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Research Article

Pathogenic Variability of Wheat Stem Rust Pathogen (*Puccinia graminis* f. sp. *tritici*) in Hararghe Highlands, Ethiopia

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Wheat is one of the important major crops of Hararghe Highlands. It is third in land coverage and total production after sorghum and maize. However, the wheat stem rust disease is threatening production of wheat in this region. So, this research was conducted with the following objective: to determine the population of *Puccinia graminis* f. sp. *tritici* in Hararghe Highlands. A total of 200 fields were surveyed and stem rust samples were collected and transported to Kulumsa Agricultural Research Center for race analysis. Inoculation of differentials carrying resistance genes Sr24 and Sr-Tmp indicated typical low infection types on all isolates. Isolates EH5, EH8, and EH3 from East Hararghe and WH2, WH1, and WH3 from West Hararghe showed high virulence of infection in all differential lines. Ten (10) races were identified by using *Puccinia graminis tritici* code system: TTGSK, PTJQK, TTSSK, TTKSK, TRSSK, and TTJQK from East Hararghe and TTTSK and TTSQK from West Hararghe zones. Race TTSSK was most frequent (25%) followed by TTKSK (25%) in East Hararghe. Race TTSSK showed 50% frequency of occurrence in West Hararghe zones. The low frequency of occurrences indicated high variability of the races in the survey areas. Therefore, monitoring of populations of pathogens is important for the national and regional research centers. Detection of pathogen virulence evolution and of currently effective resistance genes is necessary and must be applied within a system of resistance gene management.

1. Introduction

Wheat is grown in different parts of Ethiopia and it is one of the most cultivated cereal crops in the country [1, 2]. It is third in the area coverage and total production after tef and maize and in productivity after maize and sorghum [3]. Wheat is highly produced in Ethiopia from the other sub-Saharan Africa [1] with 1,025,310 hectares [3]. It is grown in different agroecologies of Ethiopia [4]. The appropriate areas for the production of wheat are ranged between 1900 and 2700 m.a.s.l. [3]. Wheat requires optimum amount of rainfall with fair distribution during the growth period. In the Ethiopian highlands, there is two-season rainfall distribution: from June to September is the main rainy season (*meher*) while short rainy season (*belg*) falling is from February to April and the amount ranges between 600 and 2000 mm per annum [3]. The crop is cultivated in both seasons though the main crop is in *meher*. Though the seasons differ, the crop growth stage overlaps in most cases. This creates favorable condition for the carryover of stem rust urediospores from one season to another and leads to the development of epidemics in wheat growing areas [5]. Hararghe Highlands are suitable areas for wheat production in the country where it is produced on a total of 50,297 ha. But, the average productivity is 1,214 kg/ha which is far from the average yield (1800kg/ha) of the other regions of the country [6]. Varieties grown in East and West Hararghe zones include Kubsa (HAR1685), Wabe (HAR710), Abola (HAR1522), ET13-A2, Pavon76, and local cultivars [7].

Even if there is large area of wheat production in Ethiopia, the average national yield is 2t/ha [6], which is lower than the average of other African countries and the world average. The same is true for Hararghe areas. The causal agents for the low yield are lower distribution of rainfall, growing of low

yielding wheat varieties, inappropriate agronomic practices, and common wheat diseases like rusts, septoria leaf and glume blotch [8]. In Hararghe Highlands rusts occur annually depending on weather conditions. At higher altitude areas (2400-2700 m.a.s.l) yellow rusts commonly occur every year and stem rusts mainly occur at medium altitude (1900-2400m.a.s.l) [7].

Epidemics of stem rust of wheat often occur in different parts of the world. Resistant cultivars are continuously being developed to prevent such epidemics, although these become susceptible to new pathogenic races sooner or later. A number of physiologic races are known to occur in *P. graminis* f. sp. *tritici* [9]. An epidemic of stem rust of wheat occurred in 1972, in Ethiopia, due to the loss of resistance in cultivar Lakech, which was grown on large area. Similarly, the cultivar Enkoy went out of production in the country after the epidemics in 1992. Currently cultivar Kubsa has become highly susceptible to stem rust. Thus monitoring of the races and their virulence is important part of rust management strategy to avoid crop losses [10–12]. There are limited reports on the distribution of stem rust races in some parts of Ethiopia [13]. Although Hararghe is one of the wheat production areas in the country, there is limited information on the distribution, incidence, severity, and race composition of wheat stem rust disease. Therefore, this study was conducted with the following objective:

(i) To detect *Puccinia graminis* f. sp. *tritici* populations and variability in Hararghe Highlands.

2. Materials and Methods

2.1. Description of the Study Area. The research field survey was conducted in East and West Hararghe zones of major wheat producing districts and the variability study was conducted in Kulumsa Agricultural Research Center. Hararghe is found in the eastern parts of Oromia Regional State, Ethiopia, and it is known by various agroecological zones. East Hararghe zones are characterized by different agroclimatic zones consisting of *dega* (7.67%), *woinadega* (24.54%), and *kolla* (67.76%). It is located at 41° 12′- 42° 53′ East longitude and between 7° 32′- 9° 44′ North latitude, at minimum and maximum elevation of 500 and 3405 m.a.s.l., respectively. The average annual minimum and maximum rainfall is 400 and 1200 mm, respectively. The minimum and maximum temperatures are 13°C and 28°C, respectively. The agroclimatic zones of West Hararghe consist of *dega* (10%), *woinadega* (38%), and *kolla* (52%). It is located at 7° 32′ - 9° 47′ North latitude and between 41° 24′ - 43° 48′ East longitude, at minimum and maximum altitude of 1200 – 3600 m.a.s.l, respectively. The average mean minimum and maximum annual rainfall is 650 – 2000 mm with temperature between 20.5°C and 24°C [7].

2.2. The Pathogen Samples Collection. The pathogen samples were collected from farmer fields and the EWRTN. Sixty nine (69) samples (39 from farmers' fields and 30 from the EWRTN) were collected during survey period of 2016 main cropping season. Sterile scissor was used in each field to cut plant samples. Three to four infected wheat stem tissues of 3 to 4 cm were collected and kept in labeled paper bags and transported to Kulumsa and stored in the refrigerator at 4-5°C until used for variability study. Collected stem rust samples were bulked together depending on their area of collection and type of cultivar from which they were collected. But, samples from EWRTN were not bulked. They were inoculated separately as they came from the field.

2.3. Growing Test Plant in the Greenhouse. Five to six seeds of the susceptible wheat cultivar (Morocco) were planted into 7 cm diameter plastic pots containing soil, sand, and compost mixtures in a 2:1:1 (v/v/v) ratio. The seedlings were allowed to grow until the first leaves fully emerged. During inoculation, leaves were firstly rubbed gently between moistened fingers to remove the waxy layer from the surface which hinders the penetration of the germ tube of the pathogen spores. Bulk spores from each sample were suspended in distilled water with a drop of Tween 20 and then sprayed until runoff using an atomizer. Hands and all materials used during inoculation were disinfested with 70% ethyl alcohol after each inoculation. The seedlings were incubated at relative humidity of about 100% and temperature of about 22°C in a plastic chamber for 24 hours. Then, they were transferred to a greenhouse bench having temperature of 18-27°C. Seedlings were kept for 11-14 days for development of symptoms. Samples with viable spores were selected to multiply inoculums for generation of monopustule isolates on the susceptible cultivar, Morocco.

2.4. Generation and Multiplication of Monopustule Isolates. The samples selected for development of monopustule isolates were again inoculated onto Morocco for generation of monopustule spores. After inoculation, individual leaves with monopustule infection were identified prior to sporulation and then isolated. In case where the pustules were aggregated and no isolated pustule occurred, inoculation was repeated on the susceptible cultivar until separate pustules developed and monopustule isolates were generated. The generated monopustule isolates were then further multiplied on Morocco until sufficient urediospores were collected for differential host test.

2.5. Determination of Pathogen Population in Wheat Stem Rust. Sets of 20 North American differential lines were used to detect race composition. These differentials were obtained from Kulumsa Agricultural Research Center. Five to six seeds of each differential line were grown in 6 cm diameter plastic pots containing soil, sand, and compost in a 2:1:1 (v/v/v/) ratio with three replications. Each set of differential lines was inoculated separately with each monopustule isolate of the pathogen, following the standard procedures [14]. Seedlings were kept in plastic cages with small layers of water at the bottom for overnight at 18-24°C. Then, after incubation, seedlings of differential lines were stored on the greenhouse benches for 11-13 days up to symptom development. Disease was recorded using 0-4 infection scale [14]: (**0**) no uredia or other macroscopic sign of infection, (**;**) no uredia, but hypersensitive necrotic or chlorotic flecks present, (**1**) small uredia surrounded by necrosis, (**2**) small to medium uredia often

Table 1: List of 20 North American stem rust differentials.

Differentials (set, line)	Sr - gene
I	
ISr5-Ra	5
Cns-T -mono-deriv	21
Vernstein	9e
ISr7b - Ra	7b
II	
ISr-11-Ra	11
ISr6- Ra	6
ISr8-Ra	8a
CnSr9g	9g
III	
W2691SrTt-1	36
W2691Sr9b	9b
BtSr30Wst	30
Combination VII	13 +17
IV	
ISr9a-Ra	9a
ISr9d-Ra	9d
W2691Sr10	10
CnsSrTmp	Tmp
V	
LeSr24Ag	24
Sr31/6∗LMPG	31
VPM1	38
McNair701	McN

Sources. Kulumsa Agricultural Research Center (KARC).

surrounded by chlorosis; green islands may be surrounded by chlorotic or necrotic border, (**x**) random distribution of variable-sized uredia on single leaf, (**3**) medium sized uredia that may be associated with chlorosis, and (**4**) large uredia without chlorosis. Infection types with 0, ";", 1, and 2 indicate low infection types while 3 and 4 indicate high infection type [14].

The international system of race nomenclature (*pgt* code) developed by Roelfs and Martens [15] was used for race designation of *P. graminis* f. sp. *tritici*. The 20 differential lines were grouped into four subsets: I, II, III, and IV (Table 1). Host lines with Sr24, Sr31, Sr38, and SrMcN were included as supplementary differential lines as V subset [16–18]. The first set includes the genes, which were the most important in the standard differentials for identifying races. The other sets include some of the more useful genes for race identification that have been identified in recent years. A letter was assigned to each of the possible combinations of interaction types. The pathogenicity of a race was coded using four letters, each indicating its pathogenicity on one set of five. The letters B through T, without the vowels, were used for race designation [15, 19].

The seedlings of all entries were inoculated with spore suspension of monopustule isolates. Each entry was inoculated separately with each monopustule isolate of the pathogen. Seedling inoculation was carried out by spraying spore suspension with an atomizer. The inoculated seedlings were incubated according to the above procedures.

2.6. Experimental Design. All differential sets were arranged in Completely Randomized Design with three replications.

2.7. Race Analysis. The 20 differential lines were grouped into five subsets for race designation. The race nomenclature of *P. graminis* f. sp. *tritici* was analyzed according to five letters systems of nomenclature (Table 2).

3. Results and Discussion

3.1. Races of Puccinia graminis f. sp. tritici Identified from East and West Hararghe Zones. The average infection types of fourteen (14) Pgt isolates detected on 20 North American standard stem rust differential lines were analyzed (Table 3). From fourteen (14) isolates detected (8 Pgt isolates were collected from East Hararghe zone whereas 6 isolates were collected from West Hararghe zone), ten (10) races were identified (Table 4). The eight (8) Pgt isolates of East Hararghe zone were grouped into 6 races (TTGSK, PTJQK, TTSSK, TTKSK, TRSSK, and TTJQK). The highly virulent race was TTKSK (Ug99), race of Sr36 and TTSSK. They were most dominant and widely distributed races with a frequency of 25% while the rest of races were detected with a frequency of 12.5% each. These two races (TTKSK and TTSSK) accounted for almost 50% of stem rust population of East Hararghe zone. The six (6) Pgt isolates were detected and grouped into four (4) races (TTSSK, TTTSK, TTSQK, and TTJQK) from West Hararghe zone. Race TTSSK was predominant with frequency of 50% while the second race occurred with a frequency of 17%. Races TTSSK and TTJQK were identified commonly in both zones. This indicated that isolates of *P. graminis* f. sp. *tritici* in both zones were genetically similar due to geographical proximity, an absence of barriers, and cultivation of similar bread wheat cultivars between two zones.

Race TTKSK (Ug99) which has additional virulence on Sr13+17 was found in East Hararghe alone whereas race TTTSK (new variant of Ug99) with virulence on Sr36 and Sr13+17 occurred in West Hararghe alone. Virulence on Sr-24 and Sr-Tmp was not found by this study. Wheat differential line with a combination of Sr gene 13 and 17 was virulent on most races, but it is avirulent on races TTKSK and TTTSK. So, it is important for breeding program to use these three resistance genes. Similar investigation indicated that stem rust resistance gene Sr24 is effective against most races of *P. graminis* f. sp. *tritici*, including race TTKSK (Ug99), and is widely used in commercial wheat cultivars worldwide [17]. In Kenya, Njoro, out of 28 single-pustule derived isolates of *P. graminis* f. sp. *tritici*, all isolates produced a near immune (IT 0 to ;) on Sr36 and low IT (2+) on line SrTmp, but high (or susceptible) ITs (3 to 4) on all other differential lines except for line combination VII (Sr13+17) [15, 19]. Therefore, this work indicates that it is comparable with the present study which indicates low infection types on Sr24 and SrTmp.

The races identified from two zones were different from each other by single-gene changes and with high frequency

Table 2: The race nomenclature mechanisms (Pgt -code) for the 20 wheat stem rust differential hosts for *Puccinia graminis* f. sp. *tritici* in order of subsets of five.

Pgt Code	Subset[a]	Infection type produced on host lines with Sr[b]			
	I	5	21	9e	7b
	II	11	6	8a	9g
	III	36	9b	30	13+17[c]
	IV	9a	9d	10	Tmp
	V	24	31	38	McN
B		Low	Low	Low	Low
C		Low	Low	Low	High
D		Low	Low	High	Low
F		Low	Low	High	High
G		Low	High	Low	Low
H		Low	High	Low	High
J		Low	High	High	Low
K		Low	High	High	High
L		High	Low	Low	Low
M		High	Low	Low	High
N		High	Low	High	Low
P		High	Low	High	High
Q		High	High	Low	Low
R		High	High	Low	High
S		High	High	High	Low
T		High	High	High	High

[a]Pgtcode consists of the designation for subset I followed by that for subset 2, etc. For examples, race TTTT is virulent (high infection type) on all 20 differential hosts and race BBBB is avirulent on all differential hosts. Low and High infection types indicate an incompatible and a compatible host-pathogen interaction, respectively; [b]Differential sets I to V are described in Roelfs and Martens [15, 16]; [c]IT 2++ produced on combination VII was considered as susceptible as indicated by Jin *et al.* [16].

of occurrence that indicates low variability of pathogen. The low variability is due to geographical similarities of two zones and cultivation of similar bread wheat cultivars between two regions. Race TTSSK was varying from TTKSK with additional virulence on Sr36 and Sr13+17 but both races are similar on the rest of Sr genes. Race TTTSK was similar to TTKSK with additional virulence on Sr13+17, but it was different with additional virulence on Sr36. Most of them are similar with the Sr genes they were virulent on. The changes in virulence between isolates were due to the main process of evolutionary change in *Pgt* populations [20]. Due to lack of molecular analysis on genotypes and R-genes in Ethiopian wheat cultivars in general and particularly in Hararghe areas, the actual evolution of *Pgt* races and their coevolution with resistance in wheat cultivars deployed cannot be determined, respectively. This generally indicates the evolution of pathogen virulence, lineage of races, and the role of host genes in virulence evolution [21, 22].

3.2. Virulence Spectrum of Puccinia graminis f. sp. tritici from East and West Hararghe Zones. The host-pathogen interactions indicated that all East Hararghe isolates of *P. graminis* f. sp. *tritici* were avirulent on differential host lines with Sr genes Sr13+17, SrTmp, and Sr24 (Table 5). Of the three Sr genes, differential genotypes carrying resistance genes Sr24 and SrTmp were resistant to 100% of the pathogen isolates whereas differential genotype carrying resistance gene Sr13+17 was resistant to 75% of the races identified in the areas. A differential line with Sr36 was resistant to 50% of the races while it was susceptible to 50%. Similar to the present study, wheat stem rust resistance gene *Sr36* was known to be effective against most races worldwide [14, 23] but it indicated high infection rates in some countries, including Ethiopia [24, 25].

Likewise, the avirulence/virulence response of wheat stem rust isolates collected from West Hararghe zone showed that differential lines with resistance genes SrTmp and Sr24 were 100% resistant to pathogen races. Differential line having resistance gene Sr13+17 was resistant to 83% of the pathogen races. Differential lines having resistance genes Sr13+17, Sr24, and SrTmp were resistant to Ug99 and to almost all of the other races. Therefore, this study recommended that further analyses of these genes will prove their effective use in Ethiopian wheat production system. It is also important to note that a variant of Ug99, detected in Kenya and virulent to Sr24, was not detected in this study. Generally, comparison of effective resistance genes against the two zones isolates showed that Sr24 and SrTmp were effective against all races of the pathogens.

The number of differential host genes on which the isolates showed avirulence/virulence was presented in Figure 1.

Table 3: The average infection types produced by East and West Hararghe isolates on differential lines for designation of races of *Puccinia graminis* f. sp. *tritici*.

Differential Sets	Sr-genes	Isolates with their infection types (IT)													
		EH1	EH2	EH3	EH4	EH5	EH6	EH7	EH8	WH1	WH2	WH3	WH4	WH5	WH6
I	Sr-5	3	3	4	3	3	4	3	4	3	3	4	3	4	4
	Sr-21	3	2	3	3	3	3	3	3	3	3	3	3	3	3
	Sr-9e	3	3	3	3	3	3	3	3	3	3	3	3	4	3
	Sr-7b	3	3	3	4	3	3	3	4	3	3	3	3	3	3
II	Sr-11	3	3	4	3	3	3	4	4	3	3	4	4	3	4
	Sr-6	3	4	4	3	3	3	3	4	4	3	3	4	3	3
	Sr-8a	3	3	3	3	3	2	4	4	3	3	3	3	3	4
	Sr-9g	4	3	3	3	3	3	4	4	3	3	3	4	4	3
III	Sr-36	2	1	3	4	2	3	2	2	3	3	3	3	3	2
	Sr-9b	3	3	4	3	3	4	3	4	3	3	3	4	4	3
	Sr-30	2	4	4	3	3	4	3	4	3	4	3	3	4	3
	Sr-13+17	2	2	2	1	3	2	2	3	2	3	2	2	1	2
IV	Sr-9a	4	3	3	3	4	3	4	3	3	3	4	4	3	3
	Sr-9d	3	3	3	4	3	3	3	3	3	3	4	4	4	4
	Sr-10	3	2	3	3	3	4	2	3	3	4	3	3	2	2
	Sr-TmP	2	2	2	2	2	2	2	2	2	2	2	2	2	2
V	Sr-24	1	;	1	1	;	1	1	;	1	1	1	;	1	1
	Sr-31	4	4	4	3	3	4	4	3	3	4	3	4	3	3
	Sr-38	4	3	4	3	3	3	3	3	3	3	4	3	3	3
	Sr-McN	4	3	4	3	4	3	4	4	4	4	3	4	4	4

; = No uredia, but hypersensitive necrotic or chlorotic flecks, 1= Small uredia surrounded by necrosis, 2= Small to medium uredia often surrounded by chlorosis; green islands may be surrounded by chlorotic or necrotic borders, 3= Medium sized uredia that may be associated with chlorosis, 4= Large uredia without chlorosis.

Table 4: The number of ineffective Sr-genes and frequency of *Puccinia graminis* f. sp. *tritici* races collected from East and West Hararghe zones in 2016 main cropping season.

Zones	Races	Virulence Spectrum (ineffective Sr resistance genes)	No.	%
East Hararghe	TTGSK	5,21,9e,7b,11,6,8a,9g,9b,9a,9d,10,31,38,McN	1	12.5
	PTJQK	5,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN	1	12.5
	TTSSK	5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN	2	25
	TTKSK	5,21,9e,7b,11,6,8a,9g,9b,30,13+17,9a,9d,10,31,38,McN	2	25
	TRSSK	5,21,9e,7b,11,6,9g,36,9b,30,9a,9d,10,31,38,McN	1	12.5
	TTJQK	5,21,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN	1	12.5
West Hararghe	TTSSK	5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN	3	50
	TTTSK	5,21,9e,7b,11,6,8a,9g,36,9b,30,13+17,9a,9d,10,31,38,McN	1	16.67
	TTSQK	5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,31,38,McN	1	16.67
	TTJQK	5,21,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN	1	16.67

4. Summary and Conclusions

The variability study of pathogen isolates resulted from fourteen (14) virulent isolates that were assigned to ten (10) races. Races such as TTGSK, PTJQK, TTKSK, and TRSSK were unique to East Hararghe zone whereas races TTTSK and TTJQK were unique to West Hararghe zone. But, races TTSSK and TTJQK were common to both zones. The highly virulent and dominant race was TTSSK with a frequency of 25% and 50% in both East and West Hararghe zones, respectively. It is noted that races such as TTKSK and TTSSK in East Hararghe and TTTSK and TTSSK in West Hararghe were known by their aggressiveness in this study. Race TTSSK was varying from TTKSK with additional virulence on Sr36 and Sr13+17 but both races are similar on the rest of Sr genes. Race TTTSK was similar to TTKSK with additional virulence on Sr13+17, but it was different with additional virulence on Sr36. Though there were some differences among races detected in two zones, the frequency of occurrence of the races in the two zones was high for most races. The high frequency of occurrence indicates the low level of pathogenic variability in the surveyed areas. This may be due to the same agroecologies of the two Hararghe zones and cultivation of similar bread wheat cultivars.

Table 5: Avirulence/virulence formula of 14 isolates of *Puccinia graminis* f. sp. *tritici* identified from both East and West Hararghe Zones.

No.	Isolates	Avirulence/Virulence of the Pathogen Isolates	Collection zones
1	EH1	Sr-36,30,13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,9b,9a,9d,10,31,38,McN**	E/Hararghe
2	EH2	Sr-21,36,13+17,10,Tmp,24//**5,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN**	E/Hararghe
3	EH3	Sr-13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN**	E/Hararghe
4	EH4	Sr-13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN**	E/Hararghe
5	EH5	Sr-36,Tmp,24//**5,21,9e,7b,11,6,8a,9g,9b,30,13+17,9a,9d,10,31,38,McN**	E/Hararghe
6	EH6	Sr-8a,13+17,Tmp,24//**5,21,9e,7b,11,6,9g,36,9b,30,9a,9d,10,31,38,McN**	E/Hararghe
7	EH7	Sr-36,13+17,10,Tmp,24//**5,21,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN**	E/Hararghe
8	EH8	Sr-36,Tmp,24//**5,21,9e,7b,11,6,8a,9g,9b,30,13+17,9a,9d,10,31,38,McN**	E/Hararghe
9	WH1	Sr-13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN**	W/Hararghe
10	WH2	Sr-Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,13+17,9a,9d,10,31,38,McN**	W/Hararghe
11	WH3	Sr-13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN**	W/Hararghe
12	WH4	Sr-13+17,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,10,31,38,McN**	W/Hararghe
13	WH5	Sr-13+17,10,Tmp,24//**5,21,9e,7b,11,6,8a,9g,36,9b,30,9a,9d,31,38,McN**	W/Hararghe
14	WH6	Sr-36,13+17,10,Tmp,24//**5,21,9e,7b,11,6,8a,9g,9b,30,9a,9d,31,38,McN**	W/Hararghe

Bold: numbers/letters indicate the virulence of the isolates on Sr genes; E = East, W = West; EH= East Hararghe, WH= West Hararghe.

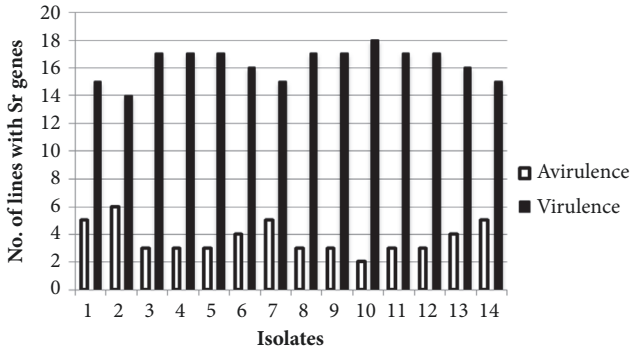

Figure 1: Response of differential lines to isolates of *P. graminis* f. sp. *tritici*. Isolates: 1= EH1; 2=EH2; 3=EH3; 4=EH4; 5=EH5; 6=EH6; 7=EH7; 8=EH8; 9=WH1; 10=WH2; 11=WH3; 12=WH4; 13=WH5; 14=WH6.

The avirulence/virulence reaction of the isolates of the pathogen collected from East and West Hararghe zones during the main season indicated that there was low variability between the pathogen isolates. The host differential lines like Sr13+17, Sr24, and SrTmp were resistant to most pathogen isolates. The resistance genes SrTmp and Sr24 were resistant to 100% of the pathogen isolates whereas differential line with resistance gene Sr13+17 was resistant to 79% of the pathogen isolates. The differential host carrying resistance gene Sr36 was effective to 43% of the isolates. Therefore, it will be helpful to another investigator to include resistance gene found in differential host lines Sr24, SrTmp, and Sr13+17 into the breeding program to manage the stem rust disease, especially by focusing on the race Ug99 which becomes virulent on different types of resistance genes and to newly emerging variant of the pathogen races. Therefore, the Ethiopian Institute of Agricultural Research and other government and nongovernment organizations must monitor and evaluate the pathogen populations over time to reduce further virulence evolution and to ensure that currently effective resistance genes are applied within a system of resistance gene management strategy.

Abbreviations

CSA: Central Statistical Authority
EH: East Hararghe
EWRTN: Ethiopian Wheat Rust Trap Nursery
HAR: Holeta Agricultural Research
KARC: Kulumsa Agricultural Research Center
Sr: Stem rust resistance gene
WH: West Hararghe.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Disclosure

There was no commercial fund provided for the research work. However, Wolkite University and Haramaya University research vice president office facilitates the fund for sample preparation and analysis service charge only.

Conflicts of Interest

We declare that we have no conflicts of interest.

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