

# Evaluation of Bread Wheat (*Triticum aestivum* L) Genotypes for yield performance and Natural Epidemics of Wheat Rust across Location in Wolaita Zone, Southern Ethiopia

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## Abstract

Bread wheat is the most important food sources and inputs as processing agro industry. Now days, the population growth and production capacity was miss matched in Ethiopia. The utilization of bread wheat genotypes has high yielders and resistance to rust disease one way of narrowing the gap. This study was conducted in 2021 main cropping season in Adekoyisha and Kokate to evaluate the yield performance and resistance for rust epidemics across locations. The field trial was laid out RCBD with three replications of three genotypes and the check cultivar Alidoro. The analysis of variance indicates the 13 agronomic traits including rust disease were highly significant ( $P \leq 0.01$ ) and significant ( $P \leq 0.05$ ) between genotypes while the leaf rust, date of 90% maturity, spike length, above ground biomass, number of kernel per spike, grain yield and harvest index were highly significant and significant the interaction of genotypes with location. The nine traits were high  $h^2b$  (70-93%) with high GAM (62-333%). These traits were easily improved and no more stressed the location. The genotype G3-238871 was earlier maturing, resistance to three rust disease and high yielder (5942.3 kg/ha) across location. For further realities, the experiment would have to be replicated over the year and location to get a conclusive result.

**Keywords:** Bread wheat genotypes; Broad sense heritability; Genetic advance; Rust resistance

## Introduction

Bread wheat (*Triticum aestivum* L.) is the most important cereal crops produced in all over the world. Currently the demand of both domestic and international export is highly increasing [1, 2]. It provides more than 35% cereal calorie intake in developing country and 74% in developed country. Now days, the daily consumption of wheat products is high compared with other cereal crops as global basis and important for source of food for making bread, biscuits and industrial inputs for many agro industry [1, 3]. The country produces both irrigated and main season wheat producing opportunity per the year and considered to be leading wheat producers in Sub-Saharan Africa [4]. Wheat is produced an altitude ranged from 1500-3000 masl and between 6-160 N, 35-420 E latitude and longitude respectively [5]. In Ethiopia the bread wheat breeding and variety improvement programme started from 1949 and since now much more have been released from national and regional research center.

The immense production potential opportunities of Ethiopia for bread wheat production despite it is very low as compared to other wheat-producing countries in the world. The production status is very low with comparison of geometrical growth of population in Ethiopia. This might be shortage of mechanized farming, in adequate utilization of full packages, lack of resistance sources [6]. The national average wheat productivity is estimated to be 3.05 t/ha [7], which is below the world average of 3.5 t/ha. The recent production increment, Ethiopia is still importing about 1.6 million tons of wheat which is estimated about 25% in deficit to fulfill domestic wheat demand [8]. The major production challenges are poor agronomic practices, disease and pest problems, and insufficient variety supplements has narrow environmental adaptation. In most of the plant breeding programs, genotype by environmental interaction effects are of special interest for identifying the most stable genotypes for mega-environments and adaptation for specific targets. The wheat producers faced lack of genotypes which have best yield performing two or more environments resistance to biotic stress such as cereal rusts. Now days the producers need multiple resistance of rust disease with minimum costs of control. Developing new durable resistance sources and best yield performing genotypes are vital for assuring wheat crop yield enhancement as well as for future rust disease resistance breeding purpose. Since now, no more research has done in this area for testing new genotypes with two or more locations in study area particularly. Hence, the aim of this study was to evaluate bread wheat genotypes under natural epidemics of wheat rusts and to identify the adaptable genotypes across location in Wolaita zone, southern Ethiopia.

## Materials and Methods

### Description of Study Area

The study was conducted in Damot gale (Adekoyisha) and Kokate (Sodo zuria) districts of Wolaita zone southern Ethiopia during 2021 main cropping season. Damote gale is located 375 Km south of Addis Ababa, with specific geographic coordinates of 6°35'0"N- 7°0'30"N latitude and 37° 52'30"E-37°54'30"E longitude. The mean annual rainfall ranges 1200-1300 mm while the average annual maximum and minimum temperature is 26°C and 13.4°C respectively has 2165 m.a.sl (Mengistu, 2020). Sodo Zuria is located 385 km south of Addis Ababa with specific geographic coordinates of 6°52'0"N-6°54'0" latitude and 37°46'0"-37°49'0"E longitude with an elevation of 2800 m.a.s.l. The mean annual rainfall has 1200 - 1365 mm and the average minimum and maximum temperatures are 13°C and 20.7°C respectively (GPS reading). Major annual crops growing in the area were haricot bean, common bean, wheat, barley, sweet potato; onset has clay loam soil characterized.

### Experimental designs

Three genotypes were selected from 48 second trial materials which were grown in preliminary yield trials at Debrezeit agricultural research center and Wolaita Zone during 2019 and 2020 cropping time respectively. Those were promoted based on the yield and other agronomic performances including diseases reactions in the previous season. The listed three genotypes, G1-226930,

G2-238133 and G3-238871 are originally obtained from Ethiopian institute of biodiversity (EIB) and one standard check (Alidoro) which is well adapted cultivar in Wolaita Zone specifically selected Woreda are used as planting materials. The genotypes were assigned in Randomized Complete Block Design (RCBD) with three replications. The single plot area was 4 m<sup>2</sup> (2 m × 2 m) and each plot consisted of 10 rows spaced 20 cm apart. The one meter distance was maintained between replication and 0.5m between plots used for the experiment. Fertilizers was applied at the rate of 100 kg/ha urea at split application and 100 kg/ha NKPS at the time of planting. The seed and fertilizer was drilled uniformly by hand and the other agronomic management practice was carried out as per recommendations for all the treatments uniformly.

## Data Collection

### Disease Severity and Assessment

The disease severity data were collected when the epidemics of rust disease were seen from time of flowering until harvesting. The disease severity is estimated as the area or volume of plant tissue usually relative to the total healthy plant tissue. From each plot whole population of plants was assessed on a scale of 1 to 9 for disease severity scale [9]. Where, 1 = very resistant, 2 = resistant, 3 = resistant to moderately resistant, 4 = moderately resistant, 5 = moderately resistant to moderately susceptible, 6 = moderately susceptible, 7 = moderately susceptible to susceptible and 8 = susceptible and 9 = very susceptible.

The average of disease severity scores for each host genotype combination was used to create reaction type classifications. Plants with disease ratings of <5% Resistant(R), (10%-15%) were regarded resistant to moderately resistant (R-MR), those with scores of (20%-30%) were considered moderately resistant and ranges between the scores 80%-90% were susceptible. The prevalent infections found during the inspection were on stem rust, leaf rust and stripe rust.

### Agronomic Trait

The data were collected either plant or raw basis. The days to 50% heading (DH) is taken by counting from the date of sowing to the date of 50% heading of the plants from each plot by visual observation. The days to 90% physiological maturity (DM) were determined as the number of days from sowing to the date of when 90% of the panicles turned to yellow straw color. It was recorded when no green color remained on glumes and panicles of the plants, i.e. when grains are difficult to break with thumb nail. Plant height (PH) was measured from the soil surface to the tip of the spike (awns excluded) of 10 randomly tagged plants from the net plot area at physiological maturity. Number of total tillers (NTT) were determined from (0.5 mx0.5m) length of two rows from the net plot and converted to per meter square of net plot at physiological maturity by counting the number of tillers. Number of productive tillers (NPT) were determined at maturity by counting all kernel bearing spikes from 0.5mx0.5m (0.25m<sup>2</sup>) length of two rows from the net plot and converted to per meter square of net plot at physiological maturity. Spike length (SPL) was measured from the bottom of the spike to the tip of the spike excluding the awns from 10 randomly tagged plants from the net plot. Above-ground dry biomass (AGB) data were taken from the net plot area were sun dried to measure consistent weight and translated to kg per hectare to calculate the above ground dry biomass. The number of kernels per spike (NKPS) was carefully counted from ten randomly selected main tiller plans from each plot. Harvest index (HI) was calculated as ratio of grain yield per plot to total above-ground dry biomass yield per plot expressed as ratio. Thousand kernel weight (TKW) was measured by counting a seeds with a seed counter sensitive balance and weighing it and grain yield (GY) was taken by harvesting and threshing the grain yield from net plot area. The grain yield was adjusted to 12.5% moisture content and the yield per plot is converted to kg/ha.

## Data Analysis

All data collected were subjected to analysis of variance procedure using Gen Stat software [10] and 2010 Microsoft excell version. Comparisons among treatment means with significant difference for measured characters were done by using fisher's protected

least significant at 0.05. Before computing the combined analysis of variances, test of homogeneity of variances were performed using F-statistics (ratio of the largest mean square error (1) to the smallest mean square error (2) in the set) compared with tabulated value of degree of freedom. The genotypic ( $\sigma_g^2$ ) and environmental variance ( $\sigma_e^2$ ) were calculated from anova table where as the sum of genotypic and environmental variations are phenotypic variations which are suggested by Burton and Devane (1953). Environmental variance ( $\sigma_e^2$ ) = MSe (error mean square), Genotypic variance ( $\sigma_g^2$ ) = (MSg-MSe)/r, Phenotypic variance ( $\sigma_p^2$ ) =  $\sigma_g^2 + \sigma_e^2$ . Where: -  $\sigma_g^2$ =Genotypic variance,  $\sigma_p^2$ =Phenotypic variance, MSg = Mean squares of genotypes, MSe = mean square due to error and r = Number of replications. Phenotypic coefficient of variation: (PCV)= $\sqrt{(\sigma_p^2)/X} \times 100$ . Genotypic coefficient of variation: (GCV)= $\sqrt{(\sigma_g^2)/X} \times 100$  where: - PCV=phenotypic coefficient of variation, GCV= genotypic coefficient of variation and X= grand mean value of the trait. The combined genotypic and phenotypic variance was computed using similar fashion the formula computed with in single location variance. The genotypic variance ( $\sigma^2g$ ) = (MSg-MSe)/lr, genotype by location interaction ( $\sigma^2_{gl}$ ) = (MSgl-MSe)/r, Environmental variance=Mse, Phenotypic variance ( $\sigma^2_p$ )=  $\sigma_g^2 + \sigma_e^2 + \sigma_{gl}^2$ . Where, MSgl = mean square of genotype by location interaction, r= replication, and l = location

Estimation of heritability:-Heritability in broad sense ( $h_b^2$ ) for all characters was computed using the formula adopted from Allard (1960).  $H_2 = \sigma_g^2 / \sigma_p^2 \times 100$ , where: -  $h_b^2$  = Heritability in broad sense,  $\sigma_g^2$  = Genotypic variance,  $\sigma_p^2$  = Phenotypic variance. Estimation of genetic advance: The genetic advance was computed using the formula adopted from Johnson et al. (1955) and Allard (1960): Genetic advance: GA= (k) ( $\sigma_p$ ) ( $h_b^2$ ) where: - GA= genetic advance, K = the selection intensity (K= 2.06 at 5% selection intensity),  $\sigma_p$  is the phenotypic standard deviation and  $h_b^2$  is heritability in broad sense. Genetic advance as percent of mean: GAM = GA/X x100 where: - GAM=Genetic advance as percent of mean, GA = genetic advance and X=Mean value of the trait.

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## Result and Discussion

The combined analysis of variance was showed that highly significant ( $P \leq 0.01$ ) and significant differences ( $P \leq 0.05$ ) of thirteen traits among genotypes except spike length (Table1). The leaf rust, plant height, above ground biomass, number of kernel per spike, thousand kernel weight were highly significant and grain yield (kg/ha), number of total tiller ( $m^2$ ), number of productive tiller ( $m^2$ ) significant different among location. The interaction of genotypes across location was highly significant of leaf rust and some traits (date of maturity, spike length, above ground biomass, number of kernel per spike, harvest index and grain yield) while the other parameters (stripe rust, stem rust, date of heading, plant height, number of total tiller, number of productive tiller & thousand kernel weight) were non-significant in two locations between the tested genotypes. The highly significant variation between genotypes of quantitative traits indicate the presence of sufficient variability of breeders to improve the traits.[11] stated that the highly significant differences ( $P \leq 0.01$ ) for traits of days to 50% heading, days to 90% maturity, number of productive tillers plant per plant, number of spikelets per spike, plant height, spike length, grain yield per plant, thousand kernel weight, biomass yield and number of kernel per spike in their previous studies on bread wheat genotypes.

When the traits were significant across location indicate there is best performing genetic potential for variability due to influence of environment [12, 13]. These study might partially agreed with some authors [14 ,15] whose described that a significant genotype by location (Gx L) effect for days of heading, days to maturity, plant height, grain filling period, spike length, aboveground biomass yield, thousand seed weight and harvest index. The stripe rust resistance, stem rust resistance, date of heading, plant height, total number of tiller, productive tiller and thousand kernel weight were non-significant with interaction of genotype by en-

vironment (GXE). These traits performing have wider adaptation of two locations [16]. The biotic influences on stripe rust and stem rust where little magnitude on the genotype by environment interaction and these genotypes have considered to be qualitative resistance genes [17].

**Evaluation of genotypes based on the mean values:** The mean performance of eleventh agronomic trait of bread wheat genotypes in Adekoysa and Kokate were indicated in tables 2-3. The average number of days to 50% heading and date of 90% maturity in both locations was more or less uniformly. In Adekoysa the mean performance of heading and maturity was 70.71, 96.7 respectively while the mean date of heading and date of maturity in Kokate was 71.63, 96.00 respectively. Kokate is cooler than Adekoysa when environmental temperature increases, crop growth hormones are more initiated and this effect hastens all physiological activities on crops because temperature has great influence on crop metabolism, which directly affects growth and maturity of the crop [18]. In the other, genotype G3- 238871 has earlier heading in both Adekoysa and Kokate were the mean value 64.1, 67.00 respectively. The genotype G2-238133 was considered late heading (77.42, 77.00) and late maturing (108.25, 104.53) in Adekoysa and Kokate respectively. The genotypes has earlier heading and early maturing is important to escape wheat rusts and drought stress [19, 20].

Comparing genotypes between the traits of plant height the check cultivar Alidoro is shortest (99.27, 81.56) in both location. The mean height (108.88) cm in Adekoysa and 94.21 cm in Kokate site. Which shows the high influence of environment determine either the plant become short, tall or intermediate based on the mean value. The altitude variation, distribution of precipitation and light intensity vary in both locations. Since, Adekoysa is mid land and Kokate is highland which has some amount high sun light intensity makes to the bread wheat genotypes become tall.

**Table 1:** Combined anova for three rust disease and agronomic parameters of their respective mean squares

Traits	SSgeno(df=3)	SSloc(df=1)	SSgl(df=3)	MSg (df=3)	MSl (df=1)	MSg*l(df=3)	MSe(df=6)
Lr	25.40	4.59	8.64	8.47**	4.59**	2.88**	0.41
Str	10.36	0.44	2.30	3.45**	0.44ns	0.77ns	0.54
Sr	36.76	0.21	2.86	12.25**	0.21ns	0.95ns	0.38
DH	2271.61	21.09	52.20	757.21**	21.09ns	17.40ns	72.07
DM	3650.10	297.20	4313.90	1216.70**	297.17ns	1437.96**	141.30
PH	6933.20	5161.20	117.80	2311.08**	5161.20**	39.27ns	190.95
NTT	71163.00	17604.00	3261.00	23720.80**	17604.20*	1087.00ns	3079.30
NPT	83508.00	19295.00	3234.00	27836.00**	19295.00*	1077.90ns	3146.70
SPL	5.91	2.38	18.93	1.97ns	2.38ns	6.31**	1.08
AGB	29360000.00	51460000.00	23590000.00	9787559.00**	51460000.00**	7863031.00**	1440665.00
NKPS	275.41	321.57	589.46	91.80**	321.57**	196.49**	21.39
HI	0.04	0.00	0.03	0.01*	0.00ns	0.01*	0.00
TKW	694.79	651.56	144.93	231.60**	651.56**	48.31ns	25.05
GY	33410000.00	10140000.00	12290000.00	11130000.00**	10140000.00**	4098025.00**	804195.00

SSgeno-sum square of genotypes, SSloc-sumsquares of location, SSgl=sum squares of genotype locatation interaction,MSg-mean squares of genotypes, MSl-mean squares of location, MSg\*l=mean squares of genotype interaction with location,MSe-mean squares of error, \*\*, \*, ns, highly significant at  $P < 0.01$ , significant at  $P < 0.05$  and non-significant respectively, Lr-leaf rust (scale), Str -stripe rust(scale),Sr-stem rust(scale),DH-date of 50% heading, DM-date of 90% maturity, PH-plant height(cm), NTT-number of total tiller/plant, NPT-number of productive tiller/plant, SPL-spike length (cm), AGB-above ground biomass(kg/ha),NKPS-number of kernel/spike, HI-harvest index(%), TKW=thousand kernel weight(g),- GY-grain yield(kg/ha).

The highest number of tiller per meter square obtained from genotype G3- 238871 (406.58) and lowest (320.83) from check cultivar with average mean of 364.48 at Adekoyisha. Similarly the highest mean (423.75) total tiller counted from genotype G3-238871 and the lowest mean obtained Alidoro (356.00) from Kokate. The genotype G3-238871 has good performing productive tiller per square meter (396.00, 428.42) in Adekoysha and Kokate. The longest spike length 8.27 cm obtained from genotype G3-238871 Adekoyisha and similarly the genotype G2- 238133 measured 7.68 cm in Kokate. The maximum above ground biomass weighted (12778.00) kg/ha from G3-238871 Adekoysha with total average (12027.00) compared with total mean (10563.00) weighted from Kokate this was significantly low. The bread wheat genotypes response uniformly across the environment is selected as stable traits which were selected as wider environment for improvement.

The traits number of kernel per spike, harvest index and grain yield were highly performing in Adekoysha sites with average (48.18, 0.43, 5257.50) comparatively in Kokate (44.52, 0.42, 4607.50) except thousand kernel weight respectively. The wheat grain yield was low at high elevations where temperatures were too low to allow the crops to mature [21, 22]. The highest yields occurred at intermediate elevations with sufficient precipitation and mild temperatures. From the combined data only significant genotype location interaction is leaf rust while both stem rust and yellow rust is no significant influence considered as yield reducing factor. The bread wheat genotypes for plant height was significantly and uniformly influenced by average temperature, altitude, and precipitation of the environment they were evaluated [23, 24]. Similar trends were also observed for traits such as number of tillers/plant, effective number of tillers/plant, spike length, aboveground biomass (g), and grain yield (g). These traits were good performance at Kokate experimental fields.

The leaf rust disease is highly significant of genotype interaction with two locations while the main effect of genotypes were highly significant for three rusts. When the comparing the cultivar Alidoro the three genotypes were susceptible for leaf rust and stripe rusts of across locations (Figure 1) while G3-238871 and Alidoro has more resistant to stem rust disease in two fields. The figure indicates that the stripe rust disease prevalent for across location. The site of experiment receives moderate rainfall, low temperature and the altitude from mid land to high land hence this situation brings more conducive environment for stripe rust epidemics than the leaf and stem rusts. The *P. striiformis* require the optimum temperature (11-23°C), cooler environment and more prevalent in mid and highland parts [25, 26]. The genotype G1-226930 was take 97.75 mean days, the genotype G2- 238133 has 106.41 mean days, G3-238871 has 90 mean days and cultivar Alidoro 91.16 mean maturity days (Table 2 & Table 3). Therefore, G3-238871 is early maturing genotypes in two locations. Selection of genotypes has wider adaptability, early maturing and high yielding genetic potential is the aim for rust disease management. The early maturing genotype shortens the number of generations available for the development rust epidemics and allows the crop to escape serious damage therefore G3-238871 performs early maturing than the rest of genotypes.

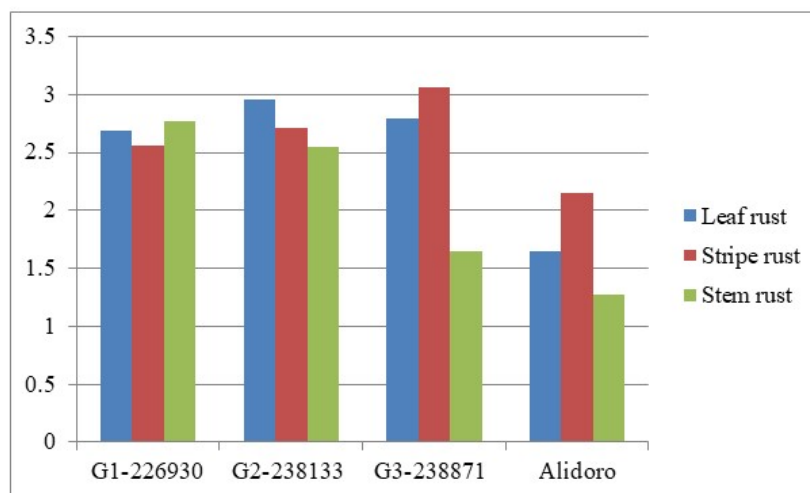


Figure 1: The mean range scale of disease severity data from three bread wheat genotypes

## Estimation of Variability Components

Genotypic and phenotypic coefficient of variation:- the genotypic coefficient was ranged between 18.25% - 169.70% for spike length and stem rust respectively (Table 6). The traits have GCV and PCV <10%, 10-20% and > 20% were considered low, medium and high coefficient of variation respectively [27, 28]. Depending on this range all traits were highest GCV except spike length which has low GCV and similarly the traits were high magnitude of PCV which has ranged from 35.13% (harvest index) and 177.91% (stem rust) across location. The leaf rust resistance (37.44, 46.45), days of 90% maturity (38.01, 51.22), spike length (18.25, 40.54), number of kernel per spike (20.27, 37.31), above ground biomass (27.36, 69.69), and grain yield (68.57, 71.38) were broad gap of magnitude variation between GCV and PCV respectively. This result indicates that the environment has greater effect of genotypes of the traits for the differences compared to the other traits which were supported by [29]. In the other hand, the stripe rust resistance (70.01, 80.89), stem rust resistance (169.70, 177.91), days to 50% heading (38.35, 40.00), plant height (47.02, 48.71), number of total tiller (40.30, 42.94), number of productive tiller (44.64, 47.16) and thousand kernel weight (34.18, 38.76) were closer GCV and PCV respectively of Adekoyisha and Kokate of little influence of environment for contribution of such variability. The all traits except spike length the GCV (>20%) these tells us the traits were improved through selection.

**Table 2:** The mean values of important agronomic traits of three bread wheat genotypes in Adekoysha sites during 2021

Genotypes	DH	DM	PH	NTT	NPT	SPL	AGB	NKPS	HI	TKW	GY
G1-226930	73.67a	92.58bc	116.67a	369.50ab	365.75a	7.42b	11357.00 b	45.87b	0.42bc	38.41b	4784.50b
G2-238133	77.42a	108.25a	115.95 ab	361.00ab	351.08ab	7.40b	11299.00b	45.00 b	0.40c	37.80b	4637.20b
G3-238871	64.17b	98.83 b	103.61 bc	406.58a	396.00a	8.27a	12778.00 a	51.60a	0.46a	45.87a	5940.20a
Alidoro	67.58b	87.00c	99.27c	320.83b	311.33 b	6.85b	12675.00a	50.23 a	0.44ab	43.98a	5668.00a
Mean	70.71	96.70	108.88	364.48	356.04	7.48	12027.00	48.18	0.43	41.52	5257.50
Lsd%	5.87	9.06	11.07	51.72	50.98	0.73	931.34	2.97	0.03	4.02	727.26
Cv	10.08	11.38	14.25	17.22	17.38	11.91	9.40	7.47	8.22	11.75	16.79

**Table 3:** The mean values of important agronomic traits of three bread wheat genotypes in Kokate during 2021

Genotypes	DH	DM	PH	NTT	NPT	SPL	AGB	NKPS	HI	TKW	GY
G1-226930	75.58a	102.92a	102.04a	383.75bc	374.25bc	7.59a	10628.00b	43.72ab	0.42ab	44.01b	4292.30b
G2-238133	77.00a	104.58a	104.49a	402.75ab	388.67ab	7.68a	10255.00b	46.42a	0.43ab	46.59ab	4377.00b
G3-238871	67.00b	81.17b	88.75 b	423.75a	428.42a	6.42b	9607.00b	39.72b	0.45a	50.38a	5944.40a
Alidoro	67.00b	95.33a	81.56 b	356.00c	346.25c	6.98ab	11762.00a	48.19a	0.38b	45.92b	3816.20b
Mean	71.63	96.00	94.21	391.56	384.40	7.17	10563.00	44.52	0.42	46.73	4607.50
Lsd%	8.10	10.38	9.47	39.39	41.16	0.97	1048.30	4.49	0.06	4.26	753.13
Cv(%)	13.73	13.12	12.2	12.21	13.00	16.45	12.05	12.25	16.99	11.05	19.84

**Table 4:** Variability estimates of bread wheat genotypes in Adekoyisha site

Traits	Mean	MSg	Mse	$\delta^2 g$	$\delta^2 p$	GCV (%)	PCV (%)	$h^2 b$ (%)	GA	GAM (%)
LR	2.30	10.10	0.26	10.02	10.28	137.47	139.24	97	6.44	279.60
STR	2.55	3.19	0.47	3.03	3.50	68.20	73.30	87	3.34	130.71
SR	2.10	9.98	0.22	9.91	10.13	149.57	151.23	98	6.41	304.74
DH	70.71	425.25	50.80	408.32	459.12	28.58	30.30	89	39.26	55.52
DM	96.67	995.94	121.06	955.59	1076.65	31.98	33.94	89	59.99	62.06
PH	108.88	922.65	240.71	842.42	1083.13	26.66	30.23	78	52.73	48.43
NTT	364.48	14860.10	3941.10	13546.40	17487.50	31.93	36.28	77	211.02	57.90
NPT	356.04	14857.40	3829.10	13581.03	17410.13	32.73	37.06	78	212.03	59.55
SPL	7.48	4.10	0.79	3.84	4.63	26.18	28.77	83	3.67	49.10
AGB	12027.00	7848980.00	1277882.00	7423019.33	8700901.33	22.65	24.53	85	5184.01	43.10
NKPS	48.18	125.35	12.96	121.03	133.99	22.84	24.03	90	21.54	44.71
HI	0.43	0.01	0.00	0.01	0.01	21.34	22.87	87	0.18	41.02
TKW	41.52	194.22	23.80	186.28	210.09	32.87	34.91	87	26.48	63.77
GY	5257.50	4972929.00	779199.00	4713196.00	5492395.00	41.29	44.58	86	4142.88	78.80

**Table 5:** The estimation of variability components of four bread wheat genotypes in Kokate site

Traits	Mean	MSg	Mse	$\delta^2 g$	$\delta^2 p$	GCV (%)	PCV (%)	$h^2 b$ (%)	GA	GAM (%)
LR	2.74	1.24	0.57	1.05	1.62	37.44	46.45	65	1.70	62.17
STR	2.69	1.03	0.63	0.82	1.46	33.77	44.92	57	1.41	52.29
SR	2.01	3.23	0.47	3.07	3.54	87.17	93.58	87	3.36	167.27
DH	71.65	349.35	96.74	317.11	413.85	24.85	28.39	77	32.11	44.82
DM	96.00	1367.94	158.64	1315.06	1473.70	37.77	39.99	89	70.57	73.51
PH	94.21	1427.70	132.13	1383.66	1515.79	39.48	41.33	91	73.21	77.71
NTT	391.56	9947.69	2286.41	9185.55	11471.96	24.48	27.35	80	176.67	45.12
NPT	384.40	14056.50	2496.30	13224.40	15720.70	29.92	32.62	84	217.27	56.52
SPL	7.17	4.17	1.39	3.71	5.10	26.87	31.51	73	3.38	47.21
AGB	10563.00	9801610.00	1619046.00	9261928.00	10880974.00	28.81	31.23	85	5784.09	54.76
NKPS	44.52	162.94	29.73	153.03	182.75	27.79	30.37	84	23.32	52.38
HI	0.42	0.01	0.01	0.01	0.02	24.02	29.42	67	0.17	40.41
TKW	46.73	85.69	26.68	76.79	103.47	18.75	21.77	74	15.55	33.28
GY	4607.50	10260000.00	835624.00	9981458.67	10817082.67	68.57	71.38	92	6251.82	135.69



**Table 6:** The estimation of combined variance components of three bread wheat genotypes between two locations during 2021

Traits	Mean	Msg	Mse	MSgxl	$\delta^2$ g	$\delta^2$ g l	$\delta^2$ p	GCV (%)	PCV (%)	$h^2$ b(%)	GA	GAM (%)
LR	2.52	8.47	0.41	2.88	8.40	2.74	11.55	114.96	134.80	73	5.09	201.96
STR	2.62	3.45	0.54	0.77	3.36	0.59	4.49	70.01	80.89	75	3.27	124.82
SR	2.06	12.25	0.38	0.95	12.19	0.83	13.40	169.70	177.91	91	6.86	333.47
DH	71.18	757.21	72.07	17.40	745.19	-6.62	810.64	38.35	40.00	92	53.92	75.75
DM	96.33	1363.89	140.54	1000.00	1340.47	953.15	2434.16	38.01	51.22	55	55.97	58.10
PH	101.54	2311.08	190.95	39.27	2279.26	-24.38	2445.83	47.02	48.71	93	94.94	93.50
NTT	378.02	23720.80	3079.30	1087.00	23207.58	60.57	26347.45	40.30	42.94	88	294.53	77.91
NPT	370.22	27836.00	3146.70	1077.90	27311.55	29.00	30487.25	44.64	47.16	90	322.22	87.04
AGB	11295.00	9787559.00	1440665.00	51460000.00	9547448.17	50979778.33	61967891.50	27.36	69.69	15	2498.45	22.12
NKPS	46.35	91.80	21.39	196.49	88.24	189.36	298.98	20.27	37.31	30	10.51	22.68
HI	0.43	0.01	0.00	0.01	0.01	0.01	0.02	25.10	35.13	51	0.16	36.94
TKW	44.12	231.60	25.05	48.31	227.42	39.96	292.43	34.18	38.76	78	27.40	62.09
GY	4932.50	11130000.00	804195.00	4098025.00	10995967.50	3829960.00	15630122.50	67.23	80.15	70	5729.54	116.16

Heritability ( $h^2b$ ) and genetic advance :- The heritability of traits ranged from 77-97% of number of total tiller ( $m^2$ ) and leaf rust resistance respectively in Adekoyisha while 57-92 % at Kokate for yellow rust resistance and grain yield respectively (Table 4-5).The heritability variation among traits were no more variation observed in both location. From combined analysis 13 traits among genotypes were significant except spike length and the heritability estimates is possible for significance traits. The heritability estimates were classified into three categories hence the heritability >60%, heritability lies 30-60% and heritability < 0-30% as high, moderate and low heritability respectively [30].The leaf rust resistance (73%), stripe rust resistance (75%), stem rust resistance (91%), days of 50% heading (92%), plant height (93%), number of total tiller (88%), number of productive tiller (90%), thousand kernel weight (78%) and grain yield (70%) were high broad sense  $h^2b$  value with comparison of number of kernel per spike (30%), harvest index (51%) and days of maturity (55%) these traits were moderate range of heritability.in the other hand, above ground biomass (15%) was low  $h^2b$  heritability.

The high broad sense heritability estimation of most of traits showed that the observed variation mainly under genetic control. The high heritability estimated from the traits of leaf rust, stripe rust, stem rust, days of heading, plant height, number of total tiller, number of productive tiller, thousand kernel weight and grain yield these might be the genotypes were selected from third cycle of progeny and the heritability could be additive genetic effects and the selection was applicable for early segregating generation of traits. The high heritability estimated from days to 50% heading, days of 90% maturity, number of spikelet's spike, number of kernel and thousand kernel weight in bread wheat which was partially supported of present finding [31, 32].

The genetic advance as percent of mean (GAM) ranged from 22.12% (AGB) to 333.47% (Sr) .These result indicates selection of the 5% base population results the advance of 22.12% to 333.47% for the base population mean over next generation (Table 6). The GAM was high (>20%), medium (10-20%) and low(<10%) which is stated by Johnson et al. (1955).The high heritability with high genetic advance as percent of mean obtained from leaf rust resistance (73% ,201.96%), stripe rust resistance (75% , 124.82%), stem rust resistance (91% , 333.47%), days of 50% heading (92% , 75.75%), plant height (93% , 93.5%), number of total tiller (88% , 77.91%), productive tiller (90% , 87.04%), thousand kernel weight (78% , 62.09%) and grain yield (70% , 116.16%) respectively. The moderate range of broad sense heritability with high GAM obtained from days of 90 % maturity (55% , 58.1%), harvest index (51% , 36.94%) respectively while number of kernel per spike (30% & 22.68%) and above ground biomass (15% , 22.12%) were high GAM but low broad sense heritability.

When the traits have high heritability with high GAM was improved through direct selection and no more influenced of across location and said to be additive gene action. The estimation of genetic advance allows the type of gene action involved in the expression of various polygenic traits. High values of genetic advance are indicative of involvement of additive gene action, whereas low values are indicative of non-additive gene action. The high broad sense heritability associated with high GAM for the traits of 50 % days to heading, date of 90% maturity, number of productive tillers per plant, number of kernel per spike, grain yield and harvest index were partially matched present finding [33, 34]. When the estimation of heritability as effective with consideration of high genetic advance. The bread wheat genotype G3-238871 were shown good performance across two locations in terms of yield and triple rust resistance.

## Conclusions

The country has great potential opportunity of bread wheat production and now started to export abroad. Considering to this, the developing the new bread wheat genotypes were adapted two or more environments is crucial activities. The three bread wheat genotypes G1- 226930, G2-238133, G3-238871 and with check Alidoro were evaluated their agronomic performance and naturally occurring cereal rusts at Kokate and Adekoyisha experiential sites. The thirteen traits including stripe, leaf and stem rusts are highly significant and significant differences between genotypes. Heritability with genetic advance is most important aspect for direct selection of genotypes and identification of the type of gene actions. Accordingly to that leaf rust, stripe, stem rust, days of 50% heading, plant height, number of total tiller, productive tiller, thousand kernel weight and grain yield were high broad sense heritability and high genetic advance as expected mean. The genotype G3-238871 was higher yielder as 5940.2 kg/ha (Adekoyisha) and 5944.4 kg/ha (Kokate) with compared in cultivar Alidoro which was 5668.0 kg/ha at Adekoyisha and 3816.2kg/ha Kokate experimental fields. Therefore, genotype G3-238871 showed good yield performance and resistance to rust disease in both locations.

## Conflicts of Interest

The authors have no conflict of interest for the publication of this article

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## References

1. FAO (Food and agriculture organization) of the united nations (2019) FAO Cereal Supply and Demand, FAO, Rome, Italy.
2. Dhillon J, Eickhoff E, Aula L, Omara P, Weymeyer G et al. (2020) Nitrogen management impact on winter wheat grain yield and estimated plant nitrogen loss. *Agronomy Journal*, 112: 564-77.
3. Obsa C, Wassu M, Firdissa E (2017) Analysis of Genetic Variability among Bread wheat (*Triticum aestivum* L.) genotypes for growth characters yield and yield components in Bore district, Oromia regional state M.Sc. Thesis, Haramaya University, Haramaya, Ethiopia.
4. Central Statistical Agency (2018) Report on Farm Management Practices (Private Peasant Holdings, Meher Season), Volume XII, Addis Ababa, Ethiopia.
5. Abu T (2012) Grain and feed annual report. Grain report number: ET1201, Addis Ababa, Ethiopia, 33-6.
6. Goshu D (2020) Adapting multidimensional poverty and inequality measures to national and regional contexts: Evidence from Ethiopia. *Tanzania Journal of Development Studies*, 17.
7. Central Statistical Agency (2020) Report on Area and Production of Major Crops: Time Series Data for National and Regional Level: Addis Ababa.
8. United States Department of Agriculture (2018) Ethiopia grain and feed annual report. In Global agricultural information network (GAIN) report ET-1813. Foreign Agricultural Service, USDA.
9. Bariana HS, Brown GN, Bansal UK, Miah H, Standen GE et al. (2007) Breeding triple rust resistant wheat cultivars for Australia using conventional and marker-assisted selection technologies. *Australian Journal of Agricultural Research*, 58: 576-87.
10. GenStat (2016) General Statistical Procedure Library Release. 22th edition. VSN International Ltd.
11. Mecha B, Alamerew S, Assefa A, Assefa E, Dutamo D (2017) Genetic diversity based on multivariate analysis for yield and its contributing characters in bread wheat (*Triticum aestivum* L.) genotypes. *Agri. Res. Tech*, 8: 555748.
12. Jacobsz MJ, Merwe WJCV, Westhuizen MMV (2015) Additive Main effects and multiplicative interaction analysis of European linseed (*Linum Ustassimum* L.) cultivars under south African conditions. *Advances in Plants & Agriculture Research*, 2: 120-4.
13. Tadesse T, Tekalign A, Sefera G, Muligeta B (2017) AMMI model for yield stability analysis of linseed genotypes for the highlands of Bale, Ethiopia. *Plant*, 5: 93-8.
14. Negasa D, Chauhan DK (2016) Variability, heritability and genetic advances in wheat (*Triticum aestivum* L.) breeding lines grown at Horro Guduru Wollega zone, Western Ethiopia. *International Journal of Advanced Scientific Research and Management*, 1: 24-8.
15. Andualem A (2022) Genotype by Environment Interaction, Variability and Stability Analysis of Ethiopian Commercial Durum Wheat (*Triticum turgidum* L) Genotypes in Southern Ethiopia. MSc thesis, Wolaita Sodo University.
16. Taghouti M, Gaboun F, Nsarellah N, Rhrib R, El-Haila M et al. (2010) Genotype x Environment interaction for quality traits in durum wheat cultivars adapted to different environments. *African Journal of Biotechnology*, 9: 3054-62.

17. Atia MA, El-Khateeb EA, Abd El-Maksoud RM, Abou-Zeid MA, Salah A et al. (2021) Mining of leaf rust resistance genes content in Egyptian bread wheat collection. *Plants*, 10: 1378.
18. Amanuel Gorfu AG, Kefyalew Girma KG, Tanner DG, Asefa Taa AT, Shambel Maru SM (2000) Effect of crop rotation and fertilizer application on wheat yield performance across five years at two locations in south-eastern Ethiopia.
19. Badebo A, Fehrmann H, Yahyuoui A (2008) Status of Wheat Yellow Rust (*Puccinia striiformis*) Races and their Virulences in major Wheat Growing areas of Ethiopia. *Pest Management Journal of Ethiopia*, 12: 1-7.
20. Mondal S, Singh RP, Crossa J, Huerta-Espino J, Sharma I et al. (2013) Earliness in wheat: a key to adaptation under terminal and continual high temperature stress in South Asia. *Field crops research*, 151: 19-26.
21. Alambo MM, Gessese MK, Wachamo EW, Melo BY, Lakore ZS et al. (2022) Performance Evaluation of Ethiopian Bread Wheat (*Triticum aestivum* L.) Genotypes in Southern Ethiopia. *Advances in Agriculture*, 2022: 1338082.
22. Thomson AM, Brown RA, Ghan SJ, Izaurralde RC, Rosenberg NJ (2002) Elevation dependence of winter wheat production in eastern Washington State with climate change: A methodological study. *Climatic change*, 54: 141-64.
23. Muhder N, Gessese MK, Sorsa Z (2020) Research Article Assessment of Genetic Variability among Agronomic Traits and Grain Protein Content of Elite Bread Wheat (*Triticum aestivum* L.) Genotypes in the Central Highlands of Ethiopia.
24. Alambo A (2022) Semantics-driven Abstractive Document Summarization (Doctoral dissertation, Wright State University).
25. Hogg WH, CE Hounam, AK Mallik, JC Zadoks (1969) Meteorological factors affecting the epidemiology of wheat rusts. *WMO Tech Note*, 99: 143.
26. Hadi MR, Karimi N (2012) THE ROLE OF CALCIUM IN PLANTS'SALT TOLERANCE. *Journal of plant nutrition*, 35: 2037-54.
27. Deshmukh SN, Basu MS, Reddy PS (1986) Genetic variability, character association and path coefficients of quantitative traits in Virginia bunch varieties of groundnut.
28. Shrigley RL (1973) The Correlation of Science Attitude and Science Knowledge of Preservice Elementary Teachers.
29. Majumder DAN, Shamsuddin AKM (2008) Genetic variability, correlated response and path analysis of yield and yield contributing traits of spring wheat. *Journal of the Bangladesh Agricultural University*, 6.
30. Robinson HF, Comstock RE, Harvey PH (1949) Estimates of heritability and the degree of dominance in corn.
31. Obsa BT, Eglinton J, Coventry S, March T, Guillaume M et al. (2017) Quantitative trait loci for yield and grain plumpness relative to maturity in three populations of barley (*Hordeum vulgare* L.) grown in a low rain-fall environment. *PloS one*, 12: e0178111.
32. Gaur SC (2019) Genetic improvement through variability, heritability and genetic advance for grain yield and its contributing traits in wheat (*Triticum aestivum* L. em Thell). *Int J Pure App Biosci*, 7: 368-73.
33. Singh P, Narayanam S (1999) *Biometrical Techniques in Plant Breeding*. New Delhi: Kalyani Publishers, 56-57.
34. Rathwa HK, Pansuriya AG, Patel JB, Jalu RK (2018) Genetic Variability, Heritability and Genetic Advance in Durum Wheat (*Triticum durum* Desf.). *International Journal of Current Microbiol. Applied Science*, 7: 1208-15.