Genetic Analysis and Performance Evaluation of Genotypes and Their Single Crosses in Bread Wheat (*Triticum aestivum* L.)

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Abstract.

The study was conducted in a farmer's field in Kirkuk province using a randomized complete block design (RCBD) with three Replications. Ten bread wheat genotypes from ICARDA (Site Moul, Kauz, Abu Ghraib, Florca, Oasis, Kalak, Milan, Sham 6, Ibaa 99, and Hadhab), were evaluated. A half-diallel crossing model was carried out in the 2022–2023 season to evaluate performance and estimate genetic parameters. In the 2023–2024 season, the genotypes and their single crosses were grown, and data were collected for number of spikelets, grains per spike, spikes per plant, 1000-grain weight, plant yield, biological yield, harvest index, and yield efficiency. The analysis of variance table showed highly significant differences ($P \leq 0.01$) among the genetic combinations for all studied traits. Regarding the parents, parent Ibaa 99 (9) excelled in number of spikelets per spike (26.27), number of spikes (37.77), and biological yield (167.76 g), while parent (2) was superior in number of grains per spike (56.44) and harvest index (0.437). Parent (4) had the highest 1000-grain weight (44.50 g), and parent (5) showed the highest plant yield (48.41 g) and yield efficiency (0.041). Among the hybrids, hybrid (3×10) performed best in number of spikelets and harvest index (0.440), hybrid (4×3) in number of grains (57.77), hybrid (7×4) in number of spikes (40.99), hybrid (6×2) in 1000-grain weight (44.90 g) and biological yield (155.42 g), hybrid (9×2) in plant yield (48.08 g), and hybrid (4×1) in yield efficiency (0.048). Estimates of genetic variances showed additive gene action prevailing in most traits, except for biological yield where dominance was more pronounced, suggesting pure line selection and hybrid breeding, respectively. These results highlight the potential of genetic variation and hybrid vigor for sustainable genetic improvement.

Keywords. Performance, Variance, Half-Diallel Crosses, Wheat.

1. Introduction

Wheat is the primary and most important crop from both a nutritional and economic standpoint, as it constitutes the main component of human food and provides substantial economic returns for producing countries [1]. It is rich in nutrients such as carbohydrates (60–80%), proteins (8–15%), fats (1.5–2%), minerals (1.5–2%), simple fibers (2.2%), in addition to amino acids and vitamins (B and E). Wheat products supply about 20% of the daily caloric intake for humans [2].

In Iraq, the average wheat yield is 2546.5 kg/hectare, which is 25.53% lower than the global yield of 3419.29 kg/hectare, and much lower than New Zealand, where the average yield is 9668.1 kg/hectare [3]. Therefore, efforts must be intensified to increase this crop's productivity in Iraq. The hybridization program is one of the most important programs for wheat development and improvement. The key step in this program is selecting parent varieties, which are pure lines, for crossbreeding, a focus of this study [4].

The scientific approach adopted in agricultural development in advanced countries involves the continuous introduction of new genotypes to ensure the availability of alternatives to local varieties, which may degrade due to continuous cultivation over several seasons. Even suboptimal genotypes can be preserved for their beneficial traits other than high yield [5]. Among the used programs is the diallel crossing program, especially the half diallel method, which is widely used in breeding programs to evaluate lines and determine the genetic variation components within them [6]. This evaluation enables the identification of new crosses, benefiting from heterosis and understanding the genetic action controlling important traits such as grain yield and its components, as well as early maturity, protein content, disease resistance, insect resistance, and other quality traits [7].

While morphological traits have been traditionally used to predict hybrid performance, they are influenced by the environment. Thus, new molecular techniques based on DNA markers, which are not affected by the environment, have been introduced in recent studies. DNA is a stable genetic material found in all plant cells at any developmental stage, and it can be extracted from any plant part. These markers follow Mendelian inheritance and can be tracked across generations [7].

The first step in evaluating any new genetic structure is comparing it with the dominant local varieties to estimate morphological variations and their components. Genetic variation is crucial in selecting superior genetic structures [8]. Studies have shown that performance and genetic variation are essential for selecting superior varieties, and genetic variation can originate from old local varieties, natural or induced mutations, or new genetic combinations resulting from hybridization. [9] was the first to divide genetic variation into additive and dominance variance. Studies by [10] showed that dominance variance was higher for spike length and grain, indicating the superiority of dominant genetic effects, while additive variance was higher for traits like the number of spikelets spike $^{-1}$and grains spike. Other studies [11] showed that 1000-grain weight did not exhibit significant differences for additive or dominance variance. The objectives of the study are to evaluate the performance of genotypes and their resulting hybrids, as well as estimate the genetic and phenotypic variations of the studied traits.

2. Materials and Methods

The study was conducted in one of the farmer fields located in Kirkuk Governorate. It included 10 wheat genetic structures introduced from the International Center for Agricultural Research in the Dry Areas (ICARDA) as shown in Table (1). The soil was prepared through leveling and modification as needed. The experiment was irrigated according to the crop's requirements, and weeds were manually controlled throughout all seasons. The hybridization and comparison program were carried out as follows:

Table 1. The genotypes used in the study and their sources

No.	Genotype Name	Genetic Composition / Source
1	Saite Mol	Research Center / Sulaymaniyah
2	Kauz	Kauz 2 / Yaco // Kauz / 3 / Ousis
3	Abu Ghraib	Ajeeba* Lian 12 * Mexico 24
4	Florca	Research Center / Sulaymaniyah
5	Ousis	Ousis / Kauz // 4 BUC
6	Klak	Research Center / Sulaymaniyah
7	Milan	Research Center / Sulaymaniyah
8	Sham 6	Plo - Ruft GTOS - RHel (M12904) – IM – SM – 14 – OSK – GAP
9	Ibaa 99	Ures / Rows / 3 / Jup / B / S / Ures
10	Hadhab	Research Center / Sulaymaniyah

2.1. Breeding Materials for Single Hybrids:

To implement the half-diallel hybridization system, as explained by [12], and to obtain first-generation hybrids, seeds of the 10 genotypes (parents) were planted in the 2022–2023 season on two different dates: December 2 and December 5, to ensure the maximum number of hybridizations. The hybridization process followed the method described by [13], resulting in 55 genetic combinations, which consisted of 45 first-generation hybrids, in addition to the 10 parent structures.

2.2. Evaluation of Genetic Structures and Individual Hybrids:

The seeds of the 10 genetic structures and their individual hybrids were planted on December 2, 2023, for the 2023–2024 season in separate plots, with four rows per genetic structure. Each row was 2.5 meters long, and the distance between rows was 30 cm. A Random Complete Block Design (R.C.B.D.) was used with three replications. Urea fertilizer (45% concentration) was applied at a rate of 20 kg nitrogen per dunum, divided into two doses: the first at planting and the second before heading. Studies were conducted on the two middle rows of each parent.

2.3. Traits Studied:

The following traits were studied: number of spikes, number of grains per spike, number of spikes per plant, 1000-grain weight, plant yield, biological yield, harvest index, and yield efficiency.

2.4. Statistical Analysis:

The statistical analysis of all the studied traits was performed according to a Random Complete Block Design (R.C.B.D.) with three replications to determine the differences between the genetic structures (Genotypes), using the method outlined by [13]. The data obtained from the 10 pure lines and their half-diallel hybrids were analyzed according to the method proposed by [12], as described by [14]. In this method, the number of genetic structures under study, represented by n(n+1)/2, equals 55 genetic structures.

The additive variance (σ^2A), dominance variance (σ^2D), environmental variance (σ^2e), and genetic variance (σ^2G) were estimated, along with the phenotypic variance (σ^{2P}), using the method described by [14].

3. Results and Discussion

Table (2) shows the results of the analysis of variance, where it is evident that the mean squares for the genetic combinations differed significantly at the 1% probability level for all traits. These differences between the genetic combinations were due to the variation in the genetic factors controlling the inheritance of these traits and their interactions with the environment, which requires continuing to study their genetic performance and understand the nature of gene action involved. This was also pointed out by [15; 16; 17; 18].

Table 2. Analysis of variance for parents, hybrids, and parents + hybrids for the studied traits.

S. o. V.	d.f	Number of spikelets	Number of grains per spike	Number of spikes per plant	1000-grain weight	plant yield	Biological yield	Harvest index	Yield efficiency
Rep.	2	38.34	698.19	1057.8	118.4	1274.5	16939.77	0.0320	0.00092
Parents	9	**7.60	**44.70	**94.58	**25.7	**68.64	**853.28	**0.006	**0.0002
Error	18	2.09	34.02	25.81	7.17	59.25	622.77	0.0018	0.00006

S. O.V	d.f	Number of spikelets	Number of grains per spike	Number of spikes per plant	1000-grain weight	plant yield	Biological yield	Harvest index	Yield efficiency
Rep.	2	196.16	3224.2	5435.8	376.2	4766.8	33356.75	0.1640	0.00704
Hybrids	44	**5.28	**55.34	**101.8	**46.3	**78.0	**783.50	**0.004	**0.0002
Error	88	2.02	27.01	47.87	3.34	60.53	330.06	0.0013	0.00013

S.o.V	d.f	Number of spikelets	Number of grains per spike	Number of spikes per plant	1000-grain weight	plant yield	Biological yield	Harvest index	Yield efficiency
Rep.	2	233.66	3874.4	6486.1	489.5	6021.	48395.83	0.1958	0.00789
Parents + Hybrids	54	**5.80	**53.32	**102.4	**42.3	**75.2	**856.89	**0.004	**0.0002
Error	108	2.01	28.57	43.44	4.01	59.57	407.93	0.0013	0.00011

Abbreviations: S.o.V. (Source of Variation), Rep. (Replicates), D.F (Degree's Freedom), **: significant at 0.01 probability level.

Tables (3 and 4) show the mean values of the studied traits for the parents and their resulting single crosses. Significant differences were observed. For the trait of number of spikelets per spike, the means ranged between 26.267 spikelets for parent (9) and 20.133 spikelets for parent (2). Among the hybrids, the means ranged between 24.667 spikelets for hybrid (10×3) and 17.967 spikelets for hybrid (10×2). The overall mean was 22.69 spikelets for parents, 21.97 for hybrids, and 22.10 for parents and hybrids combined.

For the number of grains per spike, the highest mean was recorded by parent (2) with 56.443, which is a desirable direction, while the lowest mean was 43.210 for parent (1). Among the hybrids, the highest mean was 57.767 for hybrid (4×3), and the lowest was 38.353 for hybrid (10×8). The overall mean was 49.34 for parents, 48.03 for hybrids, and 48.27 for parents and hybrids combined. The variation in this trait may be due to differences in the utilization of growth factors, especially during the flowering stage, to produce more fertile florets and consequently more grains, as well as differences in heat tolerance, which may affect pollen viability and stigma receptivity, negatively influencing pollination, fertilization, and grain set. This aligns with [4; 19]

For the number of spikes per plant, parent (9) recorded the highest mean at 37.773 spikes, while parent (1) had the lowest mean at 37.773 spikes (this repetition may be a typo). Among the hybrids, hybrid (7×4) had the highest mean at 40.993 spikes, while hybrid (5×4) had the lowest at 12.997 spikes. The overall mean was 27.20 for parents, 24.35 for hybrids, and 24.87 for parents and hybrids combined. It is well known that the number of spikes per plant is determined by the genotype and environmental conditions. Several studies have shown variability among wheat varieties in grain yield and its components, even when grown under similar environmental conditions, and that varieties differ in their response to management practices. An increase in spike number can play a compensatory role in increasing the number of grains per unit area. This is consistent with [15; 20].

For 1000-grain weight, parent (4) recorded the highest mean at 44.500 g, while parent (7) recorded the lowest at 34.167 g. Among the hybrids, hybrid (6×2) had the highest mean at 44.900 g, and hybrid (7×5) had the lowest at 30.933 g. The overall mean was 37.99 g for parents, 37.34 g for hybrids, and 37.46 g for parents and hybrids combined. The variation in 1000-grain weight may be attributed to differences in the effective green leaf area involved in photosynthesis. It was observed that genotypes maintaining green leaves for a longer time period led to increased dry matter accumulation available during grain filling, as noted by [16; 21].

The comparison of means for plant yield showed values ranging between 48.413 g for parent (5) and 31.120 g for parent (7). For the hybrids, the range was between 48.077 g for hybrid (9×2) and 30.370 g for hybrid (8×4). The overall mean was 40.36 g for parents, 41.01 g for hybrids, and 40.89 g for parents and hybrids combined. Yield per plant is determined by the average number of grains per spike and the 1000-grain weight, resulting from superior spike density, which is influenced by the total biomass at maturity and harvest index. Increasing these during the demand phase is crucial in determining source size and yield efficiency through the amount of dry matter available during spike formation and grain filling, as explained by [1; 4].

For biological yield, values ranged between 167.763 g for parent (4) and 115.543 g for parent (9). Among the hybrids, the range was between 155.420 g for hybrid (6×2) and 88.640 g for hybrid (10×7). The overall mean was 130.62 g for parents, 117.67 g for hybrids, and 120.02 g for parents and hybrids combined. This trait is important at maturity as a key physiological indicator determining yield, influenced by the increase in productive spikes. This was indicated by [21; 22].

The highest harvest index was recorded by parent (2) at 0.437, and the lowest was 0.297 for parent (10). Among the hybrids, hybrid (10×3) had the highest index at 0.440, while the lowest was 0.287 for hybrid (10×2). The overall mean was 0.36 for parents, hybrids, and combined. An increase in this trait during the demand phase is an important factor determining source size and plays a crucial role in enhancing yield components, as noted by [19; 20].

For yield efficiency, parents (3) and (5) had the highest mean at 0.041, while parent (7) recorded the lowest at 0.017. Among the hybrids, hybrid (4×1) had the highest mean at 0.048, and hybrid (2×1) had the lowest at 0.013. The overall mean was 0.029 for parents, hybrids, and combined. An increase in this trait leads to an increase in dry matter production, which in turn enhances yield components.

From the above, we observe the following regarding the parents: parent (9) excelled in number of spikelets and biological yield, parent (2) in number of grains per spike and harvest index, parent (9) in number of spikes, parent (4) in 1000-grain weight, parent (5) in plant yield, and yield efficiency.

As for the hybrids, the following stood out: hybrid (3×10) in number of spikelets and harvest index, hybrid (3×4) in number of grains per spike, hybrid (4×7) in number of spikes, hybrid (2×6) in 1000-grain weight and biological yield, hybrid (2×9) in plant yield, and hybrid (1×4) in yield efficiency.

When comparing the means of the parents and the single crosses, we notice that the hybrid means were higher than the parent means for most studied traits. This indicates differences in the performance of the hybrids, which can be utilized in breeding and improvement programs to benefit from hybrids with high and significant heterosis. These results are consistent with [23].

Table 3. Mean performance of parents for the studied traits.

Parent	**Number of spikelets**	**Number of grains per spike**	**Number of spikes per plant**	**1000-grain weight (g)**	**plant yield (g)**	**Biological yield (g)**	**Harvest index**	**Yield efficiency**
1	21.867	43.210	19.773	37.033	45.587	134.407	0.343	0.025
2	20.133	56.443	20.440	38.000	38.877	121.387	0.437	0.030
3	23.200	49.733	28.663	35.800	42.920	129.053	0.350	0.025
4	23.200	47.000	24.550	44.500	41.063	167.763	0.333	0.031
5	22.533	51.687	23.440	36.700	48.413	150.620	0.397	0.041
6	22.800	45.000	25.440	36.333	37.260	118.940	0.363	0.029
7	22.200	50.120	28.220	34.167	31.120	115.783	0.340	0.017
8	23.267	51.667	31.550	39.733	37.817	120.973	0.427	0.030
9	26.267	47.020	37.773	37.167	41.527	115.543	0.357	0.041
10	21.400	51.510	32.173	40.467	39.053	131.743	0.297	0.028
Mean	22.69	49.34	27.20	37.99	40.36	130.62	0.36	0.029
L.S.D 1%	3.400	13.71	11.942	6.296	18.092	58.651	0.101	0.019

Table 4. Mean performance of F_1 hybrids for the studied traits.

Hybrids	**Number of spikelets**	**Number of grains per spike**	**Number of spikes per plant**	**1000-grain weight (g)**	**plant yield (g)**	**Biological yield (g)**	**Harvest index**	**Yield efficiency**
2×1	**20.06**	**45.687**	**24.330**	**35.100**	**44.46**	**113.64**	**0.377**	**0.013**
3×1	**22.73**	**41.553**	**15.443**	**37.533**	**34.93**	**92.36**	**0.363**	**0.019**
4×1	**21.47**	**44.010**	**23.330**	**31.000**	**46.93**	**119.26**	**0.387**	**0.048**
5×1	**22.40**	**46.120**	**25.883**	**38.800**	**37.43**	**121.33**	**0.303**	**0.025**
6×1	**21.47**	**51.787**	**28.440**	**40.367**	**41.52**	**113.70**	**0.357**	**0.021**
7×1	**22.47**	**44.100**	**17.440**	**31.667**	**36.43**	**104.90**	**0.317**	**0.017**
8×1	**21.80**	**47.667**	**24.553**	**40.500**	**47.92**	**120.13**	**0.413**	**0.033**
9×1	**21.27**	**45.567**	**24.887**	**34.900**	**37.42**	**115.28**	**0.340**	**0.025**
10×1	**23.93**	**47.867**	**22.773**	**36.800**	**41.06**	**122.17**	**0.357**	**0.031**
3×2	**19.13**	**46.343**	**31.217**	**37.067**	**38.86**	**140.57**	**0.330**	**0.031**
4×2	**22.60**	**47.877**	**28.550**	**41.200**	**44.57**	**115.71**	**0.433**	**0.036**
5×2	**22.13**	**49.877**	**27.663**	**43.000**	**35.82**	**95.763**	**0.367**	**0.019**
6×2	**20.87**	**44.300**	**30.133**	**44.900**	**42.81**	**155.42**	**0.370**	**0.036**
7×2	**21.93**	**48.887**	**21.887**	**38.800**	**42.53**	**119.97**	**0.367**	**0.046**
8×2	**22.13**	**47.333**	**23.553**	**40.600**	**39.89**	**110.39**	**0.360**	**0.023**
9×2	**22.07**	**50.653**	**17.553**	**38.733**	**48.07**	**118.83**	**0.400**	**0.027**
10×2	**17.97**	**53.387**	**22.620**	**38.567**	**38.53**	**132.83**	**0.287**	**0.019**
4×3	**23.33**	**57.767**	**33.330**	**31.133**	**36.50**	**116.62**	**0.333**	**0.043**
5×3	**21.07**	**52.133**	**35.883**	**44.767**	**38.77**	**131.07**	**0.297**	**0.031**
6×3	**23.33**	**42.333**	**25.107**	**36.933**	**42.21**	**113.43**	**0.370**	**0.028**
7×3	**22.60**	**48.453**	**21.110**	**38.900**	**42.60**	**126.63**	**0.433**	**0.041**
8×3	**21.20**	**41.653**	**17.550**	**40.567**	**47.03**	**152.07**	**0.307**	**0.047**
9×3	**22.47**	**52.333**	**29.440**	**33.433**	**48.03**	**132.06**	**0.363**	**0.042**
10×3	**24.67**	**50.443**	**27.553**	**44.767**	**41.51**	**94.087**	**0.440**	**0.029**
5×4	**23.07**	**51.867**	**12.997**	**36.133**	**41.67**	**111.54**	**0.370**	**0.022**
6×4	**22.60**	**46.653**	**17.550**	**36.500**	**34.01**	**108.95**	**0.310**	**0.029**
7×4	**21.47**	**46.587**	**40.993**	**32.533**	**27.49**	**89.81**	**0.337**	**0.018**
8×4	**24.07**	**55.553**	**22.777**	**31.200**	**30.37**	**97.85**	**0.313**	**0.017**
9×4	**21.60**	**52.553**	**27.663**	**41.833**	**44.44**	**110.05**	**0.390**	**0.029**
10×4	**21.20**	**50.577**	**18.997**	**37.567**	**35.95**	**106.81**	**0.333**	**0.020**
6×5	**19.20**	**46.200**	**17.553**	**39.833**	**42.73**	**133.95**	**0.327**	**0.043**
7×5	**22.20**	**55.777**	**26.107**	**30.933**	**40.75**	**100.76**	**0.333**	**0.025**
8×5	**20.67**	**41.533**	**26.773**	**38.067**	**45.53**	**129.55**	**0.357**	**0.028**
9×5	**20.93**	**48.867**	**19.773**	**40.233**	**39.95**	**108.27**	**0.377**	**0.037**
10×5	**21.07**	**50.010**	**26.107**	**40.167**	**45.34**	**115.25**	**0.383**	**0.041**
7×6	**23.07**	**50.220**	**21.887**	**39.300**	**34.10**	**91.36**	**0.367**	**0.026**
8×6	**22.80**	**47.610**	**20.330**	**36.067**	**44.16**	**110.66**	**0.387**	**0.032**
9×6	**22.60**	**45.010**	**35.997**	**31.700**	**50.37**	**132.90**	**0.350**	**0.029**
10×6	**21.47**	**42.753**	**19.997**	**31.833**	**46.06**	**128.49**	**0.350**	**0.024**
8×7	**24.07**	**50.087**	**17.777**	**32.700**	**47.15**	**130.36**	**0.350**	**0.031**
9×7	**22.93**	**53.567**	**27.773**	**40.033**	**45.17**	**130.95**	**0.387**	**0.047**
10×7	**20.73**	**44.753**	**22.773**	**31.933**	**34.10**	**88.640**	**0.387**	**0.024**
9×8	**22.93**	**42.433**	**19.220**	**36.633**	**41.70**	**127.74**	**0.400**	**0.029**

10×8		**22.07**	**38.353**	**22.330**	**39.000**	**34.80**	**113.16**	**0.303**	**0.018**
10×9		**22.73**	**52.210**	**30.107**	**36.133**	**43.44**	**149.64**	**0.337**	**0.027**
Hybrids	**General Mean**	**21.97**	**48.03**	**24.35**	**37.34**	**41.01**	**117.67**	**0.36**	**0.029**
	L.S.D 0.01	**3.058**	**11.174**	**14.874**	**3.931**	**16.76**	**39.056**	**0.078**	**0.024**
Parents and Hybrids	**General Mean**	**22.10**	**48.27**	**24.87**	**37.46**	**40.89**	**120.02**	**0.36**	**0.029**
	L.S.D 0.01	**3.038**	**11.444**	**14.112**	**4.290**	**16.52**	**43.242**	**0.079**	**0.023**

Table (5) presents the estimates of additive variance (σ^2A), dominance variance (σ^2D), environmental variance (σ^2E), phenotypic variance (σ^2p), and genetic variance (σ^2G) for all the studied traits. The values of additive genetic variance were higher than the dominance genetic variance for all traits except biological yield. Therefore, the additive gene action plays a more significant role in controlling the inheritance of these traits, making pure line selection or mass selection the most suitable breeding methods. In contrast, for traits where dominance variance exceeded additive variance, dominance gene action was more influential in controlling inheritance, making hybrid production the more appropriate breeding strategy. The environmental variance values were lower than the additive and dominance variances for all the studied traits. Regarding genetic variance (σ^2G), its values increased for all traits compared to environmental variance values, indicating that an increase in genetic variance for any of these traits leads to a decrease in environmental variance. As for phenotypic variance values, they were higher for all traits compared to both genetic and environmental variances. These findings are consistent with the results reported by [24; 25; 26].

Table 5. Variances for the Studied Traits.

Traits	**Number of Spikelets**	**Number of Grains per Spike**	**Number of Spikes per Plant**	**1000-Grain Weight**	**Plant Yield**	**Biological Yield**	**Harvest Index**	**Yield Efficiency**
$\sigma^2{}_A$	7.349	0.856	50.186	29.751	66.259	303.538	0.003	1.50
$\sigma^2{}_D$	1.588	0.704	35.955	13.925	23.457	312.405	0.002	0.80
$\sigma^2{}_e$	0.671	0.362	14.483	1.339	19.857	135.979	0.001	0.40
$\sigma^2{}_G$	8.937	1.560	86.141	43.676	89.716	615.943	0.005	2.30
$\sigma^2{}_P$	9.609	1.922	100.624	45.015	109.573	751.922	0.006	2.70

4. Conclusion

The results demonstrated significant genetic variability among the studied parents and hybrids for all traits, providing ample opportunities for selection and hybridization. Additive gene action was predominant in most traits, suggesting the suitability of pure line selection to improve yield components, whereas dominance effects in biological yield favoured hybrid breeding strategies. Overall, hybrids outperformed their parents in many traits, confirming their heterotic potential and justifying their use in future breeding programs to achieve sustainable yield improvement.

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