Evaluation of Synthetic Hexaploid Wheats (*Triticum turgidum* L. x *Aegilops tauschii* L.) and their Durum Parents for Stripe Rust (*Puccinia striiformis* Westend. f. sp. *tritici* Erikson) Resistance

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Abstract. In this study, resistance to stripe rust (*Puccinia striiformis*) of 95 lines of Elite 1 synthetics, 33 lines of Elite 2 synthetics, and 51 lines of their durum parents were evaluated at the seedling stage in glasshouses at Murree, Pakistan, and at the adult plant stage under field and glasshouse conditions. Bulk inoculum collected during 2004-2005 cropping season was used in all studies. Fifty six entries (58%) of Elite 1 synthetics, 15 entries (45%) of Elite 2 synthetics, and 16 (11%) durum parental entries were found resistant at the seedling stage. In the field and glasshouse the adult plant resistance was evaluated by estimating the area under disease progress curve (AUDPC). Thirty three percent of Elite 1, 30% of Elite 2, and 41% of their durum parents had AUDPC ranging between 0-10 percent. Most of the genotypes resistant at the seedling stage were also resistant at the adult plant stage. Few lines possessed partial resistance as these lines had high infection types at the seedling stage, but low AUDPC at the adult plant stage. Resistance from *Aegilops tauschii* was identified only at seedling stage in those synthetic hexaploid wheats in which the contributing durum parent was susceptible. The synthetic hexaploid wheats found resistant in this study are potential candidates for bread wheat improvement.

Additional keywords: Yellow rust, AUDPC,

Resumen. En este estudio se evaluó la resistencia a la roya lineal (*Puccinia striiformis*) de 95 líneas sintéticas elite (grupo 1), 33 líneas sintéticas elite (grupo 2), y 51 líneas de sus líneas progenitoras de duros, en estado de plántula bajo condiciones de invernadero en Murree, Pakistán, y en estado de planta adulta bajo condiciones de campo e invernadero. El inóculo colectado en masa durante el ciclo de cultivo 2004-2005 se utilizó en todos los estudios. Cincuenta y seis entradas (58%) del grupo de sintéticos elite 1, 15 (45%) del grupo de sintéticos elite 2 y 16 (11%) de los progenitores de duros fueron resistentes durante el estado de plántula. La Resistencia en planta adulta se evaluó en campo y en el invernadero mediante la estimación el área bajo la curva del progreso de la enfermedad (ABCPE). Treinta tres porciento del grupo elite 1, 30% del grupo elite 2 y 41% de sus progenitores de duros tuvieron un ABCPE que fluctuó entre 0-10%. La mayor parte de los genotipos resistentes en la etapa de plántula también fueron resistentes en la etapa de planta adulta. Pocas líneas tienen resistencia parcial ya que tuvieron altos niveles de infección durante la etapa de plántula, pero bajo ABCPE en la etapa de planta adulta. La resistencia de *Aegilops tauschii* fue identificada solamente en la etapa de plántula en aquellos trigo sintéticos hexaploides donde el progenitor de duros era susceptible. Los trigos sintéticos hexaploides resistentes en este estudio, son candidatos potenciales para utilizarse en el mejoramiento de trigo.

Palabras clave adicionales: Roya amarilla, ABCPE,

Yellow rust or stripe rust of wheat is caused by the biotrophic fungus *Puccinia striiformis* Westend. f. sp. *tritici* Erikson. It is a common disease in many areas around the world. Most severe epidemics have been observed in cool or high altitude climates (Roelf *et al*., 1992; Zadok, 1961), but the fungus is also well adapted in countries where wheat is grown during relatively mild winter seasons with warm summers (Johnson, 1992). Tremendous losses of wheat production have been associated with yellow rust when epiphytotics occurred under favourable conditions (Yahyoui *et al*., 2002). Traditionally, crop losses from pathogen are avoided by breeding for resistance, by cultural practices, or by chemical control (Line,

1982). Use of resistant sources however, is the most suitable method. Fungicide use is costly and is a burden for many growers, especially in developing countries. Fungicide usage is known to create health problems for users; adversely affects the environment, and results in fungicide resistant strains of the pathogen. Hence, growing cultivars with adequate levels of durable resistance seems the best control strategy. Breeding for yellow rust resistance usually involves the use of major, race specific resistant genes (Robbelen and Sharp, 1978). However, the resistance obtained is often elusive, as almost all the described Yr genes have been overcome by one or more of the many yellow rust races (Beaver and Powelson, 1969; Johnson *et al*., 1969; Stubbs, 1972). The virulence factors of yellow rust races appear to increase in a stepwise manner (Stubbs, 1985) since rust fungi are living organisms with their own genetic make-up and ecological requirements. The genetic make-up of the pathogen cannot be changed at will; however, that of the host can be exploited or altered to the pathogens disadvantage. Wheat breeders and pathologists have identified resistant germplasm from wild wheat relatives and gene transfers have been made from several *Aegilops*, *Agropyron*, and *Triticum* species (McIntosh, 1988, 1992; Sharma, 1995). To sustain durable resistance to stripe rust, sources conferring resistance should be regularly identified and incorporated, as biotic stresses are a dynamic trait and volatile in change. Often genetic variability becomes limiting, so there is a need to widen search horizons beyond the readily available conventional germplasm resources. There has been growing interest over the last decade and a half amongst researchers to exploit the diploid wheat progenitor species (Mujeeb-Kazi, 2006). The D genome diploid *Ae. tauschii* L. (2n=2x=14), has received priority usage for wheat improvement (Mujeeb-Kazi *et al*., 1996; Mujeeb-Kazi, 2003a) either by bridge crossing or via direct crosses (Gill and Raupp, 1987). In bridge crossing, durum wheat cultivars (2n=4x=28, AABB) when crossed by *Ae. tauschii* accessions yield 2n=3x=21 ABD composition hybrids which upon doubling give fertile 2n=6x=42 AABBDD products called synthetic hexaploid wheats (SH). This resource of over one thousand SH´s has come into global use selectively following its production in CIMMYT, Mexico (Mujeeb-Kazi, 2006). Extensive use from this germplasm globally over the last decade has been the exploitation of an elite 1 set of 95 synthetics, and an elite 2 set of 33 entries The objective of this study was to evaluate the genetic diversity for stripe rust resistance in Elite 1 and 2 sets of synthetic hexaploid wheats (*Triticum turgidum* L. x *Ae. tauschii*) along with their durum cultivar parents.

MATERIALS AND METHODS

Host germplasm. Fifty one lines of *Triticum turgidum* (2n=4x= 28, AABB), 95 lines of synthetic hexaploid Elite 1 set and 33 lines of synthetic hexaploid Elite 2 set were used in screening against stripe rust. The germplasm was obtained from CIMMYT's Wheat Wide Crosses program. Their production has been elucidated in protocols described by Mujeeb-Kazi and Hettel (1995).

Pathogen/inoculum. The bulk inoculum collected during the 2003-2004 cropping season was used. This inoculum had virulence for genes Yr1, Yr3, Yr4, Yr5, Yr6, Yr7, Yr8, Yr9, Yr18, YrSp, YrSD, and YrCV. These genes were determined by inoculating the standard differential set with the bulk inoculum collected across the wheat growing areas within Pakistan. The differential comprised of 8 lines of the world set, 9 lines of the European set, and 16 near isogenic lines around "Avocet".

Seedling evaluation test. The test germplasm was planted in disposable pots under glasshouse conditions at Murree, Pakistan. Four to six week old seedlings were inoculated with a urediospore suspension at a concentration of approximately 2000 spores per drop of the bulk inoculum suspended in a mixture of 30:70 mineral oil: petroleum ether. Inoculated seedlings were placed in open air for two hours allowing the oil to evaporate. Plants were then transferred to a dew chamber set at 10°C with 16 h/8 h light/dark photoperiod for 48 h. Seedlings were then transferred to a glasshouse maintained at 18-20°C.

Disease scoring for seedlings. Three weeks after inoculation infection types were recorded using a 0-9 scale (McNeal *et al*., 1971) when the susceptible check was showing maximum infection. Plants having infection types 0-3 were considered as resistant, those with 4-6 as intermediate resistant, and from 7-9 as highly susceptible.

Adult plant screening. Adult plant screening was carried out both under glasshouse and field conditions. Glasshouse screening. Synthetics of Elite 1, 2, and and their durum parents, together with the susceptible check "Morocco" were evaluated for adult plant resistance under glasshouse conditions at Murree. The germplasm including Morocco was grown in plastic pots. Each pot contained 5 plants per entry. Plant growing prolifically in the glasshouse were inoculated when most of the entries were at the flag leaf stage *i.e*. Zadoks growth stage 55 (Zadoks *et al*., 1974) by spraying them with a fine mist of water containing spores of stripe rust. The spraying was done uniformly with a spray concentration that equated approximately 1 g/Liter and tween 20. Following incubation, plants were kept in a growth chamber maintained at approximately 8°C, with 98% relative humidity for 48 h. Plants were then returned to the glasshouse. Field evaluation. The germplasm was planted in 0.5 m rows which were 60 cm apart. Stripe rust epiphytotic was created approximately 6 weeks after planting by inoculating spreader rows and lines to be screened with a urediospore suspension (mineral oil:ether;30:70).

Disease scoring for adult plant resistance. Data for disease severity and infection type was recorded twice following the modified Cobb Scale (Peterson *et al*., 1948) at 10-day intervals. The first disease notes were taken when the susceptible check Morocco had reached 100% severity. Disease severity data were used to calculate the area under disease progress curve

(AUDPC) using the computer program developed at CIMMYT. The relative percentage of area under disease progress curve for each entry was calculated by setting AUDPC of "Morocco" as 100%.

RESULTS

Glasshouse evaluation for seedling resistance. Different infection types (ITs) were recorded within the SHs of Elite 1, 2, and their durum parents (Fig. 1). Fifty eight percent of Elite 1 SHs, 45% of Elite 2 SHs, and 31% of the durum parents were resistant at the seedling stage. Several synthetic hexaploid wheats were identified with good seedling resistance to stripe rust. Their resistance originated from either *Ae. tauschii* accessions or from the *T. turgidum* cultivar genomes. Of special interest was the observation that for a number of synthetic hexaploids the resistance observed seems to be from the *Ae. tauschii* parent as their durum parents were susceptible at the seedling stage (Table 1).

Adult plant screening. Elite 1 and 2 synthetic hexaploids with their durum parents were also tested for adult plant resistance under field conditions in Islamabad, plus glasshouse conditions at Murree. Thirty four percent entries from Elite 1, 33% from Elite 2, and 41% from the durum parents had less (0-10%) AUDPC's (Fig. 2). Only these entries were considered resistant. Few lines possessed only adult plant resistance (Table 2). Most synthetic entries however, possessed both seedling/adult plant resistance which are preferred candidates for use in bread wheat breeding programs (Table 3).

DISCUSSION

Close progenitors of wheat residing in same gene pool are being used to improve wheat for many biotic and abiotic stresses (Mujeeb-Kazi, 2006). In wheat breeding programs priority was assigned to *Ae. tauschii* (Coss) Schmalh, syn. *Ae. squarrosa*, 2n=2x=14, DD, because of its genetic proximity to the D genome of wheat (Kimber and Feldman, 1987). It is further attributed with a wide range of resistances/tolerances to biotic and abiotic factors (Cox *et al*., 1990; Gill *et al*., 1986; Knott, 1979; Valkoun *et al*., 1990). This D genome genetic diversity could be used via the synthetic hexaploid route of bridge crossing (Mujeeb-Kazi, 2001), or via direct crosses (Gill and Raupp, 1987) between elite but specific trait susceptible *T. aestivum* L. cultivars with resistant *Ae. tauschii* accessions. Although several genes from *Ae. tauschii* for leaf rust (*Puccinia triticina* Ericks.) (Gill and Raupp, 1987) stem rust (*Puccinia graminis* Pers.:Pers. *tritici* Eriks. and E. Henn.) (Kerber and Dyck, 1979) and yellow rust (McIntosh *et al*., 1988) have been transferred by direct crossing of *Ae. tauschii* accessions with bread wheat cultivars, synthetic hexaploid wheats have been receiving more priority in practical breeding as this route enables the breeders to harness the A and B genome diversity of the synthetic as well. For a successful trait transfer, *Ae. tauschii* should not only possess the stress resistant/tolerance, but it must also express in the wheat back-ground whether it is durum or an elite bread wheat. Sometimes the accession of *Ae. tauschii* is resistant, but its resistance may not express in the derived synthetic hexaploid under the influence of the durum genome due to suppression (Ma *et al*., 1995). Similarly, if resistant *Ae. tauschii* accessions are directly crossed with bread wheat that resistance also may not express in the bread wheat background again due to suppression by the A and B genomes of bread wheat. Accordingly, the CIMMYT program strategy that concentrated on bridge crossing was to cross elite durums with all *Ae. tauschii* accessions at random and

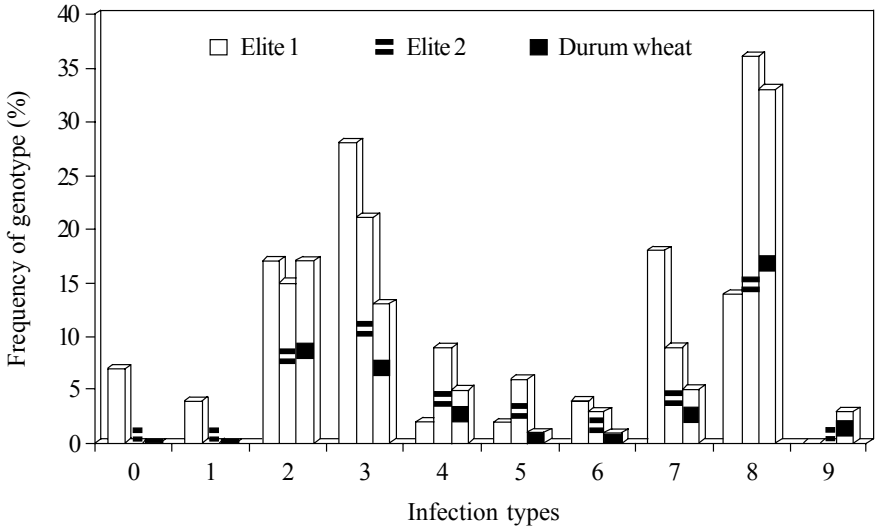

Fig. 1. Frequency distribution for infection types of durum wheat (*Triticum turgidum*), Elite 1 and Elite 2 synthetic hexaploids (*Triticum turgidum* x *Aegilops tauschii*).

Table 1. Sources of seedling resistance (0-9 scale) to stripe rust (*Puccinia striiformis* f. sp. *tritici*) identified in *Triticum turgidum* and synthetic hexaploid wheats (*Triticum turgidum* x *Aegilops tauschii*) tested under glasshouse conditions.

Sr. No.	Accession No.	Genotype	Seedling IT[x] range	Source of seedling resistance[y]
Triticum turgidum				
1		68.111/RGB-U//WARDRESEL/3/STIL	2	
2		68.111/RGB-U//WARD	2	
3		SNIPE/YAV79/DACK/TEAL	2	
4		DECOY1	2	
5		GAN	2	
6		SCOOP_1	2	
7		LCK59.61	2	
8		LARU	2	
9		CPI/GEDIZ/3/GOO//JO/CRA	3	
10		STERNA-DW	3	
11		SCAUP	3	
12		TKSN1081	2	
13		YARMUK	3	
14		STY-US/CELTA//PALS/3/SRN_5	3	
15		ACONCHI89	3	
16		YAV_2/TEZ	3	
17		6973/WARD.7463//74110	3	
ELITE I synthetic hexaploid wheats				
18	6	CROC-1/AE.SQUARROSA (205)[z]	0	At
19	37	68.111/RGB-U//WARD/3/FGO/4/ RABI/5/AE.SQUARROSA (629)	0	At
20	45	68.111/RGB-U//WARD/3/FGO/4/ RABI/5/AE.SQUARROSA (878)	0	At
21	47	68.111/RGB-U//WARD/3/FGO/4/ RABI/5/AE.SQUARROSA (882)	0	At
22	54	CETA/AE.SQUARROSA (895)	0	At
23	83	DOY1/AE.SQUARROSA (458)	0	Td and At
	24	66BOTNO/AE.SQUARROSA (625)	1	At
25	74	YAV_2/TEZ//AE.SQUARROSA (895)	1	At
26	77	RASCON/AE.SQUARROSA (312)	1	At
27	91	CROC-1/AE.SQUARROSA (517)	1	At
28	49	68.111/RGB-U//WARD/3/FGO/4/ RABI/5/AE.SQUARROSA (890)	2	At
29	50	CROC-1/AE.SQUARROSA (518)	2	At
30	52	ALTAR 84/AE.SQUARROSA (BANGOR)	2	At
31	89	STY-US/CETA //PALS/3/SRN_5 /4/ AE.SQUARROSA (502)	2	Td and At
32	90	ALTAR 84/AE.SQUARROSA (502)	2	At
33	3	ALTAR 84/AE.SQUARROSA (192)	3	At
34	5	ALTAR 84/AE.SQUARROSA(198)	3	At
35	16	ALTAR 84/AE.SQUARROSA (219)	3	At
36	28	68.111/RGB-U//WARD/3/ AE.SQUARROSA (316)	3	At
37	31	68112/WARD//AE.SQUARROSA (369)	3	At
38	34	DOY1/AE.SQUARROSA (511)	3	Td and At
39	41	68.111/RGB-U // WARD RESEL /3/ STIL/4/AE.SQUARROSA (783)	3	Td and At
40	75	ARLIN/AE.SQUARROSA (283)	3	At
41	76	FALCIN/AE.SQUARROSA (312)	3	At
42	84	GREN/AE.SQUARROSA (458)	3	At
43	93	CETA/AE.SQUARROSA (1024)	3	At
44	12	DVERD-2/AE.SQUARROSA (1027)	3	At
45	36	DOY1/AE.SQUARROSA (515)	3	Td and At

Table 1. Continuation...

Sr. No.	Accession No.	Genotype	Seedling IT[x] range	Source of seedling resistance[y]
46	12	ROK/KML//AE.SQUARROSA (214)	3	At
47	35	68.111/RGB-U//WARD/3/ AE.SQUARROSA (511)	3	At
48	38	FGO/USA2111//AE.SQUARROSA (658)	3	At
49	42	YAR/AE.SQUARROSA (783)	3	At
50	44	68.111/ RGB-U//WARD/3/FGO /4/ RABI/5/AE.SQUARROSA (878)	3	At
51	94	CETA/AE. SQUARROSA (1027)	3	At
ELITE 2 synthetic hexaploid wheats				
52	13	DOY1/AE.SQUARROSA (1027)	3	Td and At
53	16	CETA/AE.SQUARROSA (533)	3	At
54	18	CETA/AE.SQUARROSA (1031)	3	At
55	22	CROC_1/AE.SQUARROSA (212)	2	At
56	24	ARLIN_1/AE.SQUARROSA (430)	2	At
57	31	CETA/AE.SQUARROSA (417)	2	At

[x]IT = Infection types.
[y]Td = *Triticum turgidum*; At = *Aegilops tauschii*.
[z]*Aegilops tauschii* accession entry in the Wheat Wide Crossing Programmes working collection at CIMMYT, Mexico. (*Aegilops squarrosa,* syn. *Ae. tauschii* or *Triticum tauschii*).

generate a large germplasm stock since several global stresses were to be addressed. The synthetics produced upon screening would provide data around two categories: a) Dual resistance where the durum parent and the corresponding synthetic hexaploid entry showed resistance. As the *Ae. tauschii* accession seed was not available for screening we cannot categorically say whether the D genome parent contributed to the observed resistance in the synthetic. b) When the synthetic was resistant and its durum parent susceptible. This category provided unequivocal support that the resistance was a contribution of diversity that had expressed from the *Ae. tauschii* accession. The latter option was the focus in this study, and in most of the entries, sources of yellow rust resistance were *Ae. tauschii* as their durum parents were susceptible. We have identified 34 lines of synthetic hexaploid Elite 1 and 6 lines of Elite 2 wheats in which *Ae. tauschii* is the source of stripe rust resistance. The durum parents involved in the above resistant SH wheats were susceptible at the seedling stage. In the synthetics DOY1/*Ae. squarrosa* (458), STYUS/CETA//PALS/3/SRN_5/

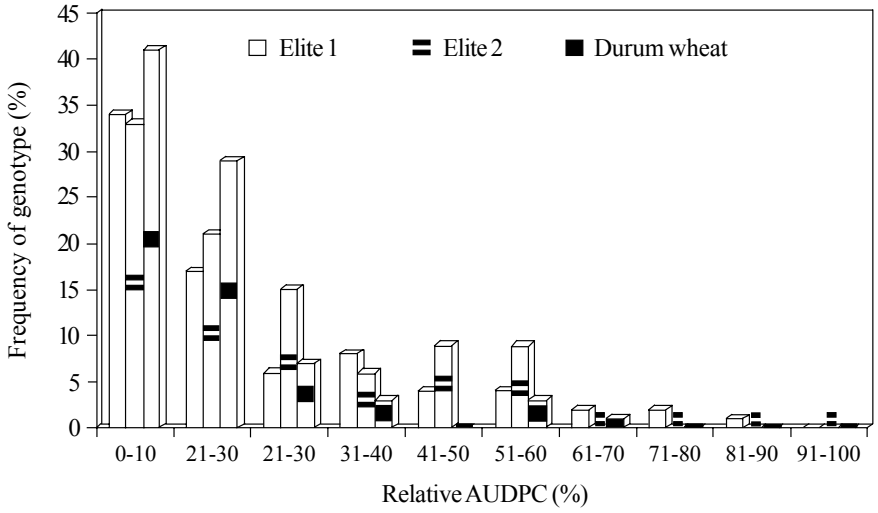

Fig. 2. Frequency distribution (%) for relative area under the disease progress curve (AUDPC) of Elite 1, 2 synthetic hexaploids (*Triticum turgidum* x *Aegilops tauschii*), and durum wheats (*Triticum turgidum*).

Table 2. Synthetic hexaploid (*Triticum turgidum* x *Aegilops tauschii*) Elite 1, 2. and durum wheat (*Triticum turgidum*) entries with good adult plant resistance to stripe rust (*Puccinia striiformis* f. sp. *tritici*).

Sr. No.	Accession No.	Genotype	Infection types	Relative AUDPC
Elite 1 synthetic hexaploid wheats				
1	1	ALTAR 84/AE.SQUARROSA (188)[z]	7	6
2	4	ALTAR 84/AE.SQUARROSA (193)	8	6
3	17	ALTAR 84/AE.SQUARROSA (220)	8	8
4	26	ACO89/AE.SQUARROSA (309)	7	10
5	48	SORA/AE.SQUARROSA (884)	8	6
6	55	GAN/AE.SQUARROSA (180)	8	1
7	61	GAN/AE.SQUARROSA (408)	8	<1
8	82	68.111/RGB//WARD/3/ AE. SQUARROSA (454)	6	<1
Elite 2 synthetic hexaploid wheats				
1	1	SORA/AE.SQUARROSA (192)	8	<1
2	6	GAN/AE.SQUARROSA (236)	8	1
Durum				
1	30	YAV_3/SCOT//JO69.CRA/3/YAV79	8	1
2	31	YAR	9	2
3	36	CIT71/CPI	8	1
4	38	TRINAKRSA	8	2
5	41	CERCETA	8	6
6	42	SCOT/MEXI-1	8	8
7	47	ARLEQUIN	7	2
8	48	CHEN-7	7	4

[z]*Aegilops tauschii* accession entry in the Wheat Wide Crossing Programmes working collection at CIMMYT, Mexico. (*Aegilops squarrosa* syn. *Ae. tauschii* or *Triticum tauschii*).

4/*Ae. squarrosa* (502),68.111/RGB-U//WARD RESEL/3/STIL/ 4/*Ae. squarrosa* (783), and DOY1/*Ae. squarrosa* (1027) the resistance appears to be from both parents. Such interpretations were made from the screening of DOY1/*Ae. squarrosa* (458) and GREN/*Ae. squarrosa* (458). DOY 1 had seedling resistance while GREN was susceptible. Thus, the resistance in the SH between GREN and 458 identifies the *Ae. tauschii* accession 458 as the contributor. From this, we concluded that in the SH between DOY and 458 both parents possess genes conferring resistance. Other *Ae. tauschii* accessions similarly identified as being resistant based upon screening of their synthetic wheats were 502, 783, and 1027. These synthetics were ALTAR 84/*Ae. squarrosa* (502), YAR/ *Ae. squarrosa* (783) and CETA/*Ae. squarrosa* (1027). In all of these, the durum parents possessed seedling susceptibility, hence resistance was attributed to the *Ae. tauschii* accession. Synthetic hexaploid wheats with resistances derived from both parents should be considered superior to those that derive the same from a single parent. This is due to the assemblage of genes from the A, B, and the D genomes and forms a good example of gene pyramiding. However, this should not undermine the benefits from a single resistance source parent as seen for various *Ae. tauschii* accessions. Such diploid accessions are excellent for targeted study and offer ease of gene characterization via direct crossing and offer simplicity when molecular diagnostics are involved. It has been recognized that lines possessing good seedling resistance also have good level of adult plant resistance (Ma *et al*., 1995). A similar result was also found in this study. Twenty four synthetics of Elite 1 and 9 of Elite 2 were found to be resistant both at seedling and adult plant stage under field and glasshouse conditions. Eight synthetic lines from Elite 1, 2 from Elite 2, and 8 durum parents were identified to possess genes for adult plant resistance. They showed high (6-8) infection types in the seedling stage but their relative AUDPC was 10%. The synthetics found resistant at both stages could possess durable resistance as compared to the lines which were found resistant only at adult plant stage. These lines could possess partial or quantitative resistance as elucidated earlier by Parleviet (1985). Once the trait resistant SH wheats have been identified, then these can be crossed with target quality bread wheats for either introgressing the value trait or for pyramiding advantage. Such outputs have been realized for many biotic stresses and abiotic tolerances. Notable are resistances/tolerances to head scab (*Fusarium graminearum* Schwabe) (Mujeeb-Kazi, 2003a), Septoria leaf blotch (*Septoria tritici* Rob. ex Desm.) (Mujeeb-Kazi, 2000), spot blotch (*Helminthosporium* spp.) (Mujeeb-Kazi *et al*.,

Table 3. Lines of synthetic hexaploid wheats (*Triticum turgidum* x *Aegilops tauschii*) from Elite 1, and 2 resistant to stripe rust (*Puccinia striformis* f. sp. *tritici*) at the seedling and adult plant stages.

Sr No.	Accesion No.	Genotype	Infection types	Relative AUDPC
Elite 1 synthetic hexaploid wheats				
1	2	DOY1/AE.SQUARROSA (188)[z]	3	1
2	3	ALTAR 84/AE.SQUARROSA (192)	3	
3	5	ALTAR 84/AE.SQUAROSA (198)	3	9
4	27	GARZA/BOY//AE.SQUAROSA (311)	3	6
5	32	DOY 1/AE.SQUAROSA (447)	3	<1
6	34	DOY1/AE.SQUARROSA (511)	3	1
7	35	68.111/RGB-U//WARD/3/AE.SQUARROSA (511)	3	2
8	42	YAR/AE.SQUARROSA (783)	3	8
9	47	68.111/RGB-U//WARD/3/FG /4 RAB /5/ AE.SQUARROSA (882)	0	<1
10	52	ALTAR 84/AE.SQUARROSA (BANGOR)	2	6
11	62	SCA/AE.SQUARROSA (518)	4	1
12	73	GAN/AE.SQUARROSSA (897)	2	<1
13	76	FALCIN/AE.SQUAROSA (312)	2	3
14	79	DOY 1/AE.SQUAROSA (333)	2	1
15	80	DOY1/AE.SQUARROSA (428)	2	<1
16	81	68.111/RGB-U//WARD/3/AE.SQUARROSA (452)	2	1
17	87	SCA/AE.SQUARROSSA (409)	2	1
18	88	CPI/GEDIZ/3/GOO//J069/CRA/4/ AE.SQUARROSA (409)	2	3
19	89	STY-US/CETA//PALS/3/SRN_5/4/ AE.SQUARROSA (502)	2	3
20	90	ALTAR 84/AE.SQUARROSA (502)	2	
21	91	CROC-1/AE.SQUARROSA (517)	1	<1
22	92	CETA/AE.SQUARROSA (1024)	3	<1
23	93	DVERD-2/AE.SQUARROSA (1027)	3	4
24	94	CETA/AE.SQUARROSA (1027)	3	2
Elite 2 synthetic hexaploid wheats				
1	9	STYUS/CELTA//PALS.3/SRM_5/4/ AE.SQUARROSA (431)	3	2
2	11	KARV_2/AE.SQUARROSA (304)	4	2
3	13	DOY1/AE.SQUARROSA (1027)	3	2
4	17	CPI/GEDIZ/3/GOO/JO/CRA/4/ AE.SQUARROSA (1018\	3	1
5	18	CETA/AE.SQUARROSA (1031)	3	1
6	30	68.111/RGB-U//WARD RESEL/3/STIL/4/ AE.SQUARROSA (385)\	2	2
7	31	CETA/AE.SQUARROSA (417)	2	1
8	32	68.111/RGB-U//WARD RESEL/3/STIL/4/ AE.SQUARROSA (431)	2	2

[z]*Aegilops tauschii* accession entry in the Wheat Wide Crossing Programmes working collection at CIMMYT, Mexico. (*Aegilops squarrosa* syn *Ae. tauschii* or *Triticum tauschii*).

1996), Karnal bunt (*Tilletia indica* Mitra) (Mujeeb-Kazi *et al*., 2001; Villareal *et al*., 1996), salinity tolerance (Pritchard *et al*., 2002), drought tolerance (Trethowan *et al*., 2003), water-logging tolerance (Villareal *et al*., 2001), leaf/stripe rust and yield (Mujeeb-Kazi, 2003a). We have so far not attempted to identify the resistant genes found in synthetics. Instead of applying single race treatment, bulk inoculum was used for evaluating the SH germplasm. This bulk inoculum was collected from farmer's field and represents all the possible virulences for the known genes in Pakistan. The inoculum used had virulence to Yr1, Yr3, Yr4, Yr5, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, YrSp, YrSD, YrCV, and was avirulent to Yr10, Yr26, Yr27, and Yr28. According to the gene for gene hypothesis (Newton and Andrivon, 1995), if the gene to which inoculum virulence is present in any of the SH, that SH would be susceptible. Accordingly, from the avirulence observations above, we can assume that resistant synthetics will have possibilities of Yr 10, Yr 26, Yr 27, Yr 28 or some other new

genes. It can also be assumed that those lines in which only *Ae. tauschii* is the sole resistance donor, these lines could posses Yr 28 as it has been transferred from *Ae. tauschii* and would thus be located on the D genome (Singh *et al*., 2000). Additional genes associated with the D genome by this same logic could be Yr 20, Yr22, Yr23 (Chen *et al*., 1995b), Yr25, and Yr33 (McIntosh *et al*., 1998, 2004). The lines in which both parents are involved could possess Yr10, Yr26, Yr27 or new genes located on A and B genomes of *T. turgidum* in addition to the above mentioned genes located on D genome. The synthetic hexaploid wheats found resistant in this study could provide a valuable source for the improvement of stripe rust resistance of Pakistani bread wheat cultivars. Further studies related to identification of molecular markers linked with the genes may provide valuable information related to marker-assisted selection and facilitate targeted breeding giving options for varietal, and gene deployment to ensure wheat productivity around a genetic diversity profile. The information obtained from this study is the backbone for initiating in the future genetic analyses that would unravel interesting information around the chromosomal/gene contribution to resistance. In case of exclusive *Ae. tauschii*'s accessional contribution a partial monosomic analysis (Mujeeb-Kazi, 2003b) would immediately identify the D genome chromosome involved, paving the way for in depth inheritance studies. The data gathered, also opens up avenues where such *Ae. tauschii* accessions can be utilized for direct hybridization onto leading high yielding wheat cultivars with DNA polymorphisms that are prone to rust susceptibility thus permitting the integration of molecular diagnostics through the use of D genome/chromosome specific markers.

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