

CHANGING BEHAVIOR OF GENE ACTION ON SELECTION EFFICIENCY ESTIMATED THROUGH GENETIC PARAMETERS IN WHEAT

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Abstract

Field based phenotypic performance along with mean biometrical variables of heritability and genetic advance guide the plant breeders to select superior genotypes. In the changing climate scenario, this is the most pivotal and challenging tasks for plant breeder to select the best plants based on desirable morphological and physiological attributes to advance to final stages of varietal development. The newly developed wheat varieties that exhibit not only early maturity but possess high potential yield and resistance/tolerance to biotic and abiotic stresses can positively contribute to food insecurity issues. To achieve this task, a set of 50 genotypes were received from CIMMYT-Mexico as Semi-arid wheat yield trial (SAWYT) and were sown at the research fields of Cereal Crops Research Institute (CCRI), Pirsabak Nowshera (74OE and 32ON), during the Rabi season of 2017-18. High Significant differences were observed in days to heading (DH), days to maturity (DM), plant height (PH) (cm) and grain yield (GY) (kg ha^{-1}). DH, DM, PH, and GY ranged from 110.02 to 118.52, 156 to 163, 85.56 cm to 110.56 cm and 1123 kg ha^{-1} to 4513 kg ha^{-1} , respectively. Genetic variation components i.e., h^2 (B.S), GCV, PCV and G.A were estimated for yield and other morphological traits. The results showed the existence of adequate genetic variability among the tested wheat genotypes. Moderate to high heritability estimates were computed for DH (0.73), DM (0.36), PH (0.49), and GY (0.37). High GCV were found in GY and PH, moderate in days to heading while low in days to maturity. Similarly, high PCV was recorded for GY and PH while moderate for DH and DM. Genetic advance, representing the potential gain through selection, was computed for GY (14.72%), PH (5.25%), DH (2.33%), and DM (0.64%), with varying levels of genetic improvement. High genetic advance with moderate heritability was recorded for GY while low genetic advance with high and moderate heritability was recorded for DH, PH and DM. The results suggested the presence of non-additive gene action, including dominance and epistasis, indicating that delayed selection may lead to more fruitful outcomes. Based on present findings the superior genotypes were SAWYT-V12, V14, V15, V17, V18, V24, V29, V37, V44, V46 and V49, which need to be further investigated for concrete results. This study emphasizes the importance of field-based evaluations and biometrical computations in selecting superior wheat genotypes, which will contribute to the development of climate resilient, high-yielding and disease resistant wheat varieties that can address the challenges of food security in changing climatic conditions.

Keywords: Genetic Advance (GA), Genotypic Coefficient of Variation (GCV), Gene Action, Heritability (h^2), Phenotypic Coefficient of Variation (PCV) and Wheat Genotypes.

INTRODUCTION

Wheat (*Triticum aestivum* L.) holds a prominent position as a vital cereal food crop and serves as a staple food in numerous countries across the globe (Li and Ali, 2022). It is a self-pollinated crop and hexaploid species having $2n$ number of chromosomes ($2n=6x=42$) (Sleper and Poehlman, 2006). The world population (820 million people) is growing at an alarming rate, posing a significant challenge in meeting the dietary needs of billions of people (FAO, 2019). Grote et al., 2021 emphasized the need of strong research and development for new green revolution to secure the supply of staple foods and diversification of improved people's diets. As one of the primary staple food crops, wheat plays a crucial role in global food security (Iqbal et al., 2023; Iqbal et al., 2020). To tackle this challenge, it is imperative for wheat breeders to spearhead advanced breeding programs that can lead to a breakthrough in increasing the yield potential of this vital crop (Singh et al., 2022). The success of these breeding programs holds the key to ensuring a sustainable and abundant supply of wheat to meet the increasing demands of the growing population. By developing high-yielding, resilient, and nutritious wheat varieties, we can fortify our global food systems and work towards alleviating hunger and malnutrition (Ali et al., 2013). Among wheat products, the most valuable is wheat flour which is being utilized to prepare various sorts of human items that not only provides food to 36% of the world population but it also gives 20% food calories (Eid, 2009). Specifically, gluten constitutes a significant portion of wheat protein, accounting for approximately 75% of the total protein content in wheat grains. This unique characteristic of gluten imparts essential qualities that are instrumental in the production of bread, noodles, and various baked goods. (Shewry and Hey, 2015). Furthermore, wheat straw finds practical applications as livestock feed and serves construction purposes in South Asian countries such as Pakistan, Afghanistan, and India (Kumar et al., 2017).

Pakistan is among the top 10 wheat producing countries of the world (Hoekstra and Mekonnen, 2016; IA et al., 2015). In the 2016-17 agricultural season, wheat was cultivated across an extensive area of 9,168.2 thousand hectares, resulting in a grain production of 27,464.1 thousand tons, with an average yield of 2,974 kg per hectare (Pakistan Economic Survey, 2020-21). Wheat's contribution to the overall GDP stood at 1.9%, while it accounted for 9.6% of the value addition in the agriculture sector (Anonymous, 2016-17). The existence of genetic variability in germplasm is the key to success of any crop improvement program. Before starting a breeding program, knowledge of the estimation of genetic parameters must be known for the heritable improvements in quantitative economic attributes of the crop plants through breeding and selection process, (Khalid et al., 2011). The processes of selection become easier and simpler with higher estimates of heritability (Khan et al., 2008). According to Eid (2009) and Shukla et al., (2004), heritability alone may not sufficiently account for significant variability in segregating generations, it is linked to a higher magnitude of genetic advance. This characteristic is crucial in the selection process, as it enables us to visualize the magnitude of heritability and generation behavior, ultimately leading to significant improvements. More heritability's estimate with high genetic advances of the

plant attributes is very necessary for the development of novel cultivars. Genetic advance estimates enhance the effectiveness of heritability and designating the character gain due to selection pressure. Therefore, estimating genetic advance explains how a gain is fixed in a character in selection pressure and it finally helps the breeders to advance the generation further (Tripathi et al., 2019; Ogunniyan and Olakojo, 2014).

Hence, this study was carried out to evaluate the genetic variation, heritability, and expected genetic advance among fifty (50) wheat genotypes during the sowing season. The objective was to identify superior wheat genotypes that demonstrate excellent adaptation to the climatic conditions of Khyber Pakhtunkhwa province.

MATERIALS AND METHODS

Experiment Location

This research work was conducted in the field conditions of Cereal Crops Research Institute (CCRI), Pirsabak, Nowshera-Khyber Pakhtunkhwa during Rabi season (30th November 2017). The climatic conditions of CCRI, Pirsabak, Nowshera is prevailed by hot relatively long summers and cold but short winters. The climatic variable, i.e., mean minimum and maximum temperature, rainfall and relative humidity during the growing period were recorded as shown in Table-5. The experimental sites were classified as “Pirsabak soil series” having USDA classification Fine, mixed, hyper-thermic according to the principle as described in key of soil taxonomy, USDA (1998). The crop was harvested on 25-26th May 2018.

Plant Materials

Forty-nine (49) promising wheat genotypes of International Semi-Arid Wheat Yield Trial (SAWYT) obtained from CIMMYT-Mexico were evaluated along with local check cultivar (Wadaan-2017). The following genotypes used in the research are given in Table-1 shown as below.

Table 1: List of the 50 SAWYT Wheat Genotypes and their Pedigree used in the Trial to assess the Genetic Variability under the Agro-Ecological Conditions of CCRI, Pirsabak, Nowshera during 2017-18

S. No.	Pedigree of the genotypes	Codes of the genotypes
1	Local Check (Wadaan-2017)	SAWYT-V1
2	FITIS	SAWYT-V2
3	MUNAL*2/WESTONIA	SAWYT-V3
4	SHORTENED SR26 TRANSLOCATION//2*WBLL1*2/KKTS/3/BECARD	SAWYT-V4
5	PSN/BOW//SERI/3/MILAN/4/ATTILA/5/KAUZ*2/CHEN/BCN/3/ MILAN/6/WBLL1*2/SHAMA/7/SAUAL/YANAC//SAUAL	SAWYT-V5
6	ATTILA*2/PBW65*2//MURGA/3/FRANCOLIN #1//WBLL1*2/KIRITATI	SAWYT-V6
7	FRANCOLIN#1/YANAC/5/KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	SAWYT-V7
8	SEHER 06/3/PBW343*2/KUKUNA//TECUE #1	SAWYT-V8
9	WHEAR//2*PRL/2*PASTOR/3/WAXBI/4/COPIO	SAWYT -V9
10	OTUS//WBLL1*2/TUKURU/3/2*PBW343*2/KUKUNA*2//FRTL/PIFED	SAWYT-V10

11	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/5/KACHU #1/6/PBW343*2/KUKUNA*2//FRTL/PIFED/7/PBW343*2/KUKUNA*2//FRTL/PIFED	SAWYT-V11
12	TACUPETO F2001/BRAMBLING//PVN/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES	SAWYT-V12
13	TACUPETO F2001/BRAMBLING//KIRITATI/5/C80.1/3 *BATAVIA //2*WBLL1/3/ATTILA/3*BCN*2// BAV92/4/WBLL1*2/KURUKU/6/ROLF07/YANAC//TACUPETO F2001/BRAMBLING	SAWYT-V13
14	WBLL1*2/KKTS//PASTOR/KUKUNA/3/KINGBIRD #1//INQALAB 91*2/TUKURU/5/KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/SAUAL	SAWYT-V14
15	ROLF07/YANAC//TACUPETO F2001/BRAMBLING*2/5/UP2338*2/SHAMA/3 /MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA	SAWYT-V15
16	ROLF07*2/KIRITATI/3/2*KINGBIRD#1//INQALAB 91*2/TUKURU	SAWYT-V16
17	FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/KINGBIRD #1//INQALAB 91*2/TUKURU	SAWYT-V17
18	TRCH/SRTU//KACHU*2/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338* 2/SHAMA	SAWYT-V18
19	TRCH/SRTU//KACHU*2/5/UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338* 2/SHAMA	SAWYT-V19
20	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVAKI/4/VORB/FISCAL//AKURI #1/5/PBW343*2/KUKUNA//SRTU/3/ PBW343*2/KHVAKI	SAWYT-V20
21	UP2338*2/SHAMA/3/MILAN/KAUZ//CHIL/CHUM18/4/UP2338*2/SHAMA*2/5/ PBW343*2/KUKUNA*2//FRTL/PIFED	SAWYT-V21
22	SAUAL/3/SW89.3064//CMH82.17/SERI/4/SAUAL/5/PBW343*2/KUKUNA*2// FRTL/PIFED/6/SAUAL/KRONSTAD F2004	SAWYT-V22
23	SAUAL/YANAC//SAUAL*2/3/TACUPETO F2001/BRAMBLING*2//KACHU	SAWYT-V23
24	KFA/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/7/BOKOTA/8/BOKOTA	SAWYT-V24
25	SAUAL/MUTUS/4/KACHU #1//WBLL1*2/KUKUNA/3/BRBT1*2/KIRITATI	SAWYT-V25
26	SITE/MO//PASTOR/3/TILHI/4/WAXWING/KIRITATI/5/KACHU #1/KIRITATI//KACHU	SAWYT-V26
27	BORL14//KFA/2*KACHU	SAWYT-V27
28	TILILA/TUKURU/4/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/KFA/2*KACHU	SAWYT-V28
29	WAXWING/2*ROLF07//BORL14	SAWYT-V29
30	BECARD/FRNCLN/3/KACHU #1/KIRITATI//KACHU	SAWYT-V30
31	CHEWINK #1/CHYAK/5/UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1	SAWYT-V31
32	CHEWINK #1/CHYAK/5/UP2338*2/VIVITSI/3/FRET2/TUKURU// FRET2/4/MISR 1	SAWYT-V32
33	MUU/KBIRD/3/PRL/2*PASTOR*2//FH6-1-7	SAWYT-V33
34	BECARD//ND643/2*WBLL1/4/ KIRITATI//ATTILA*2/PASTOR/3/AKURI	SAWYT-V34
35	ND643//2*ATTILA*2/PASTOR/3/WBLL1*2/KURUKU/4/WBLL1*2/BRAMBLING/6/BABAX/ LR42//BABAX*2/3/KUKUNA/4/CROSBILL #1/5/BECARD	SAWYT-V35
36	FRET2/TUKURU//FRET2/3/MUNAL #1/4/SUP152/AKURI//SUP152	SAWYT-V36
37	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311/6/PBW343*2/KUKUNA*2//FRT L/PIFED/7/CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311	SAWYT-V37
38	WAXWING/KIRITATI*2/3/C80.1/3*BATAVIA//2*WBLL1/4/COPIO/5/ND643//2*ATTILA*2/P ASTOR/3/WBLL1*2/KURUKU/4/WBLL1*2/BRAMBLING	SAWYT-V38
39	MUNAL #1/FRANCOLIN #1/5/KIRITATI/4/2*BAV92//IRENA/KAUZ/3/ HUITES/6/BECARD/FRNCLN	SAWYT-V39
40	FRANCOLIN #1//WBLL1*2/BRAMBLING*2/3/COPIO	SAWYT-V40
41	FRANCOLIN #1/YANAC*2/3/PBW343*2/KUKUNA*2//FRTL/PIFED	SAWYT-V41
42	NADI/3/PBW343*2/KUKUNA*2//FRTL/PIFED/4/NADI	SAWYT-V42
43	NADI/COPIO//NADI	SAWYT-V43
44	WBLL1*2/KURUKU//HEILO/3/WBLL1*2/KURUKU/4/TACUPETO F2001/BRAMBLING*2// KACHU/5/WBLL1*2/KURUKU//HEILO/3/WBLL1*2/KURUKU	SAWYT-V44

45	YAV_3/SCO//JO69/CRA/3/YAV79/4/AE.SQUARROSA(498)/5/LINE1073/6/KAUZ*2/4/CAR//KAL/BB/3/NAC/5/KAUZ/7/KRONSTADF2004/8/KAUZ/PASTOR//PBW343/9/PBW343*2/KUKUNA*2//FRTL/PIFED/10/KIRITATI//PRL/2*PASTOR/5/OASIS/KAUZ//4*BCN/3/PASTOR/4/KAUZ*2/YACO//KAUZ/6/KIRI	SAWYT-V45
46	BABAX/LR42//BABAX/3/ER2000/4/NIGHAR	SAWYT-V46
47	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PANDION//FILIN/2*PASTOR/3/BERKUT	SAWYT-V47
48	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/5/GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92	SAWYT-V48
49	WHEAR/SOKOLL/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/CHIL/6/CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA/7/PASTOR//MILAN/KAUZ/3/BAV92	SAWYT-V49
50	SUP152/6/OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI	SAWYT-V50

Experimental Conditions

Genotypes were sown in six (6) rows pattern with row length of five (5) meter long. Row to row distance was kept at 30cm and the total plot area was 9 m². Three replicates of the treatments were used under Randomized Complete Block (RCB) design. During sowing, different fertilizers like Nitrogen (50% N as urea), Phosphorus (18%-P₂O₅) and Potassium (50%-K₂O) were applied at recommended dose, while half of the dose was applied at first irrigation. There is total five irrigations applied scheduled at five different stages.

Statistical Analysis

Field data were taken on 5 randomly chosen plants from each plot. The recorded data for all traits were averaged and compiled. Analysis of variance (ANOVA) was found the procedure of Steel et al., (1997) using SAS statistical (version, 9.1) computer software and average means were compared by Least Significant Difference (LSD).

According to Farshad far et al., (2013) estimates, PCV, GCV, heritability (h²), broad sense and genetic advance (G.A) were computed from components of variance as follows:

$$V_E = MS_e$$

$$V_G = MS_g - MS_e/r$$

$$V_P = V_G + V_E$$

$$PCV = 100 \sqrt{(\sigma_p^2)/X}$$

$$GCV = 100 \sqrt{(\sigma_g^2)/X}$$

$$ECV = 100 \sqrt{(\sigma_E^2)/X}$$

$$h^2 = \sigma_g^2 / \sigma_p^2$$

$$G.A = (k. h^2 \sqrt{(\sigma_p^2)})$$

$$G. A (\text{Percent of trait mean}) = (G.A/\text{trait mean}) \times 100$$

RESULTS AND DISCUSSION

Analysis of Variance (ANOVA)

Highly significant differences ($p \leq 0.01$) were noted among all the genotypes for days to heading (Table-2). These findings are closely related to the results of Eid (2009); Yaqoob (2016); Rehman et al., (2020); Dragov et al., (2022) who worked on different wheat genotypes and quoted highly significant differences for the plant height. The mean results showed that days to heading ranged between 110.02 to 118.52 (Table-3). The genotypes with code SAWYT-V5, SAWYT-V13, SAWYT-V25 and SAWYT-V31 developed heads earlier (110.02 days) as compared to the check cultivar while, delayed heading (118.52 days) was observed in check genotype (Wadaan-2017) and SAWYT-V21 (Table-3).

Highly significant difference ($p \leq 0.01$) was noted among all the genotypes for days to maturity (Table-2). These findings are like the results reported by Kumar et al., (2014); Zerga et al., (2016); Chimdesa et al., (2017); Rehman et al., (2020); Ahmad and Guptha (2023) who observed significant difference in genotypes physiological maturity. The mean results of the genotypes showed that days to maturity ranged from 156 to 163. SAWYT-V40 was noted as the earliest maturing genotypes that got maturity in minimum days (156) as compared to the check genotype while genotypes SAWYT-V24 and SAWYT-V14 were the late maturing genotypes and got maturity in 163 days (Table-3).

Highly significant difference ($p \leq 0.01$) for days to plant height (cm) was found among all the wheat genotypes (Table-2). These findings are like the results reported by Ajmal et al. (2009) who conducted an experiment on twelve F2 wheat crop progenies and observed highly significant results for plant height. The mean data showed that plant height in the range from 85.56 to 110.56 cm. The height of taller genotype (SAWYT-V2) was 110.56 cm whereas the stature of most dwarf genotype (SAWYT-V41) was 110.56 cm (Table-3). Generic results also quoted by Khalid et al. (2011) in a study conducted on 42 winter wheat promising genotypes to find out heritability estimates and genetic advance.

Table 2: Mean Square for days to Heading, Days to Maturity, Plant Height and Grain Yield for 50 Wheat Genotypes at CCRI, Pirsabak, Nowshera, during 2017-18

SOV	D.F	Days to heading	Days to maturity	Plant height	Grain Yield
Reps	2	64.22**	56.19**	392.82**	394133.95 ^{NS}
Genotypes	49	13.15**	5.64**	90.75**	1548346.38**
Error	98	1.44	2.08	23.19	553770.70
CV	--	1.07	0.90	4.89	20.00
LSD (5%)	--	1.95	2.34	7.80	1205.80
R ²	--	0.85	0.66	0.70	0.59

* Significant at 5% level of probability, ** Significant at 1% level of probability NS: Non-significant, D.F: Degrees of freedom, C.V: Coefficient of variation, R²: Coefficient of determination

Highly significant difference ($p \leq 0.01$) was noted among all the genotypes for grain yield (Table-2). These results are in common with the results of Parveen et al. (2011) who conducted research on 13 wheat genotypes and got highly significant results for the same trait. The collected data trends exhibited range from 1123 kg ha⁻¹ to 4513 kg ha⁻¹ (Table-3). None of the genotype surpassed the check genotype for grain yield whereas the genotype SAWYT-V30 produced the minimum (Table-3).

Table 3: Mean Performance of 50 Wheat Genotypes under the Agro-Climatic Conditions of CCRI, Pirsabak, Nowshera during 2017-18

Genotype code	Days to heading	Days to maturity	Plant height(cm)	Grain yield (kg ha ⁻¹)
SAWYT-V1(check)	118.52 a	161 bac	108.56ab	4513 bac
SAWYT-V2	117.02 ba	158 ed	110.56 a	2778 ifhg
SAWYT-V3	110.52 ih	160 bdc	103.06 ejbidhagcf	4155 ebdac
SAWYT-V4	113.02 dfe	160 bdc	99.06 lejmiokhgnf	3894 ebdfc
SAWYT-V5	110.02 i	158 ed	100.06lejmidhkgnf	3413 edifhcg
SAWYT-V6	113.02 dfe	159 dc	98.06lejmiokhgn	3446 ebdifhcg
SAWYT-V7	110.52 ih	158 ed	99.56lejmiokhgnf	4169 ebdac
SAWYT-V8	114.52 dc	158ed	100.56lejmidhkgcf	3198 edifhg
SAWYT -V9	114.52 dc	159 dc	104.56 ebdhagcf	3365 edifhcg
SAWYT-V10	110.52 ih	158 ed	100.56lejmidhkgcf	3709 ebdifhcg
SAWYT-V11	112.02 gfh	159 dc	98.56 ljmiohkgnf	3667 ebdffhcg
SAWYT-V12	111.52 gifh	161 bac	93.06 pmornq	4251 bdac
SAWYT-V13	110.02 i	159 dc	101.06 lejbidhkgc	3642 ebdffhcg
SAWYT-V14	111.52 gifh	163 a	90.56prq	4359 bdac
SAWYT-V15	110.52 ih	161 bac	94.06lmponq	4338 bdac
SAWYT-V16	111.02 gih	161 bac	102.06 ejbidhkgcf	3742 ebdfcg
SAWYT-V17	110.52 ih	162 ba	93.06pmornq	4646 bac
SAWYT-V18	111.52 gifh	160 bdc	97.56lejmiokhknq	4171 ebdac
SAWYT-V19	112.52 gfe	162 ba	99.06 lejmiokhgnf	3459 ebdifhcg
SAWYT-V20	112.52 gfe	160 bdc	96.06lpjmonkq	4296 bdac
SAWYT-V21	118.52 a	161 bac	90.06 prq	3451 ebdifhcg
SAWYT-V22	111.52 gifh	160 bdc	95.06 lpjmoknq	3205 edifhg
SAWYT-V23	111.52 gifh	161 bac	92.06 porq	3901 ebdfc
SAWYT-V24	114.02 dce	163 a	98.56ljmiohkgnf	4521 bac
SAWYT-V25	110.02 i	161 bac	92.56 pmornq	4055 ebdac
SAWYT-V26	112.02 gfh	159 dc	93.56 lpmonq	2505 eifhg
SAWYT-V27	110.52 ih	160 bdc	98.56 ljmiohkgnf	3638 ebdffhcg
SAWYT-V28	114.02 dce	160 bdc	99.56 lejmiokhgnf	2996 eifhg
SAWYT-V29	111.02 gih	160 bdc	99.06 lejmiokhgnf	4355 bdac
SAWYT-V30	111.52 gifh	161 bac	96.56lepjmioknq	1123 j
SAWYT-V31	110.02 i	161 bac	92.56 pmornq	3526 ebdffhcg
SAWYT-V32	111.02 gih	160 bdc	96.06lpjmoknq	2519 ih
SAWYT-V33	111.52 gifh	160 bdc	94.06 lmponq	3784 ebdfcg
SAWYT-V34	111.52 gifh	159 dc	100.56lejmidhkgcf	2301 ij
SAWYT-V35	114.52 dc	159 dc	103.06 ejbidhagcf	2984 eifhg
SAWYT-V36	111.52 gifh	159 dc	106.56 edbac	4151 ebdac
SAWYT-V37	113.02 dfe	160 bdc	99.06 lejmiokhgnf	4317 bdac
SAWYT-V38	111.52 gifh	161 bac	93.56 lpmonq	3657 ebdffhcg
SAWYT-V39	112.02 gfh	158 ed	93.56 lmponq	5178 bac
SAWYT-V40	113.02 dfe	156 e	97.06 lejmiokhknq	3621 ebdffhcg
SAWYT-V41	113.02 dfe	159 dc	85.56 r	3459 ebdifhcg
SAWYT-V42	110.52 ih	160 bdc	90.56prq	3471 ebdifhcg

SAWYT-V43	113.02 dfe	160 bdc	93.56 lmpoq	2680 ihg
SAWYT-V44	111.02 gih	161 bac	104.56 ebdhagcf	4509 bac
SAWYT-V45	110.52 ih	161 bac	99.56 lejmiokgnf	4488 bac
SAWYT-V46	113.02 dfe	159 dc	105.56 ebdagcf	3992 ebdac
SAWYT-V47	116.52 b	160 bdc	107.56 bdac	3934 ebdfc
SAWYT-V48	113.02 dfe	160 bdc	108.06 bac	3921 ebdfc
SAWYT-V49	111.02 gih	159 dc	106.06 ebdacf	4259 bdac
SAWYT-V50	115.52 bc	158 ed	104.06 ebidhagcf	4326 bdac

Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and genetic advance (G.A)

Calculation of PCV and GCV is compulsory to get acquaintance regarding which plant attribute had maximum variability (Arphita et al., 2017). GCV and PCV was calculated according to the methods of Lush (1940), Burton's (1952); and Choudhary (1968) and was categorized according to Siva Subramanian and Madhavamenon (1973) as Low below 10%, medium 10-25% and high above 25% (Deshmukh et al. (1986). Similarly, Robinson et al. (1949) stated that magnitudes of h^2 60% and above categorized as high, 30-60% as moderate and 0-30% were as low. Johnson et al. (1955) revealed that maximum genetic advance as percent of mean (GAM) was classified as low between 0 to 10%, moderate between 10 to 20% and high more than 20%.

Estimation of all parameters of genetic diversity revealed information of variation existed among all the genotypes. This indicated that the future breeding program might be able to capitalize on the significant genetic variability in the material. Moreover, the results revealed differences among the values of PCV and GCV components. PCV component, indicating that the existent variability was due to the combination of the genotypes' inherent character and the influence of environmental factors (Ahmad and Gupta, 2023). PCV values was greater than the GCV values for all examined traits. This was due to environment influence on their expression (Dashora et al., 2020). The difference between PCV and GCV was relatively high for DH, DM, PH and GY (Table-4). These results illustrated greater environmental influence on phenotypic expression of these attributes thus selection was not effective based on phenotypic expression of the genotypes to improve these traits. Further, these findings suggested that expression of these traits were under control of non-additive gene action and dominance genetic effects predominates. These results were in close agreement with the findings of Demelash et al., (2013) who reported relatively high environmental variances than genotypic variances for DH, DM, PH and GY. In recent investigations, PCV estimates ranged from 21.80 to 1542.52 for DH to GY. Estimates of PCV found higher than GCV for all the studied traits. Moderate PCV was recorded for DH (21.80) followed by DM (14.30) (Table-4). These results are in close agreement to the finding of Dragov et al., (2022); Osekita et al., (2022); Biru and Negash (2020) whereas high PCV was recorded for PH followed by GY Table-4. These results are in close agreement to the research work done by Din et al., (2018). Biru and Negash (2020); Ghallab et al., (2016), Fellahi et al., (2013) and Tabbal, (2012) also reported high PCV values for GY.

Low difference in phenotypic variances to genotypic variances estimates and maximum in genotypic estimates as compared to environmental variances for the considered traits showed that variation is caused by genetic factors with less environmental reasons. GCV ranged from 18.63 to 943.94 for DH to GY. GCV with low magnitude (8.62) recorded for days to maturity followed by high (47.80 and 943.94) recorded for plant height and grain yield, respectively (Table-4). Similarly, moderate GCV magnitude (18.63) was recorded for days to heading. This indicates that genotypic performance of these traits reflects phenotypes. These results are like some earlier research workers (Yaqoob, 2018; Degewione et al., 2013, Khan, 2013; Shafiq et al., 2006). Further, these results are in line to the research work done by Mecha et al., (2016) who also examined very low GCV for maturity whereas recorded high values for grain yield per plant. Gauravrajsinh et al., (2021) also recorded low GCV values for DM. Ajmal et al., (2009) and Kolakar et al. (2012) also reported high PCV and GCV for grain yield in an experiment conducted on bread wheat to know the basic genetic parameters and characters association. Mecha et al. (2016) and Zareen et al. (2016) recorded medium PCV and GCV for plant height among various wheat genotypes. High and moderate magnitude of PCV and GCV of these traits portrayed scope of improvement through selection and their phenotypic expression would be good indication of the genotypic potential.

Heritability and Genetic Advance

Although the GCV discovered the range of genetic variation exist in wheat genotypes for various vital traits; it does not give complete information to know the magnitude of current heritable variability in the source population. Similarly, GCV accompanied with heritability provides authentic assessments of magnitude of expected genetic advance through phenotypic selections (Burton, 1952; Mecha, 2016). However, in the present investigations, the magnitude of heritability ranged between 36 to 73%. The high magnitude of heritability (73%) in this study was recorded for the heading while moderate was recorded for plant height (49%), maturity (36%) and grain yield (37%) (Table-4). Navin et al., (2014) also reported that higher contribution of genotypic component is represented in the form of highest heritability's observed values. Din et al., (2018) also reported moderate heritability for DM. Tabbal (2012) and Fellahi et al., (2013) also quoted high heritability for DH.

Table 4: Estimates of ranges, means, MSE, MSG, Vg, Vp, PCV, GCV, ECV, heritability, genetic advance, genetic advance percent of mean and expected gene action for four attributes of 50 wheat genotypes at CCRI, Pirsabak, Nowshera during 2017-18

Trait	Range	Mean ± standard error of mean	MSE	MSG	Vg	Vp	PVC	GVC	EVC	h ²	Genetic Advance	G.A % of mean	Expected gene action
Days to heading	110.02-118.52	112.42±2.07	1.44	13.15	3.90	5.34	21.80	18.63	11.32	0.73	2.62	2.33	Non-additive (dominance and epistasis)
Days to maturity	156-163	159.67±1.37	2.08	5.64	1.19	3.27	14.30	8.62	11.41	0.36	1.02	0.64	Non-additive (dominance and epistasis)
Plant height	85.56-110.56	98.56±5.25	23.19	90.75	22.52	45.71	68.10	47.80	48.51	0.49	5.18	5.25	Non-additive (dominance and epistasis)
Grain yield	1123-4513	3720.73±14.72	553770.70	1548346.38	331525.23	885295.93	1542.52	943.94	1219.97	0.37	547.55	14.72	Non-additive (dominance and epistasis)

MSE: Mean square of error, MSG: mean square for genotypes, Vg: Genetic variance, Vp: Phenotypic variance, PCV: phenotypic coefficient of variation, GCV: genotypic coefficient of variation, EVC: environmental coefficient of variation

Alone only heritability values do not provide indication of the initial genetic improvement resulted from process of selection of individual wheat genotype, however, some knowledge regarding expected genetic advance in line with heritability is most indispensable (Vashistha et al., 2013). Genetic advances suggest the improvement in average mean performance of selection sub family in the basic source population (Lush, 1949 and Johnson et al., 1955). Traits revealing higher broad sense heritability's might not be certainly provide higher expected genetic advance. Similarly, the magnitude of genetic advance as mean percentage ranged from 0.6 to 14.7 %. Moderated magnitude of genetic advance (14.72%) in these findings was recorded for the grain yield whereas the low magnitude of the genetic advance was recorded for days to maturity (1.02) followed by plant height (5.18) and days to heading (2.33). High heritability with low genetic advance was recorded for days to heading. These results are supported by the findings of Kumar et al., (2022); Mesele et al., (2016); Fellahi et al., (2013); Gebremariam et al., (2022). Moderate heritability with low genetic advance was recorded for DM and DH (Table-4). These results are accordance to the research findings of Din et al., (2018); Osekita et al., (2022). Moderate heritability with high genetic advance was observed for GY. These results are in line with findings of Gebremariam et al., (2022).

The heading trait exhibited non-additive gene action, as indicated by its higher heritability coupled with a low genetic advance, which suggests the involvement of dominance or epistasis gene action. This finding implies that selection based solely on this parameter may not be effective or straight forward. To enhance this trait, further testing of the population under field conditions for additional years is recommended. These results are supported by Iqbal et al. (2017), Navin et al. (2014) and Amin et al. (2015) who quoted uniform results in different wheat trails for the same attribute. Moderate heritability with relatively low genetic advance (%36, 0.64) was recorded for days to maturity (Table-4). These results exhibited that the trait is under the control of non-additive gene action (epistasis and dominance) and selection should be delayed to more advance generations. These results were in line with findings of Khan et al. (2015) who conducted trail on 24 elite wheat genotypes and reported similar results for the same parameter. Moderate heritability with low genetic advance (49%, 5.25) was also observed for plant height (Table-4). These results portrayed that these traits were under the control of non-additive gene action. This also indicates that these characters are not essential for development of variety for better yield. Saleem (2016) reported moderate heritability with low genetic advance (53.39, 4.42) for plant height in a cross Iqbal-2000×9444 in a study to estimate heritability and genetic advance in F2 population of bread wheat. Similarly, Borena (2016) also reported moderate heritability and low genetic advance for the same parameter in a study conducted on 30 genotypes of wheat crop to determine variability and association among yield and yield related attributes. Moderate heritability and moderated genetic advance (37, 14.72) was observed for grain yield (Table-4). These results manifested that the effect of environmental variance is more than the genotypic variance, hence delayed selection might be favorable for this attribute. Zareen et al. (2016) observed low level

heritability and low genetic advance while Mecha et al, (2016) and Yaqoob (2016) reported high heritability coupled with high genetic advance for the same parameter.

Table 5: Detail of Climatic Parameters at CCRI, Pirsabak, Nowshera

Longitude	74° E
Latitude	32° N
Altitude	288m
Annual rainfall	350-450mm
Temperature range	Max 42 °C, min 7 °C
Relative humidity	30 – 92 %
Soil type Alkaline	pH 7.2 – 8.7

CONCLUSION

The main objective of this study was to investigate genetic diversity among the wheat genotypes and further exploit this variation in crop development program to improve the genotypes by effective selection process and advance to varietal development program, hence, release for the end users. We found a higher significant difference among all the genotypes for studied attributes. Considerable extent of genetic variations among genotypes was observed having medium to high heritability and medium to low genetic advance which describe various types of expected gene actions. The genotypes showing more yielding potential related with higher to moderate heritability and genetic advance should be added in to the up-next breeding program to exploit their actual potential for varietal development and release. It is concluded that genotypes SAWYT-V12, V14, V15, V17, V18, V24, V29, V37, V44, V46, V49 were found superior and should be exploited in future wheat breeding program; to evolve new superior cultivars which is expected to be high yielding and play a tremendous role in food insecurity issues.

DECLARATIONS

Author's contribution statements: The original idea's conceptualization, data compilation, analysis, and manuscript drafting were carried out by MK and AI. MK, MA, AA, and UA were responsible for conducting the field trial, with MK taking the lead in data analysis. MA, AH, and UA provided technical support during the field trial. MK and AI were involved in manuscript writing, while AB and JI revised the manuscript. The study's design was a collaborative effort between CCRI Pirsabak, and CIMMYT.

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Conflict of Interest

The authors declare that there is no conflict of interest.

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