Heritability and Association among Yield Component Traits of Bread Wheat

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Abstract

This research was conducted at the Agriculture University Peshawar during rabi season 2020–21 to determine genetic parameters and correlation coefficients for flowering and yielding traits of 36 common wheat (*Triticum aestivum* L.) entries, including five check cultivars. Entries were evaluated using simple RCBD consisting of two replications. Parameters studied were Days to heading and yield component traits, such as number of spikes m^{-2}, spike length, number of seeds $spike^{-1}$, 1000-seed weight, biological and seed yield. Genotypes differed significantly for the studied traits. Estimated Heritability varied from 0.32 to 0.79. Maximum heritability was recorded for 1000-seed weight (0.79) followed by days to heading (0.73), spike length (0.54), spikes m^{-2} (0.45), biological yield (0.40), seed yield (0.38) while low and least heritability for seeds $spike^{-1}$ (0.32). Thousand grain weight and days to heading had high heritability and hence effectively can be selected. Spike length and seeds $spike^{-1}$ showed significant positive correlation (0.62**) with each other. Similarly, seed yield had positive association with spikes m^{-2} (0.64**) and biological yield (0.96**). In current study, genotypes G116-B and G51 were best for high yield and are therefore, recommended for further testing under late sowing conditions in Khyber Pakhtunkhwa.

Keywords: Spring wheat, Genetic variability, Heritability, Correlation coefficients, Genotypes

Introduction

Common wheat (*Triticum aestivum* L.) had 42 chromosomes in its genome (x=7). It is highly self-pollinated crop of the grass family Gramineae (Baenziger, 2016; Filiz, 2011). There are three species under genus Triticum. Diploid with 14, tetraploid with 28 and hexaploid (common wheat) with 42 chromosome number are known. Natural crossing between *T. monococcum* (A genome) and *Triticum. speltoides* (tauschii) with B genome or a closely related species over the period of thousands of years had resulted *Triticum durum*. This is also in accordance with morphological, geographical and cytological evidence (Abu, 2012). Bread wheat had been originated from Fertile Crescent of Southwest Asia (Mergoum *et al*., 2009). Inhabitants of Pakistan and most of the developing countries consume wheat as staple food crop. Bread wheat provide about 20% food calories and feed more than 35% of the world's population (Khan and Naqvi, 2011). It can be regarded as the strategic crop of Pakistan. Wheat crop had broad adoptability and can be grown in diversified environments with great success. It is grown in regions with freezing temperature, hot dry or water stress and normal irrigated and sub-tropical regions (Chimdesa, 2014). In Pakistan, wheat occupied an area of 8.805 million hectares during 2014-15 and per unit yield was estimated about 2867 kg per ha. In Khyber Pakhtunkhwa, wheat occupied an area of 0.76 million hectares with 1.4 million tons production and yielded 1840 kg per ha during 2014-15 (PES, 2021).

Enhancement in crop yield requires knowledge about the type and strength of association among plant traits. In this way we can do indirect selection for the trait of our interest via some other contributing traits. Previous study showed positive correlation of wheat yield with flag leaf area and productive tillers (Singh *et al*., 1995). Like this, seed yield had significant positive association with spikes m^{-2} (Singh and Dewivedi 2002). Significant negative correlation of 1000-seed weight with plant height, spikelet's $spike^{-1}$ and seed yield was reported (Shahid *et al*., 2002). In view of the pivotal importance of wheat as a national strategic and a staple food crop, the current study aimed to estimate heritability and genetic gain for yield components in bread wheat lines, determine association among traits pertaining to wheat yield and identify potential lines of wheat under late sowing conditions for further testing at multi-locations of Khyber Pakhtunkhwa.

Materials and Methods

In this research study, thirty-six spring wheat genotypes including five check cultivars (Khaista-17, Wadaan-17, Paseena, Kohat-17, and Pakistan-13) were evaluated during Rabi season 2020–21 at the Farm of Agriculture University Peshawar, Khyber Pakhtunkhwa, Pakistan. Wheat lines were sown using simple RCBD consisting of two replications. Sowing date was 15th December, 2020. There were two rows per genotype each two-meter long while distance between two rows was 0.30 m. Standard agronomic practices were followed from sowing till harvesting and recorded data on heading and yield associated characteristics.

50% heading

Days to 50% heading were calculated as the difference of days from sowing till 50% of flowering in a genotype. The difference between the sowing and date at which 50% heading were calculated by formula;

$$\text{Heading (50\%)} = \text{date of sowing-date of heading (50\%)}$$

Spikes m^{-2}

Spikes meter^{-1} was counted by putting meter rod randomly through the length of a row in an experimental unit in each replication. Spikes meter^{-1} were converted into spikes m^{-2} by formula;

$$\text{Spikes m}^{-2} = \text{Spikes meter}^{-1}/\text{ row-row distance}$$

Spike length (cm)

Ten randomly chosen spikes from each genotype were measured in centimeters for their length from the base to the tip of rachis, while not considering their awns as the part of reading. Mean length of spike was calculated.

Number of seeds spike^{-1}

Ten spikes from all genotypes were cut using scissors from the base and threshed by single spike thresher. Threshed grains were counted by seed counter.

1000-seed weight (g)

Following harvest, 500 kernels were separated from seed lot of each genotype and weighed with digital weight balance. Weight of 500 kernels was multiplied by two to get 1000-kernel weight.

Biological yield (kg ha^{-1})

Two rows of each genotype from the experimental plot were manually harvested after getting sufficient ripening, bundled, and kept for five days under sun light. These stacks of wheat were weighed with weight balance and convert data into biological yield (kg) ha^{-1} by formula;

$$\text{Biological yield (kg ha}^{-1}) = [\text{weight of individual stack (kg)/plot area (m}^2)] \times 10{,}000$$

Seed yield (kg ha^{-1})

Seed yield was determined by weighing the threshed grains that were produced after threshing stacks of wheat genotypes and convert data into grain yield (kg) ha^{-1} by formula;

$$\text{Seed yield (kg ha}^{-1}) = [\text{Grain weight (kg)/plot area (m}^2)] \times 10{,}000$$

Statistical analysis

Data for all the traits was analyzed in Excel through proper formulas. Least significant difference (LSD) test at 5% probability was used to identify minute differences between wheat genotypes. Both Genotypic (Vg) and environmental variances (Ve) were calculated from ANOVA via formula:

Variance due to Genetic factors = Vg = (GMS-EMS)/ Reps = X1

Variation due to environmental factors = Ve = EMS = X2

Variation in phenotype = Vp = Vg + Ve = X3

Heritability = h2=Vg/Vp=X1/X3

The following formula was used to determine the expected selection response for each trait:

Genetic gain = Re = $i \times \sqrt{Vp} \times h^2$

Where:

i = Constant value at a particular level of selection

$\sqrt{Vp}$= is the phenotypic standard deviation of a trait

h^2 = the trait's heritability

The following formulas were used to determine the genetic and phenotypic coefficients of variation:

Coefficient of variation (Genetic) in % = $\sqrt{V_g}$ /GM × 100

Coefficient of variation (Phenotypic) in % = $\sqrt{V_p}$ /GM × 100

Where:

GM = Grand mean of the trait

Correlation was computed by using the following formula:

Correlation = r = Cov (x_1x_2)/ √ $(Vx_1.Vx_2)$

Co-variance (x_1x_2) = (GMP-EMP)/ Reps

Where:

Cov (x_1x_2) = Co-variance between x_1 and x_2 traits

Vx_1 = Variance of first trait

Vx_2 = Variance of second trait

GMP = Genotype mean product

EMP = Error mean product

Results and Discussion

Days to 50% heading

Wheat genotypes varied significantly for days to 50% heading. Coefficients of variation (CV) and determination (R^2) for heading were 1.28% and 0.87, respectively (Table 1). Our findings for heading conform to Naik *et al.* (2015) who also observed significant variations in wheat genotypes for heading.

Wheat lines varied for days to heading and fluctuate between 89 to 97 days (Table 2). Genotype G34 took minimum days (89 days) to reach heading. This was followed by G92, G134 and G138 (each with 90 days). Genotype G140 attained this stage in 97 days followed by G123 and check cultivar KT-17 (each with 96 days).

Days to heading showed genetic and environmental variances of 3.84 and 1.41, respectively. GCV value was lower (2.12%) than PCV (2.46%) for heading of wheat genotypes. Heading had high estimates of heritability (0.73) with genetic gain of 3.46 days (Table 4). Previously, Hamza and Elhashimi (2017) found that heading had high broad sense heritability (0.87).

Correlation analysis revealed positive association of heading with the number of seeds spike^{-1} ($r_p = 0.35^*$). However, no relationship of heading was recorded with other traits like spikes per unit area, spike length, 1000-seed weight, biological and seed yield (Table 5). Our results are consistent with Zerga *et al.* (2016), who proposed that there is positive association of days to heading with seeds spike^{-1} and no association with spike length and 1000-seed weight.

Spikes m^{-2}

Wheat genotypes differed significantly for spikes m^{-2} and showed that there is enough genetic variability for spikes m^{-2}. Spikes m^{-2} had CV= 26.18% and $R^2 = 0.74$ (Table 1). Our findings are concurrent with Shah *et al.* (2007), who also noted significant variations for number of spikes per unit area among wheat genotypes.

Wheat genotypes varied in number of spikes meter^{-2}. Minimum spike meter^{-2} were recorded for genotype G130 (65 spikes) followed by genotypes G103 (148.3 spikes) and G147 (183.3 spikes). Maximum spikes m^{-2} were recorded for genotype G110-A (416.7 spikes), followed by genotypes G116-B and G120 (each with 410.0 spikes) and G138 and G148 (each with 333.3 spikes).

The genetic and environmental variances for spikes m^{-2} were 3853.13 and 4752.19, respectively. PCV was higher (35.23%) than GCV (23.57%) for spikes m^{-2} of wheat genotypes which indicate environmental influence on number of spikes per unit area. Spikes m^{-2} showed moderate heritability (0.49) and genetic gain of 85.57 spikes m^{-2} (Table 4). Our findings of heritability estimates are in conformity with Baranwal *et al.* (2012) who have also reported moderate heritability (0.40) for spikes m^{-2}.

Spikes m^{-2} had positive relationship with Biological (r_p = 0.74**) and seed yield (r_p = 0.64**). However, it was non-significantly correlated with other traits like spike length, seeds spike^{-1}, and 1000-seed weight (Table 5). Previous results also suggested that number of spikes per unit area did not show association with spike length and seeds spike^{-1} (Wani *et al*., 2011).

Spike length

Mean squares for spike length among wheat genotypes revealed highly significant variation. CV was 5.92% and R^2 was 0.77 for spike length (Table 1). Similar results for spike length among wheat genotypes were also proposed by Devesh *et al.* (2018) and Imran *et al*. (2018) in their previous research studies.

Spike length fluctuate between 7.7 and 10.4 cm among the studied wheat lines (Table 2). Genotype G103 (7.7 cm) had smallest spike. It was followed by genotypes G123 and G116-A with spike length 8.0 and 8.1 cm, respectively. Genotype G147 had longest spike (10.4 cm) and was followed by genotypes G116-B (10.3 cm) and G51 and G148 (each with 9.8 cm).

Low values of genetic variance (0.32) and environmental variance (0.28) were recorded for spike length. However, genetic variance was higher than environmental variance suggesting that role of genetic components is more than environment. PCV for spike length among wheat genotypes was higher (8.67%) than the respective GCV (6.34%). Moderate value of heritability (0.54) and genetic gain (0.85 cm) were recorded for spike length (Table 4). Previously, Arya *et al.* (2017) had proposed moderate heritability (0.57) for spike length which is agreement with our results.

Spike length was positively correlated with seeds spike^{-1} (r = 0.62**), biological (r_p = 0.42*), and seed yield (r_p = 0.41*) in our study. Also, it was not associated with heading, productive tillers per unit area and 1000-kernel weight (Table 5). Previously, positive association of spike length with seeds spike^{-1} while non-significant association with 1000-seed weight was also proposed (Ibrahim, 2019).

Seeds spike^{-1}

Mean squares from ANOVA showed that wheat genotypes varied significantly for seeds spike^{-1}. The coefficient of variance and R^2 were 12.29 % and 0.67, respectively for seeds spike^{-1}. (Table 1). Study carried by Bayisa *et al.* (2020) also proposed significant differences for kernels per spike among wheat genotypes.

Number of seeds spike^{-1} among wheat genotypes fluctuate between 38.6 and 64.7 (Table 2). Genotype G34 and G53 (each with 38.6 seeds) produced least number of seeds per spike. It was followed by genotypes G138 (39.1 seeds) and G103 and G123 (each with 39.2 seeds). Wheat genotype G116-B produced highest number of seeds (64.7) followed by genotypes G140-B (56.4 seeds) and G148 (55.2 seeds).

Variance due to genetic reason was lower (15.72) than variance due to environmental fluctuations (33.69). GCV and PCV for seeds spike^{-1} were 8.39 and 14.88%, respectively. Wheat genotypes had moderate heritability (0.32) for seeds per spike was while selection response was 4.61 seeds spike^{-1} (Table 4). Our broad sense heritability estimates are not concurrent with Baloch *et al*. (2013) who have estimated high heritability (0.97) for seeds per spike.

Seeds spike^{-1} had positive association with flowering, spike length, biological and seed yield. However, it was negatively correlated (r_p = -0.57**) with 1000-seed weight which can help us to select genotypes with more 1000-seed weight (Table 5). Previously, Ibrahim (2019) proposed significant positive association of seeds per spike with spike length and negative with 1000-seed weight and is coherent with our findings.

1000-seed weight

Wheat genotypes differed significantly for 1000-seed weight as suggested by mean square values from ANOVA. CV was 4.54 % with R^2 of 0.89 for a 1000-seed weight (Table 1). Our findings are consistent with Arya *et al.* (2017) for 1000-seed weight of wheat genotypes.

Wheat genotypes differed for 1000-seed weight and occupied values between 38.3 and 54.7 g (Table 3). Least 1000-seed weight was noticed for G142 (38.3 g) followed by G120 (39.6 g) and G110-A (40.1 g). Highest 1000-seed weight was noticed for G27 (54.7 g), followed by G53 (53.2 g) and G92 (53.0 g).

The genetic component contributes more (16.51) than environmental component (4.41) to the total variance for 1000-grain weight among wheat genotypes. GCV and PCV for 1000-seed weight of wheat genotypes were 8.79 and 9.89%, respectively. High heritability (0.79) coupled with high genetic gain (7.44 g) was estimated for 1000-seed weight (Table 4). Similar results of heritability (0.67) were also suggested by Kumar *et al.* (2017) for 1000-seedl weight.

Correlation analysis suggested negative association between 1000-seed weight and seeds spike^{-1} (r = -0.57**). However, its relationship with other traits like days to 50 % flowering, productive tillers per unit area, spike length, biological and seed yield was non-significant (Table 5). Our correlation findings are in conformity with Shah *et al.* (2007) who also proposed that there is no correlation between 1000-seed weight and seed yield.

Biological yield

Significant genetic differences exist among wheat genotypes for biological yield. CV and R^2 were 27.91 % and 0.70, respectively for biological yield (Table 1). Our findings for biological yield are in conformity with Khan *et al.* (2015), who also proposed significant variations among wheat genotypes.

Lower and upper limit of biological yield was 1250 and 11875 kg ha^{-1}, respectively for the studied wheat genotypes (Table 3). Wheat line G130 produced least biological yield (1250 kg ha^{-1}). It was followed by G103 (2931.7 kg ha^{-1}) and check cultivar Pakistan-13 (3750.0 kg ha^{-1}). Highest biological yield (11875 kg ha^{-1}) was reported for G116-B followed by G51 (10625 kg ha^{-1}) and G145 and G148 (each with 8750.0 kg per ha).

Biological yield had genetic and environmental variances of 2116587 and 3117904, respectively which predict lower value of heritability. GCV was lower (22.99%) than PCV (36.17%) for biological yield which indicate that biological yield is affected by environmental changes. Moderate heritability was recorded for biological yield (0.40) while genetic gain was 1905.75 kg ha^{-1} (Table 4). Our findings of heritability estimates for biological yield are not similar with Khan *et al.* (2015) who have recorded low heritability (0.25) for biological yield.

Seed yield (r_p = 0.96**), productive tillers (r_p = 0.74**), spike length (r_p = 0.42*), and seeds spike^{-1} (r_p = 0.39*) all were significant positively correlated with biological yield. However, it had no significant association with heading and 1000-seed weight (Table 5). Our findings are parallel with Iqbal *et al*. (2017), who also noted positive association of seed yield with biological yield. Earlier research by Baye *et al*. (2020) in wheat found a significant relationship of biological yield with spike length and no linkage with 1000-seed weight.

Seed yield

Wheat genotypes differed significantly for seed yield which showed that there is sufficient genetic variability among wheat genotypes. For seed yield, CV recorded was 28.16 % and R^2 was 0.69 (Table 1). In the prior studies, Aycicek and Yildirim (2006) also proposed significant genetic differences among wheat genotypes for seed yield.

Wheat genotype showed wide range for seed yield and fluctuate between 625 and 5000 kg per ha (Table 3). Lowest seed yield has been reported for Genotype G130 (625 kg per ha). It was followed by G103 (1041.7 kg per ha) and the control cultivar Pakistan-13 (1666.7 kg per ha). Genotype G51 produced the most seed yield (5000 kg per ha), followed by G116-B (4583.3 kg per ha) and G145 genotypes (4166.7 kg per ha).

Grain yield had genetic and environmental variances of 411018.17 and 658618.60, respectively. GCV for seed yield of wheat genotypes was 22.25 %, which is lower than the respective PCV (35.89 %). Low heritability was recorded for seed yield (0.38) while expected selection response was 818.67 kg ha^{-1} (Table 4). Same results were also reported by Dabi *et al*. (2017) who have reported moderate heritability (0.50) for seed yield.

Spikes m^{-2} (r = 0.64**), biological yield (r = 0.96**), spike length (r = 0.41*), and seeds spike^{-1} (r = 0.34*) all showed positive association towards seed yield. In this study, no association of seed yield was found with days to heading and 1000-seed weight (Table 5). Previously, Kaddem (2014) have proposed positive association between biological and seed yield.

Table 1.*Mean squares for heading and yield component parameters of 36 spring wheat genotypes in Peshawar during 2020-21.*

Source	**df**	**50 % Heading**	**Spikes per m^2**	**Spike length**	**Seeds per spike**	**1000-seed weight**	**Biological yield**	**Seed yield**
Replication	1	0.13	50.00	0.19	68.30	13.30	62031.20	38579.50
Genotype	35	9.12**	12458.50*	0.92**	65.10*	37.40**	7351078.40**	1480654.90**
Error	35	1.41	4752.20	0.28	33.70	4.41	3117903.70	658618.60
CV (%)	-	1.28	26.18	5.92	12.29	4.54	27.91	28.16
R^2	-	0.87	0.72	0.77	0.67	0.90	0.70	0.69

*= 5 % significance level

**= 1 % significance level

Table 2. *Means for heading and yield component traits of 36 spring wheat genotypes during 2020-21.*

Genotypes	**50%Heading (no. of days)**	**Spikes per m^2**	**Spike length (cm)**	**Seeds per spike**
G24	91	205.0	8.5	46.1
G27	93	278.3	9.7	44.7
G34	89	275.0	8.6	38.6
G51	95	306.7	9.8	53.2
G53	92	265.0	8.2	38.6
G55	92	286.7	9.3	43.5
G56	92	318.3	9.5	45.6
G91	91	261.7	8.6	44.3
G92	90	298.3	8.2	43.2
G103	95	148.3	7.7	39.2
G110-A	93	416.7	8.2	46.9
G110-B	94	235.0	9.2	49.3
G116-A	94	316.7	8.1	42.1
G116-B	94	410.0	10.3	64.7
G117	92	265.0	8.7	54.8
G120	93	410.0	9.6	51.6
G123	96	278.4	8.0	39.2
G124	95	250.0	8.5	46.8
G125	95	281.7	8.7	53.7
G130	95	65.0	8.9	51.0
G134	90	276.7	8.4	44.2
G135	92	238.3	8.3	44.0
G138	90	333.3	9.2	39.1
G140-A	92	266.7	9.3	47.6
G140-B	97	316.7	9.3	56.4
G141	96	225.0	8.2	44.4
G142	91	301.7	8.2	45.1
G145	93	305.0	9.7	50.0
G147	96	183.3	10.4	50.7
G148	94	333.3	9.8	55.2
G150	93	203.3	9.2	46.3
Khaista-17	95	190.0	9.2	52.5
Wadaan-17	95	223.3	8.8	49.4
Paseena	95	270.0	9.5	47.7
Kohat-17	96	251.7	9.7	47.2
Pakistan-13	95	196.7	8.7	44.2
LSD (5%)	2.4	139.9	1.1	11.8

Table 3. *Means for 1000-seed weight, biological and seed yield of 36 spring wheat genotypes during 2020-21.*

Genotypes	1000-seed weight (g)	Biological yield (kg per ha)	Seed yield (kg per ha)
G24	44.6	5000	2500
G27	54.7	5416	2500
G34	53.0	6250	3125
G51	43.9	10625	5000
G53	53.2	5833	2916
G55	48.2	5208	2291
G56	44.6	7083	3333
G91	53.1	6250	2916
G92	53.0	6041	2500
G103	47.2	2931	1041
G110-A	40.1	8333	3333
G110-B	44.4	5833	2916
G116-A	49.4	6041	2500
G116-B	43.1	11875	4583
G117	44.1	5208	2291
G120	39.6	8333	3958
G123	47.8	6250	3125
G124	45.7	5000	2291
G125	42.4	6458	3333
G130	43.4	1250	625
G134	49.1	7500	3333
G135	42.9	6875	2916
G138	50.2	6875	2916
G140-A	47.8	6041	2916
G140-B	40.2	4791	1875
G141	49.3	7291	3541
G142	38.3	5416	2500
G145	46.0	8750	4166
G147	49.8	6041	3125
G148	42.1	8750	3958
G150	41.5	6250	2916
Khaista-17	45.2	5833	2708
Wadaan-17	41.1	5833	2916
Paseena	49.7	6875	2916
Kohat-17	48.7	5625	2291
Pakistan-13	47.0	3750	1666
LSD (5%)	4.3	3584	1647

Table 4. ***Variance components, GCV, PCV, h^2 and genetic gain for heading and yield component traits of 36 spring wheat genotypes during 2020-21.***

Traits	V_g	V_e	**GCV (%)**	**PCV (%)**	h^2	R_e
Heading (days)	3.85	1.41	2.11	2.46	0.73	3.46
Spikes m^{-2} (no)	3853.13	4752.19	23.57	35.23	0.45	85.57
Spike length (cm)	0.32	0.28	6.34	8.67	0.54	0.85
Seeds $spike^{-1}$ (no)	15.72	33.69	8.39	14.88	0.32	4.61
1000-seed weight (g)	16.51	4.41	8.79	9.89	0.79	7.44
Biological yield (kg ha^{-1})	2116587.00	3117904.00	22.99	36.17	0.40	1905.75
Seed yield (kg ha^{-1})	411018.20	658618.60	22.25	35.89	0.38	818.67

Table 5. ***Correlation among heading and yield component traits of 36 spring wheat genotypes at Peshawar during 2020-21.***

Traits	**Spikes per m^2**	**Spike length**	**Seeds per spike**	**1000-seed weight**	**Biological yield**	**Seed yield**
Days to heading	0.27	0.21	0.35*	0.28	0.14	0.14
Spikes per m^2		0.21	0.22	0.17	0.74**	0.64**
Spike length			0.62**	0.10	0.42**	0.41*
Seeds per spike				-0.57**	0.39*	0.34*
1000-seed weight					0.15	0.12
Biological yield						0.96**

*= 5 % significance level

**= 1 % significance level

Conclusions and Recommendations

Mean square table showed that wheat genotypes differed significantly for the studied traits indicate sufficient genetic diversity for them. All the studied parameters other than days to heading and 1000-seed weight, showed moderate heritability. Therefore, it would also be effective to select for these highly heritable traits in early segregating generations. Correlation studies revealed a strong positive phenotypic association between biological yield and seed yield. Seeds per spike showed a negative association with 1000-seed weight. These findings of correlation study can be taken into consideration while practicing selection for improvement in yield components and ultimately yield. Wheat genotypes G116-B and G51 were found best for high yield in the current study and are therefore, recommended for further testing under late sowing conditions in Khyber-Pakhtunkhwa for possible release as new cultivars.

Author's Contribution

Aftab Jehan: Conducted the research, data analysis and wrote draft of the manuscript.

Iftikhar Hussain Khalil: Supervised the research study.

Khalil Ullah: Revise the manuscript

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