Research Article

Genetic Gain in Yield and Yield-Related Traits of Bread Wheat Over the Past 40 Years in Khyber Pakhtunkhwa

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Abstract | Periodic estimation of genetic gains in yield and associated traits is essential to know the effectiveness and impact of an ongoing crop breeding program in a specific region. Eighteen landmark wheat cultivars (Pak-81, Pirsabak-85, Suleman-96, Saleem-2000, Pirsabak-04, Pirsabak-05, Pirsabak-08, Pirsabak-13, Shahkar-13, Pirsabak-15, Pakhtunkhwa-15, Wadaan-17, Paseena-17, Gulzar-19, Pirsabak-19, Abaseen-21, Pirsabak-21 and Taskeen-22) released by the Cereal Crops Research Institute (CCRI), Pirsabak during past four decades and highly adapted by wheat growers in Khyber Pakhtunkhwa province of Pakistan were assessed at The University of Agriculture, Peshawar during 2022-23, using a randomized full block design with three replications to ascertain the genetic improvement over time in yield and associated traits of bread wheat cultivars. For all the investigated attributes, the analysis of variance revealed notable variations ($P \leq 0.05$) across wheat cultivars. Linear regression analysis revealed significant increase in plant height (0.05 cm yr^{-1}), spikes m^{-2} (0.24 yr^{-1}), grains $spike^{-1}$ (0.03 $year^{-1}$), 1000-seed weight (0.03 g yr^{-1}), biomass (biological) yield (6.3 kg $ha^{-1*}yr^{-1}$) and seed (grain) yield (2.2 kg $ha^{-1*}yr^{-1}$), while no increase was evident in spike length and single spike weight of current set of wheat cultivars released by CCRI, Pirsabak during past 40 years. Wheat cultivar Pirsabak-15 produced the highest spike count of (524.0 m^{-2}) and spike length (10.1 cm), while cultivar Pirsabak-19 had the highest 1000-grain weight (52.0g), biological yield (13326.7 $kg^{*}ha^{-1}$), and grain yield (4511.1 $kg^{*}ha^{-1}$). Moderate broad-sense heritability estimates (0.34 to 0.53) were found for most traits. Grain yield exhibited significantly positive genotypic and phenotypic correlations with single spike weight (r_g^{*}= 0.99**, r_p = 0.62**), spikelets $spike^{-1}$ (r_g^{-}= 0.99**, r_p^{*}= 0.46*), and 1000-seed weight (r_g = 0.98**, r_p = 0.60**). Grain yield also exhibited a significantly positive genetic relationship with days to maturity (r_g^{*}= 0.98**), plant stature (r_g^{*}= 0.44*), spikes m^{-2} (r_g = 0.61**), and spike length (r_g = 0.99**). It is imperative that wheat breeders should focus on improving yield-contributing traits by introgressing favourable alleles in the newly developed wheat cultivars.

Received | March 17, 2025; **Accepted** | October 16, 2025; **Published** | February 07, 2026
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Citation | Anas, M., K. Khan, H. Ali, A. Rahman, M.A. Raza, A. Wahab, M. Taimur, M.S. Afridi and I.H. Khalil. 2026. Genetic gain in yield and yield-related traits of bread wheat over the past 40 years in Khyber Pakhtunkhwa. *Sarhad Journal of Agriculture,* 42(1): 262-276.
DOI | https://dx.doi.org/10.17582/journal.sja/2026/42.1.262.276
Keywords | Genetic gain, Regression analysis, Wheat varieties, CCRI Pirsabak, Heritability, Correlation

Introduction

A traditional method of wheat breeding will forever remain a viable approach to developing exceptional wheat varieties globally. A primary goal of every breeding initiative is to create wheat genotypes with high yield potential to be introduced as cultivars to farmers. Out of all types, hexaploid (bread) wheat is the most dominant and important since it provides food for humans worldwide. In recent years, almost 95% of wheat species grown worldwide belong to bread wheat (2n =6x= 42). Wheat has become an important grain crop and provides more calories in the diet than other crops. Because of its evolutionary background and cultivation style, it is the most productive cereal crop, which actually became the king of cereals. Approximately 20% of humans' calories comes from wheat grown on approximately 30% of the global cereal-farming lands (Khan *et al*., 2015).

Wheat is one of the principal cereals, i.e., grains used in bread and pasta, that grow on the fertile soils of the Earth. Wheat production is enhanced by the green revolution in different regions around the world (Mwadzengeni *et al*., 2017). During the 2022-23 wheat season, the global crop was sown on 222.33 million hectares of wheat growing land and produced a worldwide yield of 789.86 million tons, creating an average grain productivity rate to be at around approximately 3552 kg ha^{-1} (USDA, 2022-23) for all areas (USDA, 2022-23). Pakistan has 9.0 million hectares of wheat grown, yielding a total of 26.7 million tons of wheat with an average production of roughly 2980 kg ha^{-1}. Wheat has been grown covering an area of 0.8 million ha showing a province-middling yield of 2000 kg ha^{-1} and total grain (milled) production increased up to almost 1.6 m tons in Khyber Pakhtunkhwa. The wheat was cultivated in a 6.6 m ha area of Punjab, with the production of 20.5 m tons also the average yield being 3110 kg ha^{-1}. In Sindh, wheat production totalled 4.1 mt over a cultivated land of 1.2 m ha, having an average of 3420 kg ha^{-1}. In Balochistan, wheat production was 0.9 mt from an area of 0.4 m ha, averaging 2250 kg ha^{-1} (PBS 2022-23). Punjab contributed the most to the wheat production of Pakistan (76%), followed by Sindh (15%), Khyber Pakhtunkhwa (6%) and Baluchistan (3%).

Approximately 67% of wheat in Khyber Pakhtunkhwa is cultivated in rain-fed areas; hence, the average yield is lower than the national yield (Mukhtarullah and Akmal, 2016). Because wheat supports millions of Pakistani farmers and generates money, it has become a political crop for the sustenance of the nation. Approximately 80% of the wheat grain produced in Pakistan is used to make unleavened flatbread, while 20% is used to make baked products. Wheat constitutes 60% of a person's daily diet in Pakistan, with an annual per capita consumption of around 125 kilograms (Qayyum *et al*., 2017).

A complex trait regulated by numerous genes, grain yield is influenced by the production environment (Zheng *et al*., 2011). Some of the nations in which recent research on genetic advancements in wheat yield has been carried out are Iran (Khodarahmi *et al*., 2023), Morocco (Bennani *et al*., 2023), Chili (Del-Pozo *et al*., 2022), China*(Gao *et al*., 2017; *Zhou *et al*., 2007), in Turkey (Keser et*al., 2017), in USA (Balota**et al*., 2017; *Gray-Bosch and Peterson, 2010), Canada (Clarke et*al., 2010; Hucl *et al*., 2015), Spain* (Sanchez-Garcia *et al*., 2012), Mexico (Aisawi *et al*., 2015; Manes *et al*., 2012), in Australia* (Sadras and Lawson, 2011), and in Bangladesh (Ferdous *et al*., 2011).

The ears per unit area, like any other parameter, is important for increasing the grain yield of wheat (Xiao *et al*., 2012) and a high positive correlation with it was documented by Sharma *et al*.(2009), Aisawi *et al*. (2015) and Zheng *et al*. (2011). Other research has shown a correlation between higher grain yield and both a decreased plant height and an increased harvest index (Ehdaie *et al*., 2006). By the late 1970s, Schmidt and Worrall (1983) concluded that genetic gains associated with improved wheat yield appeared to have levelled in the Great Plains of Southern USA. In contrast, the quality of winter wheat in Kansas, USA improved under variable environmental conditions (Cox *et al*., 1988). In addition, Feyerherm *et al*. (1984) studied various wheat genotypes grown in the Midwest, USA and their results revealed significant genetic gain from 1920 to 1979, leading to the conclusion that yields continuously improved during this period.

The Cereal Crops Research Institute in Pirsabak, Nowshera, has developed and made available a number of disease-resistant, high-yielding, and dwarf wheat varieties for cultivation in the primary agricultural regions of Khyber Pakhtunkhwa. These varieties cater to the needs of both traditional farmers aiming for self-sufficiency and forward-thinking farmers seeking improved yields. In Khyber Pakhtunkhwa, the area covered by approved high-yielding wheat varieties has increased to almost 80%. Semi-dwarf wheat lines developed at CCRI or received from CIMMYT and ICARDA by CCRI were evaluated as un-replicated trials annually. The chosen lines are then evaluated in one or multiple locations with RCB design A-trial. Every A-trial includes 20 wheat lines and 2 checks. Half of the selected lines from A-trials are tested at over five locations in Khyber Pakhtunkhwa sequentially as B-trials (15%). Therefore, compared to A-trials (30%), selection pressure is slighter higher in B-trials in this second stage of advancement toward further testing either by the Microplot or C- trials. A limited number of lines are selected from B-trials using 15% selection intensity to evaluate high-yielding lines in Microplot or C-trials across many locations of Khyber Pakhtunkhwa. Hence, a full cycle for a group of experimental lines entails assessing the A-experiment in the year n, the B-experiment in a year n+1, and the Microplot or C-experiment in year n+2 (Khalil *et al*., 2010). Lines selected from Microplot/ C-trials are evaluated at about 15 locations of Khyber Pakhtunkhwa under the Khyber Pakhtunkhwa Wheat Yield Trial (KPWYT) to evaluate limited lines suitable to the agroecological zones of Khyber Pakhtunkhwa. The most outstanding lines from different research centres of Khyber Pakhtunkhwa tested in KPWYT are finally submitted to the National Uniform Wheat Yield Trial (NUWYT) being evaluated by National Wheat Coordinators, NARC, Islamabad for further evaluation at more than 30 locations at national level.

Wheat varieties developed by CCRI have the best performance not only in Khyber Pakhtunkhwa and other regions of Pakistan but also in countries such as Afghanistan, Central Asian countries. Wheat cultivars Pak-81, Pirsabak-87, Khyber-87, Pirsabak-91, Kaghan-93, Suleman-96, Nowshera-96, Haider-2000, Saleem-2000, Pirsabak-2004, Pirsabak-2005, Pirsabak-2008, Pirsabak-2013,*Shahkar-2013, Pirsabak-2015, Pakhtunkhwa-2015, Wadan-2017, Paseena-2017, Khaista-2017, Gulzar-2019, Pirsabak-2019, Abaseen-2021, Pirsabak-2021, and Taskeen-2022 are some of the very popular wheat varieties released by CCRI, Pirsabak during the past 40 years.

The genetic progress (genetic gain) in wheat yield across different parts of the world has been assessed using several techniques and protocols. Traditionally, genetic improvements have been gauged by the comparative performance of cultivars in regional testing facilities (Schmidt and Worral, 1984; Schmidt, 1984), national agronomic trials (Feyerherm *et al*., 1984), or by growing cultivars from several historical periods in one place (Cox *et al*., 1988). While these strategies offer valuable insights into estimating genetic advancements at a national or regional scale, breeders are primarily interested in ascertaining the enduring genetic progress attained within their individual wheat breeding programs.

In wheat breeding and genetics, it is crucial to understand the concepts of heritability and repeatability. Heritability is the ratio of phenotypic variability that is ascribable to genetic components, indicating the extent to which a specific trait in a set of genotypes (lines) is influenced by genes rather than by environmental factors (Gandahi, 2021). Repeatability, however, measures the consistency of a trait within a specific cultivar (variety), indicating the stability and predictability of traits across different environments or periods. Heritability is often used in the early stages of wheat breeding when breeders aim to identify and select desirable traits that have a strong genetic basis (Mohsin *et al*., 2021). One of the primary reasons why repeatability, rather than heritability, is used in already-developed wheat varieties is that repeatability provides information about the stability and reliability of a trait within a variety, regardless of environmental fluctuations.

This result emphasizes the limited genetic variation commonly observed in modern wheat cultivars as a result of the recurrent utilization of the same favorable haplotypes in wheat breeding efforts (Yang *et al*., 2022). This awareness is vital for farmers, breeders, and researchers as it empowers them to make well-informed choices regarding the cultivation and selection of wheat varieties. Typically, the heritability and repeatability of complex traits like yield in wheat are lower when compared to traits such as plant height (Alipour *et al*., 2021).

The association between plant traits that result in higher yield production can be learned through correlation analysis. To increase yields, plant breeders can use correlation analysis, a statistical technique, to make selections based on secondary traits.

Additionally, it offers a useful index for forecasting how a character will change simultaneously, that is, how one trait will change at the expense of a proportionate change in other traits. Therefore, for breeders to adequately increase the yield potential of newly developed cultivars, they must have a thorough understanding of the heritability and inheritance pattern of a trait, the degree of yield correlation with various yield component traits, and the genetic potential of each genotype (Ahmad *et al*., 2008).

There has been very little research on the genetic enhancement of yield and other characteristics related to wheat cultivars developed through the wheat program by CCRI, Pirsabak, Nowshera, Pakistan. Hence, the current work was proposed to investigate genetic gain in yield and some other economical traits through regression using a pool of potential wheat cultivars released during the last 40 years by Cereal Crops Research Institute, Pirsabak, Nowshera, recommended for general cultivation following the regression procedure proposed by Cox *et al*. (1988).

The principal aims of this study were to evaluate the genetic advancement in yield and other yield-related characteristics of bread wheat varieties released by CCRI, Pirsabak over the past 40 years, compare the repeatability (heritability) of yield-contributing traits among these cultivars, and calculate the genetic and phenotypic correlations between wheat yield and other characteristics.

Materials and Methods

The research was carried out at the Research Farm of the Department of Plant Breeding and Genetics, The University of Agriculture, Peshawar, during the 2022-23 wheat season. Eighteen landmark wheat cultivars, released by the Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera, over the past 40 years, were assessed. The experiment utilized a randomized complete block design with three replications. Every cultivar in each replication was arranged on a plot including 3 rows, each 3 meters in length, with a spacing of 0.25 meters between rows. Planting occurred in the third week of November 2022. All cultivars were subjected to recommended agronomic techniques from planting to maturity. Data were taken on plant stature (height), spikes m^{-2}, spike length, individual spike weight, spikelets spike^{-1} count, number of grains spike^{-1}, 1000-seed (grain) weight, biomass (biological) yield, and seed (grain) yield.

The list of cultivars, along with their year of release, is given in Table 1.

Table 1: *List of 18 wheat cultivars with their year of release to be evaluated during 2022-23.*

S. No.	Cultivars	Year of release
1	Pak-81	1981
2	Pirsabak-85	1985
3	Suleman-96	1996
4	Saleem-2000	2000
5	Pirsabak-04	2004
6	Pirsabak-05	2005
7	Pirsabak-08	2008
8	Pirsabak-13	2013
9	Shahkar-13	2013
10	Pirsabak-15	2015
11	Pakhtunkhwa-15	2015
12	Wadaan-17	2017
13	Paseena-17	2017
14	Gulzar-19	2019
15	Pirsabak-19	2019
16	Abaseen-21	2021
17	Pirsabak-21	2021
18	Taskeen-22	2022

Statistical analysis

The data pertaining to different traits were analyzed following the model for Randomized Complete Block Design (RCBD). The total sum of squares due to cultivars for each trait was further partitioned by regressing cultivar means on the year of release for cultivars, and the residual sum of squares using a no-intercept model as proposed by Cox *et al*. (1988). The determined regression coefficient was equivalent to the yearly genetic increase per annum suggested by Cox *et al*. (1988) and Khalil *et al*. (2002). The R programming language was used to estimate the genotypic and phenotypic correlation among the different traits. Microsoft Excel was used to estimate genetic gain for each trait using the following equations:

$$Yi = bXi + \mu$$

Yi = Mean of cultivar i across three replications for a trait.

Xi = Year of release of cultivar i.

b = Regression coefficient or genetic gain per year.
μ = Residual error.

Estimation of repeatability (heritability) of yield components between traits

Repeatability of yield components traits of 18 wheat cultivars released by CCRI, Pirsabak was estimated on analogy of heritability as below:

Genetic variance of trait (V_g) = (CMS-EMS)/r
Environmental variance for trait (V_e) = EMS
Phenotypic variance for trait (V_p) = $V_g + V_e$
Repeatability of trait (h^2) = V_g/V_p

Whereas,
CMS = cultivar mean square
EMS = error mean square
V_p = phenotypic variance

Correlation analysis

Genetic and phenotypic associations among yield component traits were also worked out using the following formulas,

$$\text{Genetic correlation} = r_G = \frac{CoVg\ (X1X2)}{\sqrt{Vg\ (X1).Vg\ (X2)}}$$

$$\text{Phenotypic correlation} = r_P = \frac{CoVp\ (X1X2)}{\sqrt{Vp\ (X1).Vp\ (X2)}}$$

Where,

$CoV_{g(XIX2)}$ = Genetic covariance among traits X_1 and X_2.
$CoV_{p\ (XIX2)}$ = Phenotypic covariance among traits X_1 and X_2.
$V_{g\ (X1)}$ and $V_{g\ (X1)}$ = Genetic variance of traits X_1 and X_2.
$V_{p\ (X1)}$ and $V_{g\ (X1)}$ = Phenotypic variance of traits X_1 and X_2.

Results and Discussion

Plant height

Plant height is of significant importance in wheat breeding. Dwarf wheat tends to resist lodging, making it easier to harvest and often lead to higher grain yield. The variance analysis revealed highly significant variations (P < 0.01) in plant height across wheat cultivars (Table 2). Plant heights varied from 86.1 to 108.1 cm. Maximum plant height was observed for the cultivar Pakhtunkhwa-15 (108.1 cm), while cultivar Pak-81 had the minimum plant height (86.1 cm) (Table 3). Linear regression analysis demonstrated a significant positive genetic gain (b = 0.05, SE = 0.0006) for plant height of wheat cultivars showing an increase in plant height with high coefficient of determination (R^2 = 0.997) suggest a strong and positive correlation of plant height with year of release of cultivars (Table 6). Previously, Afridi and Khalil (2007) have reported non-significant genetic improvement of 0.03 and 0.06 cm year^{-1} in wheat cultivars tested under irrigated and rainfed environments, respectively. The genetic variance for plant height of bread wheat cultivars was lower in magnitude than the environmental variance (V_g = 15.16, V_e = 24.88), resulting in moderate heritability (repeatability) of 0.38 (Table 7). Similarly, Khan *et al.* (2003) also have reported moderate broad-sense heritability of 0.53 for plant stature in wheat. Correlation analysis showed exceedingly significant and progressive genotypic and phenotypic relationship of plant height with spike length (r_g = 0.99**, P = 0.01; r_p = 0.60**, P =0.01) and biological yield (r_g = 0.90**, P = 0.01; r_p = 0.58**, P =0.01) (Table 8). Similarly, plant stature displayed significantly positive genetic correlation with spikes m^{-2} (r_g = 0.46*, P = 0.05), single spike weight (r_g = 0.54**, P = 0.01), grain spike^{-1} (r_g = 0.91**, P = 0.01) and grain yield (r_g = 0.44*, P =0.05) (Table 8). Barman *et al.* (2020) have reported significantly positive genotypic and phenotypic correlations between plant height and various yield-related attributes, including tiller plant^{-1} (r_{g^*}= 0.920**, r_{p^*}= 0.564**), flag leaf area (r_{g^*}= 0.900**, r_{p^*}= 0.396**), and grain yield (r_{g^*}= 0.969**, r_{p^*}= 0.540**) of wheat cultivars.

Table 2: *Mean squares for agronomic and yield-related traits of 18 spring wheat cultivars evaluated at the university of agriculture, peshawar during 2022-2023.*

Traits	Reps (df=2)	Genotypes (df=17)	Error (df=34)	CV (%)
Plant height	102.39	70.36**	24.88	5.18
Spikes m^{-2}	1870.91	1495.34**	586.55	5.03
Spike length	0.07	0.42**	0.16	4.12
Single spike weight	0.15	0.10**	0.04	7.46
Spikelets spike^{-1}	0.08	2.72**	0.97	5.56
Grains spike^{-1}	1.35	4.60*	2.16	2.89
1000-grain weight	72.74	39.33**	9.69	6.60
Biological yield	371.83	597081.71**	136124.84	2.92
Grain yield	2677.29	52332.58**	15119.34	2.82

**, ** = significant at 5 and 1% probability level, respectively. NS= non-significant.*

Table 3: *Means for plant height (cm), spikes m^{-2} and spike length (cm) of 18 spring wheat cultivars evaluated at the university of agriculture, peshawar during 2022-2023.*

Cultivars	Year of release	Plant height (cm)	Spikes m^{-2}	Spike length (cm)
Pak-81	1981	86.1	441.3	8.7
Pirsabak-85	1985	94.7	477.7	9.7
Suleman-96	1996	103.5	488.0	9.8
Sal-eem-2000	2000	100.3	490.0	9.6
Pirsabak-04	2004	95.3	498.3	9.9
Pirsabak-05	2005	93.5	448.0	9.7
Pirsabak-08	2008	98.8	477.3	10.0
Pirsabak-13	2013	94.0	489.0	9.6
Shahkar-13	2013	94.7	521.3	9.8
Pirsabak-15	2015	95.1	524.0	9.9
Pakhtunkh-wa-15	2015	108.1	473.3	10.7
Wadaan-17	2017	99.3	505.3	10.1
Paseena-17	2017	96.6	473.3	10.1
Gulzar-19	2019	92.9	484.0	9.8
Pirsabak-19	2019	98.7	456.0	10.0
Abaseen-21	2021	90.5	461.7	9.9
Pirsabak-21	2021	95.3	472.0	9.9
Taskeen-22	2022	95.7	485.7	10.0
LSD (0.05)	--	4.78	23.20	0.39

Spikes m^{-2}

Analysis of variance revealed somewhat strong variations ($P \leq 0.01$) among wheat cultivars for spikes m^{-2} (Table 2). Spikes m^{-2} of wheat cultivars ranged from 441.3 to 524. Pirsabak-15 had the highest number of 524 spikes m^{-2} among the wheat cultivars. In contrast, cultivar Pak-81 exhibited the lowest spike count of 441.3 m^{-2} (Table 3). Linear regression analysis showed a highly significant genetic gain in spikes m^{-2} (b = 0.24, SE = 0.0026) of wheat cultivars. Thus, there has been an increase in more spikes production in recent wheat cultivars released by CCRI Pirsabak since 1981. Furthermore, there was a strong relationship of spikes m^{-2} with year of release of cultivar (R^2 = 0.998) (Table 6). Similarly, Donmez *et al*. (2001) and Gao *et al*. (2017) have also identified spike numbers per unit area as a key contributor to the genetic increase in grain yield. Further, Perry and d'Antuono (1989) also reported a substantial increase in grain yield potential, largely due to an increase in spikes and grain number m^{-2}. The genetic variance for spikes m^{-2} of bread wheat cultivars was lower in magnitude than the environmental variance (V_g = 302.93, V_e = 586.55), resulting in moderate heritability (repeatability) of 0.34 (Table 7). Previously, Dabi *et al*. (2019) have also reported lower genetic variance (0.11), high environmental variance (0.31) and moderate heritability of 0.34 for spikes production in wheat. Correlation analysis showed significantly positive genetic correlation of spikes m^{-2} with grains spike^{-1} (r_g = 0.54*, P^*= 0.05), biological yield (r_g^*= 0.68**, P^*= 0.01), and grain yield (r_g = 0.61**, P^*= 0.01). However, spikes m^{-2} exhibited a non-significant phenotypic association with all the studied traits (Table 8). Previously, Desheva (2016) has also reported positive genotypic and phenotypic correlation of spikes m^{-2} with other yield-aiding traits, such as the number of grains spike^{-1} (r_p^*= 0.26**), grain weight spike^{-1} (r_g = 0.36*, r_p = 0.33**), 1000-grain weight (r_p = 0.22**) and grain yield plant^{-1} (r_g = 0.82**, r_p = 0.84**).

Spike length

The analysis of variation showed highly significant distinctions ($P \leq 0.01$) among wheat varities for spike length (Table 2). Spike length of wheat cultivars ranged from 8.7 to 10.7 cm. Maximum spike length was monitored for cultivar Pakhtunkhwa-15 (10.7 cm). Whereas, minimum spike length was observed for cultivar Pak-81 (8.7 cm) among wheat cultivars (Table 4). Non-significant regression coefficient was observed for spike length (b = 0.005, SE = 3.951) of wheat cultivars indicating no increase in spike length of wheat cultivars released by CCRI Pirsabak during the past 40 years. A high coefficient of determination (R^2 = 0.998) suggests a strong relationship of spike length with year of release (Table 6). Similarly, Afridi and Khalil (2006) have also reported no significant genetic gains in spike length of wheat cultivars tested under irrigated and rainfed environments. The genetic variance for spike length of bread wheat cultivars was lower in magnitude than the environmental variance (V_g = 0.08, V_e = 0.16), resulting in moderate heritability (repeatability) of 0.34 (Table 7). Previously, Jan *et al*. (2015) reported a moderate heritability of 0.41 for bread wheat cultivars with lower genetic variance (0.24) than the environmental variance (0.34) for spike length. Spike length exhibited significantly positive genotypic correlation with spikelets spike^{-1} (r_g = 0.97**, P_*=0.01), grains spike^{-1} (r_g = 0.96**, P_*= 0.01), 1000-grain weight (r_g = 0.65**, P_*= 0.01), biological yield (r_{g^*}= 0.99**, P^*= 0.01), and grain yield (r_{g^*}= 0.99**,

P_*=0.01). However, the spike length of wheat cultivars had a positive phenotypic relationship with single-spike weight (r_p = 0.99**, P_p = 0.01) and biological yield (r_{p*}=0.50*, P_*=0.05) only (Table 8). Previously, Singh *et al.* (2023) have reported significantly positive genotypic correlation for spike length with peduncle length (r_g = 0.50**), plant stature (r_g = 0.55**), biological yield plant^{-1}(r_{g*}= 0.50**), and flag leaf area (r_{g*}=0.39**) while substantially negative association with days to flowering (r_g = -0.25*).

Single spike weight

Analysis of variation revealed highly significant distinctions (P_*≤0.01) across wheat cultivars for single-spike weight (Table 2). Single-spike weight of wheat cultivar varied from 2.15 to 2.87 g. Among the studied wheat cultivars, maximum spike weight was exhibited by cultivar Shahkar-13 (2.87 g), whereas minimum single-spike weight was recorded for cultivar Pak-81 (2.2 g) (Table 4). Regression analysis revealed a non-significant increase for the single-spike weight (b = 0.0013, SE = 2.021) of wheat cultivars released by CCRI Pirsabak since the release of Pak-81. However, the coefficient of determination (R^2 = 0.996) shows a strong correlation of spike weight with year of release of wheat cultivars (Table 6). Previously, Afridi and Khalil (2007) have documented a significant genetic enhancement in spike-weight wheat cultivars evaluated under irrigated (b = 0.012**) and rainfed (b = 0.020*) environments. The genetic variance for single-spike weight of bread wheat cultivars was lower in magnitude than the environmental variance (V_g=0.02, V_e = 0.04), resulting in moderate heritability of 0.34 (Table 7). Earlier, Asma *et al.* (2022) have reported low genotypic variance (39.29) with moderate broad-sense heritability of 0.58 for spike weight in bread wheat candidate lines cultivated in a rainfed semi-arid zone of Algeria. Correlation analysis showed significantly positive genotypic and phenotypic correlations of single-spike weight with spikelets spike^{-1} (r_{g*}=0.99**, P_*=0.01; r_{p*}=0.55**, P_*=0.01), 1000-grain weight (r_{g*}=0.99**, P_*=0.01; r_{p*}=0.62**, P_*=0.01) and grain yield (r_{g*}=0.99**, P_*=0.01; r_{p*}=0.62**, P_*=0.01). However, spike weight exhibited a considerably negative phenotypic correlation with grain spike^{-1} (r_p = -0.46*, P^*= 0.05) (Table 8). The results accord with those of Sharma *et al.* (2023), who have also stated significantly positive genetic associations of spike weight with spike length (r_{g*}=0.53**), number of spikelets spike^{-1} (r_{g*}=0.38**), number of grains spike^{-1} (r_{g*}=0.59**), grain weight spike^{-1} (r_{g*}=0.97**), biological yield plant^{-1} (r_{g*}=0.22*), and grain yield (r_{g*}=0.29**).

Table 4: *Means for single spike weight (g), spikelets spike^{-1}, and grains spike^{-1} of 18 spring wheat cultivars evaluated at the University of Agriculture, Peshawar during 2022-2023.*

Cultivars	Year of release	Single spike weight (g)	Spikelets spike^{-1}	Grains spike^{-1}
Pak-81	1981	2.15	15.3	48.1
Pirsabak-85	1985	2.44	16.9	52.3
Suleman-96	1996	2.51	17.0	51.9
Saleem-2000	2000	2.63	17.1	52.1
Pirsabak-04	2004	2.56	17.2	51.4
Pirsabak-05	2005	2.84	17.5	50.0
Pirsabak-08	2008	2.80	18.3	50.6
Pirsabak-13	2013	2.73	18.1	50.7
Shahkar-13	2013	2.87	17.7	50.9
Pirsabak-15	2015	2.77	17.1	50.1
Pakhtunkh-wa-15	2015	2.83	17.9	52.4
Wadaan-17	2017	2.75	17.4	51.9
Paseena-17	2017	2.78	19.0	52.9
Gulzar-19	2019	2.75	19.3	50.3
Pirsabak-19	2019	2.84	18.6	49.6
Abaseen-21	2021	2.86	17.6	51.5
Pirsabak-21	2021	2.82	19.1	49.3
Taskeen-22	2022	2.81	18.0	50.9
LSD (0.05)	--	0.19	0.94	1.41

Spikelets spike^{-1}

Analysis of variation displayed highly noteworthy differences (P_*≤0.01) among wheat cultivars for spikelets spike^{-1} (Table 2). Spikelets spike^{-1} of wheat cultivars ranged from 15.3 to 19.3. Maximum spikelets spike^{-1} count were noticed in cultivar Gulzar-19 (19.3), whereas cultivar Pak-81 had the lowest (15.3) number of spikelets spike^{-1} (Table 4). Thus, there was a net difference of 4 spikelets spike^{-1} in cultivars released in 1981 and 2019 by the wheat breeding program of CCRI. Linear regression analysis showed significant genetic gain for spikelets spike^{-1} (b = 0.01, SE = 0.0001) of wheat cultivars, suggesting an increase in spikelets spike^{-1} of wheat cultivars since 1981. High coefficient of determination (R^2 = 0.997) showed a strong and positive correlation of spikelets spike^{-1} with year of release of cultivar (Table 6). Similarly, Parveen and Khalil (2011) also have reported highly significant genetic gain of 0.05 spikelets spike^{-1} year^{-}

[1] as average of DI Khan, Saria Naurang and other locations of Khyber Pakhtunkhwa. Further, Zhou *et al*. (2007) also have reported significant genetic increase of 0.99 and 0.54% year^{-1} for spikelets spike^{-1} in wheat at two of four test locations in China during 2001-03. In contrast, Afridi and Khalil (2007) have reported a non-significant genetic improvement of 0.006 spikelets spike^{-1} under watered and -0.021 spikelets spike^{-1} under rainfed environments indicating no genetic gain in spikelets spike^{-1} of wheat cultivars. The genetic variance for spikelets spike^{-1} of bread wheat cultivars was lower in magnitude than environmental variance (V_g = 0.58, V_e = 0.97), resulting in moderate heritability of 0.38 (Table 7). Previously, Ali *et al*. (2008) have also reported higher environmental variance (8.15) than genetic variance (6.31) with moderate heritability of 0.54 by evaluating CIMMYT lines at Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad. Correlation analysis demonstrated significantly positive genotypic association of spikelets spike^{-1} with spike length (r_{g*}=0.97**, P_*=0.01), single-spike weight (r_{g*}=0.99**, P_*=0.01), 1000-grain weight (r_{g*}=0.99**, P_*=0.01), biological yield (r_{g*}=0.75**, P_*=0.01) and seed yield (r_{g*}=0.99**, P = 0.01). Similarly, spikelets spike^{-1} exhibited significant phenotypic relationship with single-spike weight (r_p = 0.55**, P = 0.01), 1000-grain weight (r_{p*}=0.65**, P_*=0.01) and grain yield (r_{p*}=0.46*, P_*=0.05) (Table 8). Similar to our results, Khan and Dar (2010) also have observed significantly positive correlation of spikelets plant^{-1} with tillers plant^{-1} (r_{g*}=0.871**, r_{p*}=0.780**), grain yield plant^{-1} (r_{g*}=0.759**, r_{p*}=0.617**) and test weight (r_{g*}=0.75**, r_{p*}=0.69*) both at phenotypic and genotypic levels in wheat.

Grains spike^{-1}

Analysis of variation displayed noteworthy differences (P ≤ 0.05) among wheat cultivars for grain spike^{-1} (Table 2). The number of grains spike^{-1} of wheat cultivars ranged from 48.1 to 52.9. Maximum grains spike^{-1} were produced by cultivar Paseena-17 (52.9), while cultivar Pak-81 produced the minimum grains spike^{-1} count of 48.1 (Table 4). Regression analysis revealed significant genetic improvement in number of grains spike^{-1} (b = 0.03, P = 0.0002) of wheat cultivars suggesting an increase in grains spike^{-1} of newly released wheat varieties of CCRI. There was strong correlation between year of release and grains spike^{-1} of wheat cultivars (R^2 = 0.999) (Table 6). Similar to our findings, wheat cultivars distributed from 1946 to 1992 in France showed a increase of 0.29% year^{-1} in number of grains spike^{-1} considering higher fertility and spike size (Brancourt-Hulmel *et al*., 2003). The genetic variance for bread wheat cultivars was lower in magnitude than the environmental variance (V_g = 0.81, V_e = 2.16), resulting in low heritability of 0.27 for number of grains spike^{-1} (Table 7). Previously, Prasad *et al*. (2021) have reported moderate broad-sense heritability of 0.41 for grains spike^{-1} in wheat. Significantly positive genetic correlation of grains spike^{-1} was observed with biological yield (r_{g*}=0.72**, P_*=0.01) and negative with 1000-grain weight (r_g = -0.49*, P = 0.05). Likewise, grains spike^{-1} also showed significantly negative phenotypic correlation with 1000-grain weight (r_{p*}=-0.69**, P_*=0.01) and grain yield (r_{p*}=-0.56**, P_*=0.01) (Table 8). Earlier, Meherbabu *et al*. (2023) have reported that number of grains spike^{-1} presented a substantial progressive relationship with the number of spikelets spike^{-1} but negative genetic correlation with harvest index (r_{g*}= -0.71**) at the genotypic level.

1000-grain weight

Analysis of variation displayed highly noteworthy differences (P_*≤0.01) among wheat cultivars for 1000-grain weight (Table 2). 1000-seed (grain) weight of wheat cultivars vary between 41.1 to 53.8g. Maximum 1000-grain weight was produced by cultivar Pirsabak-08 (53.8 g), whereas cultivar Pak-81 produced minimum 1000-grain weight of 41.1 g (Table 5). Regression analysis revealed significant genetic improvement (b = 0.03, SE = 0.0004) in 1000-grain weight of wheat cultivars released by CCRI, Pirsabak during past 40 years. High coefficient of determination (R^2 = 0.995) revealed a strong positive correlation between 1000-seed (grain) weight and their year of release (Table 6). Similarly, Beche *et al*. (2014) have also reported genetic gain of 0.029 g year^{-1} for 1000-grain weight among Brazilian wheat genotypes. Moreover, Underdahl *et al*. (2008) have also observed annual increase of 0.08 g year^{-1} (0.3% year^{-1}) in 1000-grain weight of hard red spring wheat bread cultivars in North Dakota, USA. Genetic variance for 1000-grain weight wheat cultivars was higher than the environmental variance (V_g = 9.88, V_e = 9.69) resulting in moderate heritability of 0.50 for 1000-grain weight (Table 7). Previously, Rahman *et al*. (2016) have observed higher genetic variance estimate (9.34) than environmental variance (3.50) for 1000-grain weight with moderate heritability of 0.54. The statistical analysis revealed significant positive genotypic and phenotypic correlation of 1000- seed (grain) weight with biological yield (r_{g*}=0.62**, P_*=0.0064) and grain yield (r_{g*}=0.98**, P_*=0.01; r_{p*}=0.60**, P_*=0.01), but negative with grains spike^{-1} (r_{g*}=-0.49*, P_*=0.05; r_{p*}=-0.69**, P_*=0.01) (Table 8). Similar to our results, Ullah *et al*. (2018) have also reported a highly significant positive phenotypic correlation between 1000-grain weight and grain yield (0.24**).

Biological yield

Analysis of variance found rather substantial variations ($P \leq 0.01$) across wheat cultivars for biological yield (Table 2). Biological yield of wheat cultivars varied between 11140.7 to 13326.7 kg ha^{-1}. Maximum biological output was achieved by cultivar Pirsabak-19 (13326.7 kg ha^{-1}), while minimum was noted for cultivar Pak-81 (11140.7 kg ha^{-1}) released by CCRI in 1981(Table 5). Regression analysis revealed highly significant genetic gain of 6.3 kg ha^{-1} yr^{-1} in biological yield (b = 6.3, SE = 0.048) of wheat cultivars released by CCRI, Pirsabak, since 1981. High coefficient of determination also revealed strong positive relationship (R^2 = 0.999) between biological yield and cultivar year of release (Table 6, Figure 1). Previously, Pask and Reynolds, (2013) have also reported similar increase of 0.42% year^{-1} in aboveground biomass for CIMMYT wheat cultivars released between 1950 and 2009. Similarly, biological yield has demonstrated a 91 kg ha^{-1} year^{-1} rise among wheat cultivars published between 1969 and 2006 (Xiao *et al*., 2012), and a 62.6 kg ha^{-1} year^{-1} increase between 1950 and 2012 in China (Gao *et al*., 2017). The genetic variability for biological yield of the studied bread wheat cultivars was greater in magnitude than the environmental variance (V_g = 153652.29, V_e = 136124.84), resulting in moderate heritability of 0.53 for biological yield (Table 7). Saini *et al*. (2019) have also reported moderate heritability of 0.59 for biological yield and yield traits in different types of bread wheat. Similarly, Hossain *et al*. (2012) also found a higher genetic variance than environmental variance with a moderate heritability of 0.61 for biological yield in wheat genotypes. Correlation analysis revealed a highly significant positive genetic correlation of biological yield with grain yield (r_g = 0.86**, P = 0.01) (Table 8). Previously, Singh *et al*. (2023) have also reported significant and positive genetic correlation of biological yield and plant height (r_g = 0.91**), peduncle length (r_g = 0.85**), spike length (r_g = 0.50**), and flag leaf area (r_g = 0.457**).

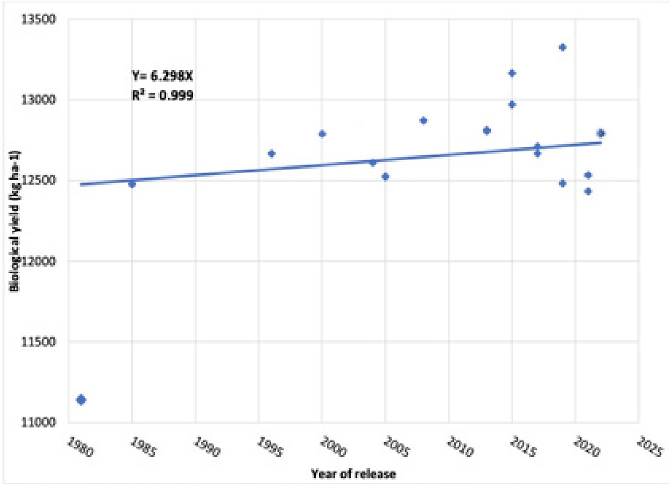

Figure 1: *Genetic gain in biological yield of 18 wheat cultivars released by CCRI pirsabak, nowshera during past 40 years*

Table 5: *Means for 1000-grain weight (g), biological yield (kg ha^{-1}) and grain yield (kg ha^{-1}) of 18 spring wheat evaluated at the university of agriculture, peshawar during 2022-2023.*

Cultivars	Year of release	1000-grain weight (g)	Biological yield (kg ha^{-1})	Grain yield (kg ha^{-1})
Pak-81	1981	41.1	11140.7	4000.4
Pirsabak-85	1985	41.7	12477.8	4214.8
Suleman-96	1996	44.0	12666.9	4285.0
Saleem-2000	2000	43.3	12788.6	4280.4
Pirsabak-04	2004	47.3	12610.3	4283.4
Pirsabak-05	2005	49.4	12524.0	4344.4
Pirsabak-08	2008	53.8	12870.6	4348.3
Pirsabak-13	2013	44.5	12814.8	4349.7
Shahkar-13	2013	48.2	12806.9	4337.0
Pirsabak-15	2015	45.8	12970.4	4496.9
Pakhtunkhwa-15	2015	46.6	13165.2	4455.7
Wadaan-17	2017	46.3	12666.3	4379.3
Paseena-17	2017	45.3	12711.1	4288.9
Gulzar-19	2019	51.8	12483.4	4515.0
Pirsabak-19	2019	52.0	13326.7	4511.1
Abaseen-21	2021	46.6	12433.3	4385.2
Pirsabak-21	2021	50.8	12533.0	4432.8
Taskeen-22	2022	50.0	12793.5	4563.0
LSD (0.05)	--	2.99	353.5	117.9

Table 6: *Regression coefficient (b) with standard error (SE) and coefficient of determination (R^2) for agronomic and yield-related traits of 18 spring wheat cultivars evaluated at the university of agriculture, peshawar during 2022-2023.*

Traits	b§	SE	R^2
Plant height (cm)	0.05**	0.0006	0.997
Spikes m^{-2} (no)	0.24**	0.0026	0.998
Spike length (cm)	0.005^{NS}	3.951	0.998
Single spike weight (g)	0.0013^{NS}	2.021	0.996
Spikelets spike^{-1} (no)	0.01**	0.0001	0.997
Grains spike^{-1} (no)	0.03**	0.0002	0.999
1000-grain weight (g)	0.03**	0.0004	0.995
Biological yield (kg ha^{-1})	6.3**	0.048	0.999
Grain yield (kg ha^{-1})	2.2**	0.013	0.999

§ = *Genetic gain per year for a specific trait.*

Table 7: *Genetic variance (V_g), environmental variance (V_e), and heritability (h^2) for agronomic and yield-related traits of 18 spring wheat cultivars evaluated at the university of agriculture, peshawar during 2022-2023.*

Traits	V_g	V_e	h^2
Plant height	15.16	24.88	0.38
Spikes m^{-2}	302.93	586.55	0.34
Spike length	0.08	0.16	0.34
Single spike weight	0.02	0.04	0.34
Spikelets spike^{-1}	0.58	0.97	0.38
Grains spike^{-1}	0.81	2.16	0.27
1000-grain weight	9.88	9.69	0.50
Biological yield	153652.29	136124.84	0.53
Grain yield	12404.41	15119.34	0.45

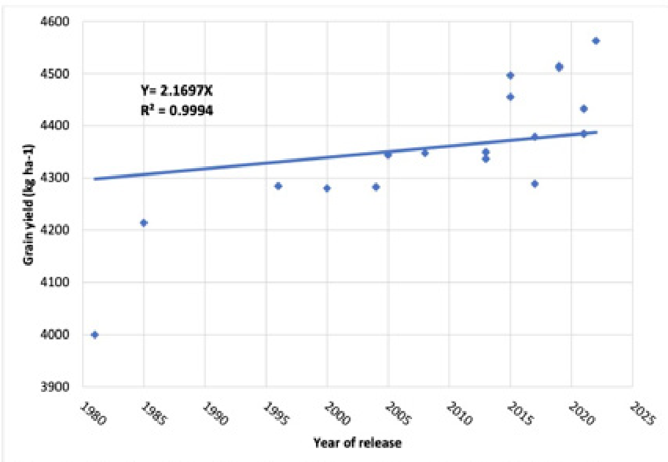

Figure 2: *Genetic gain in biological yield of 18 wheat cultivars released by CCRI pirsabak, nowshera during past 40 years*

Grain yield

Wheat cultivars of CCRI revealed highly significant differences ($P \leq 0.01$) for grain yield (Table 2). The grain yield of wheat cultivars fluctuated from 4000.4 to 4563 kg ha^{-1}. Maximum grain yield was produced by cultivar Taskeen-22 (4563 kg ha^{-1}), followed by Gulzar-19 (4515 kg ha^{-1}), Pirsabak-19 (4511.1kg ha^{-1}), and Pirsabak-15 (4496.9 kg ha^{-1}), whereas Pak-81 produced minimum grain yield (4000.4 kg ha^{-1}), which was released in 1981 (Table 5). Regression analysis showed highly significant genetic gain of 2.2 kg ha^{-1} yr^{-1}in grain yield (b = 2.2, SE = 0.013) of wheat cultivars released by CCRI in the past 40 years (Table 6, Figure 2). This is also evident from enhanced grain yield of recently released wheat cultivars compared to old ones. There was also strong association between grain yield and year of cultivar release (R^2 = 0.999). Previously, Achilli *et al.* (2022) have reported a genetic gain of 26.94 kg ha^{-1} yr^{-1} in grain yield of wheat cultivars released from 1934 to 2015 in Argentina. Similarly, Yadav *et al.* (2021) have reported an increase of 24.27 kg ha^{-1} yr^{-1} in grain yield of wheat varieties released between 1900 and 2016 in the Northwestern plain zone of India. Further, Hanif *et al.* (2021) have also reported genetic improvement of 9.03 kg ha^{-1} yr^{-1} or 0.37% in grain yield under five environments using 24 wheat cultivars released from 1911 to 2016 in Pakistan. The genetic variability for grain yield of wheat cultivars was lower in magnitude than the environmental variability (Vg = 12404.41, Ve = 15119.34), resulting in moderate heritability (repeatability) of 0.45 for grain yield (Table 7). Similarly, Dabi *et al.* (2019) have also reported moderate heritability of 0.50 for grain yield in wheat. Correlation analysis revealed significantly positive genotypic correlation of grain yield with plant height (r_g = 0.44*, P = 0.05), spikes m^{-2} (r_g = 0.61**, P = 0.01), spike length (r_g = 0.99**, P = 0.01), single spike weight (r_g = 0.99**, P = 0.01), spikelets spike^{-1} (r_g = 0.99**, P = 0.01), 1000-grain weight (r_g = 0.98**, P = 0.01) and biological yield (r_g = 0.86**, P = 0.01). Furthermore, grain yield also exhibited significantly positive phenotypic association with single spike weight (r_p = 0.62**, P = 0.01), spikelets spike^{-1} (r_p = 0.46*, P = 0.05) and 1000-grain weight (r_p = 0.60**, P = 0.01) (Table 8). Similarly, Anu *et al.* (2022) have also reported positive genotypic correlation between grain yield and number of tillers plant^{-1} (0.518**), spike weight (0.144*), number of grains spike^{-1} (0.276**), biological yield plant^{-1} (0.751**) and harvest index (0.573**) in wheat.

Table 8: *Phenotypic (above diagonal) and genotypic (below diagonal) correlation among agronomic and yield traits of 18 spring wheat cultivars evaluated at the University of Agriculture Peshawar, during 2022-2023.*

Traits	PH	SMS	SPL	SPW	SPS	GPS	1000GW	BY	GY
PH	-	0.05	0.60**	-0.20	-0.20	0.40	-0.1	0.58**	0.03
SMS	0.46*	-	-0.09	0.37	-0.36	0.11	-0.28	0.08	-0.03
SPL	0.99**	0.40	-	0.99**	0.22	0.24	0.20	0.50*	0.43
SPW	0.54**	-0.19	0.36	-	0.55**	-0.46*	0.62**	0.31	0.62**
SPS	0.29	0.02	0.97**	0.99**	-	-0.37	0.65**	0.07	0.46*
GPS	0.91**	0.54*	0.96**	0.32	0.08	-	-0.69**	-0.11	-0.56**
1000GW	0.12	-0.08	0.65**	0.99**	0.99**	-0.49*	-	0.19	0.60**
BY	0.90**	0.68**	0.99**	0.99**	0.75**	0.72**	0.62**	-	0.40
GY	0.44*	0.61**	0.99**	0.99**	0.99**	0.16	0.98**	0.86**	-

**, ** = significant at 5 and 1% probability level, respectively.PH = plant height, SMS = spikes m^{-2}, SPL = spike length, SPW = single spike weight, SPS = spikelets spike^{-1}, GPS = grains spike^{-1}, 1000GW = 1000-grain weight, BY = biological yield and GY = grain yield*

Conclusions and Recommendations

Analysis of variance exhibited significant differences among wheat cultivars for the studied traits. Highest biological yield was produced by wheat cultivar Pirsabak-19 (13326.7 kg ha^{-1}) and Pirsabak-15 (12970.4 kg ha^{-1}), while highest grain yield was produced by cultivar Taskeen-22 (4563 kg ha^{-1}), Gulzar-19 (4515 kg ha^{-1}) and Pirsabak-19 (4511 kg ha^{-1}) for the studied wheat cultivars. Significant genetic improvement was observed over time in wheat cultivars for most of the agronomic traits in the current set of wheat cultivars. Significant increase was observed in grain yield and its components i.e. spikes m^{-2} (0.24 year^{-1}), grains spike^{-1} (0.03 year^{-1}), 1000-grain weight (0.03 g year^{-1}), biological yield (6.3 kg ha^{-1} year^{-1}) and grain yield (2.2 kg ha^{-1} year^{-1}). Moderate repeatability (heritability) was observed among wheat cultivars for the studied traits. Grain yield exhibited significant positive genotypic and phenotypic correlation with single spike weight, spikelets spike^{-1} and 1000-grain weight. Breeders need to focus on genetic improvement of yield component traits to further enhance rain yield of wheat in Khyber Pakhtunkhwa.

Acknowledgements

I (Muhammad Anas) am grateful to the Cereal Crop Research Institute (CCRI) for the research materials and to my friends and family for their constant encouragement.

Novelty Statement

This study provides a novel assessment of genetic gain in bread wheat cultivars over 40 years in Khyber Pakhtunkhwa, Pakistan. By analyzing 18 landmark wheat varieties, it reveals significant improvements in key yield-related traits such as plant height, spikes per square meter, grains per spike, and grain yield, offering valuable insights into the effectiveness of local breeding programs in enhancing wheat productivity under regional conditions.

Author's Contribution

Muhammad Anas: Conceptualization, methodology, investigation, formal analysis, writing – original draft.
Iftikhar Hussain Khalil: Supervision, resources, validation, writing – review & editing.
Khushal Khan, Hira Ali, Ateeq Ur Rahman, Mian Ahmad Raza, Atta Ul Wahab, Muhammad Taimur and Muhammad Shaban Afridi: Funding acquisition

Generative AI or AI assisted technology statement

The authors declare that no generative AI or AI-assisted technologies were used in the creation of this manuscript.

Conflict of interest

The authors have no conflict of interest.

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