Screening of bread wheat (Triticum aestivum L.) genotypes resistance to yellow rust along with grain yield

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Research Article

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Abstract

Yellow rust caused by Puccinia striiformis f.sp tritici is one of the main diseases of wheat (Triticum aestivum L.) in the world, causing up to 50–100% of yield losses under favorable environmental conditions. Developing resistant cultivars is an efficient, economical, environmentally friendly and simple approach in combating wheat yellow rust. This study was carried out to evaluate spring bread wheat genotypes for their reaction to yellow rust under field conditions. Two hundred and forty spring bread wheat genotypes and seven check varieties were evaluated for their reaction to yellow rust disease under field conditions in non-replicated trials, using an augmented design. Collected data were analyzed using ANOVA. The genotypes were classified as resistant, moderately resistant, moderately susceptible and susceptible based on the percentage disease severity scored. Up to 90% disease severities were recorded from susceptible check kubsa and the other 23 genotypes. There was a significant difference of yellow rust severity, Coefficient of infections, AUDPC, yield and yield component values among genotypes, based on these parameters we identified 19 genotypes low disease severity and grain yield.

Introduction

Wheat (*Triticum aestivum L.*) is the world's leading cereal grain which is used by more than 1/3 of the population of the world as a staple food (FAO *et al.*, USDA, 2018). It is considered as one of the first domesticated food crops and for more than 80 countries has been the primary food staple of major civilizations of world and it is the most widely adapted major cereal crop that is cultivated on larger land area than any other crop worldwide (Reynolds et al., 2011; Munns and Richards, 2007). Globally wheat is grown on 220.4 million hectares with a total production of 750 million metric tons (Mt) annually, which makes it the second important grain crop after maize. China is currently the world's leading wheat producer, accounting for approximately 15% of the world's total production (FAOSTAT, 2016).

Ethiopia is the largest wheat producer in Sub-Saharan Africa (FAOSTAT, 2018) and wheat is central to achieving food and nutrition security. About 5 million Ethiopian farmers produce 5.3 million tons of wheat across 1.8 million hectares of land under rain-fed conditions (CSA, 2020).

In the period of 2009–2011, the country ranked first both in area and production of wheat in sub-Saharan Africa with a share of 55% and 47.8%, respectively (Negassa et al., 2013). In Ethiopia, wheat is cultivated on about 4.7 million hectares of land accounting for 13.5% of the total grain crop area, with an annual production of 4.54 million tons, contributing about 15.63% of the total grain production (CSA, 2017). The Bale, Arsi and Shewa areas of Oromia region are the highest wheat-producing areas of Ethiopia and they are considered as wheat belt areas. These wheat belt areas produce about 52.83% of Ethiopian wheat (CSA, 2017). Wheat is largely grown in the mid and highland areas of Ethiopia spanning at altitudes of 1500 to 3000 m a.s.l. However, it is mainly grown between 1800 to 2500 m.a.s.l in the country (Hei et al., 2017).

With the global population increasing and food security expected to become more important, wheat will continue to play a fundamental role as an important staple food crop for the vast majority of the global human population. Nationally, wheat contributes an estimated 12% to the daily per capita calorie intake, making it the third most important contributor to national calorie intake, after maize and sorghum (Guush et al., 2011). Wheat is the world-leading cereal grain serving as a staple food for more than one-third of the global population (Alemu, 2013; Hei et al., 2017).

Global wheat breeding efforts have made significant contributions to the improvement of wheat yield potential. However, the annual growth rate of wheat yield has been declining or static in the recent decade (Dixon et al., 2009; Fischer et al., 2009). The national average productivity is estimated to be 2.97 t ha^{-1} (CSA, 2020), which is by far below experimental yields of over 5 tons ha^{-1} (Mengistu et al., 2018). The sustainable productions and supply of wheat for future generations is threatened and challenged by the world population growth rate, global climate changes, various biotic and abiotic stresses (Dixon *et al.*,2009). Of biotic stress, yellow rust is one of the most devastating diseases (Chen 2005; Hovmøller et al., 2010, 2016; Wellings 2011). Over 45 million tons of wheat (valued at $9 billion) is lost due to wheat diseases and other pests annually (Oerke, 2006), among which yellow rust has become a serious threat to wheat, causing 50–100% yield losses. This is mainly due to the breakdown of existing resistance genes and gradual adaptation of new strains in warmer regions, particularly the Central and West Asia and North Africa (CWANA) region (ICARDA, 2011). Yellow rust cause significant yield losses and deteriorate quality and challenge the achievement of wheat productivity for gains needed to supply the growing demand (CIMMYT, 2011). This is mainly due to the pathogen's ability to mutate, multiply rapidly, and to use its air-borne dispersal mechanism from one field to another and even over long distances (Singh et al., 2005, Chen et al., 2014).

The Yellow rust pathogen is able to produce new races that may overcome race-specific resistance, leading to large-scale epidemics (Chen 2005). As *Berberis* and *Mahonia* have been recently found to be alternate hosts for *Pst*, sexual recombination may generate new races, in addition to mutation and somatic recombination (Jin et al., 2010; Wang and Chen 2013; Zhao et al., 2013, 2016; Lei *et al.*, 2017). Even though there is seasonal variability in the occurrence of yellow rust in Bale highlands, the main and long rainy season is ideal for yellow rust development (Bekele et al., 2002). The importance of stripe rust in the highlands of Ethiopia has been described previously (Getaneh et al., 1990; Getinet et al., 1990; Bekele et al., 2002; Dereje, 2003). Various management have been recommended like chemical, biological, cultural and other management approaches, but they are not more effective in controlling yellow rust, due to long-distance movement of spores, able to mutate and form new races (Feyissa et al., 2005).

The most effective strategy to control of yellow rust is breeding and growing resistant cultivars, as this approach has no additional cost to farmers and it is environmentally desirable (Wellings, 2011; Chen, 2013). Planting resistant cultivars is the most economical and simple approach for managing of yellow rust, However, detailed knowledge of resistance genes present in wheat cultivars is a prerequisite in resistance breeding program (Reema *et al.*,2019). The majority of Ethiopian bread wheat produced by

small holder farmers in the plains and cool high lands which are more suitable for yellow rust epidemic. There is also growing interest to produce wheat on large scale on farmer field where yellow rust is a major disease. Although Bale and Arsi are one of the wheat production areas in the country, there is no clear information on resistance variety, severity, the association of their phenotypes and genotypes against yellow rust. Therefore, searching for a new source of resistance to yellow rust from new bread wheat genotypes under field conditions in different locations is necessary to cope up with the emerging virulent races of the pathogen.

Materials And Methods

Descriptions of experimental sites

Locations	Latitude and longitude	Altitude m.s.l	Mean annual rainfall	Temperature Min and Max
KARC	08 01'7"N and 39 09'35"E	2200	800–1000 mm	10.5 C and 22.8 C
MWU	07 08'33" N and 39 59'53 E	2400	847.3 mm	8.8°C and 23°C
SARC	07° 07'29" N and 40° 13'52" E	2400	812 mm	9^0C and 21^0C

Planting materials and experimental design

Two hundred forty spring bread wheat genotypes and 7 check varieties of known and varying host responses were used (Appendix: 1) and these genotypes were obtained from ICARDA. The genotypes were planted in non-replicated trials, using an augmented design. The total experimental areas were divided into 5 blocks and each block had 48 genotypes and all the 7 check varieties, which subjected to replication in each block. The responses of genotypes were assessed in field plots comprising two rows with 1m long spaced 20 cm apart at a seed rate of 125 kg/ha and 5 plants were tagged for recording data. The pathway between plots and blocks was 40 cm and 1.1 m respectively. To facilitate uniform disease build-up within the nursery, continuous yellow rust susceptible spreader rows (using a mixture of susceptible cultivars Morocco and Kubsa in 1:2 proportion) was planted perpendicular to all entries on both sides of the plots by 20 cm to ensure sufficient production of inoculum to provide a uniform spread of yellow rust infection. A total of 11.4 m X 32.6`m, 371.64m^2, and plot size were used for each of the three locations.

Disease Assessments and Analysis

Disease severity was recorded as a percentage according to the modified Cobb scale (Peterson et al., 1948), at an interval of seven days, up to Kubsa displayed 80–100% severity about the soft to mid-dough stages. Disease severity was determined as the percentage of the ratio of the area of diseased tissue to

the total tissue area. The host response to infection in the field is scored using 'I' immune 'R' to indicate resistance or miniature uredinia; 'MR' to indicate moderately resistance, expressed as small uredinia; 'MS' to indicate moderately susceptible, expressed as moderately sized uredinia somewhat smaller than the fully compatible type; and 'S' to indicate full susceptibility(Peterson *et al*., 2001). Field responses were recorded four times and the final scoring at early-dough stage Zadoks scale 83 (Zadoks et al., 1974) was considered for analysis of variance (ANOVA). The data on disease severity and host reaction was combined to calculate the coefficient of infection (CI) following Pathan and Park (2006), by multiplying the severity value by a value of 0, 0.2, 0.4, 0.6, 0.8, or 1.0 for host response ratings of immune (I), resistant (R), moderately resistant (MR), intermediate (M), moderately susceptible (MS), or susceptible (S), respectively (Stubbs *et al*., 1986).

The area under Disease Progress Curve (AUDPC) was calculated in order to compare the genotypes' susceptibility and resistance. Yield and yield component data were subjected to ANOVA to compare the performance of genotypes. Correlation analysis was used to determine the relationship among CI, AUDPC and yield and yield components. The collected data were examined for the satisfaction of assumptions of ANOVA and remedial measures were taken for those data that violated the assumptions. Mean comparison was carried out using Dunnett's fixed range test and analysis of all these data were done with SAS software, version 9.2 (SAS, 2008), using PROC MIXED with entries as fixed and blocks as random effects. The area under the disease progress curve (AUDPC) was calculated from CI values using the formula of (Shanner and Finnery., 1977). AUDPC and CI values were used to classify the genotypes as R, MR, MS and S (Wang et al., 2005).

$$AUDPC = \sum_{i=1}^{n-1} \frac{(X_{i+1} + X_i)(t_{i+1} - t_i)}{2}$$

Where xi is the disease severity expressed in percentage at ith observation, ti is the time at the ith observation and n is total the number of days disease was assessed.

Agronomic data collected

Days to 50% heading, days to 90% maturity, grain filling period, plant height at maturity (cm), grain yield per plot, thousand seed weight and spike length were collected. Meteorological data on rainfall and temperature of experimental sites were obtained from Robe meteorological stations.

Results

Final disease severity (FDS)

There was wide variation in yellow rust severities ranging from 0 to 80% at KARC, 0 to 90% at MWU, and 0 to 90% at SARC. Diverse field reactions ranging from immune, resistance, moderately resistant, and moderately susceptible to susceptible responses were observed in all three locations. At MWU, among 240 spring bread wheat evaluated one genotype was immune, 90 R, 81 MR, 18MS, and 51 genotypes

produced S reactions. At SARC, two genotypes were immune,138 R, 50MR, 25MS, 35 S, and at KARC, 10 immunes, 0 ,115,122, and 0 shows R, MR, MS, and S, response respectively (Table1). The mean level of yellow rust severity ranged from 0 (immune) to 90 S (highly susceptible). Out of 240 genotypes tested for yellow rust, 80 genotypes (33.33%) were resistant, 94 genotypes (39.64%) were moderately resistant, 40 genotypes (16.50%) were moderately susceptible, and 26 genotypes (10.53%) were susceptible to *Puccinia striiformis f.sp. tritici* based on yellow rust severity level. There was heavy disease pressure during the seasons of testing as indicated by the susceptible checks Kubsa which had 90% susceptibility in all locations. However, some genotypes still showed yellow rust resistance at all locations.

After the final disease score, 50 genotypes showed resistance reactions and no compatible host-pathogen interactions associated with hypersensitivity that occur. In this study it was also observed that yellow rust disease directly affects the grain quality leading to shriveling of wheat grains (figure.1. genotype 82,103 and 123).

The analysis of variance for yellow rust reaction showed highly significant differences ($P \leq 0.0001$) among genotypes and the genotypes × environment interaction were also significant ($P \leq 0.01$) for disease severity across all environment. The yellow rust response calculated across sites using the data from the non-replicated experiments, the coefficient of variation reached 18.1%.

Table 1
Response of 240 spring bread wheat genotypes and 7 checks to yellow rust

locations	Spring bread wheat reactions to yellow rust				
	Immune	R	MR	MS	S
MWU	1	90	81	18	51
SARC	2	138	50	25	35
KARC	10	0	115	122	0
R-Resistance MS-Moderately susceptible					

MR –Moderately resistance S-Susceptible

Coefficient of infection (CI)

The data on final disease severity was combined to calculate a coefficient of infection (CI). In the present study, at KARC, 106 genotypes showed CI values ranged between 0–20. Eight genotypes had CI value of 21–40 and the remaining 126 wheat genotypes had CI values above 40 including susceptible checks.

The disease pressure was extremely high at the MWU site as indicated by the mean (Table 2). One hundred four genotypes show CI values ranged between 0–20. Nine genotypes had CI values 21–40, and the remaining 127 genotypes had CI value above 40 including susceptible checks. At SARC, 108 genotypes show CI values ranged between 0–20, ten genotypes had CI values 21–40, and 122 genotypes

had CI value above 40, including susceptible checks. Yellow rust infection was high in all three testing sites, allowing for clear and unambiguous scoring of field reaction. The mean CI values of the panel accessions ranged from 19.16 for MWU, 14.5 SARC, and 14.3 KARC. In all sites, a broad and continuous variation within the genotypes was noted, from close-to-immune, highly resistant reactions to highly susceptible ones, as indicated by the observed disease response ranges reported in Table 1 and the CI frequency distribution in each locations in Table 2.

Table 2
Descriptive statistics for field stripe rust response (reported as Coefficient of Infection) of the 240 elite bread wheat accessions and 7 checks evaluated on different locations in Ethiopia

Locations CI (Coefficient of infection)			
	Mean	Minimum	Maximum
KARC	14.3	0	72
MWU	19.16	0	90
SARC	14.5	1	90

The present study found considerable variation in the final rust severities of the accessions tested that could be attributed to differences in the number of resistance genes present and mode of gene action. The difference in the number of genotypes that were found to score significantly lower CI values from the susceptible check Kubsa in all three locations can be attributed to variations in environmental factors, especially to relative humidity, rainfall, and temperature. At MWU, the maximum and minimum temperatures during cropping seasons were 22.9^0C and 3.8^0C, respectively and the average relative humidity of the site were 56%. At SARC, the maximum and minimum temperatures were 23.4^0C and 3.5^0C, respectively. At KARC, on the other hand, the maximum and minimum temperatures were 23.6^0C and 8.2^0C, respectively, and the average relative humidity of the site was 55.5% during the cropping season (July to December, 2017). These clear variations in environmental factors might have potentially contributed to the difference in the number of genotypes found to score significantly lower CI values from Kubsa. The disease severity was high at MWU due to a favorable environment (continuous relative humidity and optimum temperature) for the multiplication of urediniospores.

Area under disease progress curve (AUDPC).

The area under the disease progress curve exhibited a very highly significant difference ($P < 0.001$) among the genotypes/ location. Data of each location were analyzed separately, as AUDPC data revealed significant variation between KARC, MWU, and SARC when the combined analysis was done. Areas under disease progress curves were significantly different among the genotypes at three locations ($P < 0.001$). At KARC the maximum AUDPC (1092) was recorded from 123 and 149 genotypes equally, were as genotypes number 14, 81, 90, 105, 175, 178, 196, 210, 231, and 251 show zero AUDPC. When we compare

with the checks seven genotypes (123, 149, 103, 96,116,238 and 60) show AUDPC more than the wariest check Kubsa (882) and 150 genotypes are less than the best check Shorima at KARC (138.6). At the MWU research site, a maximum of AUDPC (1715) value was obtained on three genotypes 60, 96, and 103 equally, were as genotype 151 shows zero AUDPC. When we compare with the checks, ten genotypes (60, 96, 103, 123, 160, 149, 5, 8, 56, and 57) obtained AUDPC more than the wariest check Kubsa (1358) and 139 genotypes are less than the best check Shorima (112) at MWU site. At SARC a maximum AUDPC (1820) value was recorded from two genotypes 123 and 149 similarly, were as genotype numbers 174 and 175 record zero AUDPC. At this site, when we compare genotypes with checks seven genotypes (123, 149, 103, 116, 96, 131, and 160) show maximum AUDP than the wariest check Kubsa (1463) and 159 genotypes are less than the best check Shorima (67.2) at SARC.

Yield and yield components of wheat Genotypes

In total, data for eight agronomic and physiological traits were collected during field trials and all data were collected from all three sites. The results from ANOVA for all traits indicated significant variations among genotypes, environments, and genotype × environments interactions. Average yield of the genotypes ranged from 0.58 t/ha to 10.36t/ha at KARC, 0.11t/ha to 2.25t/ha at MWU, and 0.6t/h to 7.44t/ha at SARC (Table 3). The average yield of best check cultivar Shorima was 5.35 t/ha at KARC, 1.7t/ha at MWU, and 4.212t/ha at SARC, these results clearly show that yellow rust has been a disease of great importance due to the recurrent epidemics and severe damage it caused on wheat at MWU, where disease pressure is higher. Among the top yielder, 16 bread wheat 37, 70, 117, 81, and 127 genotypes out yielded than check cultivar Shorima at all three locations. At the KARC, kubsa shows significant difference from 63 genotypes and non-significant from 177 genotypes while sixty two genotypes show significant from susceptible check Kubsa and others are not at MWU.

Although there were variations in grain yields among the entries, in case the of thousand kernel weight Kubsa had no significant from all checks and all genotypes at KARC, but at the MWU, and SARC there is a difference among checks and genotypes. At the MWU, Kubsa shows significant difference from Shorima and Hidasse but not significant from other checks and nine (93, 28, 272, 147, 144, 143, 139, 117 and 112) genotypes show significe from Kubsa. At SARC like that of the MWU site, check significant from Shorima and Hidasse but not significant from other checks and 11 genotypes are significant from Kubsa. The number of effective tillers did not show significance on Kubsa and other checks as well as all genotypes at KARC, MWU, and SARC, this may indicate that Kubsa is good in the case of the effective tiller. At KARC, for the grain filling period Kubsa not significant from other checks and genotypes, at MWU Kubsa asignificant from other checks but not from genotypes and at SARC Kubsa not a significant difference from all checks but show significant difference from one genotype (77)

Phenological parameters.

The significant difference was observed in days to heading at KARC between Kubsa and genotypes (42 genotypes), at MWU the Kubsa show significant difference from twenty genotypes and at SARC, seven

genotypes are significant from susceptible check. In the case of days to maturity at KARC, Kubsa shows significance from only one genotype (37), at MWU Kubsa show significant from eight genotypes (41, 195, 149, 123, 12, 103, 10 and 1) and at SARC Kubsa not significant different from other checks and genotypes. Mean days to heading ranged from 54–89 days at KARC, 63–96 days at MWU, and 60–92 days at SARC. Although, the of DH, 27 genotypes, 19 genotypes, and 8 genotypes show significant differences from susceptible check kubsa at KARC, MWU, and SARC respectively. For plant height, at KARC two genotypes (154 and 171), at MWU 8 genotypes and at SARC two genotypes (9 and 151) show significant differences from check. Similarly, mean plant height ranged from 62.5-102.3, 74.2-113.6 and 67.2-107.8 cm at KARC, MWU, and SARC, respectively. Days to maturity, on the other hand, present variations between environments, at KARC 3 genotypes (37, 109 and 12), at MWU and SARC there were no significant difference between all genotypes and kubsa, which may come as a result of different environmental conditions. Mean days to maturity ranges from 102–142 days at KARC, 122–149 days at MWU and 118–140 days at SARC. Mean days to grain filling period ranged from 37–65 days, 54-61days and 39-71days at KARC, MWU, and SARC respectively (Table 3).

Table 3
Mean, minimum and maximum values of the different agronomic traits with their CV and p-value.

Trait	locations	mean	max	min	CV (%)	P-value
Yield(t/ha)	KARC	5.65	10.36	0.58	12.89	< .0001
	MWU	2	2.26	0.11	23.91	0.0003
	SARC	4.34	7.44	0.6	22.46	0.0192
PH(cm)	KARC	83.3	102.3	62.5	4.61	0.0003
	MWU	94.31	113.6	74.2	3.62	< .0001
	SARC	90.80	107.8	67.2	3.58	< .0001
TKW(g)	KARC	34.51	54	18.92	18.60	0.046
	MWU	31.2	46.9	12.6	15.38	0.015
	SARC	33.1	40.9	12.8	10.09	0.003
DH(days)	KARC	68.5	89	54	1.68	< .0001
	MWU	70.9	96	54	1.48	< .0001
	SARC	68.5	92	60	1.79	< .0001
DM(days)	KARC	123.5	142	54	3.04	< .0001
	MWU	134.91	149	122	1.44	< .0001
	SARC	124.44	140	118	2.59	0.0345
GFP(days)	KARC	55.3	65	37	6.72	0.1550
	MWU	74.07	71	52	3.58	0.0068
	SARC	55.97	71	39	6.06	0.1327
SL(CM)	KARC	7.82	10.2	5.5	7.70	0.009
	MWU	9.82	12.8	7.6	7.81	0.1209
	SARC	9.05	12	7	5.89	0.0019
NET	KARC	1.11	5.6	0	15.06	0.0418

PH-plant height GFP-grain filling period

TKW-thousand kernel weight SL-Spike length

DH-days to heading NET-number of effective tillers

DM-Days to maturity

Trait	locations	mean	max	min	CV (%)	P-value
	MWU	1.58	7.4	0	18.16	0.607
	SARC	1.2	3.4	0	5.89	0.001
PH-plant height GFP-grain filling period						
TKW-thousand kernel weight SL-Spike length						
DH-days to heading NET-number of effective tillers						
DM-Days to maturity						

Correlations between epidemiological parameters and yield parameters

The epidemiological parameters CI and AUDPC were highly correlated in the present work. A positive correlation (R^2 = 0.89) at KARC, (R^2 = 0.85) at MWU and (R^2 = 0.90) at SARC was obtained between CI and AUDPC (Table 4). The Pearson correlation coefficients between the stripe rust responses recorded in the three sites were always highly significant ($P \leq 0.001$), with values ranging from 0.750 to 0.814. The correlation coefficient analysis showed that yellow rust severity was negatively correlated with all agronomic traits at SARC, MWU, and KARC (Table.4). A high negative correlation was observed between disease parameters and thousand kernel weight and yield in all locations (Table.4).

Table 4

Pearson's correlation coefficients of epidemiological parameters and among the different agronomic traits for bread wheat genotypes evaluated for reactions against yellow rust under natural field conditions at MWU, SARC and KARC, in 2017 main cropping seasons.

location		CI	AUDPC	GY	TKW	GFP	PH	NET
MWU	CI							
	AUDPC	0.85***						
	GY	-0.72***	-0.73***					
	TKW	-0.508**	-0.560**	0.69**				
	GFP	-0.114^{ns}	-0.265**	0.254**	0.33**			
	PH	-0.180*	-0.272**	0.408**	0.39**	0.35**		
	NET	-0.109^{ns}	-0.161*	0.027^{ns}	0.154*	0.25**	0.322**	
SARC	CI							
	AUDPC	0.90***						
	GY	-0.579**	-0.601**					
	TKW	-0.464**	-0.519**	0.65**				
	GFP	-0.152*	-0.213**	0.299**	0.33**			
	PH	-0.134*	-0.187*	0.266**	0.39**	0.182*		
	NET	-0.110^{ns}	-0.157*	0.246**	0.24 **	0.22**	0.205*	
KARC	CI							
	AUDPC	0.89***						
	GY	-0.514**	-0.55**					
	TKW	-0.38**	-0.38**	0.61**				
	GFP	-0.111^{ns}	-0.096^{ns}	0.048^{ns}	0.028^{ns}			

CI-coefficient of infections GFP-grain filling period

AUDPC-area under diseases progress curve PH-plant height

GY-grain yield NET-number of effective tillers

TKW-thousand kernel weight

* refers to significance level at P < 0.05; ** refers to significance level at P < 0.01;

*** refers to significance level at P < 0.001; ns refers to non-significant

location		CI	AUDPC	GY	TKW	GFP	PH	NET
	PH	0.087 ^{ns}	-0.066 ^{ns}	0.139 *	0.051 ^{ns}	0.100 ^{ns}		
	NET	-0.094 ^{ns}	-0.101 ^{ns}	0.23 **	0.140 *	-0.153*	0.106 ^{ns}	
CI-coefficient of infections GFP-grain filling period								
AUDPC-area under diseases progress curve PH-plant height								
GY-grain yield NET-number of effective tillers								
TKW-thousand kernel weight								
* refers to significance level at P < 0.05; ** refers to significance level at P < 0.01;								
*** refers to significance level at P < 0.001; ns refers to non-significant								

Discussion

The spring bread wheat genotypes evaluated for their reaction to yellow rust under natural field conditions infection at KARC, MWU, and SARC locations showed variations in their response to the disease as measured in terms of severity, CI, and AUDPC. Alemu et al. (2021) also reported that variably distributed reaction groups were demonstrated among the panel for SEV, RES, and CI across the environments. The difference in the number of genotypes that were found to score significantly lower CI value from the susceptible check kubsa in all three locations can be attributed to variations in environmental factors, especially to relative humidity, rainfall, and temperature. Yellow rust needs cooler temperatures and high relative humidity than other rusts. Similar to this finding, there are studies that (McIntosh et al., 1995; Agarwal et al., 2003) report those climatic conditions, mainly cooler temperatures, and higher humidity allowed more rapid development of yellow rust disease in susceptible wheat cultivars.

At MWU, the maximum and minimum temperatures during cropping seasons were 22.9 ^{O}C and 3.8 ^{O}C, respectively and average relative humidity of the site were 56%. At SARC, the maximum and minimum temperatures were 23.4 ^{O}C and 3.5 ^{O}C, respectively. At KARC on the other hand, the maximum and minimum temperatures were, 23.6 ^{O}C and 8.2 ^{O}C, respectively and average relative humidity of the site were 55.5 during the cropping season (July to December, in 2017). These clear variations in environmental factors might have potentially contributed to the difference in the number of genotypes found to score significantly lower and higher CI value from Kubsa. In our finding the disease severity were high at MWU due to favorable environment (continuous relative humidity and optimum temperature) for multiplication of urediniospores. According to the study conducted by, (Schröder and Hassebrauk, 1964), the minimum, optimum and maximum temperatures for urediniospore germination are 0°C, 7–12°C and 20–26°C, respectively. Many researchers (Rapilly and Fournet, 1968, Chen *et al.*, 2010; Hovmøller et al.,

2016) reported that relative humidity must exceed 50% for sporulation to occur, and that urediniospore production increased exponentially with rising relative humidity, so our field present in this interval.

Similar to this finding, other others (McIntosh et al., 1995, Agarwal et al., 2003, Shewaye and Mohammed, 2021) report those climatic conditions, mainly cooler temperatures and higher humidity allowed more rapid development of yellow rust disease in susceptible wheat cultivars. According to other experiments conducted (Chen et al., 2002, 2014, Wan et al., 2004, and Bahri *et al.*, 2008) in Pakistan, variability for pathogen population in terms of races had been reported across locations with different climatic conditions. There was heavy disease pressure during the seasons of testing as indicated by the susceptible checks Kubsa which had 90% susceptibility at MWU and SARC, but 80% at KARC locations. However, some genotypes still showed yellow rust resistance at all locations. Yellow rust infection was high in all three testing sites, allowing for clear and unambiguous scoring of field reaction. The mean CI values of the panel accessions ranged from 19.16 for MWU, 14.5 SARC, and 14.3 KARC.

The present study found considerable variation in the CI of the accessions tested that could be attributed to differences in the number of resistance genes present and mode of gene action in addition to environmental factors. Safavi, (2012) reported that wheat lines with final rust severity values of 1–30%, 31–50% and 51–70% were regarded as possessing high, moderate, and low levels of slow rusting resistance, respectively. Genotypes with a low final disease severity under high disease pressure may possess more additive genes (Singh et al., 2005). Final rust severity represents the cumulative result of all resistance factors during the progress of epidemics. Many researchers (Ali et al., 2009; Shah *et al.*, 2010, Tabassum, 2011, and Safavi and Afshari 2012), also used final severity as a parameter to assess the slow rusting behaviour of wheat lines. Previously, Ali et al. (2009) considered that lines with CI values of 0–20, 21–40, 41–60 could possess high, moderate, and low levels of slow rusting resistance, respectively.

Variation also present between genotypes and susceptible check based on AUDPC value, there is average 296.5, at MWU, 213.9 at KARC and 220.9 at SARC. Wang et al. (2005) reported that AUDPC is a good indicator of adult plant resistance under field condition. Based on the AUDPC values, (Ali et al., 2009) categorized the wheat lines into two distinct groups. According to (de Vallavieille-Pope Claude *et al.*, 1995), the epidemiological components of *Pst* are known to be affected by both temperature and light. This suggests that the variability on AUDPC present between the three locations in our study the expression of resistance genes in a given set of genotypes could be the result of variability in the prevalent races along with the climatic conditions of the area, which affect the yellow rust infection process. At three locations, the magnitude of disease severity were significantly different among genotypes, they were higher in the MWU and SARC than KARC. The observed variability could be due to the geographical features of the area affecting wind speed, direction and frequencies, along with agro climatic conditions during the study season.

Variations among genotypes were observed in their yield and yield related responses at all locations. This might be attributed to yellow rust diseases and variations in environmental factors. The average yield of

the genotypes ranged from 0.58 t/ha to 10.36t/ha at KARC, 0.11t/ha to 2.25t/ha at MWU, and 0.6t/h to 7.44t/ha at SARC. These results indicate that at the MWU site there is more reduction of yield due to high disease severity when we compare with the other two sites. Similar to this finding, Sache and Zadoks, (1994) reported that generally, yield components decreased with increasing disease severity. Wellings (2007) also reported that epidemics have been significant in some locations, causing huge yield losses, which require serious financial investment to mitigate the crops from damage. Among the top yielder 16 bread wheat genotypes 37, 70, 117, 81, and 127 are out yielded than check cultivar Shorima at all three locations.

The number of effective tillers did not show significance on Kubsa and other checks as well as all genotypes at KARC, MWU, and SARC, which may indicate that Kubsa is good in case of effective tiller even if its susceptible to yellow rust and the field has good fertility. Both, grain yield and kernel weight of the tested genotypes, were significantly affected at the MWU site than other sites. The difference in yields between the three locations could be attributed to either difference in environmental conditions or due to differences in yellow rust infection. Environmental conditions such as temperature and moisture considerably affect disease expressions and, consequently the yield. Several researchers have reported rust reducing grain yields of wheat cultivars (Wellings, 2010, Afzal *et al*., 2007). It is worth noting that yellow rust caused kernel weight reduction in the genotypes. Nzuve et al. (2012) also reported that yellow rust significantly reduces TKW in wheat. The significant differences were observed in DH and PH among genotypes and as well as among locations.

The epidemiological parameters CI and AUDPC were highly correlated in the present work. A positive correlation (R^2 = 0.89) at KARC, (R^2 = 0.85) at MWU and (R^2 = 0.90) at SARC was obtained between CI and AUDPC (Table 4). Such Similar correlation has also been reported in previous studies (Broers et al., 1996, Qamar et al., 2007; Ali et al., 2009; Safavi, 2012; Safavi and Afshari, 2012). Similar highly positive correlation results between these two parameters have also been reported by Nyamu *et al.* (2017) while evaluating Kenyan wheat genotypes against leaf rust at adult plant stage.

A high negative correlation was observed between disease parameters and thousand kernel weight and yield in all locations in our finding. Nzuve et al. (2012) also reported that yellow rust significantly reduces TKW in wheat. According to Berghaus and Reisener, (1985), the effect of rust on grain yield is due to the great injury to the photosynthetic surface of the plant. Similar findings by Smedegaard-Petersen and Tolstrup, (1985) indicate that energy expenditure in plant defense mechanisms rather than for growth and grain formation. Correlation coefficients among phenotypic traits varied depending on the environment. Lopes et al. (2012) reported weak or absence of phenotypic correlations of yield with yield components and other phenotypic traits for the same genotypes evaluated in different environments. In their report (based on combined means across 12 environments), grain yield was not correlated with thousand kernel weight, days to heading, days to maturity, and plant height; however, we found significant phenotypic correlation coefficients for yield with thousand kernel weight, days to heading, days to maturity, and other phonological traits. The resistant genotypes identified from this study could be used by the different

wheat breeding programs across the country for potential release nationally or regionally after testing over a year as well as over locations for different biotic and abiotic factors.

Conclusions

Yellow rust is one of the major diseases affecting bread wheat production in the country. To cope up these we used 240 spring bread wheat genotypes and 7 check varieties including susceptible check were evaluated in non-replicated by using augmented design for their reactions against yellow rust under natural field conditions. The genotypes showed varying levels of reactions against yellow rust at three locations and the criteria used for evaluation were disease severity, CI, AUDPC, yield and yield component. Significant variation was observed in yield and yield components among the genotypes tested. The results of this study revealed with regard to disease resistance and yield performance, the 19 genotypes are consistently ranked among the top performer, but it require further investigations over seasons and over years.

Declarations

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Figures

Figure 1

Bread Wheat reaction to yellow rust, at MWU, KARC and SARC,in Ethiopia