The appraisal of comparative genetic variability in diverse wheat genotypes for yield and yield contributing traits

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Abstract. The demand and supply of wheat for burgeoning global population reflects country's capability to accept forthcoming food security challenge to feed 9 billion peoples in coming decades with a mission for plentiful and equitably food distribution so that nobody will go to the bed hungry. Wheat is considered as the grain of life due to its indefinite and vital role to provide plentiful protein, fiber and other micronutrients. Wheat is perfectly mother of mostly offered food and feed commodities that mainly depends upon its production, consumption, wider adoptability in diverse environments. To ensure local to global food security, the durable wheat varieties are crossed for wider adoptability. Genetic diversity assessment will help the plant breeders in selecting the enhanced genotypes to deliver the propinquity in transgressive segregants. The present study was conducted in College of Agriculture, University of Sargodha, Pakistan with the aim and objective to determine the genetic diversity for the selection of candidate genotypes having much yield potential. The traits data was recorded in 20 wheat genotypes for eight morphological traits. The results showed positive diversities in all morphological traits in greater extent. These fabulous parameters depicting yield and yield related traits potentially assess the germplasm. The diverse genotypes assessed in this study will pave the path of development and provide an excellent offer a refrained paradigm shift to achieve sustainable development goals to reduce poverty and ensure food security.

Keywords: Diversity, Genetic, Germplasm, Food security, Morphology

Introduction

Wheat is the global mostly consumed and imperious staple cereal crop around the world with rich floristic diversity extended from Near East to Ethiopian Highlands. It is the prominent member of Poaceae family. It remained under cultivation throughout the globe. [1]. In SAARC countries and Pakistan particularly the wheat has vital role in daily life from the opening of eyes till the closing of the eye. It is being used as rich source of energy in our daily life and at global scenario [2]. It is enriched in protein content and considered as the most important staple food grains having the sufficient amount of fiber in flour bread. [3]. Wheat is also used as chattel, trading icon as well as 2nd to currency in Pakistan and other countries. It is used as feed for animals, poultry and birds and major food crop to combat the environmental stresses. [4]. It was observed that 1% annual food is demanded worldwide in developing countries. [5]. So the burgeoning population is demanding the abundance increase in continuous food supply for which demands concerted efforts of plant breeders, Plant physiologists, agronomists, entomologists and pathologists to conserve wheat genetic resources and change genetic architecture to achieve self-sufficiency. [6]. Wheat genetic resources coming from land races, obsolete varieties and cultivated varieties showing much characteristic diversity are crossed to get maximum genetic variability so that ultimately the yield barrier can be broken and after viable selection best adopted and good yielder genotypes would be selected to increase the genetic potential of the wheat crop. [7] It is as scientific approach now to select good wheat plant ideotype and morphological divers to enhance yield and yield related traits [8]. Genetic diversity exploration helps us in to find out the better genotypes to deliver the transgressive sergeants. This exploitation of diversity is intended to meet the current wheat production challenges and to provide the opportunities to get quantum yields to fulfill Millennium development goals to reduce hunger and poverty.

Keeping in view the current circumstances a study was initiated to check the genetic diversity among the diverse genotype of wheat with the aim to find some novel genotype having greater genetic variability for breeding the successive generation.

Materials and methods

Diverse twenty wheat genotypes including 17 advance lines and 3 checks were sown in the research area of the Department of Plant Breeding and Genetics, College of Agriculture, University of Sargodha. (Table-1). All recommended cultural practices were performed and manured accordingly. By using the Randomized complete block design with three replications to minimize the experimental error. In every plot 4 lines of 5m length was maintained with the line to line distance of 30CM.Customary agronomic practices were performed according to schedules and demands of crops for every individual single unit plot. The data was subjected to analysis of variance (ANOVA) as delineated by [9]. A Statistical software, Statistix 8.1 was employed to analyze the data to evaluate the results.

Table 1. Details of diverse wheat genotypes used in the study with their parentage

Genotype	Parentage
UOS-1	AFFTILE/2*BGN//BAA94/5/TESTOR/5/..
UOS-2	AFFTILA/2*BGN//BAA94/5/TESTOR/6/..
UOS-3	AFFTTILA/3*BON*//BAV92/3/BITTKARI/ELLWAS1/9/..
UOS-4	AT34/STAPP
UOS-5	INQILAB91//FORTOOB/JASMANN#9
UOS-6	RONALDS/G830//AB91/3/AEERI#1/4/ZD../4/FGHDDOSA
UOS-7	RONALDS/G830//AB92/3/AEERI#1/4/ZD../5/FGHDDORA
UOS-8	ATTILA/3*BCN//BAV92/3/KRITATI/WBLLI/4/..
UOS-9	SAYYED1/ALLAIVASHOREZ F1999
UOS-10	KPAKKU/GDS//ASDSAA
UOS-11	ZCSSWQ*2/THOKMMS//FADS
UOS-12	BOUT*3/CCDS//MILAN/3/KOBLW*2/4/OOPAS
UOS-13	FITTRDS//DSDSII/CM12213/2/AASCAL/1/KJ643/...
UOS-14	KACHU//WBLL1*2/BRAMBLING
UOS-15	SDDST2/CCDVDRU//FRET2/3/MUNAL#1
V-82003	SDDATI/4/2*//WDDER/TSL//QQWEW/3/KKJHGF
Pb-11	QQWSD/MMRDS//INQ.91/JASS’S’
UOS-18	BEE/ALPHA.917//GEE/3/THQ83.23327/4/QQASAS/2*WWQ95
Millat-11	CHENAB2000/INQ.91
Galaxy-13	PB96/87094//MH-97

Salient wheat plant traits selected for the recording the data

1. Plant height.
2. Tillers per meter^2
3. Peduncle length
4. Spike length
5. Number of spikelet per spike

6. Number of grains per spike
7. 1000 Grain weight
8. Grain yield per plot

Results and discussion

In order to estimate the genotypic differences, the average data for each replication for each trait i.e Plant height, peduncle length, Number of tillers per meter-2, spike length, Number of spikelet per spike, grains per spike and1000 grain weight were subjected to a analysis of variance (ANOVA).All %age data were transformed using the excel log function before the analysis. The information with respect to mean performance of 20 diverse wheat genotypes examined for eight quantitative traits of wheat were computed and shown in Table 2. A large number of the genotypes showed higher average values for each trait.

Table 2: Means values and analysis of variance (ANOVA) for yield and yield contributing traits in diverse wheat (*Triticum aestivum* L.) genotypes

Traits	**Mean Values**	**Mean squares values**		
		Replication df = 2	**Varieties df = 19**	**Error df. = 38**
Plant height	98.7	11.26	106.922**	2.58
Number of Tillers plant−1	408.68	366	1487**	572.6
Peduncle length	33.12	0.46	39.76**	2.2
Spike length	11.41	1.28	6.11**	1.23
Number of spikelets spike−1	18.6	0.65	16.11**	1.36
Number of grains spike−1	46.73	1.017	103.67**	4.16
1000 grain wt	36.62	0.003	19.78**	0.1985
Grain yield plot−1	3178	1936	727521**	4800

(*=Significant at 5% probability)

Plant height was the most important character that was negatively correlated to yield indirectly effect grain yield in wheat same was found reported by [10] It was also found that the development of short stature varieties has been desired due to lodging problems. By introducing short stature varieties grain yield was increased as a result of shorter vegetative phase and longer reproductive phase during past green revolution. There was highly significance differences were found for the trait plant height. Results revealed that plant height range was 83 to 109 cm while the grand mean value was 98.7cm.The wheat genotypes Pb-11 and Galaxy-13 had extreme number of tillers/m2 with an average of 408.68. Most minimal number of tillers per meter2 (301) were produced by UOS-10. Peduncle length is also an important yield contributing trait. Highly significant differences for the trait peduncle length were measured among wheat genotypes. The genotype UOS-7 showed highest peduncle length (40 cm)however the lowest peduncle length was recorded in wheat genotype UOS-13 as 28.33cm. The average peduncle length was recorded as 33.12cm.Spike length in wheat had more contribution in crop yield as well as the genetic diversity of the wheat genotypes. Maximum spike length 14.6 cm was recorded by the genotype UOS-18 followed by UOS-12 with spike length 13.67cm with an average of 11.41. Similarly the trait number of spikelets per spike showed very promising results, the wheat genotype UOS-18 that expressed maximum mean value of 24 spikelets per spike, while the genotype UOS-1 produced 23 spikelets per spike. The wheat genotype Millat-11 had least number of spikelets per spike. Grand mean value was 18.6. The results are in agreement with the findings of [11],[12]. Number of grains per spike is the very imperative trait to determine grain yield and has significant effect on it total grain yield. Results showed that all genotypes had significant differences for number of grains per spike. The maximum range of grains/spike was produced by the PB-11 (55) followed by UOS-12 (55).These findings are in line with the findings of earlier researchers. [13] and [14]. All of these concluded that genotypes differed significantly in number of grain per spike.

Analysis of variance demonstrated that highly significant a difference for thousand grain weight among the genotypes was estimated (Table 2). Two wheat advance lines UOS-3 and UOS-11 displayed most extreme mean value 40.4 and 40.3g for 1000 grain weight respectively, While least mean value 31.8g was showed by UOS-18 with average (36.62) Table 2. [15] and [16] findings also supported our findings. Grain yield is very complex trait and breeder utmost desire and main objective is to increase grain yield by accumulating diverse genes. In this study the analysis of variance showed that highly significant differences among genotypes for the trait grain yield/plot (Table 2). The genotype UOS-7 revealed maximum grain yield per plot (4504g) followed by UOS-11 (4314.3g) (Table 2). The average value for grain yield/plot was 3178 g. These findings are in agreement with the results of [17] and [18].

Table 3: Genetic analysis and genetical variability, heritability and genetic advance of diverse wheat genotypes

Variable	VG	V p	H2bs (%)	GA
Plant height	34.78	37.36	93.9	10.37
Number of Tillers plant−1	304	876.6	34	30
Peduncle length	12.52	14.78	85.12	6.13
Spike length	1.63	2.86	56.99	2.19
Number of spikelets per spike	4.92	6.28	78.34	3.83
No of grain per spike	33.17	37.33	88.75	9.92
1000 grain wt	4.90	5.09	96	3.82
Grain yield plot−1	0.240	0.245	97.05	0.84

Table 3.Revealed that the trait plant height depicted high heritability (93.9%) with moderate genetic. advance (10.37) so the selection of the trait at early stage will be beneficial while for the trait number of tillers per plant the phenotypic and genotypic variances showed high environmental effects depicting low heritability (34%) with high genetic advance (30). This condition showed that the trait is under the influence of additive gene affects so selection will not be effective at the moment. These results are not in agreement with [19] and [20].

The trait peduncle length showed high heritability (85.12%) with low (6.13) genetic advance depicting the breeder should delay the selection for the more precision of the trait. Our results are also supported by [21]. Spike length is very critical trait for yield enhancement. The phenotypic and genotypic variances were obtained as 2.86 and 1.63 respectively with medium heritability (56.99%) and low advance (2.19). The trait showed medium transmission of the trait and high influence of environmental effects so we should delay the selection. Similar results were earlier reported by [22] and [23] while contradictory genetic advance by [24]. High heritability (78.34%) with low (3.83) genetic advance was observed by the trait number of spikelet/spike while high heritability (96%) with low genetic advance (3.82) was also revealed for the trait 1000 grains weight. The trait number of grains per spike showed high heritability (88.75%) with moderate genetic advance (9.92) showing delayed selection. [24] and [25] results are in agreements with our results.

Grain yield/plot the prime important trait genetic response was evident from the phenotypic and genotypic variances 0.245 and 0.240 respectively. High heritability (97.05%) with low (0.84) genetic advance revealed that the selection will be useful in latter generation. Our results are also supported by the earlier researcher finding by [26] and [27].

Conclusions

The study showed that huge variations among the diverse genotypes were present for all traits. The genotypes showed maximum values for the traits plant height, peduncle length, spike length, number of tillers/meter square, number of spikelet per spike, number of grain per spike, 1000 grain weight and grain yield were shown by UOS-13, UOS-7, UOS-18, Pb-11, UOS-18, Pb-11, UOS-7 and UOS-3 respectively. Similarly much genetic variability was found when subjected to phenotypic and genotypic variance, than heritability and genetic advance. The traits like plant height, peduncle length, Number of spikelet per spike, Number of grains per spike, 1000 grains weight and grain yield/plot showed heritability but a range of high, moderate and low genetic advance respectively. So it was concluded for the trait plant height the selection will be done in early generation wile for rest of traits the selection will be more fruitful in succeeding generations. The dives genotypes showed a number of promising traits. These genotypes could be utilized for the future breeding program to exploit genetic diversity for yield and yield contributing traits. It was also revealed that genotypic performance for different traits were in line to breed for future wheat yield maximization programs.

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