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Research Article

Estimation of Genetic Parameters in F_3 Segregating Spring Wheat Populations for Yield and Yield Related Traits

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Abstract: The knowledge about genetic diversity of wheat genotypes is useful for the development of efficient cultivars adapted to diverse conditions. Various genetic parameters like broad-sense heritability, expected selection response, and correlation analysis were estimated among 12 F_3 spring wheat populations derived from eight parents. The 20 wheat genotypes exhibited highly significant differences ($P \leq 0.01$) for all the studied traits. BT4N-11 × Zam-2004 revealed maximum spikes plant^{-1}, while highest spikelets and grains spike^{-1} were obtained for BTRF-1 × Zam-2004. BTRF-17 × Kohat-2010 and BT6N-5 × Kohat-2010 revealed maximum grain yield and harvest index plant-^{1}, while BTRF-3 × Zam-2004 and BT4N-11 × Kohat-2010 showed maximum 1000-grain weight and biological yield plant^{-1} among 12 F_3 populations. Moderate to high heritability estimates were obtained for all the studied traits among the evaluated 12 F_3 populations. Principal component analysis revealed biological yield per plant (0.483), 1000-grain weight (0.586), and harvest index (0.601) as the major variability contributing traits. Correlation analysis for grain yield, biological yield, and 1000-grain weight exposed positive and significant associations among each other and also with other yield contributing traits. Hence, it is concluded that BT4N-11 × Zam-2004, BT4N-11 × Kohat-2010, BT6N-12 × Zam-2004 and BTRF-17 × Kohat-2010 exhibited high estimates of genetic parameters and multivariate analysis coupled with high mean performance for most of the yield traits among 12 F_3 populations and therefore, should be further used as F_4 populations for possible selection of desirable lines.

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Yazlık Buğdayda Verim ve Verim ile İlgili Genetik Parametrelerin F_3 Açılan Populasyonlarında Tahmini

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Anahtar Kelimeler

Çeşitlilik,
Tane verimi,
Kalıtsallık

Öz: Çeşitli koşullara adapte olmuş verimli çeşitlerin geliştirilebilmesi için buğday genotiplerinin genetik çeşitliliği hakkında bilgiye sahip olunması yararlıdır. Sekiz ebeveynden elde edilen 12 adet F_3 yazlık buğday popülasyonu arasında geniş anlamda kalıtım derecesi, beklenen seleksiyon yanıtı ve korelasyon analizi gerçekleştirilmiştir. 20 adet buğday genotipi incelenen tüm özellikler için oldukça önemli farklılıklar göstermiştir ($P \leq 0.01$). BT4N-11 × Zam-2004 ile bitki başına en yüksek başak sayısı saptanırken, BTRF-1 × Zam-2004 ile bitki başına en yüksek başakçık sayısı ve bitki başına başakta en yüksek tane sayısı saptanmıştır. BTRF-17 × Kohat-2010 ile bitki başına en yüksek tane verimi ve hasat indeksi elde edilirken, 12 F_3 popülasyonu arasında BTRF-3 × Zam-2004 ve BT4N-11 × Kohat-2010 ile en yüksek 1000 dane ağırlığı ve biyolojik verim elde edilmiştir. Değerlendirilen 12 F3 popülasyonu arasında incelenen tüm özellikler için orta ila yüksek kalıtsallık tahminleri elde edilmiştir. Temel bileşen analizi ile bitki başına biyolojik verim (0.483), 1000 tane ağırlığı (0.586) ve hasat endeksi (0.601) önemli varyasyon sağlayan özellikler olarak saptanmıştır. Korelasyon analizi tane verimi, biyolojik verim ve 1000 tane ağırlığı için birbirleri arasında ve ayrıca verime katkıda bulunan diğer özelliklerle pozitif ve anlamlı bir ilişki ortaya koymuştur. Sonuç olarak, BT4N-11 × Zam-2004, BT4N-11 × Kohat-2010, BT6N-12 × Zam-2004 ve BTRF-17 × Kohat-2010 ile üstün genetik parametreler sergilenmekle birlikte, 12 F_3 popülasyonu arasındaki verim bileşenlerinin çoğunda iyi bir performansa sahip olduğu ve bu nedenle arzu edilen hatların seçimi için ileriki çalışmalarda ayrıca F_4 popülasyonları olarak kullanılabileceği saptanmıştır.

1. Introduction

Wheat (*Triticum aestivum*) is one of the first domesticated food crops and is also known as the main source of calories and proteins in developing countries (Hossain and Teixeira da Silva, 2013). It is a widely adapted food crop around the world by providing more than half of its calories and nearly half of its protein to one-third of the world's population (Farshadfar et al., 2013). Wheat production is consistently changing under different environmental conditions, thus the adaptation of crops to changing global conditions is needed (Almeselmani et al., 2011). Wheat was cultivated in Pakistan on an area of 8972.5 thousand hectares with production and average yield of 26673.6 thousand tons and 2892 kg hectare^{-1}, respectively during 2016-17 (MNFSR, 2017).

One of the world's big concerns in the twenty-first century is the production of enough food for current and future generations while confronting climate change, and adverse environmental factors associated with biotic and abiotic stresses (Barut et al., 2021). In order to mitigate these problems, there is a need to identify the novel source of useful genetic variability. Genetic diversity can be an effective approach by providing a good source of variations (Nadeem et al., 2018; Ali et al., 2020a; Kocak et al., 2020; Balkan et al., 2021). Selection of parents and cross combinations having desirable traits is the first priority of plant breeders. The most common method of developing genetic diversity is hybridization among parental genotypes possessing traits of interest. So, the extent of variability among parents and its combinations is of huge importance in all wheat breeding programs. Estimation of genetic variance in the early generation of the various cross combinations is very fruitful to plant breeders (Ejaz-Ul-Hassan and Khaliq, 2008).

Various techniques are used to estimate the genetic basis of important plant traits and their transmission rate. Heritability is a key tool for the estimation of transmission rate from parents to offspring or from one generation to another generation. Heritability is simply the ratio of total genetic variance to the total phenotypic variance. Expected selection response has a direct relationship with heritability and can be estimated in different populations under various environmental conditions. Traits having high heritability will lead to a high expected selection response and finally genetic improvement of that desirable trait (Sial et al., 2013). The main possibilities of increasing wheat production in the last couple of years are either due to better agronomic inputs or cultivars having the potential of higher yield. 50% increment in wheat yield is only because of the development of genetically improved cultivars by wheat breeders since the green revolution by Norman Borlaug in mid-1960’s (Khalil and Afridi, 2004). Continuous wheat yield improvement programs are always important due to the consistently increasing demand for wheat. It is highly suggested to estimate phenotypic plant diversity of important morphological traits along with suitable multivariate analysis for better diversity estimation (Vollmann et al., 2005). Associations among important plant traits could be easily understood with the help of correlation analysis (Baloch et al., 2014).

This study aimed to estimate genetic parameters in 12 F_3 spring wheat populations for the identification of promising segregants which support the main objectives of the breeding program to genetically improve spring wheat in Pakistan.

2. Material and Methods

2.1. Experimental site and phenotypic evaluation

This study was conducted at Malakandher Research Farm (Lat. 34° 01′ 10.37 N″, Long. 71° 28′ 01.69″ E, Elevation 365.5m), the University of Agriculture, Peshawar-Pakistan during the wheat crop season 2016-17. Eight parents and their 12 F_3 populations were planted in randomized complete block design with three replications in the 2nd week of November 2016. Three rows of each genotype per replication were sown having a length of three meters. Plant to plant and row to row distance was maintained at 10 and 30 cm, respectively. Thus, total the plot area in each replication for each genotype was 2.7 m^2. Normal cultural practices and fertilizer doses of 120 kg nitrogen and 60 kg phosphorous ha^{-1} as recommended for wheat were applied during the growing season. Half nitrogen and full phosphorous fertilizer dose were applied at sowing time, while the remaining nitrogen was applied at the booting stage.

Data were recorded on flag leaf area, plant height, spikes $plant^{-1}$, spike length, spikelets $spike^{-1}$, grains $spike^{-1}$, 1000-grain weight, biological yield, grain yield, and harvest index. Five plants from each parental genotype and 10 plants from each F_3 population were randomly selected for data recording in each replication to compute variances of parental lines and F_3 populations, and to calculate genetic parameters and multivariate analysis.

2.2. Statistical analysis

Singh and Chaudhary (1985) approach as outlined for RCB design were subjected to analysis of variance (ANOVA) for mean data of all parameters. ANOVA was constructed in statistical software SAS 9.3 version (Statistical Analysis Software/Stat Software, 2011). The sum of squares pertaining to genotypes was further partitioned into the sum of squares due to parents, F_3 populations, and parents vs. F_3 contrast. The least significant difference (LSD) test as outlined by Gomez and Gomez (1984) was used for the mean comparison of genotypes including parental genotypes as well as F_3 populations. LSD test was also constructed in statistical software SAS 9.3 version. Frequency distribution was performed using statistical software XLSTAT (Addinsoft, 2018) (www.xlstat.com). The modified formula of Mahmud and Kramer (1951) was used to estimate broad-sense heritability (h^2_{BS}) for yield contributing traits using variances of parental genotypes and F_3 populations. Principal component analysis and Pearson correlation coefficient were calculated through the XLSTAT statistical software (www.xlstat.com).

3. Results and Discussion

3.1. Genetic diversity and morpho-agronomic performance

Analysis of variance regarding genotypes, parents, F_3 populations, and parents vs. F_3 contrast is presented in Table 1. Analysis of variance revealed that genotypes and parents display highly significant differences for all the studied traits except spikes $plant^{-1}$ in parents. F_3 populations revealed highly significant differences for plant height, spike length, grains $spike^{-1}$, 1000-grain weight, grain yield $plant^{-1}$, and harvest index. Moreover, significant differences were obtained only for spikes $plant^{-1}$ in 12 F_3 populations. Similarly, parents vs. F_3 contrast exhibited highly significant and significant differences for grains spikes^{-1}, grain yield plant^{-1}, harvest index, and biological yield plant^{-1}. Our current results are strongly supported by the findings of Azam et al. (2013) and Kumar et al. (2014) as they also reported significant differences among genotypes, parents, F_3 populations, and parents vs. F_3 contrast.

Table 1. Mean squares for various yield and related traits of 20 wheat genotypes (8 parents and 12 F_3 populations) were evaluated during 2016-17

Source	DF	FLA	PH	SPP	SL	SLPS	GPS	TGW	BYPP	GYPP	HI
Genotypes	19	48.03**	284.18**	4.85**	1.65**	1.90**	56.83**	43.19**	278.68**	48.18**	281.26**
Parents	7	85.23**	324.80**	4.39ns	1.95**	3.77**	51.78**	41.70**	384.75**	73.81**	119.38**
F_3 Pops.	11	27.47ns	280.99**	5.43*	1.50**	0.87ns	56.19**	45.26**	182.32ns	34.87**	386.09**
Parents vs. F_3	1	13.69ns	35.07ns	1.68ns	1.23ns	0.03ns	99.26**	30.93ns	596.84*	15.11**	261.27**
Error	38	14.29	25.83	2.31	0.37	0.73	2.2	9.68	109.7	0.49	0.56
CV (%)	_	9.4	4.73	13.72	4.78	3.84	2.02	8.35	16.89	3.04	1.78
R2	_	0.65	0.85	0.6	0.71	0.57	0.93	0.71	0.6	0.98	0.99

FLA: flag leaf area; PH: plant height; SPP: spikes per plant; SL: spike length; SLPS: spikelets per spike; GPS: grains per spikes; TGW: 1000-grain weight; BYPP: biological yield per plant; GYPP: grain yield per plant and HI: harvest index.

*, ** = Significant at 5 and 1% probability level, respectively.

ns = Non-significant.

Mean performances among eight parents and their 12 F_3 populations are presented in Table 2. The flag leaf area greatly contributes to grain yield, 1000-seed weight, and grain number in the wheat plant, thus a higher flag leaf area is always desirable.

Table 2. Means for various yield and related traits of 20 wheat genotypes (8 parents and 12 F_3 populations) were evaluated during 2016-17

Genotypes	FLA	PH	SPP	SL	SLPS	GPS	TGW	BYPP	GYPP	HI
I. Parents										
BT4N-11	42.4±3.3	95.8±5.5	12.9±0.8	11.7±0.5	23.5±0.6	81.5±3.8	34.3±2.8	81.2±7.6	29.0±3.0	36.8±3.7
BT6N-5	43.7±2.8	107.9±5.4	11.3±0.8	13.8±0.5	23.7±0.5	80.5±3.1	40.0±2.3	80.2±6.8	32.0±3.5	40.0±3.9
BT6N-12	47.6±2.6	113.5±4.3	10.9±0.8	12.0±0.4	20.5±0.5	71.5±2.9	41.6±2.8	73.3±6.9	23.0±3.4	31.8±3.9
BTRF-1	38.3±3.2	115.5±6.5	9.1±0.6	12.3±0.5	21.9±0.5	75.5±3.3	37.4±3.4	56.5±6.5	21.6±3.3	40.3±3.6
BTRF-3	42.4±1.1	114.4±4.3	10.5±0.7	12.0±0.5	21.9±0.3	74.2±3.4	37.6±3.3	62.7±5.5	23.5±3.6	40.0±3.7
BTRF-17	35.0±3.2	100.4±6.2	11.9±0.6	11.9±0.4	22.2±0.4	69.5±3.4	32.3±3.3	58.2±6.5	23.0±3.3	42.1±3.8
Zam-2004	45.1±2.1	116.1±4.1	12.6±0.5	13.6±0.3	23.2±0.3	72.9±2.8	37.2±2.7	64.8±5.3	23.1±2.9	35.9±2.9
Kohat-2010	31.8±2.5	88.7±4.4	10.9±0.5	12.5±0.3	21.2±0.3	73.9±2.7	30.6±2.6	50.2±5.4	15.4±2.8	38.0±3.3
Parents Mean	**40.8**	**106.5**	**11.3**	**12.5**	**22.3**	**74.9**	**36.4**	**65.9**	**23.8**	**38.1**
II. F_3 Populations										
BT4N-11 × Zam-2004	39.6±3.9	101.6±9.6	13.0±1.1	12.5±0.5	22.8±0.6	71.8±4.1	31.4±3.4	53.9±9.4	18.9±3.8	35.2±4.3
BT4N-11 × Kohat-2010	38.9±3.4	104.8±10.2	12.7±1.4	13.8±0.7	22.8±0.6	78.5±4.3	33.6±3.4	77.3±9.5	19.9±4.3	25.8±3.7
BT6N-5 × Zam-2004	40.1±4.0	104.3±9.8	10.3±1.6	13.2±0.8	22.8±0.8	69.5±4.5	38.6±3.5	61.9±9.9	22.7±4.2	37.4±3.9
BT6N-5 × Kohat-2010	33.4±4.3	98.4±9.8	11.0±1.1	12.8±0.7	22.3±0.9	67.1±3.9	40.9±3.9	51.2±9.6	24.5±4.6	48.6±4.7
BT6N-12 × Zam-2004	38.9±4.4	101.4±9.2	12.3±1.2	13.6±0.6	22.5±0.7	77.5±3.7	37.5±3.0	63.9±8.8	27.0±3.8	42.4±4.5
BT6N-12 × Kohat-2010	41.8±4.1	100.9±8.8	10.1±0.9	13.2±0.6	21.8±0.5	73.6±4.6	32.4±3.5	51.7±7.6	17.4±3.4	33.9±4.9
BTRF-1 × Zam-2004	45.1±3.5	130.5±7.9	11.3±0.7	12.9±0.8	22.9±0.6	79.7±4.0	41.3±2.0	66.6±9.3	26.8±4.3	40.3±4.3
BTRF-1 × Kohat-2010	40.5±3.4	102.3±10.3	8.9±0.9	12.3±0.5	22.0±0.7	72.2±4.1	36.0±3.4	51.8±9.5	19.6±4.7	39.6±3.7
BTRF-3 × Zam-2004	38.7±3.7	117.9±10.7	9.2±1.2	12.0±0.4	22.7±0.7	69.0±4.6	43.9±3.8	55.7±9.8	23.0±3.7	42.0±3.5
BTRF-3 × Kohat-2010	42.0±4.3	104.1±9.8	9.6±1.3	12.4±0.6	22.3±0.8	72.0±4.5	37.2±3.9	56.2±8.9	21.9±3.9	39.1±4.6
BTRF-17 × Zam-2004	36.3±4.1	117.9±9.4	11.2±1.1	11.3±0.6	21.3±0.8	66.4±3.8	40.5±4.0	58.4±10.0	23.7±4.6	40.6±4.1
BTRF-17 × Kohat-2010	42.4±4.0	113.2±7.4	11.7±0.9	13.3±0.7	21.5±0.6	70.5±4.5	40.7±3.4	64.9±8.4	28.0±4.3	43.4±4.0
F_3 Mean	**39.8**	**108. 1**	**10.9**	**12.8**	**22.3**	**72.3**	**37.8**	**59.5**	**22.8**	**39.0**
LSD (5%)	**6.2**	**8.4**	**2.5**	**1.0**	**1.4**	**2.5**	**5.1**	**17.3**	**1.0**	**1.0**

The current study reported a higher mean flag leaf area (39.8 cm^2) for the studied 12 F_3 wheat populations compared to Khan et al. (2003) (26.5 cm^2) and Azam et al. (2013) (18.3 cm^2). Khan et al. (2003) tested six parents and their six F_2 populations, while Azam et al. (2013) evaluated five parents and their 14 F_3 populations. Semi-dwarf wheat cultivars are preferred due to various reasons like lodging and yield losses. Tall wheat cultivars reduced harvestable yield up to 80% due to lodging. The current study revealed semi-dwarf wheat populations with a mean plant height of 108.1 cm and supported the results of the previous studies of Khan et al. (2003) and Azam et al. (2013) as they reported mean plant height of 110.42 and 112 cm while evaluating wheat populations respectively.

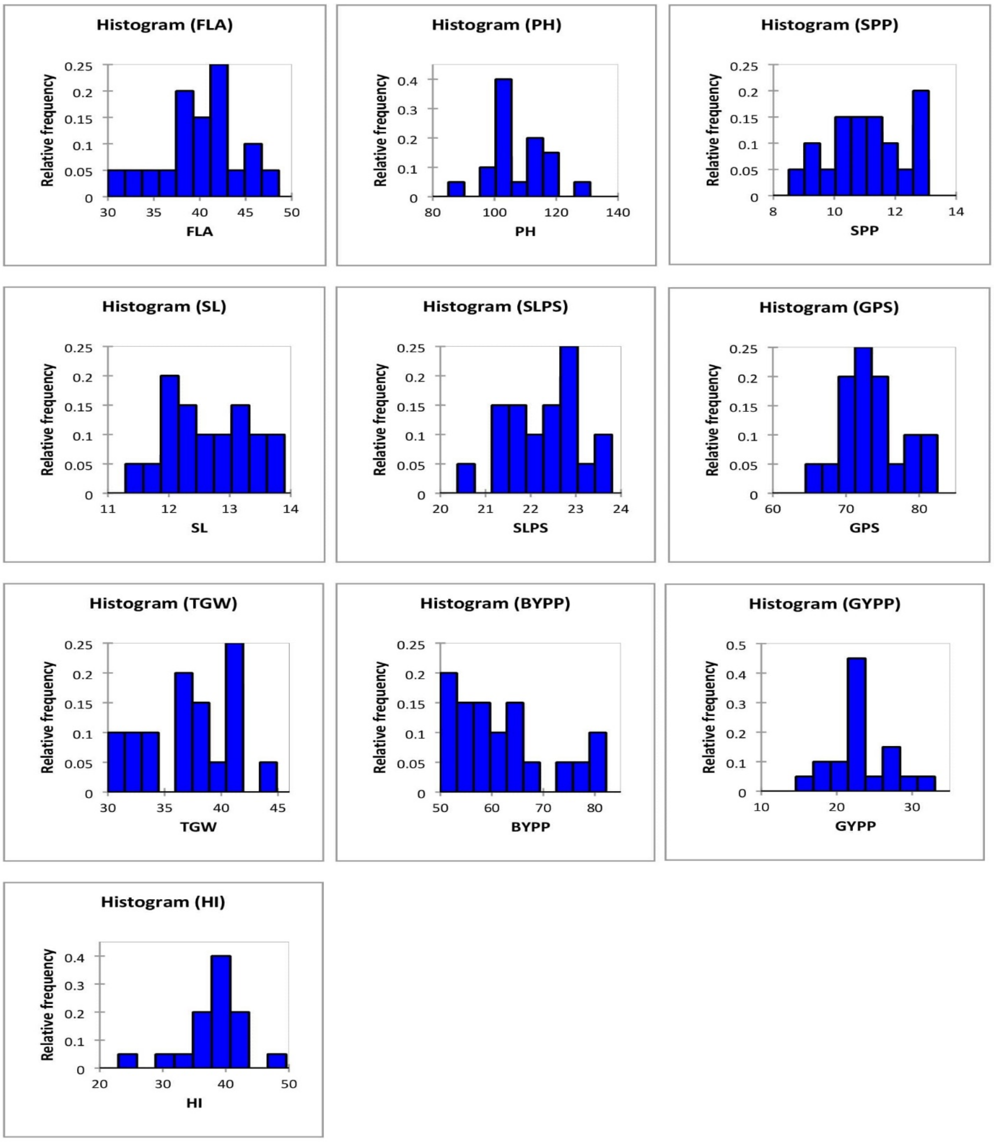

Figure 1. Frequency distribution of the studied traits among 8 parents and 12 F_3 wheat populations

Our current study supported the findings of Khan et al. (2003) by revealing the number of spikes plant^{-1} in the same range. Ahmad et al. (2007) reported a lower mean spike length (10.73 cm) in the developed five wheat crosses compared to our findings (12.8 cm). The developed F_3 populations reported a higher mean number of spikelets spike^{-1} (22.3), grains spike^{-1} (72.3), and grain yield plant^{-1} (22.8 g) compared to wheat F_3 populations developed by Memon et al. (2007) as they obtained mean spikelets spike^{-1}, grains spike^{-1}, and grain yield plant^{-1} of 18.64, 57.33, and 13.03 (g) respectively. The studied F_3 populations exhibited a higher mean harvest index (39 %) compared to the mean harvest index of F_3 populations developed by Azam et al. (2013) (30.9%). Most of the studied traits exhibited promising performance compared to various wheat populations developed previously. It clearly suggested that the investigated F_3 populations comprise good cross combinations that must be further explored. Frequency distribution was also performed to better understand the behavior of the recorded data. Frequency distribution with the help of histogram exhibited normal distribution for the studied 10 traits among 8 parents and 12 F3 populations (Figure 1).

3.2. Heritability and expected selection response of wheat derived 12 F_3 populations

Heritability and expected selection response estimation among 12 F_3 spring wheat populations are presented in Table 3. Heritability and expected selection response ranged from 0.52 (BT4N-11 × Zam-2004) to 0.78 (BTRF-1 × Kohat-2010 and BTRF-3 × Kohat-2010) and 5.29 cm^2 (BT4N-11 × Zam-2004) to 16.08 cm^2 (BTRF-1 × Kohat-2010) for flag leaf area among F_3 populations. Khan et al. (2003) tested six F_2 wheat cross combinations along with their six parents to estimate heritability and selection response for yield associated parameters in wheat. They observed high heritability (0.85) for flag leaf area in wheat cross WLRG-3 × 5039. Heritability and expected selection response among F_3 populations for plant height ranged from 0.56 (BTRF-1 × Kohat-2010) to 0.89 (BTRF-17 × Zam-2004) and 6.69 cm (B TRF-1 × Kohat-2010) to 17.61 cm (BTRF-17 × Zam-2004). Our findings are supported by the work of Ahmad et al. (2007) who also obtained high heritability of 0.89 in wheat cross WL60 × LU26S. Similarly, Memon et al. (2007) examined seven F_3 populations along with eight parents for yield contributing traits in wheat. They reported low heritability (0.56) and high heritability (0.92) for F_3 progeny RWM-9313 × Kiran 95 and Khirman × RWM-9313, which further confirm our findings. Moreover, Khan et al. (2003) also obtained high heritability (0.89) for plant height in cross WLRG-3 × LU-26S that is in accordance with our results. Heritability and expected selection response ranged from 0.32 (BTRF-3 × Zam-2004) to 0.70 (BT4N-11 × Zam-2004) and 1.50 spikes (BTRF-3 × Zam-4) to 4.72 spikes (BT4N-11 × Zam-2004) among 12 F_3 populations for spikes $plant^{-1}$. Magda and Abd El-Rahman (2013) studied three wheat crosses obtained as a result of five wheat parents crossing for yield and its contributing traits. They obtained high heritability (0.83) for spikes $plant^{-1}$ in wheat crosses, which confirms our findings. F_3 populations BT4N-11 × Kohat-2010, BT4N-5 × Zam-2004 and BTRF-3 × Kohat-2010 revealed maximum heritability (0.78) each, while BT6N-12 × Zam-2004 manifested minimum heritability (0.57) for spike length. Expected selection response ranged from 0.95 cm (BTRF-3 × Zam-2004) to 1.86 cm (BT6N-5 × Zam-2004). Memon et al. (2007) reported low heritability (0.58) for F_3 wheat progeny Marvi-2000 × Soghat-90, while high heritability (0.64) for Marvi-2000 × Khirman, which are in accordance with our finding. Furthermore, Ahmad et al. (2007) estimated high heritability (0.76) for wheat cross WL59 × LU26S. Heritability and expected selection response for spikelets $spike^{-1}$ among 12 F_3 populations ranged from 0.45 (BT6N-5 × Kohat-2010) to 0.71 (BT4N-11 × Zam-2004) and 1.22 spikelets (BT6N-5 × Kohat-2010) to 2.69 spikelets (BT4N-11 × Zam-2004) (Table 3). Memon et al. (2007) evaluated seven cross combinations of F_3 generation along with its eight parents to predict heritability and selection response for these cross combinations. They obtained low heritability (0.46) for spikelets $spike^{-1}$ in F_3 progeny of Marvi-2000 × Soghat-90. Heritability and expected selection response for grains $spike^{-1}$ among 12 F_3 populations ranged from 0.58 (BTRF-17 × Zam-40) to 0.84 (BTRF-1 × Kohat-2010) and 10.82 grains $spike^{-1}$ (BTRF-17 × Zam-2004) to 22.05 grains $spike^{-1}$ (BTRF-3 × Kohat-2010). Memon et al. (2007) evaluated eight parents and their seven F_3 populations for yield contributing traits in wheat to estimate heritability. They reported moderate to high heritability (0.57 to 0.63) for the F_3 wheat population Soghat-90 × Sarsabz and SD-1200/14 × IB 25/99. Moreover, Ahmad et al. (2007) estimated moderate heritability (0.60) for grains $spike^{-1}$ in wheat cross WL59 × LU26S. Heritability and selection response for 1000-grain weight ranged from 0.30 (BT6N-5 × Kohat-2010) to 0.75 (BT6N-12 × Kohat-2010) and 0.24 g (BTRF-1 × Kohat-2010) to 0.96 g (BT6N-12 × Kohat-2010), respectively. Our results are supported by the work of Ahmad et al. (2007) who reported high heritability (0.75) for cross WL60 × LU26S. Heritability and expected selection response magnitude ranged from 0.54 (BT6N-12 × Zam-2004) to 0.72 (BTRF-17 × Kohat-2010) and 15.60 g (BT6N-12 × Zam-2004) to 27.50 g (BTRF-17 × Kohat-2010) for biological yield $plant^{-1}$. The extent of heritability and selection response for grain yield $plant^{-1}$ ranged from 0.39 (BT6N-12 × Kohat-2010) to 0.81 (BT6N-12 × Zam-2004) and 4.65 g (BT6N-12 × Kohat-2010) to 16.84 g (BT6N-12 × Zam-2004). Ahmad et al. (2007) reported high heritability (0.87) for grain yield in wheat cross WL59 × LU26S which confirms our findings. Heritability and expected selection response for harvest index ranged from 0.36 (BTRF-1 × Zam-2004) to 0.96 (BTRF-17 × Kohat-2010) and 7.72 % (BTRF-1 × Zam-2004) to 128.59% (BTRF-17 × Kohat-2010). The explored wheat populations revealed a sufficient amount of broad-sense heritability and expected selection response for the studied traits.

Table 3. Heritability estimates (h^2) and expected selection response (R_e) for yield and yield related traits of 12 F_3 populations derived from eight parents of wheat

Traits	**PH (cm)**		**FLA (cm^2)**		**SPP (no)**		**SL (cm)**		**SLPS (no)**		**GPS (no)**		**TGW (g)**		**BYPP (g)**		**GYPP (g)**		**HI (%)**	
F_3 populations	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e	h^2	R_e
BT4N-11 × Zam-2004	0.86	14.66	0.52	5.29	0.70	4.72	0.76	1.55	0.71	2.69	0.69	14.86	0.69	0.61	0.61	19.36	0.62	8.91	0.74	15.94
BT4N-11 × Kohat-2010	0.67	7.18	0.64	7.79	0.61	3.61	0.78	1.74	0.48	1.37	0.80	20.85	0.63	0.49	0.63	21.57	0.68	11.07	0.78	18.79
BT6N-5 × Zam-2004	0.76	9.84	0.61	8.30	0.34	1.82	0.78	1.86	0.57	1.75	0.81	21.38	0.50	0.58	0.59	17.91	0.72	11.98	0.82	31.32
BT6N-5 × Kohat-2010	0.69	7.55	0.74	12.48	0.53	3.39	0.71	1.56	0.45	1.22	0.77	18.45	0.30	0.29	0.68	24.45	0.68	11.03	0.79	30.49
BT6N-12 × Zam-2004	0.87	15.35	0.64	8.73	0.39	2.01	0.57	1.00	0.65	2.03	0.77	17.65	0.40	0.34	0.54	15.60	0.81	16.84	0.93	41.19
BT6N-12 × Kohat-2010	0.77	9.73	0.72	11.58	0.57	3.55	0.72	1.62	0.54	1.43	0.80	18.94	0.75	0.96	0.58	18.81	0.39	4.65	0.83	24.73
BTRF-1 × Zam-2004	0.79	13.93	0.69	11.79	0.61	3.69	0.71	1.28	0.58	1.53	0.69	11.91	0.39	0.33	0.61	18.85	0.65	9.86	0.36	7.72
BTRF-1 × Kohat-2010	0.56	6.69	0.78	16.08	0.53	3.00	0.70	1.28	0.52	1.27	0.84	19.77	0.30	0.24	0.69	25.61	0.64	9.85	0.64	19.09
BTRF-3 × Zam-2004	0.77	9.89	0.61	8.51	0.32	1.50	0.59	0.95	0.55	1.36	0.68	13.57	0.35	0.32	0.61	19.07	0.54	8.03	0.57	14.28
BTRF-3 × Kohat-2010	0.68	7.33	0.78	14.57	0.55	3.15	0.78	1.76	0.69	2.02	0.82	22.05	0.32	0.29	0.65	22.92	0.51	7.77	0.42	9.22
BTRF-17 × Zam-2004	0.89	17.61	0.56	7.24	0.34	1.95	0.61	1.11	0.48	1.25	0.58	10.82	0.57	0.67	0.66	21.36	0.64	9.01	0.45	17.05
BTRF-17 × Kohat-2010	0.64	6.79	0.75	13.35	0.53	3.65	0.70	1.50	0.62	1.86	0.79	20.08	0.34	0.32	0.72	27.50	0.60	8.49	0.96	128.59

3.3. Correlation and principal component analysis

Correlation analysis is mainly applied to understand relatedness among various traits and evaluated information can be best used for crop improvement by an indirect selection of the components affecting crop yield (Ali et al., 2020b). Crop improvement depends upon the success of the selection criteria. The importance of the traits can be judged from their direct or indirect effects upon yield components, especially seed yield. It is therefore very important to know about the relative effects of the traits influencing the economically important traits in a desirable direction and to be selected in the crop improvement programs (Vrijendra et al., 2004). Correlation coefficients among the traits are presented in Table 4. Biological yield per plant revealed a positive and significant correlation with flag leaf area (0.563), seeds per spike (0.506), grains per spike (0.650), and grain yield per plant (0.657). Plant height exposed a positive and significant correlation with flag leaf area (0.521) and 1000-grain weight (0.690). Spikelets per spike exhibited a positive and significant correlation with grains per spike (0.504), while 1000-grain weight showed a positive and significant correlation with grain yield per plant (0.571). Present results confirmed the previous findings of Dutamo et al. (2015); Ahmad et al. (2016); Ali et al. (2017) and Adnan et al. (2017).

Principal component analysis (PCA) helps to recognize important plant traits that are used to characterize the variations among experimental materials (Chakravorty et al., 2013). Principal component analysis precisely classified 10 morphological traits into 10 principal components among which the first three principal components; PC1, PC2, and PC3 were selected along with their Eigenvalues. These three components explained nearly 72.911% of the total genetic variation (Table 5). The first principal component (PC1) contributed about 34.345% of the variation, showing the highest contributions from biological yield per plant (0.483) followed by grains per spike (0.398) and grains per plant (0.382). PC2 explained 24.505% of the variation with the highest contributions from 1000-grain weight (0.586) followed by Plant height (0.463) and harvest index (0.371). PC3 revealed 14.061% variation having the highest contributions from harvest index (0.601) followed by spikelets per spike (0.385) and grain yield per plant (0.363).

Table 4. Correlation analysis for various yield and related traits of 20 wheat genotypes (8 parents and 12 F_3 populations)

Variables	FLA	PH	SPP	SL	SLPS	GPS	TGW	BYPP	GYPP
FLA									
PH	**0.521**								
SPP	0.065	-0.162							
SL	0.207	-0.049	0.276						
SLPS	0.173	-0.003	0.352	0.410					
GPS	0.387	-0.009	0.314	0.368	**0.504**				
TGW	0.334	**0.690**	-0.311	-0.036	-0.036	-0.217			
BYPP	**0.563**	0.190	**0.506**	0.253	0.405	**0.650**	0.186		
GYPP	0.390	0.333	0.284	0.152	0.443	0.344	**0.571**	**0.657**	
HI	-0.360	0.066	-0.265	-0.194	-0.009	-0.347	0.417	-0.399	0.393

FLA: flag leaf area; PH: plant height; SPP: seeds per spike; SL: pike length; SLPS: spikelets per spike; GPS: grains per spike; TGW: 1000-grain weight; BYPP: biological yield per plant; GYPP: grain yield per plant; HI: harvest index.
Values in bold are different from 0 with a significance level alpha=0.05.

The results suggested that traits, biological yield per plant, grain yield per plant, grains per spike, 1000-grain weight, plant height, harvest index, and spikelets per spike were responsible for the genetic variation in the spring wheat genotypes. It is interpreted from the above that the traits that contributed variation in each component may contain the same genes that should be useful during selection to identify the most diverse segregants. These morphological traits having the highest variation contribution should be employed as desirable tools when screening elite populations during field studies. It is concluded that principal component analysis is very helpful to attain more accurately aware of the relationship between traits that had the highest impact on seed yield per plant and to predict the best selection indices for the yield improvement in various segregating populations. Spring wheat populations revealing best mean performance and exposed higher genetic and multivariate parameters could be effectively suggested for selection and further evaluation at later generations. The selected spring wheat populations can be used as an important source of superior cultivar development.

Table 5. PCA analysis for various yield and related traits of 20 wheat genotypes (8 parents and 12 F_3 populations)

Trait	PC1	PC2	PC3
FLA	0.366	0.168	-0.448
PH	0.173	0.463	-0.308
SPP	0.275	-0.298	0.206
SL	0.261	-0.175	0.117
SLPS	0.341	-0.113	0.385
GPS	0.398	-0.225	-0.018
TGW	0.12	0.586	0.005
BYPP	0.483	-0.03	-0.082
GYPP	0.382	0.304	0.363
HI	-0.155	0.371	0.601
Eigenvalue	3.435	2.45	1.406
Variability (%)	34.345	24.505	14.061
Cumulative %	34.345	58.85	72.911

FLA: flag leaf area; PH: plant height; SPP: seeds per spike; SL: spike length; SLPS: spikelets per spike; GPS: grains per spike; TGW: 1000-grain weight; BYPP: biological yield per plant; GYPP: grain yield per plant; HI: harvest index.

4. Conclusion

Analysis of variance exhibited highly significant differences ($P \leq 0.01$) for all the studied traits among 20 wheat genotypes. Principal component analysis revealed biological yield per plant (0.483), grain yield per plant (0.382), grains per spike (0.398), 1000-grain weight (0.586), plant height (0.463), harvest index (0.601), spikelets per spike (0.385), and grain yield per plant (0.363) as the major variability contributing traits. Correlation analysis for grain yield, biological yield, and 1000-grain yield exposed positive and significant associations among each other and with other yield contributing traits. On the basis of mean performance and genetic and multivariate parameters, F_3 populations BT4N-11 × Zam-2004, BT4N-11 × Kohat-2010, BT6N-12 × Zam-2004 and BTRF-17 × Kohat-2010 were found outstanding and hence might be suggested for further evaluation. Moreover, the parental lines involved in these crosses should be tested in later generations to achieve promising segregants across locations.

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