89.17*±22.09	1.46**±0.05	61.22**±0.98
(H <sub>1</sub> /D) <sup>0.5</sup>	5.19	1.80	1.89	1.22	3.31	1.77	1.88	1.46	2.88	3.77	3.61	2.28
H <sub>2</sub> /4H <sub>1</sub>	0.26	0.22	0.18	0.24	0.21	0.22	0.13	0.21	0.22	0.19	0.25	0.24
KD/KR	0.29	0.53	-0.54	0.78	0.59	1.03	3.86	1.34	1.12	0.60	0.55	0.94
h <sup>2</sup> (n.s)	0.16	0.53	0.51	0.57	0.41	0.42	0.18	0.41	0.28	0.43	0.28	0.35
h <sup>2</sup> (b.s)	0.72	0.83	0.45	0.86	0.84	0.86	0.58	0.83	0.88	0.83	0.83	0.99
r	0.80	-0.94	-0.72	-0.41	-0.69	-0.60	-0.88	0.62	-0.93	-0.51	0.25	-0.96
r <sup>2</sup>	0.64	0.89	0.52	0.17	0.48	0.35	0.78	0.39	0.87	0.26	0.06	0.92
t <sup>2</sup>	1.21	0.95	0.17	0.62	1.24	0.28	0.92	0.09	1.97	6.10	4.05	3.32
b	0.49	0.56	0.82	0.48	0.10	1.03	1.00	0.65	0.42	0.24	0.21	1.23

\* p> 0.05; \*\* p> 0.01

Where: E= the expected environmental component of variation, D= Variation due to additive effect, F= Refers to relative frequencies of dominant Vs recessive genes in the parents, H<sub>1</sub> = component of variation due to dominance effects, H<sub>2</sub> = Component of variation due to non-additive effects, h<sup>2</sup>= Overall dominance gene effects of the heterozygous loci in all crosses, (H<sub>1</sub>/D)<sup>0.5</sup> = mean degree of dominance at each locus over all loci, H<sub>2</sub>/4H<sub>1</sub> = measures the average frequency of positive versus negative alleles at loci exhibiting dominance, KD/KR = the ratio of total number of dominant to recessive alleles in the parents, h<sup>2</sup> (b.s) = broad sense heritability and h<sup>2</sup> (ns) = narrow sense heritability.

**Table 4. Haymans analysis for all studied traits in F<sub>2</sub> generation.**

component	DH	PH	SL	NS/P	BY/P	GY/P	HI	WS	NST/S	NG/S	WG/S	1000-GW
<b>E</b>	2.95±6.72	7.36±4.11	0.07±0.11	0.2±0.54	15.46±40.43	2.48±5.52	11.56**±1.07	0.06±0.04	0.11±0.06	8.58±11.88	0.03±0.04	4.7±7.12
<b>D</b>	6.15±17.78	13.18±10.87	1.79**±0.29	1.89±1.43	108.21±106.97	3.63±14.6	-7.76±2.84	0.53**±0.11	1.43**±0.15	31.02±31.43	0.16±0.12	4.71±18.84
<b>F</b>	47.71±86.5	-11.75±52.88	1.58±1.4	8.4±6.97	655.64±520.57	37.91±71.07	-26.75±13.82	0.29±0.55	2.03**±0.72	-43.77±152.94	0.04±0.58	42.24±91.68
<b>H<sub>1</sub></b>	287.68±180.5	143.29±110.33	8.92**±2.92	29.93±14.55	2112.94±1086.21	228.9±148.29	-134.76**±28.85	2.04±1.15	5.43**±1.49	436.02±319.13	1.35±1.21	287.99±191.3
<b>H<sub>2</sub></b>	182.07±161.24	89.94±98.56	7.35**±2.61	16.72±12.99	1181.62±970.34	148.87±132.47	-91.62**±25.77	1.3±1.03	3.35±1.33	430.66±285.09	1.13±1.08	220.33±170.89
<b>h<sup>2</sup></b>	-27.94±108.53	-83.58±66.34	-0.33±1.76	-1.75±8.75	-205.91±653.1	-17.64±89.16	-120.15**±17.34	-0.65±0.69	-1.35±0.9	-112.64±191.88	-0.26±0.73	-61.79±115.02
<b>(H1/D)<sup>0.5</sup></b>	6.84	3.30	2.23	3.98	4.42	7.95	4.17	1.96	1.95	3.75	2.86	7.82
<b>H<sub>2</sub>/4H<sub>1</sub></b>	0.16	0.16	0.21	0.14	0.14	0.16	0.17	0.16	0.15	0.25	0.21	0.19
<b>KD/KR</b>	-15.90	0.57	2.31	-18.08	-6.39	-7.33	0.09	1.77	6.41	0.45	1.17	-14.65
<b>h<sup>2</sup><sub>(n.s)</sub></b>	0.09	0.16	0.51	0.32	0.29	0.07	0.00	0.47	0.65	0.16	0.28	0.06
<b>r</b>	0.28	-0.89	0.32	-0.64	0.16	-0.77	-0.92	0.13	-0.45	-0.77	-0.17	-0.08
<b>r<sup>2</sup></b>	0.08	0.79	0.10	0.40	0.03	0.59	0.85	0.02	0.21	0.60	0.03	0.01
<b>t<sup>2</sup></b>	0.09	0.33	2.07	0.06	0.04	5.51	1.14	0.57	0.30	2.93	2.45	1.84
<b>b</b>	-0.20	0.86	0.33	0.79	0.23	-0.06	0.69	0.63	0.75	0.42	0.24	0.07

\* = The h<sup>2</sup>(n.s) value was set to zero when estimated turned out to be a negative.



### 3- Phenotypic and genotypic correlation

Phenotypic and genotypic association coefficients among the tested traits for the 21 genotypes in F<sub>1</sub> generation appeared in Table 5. Days to heading showed intermediate negative significant ( $P < 0.01$  or  $0.05$ ) phenotypic and genotypic association with SL (-0.52 and -0.64) and 1000-GW (-0.60 and -0.68). On the other hand, weak positive phenotypic and genotypic association were found between DH and BY/P by (0.06 and 0.04). Days to 50% heading showed weak negative phenotypic and genotypic association coefficients with the rest traits. Plant height showed positive phenotypic and genotypic association with SL (0.73 and 0.76), spike weight (0.68 and 0.74), NG/S (0.58 and 0.77) and 1000-GW (0.53 and 0.59). However, Plant height showed negative high significant genotypic association with NS/P (-0.57) and NST/S (-0.97). While PH exhibited negative phenotypic and genotypic association with BY/P, GY/P and HI.

Spike length showed positive significant ( $P < 0.01$  or  $0.05$ ) phenotypic and genotypic correlation with WS (0.75 and 0.76), NG/S (0.58 and 0.77), WG/S (0.49 and 0.59) and 1000-GW (0.79 and 0.91). Moreover, weak negative phenotypic and genotypic association found between SL and NS/P (-0.32 and -0.37) and GY/P (-0.04 and -0.06). Number of spikes/plant showed positive significant ( $P < 0.01$  or  $0.05$ ) phenotypic and genotypic association coefficient with BY/P (0.71 and 0.77), GY/P (0.87 and 0.92) and NST/S (0.52 and 0.52). Moreover, weak negative phenotypic and genotypic association found between NS/P and WS (-0.27 and -0.46) and 1000-GW (-0.08 and -0.08). While positive phenotypic and genotypic association coefficients was found between NS/P and the other traits, HI, NST/S, NG/S and WG/S. Biological yield/plant exhibited strong positive high

significant phenotypic and genotypic association with GY/P (0.84 and 0.89), NST/S (0.68 and 0.79) and WG/S (0.68 and 0.75). Moreover, biological yield/plant showed weak positive genotypic association coefficient with HI by (0.08), NG/S (0.24) and 1000-GW (0.28).

Grain yield per plant exhibited positive significant ( $P < 0.05$  or  $0.01$ ) phenotypic and genotypic association with HI (0.44 and 0.51), NST/S (0.64 and 0.66) and WG/S (0.58 and 0.60). Weak positive phenotypic and genotypic association were found for grain yield/plant with each of NG/S (0.33 and 0.33), and 1000-GW (0.22 and 0.22). Harvest index exhibited weak positive phenotypic and genotypic association with NST/S (0.06 and 0.03) and NG/S (0.17 and 0.23). While weak negative phenotypic and genotypic association was found between harvest index and WS (-0.06 and -0.13), WG/S (-0.07 and -0.14) and 1000-GW (-0.01 and -0.01). Spike weight showed intermediate positive significant ( $P < 0.01$  or  $0.05$ ) genotypic association with NG/S (0.59), WG/S (0.54) and 1000-GW (0.57). Spikelets/spike exhibited intermediate positive significant ( $P < 0.01$  or  $0.05$ ) phenotypic and genotypic association with WG/S (0.66 and 0.71) and 1000-GW (0.48 and 0.50). Grains per spike exhibited intermediate positive significant ( $P < 0.01$  or  $0.05$ ) phenotypic and genotypic association with WG/S (0.55 and 0.59) and 1000-GW (0.46 and 0.47). Intermediate positive significant ( $P < 0.01$ ) phenotypic and genotypic association was found between WG/S and 1000-GW (0.59 and 0.60). Our results agree with those obtained by **AbdulHamid et al. (2017)**, **Sabit et al. (2017)**, **Fouad (2018)**, **Elmassry and El Shal (2020)**, **Haridy et al. (2021)**, **Hammam et al. (2021)**, **Haleem et al. (2022)**, **Jocković et al. (2022)**, **Singh et al. (2023)** and **Saini et al. (2024)**.

**Table 5. Genotypic and phenotypic association coefficients among the studied traits in F<sub>1</sub> generation.**

Trait	R	DH	PH	SL	NS/P	BY/P	GY/P	HI	WS	NST/S	NG/S	WG/S
<b>PH</b>	rg	-0.24										
	rp	-0.32										
<b>SL</b>	rg	-0.64**	0.76**									
	rp	-0.52*	0.73**									
<b>NS/P</b>	rg	0.00	-0.57**	-0.37								
	rp	-0.10	-0.43	-0.32								
<b>BY/P</b>	rg	0.04	-0.25	0.05	0.77**							
	rp	0.06	-0.27	-0.07	0.71**							
<b>GY/P</b>	rg	-0.08	-0.39	-0.06	0.92**	0.89**						
	rp	-0.08	-0.32	-0.04	0.87**	0.84**						
<b>HI</b>	rg	-0.30	-0.35	-0.17	0.59**	0.08	0.51*					
	rp	-0.27	-0.12	0.04	0.41	-0.54*	0.44*					
<b>WS</b>	rg	-0.33	0.74**	0.76**	-0.46*	-0.07	-0.10	-0.13				
	rp	-0.28	0.68**	0.75**	-0.27	-0.07	-0.07	-0.06				
<b>NST/S</b>	rg	-0.26	-0.97**	0.20	0.52*	0.79**	0.66**	0.03	0.14			
	rp	-0.31	0.99**	0.21	0.52*	0.68**	0.64**	0.06	0.18			
<b>NG/S</b>	rg	-0.21	0.77**	0.77**	0.15	0.24	0.33	0.23	0.59**	0.09		
	rp	-0.12	0.58**	0.58**	0.15	0.24	0.33	0.17	0.52*	0.11		
<b>WG/S</b>	rg	-0.23	0.21	0.59**	0.33	0.75**	0.60**	-0.14	0.54*	0.71**	0.59**	
	rp	-0.19	0.15	0.49*	0.35	0.68**	0.58**	-0.07	0.42	0.66**	0.55**	
<b>1000-GW</b>	rg	-0.68**	0.59**	0.91**	-0.08	0.28	0.22	-0.01	0.57**	0.50*	0.47*	0.60**
	rp	-0.60**	0.53*	0.79**	-0.08	0.26	0.22	-0.01	0.51*	0.48*	0.46*	0.59**

\*,\*\* significant at 0.05 and 0.01 level of probability, respectively.

#### 4- Path analysis

Path coefficient analysis aids in estimating the influence of each variable upon the resultant variable directly as well as indirectly by partitioning the genetic correlation coefficients. It offers a good approach to identify both direct and indirect causes of association. The coefficients of determination were calculated for the indirect and direct effects of the twelve yield studied factors and transformed into percentage in order to evaluate these factors for their importance as sources of variation in grain yield Table (6).

Genotypic path coefficient analysis showed that the direct effect of days to heading on grain yield/plant was 0.054, while the indirect effects of the other traits by days to heading were -0.039 of PH, 0.033 of SL, 0.001 of NS/P, 0.030 BY/P, -0.150 of HI, -0.003 of WS, 0.081 of NST/S, 0.056 of NG/S, -0.090 of WG/S and -0.057 of 1000-GW. Plant height exhibited a positive direct effect on grain yield/plant (0.160). Furthermore, its indirect effects on grain yield/plant were negative via all other traits except WS (0.006), WG/S (0.084) and 1000-GW (0.049). on the other hand, spike length exhibited negative direct effect on grain yield/plant. Moreover, its indirect effects on grain yield/plant were positive for PH (0.122), BY/P (0.031), WS (0.006), WG/S (0.237) and 1000-GW (0.077), and negative for DH (-0.035), NS/P (-0.096), HI (-0.083), NST/S (-0.064) and NG/S (-0.204). The direct effect of NS/P on grain yield/plant was 0.262. Its indirect effects on grain yield/plant were -0.092, 0.019, 0.521, 0.291, -0.004, -0.163, -0.039, 0.133 and -0.007 for PH, SL, BY/P, HI, WS, NST/S, NG/S, WG/S and 1000-GW, respectively. Biological yield/plant exhibited high positive direct effect on grain yield/plant (0.68). Its indirect effects on grain yield were positive for DH (0.002), NS/P (0.2), HI (0.039), WG/S (0.302) and 1000-GW (0.024), and negative for the rest traits. Harvest index exhibited positive direct effect on grain yield/plant (0.954). Its indirect effects on grain yield were positive only for SL (0.009), NS/P (0.154) and BY/P

(0.053), but its negative and negligible for the rest traits. Weight of spike showed low direct effect on grain yield/plant (0.008). Its indirect effects for weight of spike on grain yield were positive via PH (0.118), WG/S (0.215) and 1000-GW (0.048), and negative via the rest traits. The direct effect of number of spikelets/spike (-0.314) and number of grains/spike (-0.265) on grain yield/plant were negative. The indirect effects of the two previous traits on grain yield were positive for PH (0.01 and 0.074), NS/P (0.136 and 0.038), BY/P (0.536 and 0.166), HI (0.014 and 0.113), WS (0.01 and 0.005), WG/S (0.286 and 0.238) and 1000-GW (0.042 and 0.04), respectively. The direct effect of WG/S on grain yield/plant was 0.401. Its indirect effects on grain yield/plant were -0.012, 0.033, -0.031, 0.087, 0.512, -0.069, 0.004, -0.224, -0.157 and 0.05 for DH, PH, NS/P, SL, BY/P, HI, WS, NST/S, NG/S and 1000-GW, respectively. 1000 grain weight showed positive direct effect on grain yield/plant (0.084). Moreover, its indirect effects on grain yield/plant were positive for PH (0.094), BY/P (0.192), WS (0.004) and WG/S (0.240), and negative for DH (-0.037), SL (-0.048) NS/P (-0.022), HI (-0.005), NST/S (-0.157) and NG/S (-0.125). Comparable findings were noted by **AbdulHamid et al. (2017)**, **Mecha et al. (2017)**, **Sabit et al. (2017)**, **Fouad (2018)**, **Elmassry and El Shal (2020)**, **Singh et al. (2023)** and **Saini et al. (2024)**.

In path analysis, the residual effect establishes how well the constituent (independent) variables explain the variance in the dependent variable, which is the grain yield/plant. (**Singh and Chaudhary, 1985**). For this reason, the residual effect in the current study was 0.00105, indicating that 99.9% of the variation in grain yield was explained by the contributing factors. This further elucidated that the choice of yield attributing traits in the study was quite perfect.

**Table 6. Estimates of genotypic path coefficient (direct effect and indirect effect) of different eleven traits on grain yield/plant of parents and F<sub>1</sub> crosses.**

Traits	DH	PH	SL	NS/P	BY/P	HI	WS	NST/S	NG/S	WG/S	1000-GW	rp
<b>DH</b>	<b>0.054</b>	-0.039	0.033	0.001	0.030	-0.150	-0.003	0.081	0.056	-0.090	-0.057	-0.083
<b>PH</b>	-0.013	<b>0.160</b>	-0.040	-0.150	-0.170	-0.172	0.006	-0.020	-0.123	0.084	0.049	-0.390
<b>SL</b>	-0.035	0.122	<b>-0.052</b>	-0.096	0.031	-0.083	0.006	-0.064	-0.204	0.237	0.077	-0.060
<b>NS/P</b>	0.000	-0.092	0.019	<b>0.262</b>	0.521	0.291	-0.004	-0.163	-0.039	0.133	-0.007	0.921
<b>BY/P</b>	0.002	-0.040	-0.002	0.200	<b>0.680</b>	0.039	-0.001	-0.247	-0.065	0.302	0.024	0.893
<b>HI</b>	-0.016	-0.056	0.009	0.154	0.053	<b>0.495</b>	-0.001	-0.009	-0.060	-0.056	-0.001	0.512
<b>WS</b>	-0.018	0.118	-0.040	-0.121	-0.047	-0.064	<b>0.008</b>	-0.043	-0.155	0.215	0.048	-0.100
<b>NST/S</b>	-0.014	0.010	-0.011	0.136	0.536	0.014	0.001	<b>-0.314</b>	-0.023	0.286	0.042	0.665
<b>NG/S</b>	-0.011	0.074	-0.040	0.038	0.166	0.113	0.005	-0.027	<b>-0.265</b>	0.238	0.040	0.329
<b>WG/S</b>	-0.012	0.033	-0.031	0.087	0.512	-0.069	0.004	-0.224	-0.157	<b>0.401</b>	0.050	0.595
<b>1000-GW</b>	-0.037	0.094	-0.048	-0.022	0.192	-0.005	0.004	-0.157	-0.125	0.240	<b>0.084</b>	0.221
<b>Residual effect</b>	0.00105											

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## تقدير المكونات الوراثية والارتباط ومعامل المرور في بعض التراكيب الوراثية لقمح الخبز

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استخدم ستة أصناف من قمح الخبز في تحليل الهجن النصف دائرية خلال ثلاث مواسم متتالية ٢٠٢٠/٢٠٢١، ٢٠٢١/٢٠٢٢، ٢٠٢٢/٢٠٢٣ لدراسة بعض المكونات الوراثية والارتباطات ومعاملات المرور. أشارت النتائج إلى أن الصنف مصر ٣ هو الأكثر تكبيراً في طرد السنابل والأقصر طولاً والأعلى في محصول الحبوب. أظهرت الهجن (P4xP6, P3xP4, P4xP5, P1xP4, P5xP6) أعلى محصول حبوب للنبات في الجيل الأول بينما أظهرت الهجن (P1xP2, P1xP6, P4xP6, P2xP4, P1xP3) أعلى محصول حبوب للنبات في الجيل الثاني. أظهر محصول الحبوب للنبات ارتباط موجب ومعنوي على المستوي المظهري والوراثي مع عدد السنابل/نبات والمحصول البيولوجي/نبات ودليل الحصاد وعدد السنييلات/سنبلة ووزن الحبوب/سنبلة. أظهر تحليل المرور تأثيرات مباشرة عالية وموجبة على محصول الحبوب/نبات عن طريق المحصول البيولوجي/نبات ودليل الحصاد ووزن الحبوب/سنبلة وعدد السنابل/نبات وطول النبات ووزن ١٠٠٠ حبة وعدد الأيام للترهير. وظهرت تأثيرات غير مباشرة موجبة عالية لصفات طول السنبلة وعدد السنابل/نبات والمحصول البيولوجي/نبات وعدد السنييلات/سنبلة ووزن السنبلة ووزن الحبوب/سنبلة ووزن ١٠٠٠ حبة على محصول الحبوب للنبات من خلال محصول الحبوب/سنبلة. مما يدل على أهميتها كصفات انتخابية في تحسين محصول حبوب القمح.