

Research Article

Identification of different types of resistance to stripe rust *Puccinia striiformis* f. sp. *tritici*, in some dryland wheat genotypes of Iran

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Abstract: Stripe (yellow) rust, caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*), is a globally devastating wheat disease and a critical yield-limiting factor in Iran, often resulting in severe production losses and necessitating costly chemical interventions. The deployment of host resistance remains the most economical and sustainable management strategy. This study aimed to identify different types of resistance to stripe rust among dryland wheat genotypes to support cultivar improvement programs. A collection of 233 dryland wheat genotypes (comprising 120 winter bread wheat, 64 spring bread wheat, and 49 durum wheat) was evaluated for adult plant resistance (APR) under field conditions at the Ardabil Agricultural Research Station, Iran. Parallel seedling resistance screenings against two prevalent *Pst* pathotypes (6E6A+, Yr27 and 142E158A+, Yr27) were conducted under controlled greenhouse conditions. The results revealed a spectrum of resistance responses. Forty-six genotypes (19.7%) exhibited all-stage resistance (ASR) at the seedling level against both pathotypes, suggesting the presence of known seedling resistance genes such as *Yr3b*, *Yr4*, *Yr5*, *Yr10*, *Yr15*, *YrSP*, *YrCV*, *YrSD*, or other unidentified genes. Fourteen genotypes were susceptible as seedlings to at least one pathotype but displayed a low relative area under the disease progress curve (rAUDPC) value (0-10) in the field, indicating effective APR. Another 10 genotypes, susceptible at the seedling stage, showed moderate rAUDPC values (11-30), characteristic of slow-rusting (SR) resistance. The remaining 163 genotypes were highly susceptible (high rAUDPC) in the field, regardless of their seedling response. The resistant genotypes identified in this study, particularly those with APR and SR characteristics, represent valuable genetic resources for breeding programs aimed at pyramiding multiple resistance genes to develop durable resistance and achieve long-term control of stripe rust in Iran.

Keywords: Dryland wheat, Race-specific resistance, Non-race specific resistance, Durable resistance

Introduction

Wheat stripe (yellow) rust, caused by the fungus *Puccinia striiformis* Westend. f. sp. *tritici*

Eriksson (*Pst*) is a major foliar disease affecting wheat in temperate, cool, and high-altitude regions worldwide (Boyd, 2005). Present on all continents except Antarctica, it is widespread

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and consistently threatens global wheat production, with documented yield losses ranging from 30 to 100% (Chen, 2005). The economic importance of wheat rusts is undeniable; however, stripe rust is often considered more devastating and widespread than leaf or stem rust due to its direct impact on photosynthetic tissue, leading to severe foliar damage and significant reductions in grain yield and quality (Line, 2002; Chen, 2005).

The high adaptability of the *Pst* pathogen, facilitated by mutation, migration, and both vegetative and sexual hybridization, allows it to overcome resistance and thrive in diverse climatic conditions (Kolmer, 2005; Jin *et al.*, 2010). This adaptability has led to frequent and severe epidemics. Over recent decades, major outbreaks have been reported across most wheat-growing areas of the world, including Iran, where epidemics in 1992 and 1994 resulted in yield reductions of 1.5 and 1 million tons, respectively (Torabi *et al.*, 1995). Significant epidemics have also been documented in Central and West Asia, China, Australia, the United States, and North Africa (Chen, 2005; Wellings, 2011; Ziyaev *et al.*, 2011; Morgounov *et al.*, 2012). Globally, annual damage from wheat rusts is estimated at up to 15.04 million tons, underscoring the persistent threat to food security (Huerta-Espino *et al.*, 2020; Basnet *et al.*, 2022).

While chemical and cultural control methods can reduce damage, they are often impractical for farmers in developing countries and are not aligned with long-term sustainable agriculture priorities (Chen, 2005). Consequently, the deployment of host genetic resistance remains the most economical, effective, and environmentally safe strategy for managing stripe rust (Chen, 2007). Two primary types of genetic resistance are recognized: race-specific (all-stage) resistance and non-race-specific (adult plant) resistance. Race-specific resistance, which operates on the gene-for-gene principle (Flor, 1942), is often effective but can be rapidly overcome by evolving pathogen races, typically within 3–5 years (Line and Qayoum, 1992). In contrast, non-race-specific resistance, often controlled by minor-effect genes, is generally

more durable. The most effective strategy for achieving long-lasting control is the pyramiding of both race-specific and non-race-specific resistance genes within a single cultivar (Singh *et al.*, 2004). This approach necessitates the identification and characterization of diverse genetic resistance resources (Bux *et al.*, 2011).

The evaluation of resistance, particularly quantitative adult plant resistance (APR) and slow rusting (SR), is best conducted under field conditions. Key parameters for quantification include final disease severity (FDS), the area under the disease progress curve (AUDPC), the relative AUDPC (rAUDPC), the apparent infection rate (*r*), and the average coefficient of infection (ACI) (Safavi and Afshari, 2012; Hei *et al.*, 2015; Mohammadi *et al.*, 2023). The rAUDPC is a particularly valuable integrated measure as it correlates strongly with components of slow rusting (e.g., latent period) and, importantly, with reduced yield loss (Sandoval-Islas *et al.*, 2007; Ochoa and Parlevliet, 2007; Safavi, 2015). Field-based assessment is crucial because the correlation between greenhouse seedling tests and the expression of APR components in the field is often low (Sandoval-Islas *et al.*, 2007).

Previous studies, both globally and in Iran, have successfully employed these methods to identify resistant sources. For instance, evaluations of international wheat collections have identified genotypes possessing all-stage resistance (ASR) genes such as *Yr5*, *Yr10*, and *Yr15*, as well as those with effective APR and SR (Bux *et al.*, 2012; Zeng *et al.*, 2014; Zahravi *et al.*, 2019). Safavi and Afshari (2017) further demonstrated the diversity of resistance responses in Iranian wheat cultivars over a multi-year study.

Given the constant threat of new *Pst* races, identifying new and diverse sources of resistance remains a cornerstone of breeding programs. This study was therefore conducted to identify and characterize different types of resistance (seedling and adult plant) to stripe rust in a diverse collection of dryland wheat genotypes from Iran. The objective was to identify promising genetic stocks possessing effective ASR, APR, and SR to

support breeding programs aimed at developing cultivars with durable resistance for sustainable wheat production.

Materials and Methods

Plant materials

A total of 233 dryland wheat genotypes (120 winter bread wheat, 64 spring bread wheat, and 49 durum wheat) provided by the Dryland Agricultural Research Institute were evaluated in this study. The characteristics of 70 selected genotypes, representing different resistance types from the initial set, are presented in Table 1.

Seedling resistance tests

Seedling reactions were assessed under controlled greenhouse conditions at the Seed and Plant Improvement Institute (Karaj, Iran). For each genotype, 5-7 seeds were sown in individual pots (7x7 cm) containing a soil: peat moss: sand mixture (7:5:5). Ten-day-old seedlings were inoculated separately with two distinct *Puccinia striiformis* f. sp. *tritici* pathotypes: **142E158A+**, **Yr27** (possessing a broad virulence spectrum) and **6E6A+**, **Yr27** (possessing a narrow virulence spectrum). The virulence/avirulence formula for these pathotypes is detailed in Table 2.

Table 1 Characteristics and stripe rust resistance responses of the evaluated dryland wheat genotypes at seedling and adult plant stages.

No.	Pedigree/Variety	Type ¹	Growth habit ²	Seedling response ³	Adult plant response ⁴			Kind of resistance ⁵
					Path. 1	Path. 2	FRS & IT	
1	WGRC10/3/KS93U69 sib/TA2455/KS93U69/4/JAGGER	BW	W	1	0	10MR	4	ASR
2	X96V107/OGALLALA	BW	W	3	0	5MR	4	APR
3	GB105	BW	W	0	0	10MR	4	ASR
4	SPII Genebank Collection -2010- 288	BW	W	0	0	10MR	4	ASR
5	Sardari/TEU2/3/Ures/Fan/kauz IRBW04-23-54-15-OSAR-OSAR-OSAR-OSAR-3SAR-OSAR	BW	W	1	0	R	27	ASR
6	Sardari/TEU2/3/Ures/Fan/kauz IRBW04-23-54-15-OSAR-OSAR-OSAR-OSAR-8SAR-OSAR	BW	W	4	0	R	1	APR
7	BUC/PVN/MILAN/3/TX96V2427	BW	W	4	0	R	1	APR
8	88 (CB-R6)/Azar2 //Un known-9/914 Gene Bank Material IRBW 05- 165-OMAR-OMAR-OMAR-5MAR-2MAR	BW	W	0	0	20MR	14	ASR
9	NGDA146/4/YMH/TOB/MCD/3/LIRA/5/F130L1.12 /6/Azar2 /7/Trakia//Maga"s"74/Mon"s"3/Shahi/4/Khazar/3/Jcam/Emu"s"//Dove..	BW	W	0	0	10MR	10	ASR
10	Fenglang15/Sefid/4/Dari-16/3/Hd2172/Bloudau//Azadi /5/10 GHAZAGESTAN 98-99/Zagros IRBW 05- 099-OMAR-0SHI-OMAR...	BW	W	0	0	10MR	10	ASR
11	ID800994W/VEE//F900K/3/PONY/OPATA/4/4848 Mashad/Tui"s" /5/Un known-2/4/Trakia//Maga"s"74/Mon"s"3/Shahi IRBW	BW	W	0	0	10MR	24	ASR
12	CH94878/BLOYKA/3/TX81V6614/SERI*3/BUC ICWH99-0468-0AP-2AP-2AP-0AP-1AP-0AP	BW	W	0	0	20MR	27	ASR
13	ERYT783-96/SHARK-1 TCI-001409030YE-030YE-2E-0E-5AP-0AP	BW	W	0	0	R	4	ASR
14	RANA96/3/RSK/CA8055/CHAM6 TCI 001093-030YE-030YE-7E -0E	BW	W	0	0	20MR	14	ASR
15	SABALAN/ALTAY	BW	W	0	0	20MR	17	ASR
16	ID800994W/FALKE/ERYT26221 TCI031020 -0E-0E-0YA-0E -6E -0E	BW	W	0	0	20MR	8	ASR
17	BLUEGIL-2/CAMPION TCI 001177 -030YE-030YE-2E-0E	BW	W	0	0	10MR	4	ASR
18	Antonisis	BW	W	2	2	20M	20	ASR
19	Luhullus	BW	W	0	0	10MR	10	ASR
20	ZARGANA-6/4/AU/CO652337//2*CA8-155/3/F474S1-1.1	BW	W	2+	2+	30MR	11	ASR
21	SHI#4414-CROWS"/... ..	BW	W	0	0	R	1	ASR
22	ATTILA*2/PBW65/YAKAR	BW	W	3	3	20MR	23	SR
23	RioBlanco/Rose	BW	W	1	0	10MR	4	ASR
24	W0405D/HGF112//W7469C/HCF012	BW	W	4	4	20MR	14	SR
25	SABALAN/ALTAY	BW	W	0	0	10MR	10	ASR
26	KS97W0935-29-15/SHARK-1/5/VEE/TSI/GRK/3/NS5503/5/C12615/COFN/3/N10B/P14/P101/4/KRC67	BW	W	0	2	10MR	10	ASR
27	KS98HW220-5-1(ARLIN/YUMA)/KS01HW162(TGO/BTY SIB)	BW	W	0;1	0	R	1	ASR
28	ZANDER-10/BOW/NKT	BW	W	0	0	R	14	ASR
29	BUC/PVN/MILAN/3/TX96V2427	BW	W	2+	3	20M	8	APR
30	KARIM	BW	S	0;1	0	10MR	6	ASR
31	PASTOR/HXL7573/2*BAU/3/SOKOLL/WBLL1PTSS02B00098T-0TOPY-0B-0Y-0B-4Y-0M-0SY	BW	S	0	0	10MR	4	ASR
32	MILAN/SHA7/3/NS732/HER/SUDAN #11ICW99-0278-12AP-0AP-0AP-37AP-0AP	BW	S	2	0	R	3	ASR
33	SHA7/VEE#5/VEE#8/JUP/BJY/3/F3.71/TRM/4/2*WEAVER/6/SKAUZ/PARUS/PBW ARUSCMS04Y01158S-099Y-099ZTM.....	BW	S	4	0	20MR	22	SR
34	QIMMA-8 CMSS93Y00332S-1AP-3AP-3AP-0APS-0AP	BW	S	0	0	10MR	4	ASR

Table 1 continued

No.	Pedigree/Variety	Type ¹	Growth habit ²	Seedling response ³	Adult plant response ⁴			Kind of resistance ⁵
				Path. 1	Path. 2	FRS & IT	rAUDPC	
35	RAMA-2 ICW99-0351-1AP-0AP-0AP-5AP-0AP	BW	S	0	0	20MR	8	ASR
36	ALSHOROQ-3 ICW99-0368-18AP-0AP-0AP-22AP-0AP	BW	S	0;1	0	R	1	ASR
37	DAMARA-6 ICW99-0427-8AP-0AP-0AP-3AP-0AP	BW	S	0;1	0	R	1	ASR
38	KLCQ/ER2000/WBLL1CMSA01M00286T-040Y-040P0M-040ZTY-040M-040SY-3M-0Y-02B-0Y	BW	S	0	0	10MR	6	ASR
39	FRET*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP/KAUZ/5/ONIX CMSA05Y00325S-040ZTP0Y-040ZTM-040SY-21ZTM-03Y-0B	BW	S	0	0	10MR	4	ASR
40	CNO79/RF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92 CMSA05Y01011T-040M-....	BW	S	3	0	R	1	APR
41	MILAN/KAUZ//PRINIA/3/BAV92/4/WBLL1*2KUKUNA CMSA04M00040S-040ZTB-040ZTY-040ZTM-040SY-2ZTM-01Y-0B	BW	S	0	0	R	1	ASR
42	TC870344/ GUI/TEMPORALERA M 87/AGR/3/ 2*WBLL1 CMSA01Y00725T-040M-030ZTM-040SY-10M-0Y-0SY	BW	S	4	0	10MR	10	APR
43	ATTILA*2/PBW65/BERCUT CMSA01M00074S-04P0M-030ZTM-040SY-040M-20Y-0M-0SY	BW	S	4	0	20MR	14	SR
44	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP/KAUZ/5/PFAU/WEAVER//BRAMBLI NGCMSS05B00480S-099Y-099M-099Y-099ZTM...	BW	S	4	0	30MR	14	SR
45	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES /7/CAL/NH/H567.71/3 /SERI/4/CAL/NH/H567.71/5/2*KAUZ/6/PASTORCMSS05B00581S-.....	BW	S	4	0	R	1	APR
46	PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNACGSS05B00256T-099TOPY-099M-099NJ-099NJ-5WGY-0B	BW	S	0	0	R	1	ASR
47	PBW343*2/KUKUNA*2//YANACCGSS05B00258T-099TOPY-099M-099NJ-2WGY-0B	BW	S	4	0	20MR	8	APR
48	HAMAM-4/ANGI-2ICW02-00621-2AP/0TS-0AP-0AP-6AP-0AP	BW	S	0	0	R	1	ASR
49	CNO79/PF70354/MUS/3/PASTOR/4/BAV92/5/FRET2/KUKUNA//FRET2/6/MILAN/KAUZ//PRINIA/3/BAV92CMSA05Y01011T....	BW	S	0	0	R	1	ASR
50	ATTILA*2/HUITES//FINSI/3/ATTILA*2/PBW65CMSS05Y00670T-099TOPM-099Y-099M-099Y-099ZTM-15WGY-0B	BW	S	4	0	40MS	20	SR
51	PBW343*2/KUKUNA//SRTU/3/PBW343*2/KHVAKICGSS05B00261T-099TOPY-099M-099NJ-099NJ-6WGY-0B	BW	S	4	0	10MR	4	SR
52	ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTORCGSS05B00290T-...	BW	S	3	0	20MR	17	SR
53	WBLL1/KUKUNA//TACUPETO F2001/5/WAXWING /4/ SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ CMSS05B00053S-099Y-099M-...	BW	S	0	0	30MR	17	SR
54	KANZ*4/KS85-8-4/5/2*FRET2*2/4/SNI/TRAP#1/3/ KAUZ*2/ TRAP//KAUZCGSS05Y00186T-099M-099Y-099M-099Y-099ZTM-2WGY-0B	BW	S	4	4	10MR	4	APR
55	SAUAL/3/MILAN/S87230//BAV92CMSS05B00593S-099Y-099M-099Y-099ZTM-14WGY-0B	BW	S	2	0	R	1	ASR
56	FRET2/KUKUNA//FRET2/3/TUKURU/4/FRET2/TUKURU//FRET2CGSS05B00149T-099TOPY-099M-099NJ-099NJ-2WGY-0B	BW	S	0	0	R	1	ASR
57	FRET2/KUKUNA//FRET2/3/PASTOR//HXL7573/2*BAU/5/FRET2*2/4/SNI/ TRAP#1/3/KAUZ*2/TRAP//KAUZCGSS05B00162T...	BW	S	3	3	20MR	17	SR
58	FRET2/KUKUNA//FRET2/3/PASTOR//HXL7573/2*BAU/5/FRET2*2/4/SNI/ TRAP#1/3/KAUZ*2/TRAP//KAUZCGSS05B00162T...	BW	S	4	0	R	1	APR
59	PBW343*2/KUKUNA//WBLL1*2/KUKUNACMSA05M00118S-0100ZTM-029(LR34 HOM+HET)ZTY-040ZTM-040SY-16ZTM-0Y-0B	BW	S	2+	1	10MR	4	ASR
60	KACHU #1/KIRITATI//KACHUCMSS06Y00778T-099TOPM-099Y-099ZTM-099NJ-099NJ-6WGY-0B	BW	S	4	0	R	1	APR
61	BECARD/KACHUCMSS06B00169S-0Y-099ZTM-099Y-099M-28WGY-0B	BW	S	0	0	R	1	ASR
62	KABY/4/TEU2/3/URES/FUN//KAUZ IRBWG-2006-001G-0G-0G-10G-0G	BW	S	2	0	20MR	8	ASR
63	KABY/4/TEU2/3/URES/FUN//KAUZ IRBWG-2006-001G-0G-0G-12G-0G	BW	S	0	0	10MR	4	ASR
64	CHEN/AEGILOPS SQUROS(AUS)/BCN/3/ VEE#7/BOW/4/PASTOR/5/CHAMRAN IRBWG-2006-008G-0G-0G-3G-0G	BW	S	3	0	20MR	8	APR
65	D94528/3/2*STOT//ALTAR 84/ALD	DW	F	0	0	R	1	ASR
66	CBC509HILE/SOMAT_3.1/3/RASCON_37/TARRO_2//RASCON_37	DW	F	0	0	R	1	ASR
67	MINIMUS/COMBDUCK_2//CHAM_3/3/CANELO_9/9/USDA595/3/D67.3/R ABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/...	DW	F	4	4	R	1	APR
68	INTER_16/SNITAN/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/POD	DW	F	3	4	R	1	APR
69	TN_12736	DW	F	1	0	R	1	ASR
70	NATIONAL CHECK (KOOHDASHT)	BW	S	0	0	10MR	10	ASR
Check	Morocco	-	-	4	4	100S	100	S

¹Wheat type: BW, bread wheat; DW, durum wheat.²Growth habit: W, winter; S, spring; F, facultative.³Seedling infection types were assessed against two *Puccinia striiformis* f. sp. *tritici* pathotypes—6E6A+, Yr27 (Pathotype 1) and 6E158A+, Yr27 (Pathotype 2)—using the scale described by McIntosh *et al.* (1995).⁴Adult plant responses were recorded as final rust severity (FRS, %) and infection type (IT) according to Roelfs *et al.* (1992). The relative area under the disease progress curve (rAUDPC) was calculated to quantify disease progression. Infection type classifications: R (resistant; no sporulation), MR (moderately resistant; small pustules with necrosis), M (moderately resistant to moderately susceptible), MS (moderately susceptible; medium pustules, possible chlorosis), S (susceptible; large pustules without chlorosis or necrosis).⁵Resistance type: ASR, all-stage resistance; APR, adult plant resistance; SR, slow rusting resistance.

Table 2 Virulence/avirulence profiles of *Puccinia striiformis* f. sp. *tritici* pathotypes employed in seedling resistance screening.

Pathotype	Avirulence pattern	Virulence pattern
6E6A ⁺ , Yr27	Yr1, Yr3, Yr4, Yr5, Yr8, Yr10, Yr15, Yr17, Yr24, Yr25, YrCV, YrSD, YrSU, YrND, YrSP	Yr2, Yr6, Yr7, Yr9, Yr18, Yr20, Yr26, Yr27, Yr28, Yr29, Yr31, YrA,
142E158A ⁺ , Yr27	Yr1, Yr4, Yr5, Yr10, Yr15, Yr24, YrSD, YrCV, YrSU, YrSP	Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr17, Yr18, Yr20, Yr25, Yr26, Yr27, Yr28, Yr29, Yr31, Yr32, YrND, YrA,

Inoculation was performed by spraying seedlings with a suspension of fresh urediniospores mixed with talcum powder (1:4 ratio). Following inoculation, the pots were placed in a dew chamber at 10 °C with 100% relative humidity for 24 hours to facilitate infection. They were subsequently transferred to a greenhouse maintained at 8-10 °C with a 16-hour light/8-hour dark cycle. Infection types (ITs) were recorded 15-17 days post-inoculation using a 0-4 scale (McIntosh *et al.*, 1995).

Adult plant resistance tests

Field evaluations were conducted during the 2018-2019 cropping season at the Agricultural Research Station in Ardabil, Iran (38.1705°N, 48.3907°E; altitude 1350 m). The same genotypes screened at the seedling stage were planted in a disease nursery. Each genotype was sown in two-row, 1-meter-long plots with 30 cm row spacing, using 8 grams of seed per plot.

To ensure uniform disease pressure, the highly susceptible cultivar 'Morocco' was planted as a spreader after every ten test genotypes and along the entire periphery of the nursery. Standard agronomic practices were followed, including flood irrigation (once in the fall and six times in the spring), weeding, and fertilization. Artificial inoculation was performed twice during the season, between stem elongation and flag leaf emergence, using a bulk mixture of urediniospores (collected from the previous season) and talcum powder applied by dusting. The bulk inoculum was virulent on seedlings carrying the resistance genes Yr1, Yr2, Yr6, Yr7, Yr9, Yr17, Yr22, Yr23, Yr24, Yr25, Yr26, Yr27, YrA, Yr21, Yr31, Yr32, and

YrSU, and avirulent against Yr3v, Yr3a, Yr4a, Yr4, Yr5, Yr10, Yr15, Yr16, YrCV, YrSD, and YrND (Safavi, 2019).

Disease assessment and data analysis

Adult plant reactions were assessed based on infection type (IT) (Roelfs *et al.*, 1992) and disease severity (DS), recorded as the percentage of leaf area affected (0-100%) (Peterson *et al.*, 1948). Assessments began when disease severity on the 'Morocco' spreader rows reached approximately 50% and were repeated at 7-8 day intervals for a total of three recordings.

The area under the disease progress curve (AUDPC) was calculated for each genotype using the following formula (Milus and Line, 1986):

$$\text{AUDPC} = [N_1(X_1 + X_2)/2] + [N_2(X_2 + X_3)/2]$$

Where X_1 , X_2 , X_3 are the rust intensities recorded on the first, second and third recording dates. N_1 is the interval day between X_1 , X_2 and N_2 is the interval day between X_2 , X_3 .

To enable comparison across genotypes, the relative AUDPC (rAUDPC) was calculated as:

$$\text{rAUDPC} = (\text{AUDPC of genotype} / \text{AUDPC of susceptible control}) \times 100$$

Classification of resistance types

Genotypes were classified into resistance groups by integrating seedling ITs with adult plant rAUDPC values, adapting methodologies from Bux *et al.* (2012) and Zeng *et al.* (2014):

All-Stage Resistance (ASR): Resistant (low IT) to both pathotypes at the seedling stage.

Adult Plant Resistance (APR): Susceptible (high IT) to at least one pathotype at the seedling stage but with low rAUDPC values (0-10) in the field.

Slow Rusting (SR): Susceptible to at least one pathotype at the seedling stage but with moderate rAUDPC values (11-30) in the field.

Susceptible: High rAUDPC values (> 30) in the field, regardless of seedling reaction.

Comparative graphs illustrating the reactions of different genotypes at both growth stages were generated using Microsoft Excel (Version 2010).

Results

Evaluation of seedling resistance

Screening 233 wheat genotypes at the seedling stage revealed distinct resistance patterns against the two pathotypes. When inoculated with pathotype **6E6A⁺, Yr27**, a total of 155 genotypes exhibited resistance. This resistant group comprised 68 winter bread wheat, 28 durum wheat, and 59 spring bread wheat genotypes. A more virulent pathotype, **142E158A⁺, Yr27**, overcame the seedling resistance of many lines, with only 113 genotypes showing resistance. This group included 66 winter bread wheat, 16 durum wheat, and 31 spring bread wheat genotypes (Fig. 1).

Notably, 97 genotypes (41.6% of the total) demonstrated resistance to both pathotypes, suggesting the presence of effective all-stage resistance (ASR) genes. This robust group consisted of 55 winter bread wheat, 12 durum wheat, and 30 spring bread wheat genotypes. However, seedling resistance alone is not always indicative of field performance. Several genotypes resistant at the seedling stage exhibited high disease severity in the field. After integrating data from both growth stages, 46 genotypes (19.7%) that were resistant to both pathotypes as seedlings also maintained effective resistance in the field and were selected for further analysis (Table 1). Furthermore, 24 genotypes (10.3%) that were susceptible to at least one pathotype as seedlings displayed various forms

of resistance in adult plants, highlighting the presence of non-seedling types of resistance.

Assessment of adult plant resistance

To mitigate the potential influence of environmental variability on disease severity, this study used artificial inoculation, maintained optimal humidity through frequent irrigation, and incorporated susceptible checks at 10-genotype intervals. Due to favourable weather conditions at the experimental site, stripe rust became well established and spread across the wheat genotypes, enabling a careful assessment. Under field conditions, 66 genotypes were susceptible while 167 (71.7%) exhibited resistance. Among the resistant genotypes, the responses of winter bread wheat, spring bread wheat, and durum wheat varieties differed according to relative area under the disease progress curve (rAUDPC) values. Specifically, within these categories, 30 (25%) winter bread wheat, 43 (67.2%) spring bread wheat, and 26 (53%) durum wheat genotypes showed low rAUDPC values (0–10) and were classified as resistant (Figure 2). Another set of genotypes demonstrated intermediate rAUDPC values (11–30), comprising 37 (30.8%) winter, 16 (25%) spring, and 15 (30.6%) durum wheat types. Finally, a group with high rAUDPC values (> 30) consisted of 53 (44.2%) winter, 5 (7.8%) spring, and 8 (16.4%) durum wheat genotypes, which were categorized as susceptible.

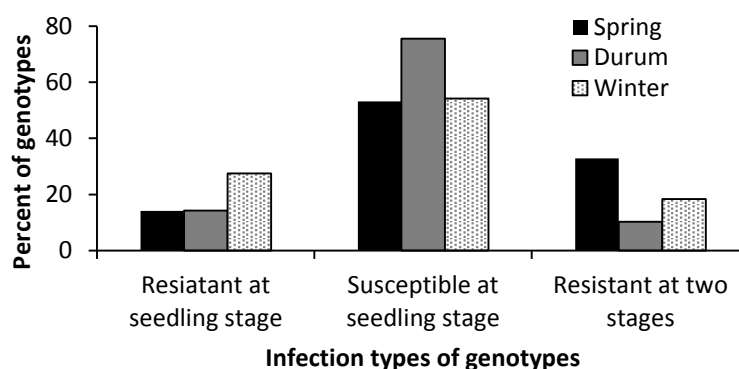


Figure 1 Seedling infection responses of dryland wheat germplasm to two prevalent *Puccinia striiformis* f. sp. *tritici* pathotypes (6E6A⁺, Yr27 and 142E158A⁺, Yr27).

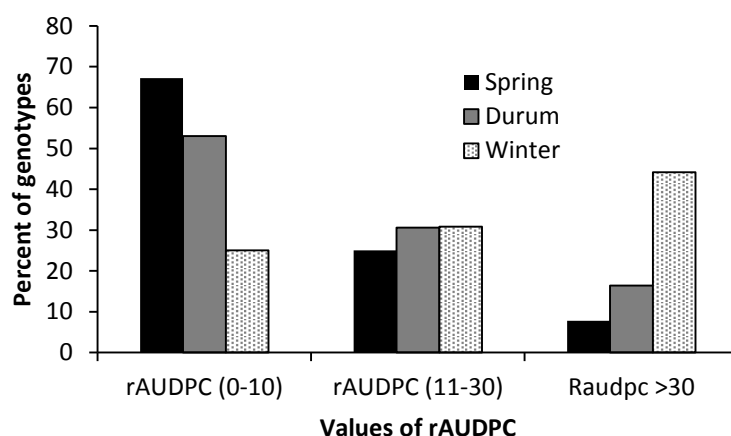


Figure 2 Evaluation of adult plant resistance to stripe rust in dryland wheat germplasm using relative area under the disease progress curve (rAUDPC).

Classification of resistance types

Integrating seedling and adult plant responses is crucial for characterizing the nature of resistance. Based on a combination of seedling infection types (ITs) and adult plant rAUDPC values, the genotypes were classified into distinct groups.

1. Adult plant resistance (APR) Group: This group consists of genotypes that were susceptible (high IT) to at least one pathotype at the seedling stage but displayed a low rAUDPC value (0-10) in the field. This phenotype is indicative of race-nonspecific adult plant resistance, which is often considered more durable. Fourteen genotypes (6%) were identified in this highly valuable category (Table 1).

2. Slow rusting (SR) group: This category includes genotypes that were susceptible at the seedling stage but exhibited moderate rAUDPC values (11-30) in the field. This pattern is characteristic of slow rusting resistance, conferred by combinations of minor-effect genes that reduce the epidemic rate. Ten genotypes (4.2%) were classified into this group, which also represents an important source of potentially durable resistance (Table 1).

3. All-stage resistance (ASR) group: This group comprised genotypes that exhibited

resistance to both pathotypes at the seedling stage, indicating the presence of race-specific or all-stage resistance (ASR) genes. Although these genotypes may also possess non-race-specific resistance genes, their effects are often masked by dominant ASR genes (Ali *et al.*, 2007; Dadrezaei *et al.*, 2013). Of the 233 genotypes evaluated, 96 (41%) belonged to this category. However, due to susceptibility observed in some genotypes at the adult plant stage, only 46 genotypes demonstrating consistent resistance (R) or moderate resistance (MR) to infection types under field conditions are listed in Table 2. While these genotypes show promise, their race-specific resistance necessitates further multi-year and multi-location evaluations—preferably within advanced breeding programs such as those at the Seed and Plant Improvement Institute (Karaj)—to assess their durability against emerging pathotypes before any cultivar release considerations.

4. Susceptible group: Genotypes in this category were susceptible to both pathotypes at the seedling stage and displayed high rAUDPC values (>30) along with moderately susceptible to susceptible (MSS) or fully susceptible (S) infection types in adult plants. This susceptibility indicates the absence of both effective race-specific resistance genes against the tested

pathotypes and functional adult plant resistance genes. A considerable number of genotypes fell into this group; however, their listings are omitted from Table 1 due to their susceptible phenotypes.

5. Seedling-specific resistance group: A subset of genotypes displayed resistance at the seedling stage but high disease severity, with moderately susceptible (MS) or moderately susceptible to susceptible (MSS) infection types, at the adult plant stage. This suggests that although these genotypes possess race-specific resistance genes, those genes are ineffective against the pathotype(s) prevalent in the field. The discrepancy between seedling and adult responses may be attributed to several factors: the field pathotype(s) might be present at low frequencies under greenhouse conditions, or may not have been included in the seedling screening panel. Alternatively, pathogen populations may overcome race-specific resistance over time and under prolonged field exposure. This underscores the limitations of relying solely on seedling tests for predicting field performance and highlights the need to incorporate adult-plant resistance into breeding programs.

Discussion

The comprehensive classification of genotypes into five distinct groups offers valuable insights into the diversity of resistance mechanisms within dryland wheat germplasm. The identification of genotypes exhibiting adult plant resistance (APR) and slow-rusting (SR) characteristics is particularly promising for developing varieties with durable resistance (Singh *et al.*, 2011), in contrast to those with only race-specific resistance, which require careful management to avoid rapid breakdown. A notable strength of this study is the concurrent evaluation of winter bread wheat, spring bread wheat, and durum wheat genotypes—a comprehensive approach not frequently employed in investigations of Iranian dryland wheat germplasm. Our resistance grouping

framework aligns with established methodologies for studying wheat-rust pathosystems (Tariq-Khan and Irfan-Ul-Haque, 2011; Dadrezaei *et al.*, 2013; Zeng *et al.*, 2014; Shah *et al.*, 2014).

This work is underpinned by the fundamental principle that resistance genes have distinct expression patterns; APR genes are typically not expressed at the seedling stage, whereas all-stage resistance (ASR) genes are functional throughout plant development (Chen, 2005). Consequently, reliance solely on seedling assays is inadequate (Sandoval-Islas *et al.*, 2007), as it may misclassify valuable sources of quantitative, non-race-specific resistance as susceptible. Our results confirm that genotypes that are susceptible as seedlings can exhibit high levels of quantitative resistance as adult plants, demonstrating that this resistance is more durable than race-specific resistance conferred by major ASR genes (Roelfs *et al.*, 1992; Nazari *et al.*, 2000). The well-documented lack of durability in monogenic race-specific resistance has driven breeders to prioritize slow-rusting resistance (Ali *et al.*, 2007; Shah *et al.*, 2010; Safavi and Afshari, 2017).

This type of race-nonspecific and durable resistance has been extensively studied in wheat, and efforts to incorporate it into elite cultivars are longstanding (Singh *et al.*, 2011; Alo *et al.*, 2018; Huerta-Espino *et al.*, 2020; Hatami-Maleki *et al.*, 2024). Notably, several genotypes identified in our study with superior resistance features are renowned international cultivars in their pedigrees, such as Tukuru, Kukuna, and Attila. These source cultivars are known to confer durable, multi-pathogen resistance through combinations of non-race-specific genes, such as Yr18, Yr29, Yr30, Yr36, and Yr46, often pyramided with resistance from germplasm such as Chapio and Kingbird (Singh *et al.*, 2005; Singh *et al.*, 2011). The genetic complexity and value of these slow-rusting genes are further underscored by their frequent pleiotropic effects and linkages with other agronomically important traits, as exemplified by research from CIMMYT showing that Yr18 (linked with the genes *Lr34/Pm38/Sr57*

/Bdv1/Stb1) is associated with leaf tip necrosis (*Ltn1*) and confers broad-spectrum resistance (Singh, 1992; Kumar *et al.*, 2019). Similarly, *Yr29* is linked with *Lr46* and *Ltn2* (Singh *et al.*, 2005; Kumar *et al.*, 2019), and *Yr46* (linked with *Lr67/Sr55/Pm46*) is associated with *Ltn3* and multi-disease resistance (Herrera-Foessel *et al.*, 2011; Singh *et al.*, 2015; Kumar *et al.*, 2019).

This expanded genetic spectrum is critically needed for Iranian dryland wheat improvement, as older cultivars were historically based on a narrow set of major ASR genes, rendering them highly vulnerable to new *Pst* pathotypes (Nazari *et al.*, 2000; Safavi and Afshari, 2017; Bux *et al.*, 2011; Safavi, 2019). This vulnerability underscores the urgent need to diversify the genetic foundation of resistance. A highly effective strategy is the pyramiding of both minor- and major-effect resistance genes within a single cultivar using molecular marker-assisted selection. The development of cultivars that combine both types of resistance is fundamental to sustainable management, as they reduce disease prevalence and slow down pathogen evolution (Randhawa *et al.*, 2012).

The choice of resistance strategy may also be informed by regional disease epidemiology (Zeng *et al.*, 2014). In regions of Iran with late disease onset, APR genes are highly recommended, whereas areas with fall or early-season infection require a combination of seedling (ASR) and adult-plant resistance genes for comprehensive protection.

The present study provides valuable resources for such a strategy. The identified seedling resistance sources are likely to carry genes such as *Yr3b*, *Yr4*, *Yr5*, *Yr10*, *Yr15*, or other unknown genes, which can be pyramided with the identified APR and SR sources. For immediate breeding applications, genotypes exhibiting APR/SR should be prioritized for advanced multi-location trials due to their non-race-specific nature and stability. Conversely, genotypes with all-stage resistance require further multi-year and multi-race validation to ensure they are not vulnerable to emerging pathotypes. Future work must include molecular validation of the putative resistance genes, and the most promising lines should enter rigorous multi-

location, multi-year trials conducted by relevant national institutes (e.g., the Seed and Plant Improvement Institute; the Dryland Agricultural Research Institute) to assess their stability against Iran's evolving *Pst* population as a prerequisite for potential cultivar release.

Conclusion

This study identified numerous wheat genotypes possessing seedling or all-stage resistance (ASR). Those resistant to both pathotypes at the seedling stage most likely carry effective genes such as *Yr3b*, *Yr4*, *Yr5*, *Yr10*, *Yr15*, *YrSP*, *YrCV*, and *YrSD*. Furthermore, a significant number of genotypes were characterized by adult plant resistance (APR) or slow-rusting (SR) resistance. The frequency of genotypes with APR and SR was notably higher in spring bread wheat than in winter bread wheat and durum wheat. These genetic resources provide a critical foundation for gene pyramiding strategies to achieve durable resistance. The integration of both APR and ASR into Iranian breeding programs is essential for the sustainable management of stripe rust.

Acknowledgments

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شناسایی انواع مختلف مقاومت به زنگ نواری *Puccinia striiformis* f. sp. *tritici* در برخی از ژنوتیپ‌های گندم دیم ایران

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چکیده: زنگ نواری (زرد) گندم، ناشی از *Puccinia striiformis* f. sp. *tritici* (Pst)، یکی از مخربترین بیماری‌های جهانی گندم و عامل کاهش شدید عملکرد گندم در ایران است که اغلب منجر به خسارات شدید تولید و نیاز به مداخلات پرهزینه شیمیایی می‌شود. استفاده از مقاومت میزبان، هم‌چنان مقرون به صرفه‌ترین و پایدارترین راهبرد مدیریتی است. هدف از این مطالعه، شناسایی انواع مختلف مقاومت به زنگ زرد در بین ژنوتیپ‌های گندم دیم با هدف افزایش موفقیت در اصلاح و معرفی رقم بود. مجموعه‌ای متشکل از ۲۳۳ ژنوتیپ گندم دیم (شامل ۱۲۰ ژنوتیپ گندم نان زمستانه، ۶۴ ژنوتیپ گندم نان بهاره و ۴۹ ژنوتیپ گندم دوروم) از نظر مقاومت گیاه بالغ (Adult plant resistance) در شرایط مزرعه‌ای در ایستگاه تحقیقات کشاورزی اردبیل، مورد ارزیابی قرار گرفت. هم‌زمان، غربالگری مقاومت گیاهچه در برابر دو پاتوتیپ (6E6A⁺, Yr27 و 142E158A⁺, Yr27) شایع Pst در شرایط کنترل شده گلخانه‌ای انجام شد. نتایج، طیفی از واکنش‌های مقاومتی را آشکار کرد. چهل و شش ژنوتیپ (۱۹/۷ درصد) در مرحله گیاهچه در برابر هر دو پاتوتیپ، مقاومت گیاهچه‌ای یا تمام مرحله‌ای (All-stage resistance) نشان دادند که احتمالاً حاکی از وجود ژن‌های شناخته شده مقاومت گیاهچه مانند Yr4، Yr3b، Yr5، Yr10، Yr15، YrSP، YrCV، YrSD یا سایر ژن‌های شناسایی نشده بود. چهارده ژنوتیپ در مرحله گیاهچه نسبت به حداقل یک پاتوتیپ حساس بودند، اما در شرایط مزرعه مقدار نسبی سطح زیر منحنی پیشرفت بیماری (rAUDPC) پایینی (0-10) نشان دادند که نشان‌دهنده مقاومت مؤثر گیاه بالغ (APR) بود. ده ژنوتیپ دیگر که در مرحله گیاهچه حساس بودند، مقادیر متوسط rAUDPC (11-30) نشان دادند که ویژگی مقاومت تدریجی (Slow rusting) است. ۱۶۳ ژنوتیپ باقی‌مانده، بدون توجه به واکنش گیاهچه‌ای، در شرایط مزرعه به شدت حساس (با rAUDPC بالا) بودند. ژنوتیپ‌های مقاوم شناسایی شده در این مطالعه، به ویژه آن‌هایی که دارای ویژگی‌های مقاومت گیاه بالغ و تدریجی هستند، نشان‌دهنده منابع ژنتیکی ارزشمندی برای ایجاد مقاومت پایدار و هدف تجمیع چندین ژن مقاومت برای ایجاد مقاومت پایدار و دستیابی به کنترل بلندمدت زنگ زرد در ایران انجام می‌شوند.

واژگان کلیدی: گندم دیم، مقاومت نژاد-اختصاصی، مقاومت غیرنژاد-اختصاصی، مقاومت پایدار