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RESEARCH ARTICLE

Field relevant resistant sources to yellow rust (*Puccinia striiformis*) and powdery mildew (*Blumeria graminis tritici*) in some exotic wheat (*Triticum aestivum* L.) and their yield potential

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Abstract

Resistance against yellow rust (YR) and powdery mildew (PM) was evaluated in 29 promising wheat (*Triticum aestivum* L.) genotypes comprising advanced breeding material from CIMMYT (24) and some popular varieties of North Hill Zone (4) and susceptible check variety PBW 343 under six and four environments at three (Malan, Kukumseri and Keylong) and two (Malan and Palampur) hot spot locations, respectively. The proportion effect of each source of variation over the total effect showed that the largest contribution to YR severity was attributed to genotype (G), i.e., 61.10%, whereas it was attributed to environment (50.84%) for PM. Genotypes E 12, E 13, E 25, HS 507, HPW 368 and TC1-24 were free from YR, whereas the rest of the genotypes, except GS 7058 and TC1-23, with a mean disease severity of <10S, were resistant. Genotypes E-11, E-12, E-13, E-14, E-25, GS 7038, HPW 368,HS 507, TC1- 17 and TC1- 27 showed multi-locational and multiyear resistance (≤5) to PM. Genotypes E-1, E-2, E-9 and TC1-7recorded significantly higher grain yield per plant than the best check HPW 368 (7.07 g/plant) whereas, genotypes E-6, E-8, E-11, E-12, E-13, E-21, E-23, GS 6012, GS 5031, HS 507, HPW 349, TC1-10, TC1-17, TC1-19, TC1-23, TC1-24, TC1-25, TC1-27 and VL 907 were at par with it.Genotypes viz. E-1, E-2, E-6, E-8, GS 6012, HPW 349, HPW 373, TC1-24, TC1-23, TC1-25 and VL 907 showed seedling resistance to races 110S84, 78S84 and 46S119 which were avirulent on genes *Yr1*, *Yr5*, *Yr10*, *Yr14*, *Yr15*, *Yr24*, *Yr26*, *Yr28* and *YrSP*. Hence, resistance in these genotypes may be attributed to any of these genes individually or in combination. Genotypes E 11, E-12, E-13, E-23, HS 507, TC1-10 and TC1-27 were high yielding and showed combined resistance to YR and PM. These could be useful donors in the breeding program to evolve PM and YR-resistant varieties. Moreover, Kukumseri and Malan could be the ideal test hotspot locations for evaluation of wheat germplasm for resistance against YR and PM, respectively.

Keywords: Powdery mildew, Yellow rust, Stripe rust, stability of resistance, GGE biplot, *Triticum aestivum*, combined resistance.

Introduction

Wheat (*Triticum aestivum* L.) is an important winter cereal in India. It is cultivated in about 31.23 m ha (14% of global area) to produce 112.92 mt of grains with an average productivity of 3615 kg/ha during the year 2024-25 (aicrpwheatbarleyicar.in). Among various factors for the low productivity as compared with the yield potential of recommended varieties, abiotic and biotic stresses take a heavy toll on the crop. Among biotic stresses, diseases pose a severe threat to wheat production, out of which yellow rust (YR) caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) and powdery mildew (PM) caused by *Blumeria graminis* f. sp. *tritici* inflict huge losses under the conducive environmental conditions (Mehta et al. 2022a, b; Camrona et al. 2020; Alemu et al. 2021; Figueroa et al. 2018; Mehta et al. 2024). Cultivation of resistant varieties is a practically feasible, eco-friendly and economically viable means to manage these diseases (Chen 2020; Sood et al. 2020; Mengesha et al. 2022). Mostly, breeders have developed resistant varieties with race-specific genes (Vechet 2006; Klymiuk et al. 2018; Kaur et al. 2020) and such resistance is frequently overcome with the appearance of new and matching virulent pathogen populations through single-step mutation and/or sexual recombination events (Kolmer and Acevedo 2016; Mehta et al. 2024), making the resistant varieties susceptible within a short period of their commercial cultivation. Most of the present-day commercially grown varieties in the epidemiologically important regions of the country, i.e., North Hill Zone (NHZ) and North Western Plain Zone (NWPZ), are susceptible (https://www.iiwbr.org). Thus, identification of YR and PM-resistant donors followed by their utilization in a breeding program to develop resistant varieties would be a holistic and systematic attempt for their management. It requires field-based assessment of resistance evaluated

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through multi-locational trials because of the differential performance of genotypes attributable to genotype-by-environment interaction (GEI) (Mehta et al. 2022a, b; Abraha et al. 2019; Mengesha et al. 2022; Abate et al. 2023). Various statistical methods are available for establishing the role of GEI in the identification of desirable genotypes (Yan and Kang 2003; Parihar et al. 2018; Abate et al. 2023), out of which the GGE biplot graphically displays genotype (G) and GEI effects, enabling the evaluation of genotypes as well as the mega environment identification (Yan et al. 2000; Huang et al. 2021; Mehta et al. 2024). Therefore, the present study was undertaken to assess the effects of genotype, environment and their interactions on the severity of YR and PM in some promising exotic advanced breeding materials through multi-location field testing at diverse hot spot sites.

Materials and methods

The experimental material comprised 24 wheat genotypes procured from CIMMYT, Mexico; varietal checks, namely, HS 507, VL 907, HPW 368 and HPW 349; and susceptible check PBW 343. The details of the materials are given in Table 1. The test genotypes were grown in one meter long row plots spaced 20 cm apart, following standard package of practices for irrigated conditions (http://www. hillagric.ac.in/extension/dee/pdf_files/Rabi_28-8-09). The susceptible check (SC) varieties PBW 343 and Agra Local were sown after every 10th test genotype and on the outer boundaries surrounding the test genotypes.

Multi-locational testing against yellow rust and powdery mildew

All the test lines were sown along with the susceptible check, i.e., PBW 343 at RWRC Malan during the cropping seasons 2015-16, 2016-17, 2017-18, 2018-19, CSKHPKV, Palampur (2017-18), Highland Agricultural Research and Extension Centre, Kukumseri (Summer 2017) and PAU, Research Station, Keylong (LahaulSpiti) during summer 2018 for YR and PM evaluations following recommended package of practices for irrigated conditions. All the locations are hot spots for YR and/or PM.

Evaluation of genotypes for yield and yield components

The experiment was carried out in randomized block design with 3 replications; with plot size of 2 x 0.4 m^2 i.e. two rows of 2m length with row to row and plant to plant spacing of 20 and 15cm, respectively at CSKHPKV, RWRC, Malan during the cropping seasons 2016-17 and 2017-18 following the standard package of practices under irrigated conditions. The observations were recorded on 5 randomly selected competitive plants in each replication for various morphometric and yield traits i.e. days to 50 % flowering, plant height (cm), tillers per plant, days to 75% maturity, biological yield per plant(g), grain yield per plant (g), harvest index (%) and 1000-seed weight (g).

Screening for yellow rust and powdery mildew resistance

Yellow rust

The field evaluation of test genotypes was carried out at CSKHPKV, Palampur; RWRC, Malanduring the cropping season 2015-16, 2016-17, 2017-18 and 2018-19, Kukumseri(Summer 2017) and Keylong(Summer 2018). These locations are hot spots for YR. Still, artificial epiphytotic of the disease was created using the mixture of yellow rust races procured from IIWBR, Research Station, Flowerdale, Shimla, at Malan. In addition to it, local field isolates were used at all the test locations for creation of epiphytotic following recommended standard practices (Mehta et al. 2022a, b). Observations on per cent of rust severity and host reaction on the foliage were recorded as per modified Cobb's scale (Peterson et al.1948).The data were recorded when the susceptible wheat variety developed terminal rust severity of >60S.

Powdery mildew

The susceptible check (SC) varieties were infected earlier in the season and with more severity. These were frequently but gently tapped with sticks to dislodge the conidia of the pathogen during the evening hours, which were blown up and served as inoculum to infect the test genotypes. The data were recorded on terminal disease reaction based on a 0-9 scale (Saari and Prescott 1975) when the susceptible varieties developed disease reaction 8-9.

Table 1. Details of the material used in the present investigation

S. No.	Genotype	Pedigree
1	TC1-7	SDSS12B00678S-0B-0B-271Y-0B, JAL95.4.3/3/KACHU#1/KIRITATI//KACHU
2	TC1-10	SDSS12B00678S-0B-0B-79Y-0B JAL95.4.3/3/KACHU#1/KIRITATI//KACHU
3	TC1-17	SDSS12B00678S-0B-0B-456Y-0B JAL95.4.3/3/KACHU#1/KIRITATI//KACHU
4	TC1-19	SDSS12B00678S-0B-0B-46Y-0B JAL95.4.3/3/KACHU#1/KIRITATI//KACHU
5	TC1-24	SDSS12B00678S-0B-0B-487Y-0B JAL95.4.3/3/KACHU#1/KIRITATI//KACHU
6	TC1-23	Early SDSS12B00678S-0B-0B-473Y-0B JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU
7	TC1-25	Early SDSS12B00678S-0B-0B-488Y-0B JAL95.4.3/3/KACHU#1/KIRITAT1//KACHU
8	TC1-27	SDSS12B009277-04-0B-0B; IG41514 /5 /SERI.1B/ KAUZ/HEVO /3/ AMAD* 2/4/ KIRITATI/6/FRET2*2 /4 / SN1/ TRAP#1/3/KAUZ*2/..
9	E-1	(KACHU) CMSS 97M03912T-040Y-020Y-030M-020Y-040M-4Y-3M-0Y
10	E-2	(BAJ#1) CGSSS 01Y00134S-099Y-099M-099M-13Y-0B
11	E-6	SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITAT 1 CGSSB00198T-099T0PY-099M-099NJ-14WGY-0B
12	E-8	HPW 234+LR34/PRINIA*2//KIRITAT1 CGSS05B00244T-099T0PY-099M-099NJ-10WGY-0B
13	E-9	WHEAR/KRONSTAD F2004 CGSS04Y00106S-099Y-099M-099Y-099M-13WGY-0B
14	E-11	CNDO/R143/ENTE/MEXI.2/3/AEGILOPSSQUARROSA(TAUS)/4/WEAVER/5/.. CMSS04M01331S-0T0PY-099ZTM-099Y-099M-3WGY-0B
15	E-12	KAUZ//ALTAR84/AOS/3/PASTOR/4/MILAN/CUPE//SW89.3064/5/KIRITAT1 CMSS04MO1386S-0T0PY-099ZTM-099Y-099M-2WGY-0B
16	E-13	SW89.5277/BORL95//SKAUZ/3/PRL/2*PASTOR/4/HEILO CMSS04M01483S-OT0PY-099ZTM-099Y-099M-1WGY-OB
17	E-14	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07 CGSS04B00025T-099Y-099ZTM-099Y-099M-8WGY-0B
18	E-21	(QUAIU #1) CGSS01B00046T-099Y-099M-099M-099Y-099M-29Y-0B
19	E-23	(VOROBEY) CMSS96Y02555S
20	E-24	CGSS00B00169T-099TOPY-099M-099Y-099M-9CEL-0B (ROELFS F2007)
21	E-25	(NAVOJOA M 2007) CMSS97404045S-040Y-050M-040SY-030M-14SY-010M-0Y-OMEX
22	GS 7038	SOKOLL/3/PASTOR//HXL7573/2*BAU*2/4/NAVJ07
23	GS 6012	KACHU/6/YAR/AE.SQUARROSA (783)/4/GOV/AZ//MUS/3/SARA/5/MYNA/VUL//JUN
24	GS 5031	PRL/2*PASTOR//KACHU
25	HPW 349	OASIS/SKAUZ//4*BCN/3/PASTOR/4/KAUZ
26	HPW 368	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR
27	HS 507	KAUZ/MYNA/VUL//BUC/FLK(4/MILAN
28	VL 907	DYBR1982-83842ABVD50/VW9365//PBW343
29	PBW 343	NORD-DESPREZ/VG-1944//KALYANSONA//BLUEBIRD/3/YACO(SIB)/4/VEERY-5

Reaction of wheat genotypes at the seedling stage against the prevalent races of yellow rust

The seedlings of 25 wheat cultivars, including varietal checks, namely, HS 507, HPW 349, HPW 368 and VL 907and susceptible checks PBW 343, were raised in aluminum trays (12x8x4 inch) filled with FYM and field soil (1:10) in uniformly fertilized soil. The three most prevalent races (110S84, 78S84 and 46S119), procured from ICAR-IIWBR Research Station, Flowerdale, Shimla, were used for screening at the seedling stage. The uredospore inoculum of above mentioned races was mass multiplied on susceptible wheat varieties PBW 343/HD 2967. Ten-day-old seedlings were inoculated with uredospore suspension of the individual pathotypes. The inoculum was prepared by mixing uredospores (1 x 10^6 spores/mL of water) with a drop of Tween-20 (used to facilitate the adhesion of spores on the leaves), and sprayed using a glass atomizer. Inoculated seedlings were kept in moist chambers for incubation at a temperature of 16 to 18°C and relative humidity of (>90% and 12 hours of daylight. The seedlings were then transferred to greenhouse benches and kept at a temperature (16 ± 2°C) and relative humidity (>80%). The data were recorded on infection type on test genotypes following the modified scale of Stakman (1962).

Statistical analysis

The contribution of environment, genotype and their interactions was determined by analysis of variance (ANOVA), using OPSTAT online statistical packages for both YR and PM. The ANOVA explained the partition of variation due to the effect of genotypes, environment, and their interaction and was used for GGE biplot model diagnosis based on goodness of fit. Among 'no-scaling' and 'standard deviation (s.d.)' scaling methods, the 'no scaling' method registered the highest goodness of fit, representing 90.06 and 84.64% of the total variation for YR and PM, respectively. The GGE biplot analysis was done using the GEA-R (Genotype x Environment Analysis with R for Windows) Version 4.1 (2017-08-3). The data on yield and yield components were statistically analyzed as per the procedure given by Panse and Sukhatme (1985).

Results and discussion

Mean performance and analysis of variance

The ANOVA was calculated across the locations using factorial randomized block design, which inferred that the mean sums-of-squares for environments, genotypes and their interaction were highly significant ($p < 0.01$) for both the YR and PM severity (Tables 2, 3). The proportion effect of each source of variation over the total effect showed that the largest contribution to disease severity was accounted for by genotype (G) and G X E interaction for YR (61.10%) and PM (43.77%), respectively (Tables 3 and 4). The multiplicative analysis revealed that the first two interaction principal components cumulatively explained 90.06 & 84.64% of the total variation for YR & PM, respectively. The highest average YR severity of 8.63% was recorded at Keylong (Summer, 2018), whereas the highest mean PM disease reaction (5.90) was recorded at Malan (2016-17). The mean YR disease severity and PM reaction were the least at location 2, i.e., Malan 2016-17 (2.43%) and at Palampur (3.60) (2017-18) (Tables 4, 5).

The best test environment (location) for wheat genotypes

Visualization of the "which-won-where" pattern of multi-environment trial data is necessary for grouping of test environments into different "mega environments," and delineation of genotypes (Gauch and Zobel 1997; Yan et al. 2000; Mehta et al. 2024). The genotypes registering the lowest and the highest disease severity/disease reaction were at different vertices of the polygon (convex hull) and contributed maximum to the interactions(Yan et al. 2007). The genotypes present at the right side of the hull showed more YR severity and those on the left side had stable resistance across the locations. The GGE biplot analysis showed that genotypes E-1, E-2, E-6, E-8, E-11, E-12, E-13, E-14, E-21, E-23, E-24, E-25, TC1-7, TC1-10, TC1-17, TC1-19, TC1-24, TC1-25, TC1-27, GS 6012, GS 5031, HPW 349, HPW 368, HS 507 and VL 907, with low level of YR severity, were highly resistant across the locations (Fig. 1). These genotypes were present near the biplot origin and on the left side of the hull. Two lines, i.e., GS 7038 and TC1-23 and one susceptible check (PBW 343) showed consistently higher YR severity, as they were the farthest on the right side of the origin of the biplot.

In the case of PM, the genotypes present at the left side of the hull showed more disease reaction, whereas those on the right side had stable resistance across the locations. The GGE biplot analysis showed that genotypes E-11, E-12, and HPW 368, which showed low PM reaction, were highly resistant across the locations. Genotypes, i.e., E-1, E-19, VL 907 and susceptible check PBW 343 showed consistently higher PM reactions were being the farthest on the right side of the origin of the biplot (Fig. 1-A, B). The scatter biplot

Table 2. Analysis of variance of yellow rust (YR) severity in 29 genotypes of wheat evaluated at six locations in Himachal Pradesh

Source of variation	DF	Sum of squares	Mean squares	Percentage of contribution	Significance
Environment (E)	5	2,212.76	442.551	2.22	***
Genotypes (G)	28	60,688.92	2,167.46	61.10	***
G X E	140	36,409.76	260.07	36.70	***

Table 3. Analysis of variance of powdery mildew (PM) severity in 29 genotypes of wheat evaluated at five locations in Himachal Pradesh

Source of variation	DF	Sum of Squares	Mean Squares	Percentage of contribution	Significance
Environment (E)	3	246.08	82.02	15.83	**
Genotypes (G)	28	627.62	22.41	40.39	**
G X E	84	680.17	8.09	43.77	**

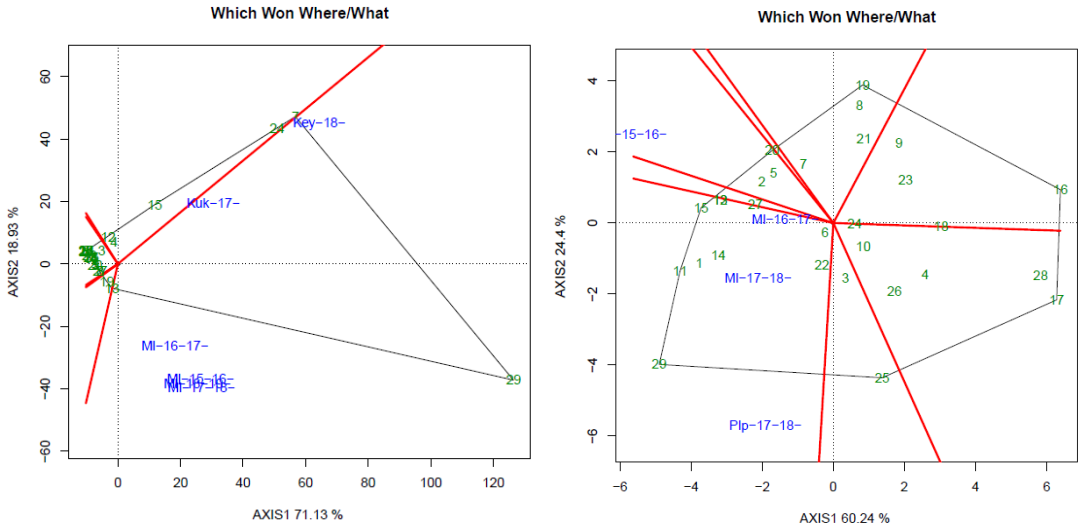
indicated only one mega-environment for YR and two mega-environments for PM (Fig. 1-A, B).

An "ideal" test environment should be both discriminating of the genotypes and representative of the mega-environment. The biplot showed that Keylong (Summer 2018) and Malan (2015-16) had greater vector length for YR and PM, respectively, inferring that these locations had the highest discrimination power and efficiency for genetic differentiation of genotypes. The angles between the test environment vectors represented the degree of relationship between the environments (Yan 2001). Acute angles (<90°) between vectors of the locations depicted a strong relationship between them and wider obtuse angles (>90°) between location vectors depicted a negative relationship between them (Yan and Kang 2003; Mehta et al. 2022a). The environment forming small angles among each other suggested a positive correlation among them, i.e. Malan during 2015-16, 2016-17, 2017-18, 2018-19 for PM and between Kukumseri (Summer 2017) and Keylong (Summer 2018) for YR (with acute angle) whereas, locations Keylong 2018 and Malan (2017-18) with an obtuse angle were slightly negatively correlated (Figs. 2-A, B).

In case of PM, the environments, i.e., Palampur (2017-18) and Malan (2017-18) and Malan (2015-16) and Malan (2016-17), forming small angles between themselves, suggested a positive correlation. The present results are in agreement with the biplot analysis as proposed by Yan and Kang (2003). Similar studies were undertaken in wheat PM and YR (Mehta et al. 2022a; Mehta et al. 2022b; Mehta et al. 2024).

In a GGE biplot, the representativeness of a target environment is determined by the angle between the test environment vector and the AEC (Average Environment Coordinate) abscissa is the single-arrowed line (ray) through the biplot origin and the average of all environments(Yan and Kang 2003; Mehta et. 2022b). The environment Keylong (Summer 2018), and Malan (2015-16) have a larger angle with the AEC abscissa for YR, and PM, respectively, indicating their low representativeness due to the highest disease pressure (Figs. 2-A, B). Therefore, this environment can be used to identify the best disease-resistant genotypes and based on the highest discriminating ability, location Kukumseri and Malan appeared to be the ideal testing sites or 'hot spots' for screening against YR and PM, respectively. Present results are in conformity with the findings of Mehta et al. (2022a), who also reported Kukumseri and Malan as the ideal or hot spot locations for evaluating wheat genotypes against YR and PM.

The single arrowed line is the AEC abscissa and the arrow points in the direction of higher disease severity(Fig. 3-A, B). The stability of the genotypes is estimated by their



A B

Fig. 1. GGE biplot of PC1 (disease severity) and PC2 (resistance stability) based on yellow rust (YR) disease severity (A)and powdery mildew (PM) disease reaction (B) of 29 wheat genotypes under 6 and 5 environments respectively, "which-won-where" pattern for genotypes and environments. Ml-15-16- = Malan 2015-16; Ml-16-17- = Malan 2016-17; Ml-17-18- = Malan 2017-18; Ml- 18-19- = Malan 2018-19; Key-18- = Keylong Summer 2018; Kuk-17- = Kukumseri Summer 2017; Pl-17-18- = Palampur 2018-19

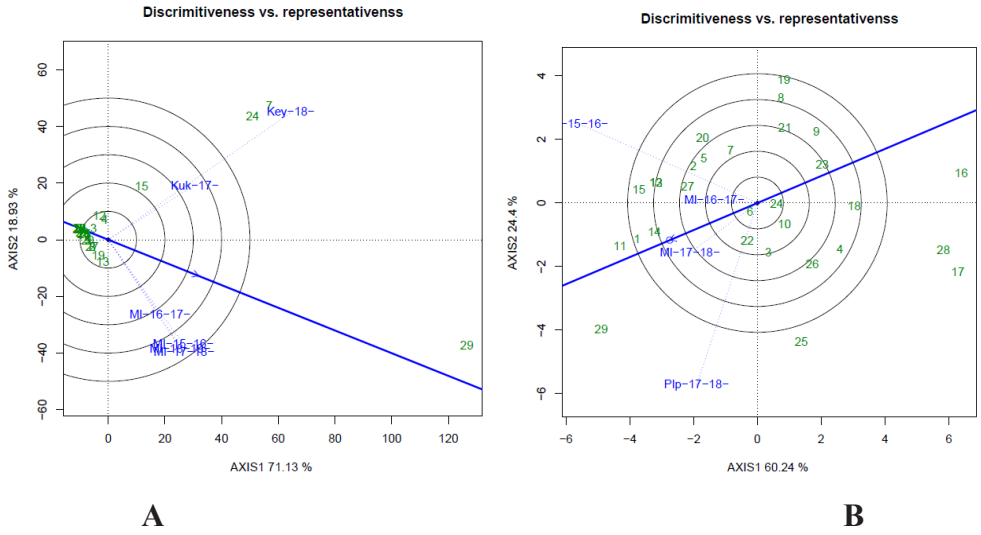


Fig. 2. GGE biplot of PC1 (disease severity) and PC2 (resistance stability) based on yellow rust disease severity (A) and powdery mildew disease reaction (B) of 29 wheat genotypes under 6 and 5 environments respectively: discriminating ability and representativeness of environments for disease severity. Ml-15-16- = Malan 2015-16; Ml-16-17- = Malan 2016-17; Ml-17-18- = Malan 2017-18; Ml- 18-19- = Malan 2018-19; Key-18- = Keylong Summer 2018; Kuk-17- = Kukumseri Summer 2017; Pl-17-18- = Palampur 2018-19

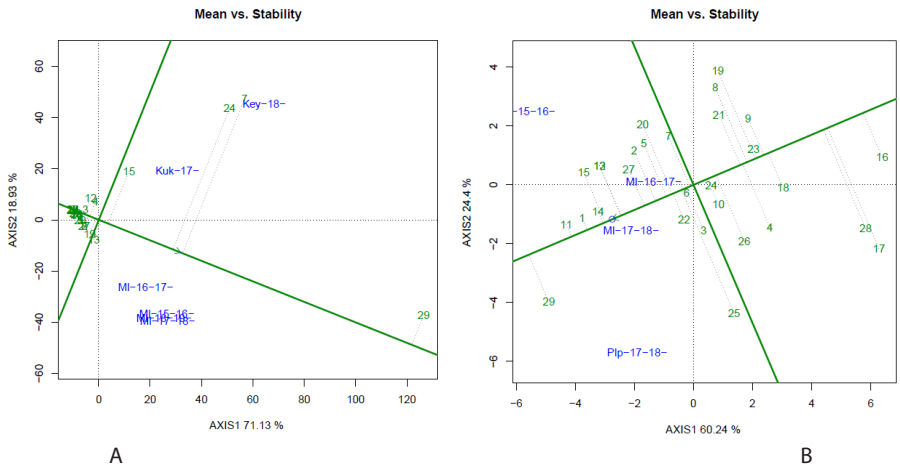


Fig. 3. GGE biplot of PC1 (disease severity) and PC2 (resistance stability) based on yellow rust (YR) disease severity (A) and powdery mildew (PM) disease reaction (B) of 29 wheat genotypes under 6 and 5 environments respectively: the relationship between mean disease severity and wheat stability. Ml-15-16- = Malan 2015-16; Ml-16-17- = Malan 2016-17; Ml-17-18- = Malan 2017-18; Ml- 18-19- = Malan 2018-19; Key-18- = Keylong Summer 2018; Kuk-17- = Kukumseri Summer 2017; Pl-17-18- = Palampur 2017-18

projection onto the middle horizontal line and the greater the absolute length of projection of a genotype, the less stable it is and vice versa (Mehta et al. 2022a; Mehta et al. 2024). The GGE biplot analysis of means vs stability, using genotype-centered data (Figs. 3-A, B) of genotypes, revealed that the overall best genotypes for YR were TC1-7, TC1-10, TC1-17, TC1-19, TC1-24, TC1-25, TC1-27, E-1, E-2, E-6, E-8, E-11, E-12, E-13, E-14, E-21, E-23, E-24, E-25, GS 6012, GS 5031, HPW 349, HPW 368, HS 507 andVL 907 whereas, for PM, the best genotypes were E-11, E-12, HPW-368 and TC1- 17 (Table 4 and 5). The present strategy to identify stable and durable YR and PM resistant lines is in agreement with the earlier successful deployment of such means for identifying stem and leaf rust resistant genotypes of wheat (Abate et al. 2023; Akcura et al 2017; Akan and Akcura 2018; Tremmel-Bede et al. 2020). As has been observed in the present studies, sources of adult plant resistance to YR have been reported by various workers in India and other parts of the world (Abraha et al. 2019; Mu et al. 2019; Kumar et al. 2020; Mehta et al. 2024). Genotypes E 11, E-12, E-13, E-23, E-25, HPW 368, TC1-17, and TC1-27 showed combined resistance to YR and PM.Sources with combined resistance to PM and YR were also reported by earlier workers (Basandrai et al. 2018; Sood et al. 2020; Mehta et al., 2024).

Race-specific resistance to yellow rust races

Seedlings of the test genotypes were evaluated using 3 races of yellow rust, i.e., 110S84, 78S84 and 46S119 (Table 7). The

Table 4. Yellow rust (YR) severity and powdery mildew (PM) disease reaction of twenty nine genotypes of wheat at Malan (2015-16, 2016-17, 2017-18, 2018-19), Keylong (summer 2018), Kukumseri (2017) and Palampur (2017-18)

S. No.	Genotype	Yellow rust severity at							Powdery mildew disease reaction at				
		Ml 2015-16	Ml 2016-17	Ml 2017-18	Ml 2018-19	Key S18-	Kuk S17-	Mean	Ml 2015-16	Ml 2016-17	Ml 2017-18	Pl 2018-19	Mean
1	TC1-7	10.00	0.00	0.00	5.00	0.00	0.00	2.50	8.00	5.00	5.00	3.00	5.30
2	TC1-10	0.00	0.00	0.00	5.00	0.00	10.00	2.50	5.00	5.00	4.00	5.00	4.80
3	TC1-17	5.00	0.00	0.00	0.00	10.00	0.00	2.50	3.00	4.00	4.00	4.00	3.80
4	TC1-19	0.00	0.00	0.00	10.00	0.00	0.00	1.67	8.00	5.00	4.00	3.00	5.00
5	TC1-24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.00	5.00	4.00	4.00	4.80
6	TC1-23	0.00	5.00	0.00	0.00	60.00	60.00	20.83	7.00	5.00	5.00	2.00	4.80
7	TC1-25	10.00	0.00	0.00	5.00	0.00	0.00	2.50	6.00	6.00	4.00	0.00	4.00
8	TC1-27	10.00	0.00	0.00	0.00	0.00	0.00	1.67	5.00	5.00	3.00	1.00	3.50
9	E-1	0.00	0.00	0.00	5.00	0.00	0.00	0.83	9.00	6.00	6.00	6.00	6.80
10	E-2	0.00	0.00	0.00	0.00	0.00	20.00	3.33	9.00	5.00	5.00	4.00	5.80
11	E-6	10.00	10.00	10.00	0.00	0.00	0.00	5.00	9.00	5.00	5.00	4.00	5.80
12	E-8	0.00	0.00	0.00	5.00	0.00	0.00	0.83	9.00	4.00	4.00	6.00	5.80
13	E-9	0.00	0.00	0.00	0.00	20.00	20.00	6.67	9.00	6.00	6.00	4.00	6.30
14	E-11	0.25	0.25	0.00	5.00	0.00	0.00	0.92	0.00	4.00	4.00	0.00	2.00
15	E-12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.00	4.00	2.00
16	E-13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	4.00	0.00	4.00	3.00
17	E-14	5.00	10.00	5.00	5.00	0.00	0.00	4.17	7.00	3.00	3.00	0.00	3.30
18	E-21	0.00	0.00	0.00	10.00	0.00	0.00	1.67	8.00	5.00	5.00	2.00	5.00
19	E-23	0.00	0.00	0.50	0.00	0.00	0.00	0.08	6.00	4.00	4.00	1.00	3.80
20	E-24	0.00	5.00	0.00	0.00	0.00	0.00	0.83	6.00	4.00	4.00	5.00	4.80
21	E-25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.00	6.00	0.00	3.00	3.50
22	GS 5031	5.00	0.00	0.00	0.00	0.00	0.00	0.83	3.00	5.00	6.00	4.00	4.50
23	GS 7038	5.00	0.00	0.00	0.00	80.00	0.00	14.17	5.00	5.00	5.00	3.00	4.50
24	GS 6012	5.00	0.00	0.00	0.00	0.34	0.00	0.89	3.00	4.00	5.00	7.00	4.80
25	HPW 349	10.00	0.00	0.00	5.00	0.00	0.00	2.50	8.00	6.00	4.00	4.00	5.50
26	HPW 368	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.00	3.00	3.00	2.50
27	HS 507	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.00	4.00	4.00	4.00	4.30
28	VL 907	0.00	0.25	0.45	0.00	0.00	0.00	0.12	9.00	5.00	5.00	6.00	6.30
29	PBW 343	60.00	40.00	60.00	60.00	80.00	40.00	56.67	8.00	7.00	8.00	8.00	7.80
General mean		4.66	4.66	2.43	2.62	4.14	8.63	5.17	4.61	5.90	4.80	4.20	3.60

Ml 2015-16 = Malan 2015-16; Ml 2016-17 = Malan 2016-17; Ml 2017-18= Malan 2017-18; Ml2018-19 = Malan 2018-19; Key S18- = Keylong Summer 2018; Kuk S17- = Kukumseri Summer 2017; Pl 2018-19 = Palampur 2018-19.

results revealed that genotypes E-1, E-2, E-6, E-8, GS 6012, HPW 349, TC1-23, TC1-24, TC1-25 and VL 907 were resistant to all the test races of yellow rust. The avirulence and virulence formula of pathotypes used in the study was given in Table 6, and all the races were avirulent on genes *Yr1*, *Yr5*, *Yr10*, *Yr14*, *Yr15*, *Yr24*, *Yr26*, *Yr28*, and *YrSP*. Hence, genotypes viz. E-1, E-2, E-6, E-8, GS 6012, HPW 349, TC1-24, TC1-23, TC1-25 and VL 907 showing resistance to all the races may carry one or more of these genes. or some other adult plant resistance genes. Genes, viz. *Yr5*, *Yr10*, *Yr15*, *Yr36*, *Yr47*, *Yr51*, *Yr57* and *Yr63* provide resistance to prevalent races of yellow rust (Sharma et al. 2022) and gene *Yr15* has been reported to be highly effective (Klymiuk et al. 2018; Kaur et al. 2020).

Evaluation for yield and yield contributing traits

Based on the pooled data of both the cropping seasons 2016-17 and 2017-18, it was observed that days to 75% maturity varied from 133.17 to 145.00 days with a mean value of 140.37 days. Fifteen genotypes, viz., E-1, E-2, E-21, E-23, E-24, GS 6012, GS 5031, HS 507, TC1-7, TC1-10, TC1-17,

Table 5. Reaction of wheat genotypes to stripe rust and powdery mildew

Reaction to			
Yellow rust		Powdery mildew	
Disease severity (%)	Genotypes	Reaction (0-9)	
0	VL 907, TC1- 17, TC1- 24, TC1- 27, HS 507, E-9, E-12, E-13, E-22, E-23, GS 7038, GS 6012, GS 5031, HS 562	0	E-11
Ts	HPW 349	1	-
5S-10S	TC1- 7, TC1- 10, TC1- 19, TC1- 23, TC1- 25, E-1, E-2, E-6, E-8, E-11, E-14, E-21, E-24	3	TC1- 10, TC1- 27, HS 507, E-8, E-12, E-13, E-14, E-22, E-23
20S	-	4-5	VL 907, TC1- 7, TC1- 17, TC1-24, TC1-23, TC1-25, TC1- 19, TC1-23, TC1- 27, E-1, E-2, E-6, E-9, E-11, E-21, E-24, E-25, GS 7038, GS 6012, GS 5031, HPW 373, HPW 349, HPW 368, HS 562
30S	-		
More than 40S	Agra local	7-9	E-8, E-9, Agra local

Table 6. Virulence/avirulence formula of yellow rust pathotypes used in the study

Race	Avirulence formula	Virulence formula
76S84	*Yr1, Y,r 3b,Yr4b, Yr5, Yr10, Yr11, Yr14, Yr15, Yr17, Yr18, Yr24/26, Yr28, Yr29, YrSD*	*Yr2, Yr3a, Yr4A, Yr6, Yr7, Yr8, Yr9, Yr12, Yr19, YrSk, YrSu, Yr31*
46S119	*Yr1, Yr5, Yr10, Yr14, Yr15, Yr24, Yr26, Yr28, YrSP*	*Yr2, Yr3a, Yr3b, Yr4a, Yr4b, Yr6, Yr7, Yr8, Yr9, Yr11, Yr12, Yr17, Yr19, Yr 29, Yr31, Yrsk*
110S84	*Yr1, Yr5, Yr10, Yr15, Yr24, Yr26, Yr28,YrSp*, Riebesel *147/51 (Yr2,9,+)*	*Yr2, Yr3a, Yr3b, Yr4a, Yr4b, Yr6, Yr7, Yr8, Yr9, Yr11,Yr12, Yr14, Yr17,Yr18, Yr19, Yr29, Yr31,Yrsk*

Table 7. Seedling infection type of the test wheat genotypes under study against yellow rust races 110S84, 78S84 and 46S119

S.No.	*Genotypes*	*Yellow rust races*		
		110S84	76S84	46S119
1	TC1-7	0	0	3+
2	TC1-10	0	2-	0
3	TC1-23	0	0	0
4	TC1-24	0	0	0
5	TC1-25	0	0	0
6	E-1	0	0	0
7	E-2	0	0	0
8	E-6	0	0	0
9	E-8	0	0	0
10	E-9	0	0	3+
11	E-11	0	0	3+
12	E-12	0	0	3+
13	E-13	0	0	3+
14	E-14	1	1	3+
15	E-21	0	0	2-
16	E-23	0	0	3+
17	E-24	3+	0	3+
18	E-25	3+	3+	3+
19	GS 5031	3+	0	0
20	GS 6012	0	0	0
21	GS 7038	0	2+	3+
22	HPW 349	0	0	0
23	HPW 368	0	3+	2-
24	VL 907	0	0	0
25	Susceptible check	4	4	3+

TC1-19, TC1-23, TC1-25 and TC1-27, matured at par with the best check HPW 368 (141.17 days). Nine genotypes viz., E-11, E-14, E-21, E-23, TC1-7, TC1-17, TC1-19, TC1-23 and VL 907 were significantly superior in height to the best check var. HPW 349 (90.59 cm). Plant height with an average value of 91.09 cm has also been reported earlier (Milkessa et al. 2022). All the genotypes tillered statistically at par with the best check. The biological yield of different genotypes varied from 11.81 to 18.34 g with a mean value of 15.43 g and only one genotype, E-1, was significantly at par with the best check.

Table 8. Estimates of mean values for 27 genotypes of *Triticum aestivum* L. for eight agro-morphological and yield components for pooled data of cropping seasons years 2016-17 and 2017-18

S.No.	Genotypes	Days to 50% flowering	Days to maturity (75%)	Plant height (cm)	Tillers per plant	Biological yield per plant(g)	Harvest index(%)	Grain yield per plant (g)	1000-seed weight (g)
1	TC1-7	109.33	140.67	104.16*	4.00	17.11	48.91*	8.06*	37.51
2	TC1-10	112.00	141.17	90.20	3.95	16.82	44.16	7.36	54.74
3	TC1-17	110.00	141.00	102.81*	4.15	15.73	48.02	7.48	50.82
4	TC1-19	110.50	138.83	96.64*	3.78	12.83	48.13	6.04	45.02
5	TC1-23	110.67	139.67	94.24*	3.72	15.43	45.15	6.84	41.03
6	TC1-24	109.00	137.83*	82.49	3.67	15.05	50.25	7.32	49.35
7	TC1-25	111.50	142.50	92.50	3.65	16.71	46.32	7.58	51.04
8	TC1-27	113.83	143.67	89.68	3.59	14.83	48.36	7.09	38.67
9	E-1	112.83	141.67	87.60	3.72	18.34	44.79	8.15*	43.18
10	E-2	111.00	140.67	87.65	3.45	16.99	48.89*	8.23*	55.40
11	E-6	108.67	135.00*	89.95	3.84	14.83	48.24	7.06	47.32
12	E-8	107.50*	133.17*	87.78	3.66	14.31	47.08	6.71	45.83
13	E-9	109.83	136.17*	93.74	4.08	15.08	53.68*	8.05*	56.45*
14	E-11	109.67	136.83*	94.72*	3.56	15.46	47.67	7.13	43.17
15	E-12	109.17	135.00*	88.61	4.07	13.22	52.07*	6.80	51.44
16	E-13	110.83	138.00*	83.70	3.87	13.69	48.84*	6.53	45.29
17	E-14	108.17	136.67*	95.61*	3.72	11.81	52.15*	6.11	51.04
18	E-21	111.00	140.00	97.60*	3.89	14.04	52.67*	7.37	44.17
19	E-23	113.67	143.5	103.32*	4.10	12.44	53.11*	6.60	48.92
20	E-24	113.17	142.67	87.67	3.77	12.33	48.49	5.91	43.59
21	GS 7038	113.17	145.00	92.89	3.84	13.58	49.00	6.60	44.71
22	GS 6012	113.17	142.83	84.11	3.73	14.40	44.41	6.25	42.01
23	GS 5031	109.17	141.00	88.89	4.43	14.65	50.29*	7.27	48.26
24	HPW 349	109.83*	145.00	90.59*	3.89*	21.29*	34.84	6.85	47.78
25	HPW 368	111.17	141.17*	87.41	3.56	20.13	37.74	7.07*	48.75*
26	HS 507	111.67	141.33	90.00	3.64	17.74	39.16	6.62	39.25
27	VL 907	108.33	144.67	95.54*	3.71	16.66	40.51	6.6	44.36
	Mean	110.61	140.37	91.98	3.81	15.43	47.14	7.01	46.55
	C.V (%)	1.6	1.73	3.1	14.19	17.59	15.15	10.1	13.16
	S.E. (m) ±	0.72	0.99	1.17	0.22	1.09	2.92	0.29	2.49
	CD(5%)	2.02	2.78	3.26	0.8	3.05	8.15	0.8	6.96

The per cent harvest index varied from 37.74 to 53.11 with a mean value of 47.14%. The grain yield per plant varied from 5.91 to 8.23 g with a mean value of 7.01 g. Four genotypes, viz., TC1-7, E-1, E-2 and E-9, were found superior to whereas 18 genotypes were at par with the best check HPW 368 (7.07 g). The 1000-seed weight varied from 37.51 to 56.45 g with a mean value of 46.55 g. About 21 genotypes were statistically at par and only one genotype, *viz*., E-9, was superior to the best check variety HPW 368 (48.75 g). Genotypes E 11, E-8, E-12, E-13, E-23, TC1-10 and TC1-27 showed combined resistance to both YR and PM. These genotypes showed high yield/plant and may prove useful donors for wheat breeding programs aiming to develop high-yielding varieties with resistant to YR and PM.

Authors' contribution

Conceptualization of research (TS, DB, AM, JK, MP, SS, AKB); Designing of the experiments (TS, DB, AKB); Contribution

of experimental materials (TS, DB, AM, JK, MP, SS, AKB); Execution of field/lab experiments and data collection (TS, DB, AM, AKB); Analysis of data and interpretation (TS, DB, AM, AKB); Preparation of the manuscript (TS, DB, AM, AKB).

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