## Second RUFORUM Biennial Meeting 20 - 24 September 2010, Entebbe, Uganda Research Application Summary

## Studies into slow rusting resistance among selected wheat lines

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## Abstract

Résumé

Wheat is an important staple crop in East Africa whose consumption outweighs its production partly due to the emergence of a virulent strain of Puccinia graminis fsp tritici, strain ug99 that cause stem rust disease. A study was carried out at Kenya Agricultural Research Institute, Njoro to identify sources of resistance to stem rust. Significant differences were noted for the final disease severity scores and their area under disease progress curve (AUPDC) values. The following lines exhibited trace response and least AUPDC values; 1168.6, SERI.1B\*2/3/KAUZ\*2/BOW//KAUZ/4/PBW343\*2/ TUKURU/5/C80.1/3\*BATAVIA//2\*WBLL1, SUNCO// TNMU/TUI and R07 F4-21258 which are entries 1, 7, 19 and 21, respectively. Lines which showed slow rusting characteristics with least disease and low AUDPC values included: CWANA 1st SR RESIS. ON - ETH - OS71, MON'S'/ ALD'S'//TOWPE'S', 87 and WHEAR/VIVITSI//WHEAR (2, 3, 4 and 14, respectively). These elite lines could form the basis for breeding for durable resistance in wheat. Identified resistance could also be introgressed into high yielding backgrounds.

Key words: Njoro, Puccinia graminis fsp tritici, ug99, wheat

Le blé est une culture vivrière importante en Afrique de l'Est dont la consommation dépasse la production, en partie à cause de l'émergence d'une souche virulente de *Puccinia graminis fsp tritici*, la souche ug99 qui cause la maladie de la rouille des tiges. Une étude a été réalisée dans un Institut de Recherche Agronomique du Kenya, à Njoro pour identifier les sources de résistance à la rouille de la tige. Des différences significatives ont été notées pour les critères finals de gravité de la maladie et de leur région sous les valeurs de la courbe de progression des maladies (AUPDC). Les lignées suivantes ont exposé la réponse de trace et au moins les valeurs AUPDC : 1168.6, SERI.1B\*2/3/KAUZ\*2/BOW//KAUZ/4/PBW343\*2/ TUKURU/5/C80.1/\*BATAVIA// 2\*WBLL1, SUNCO// TNMU/TUI et R07 F4-21258 qui sont les entrées 1, 7, 19 et

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21, respectivement. Les lignées qui ont montré les lentes caractéristiques d'enrouillement avec au moins la maladie et les faibles valeurs AUDPC ont inclus : CWANA premier SR RESIS. ON - ETH - OS71, MON'S'/ALD'S'//TOWPE'S', 87 et WHEAR/VIVITSI//WHEAR (2, 3, 4 et 14, respectivement). Ces lignées d'élite pourraient constituer la base de reproduction pour la résistance durable dans le blé. La résistance identifiée pourrait également être incorporée dans des milieux de haut rendement.

Mots clés: Njoro, Puccinia graminis fsp tritici, Ug99, blé

Wheat provides on average, one-fifth of the total calorific input of the world's population (Reynolds et al., 2008) and also forms the bulk of emergency food aid. In the developing countries, it provides 16% of total dietary calories (Dixon et al., 2009). Wheat grain yield consumption outweighs its production, calling for increased production of at least 2% per annum (Gill et al., 2004). Stem rust disease (Puccinia graminis f. sp. tritici) is currently the greatest threat to wheat production. The fungus has variable populations in terms of virulence to the various resistance genes. With migrations, mutations, recombinations and selections among the existent virulence genes, new races of the pathogens have been reported like the virulent race, ug99 currently causing heavy yield losses in East Africa (Singh et al., 2008). Countries adversely affected by rust such as in East Africa have resorted to increased importation of wheat. This study was therefore carried out to identify sources of rust resistance.

Wheat stem rust is caused by the fungus *Puccinia graminis* fsp *tritici* (Eriks and E. Henn) and exhibits high genetic diversity (Groth *et al.*, 1995). The recent breakdown of major resistance genes; sr31, sr24 and sr36 of stem rust resistant varieties has made stem rust the most important wheat disease globally. This has led to the further spread of the *ug99* pathogen spores causing epidemics in Kenya and Ethiopia (2002), Sudan, Iran and Yemen (2007) (Singh *et al.*, 2006). The emergence of virulent race *ug99* has been attributed to mutation of *Puccinia graminis* fsp *tritici* into more virulent forms possibly due to the intense solar radiation (Semenov and Halford, 2009). The pathogen could also have developed new virulence by sexual and para sexual genetic recombination (Burdon, 1993).

The East African highlands are hot spots for the new rust race due to year round availability of inoculum (Saari and Prescott, 256

Background
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1985). This is aggravated by the growing of wheat varieties with narrow genetic base (Beteselassie *et al.*, 2007). Most of the wheat farmers in the ug99 spore path are resource poor who cannot afford chemical fungicides, the equipment or the expertise to use them. The combinations of many minor resistance genes could help to provide resistance comparable to the best single major resistance gene. Sources of these genes however need to be identified.

Study DescriptionTwenty-five wheat lines selected from previous wheat<br/>screening nurseries at KARI Njoro were planted in the field on<br/> $22^{nd}$  December 2009. Other seven wheat lines with Sr 24 gene<br/>were also included as checks. This site lies at 0 20'S;  $35^{0}56'$  E,<br/>and 2166 m above sea level. Each wheat line was grown in<br/>two rows each measuring one metre in length. Irrigation was<br/>done regularly until the seeds were fully germinated. Disease<br/>spreaders were also grown perpendicular to all the entries.<br/>Artificial inoculation of the spreaders was also done using a<br/>syringe.

Disease scoring began when disease symptoms appeared weekly until physiological maturity. Scoring was done using Cobb's scale. Analysis of variance for the final disease severity scores and the mean phenotypic scores were obtained using the SAS programme. Disease progress was analyzed following the integral model of area under disease progress curve (AUPDC). The mean AUPDC values were calculated from the formula below;

$$A_k = \sum_{i=1}^{N_i - 1} \frac{(y_i + y_{i+1})}{2} (t_{i+1} - t_i)$$

Where; N=number of assessment times; y=disease measurement; t=time in days from first observation

Significant differences (P=0.05) were noted for final disease severity scores (Table 1). Plant height and maturity did not vary significantly among the wheat lines (data not shown). There were significant differences among the wheat lines with regard to the area under the disease progress curve (Table 1). The mean severity scores differed among the different wheat lines (Table 2). Though there was heavy disease pressure in the field, trace responses were noted among four entries with scores of 1 namely entries 1, 7, 19 and 21 (Table 2). Most of the other lines had resistant to moderately resistant responses.

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Table 1.	Analyses of	variance for	final disease	e severity score	and AUPDC	values among	selected
wheat lines	s.						

Source	DF	Stem rust(AUPDC values)	Stem rust (FDS)
Entry	24	108018.18**	389.66**
Error	21	5898.21	80.35
CV		18.89	42.32
Mean		406.48	21.18

\*\* = significance at 5%.

– significance at 5 /o.	Moderately resistant to moderately susceptible lines with low final disease severity (FDS) scores were also noted. The checks expressed susceptible reactions in the field. Lines which contained trace response had very low AUPDC values implying presence of a major gene. The susceptible checks had very high AUPDC values. These lines probably did not have genes for stem rust resistance. Most of the lines in this experiment had genes for stem rust resistance as exhibited by the AUPDC values. The resistant lines had pseudo black chaff on stems, suggesting presence of the Sr2 gene which could have been the probable cause of the slow rusting (Liu and Kolmer, 1998). These lines could be used as the basis for developing durable resistance in wheat.
Recommendation	The lines with FDS below 20% could be used in gene pyramiding to accumulate genes for stem rust resistance. These lines could also be used to introgress the slow rusting resistance genes to high yielding adapted cultivars through back cross. There is need for more genetic studies to determine the specific <i>Sr</i> genes contained in these promising lines.
Acknowledgement	We thank RUFORUM for funding the research, and CIMMYT and the KARI staff for the technical backstopping and use of their facilities.
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Origin	Entry	Pedigree	AUPDC *	FDS %*	FR
Argentina	1	1168.6	17.50 h	1 e	TR
Syria	7	CWANA 1st SR RESIS. ON - ETH - OS71	327.50 fg	12.5 de	Μ
CWANA	6	MON'S'/ALD'S'//TOWPE'S'	341.25fg	12.5 <sup>de</sup>	Μ
Australia	4	87	243.00 g	$10^{\text{de}}$	RMR
Mexico	5	THELIN#2/ TUKURU CGSS02Y00118S-099M-099Y-099M-16Y-OB	395.50 defg	17.5 cde	Μ
Australia	9	IGW3207	1035.00a	60 <sup>a</sup>	RMR
Mexico	7	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKUK0/5/C80.1/3*BATAVIA//2*WBLL1	35.00 h	1 e	TR
Mexico	∞	WHEAR/VIVITSI//WHEAR	603.75 bc	25 cd	RMR
Mexico	6	WHEAR/SOKOLL	458.75cdef	47.375 <sup>ab</sup>	RMR
Mexico	10	WHEAR/JARU//WHEAR	575.00 bcd	$30^{\text{bcd}}$	MR
Mexico	11	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	549.25 bcde	27.5 bed	RMR
Mexico	12	PBW343*2/KUKUNA//PBW343*2/KUKUNA/3/PBW343	448.00 cdef	25 cd	RMR
Mexico	13	SUPER SERI#1	396.25 defg	22.5 cde	RMR
Mexico	14	WHEAR/VIVITSI//WHEAR	317.25 fg	17.5 cde	RMR
Mexico	15	WHEAR/KUKUNA//WHEAR	333.75 fg	17.5 cde	Я
Mexico	16	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	626.75 bc	35 bc	RMR
Mexico	17	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	347.50 fg	20 ode	MR
Mexico	18	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	629.25 bc	35 bc	MR
Mexico	19	SUNCO//TNMU/TUI	29.00 h	1 e	TR
Mexico	20	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/5/VERDIN CMSS02	231.50 g	15 cde	RMR
		M0036IS-030M-15Y-0M-040Y-6ZTB-0Y-03B-0Y			
Uruguay	21	R07 F4-21258	29.00 h	1 e	TR
Mexico	22	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	561.75 bcde	27.5 bed	RMR
Mexico	23	WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2*WBLL1	555.50 bcde	27.5 bed	RMR
Mexico	24	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/5/VERDIN CMSS02	382.50efg	15 cde	RMR
	10			1 - 1 - 0 - 0	
Mexico	25	(yield trial 2007)	692.50b	30 0cd	RMR
Ū	heck 1	THELIN/3/BABAX/LR42//BABAX/4/BABAX/LR42//BABAX	2065	90	MSS
Ū	heck 2	THELIN/3/BABAX/LR42//BABAX/4/BABAX/LR42//BABAX	2005	90	MSS
Ū	heck 3	THELIN/3/2*BABAX/LR42//BABAX	2135	90	MSS
Ū	heck 4	THELIN/3/2*BABAX/LR42//BABAX	2230	90	MSS
Ū	heck 5	THELIN/3/2*BABAX/LR42//BABAX	2065	90	MSS
Ū	heck 6	THELIN/3/2*BABAX/LR42//BABAX	2065	90	MSS
G	heck 7	CANADIAN/CUNNINGHAM//KENNEDY	2290	90	MSS
		CV	18.89	42.32	
		Mean	406.48	21.18	
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Table 2. Means for final stem rust disease severity scores (FDS) and their AUPDC values.

CV= coefficient of variation. \*Means with the same letter are not significantly different as separated by Duncan's multiple range tests. Where, Resistant =R; moderately resistant=MR; RMR= Resistant to moderately resistant; moderately resistant =MR; moderately susceptible=MS; M= moderately resistant (MR) to moderately susceptible (MS); MSS= moderately susceptible to susceptible; susceptible =S.

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