



RESEARCH PAPER

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Detection of durable resistance against stripe rust and estimating genetic diversity through pedigree analysis of candidate wheat lines

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Key words: Stripe rust, *Puccinia striiformis* f.sp. *tritici*, Durable resistance, Coefficient of Parentage.

<http://dx.doi.org/10.12692/ijb/12.3.24-35>

Article published on March 15, 2018

Abstract

The emergence and rapid spread of virulent races of wheat stripe rust has driven a search for sources of resistance for durable resistance. This study was conducted to identify sources of stripe rust resistance among wheat advanced lines. Seventy two wheat accessions were evaluated for their resistance against stripe rust isolates at the seedling stage in a controlled environment. Forty eight lines that exhibited intermediate and susceptible reactions were further tested in 2013-14 and 2014-15 for their slow rusting characteristics in field conditions. Slow rusting resistance at the adult-plant stage was assessed on the basis of two parameters i.e. final disease severity (FRS) and area under disease progress curve (AUDPC). Thousand Kernel Weight (TKW) was also measured to assess the yield potential of slow rusting accessions. The results revealed that wheat lines PR109,11FJS310, 11FJS308,11C023, BARS 09, NRL-0913, NR-403 had low values of FRS, AUDPC and desired 1000 Kernel Weight were regarded as good slow rusting lines. High correlations were observed between different parameters of slow rusting. Among the slow rusting lines 11FJS310 and 11FJS308 had high kernel weight in both seasons. Estimation of genetic diversity revealed alarming situation of narrowing genetic base especially among the genotypes developed under the shade of same umbrella. This issue must be addressed with attention to accomplish preferred targets. The slow rusting lines identified from different clusters could be used to breed for stripe rust resistance.

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Introduction

Three rusts are the most important diseases in wheat in various parts of the world that damage wheat production significantly (Shah *et al.*, 2014; Safavi, 2012). Rusts in wheat are among the most studied of plant diseases due to the impact that have had on wheat production. (Afzal *et al.*, 2015). These studies lead to discoveries of Principles of plant breeding for disease resistance (Biffen, 1905; Stakman and Levine, 1922; Flor, 1956; Van der Plank, 1963).

Among three cereal rust diseases wheat stripe rust caused by *Puccinia striiformis* f.sp. *tritici* continues to be a restraining element of most significant importance in world wheat production across intercontinental sites (Brown, 2015). Currently, stripe rust is spreading rapidly in a region stretching from Turkey, Syria and northern Iraq to southern Uzbekistan; the potential for crop loss is in the billions of dollars (Singh *et al.* 2004). International wheat production remains exposed from periodic stripe rust epidemics (ICARDA, 2014). Yield losses caused by stripe rust have been documented from 10-70% in various wheat producing regions (Chen, 2005). Yellow rust is economically important disease capable of attacking 70% of the wheat area in the country (Yahyaoui and Rajaram 2012) and has caused 13 epidemics after independence (Welling, 2011). Four major yellow rust epidemics were recorded in 1978, 1997-98 and 2005 and caused considerable losses to the Pakistan economy (Shah *et al.*, ..(2014

Various control options are available to reduce losses caused by stripe rust (ICARDA, 2011). New, more effective fungicides like Tilt, Quadris, Stratego, Headline, and Quilt are available to control yellow rust (Chen 2005). The economical and the most biologically friendly management approach to mitigate losses to stripe rust disease would be the development of resistant wheat cultivars (Solh *et al.*, 2012).

Wheat varieties resistant to rusts have been developed through and in collaboration with International Maize and Wheat Improvement Centre

(CIMMYT) (Sehgal *et al.*, 2016) and national wheat improvement research programme in the country (Imtiaz and Rauf, 2014) but most of the varieties lack durable resistance and became prone just after their introduction (Ellis *et al.*, 2014) usually, as a result of new virulent pathotypes and deployment of the similar R-gene (s) in wheat cultivars (Admassu *et al.* 2012). In contrast slow rusting resistance is characterized by a reduced rate of epidemic development, despite a compatible host-pathogen interaction (Caldwell, 1968; Parlevliet, 1978; Parlevliet & Van Ommeren, 1975; Rubiales & Niks, 1995). Therefore, a cultivar that only has slow rusting resistance to stripe rust will display susceptible infection-type responses throughout the entire life cycle of the plant. Slow rusting resistance can be measured in the field by recording disease severity at weekly intervals and then calculating the area under the disease progress curve (AUDPC) (Wilcoxson *et al.*, 1975). This type of resistance is characterized by the combined effect of slow rusting components.

The genetic diversity in wheat (*Triticum aestivum* L.) land races also confers resistance to rust diseases (Van Ginkel & Rajaram, 1992; Hare, 1997; McIntosh *et al.*, 1998; VanDijk *et al.*, 1988; Zhang, 1995). Development of high yielding wheat varieties with narrow genetic base and influenced by farmer/consumer preference has led to cultivating fewer varieties over the large area creating genetic vulnerability to stress not only in Pakistan but in other parts of the world.

This has been observed in Pakistan when the leading cultivars Pak 81 and Pirsabak 85 were affected seriously by the emergence of virulence for the stripe rust genes Yr9 and Yr7 respectively (Ahmad *et al.*, 1991; Ahmad, 2000). The coverage of about 70% of the wheat area by the variety "Inqilab" in the country and PBW343 in the neighboring country carrying the similar genetic resistance gene (Yr 27) against stripe rust created a serious risk that favored virulence change causing epidemic. Current national focus has shifted to breed for durable resistance bearing the wide varietal genetic base.

Current study was conducted with an objective to identify durable sources of resistance characterized by slow rusting behaviour against stripe rust. The concept is based on the theory of live and let live. The genetic variability assessment of wheat advanced material in the country obtained from pedigree based distance between advanced materials will provide a basis for selection.

Material and methods

Source of seed

The test material was collected from wheat programme, NARC, Islamabad consisting of wheat candidate lines evolved in different institutes of the country. The list of test entries is enlisted in Table 1.

Source of Inoculum

A complex stripe rust race (mixture of races) was obtained from CDRP, NARC, Islamabad, for inoculation.

Methodology

Screening at seedling stage

Trial was conducted under glasshouse conditions at CDRP Sunny Bank Murree following the protocol of Shah *et al.*, 2014. Infection types were recorded three weeks after inoculation using a 0-9 scale (McNeal *et al.*, 1971), when susceptible the check "Morocco" was showing maximum infection. Material was categorized into resistant, intermediate resistant, and susceptible following Rizwan *et al.*, 2007.

Field screening

The test material comprised forty eight wheat genotypes (Carrying susceptible or moderately susceptible response at seedling stage) were used including the susceptible check cultivar, Morocco. The trial was laid out following Hovmøller, 2007. Fertilizers and supplementary agronomic practices were applied following the departmental recommendations for wheat production.

Inoculation

Inoculations were made in the evening to provide optimum darkness for germination of urediospores. The inoculum was carrying virulence to yellow rust resistance genes Yr1, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18 and Yr27.

Every experimental unit was inoculated twice by using a complex race of stripe rust fungus at tillering stage. The urediospores suspended in a lightweight mineral oil at the concentration of 1.5 mg l⁻¹ mineral oil (0.005 kg ha⁻¹) were sprayed over leaves using an ultra-low volume turbo-air sprayer (Shah *et al.*, 2014). Before inoculation, the experimental plots were irrigated to enhance humidity at micro level. "Morocco" the spreader rows of the susceptible check in between each ten genotypes was planted to establish maximum possible rust. The experimental plots were irrigated repeatedly for four weeks to boost disease severity after second inoculation (executed two weeks following the first inoculation).

Assessment of partial resistance

Partial resistance was assessed through different measures. i.e., final rust severity (FRS) (Parlevliet, 1985), area under disease progress curve (AUDPC) (Wilcoxson *et al.*, 1975). Grains were counted and weighed using conventional balance and were renovated to thousand kernel weight (TKW).

Statistical analysis

Data were analyzed by using statistical procedure, "analysis of variance" (Steel and Torrie, 1988) to determine the level of significant difference between genotypes. Duncan's Multiple Range Test ($P = 0.05$) was used to compare the genotypic means. Coefficient of correlation was done using SPSS software (SPSS, 2005) to determine the relationship between disease parameters.

Estimation of genetic diversity based on Coefficient of Parentage (COP)

Germplasm consisting of Seventy Two wheat candidate lines were evaluated for their relatedness by pedigree. Pedigree information of released cultivars was obtained from the Wheat Research Institute Faisalabad (WRI), the CIMMYT website and USDA germplasm. Initial information about the pedigree was obtained from WRI and CIMMYT and the pedigree abbreviations were decoded with CIMMYT standard catalogues. Afterward the pedigree of parents and grandparents was expanded by searching their pedigree over the website developed by CIMMYT (www.wheatpedigree.net/).

Full sketch pedigree of each cultivar was drawn and saved in separate file. The parental land races of all cultivars were scored following Almanza-Pinzon *et al* (2003). Cultivar pedigree relationships and Euclidian distance matrix was estimated from these scores using principal component analysis, statistical software Minitab 15.

Results

Seedling reaction

The greenhouse experiment revealed that the bread wheat lines differed in their reaction to the stripe rust isolates. The susceptible check, Morocco, displayed infection type 3+ at the seedling stage (data not shown). Among the 72 entries that showed susceptible and mixed reactions, 48 genotypes were advanced and evaluated for slow rusting resistance.

Table 1. List of entries screened at seedling and adult stage.

S/#	Entry	Institute	Parentage/ pedigree
1	11C007	BARI CHAKWAL	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2
2	11C023	BARI	SOKOLL/EXCALIBUR
3	11C008	BARI	MILAN//PRL/2*PASTOR
4	DH-31	BARI	GA-2002/CHAKWAL-50 (Double haploid)
5	6C002	BARI	SOKOLL
6	11C022	BARI	SOKOLL//SUNCO/2*PASTOR
7	06FJS33	BARS	PASTOR//MILAN/KAUZ
8	08FJ26	BARS	Barani-83/Bhakkar-02
9	10FJ01	BARS	03FJ22/04FJS35
10	10FJ16	BARS	8970/94-R30
11	BARS 09	BARS	PFAU/SERI//BOW
12	11FJ01	BARS	02FJ13 / KUKUNA
13	11FJ02	BARS	INQ-91 / 03FJ13//ATILA
14	11FJ07	BARS	INQ-91 / 03FJ13//ATILA
15	11FJ08	BARS	99FJ03 / 03FJ26
16	11FJ12	BARS	99FJ03 / PAK-81
17	11FJ27	BARS	REEHAB-2
18	11FJ28	BARS	BABAGA-3
19	11FJ39	BARS	HAAMA-2/QAFZAH-16
20	11FJ45	BARS	GOUBARA-1/2*SOKOLL
21	11FJS38	BARS	D67.2/PARANA
22	11FJS39	BARS	D67.2/PARANA
23	11FJS30	BARS	H45/4/KRICHAUFF/FINSI/3/URES/PRL//BAV92
24	11FJS31	BARS	VORB/SOKOL
25	11FJS33	BARS	VORB/SOKOL
26	11FJS37	BARS	EGA BONNIE ROCK/4/MILAN/KAUZ//PRINIA/3/BAV92
27	11FJS38	BARS	KRICHAUFF/2*PASTOR//2*SOKOLL
28	11FJ09	BARS	CH-86 / CH-50
29	109384	RARI Bahawalpur	UP2338/V4012
30	99172	RARI	KAUZ/PASTOR//V.3009
31	99346	RARI	MH-97/FAREED-06 (5)
32	99114	RARI	THELIN/2* WBLL-1//V.3006
33	DN-93	ARI- DI Khan	ESDA/ / ALTAR 84 / AE.AQUARROSA (211) /3/ ESDA/4/..
34	CT 09137	NIFA-Peshawar	SERI.1B*2/3/KAUZ-2/BOW//KAUZ/4/
35	SRN 09111	NIFA	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07
36	V-09082	WRI Faisalabad	INQ.91/FRET.2
37	V-09087	WRI	V-87094/2*INQ.91/3/SH88/PAK81/MH97
38	V-10104	WRI	INQ.91/AUQAB-2000
39	V-10110	WRI	KAUZ/CMH77A-308////BAU/3/INQ-91
40	V-11160	WRI	KAUZ//ALTARP194624/AE.SQUARROSA (409)//BCN/6/2*KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITE

41	TW9600	AZRI Bhakkar	BK-2002XV1076
42	TW9608	AZRI	BK2002 X LU26S/AE. cylindricaD/PAK-81
43	SD-998	NIA Tandojam	TJ-83 X 4085/3
44	NIA-MN-08	NIA	SARC-11 X Khirman
45	CIM-04-10	NIA	PBW343*2/KONK
46	ESW-9525	NIA	KAUZ/Gen
47	PR-103	CCRI-Pirsabak	WBLL1*2/4/YACO/PBW65/65/3/KAUZ*2/TRAP//KAUZ
48	PR-106	CCRI	MTRWA92.161/PRINIA/5/SERI*3//RLO6010/4*YR/3/PASTOR/4/
49	PR-107	CCRI	MTRWA92.161/PRINIA/5/SERI*3//RLO6010/4*YR/3/PASTOR/4/
50	V-11005	WRS-Tandojam	MILLION/S87230//BABAX
51	NR-413	NARC-Islamabad	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1
52	NR-421	NARC	CROC_1/AE.SUARROSA (210)//INQALAB 91*2/KUKUNA/3/PBW343*2/KUKUNA
53	NR-409	NARC	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7
54	NR-419	NARC-Isd	OASIS/KAUZ//4*BCN/3/2*PASTOR/4/T.SPELTAPI348449/5/BAV92/3/OASIS/ SKAUZ//4*BCN/4/PASTOR/6/WBLL1*2/CHAPIO
55	UAF-9452	Uni. of Agri. Fsd	LU26S X Inq. 91
56	99172	RARI – Bahawalpur	KAUZ/PASTOR//V.3009
57	DN-84	ARI- DI Khan	BYJ/COC/PRL/BOW/3/URES/JUN/KAUZ
58	09FJ34	BARS - Fatehjang	ERA F 2000/4/ FONCHAN #3 / TRT"S"//VEE#9/3/COOK/VEES//DOVE"S/SERI
59	NRL-0913	NIFA - Peshawar	PRL/SARA//TSI/VEE#5/3/WBLL1
60	v-11183	WRI - Faisalabad	SOKOLL//PBW343*2KUKUNA/3/ATTIL/ PASTOR
61	v-12001	WRI	WAXWING/4/SNI/TRAP#1/3/LAUZ*2/TRAP //KAUZ
62	PR-105	CCRI-Pirsabak	MILAN/S87230//BABX
63	PR-108	CCRI-Pirsabak	WHEAR/KRONSTAD F2004
64	PR109	CCRI-Pirsabak	PBW343*2/KUKUNA/5/CNO79//PF70354/MUS/3/PASTOR/4/BA V92
65	NIA-MB-02	NIA Tandojam	Mutant_Sarsabz (250 Gy)
66	NR-403	NARC-Islamabad	KBIRD//INQALAB 91*2/TUKURU
67	NR-407	NARC	UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/OASIS/KAUZ//4*BCN/3/2* PASTOR
68	NR-439	NARC	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/T.DICOCCON PI94625/AE.SUARROSA (372)//SHA4/CHIL/5/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1
69	NR-411	NARC	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN
70	NR-402	NARC-	KBIRD//INQALAB 91*2/TUKURU
71	AUR-0810	UAAR – Rawalpindi	WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP/KAUZ
72	AZRC-2	AZRC – Quetta	TRACHA 'S' //CMH76-252/PVN'S'

Field-Based Assessment of Partial Resistance to Yellow Rust

To assess variability among wheat breeding lines for durable resistance, parameters used as criteria to identify genotypes with partial resistance under field conditions included final rust severity, AURPC and 1000 grain weight. Results regarding these parameters are described as under.

Assessment of genetic diversity in Wheat advanced material in Pakistan

Cluster analysis was performed to elucidate the genetic diversity among wheat accessions collected from various research institutes of Pakistan.

Dendrogram obtained from the analysis showed that the accessions could be divided into two clusters at 12 dissimilarity index, wherein one cluster (A) comprised only eighteen genotypes while the remaining 55 accessions pertain to another cluster (B). However, there was a split in this big cluster wherein we observed 14, 8, 6, 21 and 5 accessions in cluster I, II, III, IV and V respectively (Fig. 1).

It was revealed that material evolved under the management of same research directorate was uniform genetically. In the pedigree of seventy two wheat candidate lines PASTOR was most frequent (13.28%) whereas, KAUZ (8.59%), INQ-91 (7.81%)

SOKOLL (7.03%), Ae. AQUARROSA (211) (6.25%), one hundred and twenty eight contributing 57.78
 WBLL-1(5.46%), KUKUNA (4.68%) and MILAN percent.
 (4.68%) were among other common parents out of

Table 2. Data of various parameters studied during 2013-14 and 2014-15.

Genotype	FDS		AUDPC		1000 Grain Weight	
	2013-14	2014-15	2013-14	2014-15	2013-14	2014-15
11C007	35.000 KL	33.33 GHI	329.3U	318.7 V	97 J	93.50G
11C023	28.33LMN	23.333 JK	238.3VW	214 Z	153 F	152.00D
DH-31	45.00 HIJ	36.67 FGH	509.0MNO	456 L	83 MN	79.67IJ
6C002	46.66 HI	36.67 FGH	517.8LMN	463 L	76 P	73.17KL
11C022	71.7 BCD	60.00 BC	666.3GHI	609.3 G	54 Z	51.00TU
06FJS3013	43.33 HIJ	43.33 EF	475.3NOPQ	429 MNO	60 V	56.00QRS
08FJ26	43.33 HIJ	43.33 EF	403.5RS	351.7 T	81 NO	78.83IJ
10FJ16	61.67 EF	56.667 CD	700.5FGH	652.7 F	54 Z	51.83STU
BARS 09	21.67 N	20.00 KL	289.0UV	234.7 Y	98 J	94.33G
11FJ02	71.7 BCD	66.67 AB	749.7DEF	723.7 D	49 a	45.67V
11FJ07	70.000 CD	66.67 AB	742.7DEF	705 E	49 a	47.67UV
11FJ27	43.33 HIJ	43.33 EF	468.7NOPQ	426.7 NOP	67 S	63.17OP
11FJ28	56.67 FG	53.333 CD	564.0KL	516 J	60 V	56.50QRS
11FJS308	26.67 MN	20.0 KL	247.5VW	189 a	197.7 B	192.83 B
11FJS309	38.33 JK	33.3GHI	402.2S	350.3 T	75.3 PQ	72.33KL
11FJS310	12.50 O	11.7 LM	136.5X	123 b	228.7 A	219.17 A
11FJS348	41.67 IJK	36.7 FGH	468.0NOPQ	376 S	87.7 L	82.67HI
99172	43.33 HIJ	40.0 FG	517.2 LMN	461.3 L	60.67 V	53.17RST
99114	70.000 CD	60.0 BC	615.0IJK	556.7 I	59.7 VW	57.00QR
DN-93	70.0 CD	66.667AB	665.3GHI	605.7 G	56.3 XY	53.50RST
CT 09137	66.7 DE	56.67 CD	703.8EFG	654 F	59.7 VW	56.33QRS
V-10104	71.67BCD	66.667AB	834.7B	754.3 B	60.67 V	55.33QRST
V-10110	71.67BCD	66.67 AB	774.5CD	699.3 E	57.7 WX	55.33QRST
V-11160	75.00BC	73.333 A	806.8BC	754.7 B	59.7 VW	56.33QRS
TW96010	78.33 AB	73.333A	742.0DEF	698.7 E	56.33 XY	54.17RST
SD-998	56.67 FG	50.000 DE	529.8LM	474.3 K	63.67 U	63.33OP
NIA-MN-08	46.667HI	40.000 FG	460.2OPQ	403 Q	63.67 U	59.83PQ
CIM-04-10	61.667 EF	56.667 CD	609.3JK	585 H	59.7 VW	54.33RST
PR-103	41.667IJK	36.67 FGH	427.0 QRS	384.7 RS	75.67 PQ	70.33 KLM
PR-107	45.00 HIJ	36.67 FGH	431.7QRS	388.7 R	45.33 b	45.17V
NR-413	48.3HI	43.3 EF	484.2MNOP	432 MN	64.67 TU	64.33 NOP
NR-409	45.0 HIJ	36.67 FGH	462.3OPQ	420.7 OP	71.67 R	70.33 KLM
NR-419	50.000 G	43.33 EF	500.3MNOP	438 M	83.67 M	79.33 IJ
UAF-9452	41.67 IJK	36.667FGH	455.0PQR	417.7 P	66.67 ST	66.33MNO
DN-84	41.66 IJK	36.7 FGH	405.8RS	350.3 T	187.33 C	166.67C
NRL-0913	21.667 N	20.000 KL	234.8 W	237.7 Y	139.67 G	132.33E
v-12001	41.67 IJK	40.00 FG	487.3MNOP	452.3 L	73.67 QR	70.00 KLM

PR-105	38.333 JK	33.3 GHI	401.7S	344.3 T	120.67 I	110.67F
PR-108	70.00 CD	66.67 AB	752.5 DE	739 C	54.7 YZ	52.33RSTU
PR109	12.50 O	8.33 M	125.8 X	111.7 c	175.33 D	170.50 C
NR-403	26.67 MN	26.67 IJK	284.7UVW	284.7 X	134.67 H	128.33E
NR-407	35.000 KL	33.33 GHI	384.2S T	350 T	90.67 K	85.33H
NR-439	41.67IJK	36.66 FGH	477.5NOPQ	428 MNOP	71.67 R	68.83 LMN
NR-411	41.67 IJK	36.67 FGH	400.0S	380.7 RS	165.67 E	147.83D
NR-402	61.667 EF	56.667 CD	652.0HIJ	566.7 I	64.33 U	59.67PQ
AZRC-2	30.00 LM	30.00 HIJ	333.7TU	331 U	79.67 O	74.83 JK
AUR-o810	26.67 MN	26.67 IJK	316.5U	306.7 W	86 L	80.50 HI
Morocco	85.00 A	73.33 A	1974.5 A	1688.3 A	27 c	23.50 W

FDS=, Final Disease severity

AUDPC=Area under disease progress curve.

Discussion]

Screening wheat advanced material in search of durable sources of resistance against stripe rust

Present study was conducted to assess the levels of partial resistance present in spring bread wheat candidate lines to stripe rust. The disease might be favored by moist conditions that prevailed during

2014 with increased rainfall humidity and lower temperature as compared to the environmental conditions persisted during 2015. Watkins (2005) also concluded greater risk for stripe rust when there are above average rainfalls and reduced chances of disease under dry conditions.

Table 3. Correlation among traits studied.

	FDS	AUDPC
AUDPC Year 1	0.7769**	
AUDPC Year 2	0.7988**	
1000 Grain Weight Year 1	-0.6938**	-0.6114**
1000 Grain Weight Year 2	0.66972**	-0.6324**

The results also suggest that the genotypes characterized by a slow disease development (low DS and AUDPC), could be considered as partially resistant for stripe rust infection. Both the DS and AUDPC seem to be reliable estimators for partially resistance in wheat to stripe rust but DS may be preferable because it is more economical (less labour-intensive and less time-consuming) than AUDPC. Epidemic growth rate seems to be unsuitable as an estimator for partial resistance because it showed a non-significant correlation with epidemic factors (DS and AUDPC).

Breeding lines with slow rusting traits are expected to possess genes that confer partial resistance which is more durable type of resistance (Parlevliet 1988) and it has been emphasized recently (Singh *et al* 2004). In the present study a high correlation was found between FRS and AUDPC which is consistent with previous studies made by Li *et al.* (2006). Genotypes showed variations in the level of slow rusting resistance in our study, implying that there could be some diversity in the number of genes involved, and/or the size of their effect, in conferring this type of resistance. Singh *et al.* (2000) showed that high yielding cultivars of bread wheat that were nearly

immune to leaf rust and stripe rust could be developed by accumulating four or five slow rusting resistance genes through intercrossing parents that show intermediate disease levels. Several slow rusting durums identified in this study are being utilized in the same way as demonstrated by Singh *et al.* (2000) to develop high yielding cultivars with high levels of slow rusting resistance to leaf rust. Broers (1989) also found a highly significant positive correlation between DS and AUDPC and reported that DS and AUDPC are the best estimators of partial resistance in wheat to leaf rust than epidemic growth rate.

Assessment of genetic diversity in wheat

Research work have exposed that reduced genetic diversity also happened attributable to exploitation of analogous type of parents or carrying similar pedigree in the development of transgressed generation. Therefore estimation of the pedigree-based distance between cultivar delivers valuable perception in the germplasm (Martin *et al.* 1995; Barrnet *et al.* 1998; Solemeni *et al.* 2002). Positive correlation between the molecular and pedigree based genetic diversity have been indicated in many studies (Martin *et al.* 1995; Barnett *et al.* 1998). Analysis of COP is one of the most common techniques of pedigree-based diversity analysis (Miranda *et al.*, 2007) provides worthwhile genetic information for the conservation of diversity, tracing genetically related phenomena from ancestor to ancestor, and the selection of parents in crop improvement programs through crossing (Souza *et al.*, 1994).

Plant breeding since the early 1900s has influenced food production intensely on and will continue to play an active role in the world food security (Borlaug 1983; Tester and Langridge 2010). However, crop uniformity across the farm fields, genetically vulnerable to stresses, occupies the status of side effect of plant breeding (Day 1973; Duvick 1984; Vellve 1993; Tripp 1996; Keneni *et al.* 2012). Occurrence of epidemics such as the Irish potato blight in the 1840s and the U.S.A. corn blight in the 1970s are examples of such risks (National Academy of Sciences 1972; Ullstrup 1972).

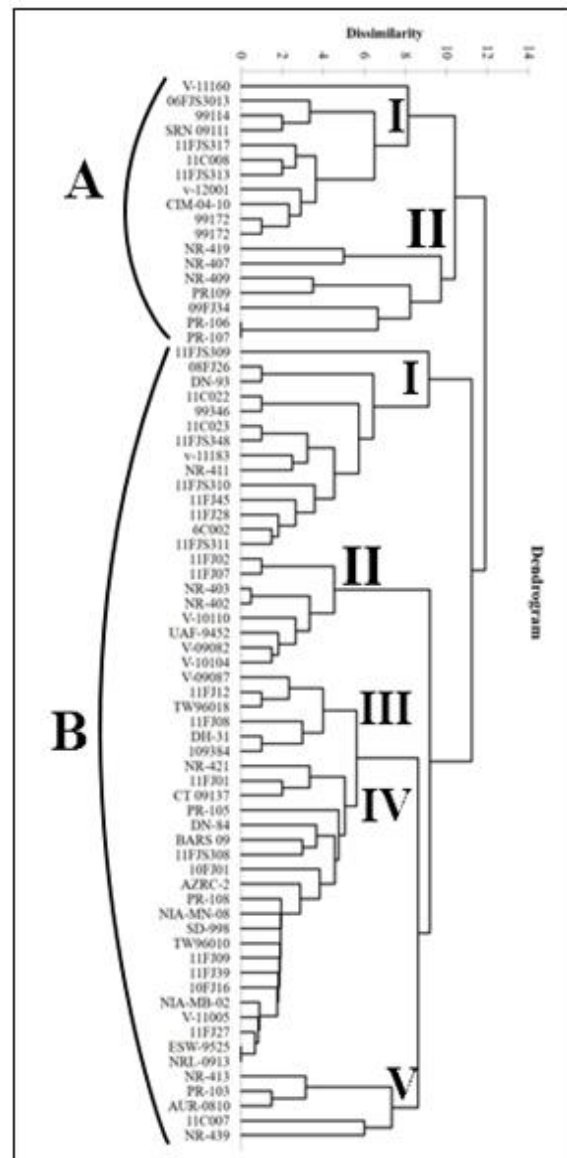


Fig. 1. Dendrogram showing clustering of wheat accessions collected from various research institutes of Pakistan.

The threat of the enormously infectious new race of stem rust Ug99 from East Africa to genetically homogeneous wheat derived from IB/IR translocation on wide area is currently evident (Borlaug 2007; Afzalet *et al.* 2015; Babiker *et al.* 2015). Pakistani wheat germplasm was judged on several criteria. i.e. contribution of land races per cultivar, total number of unique land races utilized during particular decade, proportion of unique land races to the total land races, pedigree distance between the cultivar and decades. Varietal development in Pakistan was

exclusively dependent on the introduction, acclimatization or transgressive segregation of CIMMYT breeding stock during the post green revolution period.

In most studies genetic diversity of wheat has been observed to be relatively lower than that of other self-pollinated crops like soybean and rice. This seems to be relevant observation as the common wheat (*T. aestivum*) which went through massive breeding pressure, was evolved from two progenitors, tetraploid *T. turgidum* and diploid *T. tauschii*, in limited number of accidental crosses (Reif *et al.*, 2005; Dvorak *et al.*, 1998; Talbert *et al.*, 1998). Wang and Lu (2006) have found very high genetic diversity among 100 parental lines of Indica hybrid rice in China. Similarly, huge genetic diversity among 651 Chinese soybean cultivars released from 1923 to 1995 has been observed by Cui *et al.* (2000). Similar results were found in 86 Japanese soybean cultivars indicating a potentially high degree of diversity in Japanese soybean breeding (Zhou *et al.*, 2000).

Conclusion

This study signifies identification of durable sources of resistance with broader genetic base and diversity patterns among advanced material of wheat. The information generated can direct future breeding strategies by enabling valuable crossing and/or introduction of new germplasm for better combinations of minor rust resistance genes, broadening of the genetic base, and reducing of the genetic vulnerability to the gene pool.

The issue of diversity in Pakistani wheat germplasm has argued by various author(s) (Khan *et al.* 2005; Iqbal *et al.* 2009; Zeb *et al.* 2009; Khan *et al.* 2010; Ahmed *et al.* 2010). These studies made variable conclusions based on their germplasm sample. Khan *et al.* (2005) showed narrow genetic base of Pakistani wheat germplasm. Contrastingly some studies have also indicated significant genetic diversity in cultivated wheat germplasm (Rauf *et al.* 2010). At CIMMYT, efforts are under way to expand the diversity of wheat germplasm by introgression from wild relatives (Warburton *et al.* 2006).

It seems that conventional introductions would continue from CIMMYT and diversity of Pakistani wheat germplasm will be regulated by the efforts at CIMMYT. These results may be applicable to India, which shares several cultivars with similar pedigree due to introduction from CIMMYT. Genetic diversity in the material under investigation showed interesting situation. In the country wheat research institutes have been established with a mandate to evolve wheat varieties for cultivation under specific environment. Study revealed that despite the fact genotypes evolved through introduction from CIMMYT where diversity is focused with deliberation but impact is not realized in our circumstances. This situation is attributed to the fact that our directorates select the material to achieve their targets leading to genetic uniformity in material. This is an undesired situation and must be addressed to improve output.

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