

Postulation of resistance genes and assessment of adult plant response variation for stripe rust in three international wheat nurseries

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Abstract

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is an important disease of wheat in cooler and humid geographic regions. It can cause significant yield losses. Three international nurseries, namely, 1st Australian Special Nursery (ASN), 22nd Semi-Arid Wheat Screening Nursery (SAWSN) and 12th High Temperature Wheat Yield Trial (HTWYT), were evaluated for seedling and adult plant response variation for stripe rust. A low proportion of these nurseries displayed stripe rust resistance in the seedling stage. Fifty one percent of 1st ASN, 54% 22nd SAWSN and 17% 12th HTWYT entries did not carry any seedling resistance genes. High level of APR to stripe rust was expressed in the field in all three nurseries. Stripe rust resistance genes *Yr6*, *Yr7*, *Yr9*, *Yr17* and *Yr27* were postulated either singly or in combinations across the three nurseries. Some entries carried these genes in combination with uncharacterised resistance. Based on *Lr34* and *Sr2* linked markers, *Yr18* and *Yr30* are inferred to be present in a high proportion of entries in all three nurseries. Due to the lack of robust marker, we were unable to postulate *Yr29*, this gene is however expected to be present in Pavon 76 derivatives. Results of this study can be used for strategic deployment of stripe rust resistance in new wheat cultivars.

Key words: Adult plant resistance, gene postulation, stripe rust, wheat

Introduction

Stripe rust, caused by *Puccinia striiformis* f. sp. *tritici* (Pst), is an important disease of wheat that can cause substantial yield losses. The disease is predominant in cooler and humid geographic regions [1]. Seedling/

overall resistance can be detected in the greenhouse through monocyclic rust tests. Multipathotype tests are used to postulate the presence/absence of race specific resistance genes in test genotypes. Some resistance genes express only at the post seedling stages and are referred to as adult plant resistance (APR) genes. The expression of APR genes is influenced by environmental conditions. A detailed knowledge of genetic variation for both seedling resistance and APR in target germplasm can ensure deployment of diverse sources of resistance in new cultivars to achieve durability for rust resistance.

Agriculture researchers have achieved spectacular success in the form of green revolution in the last century [2]. In the case of wheat, the success can be largely attributed to an international collaborative wheat improvement project based at CIMMYT, Mexico [3]. The advanced breeding lines developed at CIMMYT have been tested under different agro-ecological zones globally for different agronomic traits. Three international nurseries, namely; 1st Australian Special Nursery (ASN), 22nd Semi-Arid Wheat Screening Nursery (SAWSN) and 12th High Temperature Wheat Yield Trial (HTWYT) were received through the CIMMYT-Australia-ICARDA Germplasm Evaluation (CAIGE) project. This investigation was planned to postulate stripe rust resistance genes and to assess adult plant stripe rust response variation under Australian conditions.

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Materials and methods

Host and pathogen material

One hundred and fifty three entries belonging to three international nurseries were used. Forty eight entries belonged to 1st ASN, 91 to 22nd SAWSN and 14 to 12th HTWYT. The entries that showed segregation for traits under study were not included in final data compilation. The final set consisted of 129 entries with 41, 76 and 12 entries belonging to the 1st ASN, 22nd SAWSN and 12th HTWYT nurseries, respectively. Details of Pst pathotypes used in this study are given in Table 1.

Generation and management of material

Greenhouse and field sowing : Test entries were sown in 9 cm diameter plastic pots in the greenhouse. A potting mixture containing 80% composted pine bark and 20% coarse sand was used. The pots were fertilised with a water soluble fertiliser Aquasol[®] at a rate of 30g/10L of water for 200 pots. After about 20 minutes, seeds were sown and covered with potting mix. A set

of differential genotypes carrying known rust resistance genes was also sown with each experiment. Pots were transferred to a microclimate room in the greenhouse maintained at 20°C. A second application of nitrogenous fertilizer Nitram[®] was applied at the same rate as Aquasol[®] to the one week old seedlings. The infection type comparison of differential genotypes with test genotypes enabled postulation of stripe rust resistance genes.

Field sowing was done as 15-20 seeds hill plots to assess adult plant response variation among test entries. Infector rows were planted after every five experimental rows. The recommended dose of inorganic fertiliser was applied to a well prepared field to provide essential nutrients for proper germination and growth. The entire field was sprayed with herbicide Glean[®] (chlorsulfuron) after sowing at a rate of 1g/20L of water as a pre-emergence treatment to control a range of weeds. The field was irrigated with sprinkler irrigator as and when required to enhance crop growth and to create congenial conditions for rust development.

Seedling inoculations

In the greenhouse, seedlings were inoculated at the two-leaf stage. The inoculated seedlings were incubated in a dark room at a temperature of 9-12°C for 24 hours in trays filled with water and covered with polythene hoods to ensure high relative humidity.

Field inoculations

For field inoculations, urediniospores (suspended in light mineral oil Isopar L) of the Pst pathotypes (134 E16A+ and 110 E143A+) were sprayed during July and August using an ultra-low-volume applicator (Microfit[®], Micron Sprayer Ltd.) on three successive clear evenings with good expectations of dew to ensure good disease development. Inoculation of April sown infector rows of cultivars chosen selectively for multiplication of specific pathotypes by the Australian Cereal Rust Control Program staff acted as an initial source of inoculum. Experimental plots were however inoculated at the jointing stage.

Disease assessment

Stripe rust assessments in the greenhouse were performed on a 0-4 scale (4), where 0 = immune and 4 = very susceptible. In addition to the numeric value of disease score, symbols '+' and '-' were used to note deviations from standard responses. The symbols 'N' and 'C' were used to describe more than usual necrosis and chlorosis, respectively. A slash (/) was used to

Table 1. Pst pathotypes used for assessment of genetic diversity for seedling stripe rust resistance genes

Pathotype	Virulence/avirulence formula	PBI culture number
104 E137 A- Yr17+	Yr2, Yr3, Yr4, YrSD, YrSu, YrND, Yr17, Yr34/Yr1, Yr5, Yr6, Yr7, Yr8, Yr9, Yr10, Yr15, Yr24, Yr27, Yr32, Yr33, Yr35, Yr37, Yr40, Yr47, Yr51, Yr55, Yr57, YrSp, YrA	544
108 E141 A+	Yr2, Yr3, Yr4, Yr6, YrSD, YrSu, YrND, YrA, Yr34/Yr1, Yr5, Yr7, Yr8, Yr9, Yr10, Yr15, Yr17, Yr24, Yr27, Yr32, Yr33, Yr35, Yr37, Yr40, Yr47, Yr51, Yr55, Yr57, YrSp	420
110 E143 A+	Yr2, Yr3, Yr4, Yr6, Yr7, YrSD, YrSu, YrND, YrA, Yr34/Yr1, Yr5, Yr8, Yr9, Yr10, Yr15, Yr17, Yr24, Yr27, Yr32, Yr33, Yr35, Yr37, Yr40, Yr47, Yr51, Yr55, Yr57, YrSp	444
134 E16 A+	Yr2, Yr6, Yr7, Yr8, Yr9, YrA/Yr1, Yr3, Yr4, Yr5, Yr10, Yr15, Yr17, Yr24, Yr27, Yr32, Yr33, Yr34, Yr35, Yr37, Yr40, Yr47, Yr51, Yr55, Yr57, YrSD, YrSu, YrND, YrSp	572

ND = Nord Desprez, SD = Strubes Dickkopf, Su = Suwon 92/Omar, A = complementary gene from Avocet and Sp = Spladings Prolific

differentiate symptoms on the first and second leaves. Segregation for more than one infection type (IT) was separated by a comma, with the most frequent IT mentioned first. Field assessment of adult plant stripe rust responses was based on a 1-9 scale [5], where 1 denotes very resistant, 2 resistant, 3 resistant to moderately resistant, 4 moderately resistant, 5 moderately resistant to moderately susceptible, 6 moderately susceptible, 7 moderately susceptible to susceptible, 8 susceptible and 9 very susceptible.

Molecular detection of Yr18 and Yr30

DNA was extracted from 10 day-old seedlings using the SDS method (6). The adult plant resistance genes *Yr18* and *Yr30* were identified by employing molecular markers *csLv34* (7) and *csSr2* (8), respectively, across three nurseries. While *Yr18* and *Lr34* are shown to be the same gene, the extent of association of *Sr2* and *Yr30* has not been fully substantiated yet. Therefore, postulation of *Yr30* should be treated with caution.

Results and discussion

Postulation of resistance genes

Postulation of genes in elite germplasm could facilitate maintenance of genetic diversity for a given trait in breeding programs. Availability of well characterized pathogen isolates (pathotypes) is essential to generate such information. The Australian Cereal Rust Control Program at the University of Sydney maintains a historic collection of pathotypes of cereal rust pathogens. Pathotypes of Pst from this collection were used. For all three nurseries, rust response assessments were made both at the seedling and adult plant stages. Results for individual nurseries were analysed separately. To interpret results from multipathotype tests, a differential response key for a given gene based on responses of the target differential genotype against an array of pathotypes was generated (Table 2). This key was used to postulate resistance

genes which occurred singly in various entries. For postulation of combinations of resistance genes, deviations from the expected response of a given gene and pedigree records were considered. Seedling stripe rust response variation detected across three nurseries is shown in Fig. 1.

Gene postulation results for the 1st ASN are presented in Table 3. *Yr27* was postulated in five entries based on a low infection type (IT12CN) against all the four pathotypes. The blackening of pustules and high level of necrosis associated with the expression of *Yr27* were also used to support postulation. *Yr6*, *Yr9* and *Yr17* were present in one genotype each, whereas *Yr7* was postulated in three entries. *Yr17* in the 1st ASN entry (GID4894586) was contributed by cultivar Trident. Twenty one entries were susceptible to all four pathotypes and were concluded not to carry any seedling resistance genes against Pst pathotypes used in this study. Nine entries produced low infection type against all four pathotypes indicating either the



Fig. 1. Seedling stripe rust responses observed among entries of three international nurseries

Table 2. Differential responses of postulated stripe rust resistance genes to different pathotypes

Gene	104 E 137A- Yr17+	108 E141A+	110 E143A+	134 E16A+	ULI [#]
<i>Yr6</i>	L*	H [^]	H	H	;N
<i>Yr7</i>	L	L	H	H	;N-;1NN
<i>Yr9</i>	L	L	L	H	0;-;N
<i>Yr17</i>	H	L	L	L	;C-;1C
<i>Yr27</i>	L	L	L	L	;1CN-3CN

* Low infection type ^ High infection type # Usual Low Infection type expressed by the target gene. Gene combinations for two or more genes were postulated based on deviations from these responses and pedigree records of entries

presence of combinations of genes with compensating pathotypic specificities or uncharacterised resistance gene(s).

For the 22nd SAWSN, comparisons of infection types displayed by test entries and the differential lines allowed the postulation of *Yr6*, *Yr7*, *Yr9*, *Yr17* and *Yr27* (Table 3). Forty one entries did not carry any seedling resistance genes against *Pst* pathotypes used in this study. Five entries produced resistant responses (IT0; to ;NN) against pathotypes used and postulation of resistance genes was not feasible due to the lack of differential responses. *Yr27* was present in 12 entries either singly or in combination with *Yr9* or uncharacterised resistance. Stripe rust resistance genes *Yr6*, *Yr7* and *Yr9* were postulated only in a few entries and these genes are ineffective against the predominant Australian *Pst* pathotype 134 E16A+ and its derivatives. On the other hand, *Yr17* was ineffective only against one Australian *Pst* pathotype at the time of this study. *Yr17* was postulated in one entry based on a high infection type expressed against *Yr17* virulent pathotype 104 E137A-*Yr17+* (Table 3) and the presence of cultivar Milan in its pedigree.

There were only 12 entries in the 12th HTWYT. *Yr9* was postulated alone in four entries and it was present in combination with *Yr27* in three entries (Table 1). *Yr27* was postulated singly in one entry. *Yr17* carrying entries contained additional uncharacterised resistance. *Yr17* was contributed by Milan in both entries. Two entries did not carry any seedling stripe rust resistance gene against these pathotypes (Table 3).

The rye derived (1BL.1RS) stripe rust resistance gene *Yr9* was postulated in 58% of the 12th HTWYT, 17% of the 22nd SAWSN and 2% entries of the 1st ASN. Contrary to the benefits, the 1BL.1RS translocation also produces sticky dough [9, 10]. The 1st ASN carried the least number of entries with 1BL.1RS translocation due to selection against 1BL.1RS during the development of this material. Stripe rust resistance genes *Yr6*, *Yr7*, *Yr17* and *Yr27* were detected either singly or in combinations. The combination of *Yr9* and *Yr27* is present in an Indian wheat cultivar PBW343 which occupied more than six million hectares in India and *Yr27* has also been reported in entries from various agro-ecological zones [11, 12]. The presence of *Yr2*, *Yr3*, *Yr4*, *Yr6*, *Yr7*, *Yr9* and *YrA* singly or in combinations in CIMMYT derived wheat germplasm has been reported in literature [13, 14]. This study however did not detect some of these

genes in any of the nurseries. Pathotypes with virulence for *Yr6*, *Yr7* and *Yr9* exist globally. Pathotypes possessing virulence for *Yr17* have been isolated in many countries [15-17]. *Yr27* virulent pathotypes were detected in Australia after this study. Virulence for *Yr27* has been detected in Afghanistan, Iran, Kyrgyzstan, Tajikistan, Pakistan, and India [18].

A higher proportion of entries (51% for 1st ASN, 54% for 22nd SAWSN and 17% for 12th HTWYT) were susceptible to all four pathotypes and therefore lacked seedling resistance to stripe rust. The entries from the 1st ASN and the 22nd SAWSN nurseries that produced an array of intermediate ITs against all pathotypes are likely to carry either currently uncharacterised resistances genes or combinations of resistance genes with compensating pathotypic specificities.

Adult plant stripe rust response tests

All three nurseries showed high level of stripe rust resistance under field conditions. The 1st ASN entries produced moderately resistant (score 4) or lower adult plant stripe rust responses (Table 3). Almost 50% of the entries that produced a response score 2 during 2006 crop season produced a response score of 3 during 2007. In 2006, 33 entries exhibited a score 2 followed by six and two entries with scores 3 and 4, respectively (Fig. 2a).

The adult plant stripe rust response scores for 22nd SAWSN are presented in Table 3. A majority of entries exhibited low scores (Fig. 2b) during both crop seasons. Three and two entries were scored 5 and 6, respectively, during the 2006 crop season and these entries produced scores of 3 or 4 in the 2007 experiments. Nine 12th HTWYT entries were scored 2 during 2006. The remaining entries produced scores of 3 and 5. Slightly higher field scores were observed during the 2007 crop season with seven and two entries producing scores 4 and 5, respectively (Fig. 2c).

Twenty one (1st ASN), 41 (22nd SAWSN) and 2 (12th HTWYT) entries lacked seedling stripe rust resistance (Table 3). Resistance genes *Yr6*, *Yr7* and *Yr9* were not effective against the predominant pathotype 134 E16A+ during both seasons. Genotype lacking seedling resistance and those carrying ineffective resistance genes *Yr6*, *Yr7* and *Yr9* displayed high levels of adult plant stripe rust resistance during both cropping seasons indicating the presence of APR genes (Table 3).

Table 3. Postulated resistance genes, field responses and inferred presence of APR genes based on marker genotyping of three international nurseries

GID ^a	Pedigree	Seedling resistance genes	Field rust response 2006	Field rust response 2007	APR genes ^d
1st Australian special Nursery (ASN)					
4982211	FRAME/BUCHIN	Yr27	2	2	Yr30
4564446	SILVERSTAR/PASTOR	Nil	2	2	Yr18, Yr30
4564445	SILVERSTAR/PASTOR	Nil	2	3	Yr18, Yr30
4564444	SILVERSTAR/PASTOR	Nil	2	3	Yr18, Yr30
4564443	SILVERSTAR/PASTOR	Yr7	2	3	Yr18, Yr30
4557928	SILVERSTAR/PASTOR	Yr7	2	3	Yr18, Yr30
4891485	CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*FRAME	Yr7	2	3	Yr18
4809438	CROC_1/AE.SQUARROSA (205)//BORL95/3/KENNEDY	Yr27	2	2	Yr18
4809437	CROC_1/AE.SQUARROSA (205)//BORL95/3/KENNEDY	Yr27	2	2	Yr18, Yr30
4809662	CROC_1/AE.SQUARROSA (224)//2*OPATA/3/RAC655	Yr27, Unch ^c	2	3	Yr18, Yr30
4809661	CROC_1/AE.SQUARROSA (224)//2*OPATA/3/RAC655	Yr27	2	3	Yr30
4810029	D67.2/P66.270//AE.SQUARROSA (320)/3/CUNNINGHAM	Unch	2	2	Yr18, Yr30
4810028	D67.2/P66.270//AE.SQUARROSA (320)/3/CUNNINGHAM	Unch	2	2	Yr18, Yr30
4810027	D67.2/P66.270//AE.SQUARROSA (320)/3/CUNNINGHAM	Yr9, Unch	2	3	Yr18, Yr30
4972270	AUS 4930.7/2*PASTOR	Unch	2	3	Yr30
4972269	AUS 4930.7/2*PASTOR	Nil	2	3	Yr18, Yr30
4944300	WORRAKATTA/2*PASTOR	Nil	2	2	
4944299	WORRAKATTA/2*PASTOR	Unch	4	3	
4944151	WORRAKATTA/2*PASTOR	Unch	2	3	
4944150	WORRAKATTA/2*PASTOR	Unch	4	2	Yr18, Yr30
4944341	WORRAKATTA/2*PASTOR	Unch	3	3	Yr30
4944340	WORRAKATTA/2*PASTOR	Nil	2	3	Yr18, Yr30
4944615	KRICHAUFF/2*PASTOR	Nil	3	3	
4944683	KRICHAUFF/2*PASTOR	Nil	2	2	Yr18, Yr30
4972646	AUS GS50AT41//HXL8246/KAUZ/3/CUNNINGHAM	Nil	3	3	Yr18, Yr30
4912890	WORRAKATTA/PASTOR	Nil	2	3	
4912889	WORRAKATTA/PASTOR	Nil	2	4	
4912782	WORRAKATTA/PASTOR	Nil	2	2	
4913156	KRICHAUFF/PASTOR	Nil	2	3	Yr30
4913028	KRICHAUFF/PASTOR	Nil	2	2	Yr30
4913329	KRICHAUFF/PASTOR	Nil	3	2	
4913336	SUNCO/PASTOR	Nil	3	3	Yr18
4913345	SUNCO/PASTOR	Nil	2	2	Yr18, Yr30
4913344	SUNCO/PASTOR	Nil	3	3	Yr30
4913341	SUNCO/PASTOR	Nil	2	3	
4883306	HARTOG*2/ARIV92	Yr6	2	3	
4875119	BORL95/2*JANZ//JANZ	Unch	2	3	
4894586	HD29/2*WEAVER//2*TRIDENT/3/TRIDENT	Yr17	2	3	
4894611	M2A/CML//CMH78.390/3/2*JANZ/4/JANZ	Nil	2	3	Yr18, Yr30
4894675	M2A/CML//CMH78.390/3/2*GOLDMARK/4/GOLDMARK	Unch	2	3	Yr18, Yr30
4875124	HD29/2*KULIN//KULIN	Nil	2	3	

22nd Semi-Arid Wheat Screening Nursery (SAWSN)

1632809	ATTILA/3/VORONA/CNO79//KAUZ	Yr9, Yr27	2	3	Yr30
3584454	CROC_1/AE.SQUARROSA (205)//BORL95/3/2*MILAN	Yr7	2	3	
3827946	CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA	Yr27, Unch	2	3	
3864981	CASKOR/3/CROC_1/AE.SQUARROSA (224)//OPATA	Unch	3	3	Yr30
3865440	CROC_1/AE.SQUARROSA (205)//MILAN/KAUZ	Yr9	2	3	Yr30
3865439	CROC_1/AE.SQUARROSA (205)//MILAN/KAUZ	Yr9	2	4	Yr30
3865438	CROC_1/AE.SQUARROSA (205)//MILAN/KAUZ	Yr9	2	4	Yr30
3865437	CROC_1/AE.SQUARROSA (205)//MILAN/KAUZ	Yr9	2	3	Yr30
3868483	NA ^b	Nil	2	2	Yr18, Yr30
3868481	NA	Nil	6	3	Yr18, Yr30
3868480	NA	Nil	2	3	Yr30
3822954	NA	Nil	2	2	Yr30
3868513	IRENA/BABAX//PASTOR	Nil	2	3	Yr30
3868509	IRENA/BABAX//PASTOR	Nil	2	2	
3868589	DHARWAR DRY/2*PASTOR	Unch	2	3	Yr30
3868619	URES/JUN//KAUZ/3/NESSER/4/URES/JUN//KAUZ	Yr9, Unch	2	3	
3827914	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	Nil	5	4	Yr30
3868696	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	Nil	2	3	Yr30
3868700	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	Nil	3	3	Yr30
3868695	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	Nil	6	3	Yr30
3868699	SERI*3//RL6010/4*YR/3/PASTOR/4/BAV92	Nil	3	3	
3854935	MILAN/KAUZ/6/TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/ KAUZ	Yr27, Unch	2	3	Yr18, Yr30
3854946	FRTL/PIFED	Unch	2	3	Yr30
3855018	VOROBAY	Yr6	2	2	Yr30
3855013	VOROBAY	Unch	2	3	Yr18, Yr30
3827768	VOROBAY	Yr6, Unch	2	3	Yr18, Yr30
3855034	CROC_1/AE.SQUARROSA (224)//OPATA/3/ATTILA	Unch	2	3	Yr30
3827942	BJY/COC//PRL/BOW/3/URES/JUN//KAUZ	Nil	2	4	Yr30
3855088	SOROCA	Nil	3	3	Yr18, Yr30
3855083	SOROCA	Nil	2	3	Yr18, Yr30
3855080	SOROCA	Nil	2	3	Yr18, Yr30
3855082	SOROCA	Nil	2	3	Yr18, Yr30
3855090	SOROCA	Nil	2	3	Yr30
3827924	SOROCA	Nil	2	3	Yr18, Yr30
3855123	PARUS/PASTOR	Nil	2	3	Yr30
3829898	PARUS/PASTOR	Nil	2	4	Yr30
3855118	PARUS/PASTOR	Nil	2	3	Yr30
3855117	PARUS/PASTOR	Nil	2	3	Yr30
3827944	PARUS/PASTOR	Nil	2	3	Yr30
3855114	PARUS/PASTOR	Nil	2	3	
3855126	PARUS/PASTOR	Nil	2	2	Yr30
3855652	PJN/BOW//OPATA*2/3/CROC_1/AE.SQUARROSA (224)//OPATA	Nil	5	4	Yr30
3855647	PJN/BOW//OPATA*2/3/CROC_1/AE.SQUARROSA (224)//OPATA	Nil	4	4	Yr30
3855707	ASTREB	Nil	2	2	Yr30
3827934	ASTREB	Nil	2	2	Yr30
3855696	ASTREB	Nil	2	2	Yr30
3855692	ASTREB	Nil	5	3	Yr30

3827465	ASTREB	Nil	2	2	Yr18, Yr30
3830769	ASTREB	Nil	2	2	Yr18, Yr30
3855721	PIFED/2*PASTOR	Yr7	2	3	Yr30
3855789	PJN/BOW//OPATA/3/2*PASTOR	Nil	2	4	Yr30
3827945	VEE/MJI//2*TUI/3/2*PASTOR	Yr7	2	2	Yr30
3825911	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/CNDO/ R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/ 4/WEAVER/7/URES/JUN//KAUZ	Yr9, Yr27	2	2	Yr30
3855883	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/CNDO/ R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/7/URES/JUN//KAUZ	Yr9, Yr27	2	3	Yr18, Yr30
3855892	MILAN/KAUZ/5/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/6/TOB/ERA//TOB/ CNO67/3/PLO/4/VEE#5/5/KAUZ	Yr9, Yr27	2	3	Yr18, Yr30
3855902	MILAN/KAUZ/5/CNDO/R143//ENTE/MEXI_2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/6/TOB/ERA//TOB/ CNO67/3/PLO/4/VEE#5/5/KAUZ	Yr9, Yr27	2	2	Yr18, Yr30
3823821	PASTOR//HXL7573/2*BAU	Yr9, Yr27	2	3	Yr30
3888097	PASTOR//HXL7573/2*BAU	Nil	4	4	Yr30
3888095	PASTOR//HXL7573/2*BAU	Yr6, Unch	2	2	Yr30
3827750	PASTOR//HXL7573/2*BAU	Unch	2	4	Yr18
3830746	PASTOR//HXL7573/2*BAU	Yr7	2	4	Yr30
3888064	PASTOR//HXL7573/2*BAU	Yr9	2	3	Yr30
3827938	SOKOLL	Yr27	2	3	Yr30
3827751	SOKOLL	Yr27	2	3	Yr18, Yr30
3888822	SRMA/TUI//BABAX	Yr9, Yr27	2	3	
4139832	CHUM18/2*SILVERSTAR	Yr7	2	3	Yr18, Yr30
4556647	MILAN/KAUZ//PRINIA/3/BABAX	Yr17	2	3	Yr18
4340793	ALTAR 84/AE.SQUARROSA (221)//PASTOR/3/PASTOR	Unch	2	4	Yr18, Yr30
4315350	ALTAR 84/AE.SQUARROSA (221)//PASTOR/3/PASTOR	Unch	2	3	Yr18, Yr30
4557150	ATTILA/BABAX//PASTOR	Nil	2	4	Yr30
4963257	AUS GS50AT34/SUNCO//CUNNINGHAM	Nil	2	3	
4875319	SUNCO/2*PASTOR	Nil	2	3	Yr30
4874568	SUNCO/2*PASTOR	Nil	3	4	Yr30
4874564	SUNCO/2*PASTOR	Nil	2	2	Yr18, Yr30
4874570	SUNCO/2*PASTOR	Nil	2	2	Yr30
3853504	MTRWA92.91/CHOIX	Yr27	2	2	
12th High Temperature Wheat Yield Trial (HTWYT)					
3597332	KAUZ//BOW/NKT	Yr9	2	4	Yr30
4318662	RDWG/MILAN	Yr27	2	4	Yr18
3838493	TIA.4/WL6572//RL6043/3*GEN/3/LUAN	Yr9	5	5	Yr30
4318765	HD2136/SKA/5/TOB/CNO67//BB/4/NAI60*2//TT/SN64/3/ LR64A/SN64/6/HD2257/7/SPB/8/HE1/5*CNO79/9/89N2081	Yr9, Yr27	2	4	
2463808	KAUZ/WEAVER	Yr9	2	4	Yr18, Yr30
4319277	CMH84.3379/CMH78.578//MILAN	Yr17+	2	4	Yr18, Yr30
1563731	OASIS/KAUZ//4*BCN	Yr9, Yr27	2	3	Yr30
4319976	SITE/MO//MILAN	Yr17+	2	5	Yr30
4320045	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/ BOW/4/PASTOR	nil	3	3	
3628572	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3 /CMH81.38/2*KAUZ	Yr9, Yr27	2	4	Yr18, Yr30
4318130	TAM200/TUI	Yr9	2	3	Yr30
4083660	BCN/3/ALD/PVN//YMI #6	nil	3	4	Yr18, Yr30

^aNA = genotype ID from ICIS, ^bNA = not available, ^cUnch = uncharacterized, ^dbased on *Lr34/Yr18* and *Sr2* linked markers

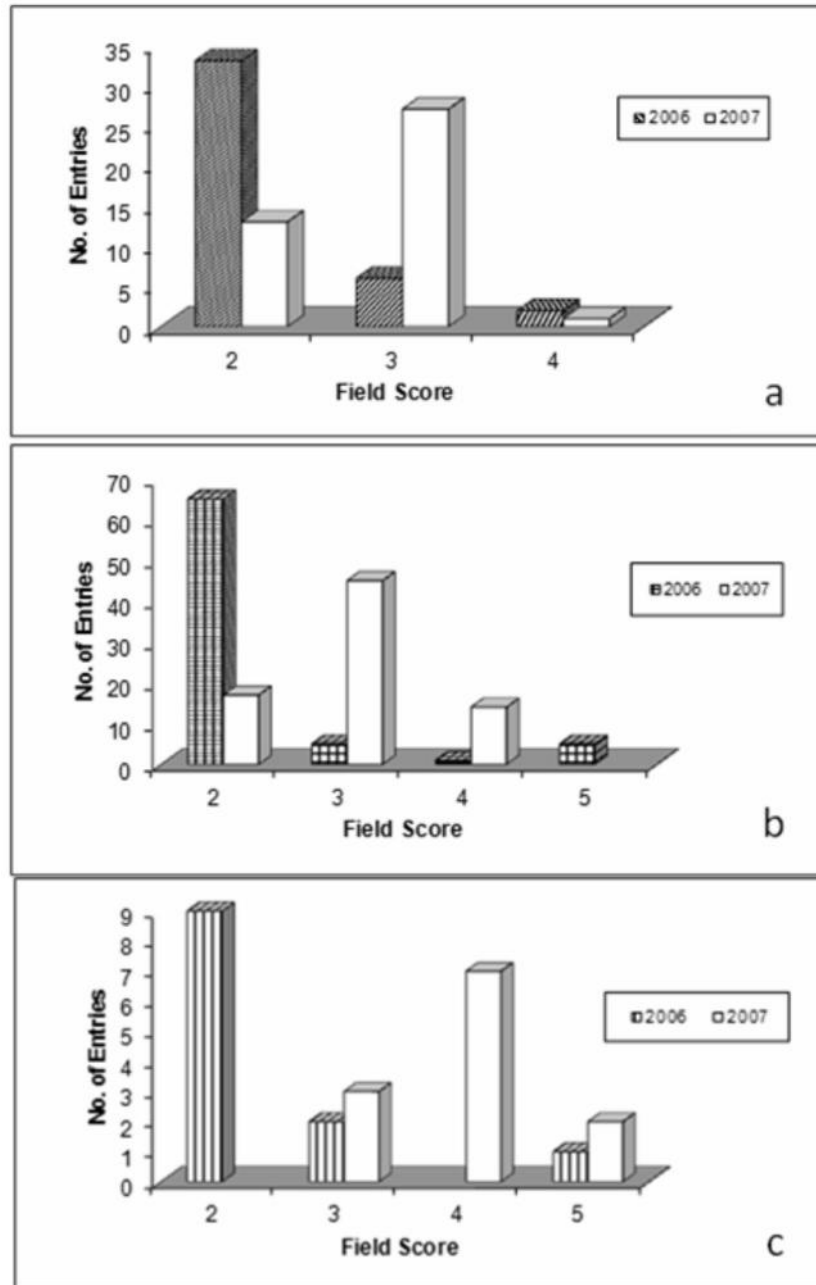


Fig. 2. Adult plant stripe rust response variation observed among a) 1st ASN, b) 22nd SAWSN and c) 12th HTWYT entries when tested with *Puccinia striiformis* f. sp. *tritici* during 2006 and 2007

Yr18 and *Yr30* were detected in a high proportion of entries through linked molecular markers. Of 41 entries, 21 and 25 carried *Yr18* and *Yr30*, respectively, in the 1stASN (Table 3). Eighteen genotypes carried *Yr18* and *Yr30* in combination. Twenty two and 65 entries from the 22nd SAWSN respectively, carried *Yr18* and *Yr30* singly and 20 genotypes carried both

APR genes. In the 12th HTWYT nursery five and nine entries carried *Yr18* and *Yr30*, respectively. One entry postulated to be devoid of any seedling stripe rust resistance genes and three other entries carried both *Yr18* and *Yr30*. Different accessions of ASTREB, Vorobey and Soroca carried *Yr18* or *Yr30* singly or in combination indicating heterogeneity among these accessions.

Detection of *Yr30* in a relatively large number of entries should be treated with caution as the extent of association between *Yr30* and *Sr2* has not been fully resolved yet. *Yr29* may be present in a high proportion of genotypes. *Yr29*-linked marker was not used due to its non-diagnostic nature. The presence of *Yr29* can however be predicted based on pedigree as Pavon 76 is known to carry this gene. Various studies dealing with CIMMYT wheat genotypes have reported combinations of two or more APR genes for stripe rust resistance [19-22].

This study provided an understanding of the stripe rust response variation across three international nurseries. Postulations based on phenotypic data were supported by pedigree records. Information reported here will facilitate the use of genotypes carrying high level of adult plant stripe rust resistance as donor sources in breeding programs.

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