



## Status of stripe (yellow) rust in Syria in 2010-2011

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### ► To cite this version:

R. El Amil, K. Nazary, Claude C. Pope de Vallavieille, Sajid S. Ali, A. Yahyaoui, et al.. Status of stripe (yellow) rust in Syria in 2010-2011. BGRI Technical workshop,, Sep 2012, Beijing, China. 2012. hal-01190827

**HAL Id: hal-01190827**

**<https://hal.science/hal-01190827>**

Submitted on 3 Jun 2020

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Context and Objectives

*Puccinia striiformis* f. sp. *tritici* (*Pst*) has become the most devastating widespread disease of wheat and could threaten food security in many countries of the CWANA region. In 2010-2011, an epidemic occurred in Syria causing 20 to 70% yield loss in wheat; important losses were also recorded in Algeria, Azerbaijan, Ethiopia, Morocco, Uzbekistan. Current study aimed to assess the evolution and changes in *Pst* virulence dynamics; the present work was thus to compare the genetic diversity of the Syrian *Pst* population with the previously described worldwide populations of the wheat yellow rust pathogen (Ali *et al.*, in prep. and Walter *et al.*, in prep.).

Materials and Methods

Extensive field surveys were conducted in major bread and durum wheat areas in Syria in 2011 using the BGRI surveillance protocols. In total, 223 samples were collected from 44 fields (Fig. 1) from which 48 isolates were pathotyped using 16 differential lines at the seedling stage and a sub-set of Avocet-based differential lines Avocet Yr1,Yr2,Yr3,Yr4,Yr5,Yr6,Yr7,Yr8,Yr9,Yr10,Yr15,Yr27,Yr32; Kalyansona, Suwon 92/Omar and TP1295 were used as source of Yr2,YrSu and Yr25 respectively. The 48 isolates were genotyped with 20 SSR markers in three multiplexes (Ali *et al.*, 2011).

Results and Discussion

Stripe rust was prevalent in wheat growing areas in northern, northeastern, and eastern parts of the country. A total of 24 races were identified prevalent in different frequency across Syria (Fig.2) where 6E0 had the highest frequency (22.90%). A group of twenty virulence phenotypes were identified from 48 isolates (Table1). The virulence profile corresponding to the phenotyped PstS2 (— (2) — — 6 7 8 9 — — — (Sd) — —; Hovmøller *et al.*,2008) was found in 25% of the samples. Microsatellite genotyping of the 48 isolates revealed very low diversity with the SSR profile closely related to the SSR profile of PstS2 (Walter *et al.*, in prep.) and specific to the Middle-East genetic group (Ali *et al.*, in prep.).

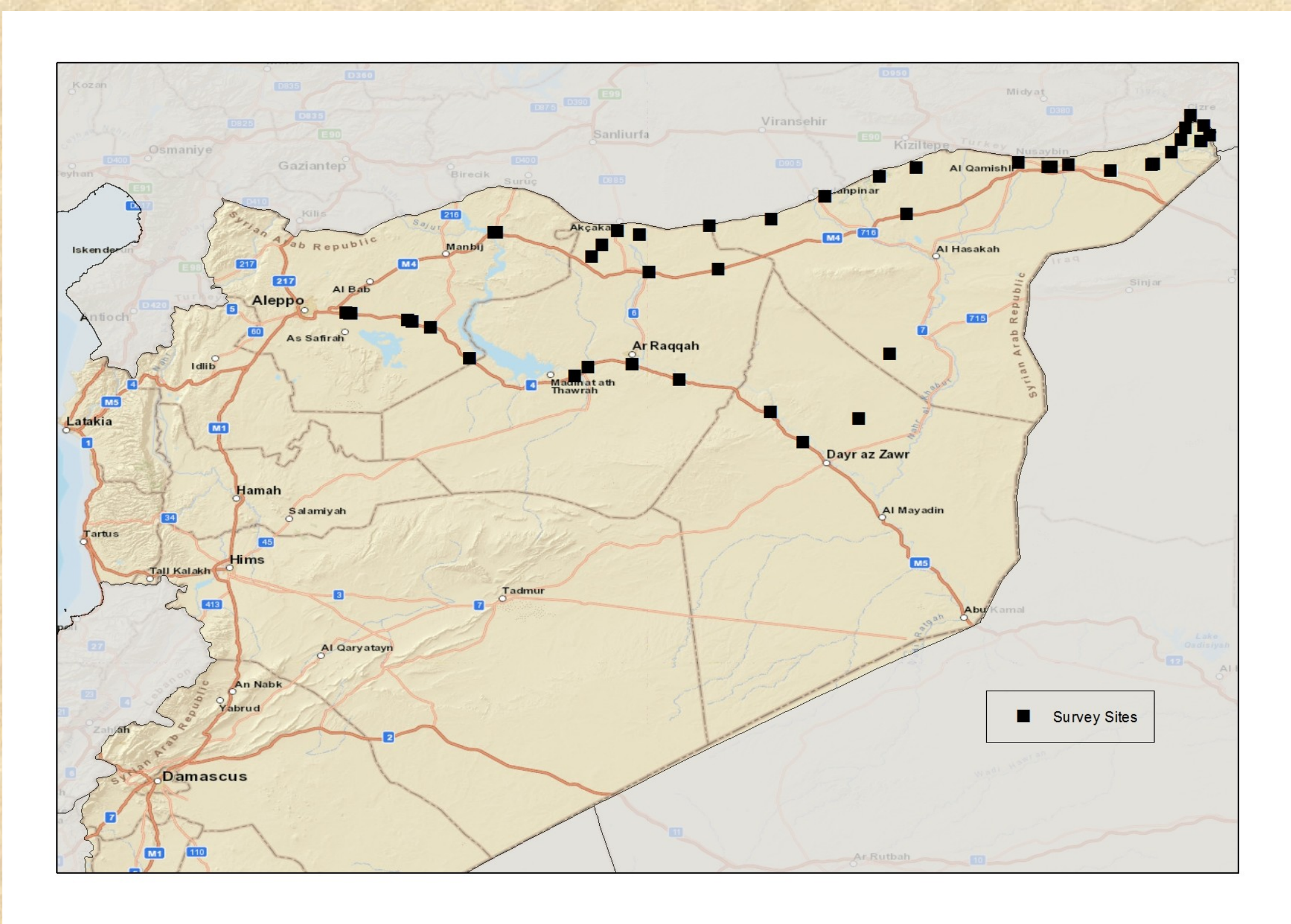


Fig. 1 : Map of 44 PST surveyed sites in Syria

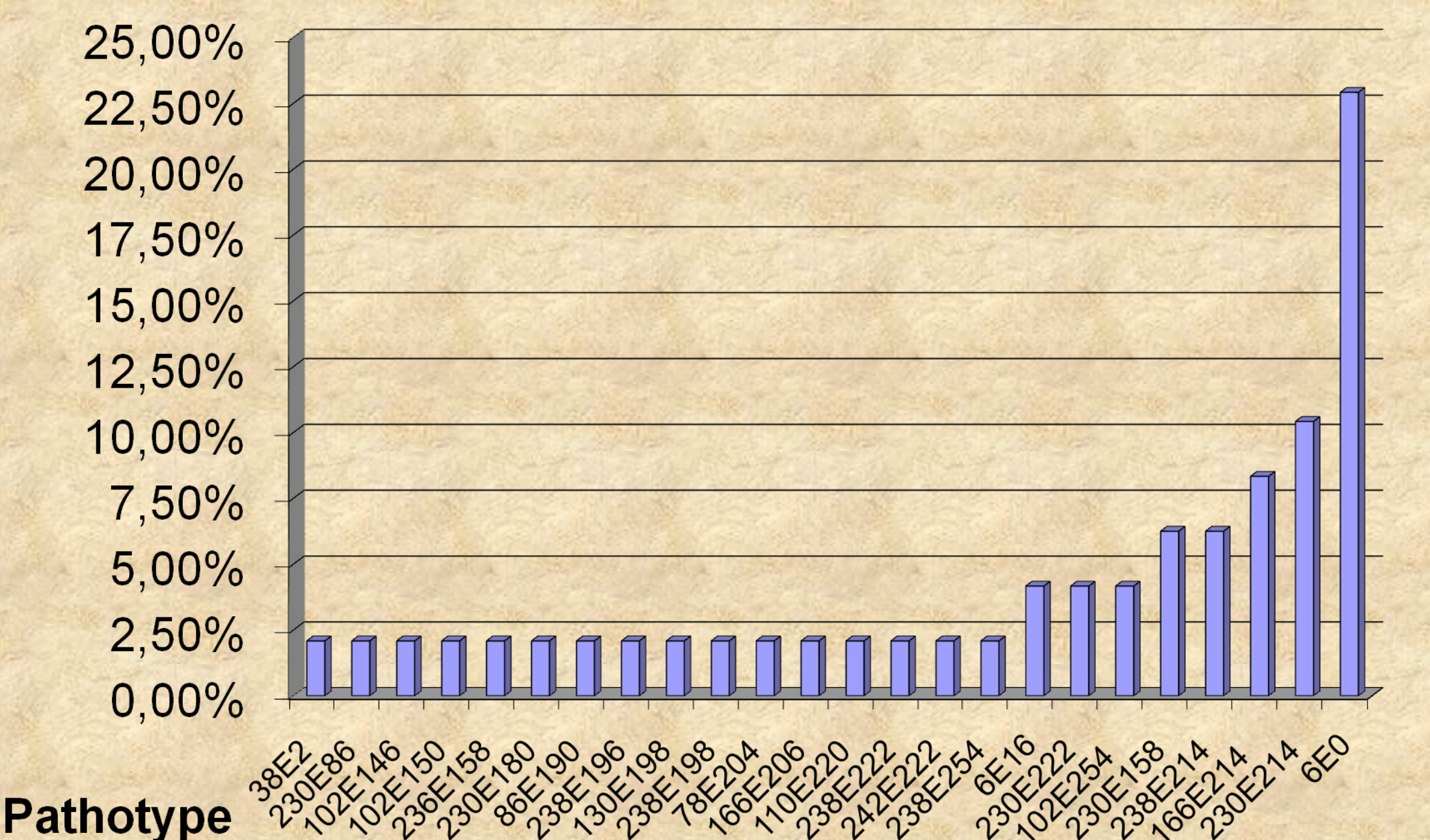


Fig. 2 : Distribution of races in percentage

Tab. 1 : Virulence profile and SSR results

		Host Origin					
	Virulence phenotype(a)				Total of	PstS2 phenotyped	PstS2 Variant genotyped
	1,2,3,4,5,6,7,8,9,10,15,25,27,32,Sd,Su,Sp				Isolates		
		BW	DW	Volunteer			
V2,7,9,25	-2,-,-,-,7,-,9,-,-,25,-,-,-,-	4	2	0	6		+
V2,7,9,25,27	-2,-,-,-,7,-,9,-,-,25,27,-,-,-	1	0	0	1		+
V2,7,8,9	-2,-,-,-,-,7,8,9,-,-,-,-,-	0	1	0	1		+
V2,7,9,25,Sp	-2,-,-,-,7,-,9,-,-,25,-,-,-,-,Sp	4	0	0	4		+
V2,6,7,8,9,25,Sp	-2,-,-,-,-,6,7,8,9,-,-,25,-,-,-,-,Sp	1	0	0	1		+
V2,7,9,25,27,Sp	-2,-,-,-,7,-,9,-,-,25,27,-,-,-,-,Sp	1	1	0	2		+
V2,7,9,25,27	-2,-,-,-,7,-,9,-,-,25,27,-,-,-,-	2	0	0	2		+
V2,6,7,,9,25,27	-2,-,-,-,(6)*,-,9,-,-,25,27,-,-,-,-	0	0	1	1		+
V2,7,8,9,25,27	-2,-,-,-,7,8,9,-,-,25,27,-,-,-,-	4	2	0	5		+
V2,6,7,9,27,-	-2,-,-,-,6,7,-,9,-,-,27,-,-,(Sd),-,-	0	1	0	1		+
V2,6,7,8,9,25,27,Sd,Sp	-2,-,-,-,6,7,8,*,-,-,25,*,-,Sd,-,-,Sp	0	0	1	1		+
V2,6,7,8,9,25,27,Sd,Sp	-2,-,-,-,6,7,8,9,-,-,25,27,-,-,Sd,-,-(Sp)	8	2	1	12	+	+
V2,6,7,9,25,27	-2,-,-,-,6,7,-,9,-,-,25,27,-,-,-,-	3	1	0	4		+
V2,6,7,9,25,27,Su	-2,-,-,-,6,7,-,9,-,-,25,27,-,-,(Sd),Su,-	2	0	0	2		+
V2,6,7,9,25,Su	-2,-,-,-,6,7,-,9,-,-,25,-,-,-,(Sd),Su,-	0	1	0	1		+
V2,7,8,9,25,27,Sp	-2,-,-,-,7,*,-,9,-,-,25,27,-,-,-,(Sp)	1	0	0	1		+
V2,7,8,9,25,27,Sp	-2,-,-,-,7,8,9,*,-,-,25,27,-,-,-,Sp	1	0	0	1		+
V2,6,7,9,25,27,Sd	-2,-,-,-,6,7,-,9,-,-,25,27,-,-,Sd,-,-	1	0	0	1		+
V2,6,7,9,25,27,Su	-2,-,-,-,6,7,-,9,-,-,25,27,-,-,(Sd),Su,-	1	0	0	1		+
		34	11	3	48		

(a) Numbers correspond to yellow rust resistance genes. Sd, Su and Sp designate resistance in Strubes Dickkopf, Suwon92/Omar and Spaldings Prolific respectively. Avirulence is shown by ‘---’ and parenthesis indicate intermediate reaction.  
 \*Asterisk refers to missing data  
 BW, DW refers respectively to Breadwheat and Durum Wheat  
 (+) refers to positive result

Conclusion

Resistance genes Yr1,Yr3,Yr4,Yr5,Yr10, Yr15 and Yr32 were still effective against all Syrian isolates whereas the virulences for almost all the widely used resistance genes Yr2, Yr6, Yr7, Yr9, Yr25 and Yr27 were found among the 48 isolates. But virulence for Yr8, YrSu, YrSd and YrSp occurred at various frequencies. The microsatellite analyses confirmed the prevalence of PstS2 type strain in the Syrian population with very low genotypic diversity.

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