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Evaluation of Bread Wheat (*Triticum aestivum L.)* Genotypes for Stripe Rust (*Puccinia striiformis f. sp. tritici*.) Resistance, Yield and Yield Attributes at Arsi High Lands, South Eastern Ethiopia

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Abstract:
The present study carried out with the objective to evaluate and identify stripe rust resistant bread wheat genotypes conducted using lattice design under natural epidemic conditions in 2021 main cropping season at Kulumsa and Meraro,South Eastern Ethiopia. Slow rusting resistance was assessed using both disease and yield and yield trait parameters. Highly significant(P<0.01) differences were noted among the 100 tested genotypes for most parameters noted above. Except genotype 231237(62.013q/ha),none of the rest tested genotypes sustained better disease reaction and grain yield than MR check Wane (61.012(q/ha).On the other hands, seven genotypes Kingbird (48.05qt/ha), 6883 (48.5qt/ha),235038 (50.21qt/ha), 231487 (49.99qt/ha), Huluka (48.47qt/ha), 20411 (44.49qt/ha, 226283(44.3qt/ha) over yielded MS check Dursa (43.88qt/ha .Genotypes with MR reaction and MS reaction and gave yield better than Dursa are recommended for yellow rust resistance breeding and yield improvement.

Keywords: Adult plant resistance, Evaluation, Bread Wheat, Stripe rust, Genotypes.

INTRODUCTION

Diseases are the main constraints for the low production and productivity of wheat in Ethiopia. Major wheat diseases are caused by both abiotic and biotic factors. Among abiotic constraints; low soil fertility and moisture stress are the principal wheat production limiting factors in Ethiopia (Hailu et al.,2012) .The major biotic factors that limit wheat production in Ethiopia include diseases, insect pests and weeds (Ayana, 2020).

Rusts including leaf rust (*P.triticina Eriks*),stem rust (*Puccinia graminis f.sp.tritici*) and yellow / stripe rust (*P.Striiformis West end f.sp.tritici*) are vital diseases reducing wheat productivity in Ethiopia (*Netsanet et al.,2014*) . Rust affects economically important plant species and usually appears as yellow, orange, red rust, brown or black powdery pustules on leaves, young shoots and fruits (*Perera et al.,2020*).

Yellow (stripe) rust that was first reported by Ciccarone (1947) is one of the major diseases of wheat in temperate regions as well as in the highlands of the tropics and subtropics including Ethiopia and it is considered as a low temperature disease. *Puccinia striiformisf.sp. tritici*. Westend: is a highly specialized obligate biotrophic fungus causing macro cyclic stripe (yellow) rust. Recently, it has been considered to be macro cyclic rust, after the identification of beriberi's species as an alternative host (Wang et al.,2009)**.** New races virulent to Yr27+resistance gene and race Pst-16 recently affected most of commercial bread wheat cultivars including the popular varieties (Galama, Kubsa and Ogolcho) and caused 70 to 100% yield losses in the major wheat producing highland areas of Ethiopia (Strait et al.,2014).

Results of different experiments conducted for the control of wheat stripe rust around the world including Ethiopia revealed that increasing resistant cultivars still a preferred approach, because it is effective, easy to use, economical and environmentally friendly strategy (Bekele et al.,2002). Therefore, searching for resistance sources against wheat yellow rusts diseases is becoming crucial to sustain wheat production through growing disease resistant and high yielding cultivars and contributing to food security. Hence this study aimed with the objective to sustain wheat production through growing disease resistant and high yielding genotypes and contributing to food security.

MATERIALS AND METHODS

Description of the Study Area

The experiment was conducted at Kulumsa and Meraro Kulumsa Agricultural research stations in Arsi zone, Oromiya Regional State, South Eastern part of Ethiopia during 2021 main cropping season. Kulumsa represents mid highlands (2200 m.a.s.l) and located at 39^{O} 09’11’’E l and 08^{O} 01’10’’N It receives mean annual rainfall of 820 mm with monthly mean minimum and maximum temperature of 10.5 and 22.8°C and also loam soil type is the dominant (Birhan, 2011). Meraro substation is located at 07°24' 27''N, 39°14 '56'' E and has an altitude of 2990 m.a.s.l.This location is a frost prone agro ecology representing the extreme highland. The minimum and maximum temperature is 5.7 and 18.1°C, respectively and it obtains 1196 mm average annual rainfall. The dominant soil type is clay soil (Nitosols) which is slightly acidic (Ph=5.0) (Birhan,2011). Both Kulumsa and Meraro are representing stripe rust hot spot areas as a result the disease pressure also increased with altitude increasing (Bekele et al.,2002).

Planting Materials

The total of 100 bread wheat genotypes consisting of 80 land race bread wheat accessions (collections), 20 commercial varieties including three checks varieties, Morocco (universal rust susceptible), Wane (MR) and Dursa (MS) varieties to yellow rust were used. Bread wheat land race accessions and commercial bread wheat cultivars used in this experiment was obtained from the Ethiopian Bio diversity Institute and Kulumsa agricultural research center respectively for their low to mid and mid to highland adaptability test to rust resistance and yield traits.

Experimental Design and Testing Procedures

The experiment was laid out in lattice design with two replications on seed-bed prepared by two rows using row makers adjusted at 20 cm spacing. Fertilizers (DAP and NPS) applied at planting with the recommended rate. Genotypes were planted manually with seed rates of 125 kg/ha in two rows 1m length and 0.4m width with 20cm spacing between rows and covered manually.

Spacing between sub blocks and two replications were 1m and 1.5m. To enhance the natural stripe rust epidemics and sufficient disease development and ensure uniform spread of inoculums, infector rows consisting of mixtures four susceptible bread wheat varieties (Morocco, Digalu, Ogolcho and Kubsa) planted bordering the plots and weeding was done manually three times.

Field Disease and Yield and Yield Component Assessment

Disease severity data were taken five times within ten days intervals on plot bases starting from the onset of rust. Severity and infection response were noted on each genotype per plot and co efficient of infection and area under disease progress curve and coefficient of infection were derived from the field data. Yield loss data traits taken interns of tillers, lodging, seed per spike, grain yield and thousand seed weight.

Analysis of Variance (ANOVA) and Mean Separation

Disease, yield and yield component epidemiological parameters were generated for each tested bread wheat genotypes and analysis of variance and mean separation were performed following the procedures of Gomez and Gomez (1984) and using SAS version 9.3 (SAS,2012) and Tukey test for mean separation (SAS,2002). Clustering of genotypes was performed by average linkage Euclidean distance using Minitab software version 17.

Correlation analysis was done for disease parameters namely terminal yellow rust severity, area under progress curve, coefficient of infection, head/spike infection and grain yield and yield attributes (thousand kernel weight, tillers, lodging, grain yield, seed per spike) using the general linear model procedure of SAS version 9.3 statistical software (SAS,2012) and Minitab software version 17,whereas principal component analysis carried out using the same software and grouped the genotypes by the clusters.

RESULT AND DISCUSSIONS

Terminal Wheat Yellow Rust Severity

Terminal/final rust severity signifies the collective result of all resistance factors during the progress of epidemics (Parlevliet and Van Ommeren,1975). According to Safavi (2012), genotypes falling into 1-30, 31-50% and above 50% severity classes possess high, moderate and low adult plant resistance level respectively. The current results indicated that there were high variations among genotypes in terms of disease development ranging from moderately resistant to highly susceptible genotypes which reveals resistant genotypes potentially reduce the disease severity while high disease severity on susceptible genotypes.In the present study 33 and 65 genotypes showed moderately and susceptible disease reaction respectively at Meraro site and 82 and 11 genotypes had moderately and susceptibility reaction at Kulumsa site respectively. Variety Wane and accession 231237 showed moderately resistant/MR with terminal rust severity ranging between 23% and 30% in variabily with test locations.

Average Coefficient of Infection

Average coefficient of infection (ACI) computed for tested genotypes from disease severities and host reactions. According to Singh et al., (2002), genotypes that show high (MR) and moderate (MS) level of final rust severity and ACI could have durable resistance, which can serve in resistance breeding as good parents. Genotypes with ACI values of 0-20, 21-40,41-100 are regarded as genotypes possessing high, moderate and low levels of adult plant resistance respectively (Ali et al.,2008). The present study result revealed that 4%, 41% and 55% of the tested bread wheat genotypes were in the category of moderately Resistant (MR), Moderately susceptible (MS) and highly susceptible (S) respectively as measured by ACI.

Area Under Disease Progress Curve

Genotypes with rAUDPC values up to 30% of the check, were grouped as genotypes having high/MR level of partial resistance. While, those having rAUDPC values up to 70% of the check were grouped as moderately resistance/MS and genotypes having above 70% of the check were grouped as susceptible/S genotypes (Ali et al.,2009). In the present study, 19 genotypes with MS (231257, 231609, 231215, 5774, 234250, 231632 ,235040, Lemmu, 222240, 231627, 6930, 6883, Dursa), MS/S (Boru, Balcha), MS/MR (234258), MR (231237, Wane) and S reactions (Kubsa) have lowered AUDPC values over Morocco by more than 60%.

Head Infection

Test genotypes differed significantly (P<0.01) and compared using LSD (least significance difference) and MSD (minimum significant difference). Response of genotypes to head infection in terms of 0-5 rating scale and percentage spike infection is summarized in figure 1 below.

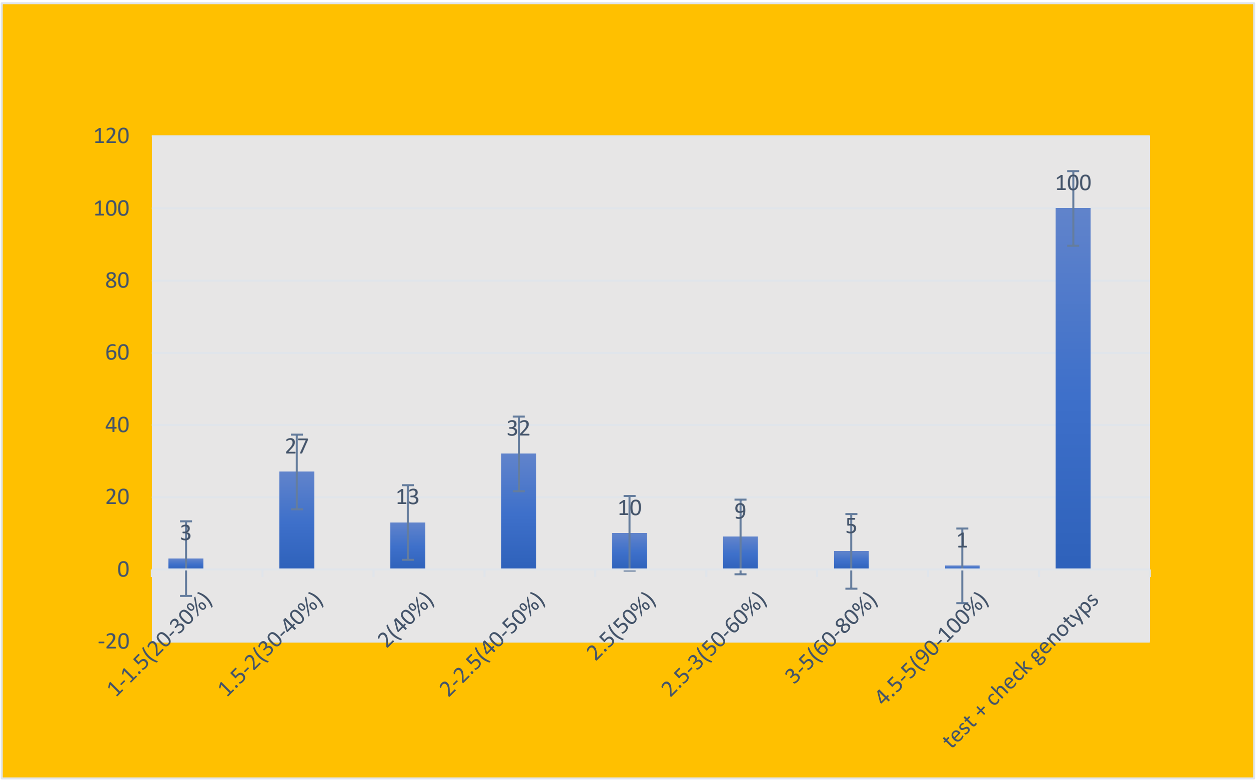


Figure 1: Response of 100 bread wheat genotypes to head infection frequency in terms of 0-5 rating scale and percentage spike infection, Meraro and Kulumsa sites average infection, main season,2021.

Analysis of Variance (ANOVA)

Combined ANOVA of agronomic and disease parameters showed significant variation among 100 evaluated bread wheat genotypes. The results showed AUDPC and all agronomic parameters were significantly different among tested genotypes. The analysis of variance showed highly significance difference at (P<0.01) except thousand seed weight and Grain yield per Quantals (GYQPH), this may be happened due to the mobility character of most of their genetic resource for disease or stress response than yield response (table1).

Table 1. Combined mean squares for seed yield, yield component and disease parameters for tested 100 wheat genotypes across two test locations, Meraro and Kulumsa,2021.

Traits	Mean Squares					
	SITE (df=1)	REP (df=1)	BLK(REP), df=18	Genotypes, df=99	SITE*Entry, df=99	Error, df=18
AUDPC	34151751.6**	3770781.42**	249361.98**	265225.05**	59816.95ns	94165.60
FRS	34399.12**	3950.12**	379.58**	334.73**	115.68ns	143.71
CI	49062.25**	6099.61**	707.25**	651.46**	131.77ns	257.83
HI	38533.69**	5520.49**	391.48**	395.76**	95.71ns	163.26
Tillers	597.80**	0.72 ns	1.40 ns	2.90**	1.40*	1.01
Lodged	564.06**	37.82*	10.98*	18.16**	3.38ns	5.83
SL	201.64**	0.49 ns	14.51**	29.02**	1.42ns	4.53
SPS	19030.20**	1.32ns	21.07*	40.05**	24.94**	12.21
TKW	539.47**	464.98**	63.01Ns	66.72ns	55.54ns	56.03
GYQPH	25115.75**	1312.72**	152.12ns	219.18**	82.13Ns	102.23

Key:AUDPC=Average Disease Progress Curve, CI=Coefficient of Infection, GQPH=Grain Yield Quantals per Hectare, HI=Head infections, MSE=Mean Squares of Error, MSB=Mean Squares of Blocks, MSG=Mean Square of Genotypes, ns=Non significance. SPS=Seed per Spike, SL=Spike Length, TRS=Terminal Rust Severity%, TKW = Thousand Kernel Weight. *= Significant at P < 0.05 and **= significant at P< 0.01, ns(non-significant) at P>0.05.

Grain Yield and Thousand Kernel Weight

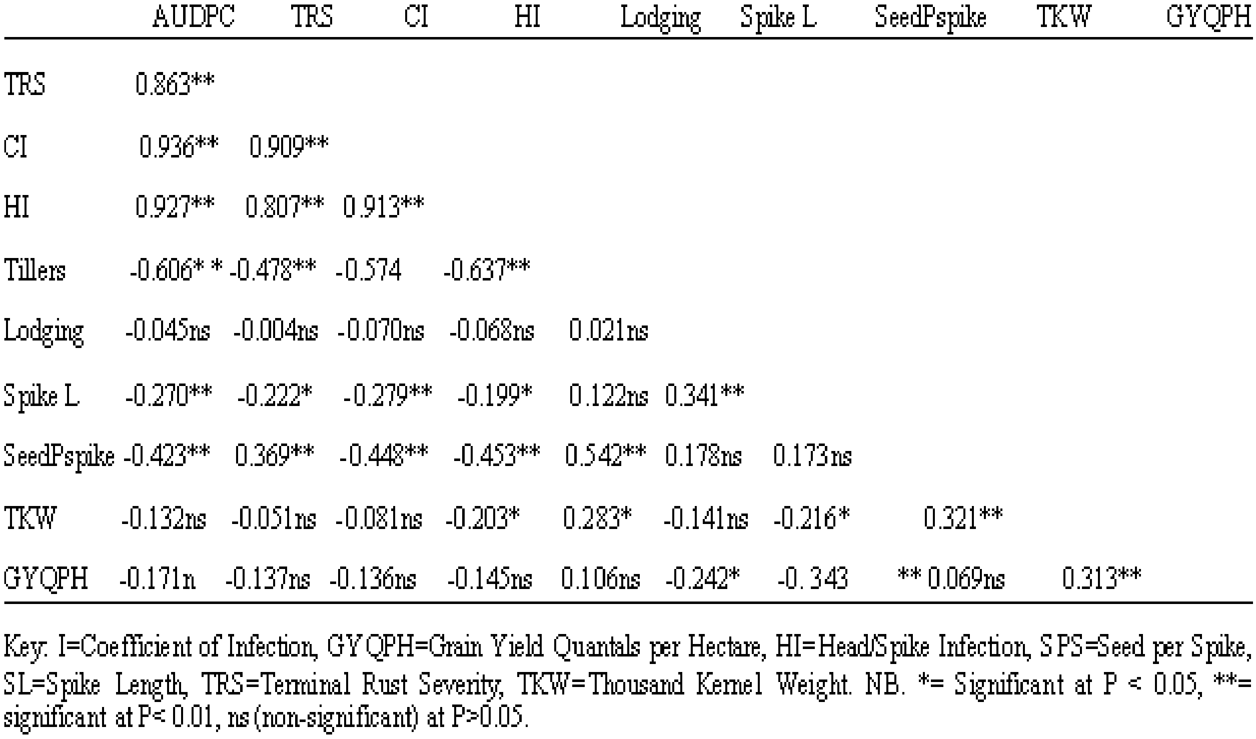
As demonstrated in figure below the yield can increase as resistance increasing from susceptibility (Morocco) to moderately resistance (Wane). The yield increment was higher at Kulumsa than at Meraro test locations, where the disease pressure registered reciprocal (figure 2). According to several authors including Krupinsky et al., (2002), yield differences can be associated with differences in the agro ecology and the level of genotypes tolerance to stresses.

Figure 2: Compared analysis for the high yielder genotype 231237 with MR (wane), MS(Dursa) and S(Morocco) checks.

Correlation of Disease, Grain Yield, Yield and Yield Components

The results showed that correlation among most of the yield and yield components are positive and significant. The disease parameter, AUDPC, was correlated with grain yield and yield components negatively (table 2). Therefore, apparently, resistant genotypes identified are reducing the disease pressure and increasing yield used as sources of stripe rust resistance breeding and high yielding and responding to agronomic practices.

Table 2. Pearson linear correlation coefficient among tripe rust disease parameters, yield and yield components,data collected from Kulumsa and Meraro sites and from 100 bread wheat genotypes,main season.2021.



	AUDPC	TRS	CI	HI	Lodging	Spike L	SeedPspike	TKW	GYQPH
TRS	0.863**								
CI	0.936**	0.909**							
HI	0.927**	0.807**	0.913**						
Tillers	-0.606* *	-0.478**	-0.574	-0.637**					
Lodging	-0.045ns	-0.004ns	-0.070ns	-0.068ns	0.021ns				
Spike L	-0.270**	-0.222*	-0.279**	-0.199*	0.122ns	0.341**			
SeedPspike	-0.423**	0.369**	-0.448**	-0.453**	0.542**	0.178ns	0.173ns		
TKW	-0.132ns	-0.051ns	-0.081ns	-0.203*	0.283*	-0.141ns	-0.216*	0.321**	
GYQPH	-0.171n	-0.137ns	-0.136ns	-0.145ns	0.106ns	-0.242*	-0. 343	** 0.069ns	0.313**

Key: I=Coefficient of Infection, GYQPH=Grain Yield Quantals per Hectare, HI=Head/Spike Infection, SPS=Seed per Spike, SL=Spike Length, TRS=Terminal Rust Severity, TKW=Thousand Kernel Weight. NB. *= Significant at $P < 0.05$, **= significant at $P < 0.01$, ns (non-significant) at $P > 0.05$.

Cluster Analysis

In the present study 100 genotypes were grouped into five clusters using average linkage Euclidean distance using MINITAB17 software (MINITAB,2003). Among the five clusters maximum inter cluster distance was found between cluster 1 and cluster 3 indicating possibility of inter crossing the genotype of the two clusters. While highest intra clusters some of square (1037.68) was recorded in cluster 1 which consists of 92 genotypes.

The cluster analysis grouped the 97 test genotypes and three check varieties into five distinct categories based on their disease and yield and yield traits obtained at Meraro and Kulumsa. Members within a single cluster were considered as similar or as having more close relationships with each other than those in distant clusters (table 3).

Table 3. Clusters of 100 Bread wheat genotypes in to different diversity classes.

			Cluster-1				Cluster2	Cluster3	Cluster4	Cluster5
G-1	G-17	G-32	G-47	G-62	G-77	G-96	G-4	G-85	G-98	G-100
G-2	G-18	G-33	G-48	G-63	G-78	G-99	G-97	G-90		
G-3	G-19	G-34	G-49	G-64	G-79			G-91		
G-5	G-20	G-35	G-50	G-65	G-80			G-93		
G-6	G-21	G-36	G-51	G-66	G-81					
G-7	G-22	G-37	G-52	G-67	G-82					
G-8	G-23	G-38	G-53	G-68	G-83					
G-9	G-24	G-39	G-54	G-69	G-84					

G-10	G-25	G-40	G-55	G-70	G-86					
G-11	G-26	G-41	G-56	G-71	G-87					
G-12	G-27	G-42	G-57	G-72	G-88					
G-12	G-27	G-42	G-57	G-72	G-88					
G-13	G-28	G-43	G-58	G-73	G-89					
G-14	G-29	G-44	G-59	G-74	G-92					
G-15	G-30	G-45	G-60	G-75	G-94					
G-16	G-31	G-46	G-61	G-76	G-95					

Key; G=Genotypes.

Cluster1:
It consisted of 92 genotypes. Among these clusters the genotype/accession, 231237 followed by Dursa (Moderately susceptible/MS check) is high yielder in seed per spike and TKW as compared to wane (Moderately Resistant check) and hence recommended for yellow rust resistance and high grain yielding variety development.

Cluster2:
It consisted of 2 genotypes with highly susceptible check (Morocco) and moderately resistance (214312) with low (16.17) to an intermediate (31.42) yield per hectare and yellow rust resistance, respectively.

Cluster3:
It consisted of 4 genotypes collected from Oromia and Amhara regional states. 214466, 226893,226898 and 231484 with an indeterminate yield of 33.11qt/ha,41.69qt/ha, 39.25qt/ha and 38.46qt/ exhibiting an intermediate resistant to yellow rust disease.

Cluster4:
It had one genotype (Ogolcho) having S to MS yellow rust reactions at Meraro and Kulumsa respectively. Exhibiting an intermediate, seed yield Quintals per hectare, number of seeds per spike, spike length,TKW and resistant to yellow rust disease.

Cluster5:
This cluster consists 1 genotype Wane (MR check) that is exhibiting high yield per hectare,spike length, seed per spike of 61.012 quintals,13.27cm,12.59 seeds, respectively and characterized by moderately resistance reaction to yellow rust.

CONCLUSION

In this study among the one hundred tested bread wheat genotypes,the Moderately resistant (MR) and moderately susceptible (MS) genetic materials identified can be used for wheat yellow rust resistance breeding,of them,genotypes Kingbird(48.05qt/ha) ,6883(48.5qt/ha),235038 (50.21qt/ha), 231487 (49.99qt /ha), Huluka(48.47qt/ha),20411 (44.49qt/ha,226283 (44.3qt/ha) were tolerant and over yielded MS check Dursa (43.88qt/ha) despite they had susceptible reaction to disease. Thus,I recommend them for further in yellow rust resistance breeding and improving yield.

On the other hand, genotype 231237 is recommended for having low terminal severity MR reaction and higher yield invariably with MR test check (Wane) across locations and thus can be used as a source germplasm to diversify the genetic base of wheat and improve durability of resistance in Ethiopia. However, "rust never sleeps", famously quoted by Norman Borlaug still initiates additional investigations of resistant genes contained in the candidate genotype, which can only be confirmed by molecular analysis. Therefore, evaluation of the wheat germplasm including land races in the field and green house, genotyping using known markers, investigating their physio chemical quality parameters to confirm the resistant Yr. gene carried with germplasm are all crucial points to be taken into consideration in the future yellow rust resistance breeding.

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