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Short Communication

The Resistance of Exotic Wheat Germplasm to Stripe Rust (*Puccinia striiformis* f. sp. *tritici*) under Nature Infection at Dera Ismail Khan, Pakistan

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Abstract. An experiment comprising of 49 exotic wheat germ plasm accessions was conducted at Arid Zone Research Institute, Dera Ismail Khan, Pakistan under rainfed condition during 2013-14 for their resistance against stripe rust disease. The trial was laid out in randomised complete block design with three replications. All entries were planted in a four-row plot with 3 m for row length and 25 cm for space among rows. A local susceptible check was repeatedly sown after every 10 test entries. The crop was maintained under rainfed conditions. Results revealed that all the exotic genotypes were genetically divergent in response to stripe rust disease. The disease score ranged from very highly susceptible to very highly resistant. Among 49 exotic lines, 27 exhibited from very highly resistant while 10 were susceptible to very highly susceptible.

Keywords: wheat germ plasm, stripe rust, *Puccinia striiformis* f. sp. *tritici*, rainfed condition

Wheat is cultivated on an area of about 21.465 million acres with production of 24.303 million tonnes annually (PBS, 2014). Stripe rust (*Puccinia striiformis* f. sp. *tritici*) is world-wide threat to wheat production, causing 10 to 70% grain losses depending on susceptibility of the cultivar, earliness of the initial infection, rate of disease development and duration of disease (Chen, 2005). Afzal *et al*. (2009) and Rattu *et al*. (2009) determined variability for yield based-partial resistance against stripe rust among wheat breeding lines. Mirza *et al*. (2003) concluded that up to 50% improvement in wheat yield has been achieved by introducing new high yielding cultivar in Pakistan. It is the genetic makeup of a variety that is expressed in a favourable environment and produces different yields in different environments (Khan *et al*., 2011). They had also screened high yielding and rust resistant wheat lines out of CIMMYT germ plasm. Rahman *et al*. (2012) released a high yielding rust resistance wheat variety BARS-09 selected from CIMMYT nursery in Pakistan. Therefore, using host plant resistance is the most economical, effective and ecologically sustainable method for controlling the disease. To diversify the resistance in wheat breeding programmes, introducing wheat grem plasm from other countries and identifying new resistance source are widely used in breeding practices. In the present study, some exotic wheat lines were evaluated under rainfed condition to identify the best source of resistance against stripe rust for further utilization in wheat breeding programme.

Forty nine exotic wheat genotypes received from CIMMYT International Wheat Improvement Network (Table 1) were planted in a triplicated randomised complete block design at Arid Zone Research Institute, Dera Ismail Khan, Pakistan in November, 2013. A local susceptible check (CBN-47) was also involved for properly assessment of disease austerity in field conditions. Each line was planted in four rows of 3 meters long plots having row to row distance of 25 cm. The crop had received enough rain during heading and grain formation stage which ultimately helped the intensification of disease pressure in field conditions. The temperature remained low from December (6 °C) to February (7 °C) while, total rain fall (118 mm) occurred in March (50 mm) and April (68 mm) during the entire cropping season.

The modified Cobb's scale (Peterson *et al*., 1948) was used to assess the wheat genotypes for adult plant stem rust resistance based on the percentage of the leaf area covered with stem rust pustules (Table 2). Disease data was recorded when susceptible check showed about 30% infection during the evaluation seasons.

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Table 1. CIMMYT wheat germ plasm accessions used in experiment at Arid Zone Research Institute, Dera Ismail Khan, Pakistan

Entry*	Cross name
1	FRANCOLIN #1/WBLL1
2	BAJ #1/TECUE #1
3	MUTUS/AKURI
4	BECARD/KACHU
5	WBLL1*2/4/SNI/TRAP#1/3/KAUZ*2/TRA P//KAUZ/5/BAJ #1
6	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU
7	WBLL1*2/BRAMBLING/5/BABAX/LR42//BABAX*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
8	MUU/5/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/6/WBLL1*2/4/SNI/TRAP #1/3/KAUZ*2/TRAP//KAUZ
9	FRANCOLIN #1//WBLL1*2/KURUKU
10	BAJ #1/AKURI
11	FRANCOLIN #1//WBLL1*2/BRAMBLING
12	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP //KAUZ*2/5/DEMAI 4
13	WBLL1/4/BOW/NKT//CBRD/3/CBRD/5/WBLL1*2/TUKURU
14	SUP152/BLOUK #1
15	MUTUS/ROLF07
16	WBLL1/FRET2//PASTOR*2/3/MURGA
17	KA/NAC//TRCH/3/DANPHE #1
18	FRET2/TUKURU//FRET2/3/MUNIA/CHTO//AMSEL/4/FRET2/TUKURU//FRET2
19	WBLL1*2/4/BABAX/LR42//BABAX/3/BABAX/LR42//BABAX
20	KA/NAC//TRCH/3/DANPHE #1
21	EMB16/CBRD//CBRD/4/BETTY/3/CHEN/AE.S Q//2*OPATA
22	FRET2/TUKURU//FRET2/3/MUNIA/CHTO//AMSEL/4/FRET2/TUKURU//FRET2
23	ROLF07*2/5/REH/HARE//2*BCN/3/CROC/AE.SQUARROSA (213)//PGO/4/HUITES
24	TILILA/JUCHI/4/SERI.1B//KAUZ/HEVO/3/AMAD
25	BAV92//IRENA/KAUZ/3/HUITES/4/2*ROLF07
26	KA/NAC//TRCH/4/MILAN/KAUZ//DHARWAR DRY/3/BAV92
27	KA/NAC//TRCH/3/VORB
28	OB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAU /FRET2/7/PASTOR//MILAN/KAUZ/3/BAV92
29	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAU6/FRET2/7/PASTOR//
30	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KA UZ/6/FRET2/7/MINO
31	METSO/ER2000//MUU
32	CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*JANZ/6/SKAUZ/BAV92
33	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
34	SNLG/3/EMB16/CBRD//CBRD/4/KA/NAC//TRCH
35	SLVS/3/CROC_1/AE.SQUARROSA(224)//OPATA/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/2*KA/NAC//TRCH
36	C80.1/3*BATAVIA//2*WBLL1/3/EMB16/ CBRD//CBRD/4/CHEWINK #1
37	1447/PASTOR//KRICHAUFF/5/2*SERI*3 /RL6010/4*YR/3/PASTOR/4/BAV92
38	METSO/ER2000//MONARCA F2007/3/WBLL1*2/KKTS
39	BERKUT/MUU//DANPHE #1
40	QING HAIBEI/WBLL1//BRBT2/3/PAURAQ
41	KA/NAC//TRCH/3/DANPHE #1
42	WORRAKATTA/2*PASTOR//DANPHE #1
43	METSO/ER2000/5/2*SERI*3//RL6010/4 *YR/3/PASTOR/4/BAV92
44	MILAN/KAUZ//DHARWAR DRY/3/BAV92/4/PAURAQ
45	1447/PASTOR//KRICHAUFF/3/PAURAQ
46	DHARWAR DRY
47	HIDDAB
48	SUNCO.6/FRAME//PASTOR/3/PAURAQ
49	CHAM 6
50	Local Check " CBN-47"

*wheat genotypes have been arranged according to their merit of resistance against stripe rust disease.

Table 2. A modified disease rating scale for recording stripe rust in wheat genotypes

Symptoms	Infection (%)	Rating
No visible signs or symptom	0	VHR
Necrotic and/or chlorotic flecks; no sporulation	5	HR
Necrotic and/or chlorotic blotches or stripes; no sporulation	6-10	R
Necrotic and/or chlorotic blotches or stripes; trace sporulation	11-15	MR
Necrotic and/or chlorotic blotches or stripes; light sporulation	16-25	MS
Necrotic and/or chlorotic blotches or stripes; intermediate sporulation	26-40	MS to S
Necrotic and /or chlorotic blotches or stripes; moderate sporulation	41-70	S
Necrotic and/or chlorotic blotches or stripes; abundant sporulation	71-90	HS
Chlorosis behind sporulating areas; abundant sporulation	91-100	VHS

VHR = very highly resistance; HR = highly resistant; R = resistant; MR = moderately resistant; MS = moderately susceptible; MS to S = moderately susceptible to susceptible; S = susceptible; HS = highly susceptible; VHS = very highly susceptible.

A set of 49 wheat genotypes was studied to evaluate their response against stripe rust disease. A local cultivar (CBN-47) was also involved as susceptible check for properly assessment of disease severity in the field conditions. The crop had experienced severe drought stress up to month of February as it was maintained under rainfed conditions. The frequent rain (50 to 68 mm in March and April, respectively), high relative humidity (67 to 83%) coupled with cool temperature (12 - 24 °C in March, and 18 - 23 °C in April) during heading and grain formation stage had created quite favourite conditions for stripe rust infection and spread on wheat. Imported germ plasms were screened under high disease pressure in field conditions. Therefore, a narrow disease rating scale (0-100) was used for most opposite evaluation and rating of genotypes. Recorded data revealed highly significant variability among the genotypes regarding their response to stripe rust disease. The reaction of various entries ranged from very highly resistant to very highly susceptible depending upon the genetic makeup of genotypes. Out of 49 test entries, 11 remained very highly resistant, 4 highly resistant, 12 resistant, 3 moderately resistant, 2 moderately susceptible, 8 moderately susceptible to susceptible, 1 susceptible, 2 highly susceptible and 6 were very highly susceptible to yellow rust disease (Table 3). Similar results have been reported by Afzal *et al*. (2009), who determine significant variability for field based-partial resistance against stripe rust among 188 wheat breeding lines. Rattu *et al*. (2009) have also found three resistant lines against leaf and yellow rust among 29 wheat candidate lines with desirable Relative Resistance Index (RRI). The expression of resistance and production of different yields in different environments depends upon the genetic makeup of a variety (Khan *et al*., 2011).

Mirza *et al*. (2003) reported that, up to 50% yield improvement in wheat has been attained through introducing new high yielding disease resistance cultivars in Pakistan. Kolmer (2003) and Oelke and Kolmer (2004), suggested that prior to exercising any gene pyramiding approach, it is necessary to identify the effective and genetically diversified sources of resistance. Host resistance is the most economical, effective and ecologically sustainable method of controlling the disease (Vanzetti *et al*., 2011). Rajaram *et al*. (1996) suggested simultaneous evaluation of germ plasm for drought tolerant and disease resistance genotypes. In present studies, all the entries have shown quite inimitable and incomparable response to disease. The entries No. 1 to 27 possessing resistant genes against stripe rust disease may be conceivably exploited; either through direct selection and/or involving them in wheat hybridization programme for development of stripe rust resistant varieties.

Table 3. Disease scoring of CIMMYT wheat accession at AZRI, Dera Ismail Khan, Pakistan

Entry	Disease infection	Genotypic reaction
1	0 J	VHR
2	0 J	VHR
3	0 J	VHR
4	0 J	VHR
5	0 J	VHR
6	0 J	VHR
7	0 J	VHR
8	0 J	VHR
9	0 J	VHR
10	0 J	VHR
11	0 J	VHR
12	3.3 IJ	HR
13	3.3 IJ	HR
14	3.3 IJ	HR
15	3.3 IJ	HR
16	6.7 HIJ	R
17	6.7 HIJ	R
18	6.7 HIJ	R
19	6.7 HIJ	R
20	6.7 HIJ	R
21	6.7 HIJ	R
22	6.7 HIJ	R
23	6.7 HIJ	R
24	6.7 HIJ	R
25	6.7 HIJ	R
26	10 HIJ	R
27	10 HIJ	R
28	13 HI	MR
29	13 HI	MR
30	15 H	MR
31	17 GH	MS
32	17 GH	MS
33	27 FG	MS to S
34	28 F	MS to S
35	30 EF	MS to S
36	33 EF	MS to S
37	33 EF	MS to S
38	33 EF	MS to S
39	37 EF	MS to S
40	40 E	MS to S
41	70 D	S
42	83 C	HS
43	87 BC	HS
44	93 ABC	VHS
45	97 AB	VHS
46	100 A	VHS
47	100 A	VHS
48	100 A	VHS
49	100 A	VHS
50	100 A	VHS

Genotypes sharing common letter(s) are statistically similar at 5% probability level.

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