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التحليل الوراثي و تحليل المكونات الرئيسية للنمو والمحصول ومكوناته في هجن القمح في الجيلين (الأول والثاني)

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Genetical and Principal Component Analyses for Growth, Yield and Yield Components of Wheat (*Triticum aestivum* L.) Genotypes in F1 and F2 Generations

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الملخص:

أُستخدمت ثمانية تراكيب وراثية من قمح الخبز متباعدة وراثيًا وتم تنفيذ جميع التهجينات الممكنة بطريقة التهجين نصف الدائري لإنتاج 28 هجين بهدف التحليل الوراثي والمكونات الوراثية للنمو والمحصول ومكوناته في بعض هجن القمح، بالإضافة إلى تقدير طبيعة العلاقات الارتباطية بين صفة المحصول وبعض الصفات الاقتصادية الأخرى للاستفادة منها في برامج تحسين القمح.

أظهر تحليل التباين وجود فروق معنوية عالية بين التراكيب الوراثية (الأباء والهجن) في كلا الجيلين في جميع الصفات المدروسة مما يدل على وجود تنوع وراثي واسع يمكن استغلاله في برامج التحسين الوراثي._أظهرت النتائج أن المكون المضيف (D) كان معنوى أو عالى المعنوية لكل الصفات تحت الدراسة لكلا الجيلين ما عدا صفة عدد حبوب السنبلة فى الجيل الأول ، وبالنسبة للمكون السيادى (H1) كان معنوي أو عالي المعنوية لكل الصفات المدروسة أما بالنسبة للمكون السيادي (H2) كان معنوي أو عالي المعنوية لكل الصفات المدروسة ما عدا صفة محصول حبوب النبات فى الجيل الأول والجيل الثانى و صفة طول النبات في الجيل الثاني، كما أظهرت النتائج أن قيمة المكون السيادى (H2) كانت أقل من المكون السيادى (H1) لكل الصفات المدروسة فى كلا الجيلين مما يدل على عدم تساوي تكرار الأليلات الموجبة والسالبة التي تتحكم في هذه الصفات وهذه النتائج تدل على أن وراثة هذه الصفات تعتمد على كل من الفعل المضيف والسيادي.تراوحت درجة التوريث بالمعنى الواسع بين 92.46 و98.92% في الجيل الأول، وبين 91.14

و98.65% في الجيل الثاني، ما يشير إلى أن معظم التباين الظاهري ناتج عن عوامل وراثية.بناءً على نتائج PCA كان تحليل PCA مفيدًا في تحديد الآباء P2 و P4 و P6 و هجن الجيل الأول (C2 و C14 و C20 و C11 و C3) وهجن الجيل الثانى (H2 و H4 و H3 و H15 و H14) كأفضل التراكيب الوراثية مع أكبر إمكانية لإنتاج قمح عالي المحصول في هذه الدراسة. وبالتالي يمكن استخدام هذه التراكيب الوراثية في برامج التربية المستقبلية لزيادة محصول حبوب القمح عبر البيئات المختلفة.

الكلمات المفتاحية . تحليل التباين ، التراكيب الوراثية ،الاباء ، الهجن

Abstract:

Eight bread wheat genotypes were crossed using a half diallel design to explore the genetic patterns of grain yield and several agronomic characteristics in the F1 and F2 generations. The additive genetic variance (D) showed significant effects for all studied traits in both generations, except for the number of kernels per spike in F1. The dominance variance (H1) was significant for all traits in both generations, while the second dominance component (H2) was significant for all traits except grain yield per plant in F1 and F2, and plant height in F2. This indicates an unequal distribution of positive and negative alleles among the loci controlling these traits and confirms that both additive and dominance gene actions influence their inheritance. The distribution of positive and negative alleles differed among parents for all evaluated traits. The mean degree of dominance $(H1/D)^{½}$ was below unity for plant height, number of spikes per plant, and spike length, suggesting partial dominance in their inheritance. The ratio of dominant to recessive alleles (KD/KR) exceeded unity for all traits, showing that dominance alleles were more frequent in both generations. The relative frequency of dominant to recessive alleles (F) was significant for all traits except 100-kernel weight, which indicated an equal gene distribution among parents. Broad-sense heritability showed very high values, ranging from 92.46% to 98.92% in F1 and from 91.14% to 98.65% in F2, revealing that most phenotypic variation was genetically controlled. The combination of high broad-sense and moderate narrow-sense heritability indicates that non-additive gene effects contributed substantially to trait variation. Principal Component Analysis (PCA) demonstrated that selecting superior genotypes can enhance yield and its related traits. Based on PCA, parents P2, P4, and P6; F1 crosses C2, C14, C20, C11, and C3; and F2 hybrids H2, H4, H3, H15, and H14 were identified as the best performing genotypes for yield potential. These genotypes are recommended for use in future wheat breeding programs to improve productivity under varying environmental conditions. The results confirm that the studied yield traits in wheat are controlled by both additive and dominance genetic effects. The high heritability values indicate the possibility of achieving successful early selection programs to improve wheat productivity using these superior genetic combinations.

Keywords: Analysis of variance; genotypes; parental; F1and F2 .

Introduction

Wheat (*Triticum aestivum L.*) is one of the most vital cereal crops worldwide and belongs to the *Poaceae* family, which includes several major food plants. In Egypt, wheat is the main staple food for almost the entire population, making it crucial to boost national wheat production by increasing grain yield per unit area .Hybridization serves as the key breeding method to create genetic diversity in wheat. Through crossing genetically different parents, breeders can generate hybrid populations with wide variability, from which favorable gene combinations can be selected for improvement (Singh, 2000). The choice of an appropriate breeding strategy largely depends on accurate knowledge of the genetic structure of the population, including the nature and magnitude of genetic effects influencing various traits. Understanding how genes function, interact, and influence specific agronomic traits helps plant breeders design efficient selection programs. Moreover, evaluating how much of the total variability is genetically controlled and heritability is essential, since successful selection depends mainly on additive genetic variance, environmental impact, and genotype × environment interaction. Previous studies have estimated the types of gene actions and heritability in wheat (Mari *et al.*, 2015; El-Hosary and Gehan, 2015; Pavlovic *et al.*, 2016; El-Gammal and Yahya, 2018). Heritability estimates provide valuable guidance for predicting the performance of subsequent generations, making efficient selections, and assessing the potential for genetic improvement.

The main objectives of the present study were to:

1. Estimate the genetic components of variance and heritability (both broad and narrow sense).
2. Conduct Principal Component Analysis (PCA) to evaluate the relationships among yield and its components in *F1* and *F2* wheat generations.

Materials and Methods

Plant Material

Eight bread wheat (*Triticum aestivum L.*) genotypes — Misr-1, Misr-2, Gemmeiza-12, Giza-171, Sakha-94, Sids-14, Line-1, and Line-2 — were selected to represent a wide spectrum of genetic variation. Details about their pedigree, origin, and code numbers are summarized in Table 1.

Table 1 the code number, name, pedigree and origin of the studied parental bread wheat varieties and lines.

Code no.	Genotype	Pedigree	Origin
1	Misr-1	OASIS/SKAUZ//4×BCN/3/2×PASTOR.CMs s00Y01881T-050M-030Y-030M-030WGY-33M- 0Y-0S	Egypt
2	Misr-2	SKAUZ /BAV92 CMSS96 M03611 S- 1M – 010SY-010M -010SY- 8M-0Y -0S.	Egypt
3	Gemmeiza-12	OTUS /3 /SARA /THB /VEE GMSS 97 YOO227S - 5Y-010Y -010M- 2Y - 1M - 0Y -OGM.	Egypt
4	Giza-171	Sakha 93 /Gemmeiza 9 Gzoo3- 101-IGZ - IGZ - 2GZ -0 GZ	Egypt
5	Sakha-94	OPATA/ RAYON// KAUZ. CMBW 90 Y3180- 0 TOPM-010M - 010M -010Y -10M-015Y - 0Y - AP -0S.	Egypt
6	Sids-14	BOW"S"/ VEE"S" //BOW'S'/TSI /3 / BANI SUEF 1SD239-ISD-2SD- 4SD -0SD.	Egypt
7	Line-1	112579.	Egypt
8	Line-2	112706.	Egypt

Experimental Design and Hybridization

The experiment was carried out at the Agronomy Department Farm, Faculty of Agriculture, Al-Azhar University, Nasr City, Cairo, Egypt, across three consecutive seasons (2019/2020, 2020/2021, and 2021/2022). During the first season (2019/2020), all possible crosses among the eight parents (excluding reciprocals) were produced following a half-diallel mating design, yielding 28 *F1* hybrids. In the second season (2020/2021), these *F1* plants, along with their parents, were grown and self-pollinated to obtain *F2* seeds. The third season (2021/2022) involved the evaluation of the parental lines, *F1*, and *F2* generations using a Randomized Complete Block Design (RCBD) with three replications. Each row was 3 meters long, spaced 20 cm apart, with 15 cm between plants within the row. Two rows were used for each parent and *F1* cross, while *F2* populations were grown in 10 rows per replicate. Data were collected from individual plants for yield and related agronomic traits.

-Genetic Components and Heritability

Genetic analysis was performed using Hayman's diallel model (1954a, 1954b) to estimate the key genetic parameters:

- **D:** additive genetic variance
- **H1:** dominance variance
- **H2:** a modified dominance variance accounting for unequal allele frequencies
- **F:** average frequency of dominant vs. recessive alleles

Derived ratios and formulas included:

1- $(H_1/D)^{½}$ = measures the average degree of dominance overall loci, for the F_2, this formula was $(H_1/4D)^{½}$.

When

$(H_1/D)^{½} = 0$ indicates no dominance.

$0 < (H_1/D)^{½} < 1$ indicates partial dominance.

$(H_1/D)^{½} = 1$ indicates complete dominance.

$(H_1/D)^{½} > 1$ indicates over dominance.

2- $(H_2/4H_1)$ = measures the mean value of the product U and V which are the frequencies of positive (U) and negative (V) alleles in the parents. It has a maximum value of 0.25 when P = q = ½

3- $[(4DH_1)^{½} + F/(4DH_1)^{½} - F]$ = KD/KR = refers to the ratio of the total number of dominance to recessive genes in all parents.

$¼\,(4DH_1)^{½} + ½\,F$

For $F_2 = \frac{¼\,(4DH1)^{½} + ½\,F}{¼\,(4DH1)^{½} - ½\,F}$

The least significant difference (LSD) at 5% and 1% levels of probability according to Gomez and Gomez (1984). Broad-sense h^2 (b.s) and narrow-sense h^2 (n.s) heritability were calculated according to Warner (1952) as follows:

h^2 (b.s) = [VF2 – (Vp1 + Vp2 + F1)/3]/VF2

h^2 (n.s) = [2VF2 – (VBC1 + VBC2)]/VF

Principal components analysis (PCA):

Principal component analysis (PCA) was applied for a better understanding of the relationship between studied traits across the parents, F_1 and F_2 crosses. PCA was performed using the computer software programs Origin Pro 2018 b9.5.0.193. The principal component analysis (PCA) method explained by Harman (1976) was followed in the extraction of the components.

Results and Discussion

The analysis of variance (ANOVA) revealed highly significant differences among genotypes, parents, and their crosses for all the studied traits in both *F1* and *F2* generations. This indicates the presence of wide genetic diversity among the tested materials. Moreover, significant differences were also found between parents and crosses for most traits in both generations, except for grain yield per plant. These results suggest that substantial variability exists among the genotypes, providing good opportunities for selection and genetic improvement. The observed variation confirms the efficiency of the crossing design in generating new genetic combinations, which are essential for enhancing yield-related traits in wheat breeding programs. The genetic components and heritability were analyzed using a half-diallel cross following the method described by Hayman (1954a, b). This approach provided six genetic parameters: D, H1, H2, h^2, F, and E (Table 2). In addition, several genetic ratios were calculated according to the procedures outlined by Hayman (1954b) and Jinks (1954) to obtain deeper insights into the inheritance pattern of each trait.

1-Days to Heading (DH)

The various components of genetic variance and their relative contributions for the SL trait in both the *F1* and *F2* generations are shown in Table 2 The genetic analysis for days to heading revealed that the additive component (D) was significant in both *F1* and *F2* generations, confirming that additive gene effects were involved in the inheritance of this trait. Dominance components (H1 and H2), along with the F and h^2 parameters, were also highly significant in both generations. The dominance components were larger than the additive variance, indicating that non-additive gene action predominated in the control of this trait. This agrees with previous findings by Rania El-Said (2018) and Gita Chaudhari *et al.* (2023). For both generations, H2 values were smaller than H1, showing unequal frequencies of alleles among parents, consistent with Hayman's (1954b) observations. The ratio KD/KR exceeded unity, demonstrating that dominant alleles were more common. The significant F-values in both *F1* and *F2* also confirmed unequal allele distribution. Significant dominance effects (h^2) for HD in the F2 generation indicated that heterozygosity played an important and unidirectional role, with strong effects from heterozygous loci. The mean degree of dominance $(H1/D)^{0.5}$ was greater than one, suggesting overdominance for days to heading. Hence, early-generation selection for this trait would be ineffective. Broad-sense heritability was high, indicating strong genetic control; however, the moderate narrow-sense heritability values suggest that much of the variation resulted from non-additive gene action. Hence, selecting any of these traits during the early segregating generations would have limited effectiveness. Heritability estimates in both the broad and narrow sense were calculated for the studied traits following Mather and Jinks (1982). High broad-sense heritability values were recorded for the DH trait, indicating that most of the phenotypic variation was attributed to genetic factors. However, when high broad-sense heritability was accompanied by medium or low narrow-sense heritability in both generations, it suggested that non-additive genetic effects were predominant. These results align with the earlier findings on genetic components, where H1 played a major role in the inheritance of this trait. Therefore, applying the bulk method for improving these traits could be a promising approach, as suggested by Bakhsh *et al.* (2003), Rania El-Said (2018), and El-Hosary (2020).

2-Plant Height (PH)

The various components of genetic variance and their relative contributions for the SL trait in both the *F1* and *F2* generations are shown in Table 2..Analysis of variance for plant height showed that the additive component (D) was significant in both *F1* and *F2*, indicating that additive genetic effects played an important role in inheritance. In the *F1* generation, F, H1, and H2 were all significant, while in *F2*, only H1 remained significant. Unlike the previous trait, dominance effects were smaller than additive ones, suggesting that additive gene action was predominant for plant height. These results agree with those of Ashoush (2006), Seleem and Koumber (2011), and El-Hosary & Nour El-Deen (2015). The H2 values were smaller than H1, confirming unequal allele frequencies among parents. The KD/KR ratio was greater than one, revealing the prevalence of dominant alleles. The mean degree of dominance $(H1/D)^{0.5}$ was less than one in both generations, indicating partial dominance. High heritability in both broad and narrow senses confirmed that most variation in plant height was due to additive genetic effects, suggesting that direct selection for this trait could be effective in early generations. Therefore, this trait may be promising for (Bakhsh *et al*., 2003, Allah *et al*., 2010 and Koumber 2011and EL-Hosary and Gehan Nour El- Deen 2015 and El- Hosary 2020).

3- Number of Spikes per Plant (NSP)

The various components of genetic variance and their relative contributions for the SL trait in both the *F1* and *F2* generations are shown in Table 2. The additive component (D) was significant for the number of spikes per plant in both *F1* and *F2* generations, meaning additive effects influenced this trait. Dominance components (H1 and H2) were also significant and generally greater than the additive component, showing that non-additive gene action was more important. H2 was smaller than H1, indicating unequal allele distribution among parents. Significant dominance effects (h^2) for NSP in the *F2* generation indicated that heterozygosity played an important and unidirectional role, with strong effects from heterozygous loci. The ratio KD/KR exceeded one, implying a higher number of dominant alleles. The mean degree of dominance $(H1/D)^{0.5}$ was less than unity, which points to partial dominance. Therefore, selection for these traits during the early segregating generations would not be effective. High broad-sense heritability values were recorded for the NSP trait, indicating that most of the observed variation in this trait was primarily genetic in nature. The combination of high broad-sense heritability with medium to high narrow-sense values in both generations suggests that non-additive gene actions were predominant. These outcomes align with the genetic component analysis, where the H1 parameter had a major influence on the inheritance of the NSP trait. Consequently, applying the bulk method could be an effective breeding approach for improving this trait (Rania El-Said, 2018; Zaazaa, 2017; El-Hosary, 2020).

4-Spike Length (SL)

The various components of genetic variance and their relative contributions for the SL trait in both the *F1* and *F2* generations are shown in Table 2.The additive variance (D) was significant for spike length in both *F1* and *F2*, indicating additive influence. However, H1 and H2 dominance components were higher, suggesting a stronger role of non-additive gene action. These results agree with Naglaa Qabil (2017) and El-Hosary (2020). Significant dominance effects (h^2) for SL in the F2 generation indicated that heterozygosity played an important and unidirectional role, with strong effects from heterozygous loci .The $H2 < H1$ relationship confirmed unequal allele frequencies, while $KD/KR > 1$ indicated dominance of favorable alleles. The mean dominance degree $(H1/D)^{0.5}$ was below one, implying partial dominance. Therefore, selection for these traits during the early segregating generations would not be effective. High broad-sense heritability values were recorded for the SL trait, suggesting that genetic factors largely contributed to its phenotypic variation. The combination of high broad-sense heritability with medium to high narrow-sense heritability in both generations indicates that non-additive genetic effects were predominant. These outcomes align with the genetic component analysis, where H1 estimates had a major influence on the inheritance of the SL trait. Consequently, using the bulk method for improving this trait appears to be effective, as supported by the findings of Zaazaa (2017), Rania El-Said (2018), El-Hosary (2020), and Mohammed (2020).

5-Number of Kernels per Spike (NKS)

The various components of genetic variance and their relative contributions for the SL trait in both the *F1*and *F2* generations are shown in Table2. The additive variance (D) was significant in *F2* only, showing additive effects mainly expressed in later generations. The dominance variances (H1 and H2) were both significant in *F1* and *F2*, being greater than D, which reflects the dominance nature of inheritance for this trait. These findings are consistent with those reported by Hayman (1954b). The significant overall dominance effects of heterozygous loci (h^2) observed for NKS in the F2 generation suggest that the dominance was mainly due to heterozygosity, showing a clear unidirectional and notable heterozygous influence. The H2 < H1 relationship revealed unequal allele frequencies. KD/KR values above one suggested dominance of positive alleles. The mean dominance value $(H1/D)^{0.5}$ exceeded one, indicating overdominance. High broad-sense heritability values were recorded for the NKS trait, suggesting that most of its phenotypic variation resulted from genetic factors. The occurrence of high broad-sense heritability along with moderate to high narrow-sense values in both generations indicates that non-additive genetic effects were predominant. These results agree with the previous analysis of genetic components, where the H1 estimates showed a major role in controlling the inheritance of this trait. Hence, applying the bulk method could be an effective approach for improving this character (Zaazaa 2017; Rania El-Said 2018; El-Hosary 2020; Mohammed 2020).

6- 100-Kernel Weight (KW)

The different components of the genetic variance and their proportions for KW trait in the *F1* and *F2* generations are presented in Table (2). The additive component (D) reached a significant level of probability for KW in both generations. These results indicate that additive genetic influences were involved in the inheritance of this trait in both generations. Also, f, H1 as well as H2 were significant or highly significant in *F2* generation, while f were not significant in *F1* generation. Dominance components (H1 and H2) were more than additive component in both generations for this trait. This suggests that the non–additive type of genetic action is the most prevalent genetic component in the inheritance of this trait. The genetic variance components and their proportions for the KW trait in both the *F1* and *F2* generations are shown in Table (2).The additive genetic component (D) was statistically significant for KW in both generations, suggesting that additive gene effects play a role in the inheritance of this trait. In the F2 generation, f, H1, and H2 were significant or highly significant, whereas f was not significant in F2. The dominance components (H1 and H2) were greater than the additive component in both generations, indicating that non-additive gene action was the major factor influencing this trait. These outcomes are consistent with the findings of El-Hosary and Gehan Nour El Deen (2015), Rania El-Said (2018), El-Hosary (2020), and Gita Chaudhari et al. (2023).Highly significant H2 values, related to gene distribution, were detected for KW in both generations. The fact that H2 values were smaller than H1 implies unequal allele frequencies among the parents, which aligns with Hayman (1954b). The overall dominance effects (h^2)

were significant for KW in the F2 generation, suggesting that dominance was mainly due to heterozygosity and acted in one direction with noticeable heterotic effects.The KD/KR ratio was greater than one in both generations, meaning that dominant alleles were more influential in controlling the KW trait. The F-values were significant in the F2 generation, showing consistent gene frequency patterns between the parental groups. The mean degree of dominance $(H1/D)^{0.5}$ exceeded one for KW in both generations, pointing to overdominance in this trait. Therefore, selection for KW in early segregating generations would not be very effective. The broad-sense heritability for KW was high, indicating that genetic factors strongly influence this trait. However, the narrow-sense heritability was moderate or low, suggesting that non-additive genetic variance plays a larger role than additive variance. Thus, the additive effect is relatively small. These conclusions are in agreement with the reports of Naglaa Qabil (2017), Zaazaa (2017), Rania El-Said (2018), and El-Hosary (2020). These findings support the above findings on genetic components in which H1 estimates played a greater role in the inheritance of KW trait. Therefore, the bulk method program to improve these traits may be promising for EL-Hosary and Gehan Nour El Deen (2015), Rania El- Said (2018) and El- Hosary (2020).

7- Biological Yield per Plant (BY/P)

The different components of the genetic variance and their proportions for BY/P trait in the *F1* and *F2* generations are presented in Table 2.The additive component (D) reached a significant level of probability for BY/P in both generations. These results indicate that additive genetic influences were involved in the inheritance of this trait in both generations. Also, H1and H2 was highly significant in both generations. Dominance components (H1 and H2) were more than additive component in both generations for this trait .This suggests that the non–additive type of genetic action is the most prevalent genetic component in the inheritance of this trait. These results are in agreement with those reported by Ashoush (2006), Seleem and Koumber (2011), Farshadfar *et al*., (2012).H2 values were smaller than H1 values for BY/P trait indicating unequal allele frequency in the parents. These are in agreement with the results obtained by Hayman (1954b). The overall dominance effects of heterozygous loci (h2) proved significant for BY/P in *F2* generation, indicating that the dominance was due to heterozygosity and was unidirectional with an appreciable heterozygous effect. The proportion of dominant to recessive gene in parents KD / KR were more than unity for BY/ P indicating that the dominant alleles govern these in both generations. The distributions of the relative frequencies of the dominant gene versus the recessive gene (F) were significant for BY/P in *F2*. Statistically significant F-values indicating a consistency in gene frequency were obtained between the two parental populations. The weighted measure of mean degree of dominance $(H1/D)^{0.5}$ exceeded unity for BY /P trait in both generations, indicating an over-dominance of these trait. Thus, selection this trait in the early segregating generations would be of little use for BY/P trait in both generations. High values of heritability in the broad sense were obtained for BY / P trait, revealing that most of the phenotypic variance in the trait was due to genetic causes. High values of broad-sense heritability were shown together with medium values in the narrow sense in both generations, indicating that most of the genetic variances were due to non-additive genetic effects. These findings support the above findings on genetic components in which H1 estimates played a greater role in the inheritance of BY/P trait. Therefore, the bulk method program to improve these traits may be promising for (Bakhsh *et al.*, 2003, Allah *et al.*, 2010 and Koumber 2011 and El- Hosary 2020 and Mohammed (2020).

8- Harvest Index (HI)

The genetic variance components and their proportions for the HI trait in both *F1* and *F2* generations are presented in Table 2. The additive component (D) was statistically significant in both generations, showing that additive genetic effects contributed to the inheritance of this trait. Likewise, the dominance components (H1 and H2) were highly significant in both generations and exceeded the additive component, suggesting that non-additive genetic effects were predominant in controlling this trait. These observations are in line with those of Ashoush (2006), Seleem and Koumber (2011), and Gita Chaudhari *et al.* (2023).The H_2 values were lower than H1 values, indicating unequal frequencies of positive and negative alleles among parents, which agrees with Hayman (1954b). The overall dominance effect (h^2) was significant in the F2 generation, suggesting that heterozygosity had a unidirectional and strong influence on the HI trait.The KD/KR ratios were greater than one in both generations, implying that dominant alleles played a major role in controlling this trait. The f-values, representing the balance between dominant and recessive gene frequencies, were significant in F2, indicating consistency between the two parental populations. The mean degree of dominance $(H1/D)^{0.5}$ exceeded unity in both generations, pointing to over-dominance for HI. Therefore, selecting for this trait in early segregating generations would be ineffective. High broad-sense heritability values were observed, meaning that most phenotypic variation was genetically determined. However, the combination of high broad-sense and medium to low narrow-sense heritability suggested that non-additive effects were the main source of genetic variation. These results reinforce the conclusion that H1 estimates had a larger influence on the inheritance of the HI trait. Consequently, the bulk method appears to be a suitable breeding approach for improving this trait, as supported by Bakhsh *et al.* (2003), Zaazaa (2017), El-Hosary (2020), and Mohammed (2020).

9- Grain Yield per Plant (GY/P)

The genetic variance components and their relative contributions for the GY trait in both F1 and F2 generations are presented in Table 2. The additive variance (D) showed a significant effect for GY in both generations, suggesting that additive gene action played a role in its inheritance. Moreover, the parameters F and H1 were significant or highly significant in both generations. Since the dominance components (H1 and H1) exceeded the additive one, this indicates that non-additive gene effects were predominant in controlling this trait. Similar observations were recorded by El-Hosary and Gehan Nour El Deen (2015), Naglaa Qabil (2017), Rania El-Said (2018) and Gita Chaudhari *et al.* (2023).The smaller H_2 values compared to H1 revealed an unequal distribution of alleles among parents, consistent with the findings of Hayman (1954b). The dominance effect of heterozygous loci (h^2) was significant in the F2 generation, showing that dominance was mainly due to heterozygosity and acted in one direction with a strong heterozygous influence. The ratio of dominant to recessive alleles (K^D/K^R) exceeded one for GY, indicating that dominant alleles were more frequent in both generations. The significant F values for GY in *F1* and *F1* reflected a stable gene frequency across parental lines. The mean degree of dominance $(H1/D)^{0.5}$ being greater than one also suggested over-dominance for this trait. Therefore, selecting for GY in early segregating generations would not be effective. High broad-sense heritability estimates were obtained for GY, showing that most of the observed variation was due to genetic factors. However, the combination of high broad-sense but moderate to low narrow-sense heritability in both generations indicated a strong influence of non-additive effects, with limited additive contribution. These results align with the dominance-related findings (high H1 values) and imply that the bulk breeding method could be beneficial for improving this trait. Similar conclusions were also drawn by Zaazaa (2017), Rania El-Said (2018), El-Hosary (2020) and Mohammed (2020).

Table(2). Hayman's genetic (D, H1, H2, F, h², and E and their derivatives) analysis for all studied traits in the F1 and F2 generations.

component	Days to heading /day(DH)	Plant height in cm (PHcm)	No of spikes / plant (NS/P)	Spike length in cm (SL)	No of kernels / spike (NK/S)	100 kernel weight in g (kw)	Biological yield per plant in g (B.Y/P)	Harvest index (H.I)%	Grain yield per plant in g (G.Y/P)
F_1									
E	**1.22**	**688.09**	**0.38**	**0.04**	**3.2**	**0.03**	**5.16**	**6.81**	**0.8**
D	**93.161****	**472.65****	**12.85****	**7.80****	**217.4**	**0.60****	**288.13****	**395.56****	**23.4****
F	**109.066****	**473.76****	**11.34****	**4.99****	**174.9****	**0.44**	**420.84**	**630.05****	**33.0***
H_1	**127.239****	**276.56****	**11.59****	**7.04****	**273.6***	**0.84****	**881.43****	**754.48****	**76.3****
H_2	**-304.861****	**19.84***	**-15.99****	**-63.94****	**82.1****	**-19.95****	**582.60****	**385.06****	**13.2**
h^2	**47.311****	**688.09**	**1.45**	**0.22**	**41.8**	**0.27**	**14.12**	**8.26**	**-0.1**
s2	**124.198**	**3735.52**	**2.02**	**0.34**	**722.5**	**0.02**	**7525.33**	**2949.65**	**32.7**
Bh2	**99.083**	**97.50**	**96.50**	**99.83**	**97.7**	**99.49**	**97.79**	**96.00**	**97.4**
$(H1/D)^{0.5}$	**1.169**	**0.83**	**0.95**	**0.95**	**1.1**	**1.18**	**1.75**	**1.38**	**1.8**
UV	**-0.599**	**0.15**	**-0.35**	**-2.27**	**0.1**	**-5.94**	**0.17**	**0.13**	**0.0**
KD/KR	**3.007**	**2.41**	**2.74**	**2.02**	**2.1**	**1.90**	**2.43**	**3.72**	**2.3**

r Y& Wr+Vr	**0.317**	**0.36**	**0.04**	**-0.11**	**-0.3**	**0.65**	**0.39**	**0.62**	**0.4**
r^2	**0.101**	**0.13**	**0.00**	**0.01**	**0.1**	**0.42**	**0.15**	**0.39**	**0.1**
h2/H2	**-0.155**	**0.07**	**-0.09**	**0.00**	**0.5**	**-0.01**	**0.02**	**0.02**	**0.0**
h^2b%	**98.55**	**97.54**	**92.46**	**98.92**	**97.26**	**94.57**	**95.67**	**95.81**	**95.64**
h^2n%	**23.89**	**65.63**	**45.24**	**58.54**	**50.03**	**47.80**	**10.27**	**8.29**	**6.12**
F_2									
E	**2.32**	**45.59**	**0.26**	**0.13**	**2.67**	**0.02**	**4.32**	**10.06**	**0.74**
D	**91.74****	**649.58****	**12.94****	**7.71****	**245.57****	**0.60****	**286.80****	**392.31****	**23.94****
F	**146.81****	**335.69**	**12.28****	**8.09****	**221.89****	**0.62***	**340.11****	**467.92****	**26.43****
H_1	**144.42****	**503.12****	**12.37****	**6.55****	**264.93****	**0.97****	**341.68****	**501.14****	**40.59****
H_2	**-314.91****	**403.12**	**-11.27****	**-60.52****	**84.18****	**-16.43****	**148.30****	**310.62****	**-1.46**
h^2	**149.12****	**-4.90**	**11.37****	**7.16****	**176.28****	**1.14****	**237.18****	**131.89***	**36.47****
s2	**115.29**	**12520.05**	**1.59**	**0.28**	**183.23**	**0.01**	**553.14**	**2110.39**	**9.77**
Bh2	**98.16**	**87.10**	**97.34**	**99.31**	**97.88**	**99.48**	**96.12**	**93.07**	**96.32**
$(H1/D)^{0.5}$	**1.26**	**0.88**	**0.98**	**0.92**	**1.04**	**1.27**	**1.09**	**1.13**	**1.30**
UV	**-0.55**	**0.20**	**-0.23**	**-2.31**	**0.08**	**-4.25**	**0.11**	**0.155**	**-0.01**

KD/KR	**4.52**	**1.83**	**2.89**	**3.65**	**2.54**	**2.35**	**3.38**	**3.23**	**2.47**
r Y& Wr+Vr	**0.81**	**0.41**	**0.77**	**0.60**	**0.81**	**0.94**	**0.91**	**0.79**	**0.76**
r^2	**0.66**	**0.16**	**0.60**	**0.36**	**0.66**	**0.88**	**0.83**	**0.63**	**0.58**
h2/H2	**-0.47**	**-0.01**	**-1.01**	**-0.12**	**2.09**	**-0.07**	**1.60**	**0.425**	**-25.04**
h^2b%	**98.21**	**97.74**	**91.14**	**98.65**	**97.08**	**93.66**	**92.12**	**95.55**	**93.86**
h^2n%	**1.57**	**71.68**	**45.45**	**43.10**	**39.95**	**18.43**	**27.03**	**38.86**	**14.97**

-Principle components analysis (PCA):-

Principal Component Analysis (PCA) Principal Component Analysis (PCA) was applied to determine the most promising genotypes and to clarify the relationships among the evaluated traits in the parental and hybrid generations (F1 and F2). Table 3 presents the nine principal components (PCAs) obtained for the studied traits based on the genetic variations among parents and hybrids. The first three components (PCA1, PCA2, and PCA3) had eigenvalues greater than one (3.06, 2.29, and 1.13, respectively) and together accounted for 72.02% of the total variance observed in this study. This indicates that most of the variation represented by these components originated from the genetic differences among the parents, F1, and F2 crosses for the measured traits. In contrast, the remaining six components had eigenvalues below one and explained only 27.98% of the total variation. Overall, the first three axes of the PCA described more than 77.93% of the total variability in the wheat dataset, similar to the results of Fellahi et al. (2018). The first component (PCA1) alone explained 33.98% of the total variation and showed strong positive associations with NKS (0.42), HI (0.41), SL (0.37), GY (0.26), and 100 KW (0.17). The second component (PCA2) accounted for 25.47% of the variance and was positively correlated with BY (0.46), GY (0.44), DH (0.43), NSP (0.39), and 100 KW (0.39). The third component (PCA3) contributed 12.57% of the total variation and had strong positive correlations with 100 KW (0.42), SL (0.37), and NKS (0.35).Because PCA1 and PCA2 had eigenvalues greater than one and together explained more than 59% of the total variability, they were selected for further analysis to evaluate genotype performance and inter-trait relationships. These outcomes align with the findings of Kamara *et al.* (2022) and Shamuyarira *et al.* (2022), who also reported that the first two PCAs captured most of the variation in similar studies.

Table (3). Results of principal component analysis (PCA) for the studied traits in parents and their hybrids (*F1* and *F2*).

Traits	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7	PCA8	PCA9
DH	-0.23	0.43	-0.16	0.48	-0.09	-0.60	0.02	0.36	-0.12
PH	-0.46	0.09	0.10	-0.15	0.38	0.39	0.41	0.52	-0.11
NSP	-0.29	0.39	-0.10	0.50	0.04	0.53	-0.17	-0.44	0.06
SL	0.37	0.30	0.37	0.13	-0.04	-0.05	0.74	-0.28	-0.02
NKS	0.42	0.09	0.35	0.27	-0.35	0.38	-0.26	0.53	-0.02
100 KW	0.17	0.39	0.42	-0.17	0.64	-0.18	-0.41	-0.04	0.03
BY	-0.25	0.46	0.11	-0.49	-0.46	-0.02	-0.03	0.02	0.52

HI	0.41	0.10	-0.56	0.08	0.31	0.10	0.13	0.20	0.58
GY	0.26	0.44	-0.44	-0.38	-0.09	0.16	-0.04	-0.01	-0.61
Eigenvalues	3.06	2.29	1.13	0.71	0.66	0.52	0.36	0.24	0.02
Variance %	33.98	25.47	12.57	7.93	7.33	5.82	3.99	2.67	0.24
Cumulative%	33.98	59.45	72.02	79.95	87.28	93.10	97.09	99.76	100.00

The first two principal components (PCA1 and PCA2) were used to construct a biplot illustrating the relationships among the studied traits and genotypes (Fig. 1). The biplot revealed that most of the examined traits formed acute angles, indicating positive correlations, though the strength and consistency of these associations varied among traits. For instance, strong positive correlations were detected between 100-kernel weight (100-KW) and grain yield (GY), as well as between harvest index (HI) and number of kernels per spike (NKS), and among days to heading (DH), biological yield (BY), and number of spikes per plant (NSP). Conversely, obtuse angles represented negative associations, which also differed in magnitude and stability. Plant height (PH) showed negative relationships with spike length (SL), NKS, HI, and GY. The strong positive correlations observed between NKS, 1000-grain weight, and grain yield emphasize their importance as key traits for indirect selection to improve yield in wheat (Thapa *et al.,* 2018; Qaseem *et al*., 2019; Morsy *et al.,* 2021; Kamara *et al.,* 2022).

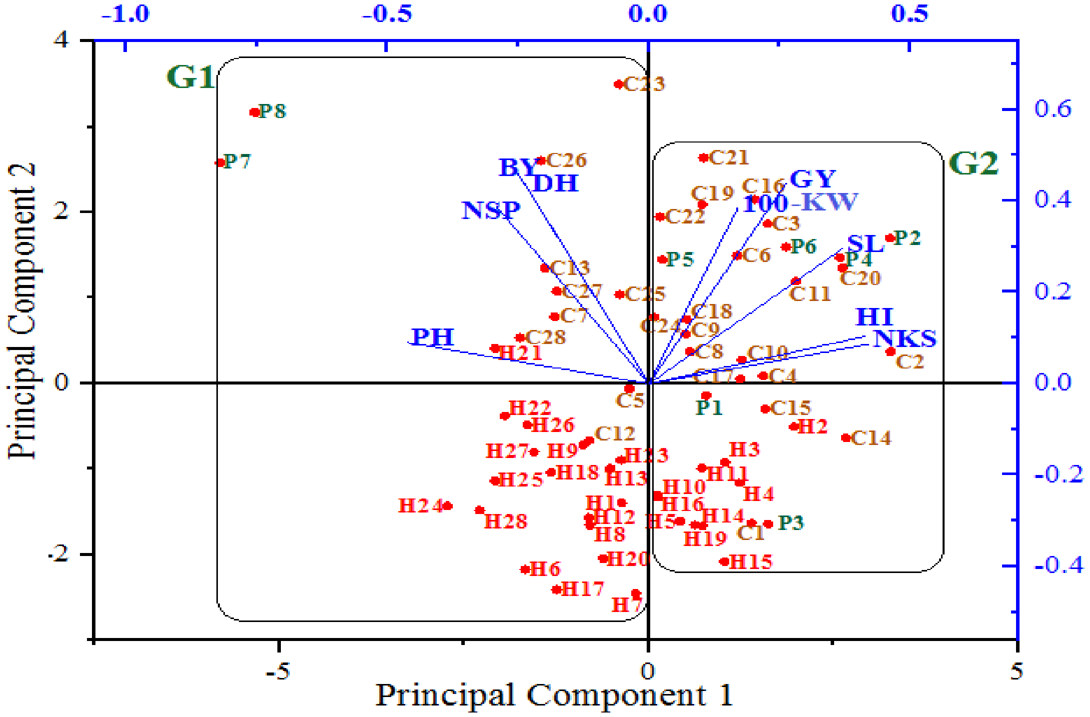

Fig. 1. Biplot diagram based on PC1 and PC2 shows similarities and dissimilarities relationships among the studied traits for the parents (green color), F1 crosses (brown color) and F2 hybrids (red color). The F1 Crosses: C1: P1*P2; C2: P1*P3; C3: P1*P4; C4: P1*P5; C5: P1*P6; C6: P1*P7; C7: P1*P8; C8: P2*P3; C9: P2*P4; C10: P2*P5; C11: P2*P6; C12: P2*P7; C13: P2*P8; C14: P3*P4; C15: P3*P5; C16: P3*P6; C17: P3*P7; C18: P3*P8; C19: P4*P5; C20: P4*P6; C21: P4*P7; C22: P4*P8; C23: P5*P6; C24: P5*P7; C25: P5*P8; C26: P6*P7; C27: P6*P8; C28: P7*P8. The F2 Hybrids: H1: P1*P2; H2: P1*P3;

H3: P1*P4; H4: P1*P5; H5: P1*P6; H6: P1*P7; H7: P1*P8; H8: P2*P3; H9: P2*P4; H10: P2*P5; H11: P2*P6; H12: P2*P7; H13: P2*P8; H14: P3*P4; H15: P3*P5; H16: P3*P6; H17: P3*P7; H18: P3*P8; H19: P4*P5; H20: P4*P6; H21: P4*P7; H22: P4*P8; H23: P5*P6; H24: P5*P7; H25: P5*P8; H26: P6*P7; H27: P6*P8; H28: P7*P8.

As shown in Fig.1, the parents and hybrids (F1 and F2) were primarily distributed and separated into two groups based on the first two PCAs. The first two principal components of each panel were depicted in two dimensional space to show the clustering of wheat genotypes by Muqaddasi *et al*., (2017). The first group (G1) was related to PCA2 (the second and third quarters) and includes BY, DH, NSP and PH traits, which are strongly positively associated with the two parents P7 and P8, some F1 crosses and most F2 hybrids. While the second group is related to PCA1 (the first and fourth quarters) and includes the other traits, which are strongly positively correlated with the other parents, F1 and F2 hybrids in this study. These results indicated the traits studied inside each group introduced a contrasting genetic pattern during the genotypes development in each group. Based on PCA, some crosses may have a positive influence on the grain yield of wheat (Shamuyarira *et al*., 2022).

In the first quarter (the highest PCA1 and PCA2), the parents P2, P4, P5 and P6 as well as some F1 hybrids are related to the traits of GY (C6, C16), 100-KW (C14 and C20), SL (C19), HI (C6 and C11) and NKS (C2 and C4), which showed high values for these traits. While, the two parents P1 and P3 as well as the F2 hybrids (H2, H3, H4, H15, H14, H11 and H19) had high values for the previous traits, which were located in the fourth quarter (the highest PCA1 and the lowest PCA2). The second quarter (the Highest PCA2 and the lowest PCA1) comprised the parents P7 and P8 as well as the F1 crosses including C23, C26 and C13, which produced good values for BY, DH, NSP and PH traits. During the third quarter (the lowest PCA1 and PCA2), the F2 hybrids including H24, H28, H21, H25, H22, H6, H26 and H 27 produced good values for previous traits. Similar to our results, PCA identified some crosses as the most promising populations of wheat according to (Fellahi *et al.,* 2018 and Shamuyarira *et al.,* 2022). From PCA results, it could be concluded that the effective selection of superior individuals contributes to the improvement of yield and yield components, in a semi-late genetic background (Fellahi *et al.,* 2018). Based on PCA results, the parents P2, P4 and P6, the F1 crosses (C2, C14, C20, C11 and C3) and the F2 hybrids (H2, H4, H3, H15 and H14) have the potential to improve plant growth and increase the sustainable productivity of wheat.

الخلاصة :

تؤكد النتائج أن الصفات المحصولية المدروسة في القمح يتحكم فيها كل من الفعل الوراثي المضيف والسيادي وأن ارتفاع قيم التوريث يشير إلى إمكانية نجاح برامج الانتخاب المبكر لتحسين إنتاجية القمح باستخدام هذه التراكيب الوراثية المتميزة.

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