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Evaluation of Bread Wheat (*Triticum aestivum* L.) Germplasm for Wheat Rust Diseases Resistance and Yield Perforamance

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ABSTRACT

The experiment was conducted from July to December, 2023 at Melkasa Agricultural Research Center (MARC) and Kulumsa Agricultural Research Center (KARC) to evaluate the performance of introduced bread wheat materials from CIMMYT against wheat rust diseases and yield. A total of fifty advanced lines were brought from CIMMYT. The trial was planted in an alpha-lattice design with two replications. Data were collected for stem rust, yellow rust, and some agronomic traits, including grain yield. The ANOVA showed highly significant genotypic variation (p<0.05) in days to heading (DTH), Hectoliter weight (HLW), Thousand Kernel Weight (TKW), and Yield (YLD). Then, results from LSD revealed that genotypes: EBW222102 YLD=7.7 t ha^{-1}, EBW222106 YLD=7.61 t ha^{-1}, EBW222108 YLD=7.66 t ha^{-1}, EBW222136 YLD=7.76 t ha^{-1} significantly higher than the check variety Daka at (p<0.05). Eighteen genotypes were susceptible to stem rust disease, with a coefficient of infection (YRCI) >30 at Melkasa. Genotypes: EBW222111, EBW222126, EBW222129, EBW222134, and EBW222142 delivered high yield, greater than or equal to 2 t ha^{-1} at Melkasa. These genotypes therefore represent promising candidates for the development of widely adapted, high-yielding, and disease-resistant wheat varieties. Accordingly, their advancement to the next stage of the breeding pipeline is strongly recommended.

KEYWORDS: CI, CIMMYT, genotype, SAWYT, pipelines, resistance YLD

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1. INTRODUCTION

Wheat productivity and production have increased for the past two decades in Ethiopia. The productivity increased from 2.4 t ha^{-1} in 2013 to 3.1 t ha^{-1} in 2023 (Anonymous, 2023). The wheat production in 2022/2023 is about 5.8 mt (Anonymous, 2023). Still, the country has higher potential beyond the present productivity and production. However, wheat in Ethiopia is behind the existing potential due to biotic, abiotic, and post-harvest losses (Mulu et al., 2022; Yared et al., 2021; Zewdie et al., 2022).

The major biotic constraints for wheat production in Ethiopia are Wheat rust diseases, insects, and weeds. Among the biotic constraints, wheat rust diseases (mainly stem rust and yellow rust) are more limiting factors (Jaleta et al., 2019; Daved et al., 2010). Similarly, the most important abiotic stresses are terminal drought, soil acidity, erosion, poor soil fertility, prolonged high rainfall, water-logging and pre-harvest sprouting.

The occurrences and outbreaks of stem rust and yellow rust diseases in Ethiopia varied from year to year in severity (Meyer et al., 2021). The prevalence of wheat rusts also differed significantly amongst bread wheat varieties under production (Ali et al., 2017; Worku et al., 2016; Hovmøller, 2012). Some variety shows resistance (Balcha for yellow rust) and moderate resistance (Daka for yellow rust). Others show susceptibility (Hidasse for yellow and stem rusts) and highly susceptible (Kubsa for yellow and stem rusts). The country experiences recurrent epidemics of stem rust due to the evolution of new stem rust races (Meyer et al., 2021; Olivera et al., 2015). Stem rust caused by the basidiomycete *Puccinia graminis* f.sp. tritici (Pgt) causes a total crop loss during epidemic years (Olivera et al., 2015). Yellow rust caused by the basidiomycete fungus *Puccinia striiformis* f. sp. tritici (Pst) causes significant yield loss. In 2010, the outbreak of this disease seriously damaged popular adapted varieties: Kubsa and Galema. It affected more than 600,000 ha of wheat growing areas and reduced up to 20% production (Sanders et al., 2011; Daved et al., 2010; Teklay et al., 2013). Due to these rusts, farmers in the area expended additional expenses for fungicides, which they spray three to four times per cropping season.

Different wheat rust disease-controlling options are available for wheat farmers, such as cultural practices, fungicides, and growing resistance varieties (Jushi et al., 2011; Singh et al., 2015). Due to the high pressure of yellow and stem rust pressure, farmers in the country use fungicides extensively to control wheat rust diseases (Ayele et al., 2008; Hailu and Fininsa, 2009). However, due to the cost of the chemicals, the lack of skill when and how to use the fungicides, and the poor quality of the chemicals to control the diseases effectively, the farmers still lose their crops. The other management option is Growing resistance varieties for wheat rust diseases. It is an environmentally and economically safe option for the farmers. However, the lack of availability of the resistance varieties forced the farmers to grow obsolete varieties.

To overcome the problem, the continuous development and release of wheat rust disease-resistant noble bread wheat varieties is crucial.

The generating and releasing of noble bread wheat varieties for the wheat-producing community goes through different breeding procedures. Getting germplasm from diverse sources, evaluating the genotypes on the field, and selecting among the lines for better performances are the activities practiced by the wheat research program. The national wheat research program has been introducing germplasm from CGIAR centers besides its crossing materials. Consequently, the program has released many widely adopted bread wheat varieties. The released resistance varieties so far delivered a significant impact on wheat productivity and production (Hodson et al., 2020). Therefore, the objective of this study was to evaluate the performance of introduced bread wheat materials from CIMMYT for wheat rust diseases and yield.

2. MATERIALS AND METHODS

2.1. Material, design, description of the study area

In 2022, the national wheat research program introduced the 29 Semi-arid wheat yield trials (29SAWYT) along other trials from CIMMYT, Mexico. A total of fifty genotypes, including one local check variety, Daka planted in alpha lattice design with two replications. The rep/block had five sub-blocks, and a sub-block had ten plots. The size of a plot was 1.2 m width by 2.5 m length. A plot had six rows with a total area of 3 m^2. All agronomic practices applied equally to all plots.

The experiment was conducted at Melkasa Agricultural Research Center (MARC) and Kulumsa Agricultural Research Center (KARC) from July to December, 2023. MARC is located at 8°24′N 39°12′E latitude and longitude with an Altitude of 550 m.a.s.l. The minimum and maximum temperatures are 14°C and 280°C respectively. The area received an annual rainfall of about 763 mm. KARK is located at 8°02′N 39°10′E latitude and longitude with an Altitude of 2200 m.a.s.l. The minimum and maximum temperatures are 100°C and 220°C respectively. Annual rainfall in kulumsa is about 840 mm.

2.2. Data collection and analysis

2.2.1. Wheat rust diseases

Stem rust and yellow rust diseases were collected two rounds. The first score was taken a week after the symptom had seen on the plot. The second was taken at the pick time of the disease's pressure on the trial. The severity of the rust was taken in percent using 5% 10% 20% 30% … 100%. The reaction of the host for the pathogen designates using the English letters where: 0=No visible infection on the plant; R=Resistant: visible chlorosis or necrosis, no uredia are present; MR=Moderately resistant: small uredia are present and surrounded by either chlorotic or necrotic areas; M=Intermediate: variable-sized uredia are present; some with chlorosis, necrosis, or both; MS=Moderately susceptible: medium-sized uredia are present and possible surrounded by chlorotic areas; S=Susceptible: Large uredia are present, generally with little or no chlorosis and no necrosis (Muhammad et al., 2017; Mulu et al., 2022). Severity and field response readings are usually combined. For example, tR=Trace severity with a resistant field response. 10MS= 10% severity with moderately susceptible field response. For the purpose of analysis, the diseases data changed to Coefficient of infection (CI) as outlined by (Stavely, 2022; Olivera et al., 2015) in which the host reaction changed to numeric and then multiplied by severity. Immunity (O)=0.05, resistant (R)=0.1, moderately resistant (MR)=0.2, intermediate (M)=0.4, moderately susceptible (MS)=0.6, and susceptible (S)=1. For example: CI for 10MS=10*0.6= 6; CI=6.

The analysis of variance, ANOVA is computed to compare the variance related to genotypes to that of variance environmentally occurring between plots (Peterson et al., 1948).

The broad-sense heritability of a given trait at an individual environment is calculated as {5}

$H^2=(\delta^2 g)/(\delta^2 g+\delta^2 E/nRep)$

where σg^2 and $\sigma \varepsilon^2$ are the genotype and error variance components, respectively, and nRep is the number of replicates

The LSD at 5% of significance is calculated as $LSD=t_{(1-0.05,df\mathrm{Err})}\times ASED$, where t is the cumulative Student›s t distribution, 0.05 is the selected α level (5%), df Err is the degrees of freedom for error in the linear mixed model, and ASED is the average standard error of the differences of the means (R Core Team, 2015; Roelfs et al., 2015).

ALL the analysis computed using R software 3.6.0 and META-R (Henderson, 1975; Hodson et al., 2020).

3. RESULTS AND DISCUSSION

In field experiments, variation among experimental units or plots arises from both genotypic effects and unexplained sources of variation (error). The presence of such variability among tested genotypes provides an opportunity for effective selection by breeders. Data from the two locations were combined and subjected to analysis of variance (ANOVA). The results revealed significant genotypic variation (p<0.05) for days to heading (DTH), hectoliter weight (HLW), thousand kernel weight (TKW), and grain yield (YLD), indicating the existence of sufficient genetic variability among the evaluated genotypes. This suggests that selection for these traits can be effective in crop improvement (Verma et al., 2023). Furthermore, highly significant differences (p<0.05) with large mean squares were observed for test sites across all traits (Table 1), highlighting the substantial contribution of environmental factors to the total variation Table 1. Analysisi of variance (ANOVA) for Genotype (G), Environment (SITE) means squares for yield (YLD), days to heading (DTH), days to maturity (DTM), Plant height (PHT), thousand kernel weight (TKW), and hectoliter weight (HLW)) of fifty bread wheat genotypes tested across two locations.

Heritability is an important quantitative parameter that evaluates how genetics and environment interact to determine a trait's expression. Heritability in this study computed for each environment separately to see the responses of the locations in heritability of the traits and for the combined environments to see how heritability of the traits responses across the two locations. Result from the experiment showed different responses from Very low heritability 2.3% for yield to high heritability 79.2% for plant height across locations (Table 2). At kulumsa, high heritability gained for all traits in the study: YLD, DTH, TKW, HLW, DTM and PHT (Table 3) tha at Melkasa. Similar result was reported by Uttej et al. (2023). This showed that environmental effect on the traits to phenotypically express was higher at melkasa. At Kulumsa, the genotypes were able to phenotypically express the traits more of due to their genetic makeup.

Higher heritability for yield and yield component enable to select and advance promising genotypes for release. Grain yield and wheat rust resistance are the two important traits in the breeding program. Hence, in addition to diseases resistance considering the yield performance helps to select better genotypes.

The check variety Deka used to mean yield comparison. The average yield across locations for Deka was 3.2 t ha^{-1}. The least significant difference LSD across location was 0.277 (Table 2). About thirty three genotypes delivered higher average grain yield than the check, Deka variety across the locations. Moreover, thirty one out of thirty three genotypes were significantly different in grain yield than the check variety Deka at (p<0.005) (Table 2 and 3).

The least significant difference LSD for yield at Kulumsa was 1.37 (Table 2). The average yield of the check variety Daka

Table 1: Analysis of variance (ANOVA) for yield and related traits of fifty bread wheat genotypes tested across two locations

Source of variation	DF	DTH	DTM	PHT	HLW	TKW	YLD
Genotype (G)	49	27.9^{***}	6.8^{**}	53^{*}	24.6^{***}	35.7^{***}	1.7^{***}
Environment (E)	1	3553.2^{***}	28962.6^{***}	73345^{***}	1513.44^{***}	4608.0^{***}	945.17^{***}
Genotype: Environment G×E	49	5.8^{***}	6.5^{**}	44^{ns}	9.92^{*}	19.0^{***}	1.66^{***}
Environment: Rep	2	9.6^{*}	0.4^{ns}	131^{*}	30.74^{**}	66.6^{***}	3.20^{***}
Environment: Rep: Block	2	0.6^{ns}	3.1^{ns}	0^{ns}	3.35^{ns}	25.9^{*}	0.65^{ns}
Residual	96	2.1	3.5	35	6.26	7.1	0.41

Since, variations among genotypes, environments, genotypes by environments was observed, other statistics broad sense heritability, Least Significant Difference LSD, Coefficient off variance CV were computed

Table 2: Broad sense heritability, genotypic and residual variance, grand mean, LSD, CV, and level of genotypic significance for fifty genotypes evaluated across Kulumsa and Melkasa

Statistic	DTH	DTM	PHT	SR	TKW	HLW	YLD
Heritability	0.792	0.039	0.173	0.444	0.468	0.638	0.023
Genotype variance	5.426	0.058	2.296	44.211	4.173	4.166	0.010
GenxLoc variance	1.824	1.415	5.075	36.247	5.740	1.806	0.621
Residual variance	2.037	2.862	33.870	149.070	7.499	5.830	0.415
Grand mean	63.245	109.121	84.150	15.976	29.520	62.983	3.533
LSD	3.051	0.674	3.922	14.265	4.258	3.581	0.277
CV	2.257	1.550	6.916	76.422	9.276	3.834	18.238
n replicates	2	2	2	2	2	2	2
n environments	2	2	2	2	2	2	2
Genotype significance	***	ns	ns	ns	*	***	ns
Gen×Env significance	***	*	ns	ns	***	ns	***

KU: Kulumsa; MK: Melkasa; DTH: Date of heading; DTM: Date of maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield; Genotype significance for the traits at: ns: non significance, *,**, and *** significant (p=0.05), (p=0.01), and (p=0.001) level of significance, consecutively

was 6.22 t ha^{-1} at Kulumsa. Yield at Kulumsa for Genotypes: EBW222102 YLD=7.7 t ha^{-1}, EBW222106 YLD= 7.61 t ha^{-1}, EBW222108 YLD=7.66 t ha^{-1}, EBW222136 YLD= 7.76 t ha^{-1} significantly higher than the check variety Deka at (p<0.05) (Table 3). The check variety Deka delivered the lowest yield, 0.17 t ha^{-1} at Melkasa. The least significant difference at melkasa was 0.577. Unexpectedly, all genotypes but EBW222119 are significantly different than Deka for yield at (p<0.05) (Table 3).

The other important traits to evaluate and select better genotypes are wheat rust diseases resistance. Especially, at the early stage of breeding pipe line, performance of the genotypes for the existing important wheat rust diseases is more important than the other traits. The trial is at nursery stage; it is early to look for yield and stability across different environment. But, later, genotypes selected here will be advanced to yield trial and evaluated at different stages of breeding pipelines across different locations before released as a variety. Genotype EBW222099 scored the highest stem rust coefficients: SRCI=55 at Kulumsa and SRCI=60 at Melkasa. In contrast, this genotype showed very low coefficient of infection YRCI=1.1 for yellow rust disease at Kulumsa site. Hence, this genotype is highly susceptible for stem rust but resistance for yellow rust. Genotype EBW222146 had the highest coefficient of infection YRCI=35 for yellow rust at Kulumsa. Also, it had higher coefficient of infection SRCI=40 for stem rust at Melkasa. These told us the genotype is highly susceptible for both diseases. Genotypes: EBW222147, EBW222135, EBW222131, EBW222128, EBW222124, EBW222122, EBW222120 scored YRCI=1.5, 1, 0.6, 0.6, 0.6, 0.2, and 3 for yellow rust successively at Kulumsa. The same genotypes successively scored SRCI=3.5, 0.2, 1.03, 0.05, 0.13, 0.13, and 0.23 for stem rust at Kulumsa. So, they were resistance

Table 3: Broad sense heritability, genotypic and residual variance, grand mean, LSD, CV, and level of genotypic significance for fifty genotypes evaluated at Kulumsa and Melkasa, for each site separately

Statistics	DTH		DTM		PHT		YRCI
	KU	MK	KU	MK	KU	MK	KU
Heritability	0.96	0.64	0.75	0.32	0.63	0.10	0.66
Genotype variance	11.62	2.69	1.88	1.03	10.60	3.10	59.97
Residual variance	1.02	2.97	1.27	4.46	12.25	55.17	60.57
Grand mean	67.46	59.03	121.21	97.01	103.30	65.00	6.20
LSD	2.07	2.84	2.07	2.43	5.63	4.77	12.98
CV	1.49	2.92	0.93	2.18	3.39	11.43	125.48
n Replicates	2	2	2	2	2	2	2
Genotype significance	***	**	***	ns	**	ns	**

Table 3: Continue...

Statistics	SRCI		TKW		HLW		YLD	
	KU	MK	KU	MK	KU	MK	KU	MK
Heritability	0.80	0.08	0.81	0.57	0.90	0.41	0.81	0.32
Genotype variance	136.95	10.45	14.39	5.25	8.26	3.50	1.19	0.06
Residual variance	68.97	229.86	6.94	7.85	1.94	10.05	0.57	0.25
Grand mean	7.91	24.04	34.32	24.72	65.79	60.17	5.71	1.36
LSD	15.26	8.87	4.77	4.33	2.73	NA	1.37	0.58
CV	104.96	63.07	7.67	11.33	2.12	5.27	13.28	36.67
n Replicates	2	2	2	2	2	2	2	2
Genotype significance	***	ns	***	**	***	ns	***	ns

KU: Kulumsa; MK: Melkasa; DTH: Date of heading; DTM: Date of maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield; Genotype significance for the traits at: ns: non significance, *,**, and *** significant (p=0.05), (p=0.01), and (p=0.001) level of significance, consecutively

for both yellow rust and stem rust at kulumsa. Nonetheless, they scored high coefficient of infection from SRCI=30 to SRCI=45 for stem rust at Melkasa. Probably, it is due to the occurrence of different stem rust races between Kulumsa and Melkasa during the study (Singh et al., 2006).

The reason for testing genotypes for their disease response across different locations is to examine their performance for the existing wheat rust races across different wheat producing agro-ecology. Genotypes: EBW222108 with YRCI=0.13 for yellow rust at Kulumsa, SRCI=0.4 for stem rust at Kulumsa, and SRCI=3 for stem rust at Melkasa; EBW222109 with YRCI=0.13 for yellow rust at Kulumsa, SRCI=5.5 for stem rust at Kulumsa, and SRCI=4 for stem rust at Melkasa; EBW222111 with YRCI=1.1 for yellow rust at Kulumsa, SRCI=0.05 for stem rust at Kulumsa, and SRCI=3 for stem rust at Melkasa; EBW222112 with YRCI=1.5 for yellow rust at Kulumsa, SRCI=0.05 for stem rust at Kulumsa, and SRCI=4 for stem rust at Melkasa; EBW222114 with YRCI=3 for yellow rust at Kulumsa, SRCI=4 for stem rust at Kulumsa, and SRCI=6 for stem rust at Melkasa; EBW222125 with YRCI=0.6 for yellow rust at Kulumsa, SRCI=0.05 for stem rust at Kulumsa, and SRCI=6 for stem rust at Melkasa; EBW222142 with YRCI=4 for yellow rust at Kulumsa, SRCI=1.05 for stem rust at Kulumsa, and SRCI=8 for stem rust at Melkasa; EBW222143 with YRCI=3.5 for yellow rust at Kulumsa, SRCI=2.15 for stem rust at Kulumsa, and SRCI=8 for stem rust at Melkasa showed resistance to moderately resistance for yellow rust and stem rust across both locations. The above genotypes probably had more resistance genes for more wheat rust races, which expected across different locations. Therefore, advancing these genotypes to the next stage of breeding pipelines enable breeders to develop and release widely adapted varieties especially for diseases prone areas (Table 4).

The top six high yielder genotypes, which gave seven tons per hectares and above, were EBW222102, EBW222106, EBW222108, EBW222127, EBW222128,

Table 4: Average grain yield, wheat rust disease score, DTH, DTM, PHT, TKW, and HLW of fifty bread wheat lines evaluated across Kulumsa and Melkasa

Entry	Genotype	DTH	DTM	PHT	YRCI	SRCI		TKW	HLW	YLD		Average yield
					KU	KU	MK			KU	MK	
1	Deka	64.50	111.00	87.50	1.50	18.00	17	26.00	66.81	6.22	0.17	3.20
2	EBW222099	65.50	109.75	79.75	1.10	55.00	60	25.50	61.48	5.49	1.07	3.28
3	EBW222100	59.25	107.50	87.75	0.60	29.00	40	32.00	60.61	4.65	1.14	2.89
4	EBW222101	59.50	108.25	84.50	0.70	4.00	30	31.50	64.80	6.86	0.91	3.89
5	EBW222102	60.75	108.50	87.00	0.13	0.05	40	32.00	68.85	7.70	1.23	4.47
6	EBW222103	63.75	109.25	88.75	6.10	30.50	26	25.50	59.16	4.49	1.33	2.91
7	EBW222104	65.00	109.00	82.75	10.50	1.10	22	27.50	62.60	4.04	0.97	2.51
8	EBW222105	61.00	107.75	78.00	21.00	6.10	40	27.00	59.72	3.67	0.95	2.31
9	EBW222106	60.00	109.50	82.25	0.30	7.00	17	32.50	64.93	7.61	1.07	4.34
10	EBW222107	59.75	107.50	87.00	5.50	6.50	34	34.00	63.17	6.33	0.96	3.65
11	EBW222108	59.75	108.00	81.75	0.13	0.40	3	30.50	64.98	7.66	1.28	4.47
12	EBW222109	60.75	108.75	79.25	0.13	5.50	4	30.50	66.25	6.73	0.96	3.85
13	EBW222110	62.25	108.25	88.75	0.05	5.50	17	32.00	65.43	6.47	1.00	3.74
14	EBW222111	69.00	109.50	86.25	1.10	0.05	3	29.00	63.73	6.30	2.00	4.15
15	EBW222112	68.75	80.75	82.25	1.50	0.05	4	29.00	63.19	6.28	1.38	3.83
16	EBW222113	61.75	107.75	81.00	1.20	0.13	27	32.50	63.45	6.05	1.97	4.01
17	EBW222114	63.50	111.00	85.50	3.00	4.00	6	30.50	62.87	5.48	1.95	3.72
18	EBW222115	62.25	108.00	83.75	25.00	1.03	27	24.00	56.89	3.89	1.20	2.54
19	EBW222116	61.50	108.50	83.00	2.50	0.05	17	28.00	62.87	5.45	1.15	3.30
20	EBW222117	66.75	112.00	85.50	2.10	6.00	17	37.00	62.09	5.72	1.69	3.71
21	EBW222118	66.25	108.50	80.75	11.00	45.00	17	31.00	59.68	5.40	0.98	3.19
22	EBW222119	66.50	108.75	83.50	3.10	21.00	40	24.50	57.12	4.98	0.72	2.85
23	EBW222120	66.25	110.00	87.25	3.00	0.23	30	29.50	63.22	5.53	1.64	3.58
24	EBW222121	64.50	109.25	85.75	2.00	0.05	21	29.00	63.30	6.68	0.80	3.74
25	EBW222122	65.00	108.75	87.75	0.20	0.13	30	29.50	61.60	5.83	1.15	3.49
26	EBW222123	62.00	107.00	81.25	25.50	0.05	31	25.00	62.41	5.30	0.89	3.10
27	EBW222124	66.00	108.75	88.75	0.60	0.13	30	27.50	65.66	5.89	1.38	3.63
28	EBW222125	67.25	109.50	86.50	0.60	0.05	6	28.50	64.39	6.67	1.53	4.10
29	EBW222126	60.50	108.50	89.00	14.00	0.05	4	30.50	63.53	5.32	2.30	3.81
30	EBW222127	63.00	109.75	84.75	0.60	40.00	17	28.00	63.72	7.49	1.52	4.51
31	EBW222128	63.75	109.25	84.75	0.60	0.05	30	34.50	66.81	7.37	1.52	4.45
32	EBW222129	62.25	108.75	82.50	0.60	0.05	16	31.00	65.46	5.82	2.15	3.99
33	EBW222130	66.00	108.00	78.00	0.60	22.50	29	30.00	59.11	6.36	1.43	3.89
34	EBW222131	63.25	109.25	87.25	0.60	1.03	45	32.50	65.05	6.21	1.40	3.80
35	EBW222132	64.75	108.00	80.75	3.00	0.30	21	28.50	62.50	5.28	1.04	3.16
36	EBW222133	63.25	107.75	79.25	1.50	0.23	21	29.50	59.41	4.06	1.01	2.53
37	EBW222134	65.50	110.00	90.25	34.00	6.00	30	27.50	61.79	4.48	2.15	3.32
38	EBW222135	65.25	111.25	88.75	1.00	0.20	35	30.00	65.83	6.75	1.44	4.10

Table 4: Continue...

Entry	Genotype	DTH	DTM	PHT	YRCI	SRCI		TKW	HLW	YLD		Average yield
					KU	KU	MK			KU	MK	
39	EBW222136	64.75	111.25	86.50	1.00	37.00	35	34.00	67.92	7.76	1.89	4.82
40	EBW222137	66.75	110.50	81.00	14.00	2.50	24	29.00	60.01	5.88	1.75	3.81
41	EBW222138	60.75	110.50	80.25	0.30	1.03	22	34.50	65.14	6.39	1.66	4.03
42	EBW222139	59.50	110.00	82.25	0.20	0.23	26	30.00	64.46	6.10	1.60	3.85
43	EBW222140	64.25	108.50	77.00	34.00	0.13	11	28.50	63.18	2.81	1.48	2.14
44	EBW222141	61.00	110.50	88.50	9.00	0.05	30	33.50	61.52	6.52	0.89	3.70
45	EBW222142	64.25	109.75	91.50	4.00	1.03	8	31.00	65.85	5.77	2.37	4.07
46	EBW222143	63.50	110.25	81.00	3.50	2.15	8	25.50	62.02	3.94	1.14	2.54
47	EBW222144	60.50	78.75	81.25	10.00	6.00	19	23.00	58.96	3.54	1.80	2.67
48	EBW222145	61.00	108.50	80.75	11.00	16.50	35	27.00	63.02	4.70	0.97	2.83
49	EBW222146	59.25	106.00	80.75	35.00	7.50	40	28.50	61.62	3.38	1.48	2.43
50	EBW222147	60.25	109.00	87.75	1.50	3.50	40	28.50	63.36	6.11	1.50	3.80

KU: Kulumsa; MK: Melkasa; DTH: Date of heading; DTM: Date of maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight; GYLD: Grain yield; Genotype significance for the traits at: ns: non significance, *,**, and *** significant (p=0.05), (p=0.01), and (p=0.001) level of significance, consecutively

and EBW222136. Four of these genotypes: EBW222102, EBW222106, EBW222108, and EBW222128, were highly resistance for stem rust and yellow rust at Kulumsa. The remaining two genotypes, EBW222127 SRCI=40 and EBW222136 SRCI=37, were resistance for yellow rust but susceptible for stem rust at Kulumsa (table 3). Giving high yield in the presence of the disease on the genotypes is linked with adult plant resistance gen APR gene (Solomon et al., 2023; Dinglasan et al., 2022). It is a durable rust resistance,sometime called slow rusting, in which the genotype may be susceptible at seedling stage but give high yield without significant yield loss due to the diseases(Huerta et al., 2020; Singh et al., 2008; Muhammad et al., 2017). All the above six genotypes were resistance for yellow rust at Kulumsa. On the other hand, the five top highly susceptible genotypes for yellow rust, EBW222115 YRCI=25, EBW222123 YRCI=25.5, EBW222134 YRCI=34, EBW222140 YRCI=34, and EBW222146 YRCI=35 delivered lower yields 3.89 t ha^{-1}, 5.3 t ha^{-1}, 4.48 2.81 t ha^{-1}, and, 3.38 consecutively (Table 3).

Most of the time, yellow rust doesn't occur at Melkasa. Stem rust is an important wheat rust disease across low land wheat producing areas like Melkasa. About eighteen genotypes were susceptible for stem rust diseases with coefficient of infection YRCI≥30. Genotypes: EBW222111, EBW222126, EBW222129, EBW222134, and EBW222142 delivered high yield, greater than or equal to 2 t ha^{-1} at Melkasa (Table 3). Their responses for stem rust disease at Melkasa were resistance to moderately resistance except EBW222134, which was susceptible. Stem Rust Coefficients of Infection SRCI for the above genotypes were: EBW222111 SRCI=3, EBW222126 SRCI= 4, EBW222129 SRCI=16, EBW222134 SRCI=30, EBW222142 SRCI=8.

4. CONCLUSION

Genotypes EBW222106 and EBW222108 exhibited significantly higher grain yield than the check variety and showed resistance to moderate resistance against both stem rust and yellow rust at Kulumsa and Melkasa. In addition, genotypes EBW222109, EBW222111, EBW222112, and EBW222125 combined high grain yield with resistance to both diseases across the two locations. These genotypes therefore represent promising candidates for the development of widely adapted, high-yielding, and disease-resistant wheat varieties. Accordingly, their advancement to the next stage of the breeding pipeline is strongly recommended.

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