

EVALUATION AND SCREENING OF DURUM WHEAT GERMPLASM TO STEM RUST RACES AT SEEDLING STAGE

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ABSTRACT

Wheat stem rust rapidly evolves a new virulence to resistance genes. Recently emerging races in East Africa, such as TTKSK (or Ug99), possess broad virulence to durum cultivars, and only a limited number of genes provide resistance. In attempts to identify and characterize stem rust resistance genes effective against four *pgt* races with broad virulence (TRTTF, TTTTF, TTKSK and JRCQC) at the seedling stage, a panel of durum wheat germplasm collected from major durum growing countries were evaluated.

In this study, 183 durum wheat germplasm were screened for seedling resistance to stem rust races under controlled condition with the aim of identifying source of resistance to stem rust in the future breeding activity. The seedling stage infection types were scored based on standard scoring method. The germplasm showed diverse seedling resistance responses to the four races. Germplasm with high resistance to multiple races were identified. The current result of this study identified suitable parental lines for further improving stem rust resistance in durum wheat in Ethiopia where such races are prevalent.

Keywords: Durum wheat, stem rust, Ug99, races

INTRODUCTION

Durum wheat [*Triticum turgidum* ssp. *durum* (Desf.) Husn.] is an important crop in the Mediterranean Basin, particularly in West Asia and North Africa, where it is grown annually on >13 million hectares. Mediterranean countries account for approximately 75% of global worldwide durum wheat production. In Sub-Saharan Africa, Ethiopia is the largest wheat-growing country and is one of the centers of diversity for tetraploid wheat. Durum wheat represents approximately 40% of the total wheat area in Ethiopia, with a tendency to increase in response to the growing internal demand for pasta (Badebo et al. 2009).

Durum wheat is a major staple food used for pasta, couscous, bread and more across the globe, especially in developing countries. It is especially important in developing countries where it often represents a large portion of total wheat planted as well as a major staple food. It is also attractive to farmers due to its adaptability to arid climate conditions, marginal soils and relatively low water requirements. Despite this broad adaptability, durum wheat production is often limited by various fungal diseases including rusts.

Durum production and kernel quality can be negatively affected by rust diseases (Singh et al., 2005). Historically, stem rust infections of *Puccinia graminis* Pers. f. *sp. tritici*, (*Pgt*) have caused severe losses to wheat production (McIntosh and Brown, 1997; Eversmeyer and Kramer, 2000; Singh et al., 2011). While >50 *Sr* loci have been identified in cultivated wheat and wild relatives, only a few of them remained effective against the newly emerged races in East Africa, including TTKSK = Ug99 (Pretorius et al., 2000) and its variants, and even fewer are effective against the durum-specific Ethiopian races (Admassu et al., 2009; Rouse et al., 2012). In Ethiopia, Ug99 was, in fact, added to previously existing races, several of them specifically virulent on durum wheat (Admassu and Fekadu, 2005; Haile et al., 2012). Two such races, typed as TRTTF and JRCQC, have a combined virulence on stem rust resistance genes *Sr9e* and *Sr13* (Olivera et al., 2012). Virulence on *Sr13* appears to be widespread in Ethiopia (Admassu et al., 2009). Very limited effective resistance (5.2%) to races TRTTF and JRCQC was found in a highly diverse collection of 996 tetraploid genotypes evaluated for field reaction at the Debre Zeit Research Center in Ethiopia (Olivera et al., 2012). Therefore, the combination of Ug99 with *Sr9e*- and *Sr13*-virulent Ethiopian races represents a major threat to the viability of the Ethiopian durum wheat production. Achieving higher and more durable stem rust resistance requires the characterization of improved durum wheat germplasm or in exotic sources used for introgression in breeding. Only then can breeding programs develop strategies to preemptively counter the emerging new virulence types in the pathogen populations. Whereas field resistance is the ultimate goal sought in breeding programs, seedling tests are a good complement for resistance characterization, as they allow screening a large number of lines for reaction to multiple races, one race at a time, in relatively short periods and with modest space requirements. Seedling screening provides information for postulating the presence of designated loci based on the series of available races and/ or the presence of novel loci, avoiding the confounding effects of having several races acting at the same time, as is usually the case in field experiments.

Among more than 50 stem rust resistance genes catalogued, only few of them are adult plant resistance gene, while the rest are race specific. The race specific stem rust resistance genes are expressed at both seedling and adult stages. These genes show resistance to some stem rust races but are susceptible to others.

The replacement of currently susceptible wheat varieties with more stem rust resistance varieties remains a high priority given the favorable climatic conditions in East African region for the infection and spread of stem rust. Urgent interventions in identifying good sources of resistance to stem rust will offer an indispensable relief. Hence, the objective of this study was to evaluate 183 durum wheat germplasms against four aggressive stem rust races of *Pgt* races TRTTF, TTTTF, TTKSK, and JRCQC at the seedling stage and to identify new sources of stem rust resistance for future durum wheat breeding program.

MATERIALS AND METHODS

Plant Materials

Host materials comprised of one-hundred-eighty-three cultivars from different durum wheat-growing regions of Mediterranean countries (Italy, Morocco, Spain, Syria, and Tunisia), the Southwestern United States, and Mexico (Appendix 1). A set of the standard North American stem rust differentials with known genes for resistance to stem rust was included in each inoculation with each isolate.

Pathogen Races and their virulence

The durum wheat cultivars were tested against four *Pgt* races: TRTTF, TTTTF, TTKSK, and JRCQC with broad virulence and different geographic origin. The race designation is based on the letter code nomenclature system (Roelfs and Martens, 1988; Roelfs et al., 1993), modified to further delineate races in the TTKS lineage (Jin et al., 2008). These races were selected based on their differential virulence pattern and/or importance for durum wheat. Race TTKSK (Ug99) has a wide virulence spectrum and is rapidly evolving in East Africa. Race TTTTF is the most widely virulent race known in the United States, producing high infection types (ITs) on the majority of stem rust differential lines (Jin et al., 2007). Races TRTTF and JRCQC, both present in Ethiopia, possess a virulence combination that overcomes both the resistance genes *Sr13* and *Sr9e*, two genes present at high frequency in durum wheat (Klindworth et al., 2007). All isolates were derived from single pustules, increased in isolation, and stored at -80°C. Information about the stem rust isolates used in the disease phenotyping test is summarized in Table 1.

Table 1. Origin and virulence properties of the *Puccinia graminis f.sp. tritici* races used to evaluate the durum varieties.

Race	Isolate	Origin	Virulence/avirulence formula
TRTTF	06YEM34-1	Yemen	<i>Sr5, 6, 7b, 9a, 9b, 9d, 9e, 9g, 10, 11, 17, 21, 30, 36, 38, McN/ Sr8a, 24, 31</i>
TTTTF	01MN84A-1-2	United States	<i>Sr5, 6, 7b, 8a, 9a, 9b, 9d, 9e, 9g, 10, 11, 17, 21, 30, 36, 38, McN/ Sr24, 31</i>
TTKSK (Ug99)	04KEN156/04	Kenya	<i>Sr5, 6, 7b, 8a, 9a, 9b, 9d, 9e, 9g, 10, 11, 17, 21, 30, 31, 38, McN/ Sr24, 36, Tmp</i>
JRCQC	09ETH08-3	Ethiopia	<i>Sr21, 9a, 9d, 9e, 9g, 11, 6, 17, McN/ Sr5, 7b, 8a, 36, 9b, 30, Tmp, 24, 31, 38</i>

Inoculation, Incubation, and Disease Assessment

The durum cultivars were evaluated under controlled conditions using a Completely Randomized Design with two replications (over time) for each of the four races. Five to six seedlings per line were inoculated on the fully expanded primary leaves 8 to 9 d after planting. This work was conducted at the Cereal Disease Laboratory, St. Paul, MN, and the experimental procedures in inoculation and disease assessment were performed as described by Jin et al. (2007). Wheat cultivar McNair 701 (Citr 15288) was used as susceptible control in all evaluations. Plants were evaluated for their Infection Types (ITs) 14 days post inoculation using the 0 to 4 scale according to Stakman et al. (1962), where ITs of 0, ;, 1, 2, or X are considered as incompatible (low ITs), where as ITs 3 or higher were considered as compatible (high ITs) (Table 2). Lines giving variable reactions between experiments were repeated again to confirm the most likely reactions.

Table 2. Description of infection type and symptoms based on stakman et al (1962) scale of seedling score

Infection type	Symptoms
0	No uredinia or other macroscopic sign of infection
0;	Few faint flecks
;	No uredinia but hypersensitive necrotic or chlorotic flecks are present
1	Small uredinia often surrounded by a necrosis
2	Small to medium uredinia often surrounded by chlorosis
3	Medium sized uredinia without chlorosis or necrosis
4	Large uredinia without chlorosis or necrosis

RESULTS AND DISCUSSION

Seedling Evaluations

Seedling Infection Types (ITs) for each of the 183 durum germplasms is presented in Appendix 2. The result of seedling test indicates that there is successful inoculation as shown by the susceptible infection types of the check cultivar 'McNear with IT score of 33+. The 183 durum germplasm displayed a wide range of seedling infection types to all four races. The ITs frequency distribution presented in Figure 1 depicts a continuous variation for all four races, with that for JRCQC being skewed toward susceptibility scores (3 and 4). The frequencies of the cultivars categorized as resistant, susceptible, and heterogeneous in their reaction to the four races varied markedly depending on the race. The presence of highly virulent pathotypes in the population of stem rust represents a great threat to commercial varieties in durum wheat cultivation. The results of tests of the durum wheat genotypes to four races showed that the tested entries differ in their resistance to disease (Table 3). For example, seedling resistance to TRTTF, TTTTF, TTKSK, and JRCQC was observed in 149 (81.4%), 117 (63.9%), 106 (57.9%), and 87 (47.5%) cultivars, respectively (Table 3). The ranking values of the four races based on their frequencies of avirulence/ virulence interactions considering the germplasm collection as a whole (with TRTTF showing the highest degree of avirulent interactions, followed by TTTTF, TTKSK and finally JRCQC, which showed the highest frequency of virulent interactions). Sixty-six (36.1%) accessions were resistant (IT = 0 to 2) to all four races. Generally, the high variability in response to seedling infection to different races supports the significance of the race

× genotype interaction. The current results reveal that these durum wheat germplasm are rich source of stem rust resistance. Resistance to wheat stem rust at the seedling stage was reported in cultivated tetraploids by Olivera et al. (2011). Similar results were also reported by Beteselassie et al. (2007) in Ethiopian emmer wheat, as 18 of 41 accessions were resistant to a bulk of six local isolates of stem rust. Similarly, the predominance of infection types ranging from 2= to 2+ appears to be a common feature in cultivated tetraploid wheat and similar results were observed in wild emmer (Olivera et al 2012).

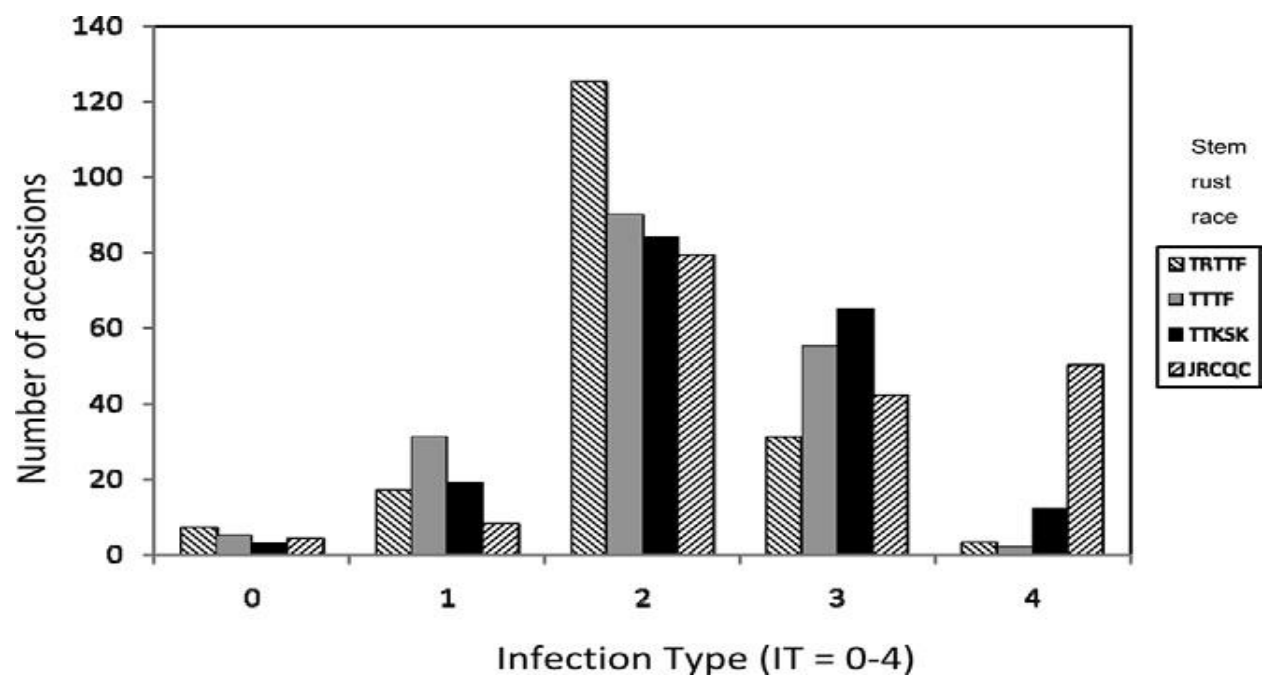


Figure 1. Frequency distribution of infection types (ITs) of 183 durum germplasms evaluated at the seedling stage with four stem rust races.

Table 3. Numbers and frequencies of infection types (IT) and resistant, susceptible and heterogeneous reactions of the 183 durum genotypes included in this study to four races of *Puccinia graminis* f. sp. *tritici* and the combined reaction to all races.

IT ¹ / Reaction	TRTTF		TTTTF		TTKSK (Ug99)		JRCQC		All races	
	Lines	%	Lines	%	Lines	%	Lines	%	Lines	%
"0" or "1"	10	5.5	3	1.6	2	1.1	4	2.2	0	0
"1"	1	0.5	10	5.5	1	0.5	5	2.7	0	0
"2" or "23" or "X"	138	75.4	104	56.8	103	56.3	78	42.6	66	36.1
Resistant Reaction	149	81.4	117	63.9	106	57.9	87	47.5	66	36.1
"3"	22	12.0	47	25.7	53	29.0	39	21.3	10	5.5
"4"	4	2.2	2	1.1	13	7.1	50	27.3	2	1.1
Susceptible Reaction	26	14.2	49	26.8	66	36.1	89	48.6	12	6.6
Heterogeneous ²	8	4.4	17	9.3	11	6.0	7	3.8	1	0.5

¹Infection types observed on seedlings at 14 days post-inoculation using a 0 to 4 scale according to Stakman et al. (1962), where infection types of ; 1, 2, or X are considered as a low IT and ITs of 3 or higher are considered as a high IT

²Cultivars that contained both resistant and susceptible plants

Breeding Perspectives and Conclusions

Identifying new sources of resistance to stem rust including Ug99 and other virulent races provides wheat breeders with an increased diversity of *Sr* genes to be combined in new cultivars. With proper planning and an accurate selection of *Sr* genes, long-term, broad-spectrum resistance can thus be attained. Attaining adult plant resistance is essential for the release of novel cultivars of durum wheat because stem rust susceptibility is not high until heading. Nonetheless, stem rust resistance at the seedling stage, while easy and fast to assay, may not be indicative of the reaction at the adult plant stage because some genes are effective only at specific growth stages. Combining the results of this study with those in adult plant resistance in the field at Debrezeit where races such as TTKSK, TRTTF and JRCQC are prevalent will provide valuable indications to select suitable parental lines for further improving stem rust resistance of durum wheat. Additionally, accessions carrying resistant genes against the four races should be tested against a collection of other different stem rust isolates in the greenhouse to determine whether they possess a broad-based resistance.

A better understanding of the genetic basis underlying the naturally occurring genetic diversity for stem rust response in durum wheat could help to accelerate the progress of enhancing stem rust resistance in this crop while shedding light on the evolution of the host–pathogen relationships. Along this line, the panel of durum wheat germplasm herein evaluated surveys the genetic variation present in elite germplasm pool commonly used by durum breeders, a feature that makes our results more readily transferable to breeding activities. The survey was performed based on a set of *Pgt* isolates belonging to four races chosen to represent the most virulent, diverse, and aggressive pathotypes challenging durum wheat worldwide, that is, the TTKSK (= Ug99) race now diffused throughout Central and Northeast Africa and Iran in Asia (Singh et al., 2006), The North American TTTTF race (Jin et al., 2008) and two recently described and highly virulent Ethiopian races (TRTTF and JRCQC) that overcame some of the few resistance genes effective against Ug99 (Olivera et al., 2012). These four races complement each other in terms of their virulence/avirulence formula, thus providing a nearly complete spectrum of virulence against known resistance loci (Pretorius et al., 2000; Rouse et al., 2012).

This collection of durum wheat is a potential reservoir for several novel resistance genes of seedling resistance. The present study was carried out to identify wheat genetic resources for stem rust resistance to enhance cultivar improvement efforts. Both types of seedling and adult plant resistance identified in wheat germplasm offer promising genetic stocks for accumulating both resistances to acquire durable resistance and long lasting control against stem rust pathogen in Ethiopia.

Stem rust is among the most destructive of wheat diseases and can cause heavy yield loss if uncontrolled. It is however possible to mitigate this yield loss through the use of fungicides, but this has a serious cost implication to a resource poor farmers. Consequently, the plant breeders have emphasized the use of genetic sources of resistance. Major gene resistance/seedling resistance can offer complete protection and significant economic benefits to farmers. Nevertheless, this kind of resistance is known to lack durability. Adult plant resistance (APR) is not complete and not limited to specific physiological races of the pathogen but unlike major gene resistance, it can be durable, hence a major concentration for wheat breeders and valuable to farmers. However, the APR genes can render the plant completely susceptible to the pathogen at seedling stage. Thus, if major genes/seedling resistances genes are identified and systematically employed through gene pyramiding (pyramiding 3-4 major genes using Marker assisted selection by the aid of diagnostic markers), they provide resistance to stem rust for adequate period of times.

In, this study provides novel information that can be exploited for pre-emptive breeding efforts to reduce the vulnerability of durum wheat to stem rust.

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APPENDIXES**Appendix 1.** Name and origin of durum wheat genotypes used in this study.

Genotype code	Genotype name	Origin
1.	CANNIZZO	ITALY
2.	CLAUDIO	ITALY
3.	LESINA	ITALY
4.	MERIDIANO	ITALY
5.	MONGIBELLO	ITALY
6.	NORBA	ITALY
7.	PIETRAFITTA	ITALY
8.	TORREBIANCA	ITALY
9.	BISU_1/PATKA_3	CIMMYT
10.	CMH82A.1062/3/GGOVZ394//SBA81/PLC/4/AAZ_1/CREX/5/HUI//CIT71/CIH	CIMMYT
11.	DUKEM/3/RUFF/FGO//YAV79	CIMMYT
12.	KULRENGI-BALIKCIL_8	CIMMYT
13.	PLATA_16	CIMMYT
14.	PORTO_5	CIMMYT
15.	ROK/FGO//STIL/3/BISU_1	CIMMYT
16.	ACUATICO/YAZI_1	CIMMYT
17.	FOCHA_1/5*ALAS	CIMMYT
18.	BUSHEN_4/TARRO_2//BUSHEN_4	CIMMYT
19.	GS/CRA//SBA81/3/HO/4/MEXI_1/5/MEMO/6/2*ALTAR 84	CIMMYT
20.	RASCON_37/2*TARRO_2	CIMMYT
21.	SRN_3/AJAIA_15//DUKEM_1/3/DION_2	CIMMYT
22.	ALDEANO	IRTA-SPAIN
23.	ARIESOL	IRTA-SPAIN
24.	ARTENA	IRTA-SPAIN
25.	ASTIGI	IRTA-SPAIN
26.	BOABDIL	IRTA-SPAIN
27.	BOLENGA	IRTA-SPAIN
28.	BOLIDO	IRTA-SPAIN
29.	BOLO	IRTA-SPAIN
30.	BOMBASI	IRTA-SPAIN
31.	BORLI	IRTA-SPAIN
32.	CANYON	IRTA-SPAIN
33.	DURCAL	IRTA-SPAIN
34.	DUROI	IRTA-SPAIN
35.	GALLARETA	IRTA-SPAIN
36.	ILLORA	IRTA-SPAIN
37.	SENADUR	IRTA-SPAIN
38.	SULA	IRTA-SPAIN
39.	NASSIRA (MOROCCO_1805)	INRA-MOROCCO
40.	CHAOUI (MOROCCO_1807)	INRA-MOROCCO
41.	AMRIA (MOROCCO_1808)	INRA-MOROCCO
42.	MAROUANE (MOROCCO_1809)	INRA-MOROCCO
43.	JAWHAR	INRA-MOROCCO
44.	MARJANA	INRA-MOROCCO

45.	MARZAK	INRA-MOROCCO
46.	OURGH	INRA-MOROCCO
47.	TAREK	INRA-MOROCCO
48.	AWALBIT	ICARDA
49.	BCR/3/CHAM 1//GTA/STR	ICARDA
50.	CHHB88/DERAA	ICARDA
51.	CHACAN	ICARDA
52.	KARIM	ICARDA
53.	HML/CHHB88	ICARDA
54.	KRS/HCN	ICARDA
55.	MURLAGOST-3	ICARDA
56.	MOULSABIL 2	ICARDA
57.	OMBAR	ICARDA
58.	MRB589 5	ICARDA
59.	QUADALETE//ERP/MAL/3/UNKNOWN(VSGI,ODESSA)	ICARDA
60.	SEBAH	ICARDA
61.	STOJOCRI 3	ICARDA
62.	ZEINA 1	ICARDA
63.	ANTON	ICARDA
64.	APPIO	ITALY
65.	ARCANGELO	ITALY
66.	ARCOBALENO	ITALY
67.	BRAVADUR	DESERT
68.	BRONTE	ITALY
69.	CAPEITI 8	ITALY
70.	CAPPELLI	ITALY
71.	CICCIO	ITALY
72.	COLORADO-DW	DESERT
73.	COLOSSEO	ITALY
74.	CORTEZ	DESERT
75.	CRESO	ITALY
76.	DON PEDRO	ITALY
77.	DUILIO	ITALY
78.	FLAMINIO	ITALY
79.	FORTORE	ITALY
80.	GARGANO	ITALY
81.	GRAZIA	ITALY
82.	IRIDE	ITALY
83.	ITALO	ITALY
84.	IXOS	ITALY
85.	KRONOS	DESERT
86.	MESSAPIA	ITALY
87.	MEXICALI 75	ITALY
88.	MOHAWK	ITALY
89.	OFANTO	ITALY
90.	PLATANI	ITALY
91.	PLINIO	ITALY
92.	PRODURA	ITALY

93.	REVA	ITALY
94.	ROQUENO	ITALY
95.	SVEVO	ITALY
96.	TRINAKRIA	ITALY
97.	VALBELICE	ITALY
98.	VALNOVA	ITALY
99.	WESTBRED 881	DESERT
100.	WESTBRED TURBO	DESERT
101.	AGHRASS_1	ICARDA
102.	AINZEN_1	ICARDA
103.	ANGRE	ICARDA
104.	AMEDAKUL-1	ICARDA
105.	AMMAR-1	ICARDA
106.	ARISLAHN-5	ICARDA
107.	ATLAST-1	ICARDA
108.	AUS1	ICARDA
109.	AWALI_1	ICARDA
110.	RADIO SO	ITALY
111.	AZEGHAR_2	ICARDA
112.	BICRE	ICARDA
113.	BICREDERAA_1	ICARDA
114.	BIGOST-1	ICARDA
115.	BELIKH 2	ICARDA
116.	BRACHOUA	ICARDA
117.	CHAHBA88	ICARDA
118.	CHAM_1	ICARDA
119.	DERAA	ICARDA
120.	GEROMTEL-1	ICARDA
121.	GEZIRA-17	ICARDA
122.	GIDARA_2	ICARDA
123.	GUEROU_1	ICARDA
124.	HAURANI	ICARDA
125.	HEIDER	ICARDA
126.	OSL_1/4/BUC/CHRC//PRL/3/PVN/5/HEL/3/YAV/CORM//SHWA	ICARDA
127.	SEBOU	ICARDA
128.	BLK2//134XS-69-186/368-1/3/MRB589_5/4/ALBT_3	ICARDA
129.	ARIC31708.70/3/BO-DW//CDECH/BR-DW/4/CIT71/GTA	ICARDA
130.	JORDAN	ICARDA
131.	KABIR_1	ICARDA
132.	KHABUR_1	ICARDA
133.	KORIFLA	ICARDA
134.	LAGONIL-2	ICARDA
135.	LAHN	ICARDA
136.	LOUKOS_1	ICARDA
137.	MAAMOURI-1	ICARDA
138.	MARSYR-1	ICARDA
139.	MASSARA_1	ICARDA
140.	MIKI-1	ICARDA

141.	MURLAGOST-1	ICARDA
142.	NILE	ICARDA
143.	OMGENIL_3	ICARDA
144.	OMLAHN-3	ICARDA
145.	OMRUF-2	ICARDA
146.	OMSNIMA-1	ICARDA
147.	ORONTE 1	ICARDA
148.	OTB-6	ICARDA
149.	OUASERL_1	ICARDA
150.	OUASLAHN-1	ICARDA
151.	QUABRACH-1	ICARDA
152.	QUADALETE	ICARDA
153.	RAZZAK	INRAT
154.	SAADA3/DDS//MTL-1	ICARDA
155.	SAJUR	ICARDA
156.	SHABHA	ICARDA
157.	TELSET_5	ICARDA
158.	TENSIFT_1	ICARDA
159.	TERBOL_97_3	ICARDA
160.	TUNSYR-1	ICARDA
161.	WADALMEZ_1	ICARDA
162.	YOUNES-1	ICARDA
163.	YOUSEF_1	ICARDA
164.	KOFA	ITALY
165.	1A.1D 5+10-6/3*MOJO//RCOL	CIMMYT
166.	SOOTY_9/RASCON_37	CIMMYT
167.	STOT//ALTAR 84/ALD	CIMMYT
168.	SOMAT_4/INTER_8	CIMMYT
169.	CHEN_1/TEZ/3/GUIL//CIT71/CII/4/SORA/PLATA_12/5/STOT//ALTAR 84/ALD	CIMMYT
170.	MALMUK_1//LOTUS_5/F3LOCAL(SEL.ETHIO.135.85)	CIMMYT
171.	1A.1D 5+10-6/2*WB881//1A.1D 5+10-6/3*MOJO/3/BISU_1/PATKA_3	CIMMYT
172.	HESSIAN-F_2/3/STOT//ALTAR 84/ALD	CIMMYT
173.	AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37	CIMMYT
174.	USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV 79/8/POD_9	CIMMYT
175.	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN	CIMMYT
176.	GEDIZ/FGO//GTA/3/SRN_1/4/TOTUS/5/ENTE/MEXI_2//HUI/3/YAV_1/GEDIZ /6/SOMBRA_20/7/STOT//ALTAR 84/ALD	CIMMYT
177.	VANRRIKSE_6.2//1A-1D 2+12-5/3*WB881	CIMMYT
178.	RANCO//CIT71/CII/3/COMDK/4/TCHO//SHWA/MALD/3/CREX/5/SNITAN	CIMMYT
179.	PLATA_10/6/MQUE/4/USDA573//QFN/AA_7/3/ALBA-D/5/AVO/HUI/7/PLATA_13/8/THKNEE_11/9/CHEN/ALTAR 84/3/HUI/POC//BUB/RUFO/4/FNFOOT	CIMMYT
180.	EUDO//CHEN_1/TEZ/3/TANTLO_1/4/PLATA_6/GREEN_17	CIMMYT
181.	ROLA_5/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/4/MALMUK_1/SERRATOR_1	CIMMYT
182.	ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1	CIMMYT

183. SOMAT 3/PHAX 1//TILO 1/LOTUS 4 CIMMYT

Appendix 2. Phenotypic response to four races (TRTTF, TTKSK, TTTTF and JRCQC) of the 183 durum germplasm included in the study.

Genotype	Stem rust response			
	TRTTF	TTKSK	TTTTF	JRCQC
1.	3- / 2-	2 / 3	2-;	1;
2.	22-	2 / 3	2-	2
3.	2	33+	2-; / 33+	1; / 3+
4.	2-	4	4	4
5.	3	2+/2+3-	2+ / 3-	2-
6.	2-	;2-	2-	3+ / 2-;
7.	33+	3	2+	;N
8.	33+	33+	3+	4
9.	2-	2-	2-	2-
10.	2-	2	2-	4
11.	2	3+	3+	3+
12.	2-	2	2-	2-
13.	2-;	2	2-;	2
14.	2-	2	2-	2
15.	2-	2	2-	22+
16.	2-	2-;	2-	4
17.	2-	2	2-	2
18.	2-	22-	2-	2
19.	2-;	2	2-	2-
20.	2-	2-	2-	2-
21.	;N	2-;	;N	22+
22.	2-	2-	2-	0; / 3+
23.	;	2-;	2-	2-
24.	3+	3	3+ / 2	4
25.	2-	3	33+	4
26.	2-	4	3+	0
27.	;N	;	;1-	2+
28.	2-	2-	2	2+
29.	2-	2	2-;	2-
30.	2-	2	2-	2-
31.	2-	2-;	2-	2-
32.	2-	2-	2-	3+1;N
33.	22-	3+	3+	3+
34.	2-	2-	22-	22+
35.	2-	;2-	2-;	2-
36.	2-;	2-	2-	2-

Genotype	Stem rust response			
	TRTTF	TTKSK	TTTTF	JRCQC
37.	;N	0;	;1	2+3-
38.	2-	2 / 2+	2-;	2-
39.	2	3++	3+	4
40.	2	2-	22-	3
41.	2-	;	2-	2-
42.	33+	3	3+	3+
43.	2- / 22+	2-	2-	2-
44.	2-	2-	2-	2-
45.	2+	2-	2-	2
46.	2	2+3- / 3	3+	3+
47.	;2-N	33+	22-	3+
48.	2	3-	3	3+
49.	2-	3+	2 / 3	3+
50.	2-	3	3	4
51.	22-	3-	2-	3+
52.	22-	3-	3+	4
53.	2 / 3+	2- / 3	2 / 3+	2+ / 4
54.	2-	2-	;1-	2-
55.	0; / ;1	2+3- / 22-	2+3-	3+
56.	4	3	33+	3+
57.	2 / 2-;	2- / 3+	;2- / 3	2
58.	22+	3+	3	4
59.	2-	2-	2-	2-
60.	22- / ;	2-	2-	2+
61.	22-	2-	2	22+
62.	3	3	2-	;N
63.	3	3	2-	11+;
64.	X	2+	2+	4
65.	3-	2+3-	3-	33+
66.	2-	22+	2-;	2-
67.	2-	2-;	2-	3+
68.	2	3	33+	4
69.	2+3	2+	22+	33+
70.	3- / 4	2+3	2+	4
71.	33+	3	33+	4
72.	3+ / 2;	4	2+	4

Genotype	Stem rust response			
	TRTIF	TTKSK	TTTIF	JRCQC
73.	3+	3+	3	4
74.	33+	3	33+	4
75.	23	3	2-	33+
76.	2-	2-	2-;	4
77.	2	3	3	4
78.	2	33-	3	4
79.	3+	2+3 / 3	33+	4
80.	3+	3	33+	3+3
81.	2-; /;	2-	;	2-
82.	2-	2	2-	2
83.	;N	2-N	;2-	2
84.	33+	3	2+	2-
85.	2-	2-	2- / 3+	2-
86.	2	2-	2-	2-
87.	2-	2-	2-	2
88.	2-	3	22+	1
89.	33+ / 2+	3+	2-	2-
90.	2-	2+2	2	22+
91.	3+3	3	33+	4
92.	22+	22+	22-	2+
93.	2-;	2- / 3	;2-	3+
94.	32+; / 2;	2+3	31+;	4
95.	2-	2-	2-	4
96.	2+3-	22+	2+	3
97.	2+3-	22+	2+	3
98.	3	2+3-	2	;1
99.	2-;	2-	22-	2+
100.	22-	3	3	3+
101.	2-	2-	2- / 3+	22+
102.	2-	2-	2-	2-
103.	2-	2-	2+	33+
104.	2-	2-;	2-;	4
105.	2	2	22+	22+
106.	2-;	2-;	2-;	33+
107.	2-	4/X	3	4

Genotype	Stem rust response			
	TRTTF	TTKSK	TTTTF	JRCQC
108.	3+	3+	3+	4
109.	2-	2-;	2-;	4
110.	2	2+	2-	2-;
111.	2	4	3+	4
112.	2	3	2+ / 3	4
113.	2-	3+	2-	3+
114.	2-	2-	2-	2+3-
115.	2-;	2-	2-;	2-
116.	2-;	2-;	2-;	33+
117.	2-	4	3+	3+
118.	22+	2-	2- / 3-	1; / 4
119.	3-	4	2-;	2
120.	2-	3	2-	2+
121.	2-2	3	22+	3
122.	2-	3+	3+	4
123.	2-	2-	2- / 3+	2-
124.	4	4	4	4
125.	2 / 2+	2-	2	2+
126.	2	3	2-	2-
127.	;N	2	2- / ;N1	2- / 3
128.	2-	;2-	2-;	2-;
129.	;N / 2-	2-;	;N	2-
130.	2	2	22-	22+
131.	2-	2-;	2-	4
132.	2-	2-	2-	33+
133.	33+	3+	3 / ;2-	3+
134.	;2- / ;N	2+ / 3	3 / 2;	3+
135.	2- / 3-	2-	2	4
136.	2-	4	3	4
137.	2-	2-	2-	2-
138.	2	3+	3+	4
139.	2-	3+	3	4
140.	2-	2	;2-	2-
141.	2-;	2-	2-;	2-
142.	2-	2-	2	22-
143.	2-;N	3+	2+3-	4

Genotype	Stem rust response			
	TRTTF	TTKSK	TTTTF	JRCQC
144.	2-	4	33+	4
145.	2-	2-	2-;	2-
146.	4	3+	3+	4
147.	2-;	2-;	2-;	2-
148.	2 / 3-	3+	2-	2
149.	2-	2+	3+	3+
150.	2-	3 / 2	;2-	;1 / 4
151.	2-	2-	2-	2
152.	3+3	X-	3	4
153.	22+	;2-	2-	4
154.	2- / 3+	2-	2- / 3	3+
155.	2-	2-;	2-;	2-
156.	3+3	3	3	3+
157.	2-	22+	2- / 3	2-
158.	2-	2-;	2-	3+
159.	2-	2-	2- / 3-	2-
160.	2-	4 / 2-	2-	3+
161.	2-	2-	2-	;2-
162.	2-	33+	3+	4
163.	2-	3+	3+	4
164.	2-	2-	;2-	2-
165.	;N	33+	3	3+
166.	2-	4	3	3+
167.	2-	2-	2-;	2
168.	2	4	3+	4
169.	2-	2	2	2+
170.	2-	2-	2-	22+
171.	2-	;2= / 3	;2-	;
172.	2-	2-	2-;	2-
173.	2-	2-	2-	4
174.	2-	2-	2	2
175.	2-	3	3+	4
176.	2-	2-	2-	3
177.	2-	2	2-	2
178.	2-	3	3+	4
179.	2-	2-	2-;	4
180.	2-	2-	2-	3+
181.	2-;	2	2- / 3	2
182.	2-	2	2+	2+
183.	2-	3	3+	4