PJMLS

Print ISSN: 2707-4471. Online ISSN: 2707-448X

Research Article	Pak-Euro Journal of Medical and Life Sciences
DOI: 10.31580/pjmls.v7i3.3091	Copyright © All rights are reserved by Corresponding Author
Vol. 7 No. 3, 2024: pp. 401-410	
www.readersinsight.net/pjmls	**Revised:** September 26, 2024 **Accepted:** September 29, 2024
Submission: May 31, 2024	**Published Online:** September 30, 2024

ADAPTABILITY AND QUALITY EVALUATION OF WHEAT GERMPLASM SELECTED FROM CIMMYT NURSERY ELITE SPRING WHEAT YIELD TRIAL FOR BALOCHISTAN

Sultan Muhammad[1], Zafar Ullah Malghani[1], Muhammad Ejaz[2], Naseer Ahmed[3], Muhammad Saleem[4], Noor Ullah Kakar[1], Tahira Nisa[5], Muhammad Nouman Irshad[1], Manzar Khan[1], Abdul Qadir[6]

[1]**Department of Agronomy,** Balochistan Agriculture College Quetta, Pakistan
[2]**Balochistan Agricultural Research and Development Centre, (BARDC),** Quetta, Pakistan
[3]**Department of Agriculture Extension,** Balochistan Agriculture College Quetta, Pakistan
[4]**Department of Food Technology,** Balochistan Agriculture College Quetta, Pakistan
[5]**Department of Plant Pathology,** Balochistan Agriculture College Quetta, Pakistan
[6]**Productivity Enhancement of Sugarcane,** Pakistan Agricultural Research Council, Islamabad, Pakistan

***Corresponding Author:** Abdul qadir E. mail: abdulqadirjan@gmail.com

Abstract

Wheat (Triticum aestivum) covers 21% of the world's food and develops on 200 million hectares of farmland around the world. Despite the fact that wheat is exchanged universally, and agricultural nations are significant merchants (43% of food imports), actually 81% of wheat ate in the creating scene is delivered and used inside a similar nation, in the event that not a similar local area. An experiment on the adaptability and evolution of wheat germplasm selected from CIMMYT nursery elite spring wheat yield trail for Balochistan consisting of 25 genotypes was conducted in Balochistan Agricultural Research and Development Centre, Quetta (BARDC). The experiment followed an alpha lattice design with two replications, utilizing a total experimental area of 150 m2, divided into two halves of 75 m2 each for replication purposes. There were a total of 25 plots, each with a size of 3 m2 (arranged in 4 rows, spaced 0.25m apart, and measuring 3m in length). Several parameters were measured in this study, including plant height (in centimetres), days to reach 50% heading, days to maturity, spike length (in centimeters), number of tillers per square meter, number of grains per spike, 1000-grain weight (in grams) or seed index, biological yield (in kg per hectare), canopy temperature (in degrees Celsius), and chlorophyll content (in mg per cm2). The collected data underwent statistical analysis using Statistix Ver. 8.1 Software. The results of the study revealed that genotype number BARDC-9 exhibited the maximum number of days required to 50% heading, while genotype number BARDC-4 had the minimum, achieving this milestone in just 117 days. Genotype number BARDC-21 displayed the tallest plants, reaching a height of 84 cm, whereas genotype number BARDC-22 had the shortest plants, measuring 70 cm in height. Genotype number BARDC-10 took the most time to reach maturity, with a maximum of 189 days, while genotype number BARDC-15 reached maturity in the shortest time, at 174 days. Among the observed parameters, genotype number BARDC-16 had the maximum spike length, measuring 14 cm, while five genotypes (1, 2, 3, 18, and 19) had the minimum spike length, which was 9 cm. Genotype number BARDC-8 had the highest average number of grains, with 65 grains per spike, while three genotypes (3, 17, and 25) had the lowest average, with 51 grains per spike. Regarding thousand grain weight, genotype number BARDC-25 recorded the maximum weight, while genotype number BARDC-8 had the minimum weight. Maximum mean result of total dry matter was noted in genotype number BARDC-21 and minimum mean total dry matter was recorded in genotype number BARDC-6. The result of the canopy temperature of different genotypes was different. The mean maximum canopy temperature was noted in genotype number BARDC-10 and the minimum mean canopy temperature was recorded in genotype number BARDC-24. Maximum chlorophyll content was found in genotype number 25 while minimum chlorophyll content was found in BARDC-2 genotypes i.e., BARDC-17, and BARDC-22. Extreme grain yield was recorded in genotype number BARDC-8 while lowest grain yield was recorded in genotype number BARDC-6.

Keywords: *Antioxidant activity, Brine shrimp lethality, Cytotoxicity potential, Methanolic extract, Phytochemical composition, Thymus vulgaris L.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the predominant crop in the West and central Asia and North Africa, covering a yearly creation part of around 52 million hectors, which represents over half of the wheat creation region universally in the creating world (1). Creating and conveying hereditarily safe varieties adjusted to target developing conditions is the best practical and harmless to the ecosystem methodology for rust illnesses, especially for asset unfortunate ranchers. To this end, sending of safe qualities into adjusted cultivars trailed by thorough genotype execution assessment across areas and years are attempted by maximum plant reproducing programs (2).

Wheat reproducing all over the planet for yield improvement has been founded essentially on the experimental choice measures of yield fundamentally. In any case, yield has exhibited low genetic and a high genotype-climate connection (3). A sufficient reproducing procedure requires a superior comprehension of the variables liable for improvement and development since grain yield in a given climate is straightforwardly and in a roundabout way impacted by hereditary, morphological, physiological, and ecological components (4). Hereditary enhancement in yield is especially effective for spring wheat in watered conditions, which chiefly has been ascribed to better parceling of photosynthetic items (5). But,there has been critical advancement under intensity focused and drought conditions in the creating scene utilizing the Global Wheat and Maize Improvement Center's (CIMMYT) germplasm for production of nearby peevish. Promising extreme-yielding genotypes can be distinguished in reproducing programs before the yield is reaped (yield forecast) and many high-yielding genotypes could be recognized in isolating populaces (6). For minimizing the laborious process of yield choice, a simple, quick, and cheap selection device is attractive for assisting breeders with screening an enormous no. of genotype in a generally rapid time. Moreover, this selection instrument could have to have high genetic and a solid relationship with wheat yield for recognizing high yielding genotypes quickly and productively from an enormous number of early age lines & for cutting edge genotypes. Breeders frequently need to recognize an absolute best yielding genotypes from among an example of currently predominant lines. A technique that coordinates the entire canopy temperature is profoundly attractive to survey numerous genotypes in a short time (7). Carbon isotope discrimination (CID) is additional method used effectively to enhance wheat yield potential in wheat beneath water stress condition.

CIMMYT's worldwide spring wheat breeding program uses a two-step yield testing method to find promising parent lines for the next breeding cycle. These lines are evaluated for advancement according to how consistently high their yields are in controlled selection environments (SEs) (8). Partners choose elite lines to use as parent material in national breeding programs or for variety release after these candidates undergo global evaluation via cooperative trials. Different planting periods and management circumstances characterize the SEs, which are found in one place, Ciudad Obregon, Mexico. Despite being first developed in one place, these SEs are made to forecast performance for circumstances that are targeted globally (9). In the first stage of yield testing, sometimes called PYT or stage 1, lines with good agronomic characteristics and disease resistance, especially to rusts, are tested for yield in five separate irrigation beds under ideal circumstances. During this phase, low-yielding lines are weeded out but a variety of genetic variations are preserved. According to (10), determining which lines have the best chance of succeeding in international trials requires precise capture of genotype-environment (GxE) interactions. After that, over six SEs, an Elite Yield Trial (EYT) is carried out to further assess the lines that were chosen in stage 1. The two-step procedure for finding productive lines is expensive and labour-intensive since it calls for two sets of yield testing in one go. Thus, one of the main goals of the CIMMYT spring wheat program is to expedite the selection process by sending lines straight to multi-climate trials in the first year. This is done by using genomic predictions, such GBLUPs, for wheat yield and other important characteristics (11).

MATERIALS AND METHODS

Adaptability and quality evolution of wheat germplasm selected from CIMMYT nursery elite spring wheat yield trail for Balochistan consisting of 24 entries and one check variety Shalkot-14 was conducted during 2021 Rabi season in Balochistan Agricultural Research and Development Centre, Quetta (BARDC).

EXPERIMENTAL DESIGN

The experiment was designed in an alpha grid design with two replications. The total experimental area was 150 m^2 divided into two halves 75 $m^2$for each replication. There was 25 plots, and each plot size was 3 m^2 (4 rows x 0.25m x 3m long apart).

Total plots 3x1 = 3 m^2 each plot
3 m^2 x 25 entries = 75 m^2
75 m^2 x 2 replications = 150 m^2

The Recordings of Data were made on the following parameters.

Days to heading (50%): For each plot, the days to heading were determined by counting the number of days from planting to the day when half (50%) of the heads completely emerged from the flag leaf container.

Plant height (cm): During maturity, the height of the plant was measured at random intervals from the ground level to the very tip of the spike.

Days to Maturity: The Days to Maturity were calculated as the number of days from the date of sowing to the date on which the wheat peduncle of the spike in each tract becomes completely yellow.

Number tillers m^{-2}: Use a quadrant to measure the harvested crop area and the number of tillers per square metre.

Spike length (cm): Using a measuring rod, we randomly selected three spikes from each treatment and recorded their length (cm) without the awns.

Number of grains per spike: Three spikes were randomly selected from each treatment and tallied the number of grains per spike

1000 grain weight (g): The three samples, consisting of one thousand grains from each treatment, were combined and then measured using an electric balance.

Total dry matter (Kg ha^{-1}): The total dry matter per plot was measured after crop harvesting for each plot size and reflected to kilo grams per hectare.

Grain yield (Kg ha^{-1}): The grain yield was determined by harvesting data per plot area for each treatment and then converting it to kilo grams per hectare.

Chlorophyll content (mg/cm^2): A chlorophyll meter was used at the leaf to record the total chlorophyll content in milligrams per square centimeter. Three samples were taken from each treatment.

QUALITY PARAMETERS

The following quality parameters were recorded by analyzer (inframatic 9500).

Moisture %, Wet Gluten %, Starch %, Zeleny (ml), Protein %

STATISTICAL ANALYSIS

The data was processed statistically through Statistix Ver. 8.1 Software (12)

RESULTS

DAYS TO HEADING 50%

Table I has shown mean results of days to heading 50% of various tested genotypes. Maximum days to heading 50% was noted in genotype number 9 while minimum days to heading 50% was recorded in genotype number 4 which bear 50% heading in 117 days. There was a significant difference found between genotypes of maximum and minimum days to heading 50%.

PLANT HEIGHT (CM)

Table II has shown mean result of plant height of various tested genotypes. Maximum plant height 84.5 cm was noted in genotype number 21 while minimum plant height 70 cm was recorded in genotype number 22. There was significant difference found between genotypes number 21 and 22 and no significance difference was found between various other genotypes.

DAYS TO MATURITY

Mean result of different genotypes tested for days to maturity is shown in Table III, maximum 189 days was taken by genotype number 10 for maturity while minimum 174.5 days was taken by genotype number 15 for maturity. There was significant difference between genotype number 10 and 15 for days to maturity.

TILLERS m^{-2}

There were substantial differences between the treatments, according to the data in Table I. Out of all the treatments, treatment no. 8 had the most tillers (435 tillers m-2), which is 58 more than shalkot-14. For treatments no. 7 and 10, the bare minimum in tillers generated was 276, 289 tillers m-2. Also, genotype 8 produces 477 tillers m-2, but tick variety 25 shalkot-14 only manages 377.

SPIKE LENGTH (CM)

Mean result of different genotypes tested for Spike length (cm) is shown in Table I. Maximum spike length 14 cm was noted in genotype number 16. Minimum 9 cm spike length was noted in five genotypes i.e., 1, 2, 3, 18, and 19, there was significant difference between genotypes bearing maximum and minimum spike length.

Table I. Genotypic responses to days to heading (50%), plant height (cm), days to maturity, number of tillers per m², and spike length (cm)

Sr.#	Genotypes	Days to heading	Plant height (cm)	Days to Maturity	No. tillers m^{-2}	Spike Length (cm)
1	BARDC-1	122 ABCD	80.5 AB	183 AB	357 AB	10.5 ABC
2	BARDC-2	124.5 ABCD	81AB	183.5 AB	381 AB	11 ABC
3	BARDC-3	125 ABC	84A	182.5 AB	294 B	9 C
4	BARDC-4	117 D	80.5 AB	182.5 AB	333 AB	10 BC
5	BARDC-5	121 ABCD	83 A	176 AB	385 AB	12ABC
6	BARDC-6	120.5 BCD	76 AB	176.5 AB	374 AB	10 ABC
7	BARDC-7	127.5 AB	74 AB	187 AB	276 B	9 C
8	BARDC-8	127 AB	80 AB	181 AB	435 A	14 A
9	BARDC-9	128.5 A	83.5 A	187 AB	374 AB	10.5 ABC
10	BARDC-10	118 DC	76.5 AB	189 A	289 B	9 C
11	BARDC-11	118 DC	80 AB	180.5 AB	294 B	9 C
12	BARDC-12	124 ABCD	79.5AB	186.5 AB	393 AB	13 AB
13	BARDC-13	122.5 ABCD	75 AB	181.5 AB	366 AB	10.5 ABC
14	BARDC-14	125 ABC	75 AB	184.5 AB	353 AB	10.5 ABC
15	BARDC-15	126.5 AB	70.5 B	174.5 B	299 B	9.5 BC
16	BARDC-16	124 ABCD	74 AB	188 AB	377 AB	10.5 ABC
17	BARDC-17	124.5 ABCD	77 AB	179 AB	381 AB	11 ABC
18	BARDC-18	124.5 ABCD	78.5 AB	179 AB	344 AB	10.5 ABC
19	BARDC-19	124.5ABCD	74 AB	182.6 AB	334 AB	10 BC
20	BARDC-20	121 ABCD	79 AB	177 AB	361 AB	10.5 ABC
21	BARDC-21	120 DC	84.5 B	179 AB	384 AB	12 AB
22	BARDC-22	118 DC	70 B	179.5 AB	287 B	9 BC
23	BARDC-23	122 ABCD	75.5 AB	179 AB	316 AB	10 ABC
24	BARDC-24	126.5 AB	69.5 B	176 AB	346 AB	10.5 ABC
25	BARDC-25	118 DC	76.5 AB	180.5 AB	377 AB	10.5 ABC
Grand mean		116.14	77.02	179.38	276.4	10.04
LSD value (0.05)		1.69	1.41	1.92	4.32	3.21
Standard error		3.80	3.21	1.39	2.37	2.63
CV%		0.74	0.48	0.96	1.23	0.57

*Values within the same column followed by the same letters are not significantly different, using LSD Range Test at 5% level

NUMBER OF GRAINS PER SPIKE

The average result of different genotypes tested for number of grains per spike is shown in II. Maximum average number of grains 65.5 was recorded in genotype number 8 and minimum average number of grains 51.5 per spike was recorded in three genotypes viz. 3 , 17 and 25. A significant difference was found between the genotypes producing the minimum and maximum number of grains per spike

PER SPIKE GRAIN WEIGHT (G):

There were statistically significant variations in the treatment averages, as shown in Table II. Treatment No. 8 outperformed shalkot-14 with a 2.31 g grain weight per spike, a 0.39 g increase. Treatments Nos. 3 and 7 had minimum grain weights of 1.63 g, which was 29 g less than shalkot-14. Although genotypes 8 had a grain weight per spike of 2.38 g, the control variety shalkot-14 had a weight of 1.92 g.

THOUSAND GRAIN WEIGHT GM

Table II shows the average result of the different genotypes tested for the weight of one thousand grains. The highest thousand grain weight was obtained by genotype number 25, while the lowest was reported by genotype number 8, a significant difference was found between genotype number 25 and genotype number 8. There was no significant difference among genotypes number 1, 3, 10, 15 and 21.

CANOPY TEMPERATURE

Mean result of various genotypes tested for canopy temperature is shown in Table II, the result of canopy temperature of different genotypes was different. Variegate genotype 10 had the highest mean canopy temperature, whereas genotype no. 24 had the lowest was significant difference between genotype number 10 and 24.

Table II. Genotypic response to the number of grains per spike, per spike grain weight, 1000 grain weight (g), and canopy temperature

Sr.#	Genotypes	No. grains per spike	Per Spike grain weight	1000 grain weight (g)	Canopy temperature
1	BARDC-1	55.5 BC	2.24	37 ABC	31.5 ABCD
2	BARDC-2	57 ABC	1.9	39 ABC	29.5 ABCD
3	BARDC-3	51.5 C	1.63	37.5 ABC	31 ABCD
4	BARDC-4	58 ABC	2.14	36 BC	30.5 ABCD
5	BARDC-5	61.5 AB	1.83	36 BC	31.5 ABCD
6	BARDC-6	55.5 BC	2.09	39.5 ABC	29.5 ABCD
7	BARDC-7	49 C	1.63	36 ABC	31 ABCD
8	BARDC-8	65.5 A	2.31	41.5 A	33 AB
9	BARDC-9	57.5 ABC	1.75	37 ABC	30 ABCD
10	BARDC-10	57 ABC	2.2	39 ABC	34 A
11	BARDC-11	50 C	1.75	37 ABC	31.5 ABCD
12	BARDC-12	58 ABC	1.97	41 A	30 ABCD
13	BARDC-13	53 BC	1.96	40 AB	33 AB
14	BARDC-14	52 BC	1.93	38 ABC	28.5 CDE
15	BARDC-15	56.5 ABC	2.09	37 ABC	30.5 ABCD
16	BARDC-16	54 BC	1.99	38 ABC	32.5 ABC
17	BARDC-17	62.5 AB	2	39.5 ABC	30 ABCD
18	BARDC-18	54.5 BC	2.12	36.5 BC	32 ABC
19	BARDC-19	55 BC	2.13	38 ABC	31 ABCD
20	BARDC-20	54 BC	1.97	36.5 BC	32 ABC
21	BARDC-21	63.5 AB	1.93	40 AB	28.5 CDE
22	BARDC-22	49.5 C	1.72	36 BC	27.5 DE
23	BARDC-23	56 ABC	1.97	38.5 ABC	31 ABCD
24	BARDC-24	55.5 BC	1.99	40 ABC	25.5 E
25	BARDC-25	51.5 C	1.92	41.5 A	31 ABCD
	Grand mean	54.7	1.95	38.32	30.1
	LSD value (0.05)	2.65	1.82	2.19	1.03
	Standard error	3.28	3.21	2.31	1.37
	CV %	0.86	0.76	0.79	0.69

*There was no statistically significant difference between values in the same column that follow the same letters, according to the LSD Range Test at the 5% level

TOTAL DRY MATTER KG H^{-1}

Table III shows mean result of various genotypes tested for total dry matter. Maximum mean result of total dry matter was noted in genotype number and minimum mean total dry matter was recorded in genotype number 6. There was significant difference found between genotypes producing maximum and minimum total dry matter.

CHLOROPHYLL CONTENT MG CM^{-2}

Table III shows mean result of different genotypes tested for chlorophyll content. Maximum chlorophyll content was found in genotype number 25 while minimum chlorophyll content was found in 2 genotypes i.e., 17, and 22. There was significant difference found between genotypes having maximum and minimum chlorophyll content.

GRAIN YIELD KG H^{-1}

The average result of different genotypes tested for grain yield is shown in Table III. Maximum grain yield was recorded in genotype number 8, minimum grain yield was recorded in genotype number 6. Significant difference in grain yield was found between different genotypes.

Table III. Genotypic responses to Total Dry Matter (kg ha-1), Grain Yield (kg ha-1), and Chlorophyll concentration

Sr.#	Genotypes	Total Dry Matter (Kg ha^{-1})	Chlorophyll content(mg/cm^2)	Grain Yield (Kg ha^{-1})
1	BARDC-1	19170 ABC	55.5 AB	5100 AB
2	BARDC-2	14410 ABCD	56.5 AB	5120 AB
3	BARDC-3	18370 ABCDE	58.5 AB	4790 AB
4	BARDC-4	18550 ABCDE	55 AB	5080 AB
5	BARDC-5	14240 BCDE	57.5 AB	4610 ABC
6	BARDC-6	12390 E	55.5 AB	3960 BC
7	BARDC-7	14410 BCDE	54 AB	3410 C
8	BARDC-8	21030 A	58 AB	5640 A
9	BARDC-9	13800 BCDE	60 A	4830 ABC
10	BARDC-10	13580 CDE	58.5 AB	4530 ABC
11	BARDC-11	14030 BCDE	54 AB	3550 BC
12	BARDC-12	18830 ABCDE	57 AB	5150 AB
13	BARDC-13	13970 BCDE	56 AB	3980 ABC
14	BARDC-14	15930 ABCDE	55 AB	4325 ABC
15	BARDC-15	16360 ABCDE	56 AB	4390 ABC
16	BARDC-16	17400 ABCDE	56.5 AB	4880 ABC
17	BARDC-17	20520 ABCDE	53.5 AB	5480 AB
18	BARDC-18	15780 ABCDE	58.5 AB	4370 ABC
19	BARDC-19	16620 ABCDE	55 AB	4380 ABC
20	BARDC-20	19140 ABC	55.5 AB	4650 ABC
21	BARDC-21	20480 AB	56 AB	5390 AB
22	BARDC-22	14955 BCDE	53.5 B	3550 BC
23	BARDC-23	17230 ABCD	57 AB	4650 ABC
24	BARDC-24	12500 DE	55 AB	3845 BC
25	BARDC-25	20130 AB	60.0 A	4560 ABC
	Grand mean	6975.8	55.9	4703
	LSD value (0.05)	5.65	4.82	7.19
	Standard error	8.48	9.80	6.05
	CV %	3.40	5.67	4.47

MOISTURE %

Mean result of moisture percentage of different tested genotypes. Highest moisture percentage was recorded in genotype number 4, 10 and genotype number 15. While the minimum moisture percentage was recorded in genotype numbers 9 and 18. Significant difference was found between various different genotypes tested for moisture percentage.

WET GLUTEN%

Mean result of wet gluten percentage tested for various genotypes. Highest wet gluten percentage (39.2 %) was noted in genotype no 16. While the lowest wet gluten % was found in genotype number 15. There was significant difference found between various genotypes tested for wet gluten percentage.

STARCH %

Mean result of starch percentage tested for various genotypes. Highest starch percentage (69.8 %) was noted in genotype no 15. While the lowest starch % was found in genotype number 19. There was significant difference found between various genotypes tested for starch percentage.

ZELENY (ML)

The result of zeleny (ml) in different genotypes. The result indicated that among the tested different genotypes the highest 96.7 zeleny (ml) was recorded in genotype number 16. And the minimum 48.3 zeleny (ml) was recorded in genotype number 15. There was significant difference found between the tested genotypes for zeleny (ml).

PROTEIN %

Mean result of protein percentage of different tested genotypes. Highest protein percentage was recorded in genotype number 1. While the minimum protein percentage was recorded in genotype number 12. Significant difference was found between various different genotypes tested for protein percentage.

DISCUSSION

The rationale for cultivating the wheat germplasm was to assess its performance under highland agro-climatic conditions. (13) contend that earliness is a genetic characteristic that facilitates early maturation in crops, thereby offering defence against several abiotic stresses and (14) also viral diseases. (15) (2000) established a favourable link between the duration to heading and grain production. (16) et al. and (17) 2003) discovered that genotypes exhibited considerable variance in the duration until heading. (18). (1994) indicate that pre-harvest circumstances may influence grain weight, either via stem storage or parameters established soon after anthesis. (19) and (20) assert that inadequate water supply post-anthesis results in decreased grain filling time, kernel weight, and total crop output. The significant decrease in grain yield seen under the I4 treatment seems to be associated with a fall in MD and other yield components, such as TKW and kernel weight per spike.

Improved climatic conditions, particularly temperature and sun radiation, together with an extended vegetative development phase, promote increased plant height (21) According to (22), genetic variety may explain why different types of plants have different average heights. Plant height was positively and significantly correlated with grain production in phenotypic studies (23). In terms of plant height, (24) found no statistically significant differences between genotypes. However, there was strong evidence of a genotypic link between plant height and other variables (25). Variations in genetic composition account for observed variations in plant height (26). (27) replicated the findings.

When it comes to drought stress, the early maturing attribute of genotypes is a great asset. This means that crops may finish their life cycles before the drought starts and avoid both biological and environmental pressures (28).

Tillering is largely dependent on the green photosynthetic area, which is responsible for carbohydrate generation, grain filling, and ultimate grain yield; this area also dramatically boosted the number of tillers, with tillers contributing the most to final output. Finding positive and statistically significant relationships between grain yield and number of tillers m-2, the current results are in accordance with those of (29) and (30). According to Dhonde *et al.*, (2000), tiller m^{-2} and grain yield have an extremely substantial positive correlation (15, 31). Since comparatively higher temperatures delayed the interval between anthesis and senescence, they also lowered the number of tillers in late-sown crops (32). The genetic variety across cultivars might explain why some have more tillers than others (33).

There is a substantial correlation between the weight of one thousand grains and the ultimate grain yield. This finding is supported by the research of (34), who found that kernel weight is a key factor in predicting the final grain yield. Reduced test weight and forced maturity of wheat are outcomes of the warmer weather and drying winds that hit the region in March and April (35).

Grain yield is significantly affected by the quantity of kernels per spike. One study found that increasing the number of kernels per spike or unit area increased durum wheat output. Research has shown that new types of durum and bread wheat have a higher yield when there are more kernels per spike or unit area (36). From what they can tell, the most vulnerable time for the kernel under water-limited conditions was from the floral initiation to anthecias stage. They also noticed that the quantity of kernel spikes per spike is determined at this time. This stage is the most critical era for growth and development of the ultimate grain yield.

Better grain output was the result of a combination of factors, including a greater or similar number of tillersm-2, more grains per spike, and a higher mean grain weight, all of which were caused by the plants' genetic make-up and the increased photosynthesis that occurred during a longer period of development (37).

CONCLUSION

Many different types of wheat varieties, including modern cultivars, hybrids, traditional cultivars, landraces, genetic strains, introgressed lines, mutants, and central wheat varieties (CWRs), are stored in gene banks across the globe. World Information and Early Warning System (WIEWS) data from the Food and Agriculture Organisation (FAO) indicates that 218 gene banks in 88 different countries have around 855,000 Triticum accessions. Prior to this, there was an overview based on more sources of information.

Adaptability and evolution of wheat germplasm selected from CIMMYT nursery elite spring wheat yield trail for Balochistan consisting of 24 entries and one check variety Shalkot-14 was conducted in Balochistan Agricultural Research and Development Centre, Quetta (BARDC). Results of the study showed that heading genotype number 9 while minimum days to heading 50% were recorded. Maximum plant height 84.5 cm was noted in genotype number 21. Maximum spike length 14 cm was noted in genotype number 16 and Maximum average 65.5 numbers of grains was recorded.

In genotypes tested for thousand-grain weight, maximum thousand-grain weight was recorded in genotype number 25. The maximum canopy temperature was recorded in genotype number 10. Maximum chlorophyll content was found in genotype number. Maximum grain yield was recorded in genotype number 8. Moisture % was determined in the tested genotypes and the mean highest moisture percentage was found in the genotype number 4, 10 and 11. Wet gluten is an important characteristic of wheat grain. The highest wet gluten percentage (39.2 %) was noted in genotype no 16. Among the tested genotypes highest starch percentage (69.8 %) was noted in genotype no 15. Among the tested different genotypes the highest 96.7 zeleny (ml) was recorded in genotype number 16. Protein percentage of the tested genotypes was determined highest protein percentage was recorded in genotype number 1.

References:

1. El Hanafi S, Backhaus A, Bendaou N, Sanchez-Garcia M, Al-Abdallat A, Tadesse W. Genome-wide association study for adult plant resistance to yellow rust in spring bread wheat (Triticum aestivum L.). Euphytica. 2021;217(5):87.
2. Tadesse W, Abdalla O, Ogbonnaya F, Nazari K, Tahir I, Baum M. Agronomic performance of elite stem rust resistant spring wheat genotypes and association among trial sites in the Central and West Asia and North Africa Region. Crop science. 2012;52(3):1105-14.
3. Liu X, Wang H, Wang H, Guo Z, Xu X, Liu J, Wang S, Li WX, Zou C, Prasanna BM, Olsen MS. Factors affecting genomic selection revealed by empirical evidence in maize. The Crop Journal. 2018;6(4):341-52.

4. Akter N, Rafiqul Islam M. Heat stress effects and management in wheat. A review. Agronomy for sustainable development. 2017;37:1-7.
5. Reynolds M, Foulkes J, Furbank R, Griffiths S, King J, Murchie E, Parry M, Slafer G. Achieving yield gains in wheat. Plant, cell & environment. 2012;35(10):1799-823.
6. Cairns JE, Prasanna BM. Developing and deploying climate-resilient maize varieties in the developing world. Current Opinion in Plant Biology. 2018;45:226-30.
7. Hassan MA, Yang M, Rasheed A, Yang G, Reynolds M, Xia X, Xiao Y, He Z. A rapid monitoring of NDVI across the wheat growth cycle for grain yield prediction using a multi-spectral UAV platform. Plant science. 2019;282:95-103.
8. Velu G, Singh RP, Crespo-Herrera L, Juliana P, Dreisigacker S, Valluru R, Stangoulis J, Sohu VS, Mavi GS, Mishra VK, Balasubramaniam A. Genetic dissection of grain zinc concentration in spring wheat for mainstreaming biofortification in CIMMYT wheat breeding. Scientific reports. 2018;8(1):13526.
9. Atanda SA, Govindan V, Singh R, Robbins KR, Crossa J, Bentley AR. Sparse testing using genomic prediction improves selection for breeding targets in elite spring wheat. Theoretical and Applied Genetics. 2022;135(6):1939-50.
10. Robert P, Auzanneau J, Goudemand E, Oury FX, Rolland B, Heumez E, Bouchet S, Le Gouis J, Rincent R. Phenomic selection in wheat breeding: identification and optimisation of factors influencing prediction accuracy and comparison to genomic selection. Theoretical and Applied Genetics. 2022:1-20.
11. Singh RP, Juliana P, Huerta-Espino J, Govindan V, Crespo-Herrera LA, Mondal S, Bhavani S, Singh PK, He X, Ibba MI, Randhawa MS. Achieving genetic gains in practice. InWheat improvement: food security in a changing climate 2022 Jun 3 (pp. 97-123). Cham: Springer International Publishing.
12. Şahin İ, Gümez Y. Efficiency of education: The case in eastern and south-eastern Turkey. Social Indicators Research. 2000;49:213-36.
13. Eticha F, Belay G, Bekele E. Species diversity in wheat landrace populations from two regions of Ethiopia. Genetic Resources and Crop Evolution. 2006;53:387-93.
14. Qadir A, Hameed S, Munir A. First report of barley yellow dwarf virus PAV in uncultivated grasses of Pakistan. Journal of Plant Pathology. 2019;101(3):769-.
15. Dhonde SH, Kute NS, Kanawade DG, Sarode ND. Variability and characters association in wheat (Triticum aestivum). Agricultural science digest. 2000;20(2):99-101.
16. Mohammad A, Mitra B, Khan AG. Effects of sheared-root inoculum of Glomus intraradices on wheat grown at different phosphorus levels in the field. Agriculture, ecosystems & environment. 2004;103(1):245-9.
17. Ahmad M, Niazi BH, Zaman B, Athar M. Varietals differences in agronomic performance of six wheat varieties grown under saline field environment. International Journal of Environmental Science & Technology. 2005;2:49-57.
18. Ortiz-Monasterio JI, Peńa RJ, Hede AH, Pfeiffer WH. Nitrogen and water stress in triticale and durum wheat yield and quality. 2002:11-26.
19. Donaldson E. Crop traits for water stress tolerance. American Journal of Alternative Agriculture. 1996;11(2-3):89-94.
20. Nazeri M. Effect of post anthesis water deficit on yield potentional and effective traits in promising winter and facultative bread wheat genotypes. Environmental Stresses in Crop Sciences. 2016;9(2):109-19.
21. Qasim M, Ahmed W, Safdar U, Maqbool R, Sajid HB, Noor H, Ul Haq MI. Effect of drought stress on fertile tillers of wheat genotypes (Triticum aestivum L.). 2022:172-180.
22. Shahzad M, Saqib ZA, Hafeez F, Bilal M, Khan SA, Asad SA, Akhtar J. Growth-related changes in wheat (Triticum aestivum L.) genotypes grown under salinity stress. Journal of Plant Nutrition. 2016;39(9):1257-65.
23. Chaves MM, Oliveira MM. Mechanisms underlying plant resilience to water deficits: prospects for water-saving agriculture. Journal of experimental botany. 2004;55(407):2365-84.
24. Upadhyay PN, Dixit AG, Patel JR, Chavda JR. Response of summer pearlmillet (Pennisetum glaucum) to time and method of planting, age of seedling and phosphorus grown on loamy sand soils of Gujarat. Indian Journal of Agronomy. 2001;46(1):126-30.
25. Khan MJ, Rashid H, Rashid A, Ali R. Intravarietal variability in wheat grown under saline conditions. Pak. J. Biol. Sci. 1999;2:693-6.

26. Ashiq M, Muhammad N, Ahmad N. AGAI NST BROAD LEAF Weeds IN Wheat. Pak. J. Weed Sci. Res. 2007;13(3-4):149-56.
27. Hassan FU, Ahmad M, Ahmad N, Abbasi MK. Effects of subsoil compaction on yield and yield attributes of wheat in the sub-humid region of Pakistan. Soil and Tillage Research. 2007;96(1-2):361-6.
28. Saleem B, Khan AS, Shahzad MT, Ijaz F. Estimation of heritability and genetic advance for various metric traits in seven F2 populations of bread wheat (Triticum aestivum L.). Journal of Agricultural Sciences, Belgrade. 2016;61(1):1-9.
29. Dautani MA, Ahmad HK, Sadiq M. Performance of different wheat (Triticum aestivum L.) varieties under the agro-climatic conditions of Dera Ismail Khan.1997:527-532
30. Ullah R, Mohammad Z, Khalil IH, Ullah A. Heritability for heading, maturity, plant height, spike length and tillers production in winter wheat (Triticum aestivum L.). Pak. J. Pl. Sci. 2007;13(1):67-73.
31. Khalifa MA, Akasha MH, Said MB. Growth and N-uptake by wheat as affected by sowing date and nitrogen in irrigated semi-arid conditions. The Journal of Agricultural Science. 1977;89(1):35-42.
32. Rasol HO. *Effect of different quantities of irrigation water on growth and yield of wheat (Tritcumaestivum L.)* (Doctoral dissertation, MS thesis, Dept. of Agron., Univ. Khartoum, Khartoum, Sudan). 2003
33. Shah AR, Shah RK, Madamwar D. Improvement of the quality of whole wheat bread by supplementation of xylanase from Aspergillus foetidus. Bioresource technology. 2006;97(16):2047-53.
34. Peltonen-Sainio P, Kangas A, Salo Y, Jauhiainen L. Grain number dominates grain weight in temperate cereal yield determination: evidence based on 30 years of multi-location trials. Field Crops Research. 2007;100(2-3):179-88.
35. Dhaliwal SS, Singh CB, Toor AS. Wheat yield as influenced by moisture conservation practice through ploughing and planking after maize harvest under rainfed conditions. International Journal of Science, Environment and Technology. 2013;2(2):176-84.
36. Calderini DF, Ortiz-Monasterio I. Are synthetic hexaploids a means of increasing grain element concentrations in wheat?. Euphytica. 2003;134:169-78.
37. Ali M, Jensen CR, Mogensen VO, Andersen MN, Henson IE. Root signalling and osmotic adjustment during intermittent soil drying sustain grain yield of field grown wheat. Field Crops Research. 1999;62(1):35-52.