

Genetic Variability for Yield and yield component characters in Triticale (*XTritiosecale wittmack*) Genotypes grown in Jima Geneti, Guduru and Horo Districts of Horro Guduru Wollega Zone, Western Ethiopia

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Abstract

A total of eighteen triticale (*XTritiosecale wittmack*) genotypes were evaluated at three different environments to assess the genetic variability, for yield and yield component characters. The results of the analysis of variance for individual locations and combined analysis indicated that the tested genotypes were significantly ($p < 5\%$) different for all traits except grain per spikelet's at Guduru. Phenotypic coefficient of variability was generally slightly higher than the genotypic coefficient of variability. High phenotypic and genotypic coefficient values were recorded at Gitilo and Hareto than at Guduru. Thousand-kernel weight, tillers per plant, spikes per plant and kernels per spike had high phenotypic and genotypic coefficient of variability at both locations compared to Guduru. Higher heritability estimates (for five characters out of twelve) were recorded at Guduru, (for six characters out of twelve) at Hareto, and (for seven characters out of twelve) at Gitilo indicating that Guduru growing environment was less favorable than that of Hareto and Gitilo. Gitilo growing environment was more favorable than the other two locations. Estimated genetic advance for grain yield indicated that the appropriate environment for improving grain yield for the genotypes grown at high land environment ; Gitilo than Hareto and then Guduru even if higher yield was recorded at Guduru than Hareto. Generally, for

most characters higher genetic advance as percent of mean was recorded at Gitilo and Hareto than at Guduru. Since thousand-kernel weight, grain yield, harvest index and grain filling period had relatively high genetic advance as percent of mean and high heritability at all locations; hence, they can be used as a selection criterion, but ultimate evaluation must be performed in the target environment prior to using them.

Keywords: Variability, Heritability, Genetic Advance, Triticale Genotypes

1. Introduction

Hexaploid triticale (*XTritiosecale wittmack*) is a synthetic species. Triticale is a crop developed by crossing wheat (*Triticum turgidum* or *aestivum*) with rye (*Secale cereal*). Triticale introduced from CIMMYT to Ethiopia in 1999. Triticale (*X Tritiosecale wittmack*) is a cereal crop developed by human intervention from crosses between wheat and rye. It has high yield potential and is adapted to a wide range of soil types and environments. Triticale has an aggressive root system that binds light soils better than wheat, barley or oats. Under ideal conditions, triticale can out-yield wheat and barley and sometimes oats (Castleman, 1996). Research on triticale actually began

at CIMMYT in 1966 (Varghese, *et al.*, 2001). The first breakthrough in producing fertile primary triticale came in 1937 with the discovery of colchicine. Triticale is the stabilized hybrid of wheat (*Triticum*) and rye (*Secale*). Poland, Germany, China, and France account for nearly 90 percent of world triticale production (Gibson, 2002). Globally, triticale is used primarily for livestock feed. In Mexico, which grows the crop, triticale is used mostly for whole-grain triticale breads and tortillas. In the US, triticale is harvested mostly for forage, but there is a small market for pancake mixes and crackers due to a savory, nutty flavor. Ethanol plants will pay a premium for triticale over barley since it has more starch and no hull, making alcohol production more efficient. Although wheat-rye hybrids date back to 1875, it was only in 1953 that the first North American triticale-breeding program was initiated, at the University of Manitoba (Salmon *et al.*, 2001). Triticale is less susceptible to the common fungal diseases of cereals which make it suitable for use in rotations where stubble is retained (Jessup and Wright, 1991). Of all the cereals available to farmers, triticale has the best adaptation to water logged soils and those of high pH (alkaline soils) Triticale is also tolerant of low pH (acid soils), grows well on sodic soils and tolerates soils high in boron. In nutrient deficient soils, triticale appears to respond better to applied fertilizers than other cereals. Triticale has the capacity to survive utilizing trace elements in soils which would be considered nutrient deficient for any other type of crop (Castleman, 1996). Past studies indicate that while the nutritional quality of triticale is considered superior to wheat, the higher ash content, lower milling yields of flour, and inferior loaf volume and texture distract from commercial baking use of triticale (Stallknecht, *et al.*, 1996). Pena and Amaya (1992) indicate that triticale flour blends of up to 50% with wheat flours produce breads with quality similar to breads made from wheat flours only. In some livestock industries triticale has become the preferred cereal, in part due to its high lysine and methionine content and its reduced problems associated with acidosis in feeding the grain to ruminants. It has a similar protein, energy and digestibility to wheat. The grain has potential as a cereal for human food consumption domestically and as an export commodity. Uses include a flour supplement to wheaten flour for bread, biscuits and cakes, as rolled whole grains for breakfast cereals and in the brewing and distilling industries (Castleman, 1996). Organized research on triticale started in Ethiopia in 1999 when the national wheat research project introduced several triticale germplasm from CIMMYT. Studies have

indicated that the grain production of newer and improved triticale cultivars both as a mono-crop and in small grain mixtures was acceptable in a wide range of genetic diversity available and the response of environments (ASHS *et al.* 2000). The forage production and silage yield and quality of hexaploid triticale's both as a monocrop and in small grain mixtures were reported to be favorable in comparison with other small grains (Sun *et al.* 1996; Juskiw *et al.* 2000 a,b; Rao *et al.* 2000).

Heritability is the proportion of observed variability, which is due to heredity, the remainder being due to environmental causes (Allard, 1960). The effectiveness of selection for a trait depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among genotypes in a population (Fehr, 1987).

The phenotypic variance can be sub-divided into components of variance attributable to factors that cause differences in the performance among individuals. This relationship can be written as $\sigma_p^2 = \sigma_e^2 + \sigma_{ge}^2 + \sigma_g^2$, where σ_p^2 is phenotypic variance, σ_e^2 is environmental variance, σ_{ge}^2 variance due to genotype by environment interaction, and σ_g^2 is genotypic variance. The total genetic variance can be further subdivided into additive genetic variance, dominance genetic variance and epistatic genetic variance (Suzuki *et al.*, 1981).

Generally, heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. If heritability were 100%, that is genotypic variance (σ_g^2) is equal to phenotypic variance (σ_p^2), then phenotypic performance would be a perfect indication of genotypic value (Johnson *et al.*, 1955b); but, even in such a hypothetical situation, the heritability value in itself provides no indication of the amount of genetic progress that would result from selecting the best individuals. However, genetic progress would expect from selection increase with an increase in the genotypic variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential leading to concomitant estimate of genetic advance expectations from selection.

The heritability of a character is not a constant value; hence, an understanding of the factors that contribute to heritability permits the breeder to develop a breeding programme that maximizes the genetic improvement with available resources (Hallauer, 1987). Factors influencing the magnitude of heritability estimates include characteristics of the population (amount of genetic variance), number of genotypes evaluated, methods of calculating heritability, linkage disequilibrium and conduct of experiment (Hohenboken, 1985).

Genetic advance is the expected gain in the mean performance of a population for a particular trait by one generation of selection of a specified percent of the highest-ranking plants.

It measures the difference between the mean genotypic value of the selected lines and the mean genotypic value of the original population.

Selection intensity refers to the percent of the population selected, (n/N) . The selection intensity used in prediction of equation expressed in standard units and is often denoted as k .

Genetic advance under selection $(G_s) = k (\sqrt{\sigma_p^2}) h^2$ Where, G_s is the predicted genetic advance; K is a constant based on selection intensity in standard deviation units, $\sqrt{\sigma_p^2}$ is the square root of the phenotypic variance, h^2 is the heritability, broad or narrow, as the case may be. The net gain from selection depends on upon the combined effect of the heritability, the amount of the genetic variance present, and the selection intensity.

Hexaploid triticale has many advantages over both parental species for both grain and forage production in certain environments. Additional information on environmental stability and heritability would be desirable to develop appropriate selection strategies in the production of superior widely adapted cultivars. Even though the environment of the study area is favorable for triticale production and its importance is well known, little research had been conducted concerning the crop in this area and productive varieties were not yet known. Therefore, the purpose of this study was;

- To identify the variability of triticale genotypes under the study

- To determine heritability and genetic advance for the characters studied

2. Materials and Methods

Eighteen genotypes of triticale constituted the experimental material of this study. Planting was done in Randomized Complete Block Design. Each genotype was planted in 5row plot where row to row and plant to plant distance maintained at 20 cm and 5cm respectively. The experiment was planted at Gitilo, Horro district, Shambu campus research site, Guduru and Hareto, Western Ethiopia. The locations are characterized in long, short and medium maturity duration environments respectively. The experiment was planted from mid August and raised under rain fed condition. Data were collected on 12 morphological and yield characters. Site was kept weed free by manual weeding.

Table 1: Spring triticale genotypes used in the experimental areas

No	Seed Source (Genotypes)	Sectional code
1	2012MS#2	02L008002
2	2012MS#110	10P154
3	2012MS#100	10P028
4	2012MS#102	10P104
5	2012MS#51	09P144
6	2012MS#94	04L064010
7	2012MS#26	03L032018
8	2012MS#85	10P139
9	2012MS#59	09P167
10	2012MS#15	03L003006
11	2012MS#62	09P019
12	2012MS#88	10P022
13	2012MS#81	10P009
14	2012MS#38	04L018011
15	2012MS#101	10P030
16	2012MS#64	09L0302
17	Moti	Released
18	Abdisa	Release

3. Results and Discussion

The result of pooled analysis of variance shows there is highly significance difference between all genotypes ($P < 0.01$) except tiller number per plant and grain per spikelet's which shows significance at ($P < 0.05$) indicating the existence of great variability of triticale genotypes under different environments. In addition, location effect was highly significant for nine of the variables out of 12, one variable (spike length) shows none significance difference and plant height and tiller number per plant shows significance ($P < 0.05$). This indicates that most of the characters studied were not affected by environment. In other case the interaction of genotype and location shows highly significance for all of the 12 characters studied (days to heading, days to maturity, grain filling period, tiller number per plant, plant height, spike length, spikelet per spike, grain per spike, biological yield, thousand grain weight, grain yield per plot and harvest index), significance ($P < 0.01$) (Table 2 below).

Table 2: Mean square analysis of variances for 12 characters analyzed in combined location

Variables	Gen.	Env.	Rep	GXE	Error	CV	SE	Mean
Df	17	2	2	34	105			
DH	110.6*	5568.9*	22.4*	25.9**	2.7	2.3	1.6	71.24
DM	92.3**	1838.7*	10.8*	38.6**	3.6	1.5	1.9	126
GFP	37.5**	2822**	2 ^{ns}	47.9**	5.3	4.2	2.3	55
Till	0.76*	1.55*	0.55 ^{ns}	1.42**	0.42	27	0.6	2.3
PH	416.9*	21*	12*	245.6*	6	3.5	2.4	69
SL	5.2**	0.27 ^{ns}	0.74 ^{ns}	2.8**	0.73	11.7	0.85	7.2
SPS	19.8**	394.6**	2.3 ^{ns}	15.3**	2.1	7.8	1.4	18.6
GPS	0.6*	4.7**	0.1	0.67**	0.27	20	0.52	2.6
BY	37507**	188036**	384 ^{ns}	16862*	6673	10.6	81	791
TGW	45.4**	18.3**	6.2	32.4**	3.3	4.3	1.8	42.3
GY	32497**	243022**	399	8017.8**	668.8	9.5	25.8	271
HI	0.02**	0.18**	0.002	0.01**	0.0001	10.5	0.34	0.33

Where, Dh=days to heading, DM= days to maturity, GFP=grain filling period, Till= tiller number per plant, PH=plant height, SL=spike length, SPS=spikelet per spike, GPS=grain per spike, BY=biological yield, TGW=thousand grain weight, GY=grain yield per plot and HI=harvest index

This indicated that for all traits the genotypes showed differential performance at the three locations. Significant genotypes by environment interactions are commonly reported in wheat either in vitro or in vivo experiments in different types of stress including drought (Sivapalan et al., 2001; Desalegn et al.,

2000; Prakash and Sastry, 1999). Because of significant genotype by environment interaction for most of the characters, the analysis of variance and other estimates were done location-wise.

The result of analysis of variance for mean square of the traits for individual location was presented in (Table 3) for Guduru, Hareto and Gitilo respectively. At Guduru, Ten characters out of 12 shows highly significance ($P < 0.01$). The rest, tiller number per plant and Grain per spikelet's showed significance ($P < 0.05$). Similarly, at Hareto location, number of tiller per plant showed significance ($P < 0.05$) and grain per spikelet's showed non-significant, while the rest of all of the characters studied showed highly significance ($P < 0.01$). In Gitilo case, all of the characters responded differently showing significance difference between the traits. As general, all results at all locations showed there is high variability in triticale genotypes studied for farther investigations.

Table 3: Mean square analysis of variances for 12 characters analyzed in RCBD at Guduru, Hareto and Gitilo location separately

Variable	Gen	Rep	Error	CV%	Mean
Df	17	2	33		
DH Guduru	31.6**	406	1.9	2.2	62.3
Hareto	58.5**	16.3*	3.6	2.7	69
Gitilo	76.6**	11**	2.5	2	82
DM Guduru	105.9**	1.7	2.2	1.2	125.7
Hareto	12.4**	25**	2.5	2	120
Gitilo	51.6**	0.4	5.3	2.1	132
GFP Guduru	48**	7.8	2.5	2.5	63.2
Hareto	1048**	6	6.3	4.8	51.7
Gitilo	24.8**	7.5	7	5.2	50.1
Till Guduru	1.4*	0.2	0.3	24.7	2.5
Hareto	1.2	0.62	0.6	31	2.4
Gitilo	0.93*	0.2	0.3	26	2.2
Variable	Gen	Rep	Error	CV%	Mean

PH Guduru	408**	2	6.3	3.6	69.8
Hareto	234.5**	10.2*	5.2	3.3	68.7
Gitilo	265.9**	2	7.8	4	69
SL Guduru	9**	2.9	2.2	19.8	7.4
Hareto	2.2*	0.9	0.7	11.6	7.3
Gitilo	3.4*	1.3	0.7	11	7.3
SPS Guduru	13.4**	0.4	4.9	12.9	17.2
Hareto	16**	1.3	1.8	8.1	16.7
Gitilo	26.8**	4.6*	2.7	7.5	21.7
GPS Guduru	0.37	0.4	0.35	1.3	2.5
Hareto	0.88*	0.3	0.2	19.8	2.3
Gitilo	0.6*	0.5	0.2	16	2.9
BY Guduru	44036**	14485	10949	12.5	740
Hareto	22254.7**	7266.9*	16202	17.3	735
Gitilo	25524**	958	2101	5.8	784
TGW Guduru	21.8**	13.6	2.8	3.9	42.7
Hareto	36.2**	0.24	4.9	5.3	42
Gitilo	52**	1.58	2.1	3.5	41.2
GY Guduru	14660**	627	401	7.9	251
Hareto	9632.3**	3187.7	335	8.5	215.7
Gitilo	24240**	1612.2	1268	10.23	345
HI Guduru	0.014**	0.0004	0.001	10.2	0.32
Hareto	0.017**	0.002	0.0013	12.7	0.28
Gitilo	0.0097**	0.0004	0.0013	9.3	0.39

3.1 Range and Mean of Different Characters

Estimated range, mean, and standard error of the mean are presented in Tables 4. Wide ranges were recorded for grain yield, plant height, days to heading, days to maturity, thousand-kernel weight, and kernels per spike. The highest grain yield (3780.2kg/ha) was recorded from genotype Moti, while

low yield of (2126.3kg/ha) was obtained from genotype 2012MS#62 in average of the three locations. At Hareto, the highest grain yield of (3780.2 kg/ha) was recorded from Genotype Moti and the lowest yield of (1560.8 kg/ha) was obtained from genotype 2012MS#26. At Gitilo, genotype Abdissa records the highest grain yield (5160kg/hac) while, genotype 2012MS#102 records the list grain yield (2340kg/hac). Most of the genotypes matured earlier at Guduru than at Hareto and Gitilo with the mean days to maturity of 120 for Guduru, 125.7 for Hareto and 132 for Gitilo. This is due to the effect of uncertain amount of soil moisture and air temperature during the crop-growing season: it also affected other traits like plant height, grain filling period and effective tiller. Higher mean plant height (69.7 cm) was recorded at Guduru. At Hareto, mean plant height was little shorter (68 cm) as to Guduru growing season and at Gitilo, mean plant height was higher compared to the others as the result of long moisture reservation of the growing soil. The highest mean for grain yield (5160kg/ha) and biological yield (840.3 gm/plot) were recorded at Gitilo as compared to mean grain yield (3630 kg/ha) and biological yield (740 gm/plot) that were recorded at Guduru and (3360kg/hac) of grain yield and (785gr/plot) recorded at Hareto. This indicated that the crop performance was much better at Gitilo than at Hareto and Guduru.

Some of the genotypes had equal or higher-thousand kernel weight at Gitilo in comparison to Hareto and Guduru. Observation made in this study suggests that as moisture retention of the soil long, after rainy condition stops such as end of September and mid October, certain genotypes namely, 16 and 2 and 4 stayed greener and produced better grains Other genotypes had longer grain filling period and as a result they had higher thousand-kernel weight. Highest mean of thousand-kernel weighs was recorded for genotypes 2012MS#64 (50), 2012MS#110 (48) and lower thousand-kernel weighs was recorded for genotype 2012MS#88 (33) and 2012MS#94 (35) at Gitilo. Whereas, higher thousand-kernel weight was reordered for genotype 2012MS#85 (46.23) and the lowest thousand-kernel weight was recorded for genotype 2012MS#94 (31.5) at Guduru. Generally, low rainfall or drought stress can affect many traits such as tillering and plant height (Richards *et al.*, 2001) but the result obtained for tillers per plant at Hareto had higher value this indicate the amount of rain during planting was enough for proper and normal crop establishment and growth .

3.2 Phenotypic and Genotypic Variations

The amount of genotypic and phenotypic variability that exists in a species is of utmost importance in breeding better varieties and in initiating a breeding program. Genotypic and phenotypic coefficients of variations are used to measure the variability that exists in a given population (Burton and Devane, 1988). Estimated variance component, phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) of the characters studied at Guduru, Hareto and Gitilo are presented in Tables 4.

In general, the PCV values were greater than GCV values across environments and in combined although the differences were small. This indicated that the environmental effect was small for the expression of most characters. Among all characters, higher GCV and PCV values (>10%) were observed for tillers per plant, spikes length, kernels per spike and grain yield, harvest index and biological yield for combined and the rust characters records medium GCV and PCV value (>5% and <10%). At Hareto, higher GCV and PCV values were observed for grain yield, thousand-kernel weight, harvest index, tillers per plant, spikes per plant, spike length and kernels per spike: at Gitilo, higher GCV and PCV values were observed for grain yield, thousand-kernel weight, harvest index, tillers per plant, spikes per plant, spike length and kernels per spike. Lowest GCV and PCV values (<5%) were observed for days to maturity and grain per spikelet's at Guduru, and for days to maturity at Hareto and days to maturity and Grain filling period at Gitilo. Days to heading, thousand grain weight and spikelet's per spike at Guduru, and Days to heading, Spike length, thousand grain weight and biological yield at Hareto and days to heading, thousand grain weight and grain filling period at Gitilo showed intermediate (>5% and <10%) coefficients of variability. Among the yield components, tillers per plant, kernels per spike and spikes per plant had considerable variation at three of the locations.

3.3 Heritability

Estimated heritability for the characters considered at Guduru, Hareto, and Gitilo and in combined calculated. The heritability values were sufficiently high for most of the traits at three of the locations, indicating the possibility of progress from selection. The high heritability values for most of the characters

could be attributed to the relatively favorable environment at all locations. Heritability estimates are expected to be lower in environments where heritability is concealed due to a greater genotype by environment interaction component.

Grain yield at three of the locations had higher heritability estimate. High heritability values (>80%) were found for grain yield (94%), plant height (95.7%), harvest index (98%), Harvest index (98%) and Moderately high heritability value (>40% and <80%) were recorded for grain filling period(66.8%), days to maturity (76.8%), spikelet per spike (73%) and spike length ((67%) and low heritability value (<40%) were recorded for tiller number per plant (34.2%) and grain per spikelet (30.7%) . Moderately high heritability values were obtained for most of the traits including grain yields as reported by previous workers (ICARDA, 1990; Whan *et al.*, 1991; Desalegn *et al.*, 2000).

Generally, higher heritability estimates (for five characters out of twelve) were recorded and moderately high Heritability value was recorded four variables out of 12 and low heritability values were recorded for two variables out of 12. According to Singh (1990), if heritability of a character is very high, say 80% more, selection for such a character should be fairly easy, because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. But for a character with low heritability, say less than 40%, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects.

3.4 Estimates of Expected Genetic Advance

The estimated genetic advance and expected genetic advance as percent of the mean for the characters considered at Guduru, Hareto Gitilo and combined were evaluated. Expected genetic advance as percent of the mean was generally high for most characters at all locations. Among the characters, the highest genetic advance (>10) was recorded for days to heading (11.9), plant height (23.3) biological yield (12.3) and grain yield (20.5). Intermediate genetic advance (>5 and <10) was obtained from days to heading (9.1), grain filling period (5.5) and thousand grain weight (6.9). The other five characters out of 12 shoes low genetic advance in combined.

In other way, days to maturity and biological yield at two locations, and grain-filling period, at Gitilo, depicted genetic advance in percentage of mean values

lower than 10%. As opposed to these, most characters as grain yield, harvest index, tillers per plant, and kernels per spike at Hareto and Guduru locations and days to heading, spikes per plant, spike length and at Gitilo, except days to heading, grain filling period and spikelet's per spike the others showed relatively high (>15%) genetic advance as percentage of the mean values.

Table 4: Range, mean, variance, broad sense heritability, genotypic and phenotypic coefficient of variability, genetic advance as percent of mean for the 12 characters of Triticale Genotypes tested as combined

Character	Range	Mean	σ^2_g	σ^2_{ph}	GCV	PCV (%)	h^2 (%)	GA	GA as % Mean
DH	66.5-77.5	71.24	36	38.7	8.4	8.7	93	11.9	16.7
DM	121-130	126	29.5	33.1	4.3	4.6	76.8	9.1	7.2
GFP	52.4-59.3	55	10.7	16	5.9	7.2	66.8	5.5	10
Til	1.8-2.7	2.3	0.2	0.62	14.6	34.2	32.3	0.52	31.3
PH	60.2-85.3	69	136	142	16.2	17.2	95.7	23.5	7.02
SL	5.8-8.9	7.2	1.49	2.22	17	20.7	67	2.05	28.8
SPS	15.3-21.7	18.6	5.9	8	13.1	15.2	73.2	4.3	23.1
GPS	2.2-3.3	2.6	0.12	0.39	12.7	24	30.7	0.4	15.3
BY	653.5-982.5	791	10278	16951	12.8	16.4	60.6	163	20.7
TGW	37.6-45.4	42.3	14	17.3	8.8	9.8	80.9	6.9	16.3
GY	211-378.2	271	10609	11277	38	39.2	94	206	75.6
HI	0.25-0.43	0.33	0.007	0.007	24.6	25.5	98	0.2	60

However, plant height, grain filling period, thousand grain weight and spike length at Hareto, and days to heading and spikelets per spike at Gitilo depicted, genetic advance as percentage of the mean values between 10 and 15%.

Estimated genetic advance for grain yield indicated that the appropriate environment for improving grain yield for the genotypes grown at high land environment ; Gitilo than Hareto and then Guduru even if higher yield was recorded at Guduru than Hareto. Generally, for most characters higher genetic advance as percent of mean was recorded at Hareto than at Guduru. Since thousand-kernel weight, grain yield, harvest index and grain filling period had relatively high genetic advance as percent

of mean and high heritability at all locations; hence, they can be used as a selection criterion, but ultimate evaluation must be performed in the target environment prior to using them.

4. Summary and Conclusions

A total of eighteen triticale genotypes were evaluated at three different environments to assess genetic variability heritability and genetic advance after ANOV. The results of the analysis of variance for individual locations and combined analysis indicated that the tested genotypes were significantly ($p < 5$ percentage) different for all traits except grain per spikelet's at Guduru.

The phenotypic coefficient of variability was generally slightly higher than the genotypic coefficient of variability. High phenotypic and genotypic coefficient values were recorded at Gitilo and Hareto than at Gitilo. Thousand-kernel weight, tillers per plant, spikes per plant, kernels per spike and grain protein yield had high phenotypic and genotypic coefficient of variability at both locations compared to Guduru. The high PCV and GCV observed are evident from their high variability that in turn offers good scope for selection.

Generally, higher heritability estimates (for characters five out of twelve) were recorded at Guduru, for six characters out of twelve at Hareto, and seven characters out of twelve at Gitilo indicating that Guduru growing environment was less favorable than that of Hareto and Guduru and Gitilo growing environment was more favorable than the other two locations. Estimated genetic advance for grain yield indicated that the appropriate environment for improving grain yield for the genotypes grown at high land environment ; Gitilo than Hareto and than Guduru even if higher yield was recorded at Guduru than Hareto. Generally, for most characters higher genetic advance as percent of mean was recorded at Hareto than at Guduru. Since thousand-kernel weight, grain yield, harvest index and grain filling period had relatively high genetic advance as percent of mean and high heritability at all locations; hence, they can be used as a selection criterion, but ultimate evaluation must be performed in the target environment prior to using them. High estimates of heritability coupled with high genetic advance were also observed for these characters, indicating that they can be effectively improved through selection.

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