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Screening some durum wheat germplasm to strip rust (*Puccinia striimorfis* spp.) in field and greenhouse condition

Naser Mohammadi[1], Hamid Hatami Maleki[2*], Fatemeh Mohammadzadeh[2], Safar Ali Safavi[3], Mohsen Yassaie[4], Farzad Afshari[5]

[1]*Dryland Agricultural Research Institute, Agricultural Research, Education and Extension Organization (ARREO), Maragheh, Iran.*
[2]*Department of Plant Production and Genetics, Faculty of Agriculture, University of Maragheh, Maragheh, Iran.*
[3]*Ardebil Agricultural and Natural Resources Research and Education Center; Agricultural Research, Education and Extension Organization (AREEO), Ardebil, Iran.*
[4]*Fars Agricultural and Natural Resources Research and Education Center; Agricultural Research, Education and Extension Organization (AREEO), Zarghan, Iran.*
[5]*Seed and Plant Improvement Institute; Agricultural Research, Education and Extension Organization (AREEO), Karaj, Iran.*
[*]*Corresponding author, 0000-0001-7179-861X. Email: hatamimaleki@maragheh.ac.ir, hatamimaleki@yahoo.com.*

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ABSTRACT

Durum wheat is the second most widely cultivated wheat species after bread wheat. Yellow rust, caused by *Puccinia striiformis* Westend. f. sp. *tritici* Eriks. (*Pst*), severely impacts global wheat production. This study screened 45 durum wheat genotypes for yellow rust resistance through field inoculations in Ardabil and Zarghan, Iran, as well as greenhouse tests. Two *Pst* isolates, 6E158A+ (from Ardabil) and 14E158A+,YR27 (from Zarghan), were used for inoculations in both field and greenhouse conditions. The slow rusting parameters—area under the disease progress curve (AUDPC), coefficient of infection (CI), and adult plant reaction (APR)—revealed varying genotypic responses between the two regions. Results indicated that climatic factors, particularly temperature in rainfed areas, affected yellow rust development. The greenhouse experiment identified the roles of resistance genes *Yr1*, *Yr4*, *Yr5*, *Yr10*, *Yr15*, *Yr24*, *Yr26*, *Yr32*, *YrSD*, *YrSU*, *YrCV*, and *YrSP* in the resistance of durum wheat genotypes. Both field and greenhouse assays showed that genotypes G01, G04, G28, and G30 exhibited minimal slow rusting values in both locations and susceptible reactions to both *Pst* isolates in the greenhouse, suggesting race non-specific resistance. Conversely, genotypes G25, G26, G27, and G38 displayed lower slow rusting values and resistance to both *Pst* isolates in the greenhouse, indicating the presence of race-specific or race-non-specific resistance. The identified resistant genotypes can replace susceptible ones in rainfed regions after yield trials and may serve as resistant parents in wheat breeding programs.

Key words: Durable resistance, Race-nonspecific resistance, Race specific resistance, Yellow rust.

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INTRODUCTION

Rust agents' adaptability to various climatic conditions through sexual and asexual reproduction, mutation, and migration contributes to their significance as a serious wheat disease (Jin *et al.,* 2010). There are three types of rust: yellow rust, stem rust, and brown rust, with yellow rust being the most devastating due to its wide range. Yellow rust, caused by the biotrophic fungus *Puccinia striiformis* f. sp. *tritici* (*Pst*), is a major wheat disease found in cold, moderate, and high-altitude regions (Boyd, 2005). It affects wheat production globally, potentially reducing yields by 10% to 100% during epidemics (Chen, 2005; Pouralibaba *et al.,* 2021). The pathogen primarily attacks the aerial parts of the wheat plant, resulting in wrinkled seeds and diminished yield quality (Line, 2002). Wheat can be infected at any growth stage, from the one-leaf seedling to mature plants (Chen, 2005). Symptoms include orange-yellow urediniospores in long stripes along the leaf veins. Developing resistant varieties is a cost-effective control method (Vergara-Diaz *et al.,* 2015; Li *et al.,* 2021). Rust resistance can be classified into race-specific and race-nonspecific types. Race-specific resistance, based on gene-for-gene action (Flor, 1942), may last only 3 to 5 years before breaking down. In contrast, race-nonspecific resistance is governed by minor genes and is more durable. Therefore, combining both resistance types in wheat varieties can enhance disease management (Singh *et al.,* 2004). In summary, genetic resources with diverse resistance genes are essential for optimal management of yellow rust. To date, over 78 stripe rust resistance genes (*Yr1* to *Yr78*) have been identified in various hexaploid bread, durum wheat, and wild species backgrounds (Miedaner *et al.,* 2019).

Durum wheat, a tetraploid species (2n=4x=28), traces its origins to the domesticated form of wild emmer wheat (*Triticum dicoccum* Koern.) 12,000 to 10,000 years ago (Ozkan *et al.,* 2011). Primarily used for pasta, it is cultivated in many countries alongside common wheat, with Italy producing 4.95 MT and Turkey producing 3.62 MT, along with significant contributions from the Commonwealth of Independent States (CIS), North America, South America, Asia, Africa, and Oceania (International Grains Council, 2020). Previous studies indicate that durum wheat possesses valuable rust resistance genes that could benefit bread wheat (Miedaner *et al.,* 2019). While several studies have screened bread wheat germplasm against *Pst* isolates (Kumar *et al.,* 2020; Saeed *et al.,* 2022), research on durum wheat remains limited. Liu *et al.* (2017) evaluated 182 durum wheat landraces and contemporary varieties from Ethiopia against *Pst* races, finding that landraces were more resistant at the seedling stage and cultivars at the adult stage. Recently, Alemu *et al.* (2019 and 2021) screened 300 durum wheat lines (landraces and cultivars) against three virulent isolates (*Pst_Is1*, *Pst_Is4*, and *Pst_Is8*), revealing that 59.3%, 67.3%, and 46.3% of the lines exhibited a highly resistant infection type (0 to 3), respectively. Consistent with Liu *et al.* (2017), Alemu *et al.* (2019 and 2021) noted that most resistant genotypes were landraces, while commercial cultivars tended to be more susceptible.

Water resources are limited, and many dryland- and semi-dryland regions exist worldwide. Therefore, cultivating durum wheat, which constitutes 10% of wheat production area and offers nutritional and industrial benefits as well as resistance to rust diseases, is advantageous. This study aimed to evaluate and screen durum wheat germplasm from International Maize and Wheat Improvement Center (CIMMYT) and its related institutes for resistance to yellow rust in greenhouse conditions and in two yellow rust hotspots in Iran.

MATERIALS AND METHODS

Plant material

This study examined 43 durum wheat genotypes along with two internal varieties (Saverz as resistant and Dehdasht as susceptible) as controls under field and greenhouse conditions (Table 1).

Table 1. Code and pedigree of durum wheat genotypes screened for strip rust (*Puccinia striiformis*) under field and greenhouse conditions.

Genotype	Pedigree
G01	ALTAR84/STINT//SILVER_45/3/LLARETAINIACDSS99 Y00376S-0M-0Y-13Y-0M-0Y-2M-0Y
G02	OROBEL//BUSHEN_4/2*GREEN_18/8/GEDIZ/FGO//GTA/3/SRN_1/4/TOTUS/5/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/6/SOMBRA_20/7/JUPARE C 2001CDSS07Y00746T-099Y-099M-5Y-3M-04Y-0B
G03	Bezajihan*Ossl1/Stj5/5/Bicrederaa1/4/BezaizSHF//SD19539/Waha/3/Stj/Mrb3/6/Icajihan12
G04	BCRIS/BICUM//LLARETA INIA/3/DUKEM_12/2*RASCON_21/5/1A.1D 5+1 -06/3*MOJO//RCOL/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1 CDSS07Y00068S-099Y-099M-4Y-3M-04Y-0B
G05	MÂALI/6/MUSK_1//ACO89/FNFOOT_2/4/MUSK_4/3/PLATA_3//CREX/ALLA/5/OLUS*2/ILBOR//PATKA_7/YAZI_1/10/SELIM/9/ALTAR 84/860137 //YAZI _1/4/LIS_8/FILLO_6/3/FUUT// HORA/JOR/8/GEDIZ/FGO//GTA/3/ SRN_1/4/ TOTUS/5/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60// JO69/6/SOMBRACDSS07Y00784D-2B-07Y-07M-8Y-1B-04Y-0B
G06	WID22202/4/SORA/2*PLATA_12//SOMAT_3/3/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/5/CF4-JS 21//TECA96/TILO_1CDSS07B00 683T-0TOPY-099Y-014M-20Y-1M-0Y
G07	EXELDUR/8/GEDIZ/FGO//GTA/3/SRN_1/4/TOTUS/5/ENTE/MEXI_2//HUI/4/YAV_1/3/LD357E/2*TC60//JO69/6/SOMBRA_20/7/JUPARE C 2001/9/ SOMAT_3/ PHAX_1//TILO_1/ LOTUS_ 4/3/RASCON_22/RASCON_21// MOJO_2 CDSS08Y00900T-0TOPB-099Y-07M-13Y-3M-0Y
G08	PLATA_6/GREEN_17//SNITAN/4/ARMENT//SRN_3/NIGRIS_4/3/CANELO_9.1/11/ARTICO/AJAIA_3//HUALITA/10/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 CDSS08Y00518S-099Y-025M-11Y-1M-0Y
G09	SOMAT_3/GREEN_22/4/GODRIN/GUTROS//DUKEM/3/THKNEE_11/7/CMH83.2578/4/D88059//WARD/YAV79/3/ACO89/5/2*SOOTY_9/RASCON_37/6/1A.1D 5+1-06/3*MOJO/3/AJAIA _12/F3LOCAL(SEL.ETHIO.135.85)// PLATA_13 CDSS08Y00394S-099Y-025M-9Y-2M-0Y
G10	TOPDY_18/FOCHA_1//ALTAR 84/3/AJAIA_12/F3LOCAL(SEL.ETHIO. 135.85)// PLATA_13/4/SOMAT_3/GREEN_22/6/LAHN/HCN//PATA_2/3/ SOMAT_4/INTER_8/5/CREX//BOY/YAV_1/3/PLATA_6/4/PORRON_11CDSS07B00051S-099Y-018M-1Y-2M-0Y
G11	Mrf1/Stj2/3/1718/BT24//Karim = Icajihan*ICD01-0251-T-8AP-TR-8AP-0AP-5AP-0AP-2AP-0AP-2AP-0AP-0TR
G12	Terbol975/Geruftel2*ICD06-1790-0AP-4AP-0AP-4AP-0THTD-0TR
G13	Maamouri1/5/IcamorTA0462/4/Stj3//Bcr/Lks4/3/Icamor"s"/6/Mgnl3/Ainzen1*ICD06-0367-BLMSD-0AP-2AP-0Tr-2AP-0Tr-4AP-0THT-0AP-0TR
G14	Mgnl3/Ainzen1/3/IcamorTA0463//H.mouline/Sbl2/4/Mgnl3/Ainzen1*ICD06-0261-BLMSD-0AP-1AP-0Tr-4AP-0Tr-2AP-0THT-0AP-0TR
G15	PH896-21/5/BRAK_2/AJAIA_2//SOLGA_8/3/CANELO_8//SORA/2*PLATA_12/4/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN/6/HUBEI// SOOTY_9/RASCON_37/3/2*SOOTY_9/RASCON_37/4/SOOTY_9/ RASCON_37CDSS07Y00461T-099Y-099M-1Y-3M-04Y-0B
G16	Dehdasht
G17	Saverz
G18	CBC 509 CHILE/5/2*AJAIA_16//HORA/JRO/3/GAN/4/ZAR/6/AJAIA _12/F3LOCAL (SEL.ETHIO.135.85)//PLATA_13/4/CHEN_1/TEZ/3/ GUIL//CIT71/CII/5/SORA/2*PLATA_12//SOMAT_3CDSS09Y00310S-099Y-034M-12Y-0M-04Y-0B

Table 1 (Continued). Code and pedigree of durum wheat genotypes screened for strip rust (*Puccinia striiformis*) under field and greenhouse conditions.

Genotype	Pedigree
G19	SNITAN/5/AJAIA_12/F3LOCAL(SEL.ETHIO.135.85)//PLATA_13/3/SOMAT_3/4/SOOTY_9/RASCON_37/6/SNITAN/11/CANELO_9.1/SNITAN/10/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/12/CBC 509CDSS09Y00771T-099Y-040M-3Y-0M-04Y-0B
G20	MOHAWK/3/SOMAT_3/PHAX_1//TILO_1/LOTUS_4/5/SOMAT_3//SOOTY_9/RASCON_37/3/BINTEPE 85/SULA/4/SOOTY_9/RASCON_37 /3/SOOTY_9/ TARRO_1//AJAIA_2/6/ SOOTY_ 9/ RASCON_37// GUAYACAN INIACDSS09Y00991T-099Y-022M-18Y-0M-04Y-0B
G21	D86135/ACO89//PORRON_4/3/SNITAN/10/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/11/ CANELO_8//SORA/2*PLATA_ 12/12/ TADIZ/9/USDA595/3/D67.3/ RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENT CDSS08Y00433S-099Y-016M-26Y-4M-0Y
G22	Stj3//Bcr/Lks4//dehdast-IRDWG-2009-2309-0GACH-0GACH-0GACH-0GACH—0GACH93_0GACH94—0GN95
G23	SOOTY-9/RASCON-37/3/SOOTY-9/TARRO-1//AJAIA-2 /7/ AJAIA_16//HORA/ JRO/3/GAN/4/ZAR/5/SUOK_7/6/STOT//ALTAR 84/ALD- IRDWG-2009-2322-0GACH-0GACH-0GACH-0GACH—0GACH93_0GACH94—0GN95
G24	Dehdasht /5/ LLARETA INIA/3/STOT//ALTAR 84/ALD/4/…- IRDWG-2009-2372-0GACH-0GACH-0GACH-0GACH—0GACH93 _0GACH94—0GN95
G25	Geromtel-1/Icasyr-1—ICD04-1101-TA-0AP-1AP-0AP-6AP-0AP0GN-0GN*5GN
G26	Sebatel-2//Wdz6/Gil4—ICD02-0992-C-12AP-0AP-7AP-0AP-11AP-0AP-3AP-0AP0GN-0GN*4GN
G27	BRENNUR/CIRNO C 2008CDSS09B00077S-099Y-014M-4Y-3M-06Y-0B
G28	GEROMTEL-3/7/ALTAR 84/BINTEPE 85/3/STOT//ALTAR 84/ALD/4/ POD_11/YAZI_1/5/VANRRIKSE_12/SNITAN/6/SOOTY_9/RASCON_37//WODUCK/CHAM_3CDSS10Y00288S-099Y-038M-17Y-1M-06Y-0B
G29	Mikikassem-Icamilmus5/Miki2//Geromtel1/Icasyr1-ICD10-099-BLMSD-0AP-3AP-0TR-2STR-0TR-0AUB-0AUB
G30	Magrour-Amedakul1/TdicoSyrCol//Cham1-ICDJMC04-005-BThL (Bulksel)-0sTh-0wTh-0sTh-18wTh-0sTh-0MCH-0MCH[MtAJDSZ] [MMkJT]-0AUB
G31	Cucaraja-Tdicoccum1/Ch1//IcamorTA0469/3/IcamorTA0459// CandocrossH25 /Blk204144/4/ Mrf1/Stj2//Bcrch1/5/F413/3/ Arthur71/Lahn//Blk2/Lahn/4/ Quarmal -ICD07-785-BLMSD-0AP-0T-2AP-0T-7AP-0APT-1AP-0AP-0AN-0MCH[TIMSJGAA][MTrJTs]-0AUB
G32	SORA/2*PLATA_12/3/SORA/2*PLATA_12//SOMAT_3/4/AJAIA_13/YAZI//DIPPER_2/BUSHEN_3CDSS02B00849T-0TOPB-0Y-0M-7Y-2M-04Y-0B
G33	GEROMTEL-3/7/ALTAR 84/BINTEPE 85/3/STOT//ALTAR 84/ALD/4/POD_11/YAZI_1/5/VANRRIKSE_12/SNITAN/6/SOOTY_9/RASCON_37//WODUCK/CHAM_3CDSS10Y00288S-099Y-038M-17Y-1M-06Y-0B
G34	Ter1//Mrf1/Stj2/3/Icasyr1-ICD07-349-BLMSD-0AP-0T-6AP-0T-8AP-0APT-1AP-0AP-0AN-0MCH[TIMSJGAA]-0AUB[MTrJTs]-0AUB
G35	Ossl1/Stj5/5/Bicrederaa1/4/BEZAIZSHF//SD19539/Waha/3/Stj/Mrb3/6/Stk/Hau//Heca1-ICD06-1529-BLMSD-0AP-5AP-0T-2AP-0T-2AP-0APT-1AP-0AP-0AN-0MCH[TIMSJGAA]-0AUB[MTrJTs]-0AUB
G36	Mrb5/TdicoAlpCol//Cham1-ICDJMC04-010-BThL(Bulksel)-0sTh-0wTh-0sTh-3wTh-0sTh-0MCH-0MCH[MtAJDSZ]-0AUB[MMkJT]-0AUB
G37	Amedakul1/TdicoJCol//Cham1-ICDJMC04-005-BThL(Bulksel)-0sTh-0wTh-0sTh-10wTh-0sTh-0MCH-0MCH[MtAJDSZ]-0AUB[MMkJT]-0AUB
G38	Korifla/AegSpeltoidesSyr//Lahn-ICDJMC04-031-BThL(Bulksel)-0sTh-0wTh-0sTh-10wTh-0sTh-0MCH-0MCH[MtAJDSZ]-0AUB[MMkJT]-0AUB

Table 1 (Continued). Code and pedigree of durum wheat genotypes screened for strip rust (*Puccinia striiformis*) under field and greenhouse conditions.

Genotype	Pedigree
G39	Ysf1/Otb6/6/Ouasloukos1/5/Azn1/4/BEZAIZSHF//SD19539/Waha/3/Gd2-ICD11-016-0TR-10STR-0TR-2TR-0STR-5TR-0STR-0AUB
G40	SOOTY_9/RASCON_37//GUAYACAN INIA/4/BCRIS/BICUM//LLARETA INIA/3/DUKEM_12/2*RASCON_21/9/CBC 509 CHILE/6/ECO/CMH76A.722//BIT /3/ALTAR 84/4/AJAIA_2/5/KJOVE_1/7/AJAIA_12/F3LOCAL (SEL.ETHIO.135.85)//PLATA_13/8/SOOTY_9/RASCON_37//WODUCK/CHAM_3CDSS10Y00500T-099Y-028M-1Y-4M-06Y-0B
G41	Mammachan-Icamilmus2/Ammar8/3/Marsyr3//Saadi1989/Chan-ICD10-058-BLMSD-0AP-1AP-0TR-2STR-0TR-0AUB-0AUB
G42	GUAYACAN INIA/2*SNITAN/10/TADIZ/9/USDA595/3/D67.3/RABI//CRA/4/ ALO/5/ HUI/YAV _1/6/ARDENTE/7/HUI/YAV79/8/POD_9-CDSS11Y00160S-099Y-048M-32Y-0M-06Y-0B
G43	ALTAR 84/STINT//SILVER_45/3/GUANAY/4/GREEN_14//YAV_10/AUK/5/ SOMAT_4/ INTER_8/6/SILK_3/DIPPER_6/3/ACO89/DUKEM_4//5*ACO89/4/PLATA_7/ILBOR_1//SOMAT_3-CDSS11Y00207S-099Y-027M-30Y-0M-06Y-0B
G44	CBC 509 CHILE/SOMAT_3.1//BOOMER_18/LOTUS_4/6/SOMAT_3/PHAX_1// TILO_1/ LOTUS_4/3/GUANAY/5/NETTA_4/DUKEM_12//RASCON_19/3/SORA /2*PLATA_12/4/GREEN_18/FOCHA_1//AIRON_1/9/CBC 509 CHILE/6/ECO/ CMH76A.722//BIT/3/ALTAR 84/4/AJAIA _2/5/KJOVE_1/7/AJAIA_12/ F3LOCAL(S-CDSS10Y00493T-099Y-035M-9Y-4M-06Y-0B
G45	ADAMAR_15//ALBIA_1/ALTAR 84/3/SNITAN/4/SOMAT_4/INTER_8/5/SOOTY _9/ RASCON_37/6/BICHENA/AKAKI_7/4/LIS_8/FILLO_6/3/FUUT//HORA/JOR/5/YAZI_1/AKAKI_4//SOMAT_3/3/AUK/GUIL//GREEN/10/TADIZ/9/USDA595/3/D67.3/RABI//CRA/4/ALO/5/HUI/YAV_1/6/ARDENTE/7/HUI/YAV79/8/P-CDSS11Y00230S-099Y-040M-22Y-0M-06Y-0B

Inoculum preparation and greenhouse assays

Seeds of the susceptible bread wheat cultivar Bolani were grown in 6 cm plastic pots. Ten-day-old seedlings, with fully emerged first leaves, were treated with distilled water mixed with one drop of Tween 20 per liter (Knott, 1988). For inoculation, the seedlings were dipped in a uredospore suspension prepared with industrial oil Saltrol 170 at a concentration of 0.1 g. mL^{-1} of uredospores. The seedlings were misted again, covered with transparent plastic bags, and incubated at 10 °C in the dark for 48 hours. They were then transferred to a greenhouse set at 18 °C with a 16:8-hour light/dark photoperiod at an intensity of 10–15 lux. Spores were collected starting 15 days post-inoculation every three days until the seedlings failed, with uredospores stored at -17 °C.

Ten seeds from each wheat genotype were planted in 6 cm pots in the greenhouse. The experimental design was completely randomized with three replications. After 10 days, the seedlings were inoculated with rust spores identified from the studied regions using a hand sprayer at the stage when the first leaf was complete. The inoculated seedlings were incubated under standard conditions (dark, 10 °C, 100% RH) to promote infection and development of *P. striiformis* f. sp. *tritici*. Following 17 days, seedling reactions to yellow rust disease were recorded using a 0-4 scale (McIntosh *et al.,* 1995).

Multi-environmental assays

Field experiments were conducted in two regions: Ardebil and Zarghan. Seven grams of seeds from each wheat line/variety were planted in two 1-meter-long rows, surrounded by the highly susceptible cultivar Bolani to facilitate pathogen distribution. Inoculation began after tillering and continued until the flag leaf stage for three cycles, using a mixture of regional yellow rust uredopsores and talc powder (1:3) applied with a backpack atomizer. Disease progression was recorded three times after the appearance of symptoms on the flag leaves at seven-day intervals, assessing the percentage of infected leaf area (ILA, 0-100%) using a modified Cubb's method (Peterson *et al.,* 1948). Plant reactions to yellow rust infection were categorized according to Roelfs (1992) into five classes: resistant (R), moderately resistant (MR), moderate (M), moderately susceptible (MS), and susceptible (S).

Data analysis

The area under the disease progress curve (AUDPC) was calculated in Microsoft Excel using the formula:

$$(1) \qquad AUDPC = \frac{\sum_{i=1}^{n-1} y(i)+y(i+1)}{2} \times [t(i+1)-t(i)]$$

Where y_i measures disease (percentage, proportion, ordinal score, etc.) at the *i*th observation, t_i is the time at that observation, and n is the total number of observations. The coefficient of infection (Stubbs, 1986) was calculated by multiplying a fixed value representing host reaction (immune=0, R=0.2, MR=0.4, M=0.6, MS=0.8, S=1) with the final disease severity score. Statistical analysis included T-tests and biplot representations performed in Minitab 16.0.

RESULTS

Adult plant resistance

This study evaluated 43 advanced inbred lines of durum wheat, known for their drought and salinity resistance, along with resistant (Savrez) and susceptible (Dehdasht) control genotypes, for their response to yellow rust under field and greenhouse conditions. The parameters used to assess yellow rust included AUDPC, CI, and APR in the studied regions of Ardebil and Zarghan. In Zarghan, CI values ranged from 1 to 56, with an average of 12.1; resistant controls had a CI of 2 while susceptible controls had a CI of 24. The lowest CI values were observed in genotypes G01, G17, G255, G26, G27, G30, G38, G42, G43, and G45, all exhibiting an R type of adult plant reaction with final disease severity ratings of 5 or 10. Field observations in Zarghan included various types of genotypes: R, MR, M, and MS. The AUDPC values, indicating disease progression, ranged from 70 for most R genotypes to 830 for an MR genotype, with many durum wheat genotypes recording an AUDPC of 70 in Zarghan. In contrast, in Ardebil, CI and AUDPC values were generally higher, with AUDPC ranging from 240 for most R genotypes to 900 for MSS genotypes, and CI values ranging from 8 to 72 with an average of 30.57. There was variability in AUDPC values in Ardebil, with the minimum AUDPC observed at 8 for MR genotypes and a maximum of 900 for MSS genotypes. No durum wheat genotype with R type reaction was detected in Ardebil, where the adult plant reactions were MR, M, MS, and MSS.

Results on adult plant reactions in field conditions showed discrepancies across studied regions regarding slow rusting parameters (Table 2). For instance, a genotype classified as resistant in the Zarghan region was rated as moderately resistant in the Ardebil region. A mean comparison of CI and AUDPC values across regions revealed significant differences (Table 3) at a 1% probability level, indicating non-homogeneity in climatic conditions. The analysis of durum wheat genotypes based on these parameters demonstrated genetic variability between the regions. As shown in Figure 1, CI and AUDPC values in Zarghan (blue) were lower than in Ardebil (brown), with most genotypes in Zarghan being resistant compared to Ardebil. However, some genotypes exhibited similar susceptibility and resistance reactions in both environments. The two-dimensional plot allows for clear separation of susceptible, moderately resistant, and resistant genotypes (Figure 1). For example, genotype G16, a susceptible control with high CI and AUDPC values, is distinct from the others in both regions.

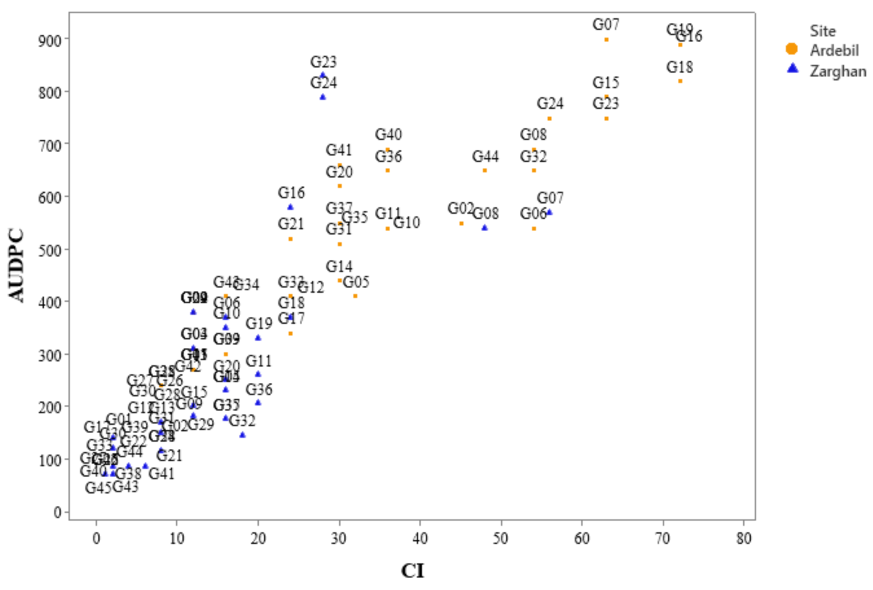

Figure 1. Dispersion of durum wheat genotypes using AUDPC and CI attributes across two regions.

Table 2. Field response of durum wheat genotypes to *Puccinia striiformis* Westend. f. sp. *tritici* Eriks.

Zarghan				Ardebil			
Genotype	AUDPC	CI	APR	Genotype	AUDPC	CI	APR
G01	140	2	10R	G01	270	12	30MR
G02	170	8	20MR	G02	550	45	50MSS
G03	310	12	30MR	G03	300	16	40MR
G04	380	12	30MR	G04	310	12	30MR
G05	230	16	40MR	G05	410	32	40MS
G06	370	16	40MR	G06	540	54	60MSS
G07	570	56	70MS	G07	900	63	70MSS
G08	540	48	60MS	G08	690	54	60MSS
G09	200	12	30MR	G09	380	12	30MR
G10	350	16	40MR	G10	540	36	60M
G11	260	20	50MR	G11	540	36	60M
G12	170	8	20MR	G12	410	24	40M
G13	170	8	20MR	G13	270	12	30MR
G14	230	16	40MR	G14	440	30	50M
G15	200	12	30MR	G15	790	63	70MSS
G16	580	24	60MR	G16	890	72	80MSS
G17	140	2	10R	G17	340	24	40M
G18	370	24	40M	G18	820	72	80MSS
G19	330	20	50MR	G19	890	72	80MSS
G20	250	16	40MR	G20	620	30	50M
G21	85	6	10M	G21	520	24	40M
G22	85	4	10MR	G22	380	12	30MR
G23	830	28	70MR	G23	750	63	70MSS
G24	790	28	70MR	G24	750	56	70MS
G25	70	1	5R	G25	240	8	20MR
G26	70	1	5R	G26	240	8	20MR
G27	70	1	5R	G27	240	8	20MR
G28	115	8	20MR	G28	240	8	20MR
G29	180	12	30MR	G29	380	12	30MR
G30	120	2	10R	G30	240	8	20MR
G31	150	8	20MR	G31	510	30	50M
G32	145	18	30M	G32	650	54	60MSS
G33	85	2	10R	G33	410	24	40M
G34	115	8	20MR	G34	410	16	40MR
G35	175	16	40MR	G35	550	30	50M
G36	205	20	50MR	G36	650	36	60M
G37	175	16	40MR	G37	550	30	50M
G38	70	1	5R	G38	240	8	20MR
G39	140	2	10R	G39	300	16	40MR
G40	70	2	5MR	G40	690	36	60M
G41	85	4	10MR	G41	660	30	50M
G42	70	1	5R	G42	270	12	30MR
G43	70	1	5R	G43	410	16	40MR
G44	85	4	10MR	G44	650	48	60MS
G45	70	1	5R	G45	270	12	30MR

Table 3. Differences in yellow rust resistance among field experiment sites in Zarghan and Ardebil based on their constituents.

	Mean $_{\text{Zarghan}}$	Mean $_{\text{Ardebil}}$	Standard deviation	|t|	Pvalue
AUDPC	185	203	194.2	6.5	0.0
CI	12.1	30.6	16.6	5.3	0.0

Table 4. Races of *Puccinia striiformis f. sp. tritici* used for greenhouse seedling tests.

Pst race	**Avir**/vir **formula**	Origin
6E158A+	***Yr1, Yr3, Yr4, Yr5, Yr10, Yr15, Yr24, Yr26, Yr27, YrSD, YrSU, YrCV, YrSP***/ *Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr25, Yr32, YrA, YrND*	Ardebil
14E158A+,YR27	***Yr1, Yr4, Yr5, Yr10, Yr15, Yr24, Yr26, Yr 2, YrSD, YrSU, YrCV, YrSP***/*Yr2, Yr3, Yr6, Yr7, Yr8, Yr9, Yr17, Yr25, Yr27, YrA, YrND*	Zarghan

In this study, G24, G15, G8, G07, G19, G33, and G18 were identified as susceptible in Ardebil, while G07, G08, G23, and G24 were categorized as susceptible in Zarghan due to higher CI and AUDPC than the control. Conversely, genotypes like G45, G43, G40, and G38 exhibited average CI and lower AUDPC values in Zarghan, confirming their resistance to yellow rust in this climate (Figure 1).

Seedling stage resistance

Yellow rust-infected samples were collected from field conditions and genotyped using a differential set with various resistance genes (Johnson *et al.,* 1972) at the Dryland Agriculture Research Institute (DARII) (data not shown). The genetic compositions of the studied isolates were 6E158A+ and 14E158A+,YR27 for the Ardebil and Zarghan regions, respectively (Table 4). The isolates 6E158A+ and 14E158A+,YR27 displayed 10 and 11 virulent genes, respectively, and were pathogenic to the *Yr2*, *Yr6*, *Yr7*, *Yr8*, *Yr9*, *Yr17*, *Yr25*, *YrA*, and *YrND* genes in both regions. Examination of durum wheat genotypes using these isolates revealed genetic variability at the seedling stage (Table 5). Resistance was categorized into three types: resistant to isolate 6E158A+, resistant to isolate 14E158A+,YR27, and resistant to both isolates. Results indicated that genotypes G3, G9, G10, G25, G26, G27, G38, G39, G41, and G42 were immune or very resistant to both isolates, while G6, G8, G13, G22, G33, G34, G40, G41, G43, and G45 were resistant or immune to one isolate. Overall, 23 of the genotypes studied were susceptible to both *Pst* isolates (Table 5).

DISCUSSION

This project identified significant genetic variability among durum wheat genotypes in their resistance to yellow rust under both rainfed and controlled conditions. Such variability is crucial for breeding programs aimed at enhancing rust resistance, given the potential for fungi to evolve and produce new isolates (Aktar-Uz-Zaman *et al.,* 2017). Consequently, there is a continuous need to explore new resistance sources and integrate them into compatible genotypes. We selected two rainfed hotspot regions for yellow rust, Zarghan and Ardebil, to evaluate adult plant responses under different conditions. Results indicated that the slow rusting traits in the Ardebil region surpassed those in Zarghan, suggesting Ardebil is more conducive to stripe rust development. This observation aligns with the region's colder temperatures and higher cloud cover compared to Zarghan, and corroborates previous findings regarding the influence of environmental factors on rust proliferation (Hassan *et al.,* 2022). In our field evaluations, similar to the findings of Singh *et al.* (2017), genotypes exhibiting lower values of area under the disease progress curve (AUDPC) also showed reduced disease severity across regions, resulting in moderate to resistant reactions (MR, M, and MS). These genotypes likely possess minor effect genes that contribute additively to durable strip rust resistance (Chen *et al.,* 2013). Additionally, these genotypes may harbor previously identified slow rusting genes, Yr18 and Yr36, or genes associated with high-temperature tolerance (Singh *et al.,* 2011).

Adult plant resistance genes may overlap with seedling stage resistance genes, making field evaluations alongside seedling assessments essential (Sandoval-Islas *et al.,* 2007; Pretorius *et al.,* 2007). This study investigated host-pathogen interactions with two *Pst* isolates, 6E158A+ and 14E158A+, from the Ardebil and Zarghan regions under greenhouse conditions. It was concluded that isolate 6E158A+ is more aggressive, likely due to the favorable climatic conditions in Ardebil, which could drive fungal genomic evolution (Aktar-Uz-Zaman *et al.,* 2017). Such aggressive isolates like 6E158A+ could be beneficial for future durum wheat breeding programs through phenotyping of bi-parental mapping populations and germplasm screening (Bokore *et al.,* 2021).

Greenhouse assays indicated that resistant genotypes likely possess the *Yr1*, *Yr4*, *Yr5*, *Yr10*, *Yr15*, *Yr24*, *Yr26*, *Yr32*, *YrSD*, *YrSU*, *YrCV*, and *YrSP* genes. Similar studies (Maccaferri *et al.,* 2015; Jan *et al.,* 2021) highlighted the importance of *Yr4*, *Yr5*, *Yr10*,

Table 5. Seedling stage response of durum wheat genotypes to two *Puccinia striiformis* Westend. f. sp. *tritici* Eriks isolates.

Genotype	Seedlings infection type against races[a]		Genotype	Seedlings infection type against races	
	6E158A+	14E158A+,YR27		6E158A+	14E158A+,YR27
G01	3	3	G24	3	3
G02	3	3	G25	0;CN	;CN
G03	0;1	0;CN	G26	;1CN	0;
G04	3	3	G27	0;CN	0;
G05	3	3	G28	4P;1 , 2P3 MIX	3
G06	2-3C	0	G29	0;CN	4P0; , 2P3 MIX
G07	3	3	G30	3	3
G08	0	3	G31	3	3
G09	0	0;	G32	3	;1C
G10	0	0	G33	0;CN	3
G11	3	4	G34	;1CN	2+C
G12	3	4	G35	3	3
G13	0;	4	G36	3	3
G14	3	;1CN	G37	;1CN	4P0; , 3P3 MIX
G15	4P0; , 2P3 MIX	4P0; , 2P3 MIX	G38	0;	0;
G16	4	4	G39	0;	0;
G17	3?	3?	G40	0;	3
G18	3	3	G41	0;	;1CN
G19	3	3	G42	0;	0;
G20	3	4	G43	3	;1CN
G21	3	4	G44	3	4
G22	0;	3	G45	0;1CN	6P0;1 , 2P3 MIX
G23	4	4			

[a]Infection types were determined according to a 0 to 4 scale (McIntosh *et al.,* 1995) and ';', 'c' and 'n' indicate a fleck reaction, chlorosis and necrosis, respectively. Plus, or minus signs signify larger or smaller pustule variations within an accepted infection type class.

Yr15, *YrCV*, and *YrSD* genes in the resistance of both bread and durum wheat genotypes. Consistent with field evaluations, high genetic variability was observed among durum wheat genotypes in response to the two *Pst* isolates. In greenhouse experiments, genotypes G01, G04, G28, and G30 are prioritized due to their susceptibility to at least two *Pst* isolates and low slow rusting parameters across both regions, likely carrying adult plant resistance gene(s) (Basnet *et al.,* 2013).

Additionally, genotypes G25, G26, G27, and G38 exhibited simultaneous resistance to both *Pst* isolates and low slow rusting parameters across regions, making them significant for conferring specific resistance. These genotypes may also include nonspecific resistance genes that could be masked by the effects of specific resistance genes (Safavi, 2015).

CONCLUSION

This project examined the variable responses of durum wheat germplasm to yellow rust across two rainfed regions, indicating that selection breeding methods can yield significant genetic gains. Field evaluations revealed a spectrum from completely resistant to sensitive genotypes, depending on the region. In the Ardebil region, where environmental conditions favor the rust agent, completely resistant genotypes were not identified. Given the aggressive *Pst* isolate in Ardebil, this area is ideal for screening durum wheat germplasm under high selection pressure. Comparing slow rusting data from both regions can help identify genotypes with adult plant resistance (non-race specific resistance). In combination with greenhouse experiments, genotypes G01, G04, G28, and G30 exhibited non-race specific resistance genes, while G25, G26, G27, and G38 showed both non-race and race specific resistance genes. These genotypes demonstrated varying degrees of durable or slow rusting resistance and could be utilized in durum wheat breeding programs after further evaluation for relevant diseases and yield trials.

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