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RESEARCH ARTICLE

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Deciphering field resistance to powdery mildew and yellow rust among popular cultivars of wheat and set of differential lines

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Abstract

The analysis of data on disease severity using genotype (G) and genotype by environment interaction (GGE) biplot revealed that the highest contribution to disease severity was due to genotype (G) 50.75 and 47.56 followed by G X E interaction 44.38; 37.70 and environment (E) 4.8 and 14.74 for powdery mildew (PM) and yellow rust (YR), respectively. Sixteen genotypes showing mean TDS ≤15% and Area under Disease Progress Curve (AUDPC), relative Area Under Disease Progress Curve (rAUDPC) and 'r' ranging between 20.63-494.44, 2.75-40.05 and 0.01-0.04, respectively in comparison with TDS, AUDPC, rAUDPC and 'r' of 41%, 1510.88, 99.18 and 0.04 respectively, in susceptible cultivar Lehmi, were slow mildewing genotypes. Six genotypes Maris dove, Rye, Aldan, CMH 77.308, SAW 71 and SAW 74 showed multiple resistances to PM and YR, of which ALDAN and CMH 77.308 were reported to be resistant to Karnal bunt (KB) also. Hence, these can be used as potential donors aimed to develop cultivars with combined resistance to PM, YR and /or KB and Kukumseri could be used as an ideal hot spot for screening against PM and YR.

Keywords: GGE biplot, Karnal bunt, multiple resistance, powdery mildew, resistance, slow mildewing, wheat, yellow rust.

Introduction

Wheat (*Triticum aestivum* L.), one of the most widely cultivated cereal crops worldwide (Yang et al. 2016), is threatened by many diseases. Out of these, powdery mildew (PM) and yellow rust (YR), caused by *Blumeria graminis* f. sp. *tritici* (*Bgt*) (syn. *Erysiphe graminis* (DC) f.sp. *tritici*) and *Puccinia striiformis* f. sp. *tritici* (*Pst*), respectively are the most devastating in cool climatic regions (Bennett 1984; Wan et al. 2004; Han et al. 2020). Powdery mildew is typically decreasing wheat yield by 10–15% and up to 50% in severe cases (Morgounov et al. 2012; Xu et al. 2015).

Both the diseases have emerged as a potential threat in Northern Hill Zone (NHZ) and North-Western Plain Zones (NWPZ) of India and can be partially managed by the use of fungicides. However, increased awareness on ill effect of fungicides on human and animal health, pollution of environment, water and soil discourage their use. Contrarily, resistant varieties offer an economically and ecologically viable, environmentally safe, and practically feasible alternative to manage these diseases. Majority of the varieties released for the disease prone areas in India are susceptible to PM and YR. Boom-and-bust cycle (Todorovska et al. 2009) in most of the major resistance genes exerting a strong selection pressure result in emergence of pathotypes with new and matching virulences (Parks et al. 2008) rendering resistant varieties susceptible. Understanding the role of environments and genotype by environment interaction (GEI), pertaining to the pathosystem and host genotype stability across diverse locations, is imperative for an efficient resistance breeding program (Das et al. 2019; Sankar et al. 2021). Out of various statistical methods employed to

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analyze GEI for predicting genotypic performance across the environments, genotype X genotype by environment (GGE) biplot analyses has been widely used (Parihar et al. 2018; Abraha et al. 2019). Accurate understanding of GxE interaction is essential to optimize the use of host-plant resistance in disease management and for analysis of multi-environment data. Partial resistance or slow mildewing, expressed in adult plants as slow disease development is often associated with race non-specificity and compatible host–pathogen interaction (Parlevliet 1985; Herrera-Foessel et al. 2014) and it is reported to be durable and stable. Although, more than 60 OM and 83 YR resistance loci have been identified and/or mapped in wheat and their wild relatives (named from *Pm1* to *Pm64*) (McIntosh et al. 2017; Zhao et al. 2018; Singh et al. 2018; Zhang et al. 2020; Alemu et al. 2021) but we have taken available germplasm for the investigation. The present study was, therefore, undertaken to assess the effect of genotype, environment, and their interactions on severity of PM and YR in some PM, leaf rust (LR), and loose smut (LS) differential lines with known genes for resistance through multi-location field testing at hot spot sites and slow mildewing resistance. The results are reported herein.

Materials and methods

The material included 71 genotypes comprising some international PM, LR and LS differential lines with known genes, and some promising genotypes including rye (*Secale cereale* L.). The lines were evaluated at seedling stage in the poly-house at RWRC, Malan against the local field populations of Bgt, whereas, APS studies on PM and YR were carried out at the experimental fields of Department of Plant Pathology, CSKHPKV, Palampur (2016-17 and 2017-18); RWRC, Malan (2016-17), Highland Agricultural Research and Extension Centre, Kukmseri (Summer, 2016) and PAU, Research Station, Keylong (Summer 2017).

Evaluation against powdery mildew at seedling and adult plant stages

Seedlings of test entries along with susceptible check HPW155 were raised in the iron trays (20 x 15 x 4 cm) filled with a mixture of field soil and FYM (10:1). Ten days old seedlings (at one leaf stage) were dust inoculated and incubated for the disease development as per Basandrai et al. (2016). The data were recorded on infection - type (IT) based on modified 0-4 scale (Smith and Blair 1950), 10 days after the inoculations.

The experiments were conducted to evaluate the test genotypes for PM and YR resistance at adult plant stage at Palampur, Kukumseri, Keylong and Malan. The test genotypes were grown in 1 m long rows following standard package and practices. The susceptible check (SC) variety Lehmi was sown after every 20th test genotypes and on the outer boundaries of the experimental plots which served as spreader for the multiplication of inoculum and its spread. The disease appeared earlier in the season on the susceptible check variety, which were tapped with wooden sticks in the evening hours to dislodge conidia which could infect the healthy plants. The data were recorded periodically on % disease severity on randomly selected five plants in each test line based on the modified scale of Mayee and Datar (1986) and it was used to determine Area under Disease Progress Curve (AUDPC), rate of disease increase (r) and relative Area Under Disease Progress Curve (rAUDPC) to identify lines with slow mildewing resistance.

The AUDPC was calculated using formula of Shaner and Finny (1977):

$$AUDPC = \sum_{i=1}^{n-1} \frac{(y_i + y_{i+1})}{2} \times (t_{i+1} - t_i)$$

Where *yi* is an assessment of a disease (percentage, proportion, ordinal score, etc.) at the *i*th observation, *ti* is time (in days etc.) at the *i*th observation, and *n* is the total number of observations.

The infection rate (r) was calculated by using the equation given below (Vander Plank (1963).

$$r = \frac{2.3}{t_2 - t_1} \times \text{Log } 10 \frac{X_2 (1-X_1)}{X_1 (1-X_2)}$$

where,

X_1 = Proportion of infected tissues at time t_1

X_2= Proportion of infected tissues at time t_2

t_2-t_1= time interval

Relative Area Under Disease Progress Curve (rAUDPC) was calculated using AUDPC of the test genotype divided by the AUDPC of the susceptible check var. multiplied by hundred (Ma and Singh 1996).

Evaluation for yellow rust

All the test locations except Palampur are hot spots for YR. However, to avoid escape artificial epiphytotics were created by using inoculum procured from ICAR-IIWBR, Regional Station, Shimla at Malan. It was mass multiplied on the susceptible check variety Lehmi and was sprayed ($1x10^6$ uredospores/mL of water) onto the test genotypes and susceptible vars. grown after every 20th test row. Additionally, mixture of local field populations of YR was also used especially at Kukumseri and Keylong. The data were recorded simultaneously using infection-type (IT) at the flag leaf stage as per Roelfs et al. (1992), and on percentage severity using the modified Cobb' s scale (Peterson et al. 1948).

Statistical analysis

The contributions of environment, genotype and their interactions were determined by analysis of variance (ANOVA), using OPSTAT online statistical packages for both PM and YR. The ANOVA explained the partition of variation

due to the effect of genotypes, environment, and their interaction and were used for GGE biplot model diagnosis based on goodness of fit. Among no-scaling and standard deviation (SD) scaling methods, the no scaling method registered the highest goodness of fit representing 73.29 and 86.42% of the total variation for PM and YR, respectively, compared with 72.4 and 84.21% in the standard deviation method. The GGE biplot analysis was done using the GEA-R (Genotype x Environment Analysis with R for Windows) Version 4.0 (Pacheco et al. 2015) and Spearman's correlation between the locations was also determined and graphically represented by using R version 4.0.5 (R Core Team 2021).

Results and discussion

Testing of materials at seedling and adult plant stages

The genotypes Amigo (*Pm17*), Maris Dove (*Pm2, Mld*), near isogenic (NIL) *Pm1* and rye were free from disease at seedling stage (Supplementary Table S1). Three genotypes i.e. NIL *Pm2*, NIL *Pm3b* and H 56771 with IT= '1' were highly resistant whereas, genotypes NIL *Pm3c*, CITR 15888 (*Pm3f*), Soissons (*Pm3g*), Wembley (*Pm12*), NC96BGTA5 (*Pm 25*), IWP 94 (*Lr 23*), *TD 1, TD 4, TD 5, TD 6, TD 8, TD 12, TD 19, TD 20,* UP 2382 and CMH 77.308 showing IT= '2' were moderately resistant. As has been observed in the present studies, seedling resistance to PM was reported in four Egyptian cultivars (Draz and El-Kreem 2021) and eight CIMMYT and 6 wheat 'Alcedo'-*Ae. markgrafii* chromosome disomic addition lines (Niu et al. 2018), Indian advanced wheat breeding material (Basandrai et al. 2016; Sood et al. 2020). Emara et al. (2016) also observed that eight *Pm* genes i.e., *Pm2, Pm6, Pm12, Pm16, Pm24, Pm35, Pm36* and *Pm37* were resistant to 42 isolates of PM at seedling stage. Basandrai and Basandrai (2017) reviewed seedling resistant donors identified among *Triticum* spp. from various countries throughout the world.

Mean performance and analysis of variance

The ANOVA was performed via factorial randomized block design (FRBD) which elaborated that the mean sum-of squares for environments, genotypes and genotype x environment interaction was highly significant ($P < 0.001$) for both PM and YR. Proportion effect of each source of variation over the total effect inferred that among the three sources of variation, the largest contribution to disease severity was by genotype (G) i.e., 50.75 and 47.56 followed by genotype by environment (G x E) interaction i.e., 44.38 and 37.70 and environment (E) 4.8 and 14.74 for PM and YR, respectively. The mean PM and YR severity of each genotype over the locations is given in Supplementary Table S1. The disease severity in the susceptible check varieties varied from 25 to 70% and 60 to 80% for PM and YR, respectively, with mean of 41.25 and 70%, demonstrating the substantial disease pressure across locations. Among the 4 and 3 test locations for PM and YR, respectively, Palampur 2017-18 recorded the highest mean PM (26.57%) and Kukumseri mean YR (32.68%), severity whereas, the mean disease severity was the least (19.04%) at Palampur (2016-17) and Malan (8.42%) for PM and YR, respectively. Mean PM severity at Palampur (2017-18) was much higher whereas, disease pressure based on individual genotypes was higher at Kukumseri. Mean severity of YR was highest at Kukumseri and the lowest at Malan. The maximum and minimum temperature of 23.60°C and 13.4°C and RH 45.08% at Kukumseri and Palampur (2017-18) i.e., 22.50°C and 9.67°C and RH of 51.78% were highly favorable for the development of PM and YR as the diseases require low temperature for development (Singh and Pannu 2014; El Jarroudi et al. 2020) (Table 1). The inconsistency in disease severity at different locations might be due to evolution in the pathotypes of the pathogens in NHZ, variability among the genotypes, or both (Aggarwal et al. 2018; Vikas et al. 2020). The association between locations with respect to mean disease severity was tested by Spearman's correlation analysis and there was strong positive correlation among all the locations for PM severity (Fig. 1) whereas, for YR it was non-significant between Malan and Kukumseri and significantly positive for Kukumseri, and Malan, (Fig. 2).

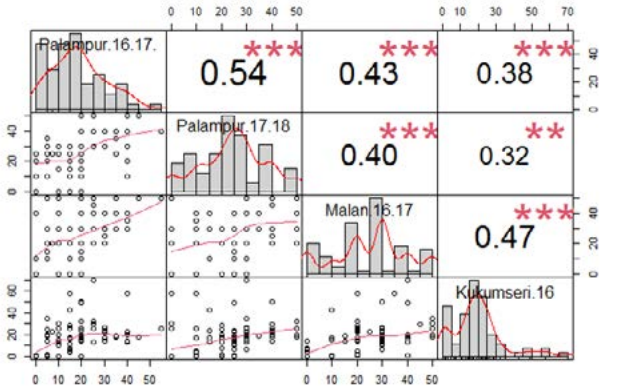

Fig. 1. Spearman's correlation between four test locations for wheat powdery mildew severity during the cropping seasons. *p < 0.05; **p < 0.01; ***p < 0.001 (Palampur 2016-17, Palampur 2017-18, Kukumseri 2016, Malan 2016-17)

Table 1. Mean weekly minimum and maximum temperature and relative humidity during experimental period February to April (Palampur 2016-17 and 2017-18, Malan 2016-17), August to I[st] week of September (Kukumseri 2016) and second fortnight of August to September (Keylong 2017)

S. No.	Locations	Min. Temp	Max. Temp	R.H.
1	Kukumseri (2016)	13.4	23.60	45.08
2	Malan (2016-17)	8.30	29.26	62.69
3	Palampur (2016-17)	8.93	19.85	53.86
4	Palampur (2017-18)	9.67	22.50	51.78
5	Keylong (2017)	10.9	23.1	43.87

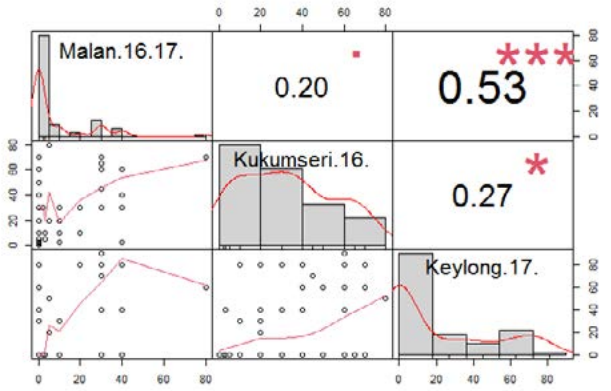

Fig. 2. Spearman's correlation between three test locations for wheat yellow rust severity during the cropping season. *p < 0.05; **p < 0.01; ***p < 0.001 (Malan 2016-17; Kukumseri 2016, Keylong 2017)

Mega-environment investigation of genotypes based on GGE biplot

The 'which-won-where' view of the GGE biplot of multilocation trial data of PM and YR was drawn using the symmetrical (row metric preserving) singular value partitioning method to display the biplot of PC1 (disease severity) against PC2 (stability of resistance) for both the genotypes and environments, which is useful for interpreting the interaction between genotypes and environments. Moreover, the polygonal view of a biplot is the best way to visualize the patterns of interaction between genotypes and environments and interpret a biplot effectively (Yan and Kang 2003). The GGE biplot showed that PC1 and PC2 accounted for 51.37 & 57.42%, and 21.29 & 29.00% of the total variation for PM and YR, respectively (Figs. 3 A and B). The vertex genotypes in each sector represented the best and the worst performing genotypes of the location that fell within that particular sector (Yan and Tinker 2006; Yan et al. 2007). The genotypes registering the lowest and the highest PM and YR severity were at different vertices of the polygon (convex hull) and contributed maximum to GE interactions. The genotypes within the polygon were notably less responsive for GE interaction than the vertex genotypes. The genotypes present at the right side of the hull showed more PM severity and those on the left side had stable resistance across the locations. GGE biplot demonstrated that genotypes i.e. G-1 (CROC_1/*Ae. squarrosa* (662), G-2 (68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. squarrosa* (905), G-6 (Maris Dove, *Pm2, Mld*)), G-9 (NIL *Pm1*)), G-14 (NIL *Pm2*) and G-61 (Rye) had low levels of PM severity by being the farthest to the left side of the origin of biplot (Fig. 3-A). As has been observed in the present studies, resistance to PM has been reported in India by various workers (Basandrai et al. 2016; Gupta et al. 2016; Vikas et al. 2020), Pakistan (Muhammad et al. 2014), China (HaiRong et al. 2011), Egypt (Draz et al. 2019); and it has been extensively reviewed from other countries of the

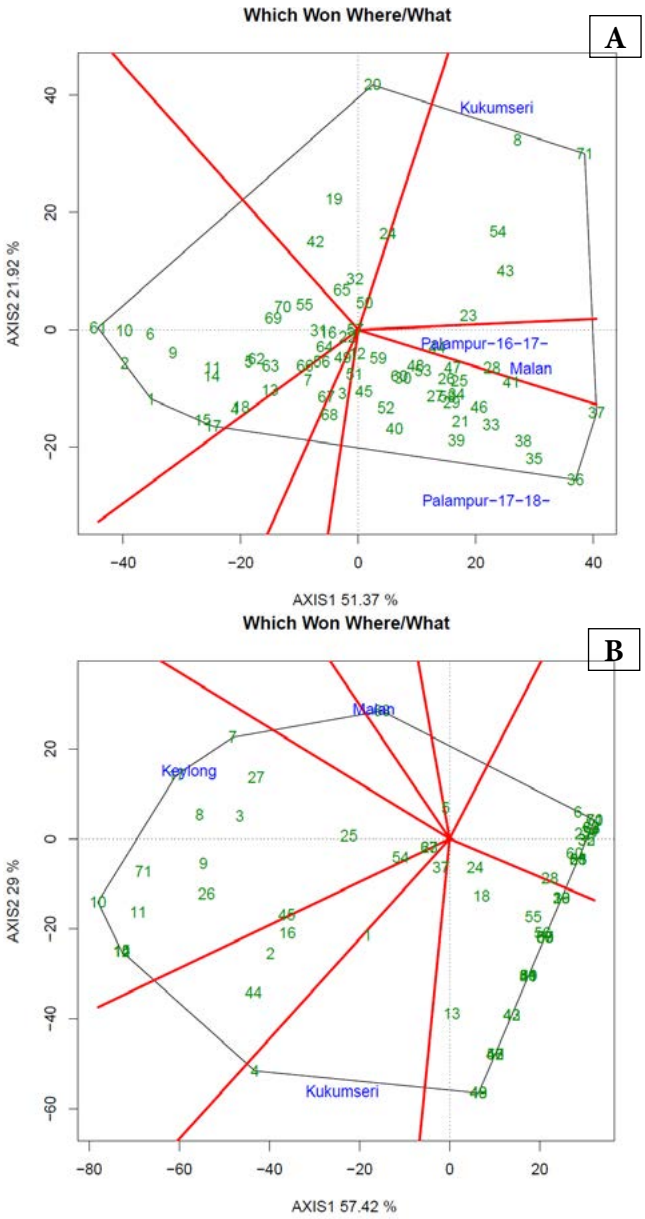

Fig. 3. Which-won-where' view of the unscaled GGE biplot based on powdery mildew and yellow rust disease severity on 71 genotypes of wheat under four and three environments, respectively, A. powdery mildew B. yellow rust. There was no transformation of data. Data were centered by means of the environments (centering = 2). Biplot was based on 'row metric preserving', i.e. genotype-focused singular-value partitioning. Green numbers correspond to genotypes as listed in (Supplementary Table S1).

world (Basandrai and Basandrai 2017). Genotypes, G-36 (*TD 4*), G-37 (*TD 5*) and Lehmi (G-71) constantly showed higher disease severity of PM and were located outermost to the right side of the origin of the biplot (Figs. 3-A).

In case of YR, the genotypes present at the left side of the hull showed more disease severity whereas, those on the right side had stable resistance across the locations. Genotypes i.e. G-6 (Maris Dove, (*Pm2, mld*)), G-19 (IWP 94, *Lr23*), G-20 (Kharchia Local), G-21 (Raj 3765), G-22 (HD 2189),

G-32 (Thew, *Lr20*), G-33 (HP 1633, *Lr9*), G-34 (*TD1*), G-35 (*TD2*),G-36 (*TD4*), G-58(SHANGAI), G-60 (TL 1210), G-61 (Rye), G-62 (ALDAN), G-63 (CMH 77.308), G-64 (H 56771), G-65 (HD 29) and G-70 (SAW 74) had low levels of YR severity by being farthest to the right side of the origin of the biplot (Fig. 3-B). As has observed in the present studies, sources of resistance to YR have already been reported in India (Rani et al. 2019; Sood et al. 2020) Egypt (Elbasyoni et al. 2019; El-Orabey et al. 2020) and it has been extensively reviewed from India and other countries of the world (Bhardwaj et al. 2019; Jamil et al. 2020; Figlan et al. 2020). Ten genotypes, viz., G-4 (Amigo, *Pm17*), G-8 (Chancellor, *Pm 10,15*)), G-9 (NIL*Pm1*), G-10 (NIL *Pm2*), G-11 (NIL *Pm3a*), G-12 (NIL *Pm3b*), G-14 (NIL *Pm4*), G-15 (CITR 14125), G-16 (Wembley, *Pm12*) and G-17 (NC96BGTA5, *Pm 25*) and susceptible check var. Lehmi (G-71) consistently showed high level of disease severity and were located outermost to the left side of the origin of the biplot (Fig. 3B). Similar studies to identify stable resistance donors were also conducted in different crops i.e. wheat, lentil and pea (Mehari et al. 2015; Parihar et al. 2017; Das et al. 2019). The polygon view had a set of lines perpendicular to each of the polygons which partition the biplot into several sectors. Consequently, environments for PM and YR could be divided into three mega-environments each based on repeatable 'which-won where' representing the variability of the environments. Mega environments I (ME-I) comprised locations Palampur (2016-17) and Malan (2016-17) whereas, ME-II and ME-III comprised Kukumseri and Palampur (2017-18), respectively, for PM. ME I, ME-II and ME-III comprised locations Malan, Kukumseri and Keylong, respectively for YR.

Mean vs Stability

GGE biplot ranked the genotypes along the average environment coordinate (or AEC abscissa), based on their average performance across 4 and 3 locations for PM and YR, respectively (Figs. 4 A and B). The single arrowed line was the AEC abscissa and the arrow was pointed in the direction of higher disease severity (Yan and Tinker 2006; Parihar et al. 2018). The stability of the genotypes was approximated by their projection onto the middle horizontal line. The GGE biplot revealed that, in terms of the least disease occurrence for PM, the overall best performing genotypes with wider adaptability were G-1 (CROC_1/*Ae. squarrosa* (662), G-2 (68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. squarrosa* (905), G-6 (Maris dove, *Pm2, Mld*)), G-9 (NIL *Pm1*), G-14 (NIL *Pm2*) and G-61 (Rye) (Fig. 4-A). In case of YR, i.e. G-6 (Maris Dove, *Pm2, mldb*)), G-19 (IWP 94, *Lr23*), G-20 (Kharchia Local), G-21 (Raj 3765), G-22 (HD 2189), G-32 (Thew), G-33 (HP 1633 (*Lr9*)), G-34 (*TD1*), G-35 (*TD2*), G-36 (*TD4*), G-58 (SHANGAI), G-60 (TL 1210), G-61 (Rye), G-62 (ALDAN), G-63 (CMH 77.308), G-64 (H 56771), G-65 (HD 29) and G-70 (SAW 74) were the overall best genotypes (Fig. 4B). These genotypes showed a short absolute length of projection in either of the two directions of AEC ordinate (located closer to AEC abscissa), and higher negative projection on AEC inferring that these were the most stable genotypes across different environments and vice versa and these findings were in the agreement with biplot analysis studies conducted by earlier workers (Yan 1999; Yan et al. 2007; Das et al. 2019)

Evaluation of best test-environment based on discrimination ability and representativeness

During a multi-environment trial, testing locations should be screened out considering their "discrimination" power to categorize the genotypes and "representativeness" of the mega-environment of interest (Yan et al. 2011). The

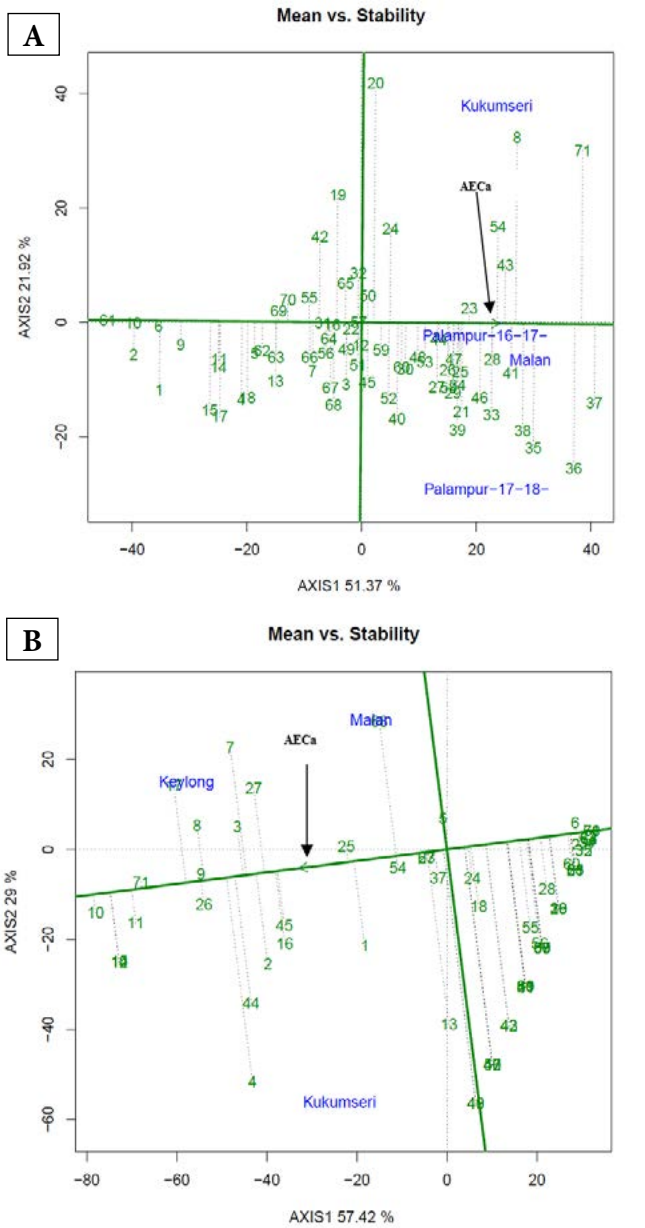

Fig. 4. Mean *vs* stability view of the unscaled GGE biplot based on, A. powdery mildew B. yellow rust severity on 71 genotypes of wheat under four and three environments respectively. AECa: abscissa of the average environment coordination axis, which connects the origin with the environmental average

GGE biplot of 'discrimitiveness vs representativeness' of test locations explained that location '2' i.e., Kukumseri had greater vector length for both PM and YR, than other locations indicating that this location had the highest discrimination power and competence for genetic differentiation of genotypes. The smallest vector length of location '1' (Palampur, 2016-17) for PM and '1' (Malan, 2016-17) for YR suggested that these to be the least discriminatory. In a GGE biplot, the representativeness of a target environment is determined by the angle between the test environment vector and the AEC. Smaller angle between the environment vectors is indicative of the stronger representativeness of the respective environment (Parihar et al. 2017; Das et al. 2019). Small angles between Palampur (2016-17) and Malan, and Malan and Keylong for PM and YR, respectively (with an acute angle) were indicative of a positive association. Kukumseri and Palampur (2017-18) and Malan & Kukumseri with an obtuse angle, were negatively associated; accordingly (Fig. 5-A, B). In addition, wider obtuse angles between test locations indicated a strong GE component. Hence, in case of PM, and YR, Kukumseri and Palampur (2017-18), and Malan and Kukumseri, respectively could be ideally used for identification of disease-resistant genotypes. Earlier the "representativeness" has been reported as the key factor to decide how a test location used in genotype evaluation, assuming adequate discriminating ability (Yan et al. 2007).

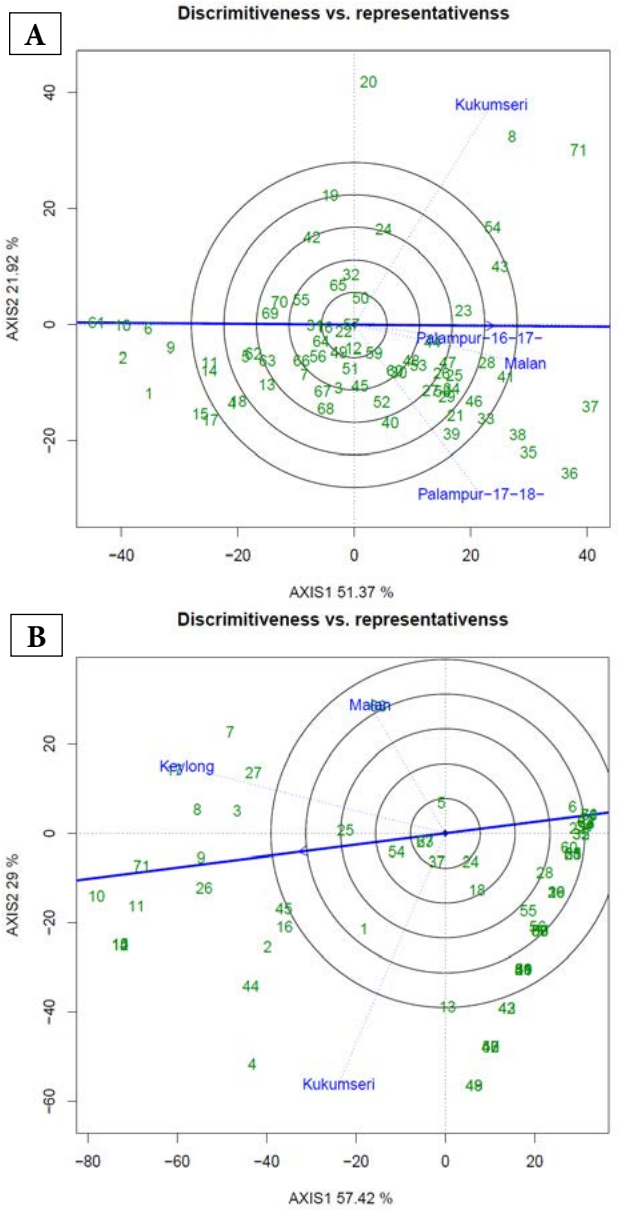

Fig. 5. Discrimitiveness *vs* representativeness view of the unscaled GGE biplot based on, A. powdery mildew B. yellow rust severity on 71 genotypes of wheat under four and three environments, respectively

Slow mildewing resistance sources

Sixteen genotypes namely, CROC_1/*Ae. squarrosa* (662), 68.111/RGB-U//WARD/3/FGO/4 /RABI/5/*Ae. Squarrosa* (905), Amigo (*Pm17)*, Kavkaz (*Pm8*), NIL *Pm1*, NIL *Pm2*, NIL *Pm3a*, NIL *Pm3c*, CITR 15888 (*Pm3f*), NIL *Pm4a*, CITR 14125, NC96BGTA5 (*Pm 25*), ALDAN, CMH 77.308, SAW 71 and SAW 74 developed mean disease severity ≤15, AUDPC of ≤600,rAUDPC between 2.74-50.61 and infection rate between 0.01-0.06 unit/day, respectively in comparison to the susceptible cultivar Lehmi showing mean TDS, AUDPC, rAUDPC and 'r' of 41.25%, 1510.88, 99.18 and 0.04, respectively, and were categorized as slow mildewing genotypes (Supplementary Tables S1 and S2). The results were in conformity with the results of various researchers (Shaner and Finney 1977; Nass et al. 1981); Sharma et al. 1991) attributed rate reducing resistance in NIL *Pm3a*, *Pm3b*, *Pm3c* and *Pm4a* & *Pm7*, *Pm 8* and *Pm17* to the longer incubation and latent period, development of less number of smaller colonies/area, low sporulation, as compared to susceptible cvs. Agra Local. These genotypes may be used as donors for combining high level of race specific and low level and durable race non-specific or rate reducing resistance to breed varieties with durable and stable resistance to PM as has been earlier advocated (Lilemo et al. 2010).

Multiple disease resistance genotypes

Rye was free from PM and YR at all the locations. Genotype 'Maris Dove' showed mean TDS of ≤10 for PM and YR. Genotypes ALDAN, CMH 77.308, SAW 71 and SAW 74 with mean TDS ≤15 for PM and YR, at all the locations, were moderately resistant to both the diseases (Table 4). The present results of combined resistance to PM and YR have been corroborated by reports of combined resistance to leaf and yellow rust (Kochumadhavan et al. 1980; Shrestha and Mahto 2021), PM and YR (Sood et al. 2020; Vikas et al. 2019). Among loose smut (LS) differential no genotypes was found resistant to PM whereas, *TD 1* (Mindum), *TD 2* (*Renfrew*) and *TD 4* (*Kota*) showed YR severity <10S. Hence, these genotypes may be desirable donors for LS and YR and may be used

in breeding program aimed to develop genotypes with combined resistance to YR and LS. Genotypes UP 2382, HD 29, HD 30, SHANGAI, PBW 233, TL 1210, Rye, ALDAN, CMH 77.308, H 56771, SAW 71 and SAW 74 have been suggested as promising wheat genotypes out of which lines ALDAN, CMH 77.308, Rye, ALDAN, CMH 77.308, HD 29, HD 30 and SHANGAI had proven resistance to Karnal bunt (Fuentes-Dávila et al. 1995; Singh et al. 1999; Sharma et al. 2005; Emebiri et al. 2019; Bishnoi et al. 2020). These lines developed mean YR TDS of ≤10 and genotypes i.e., Maris Dove, ALDAN, CMH 77.308, SAW 71 and SAW 74 showed multiple resistance to both PM and YR. The present results have been corroborated by the earlier reports (Yang et al. 2017; Vikas et al. 2020; Sood et al. 2020) of wheat genotypes with multiple resistance to various diseases including PM and YR. In the present studies, genotypes with multiple resistance to PM and YR have been identified and incidentally some genotypes have been reported to have proven resistance to other important prevailing diseases like Karnal bunt and loose smut. The donors with multiple resistance to various diseases and designated effective genes may be used in breeding programme to develop cultivars with combined resistance to PM, YR, LS and/or KB. Moreover, Kukumseri could be the ideal test site or hotspot for screening wheat germplasm against PM and YR.

Authors' contribution

Conceptualization of research (AKB, AM, DB); Designing of the experiments (AM, AKB, DB); Contribution of experimental materials (AKB, VR); Execution of field/lab experiments and data collection (AM, AKB, DB, MK); Analysis of data and interpretation (AM, AKB); Preparation of manuscript (AM, AKB, DB, VR).

Supplementary materials

Supplementary Tables S1 and S2 are presented

Declaration

The authors declare no conflict of interest.

References

Abraha M. T., Shimelis H., Solomon T. and Hailu A. 2019. Genotype-by-environment interaction and selection of elite wheat genotypes under variable rainfall conditions in northern Ethiopia. J. Crop Improv., **33**(6): 1-17.

Aggarwal R., Sharma S., Gupta S., Banrjee S., Bashyal B. M. and Bhardwaj S. C. 2018. Molecular characterization of predominant Indian wheat rust pathotypes using URP and RAPD markers. Ind. J. Biotech., **17**: 327-336.

Alemu S., Huluka A.B., Tesfaye K., Haileselassie Y and Uauy C. 2021. Genome-wide association mapping identifies yellow rust resistance loci in Ethiopian durum wheat germplasm. PLoS One, **17**16(5): e0243675. Doi. 10.1371/journal.pone.0243675.

Bhardwaj S. C., Singh G. P., Gangwar O. P., Prasad P. and Kumar S. 2019. Status of wheat rust research and progress in rust management-Indian context. Agronomy, **9**: 892.

Basandrai D., Basandrai A. K., Rana S. K., Sharma B. K., Singh A., Singh D. and Tyagi P. D. 2016. Resistance to powdery mildew (*Blumeria graminis* f. sp. *tritici* E. Marchal.) in bread wheat, durum, dicoccum and triticale genotypes. Indian J. Gen. Plant Breed., **76**: 205-208.

Basandrai A. K. and Basandrai D. 2017. Powdery mildew of wheat and its management. In: Management of wheat and barley diseases (Ed. Devender Pal Singh). Apple Academic Press, Canada, pp-173-181.

Bennett F. G. A. 1984. Resistance to powdery mildew in wheat: a review of its use in agriculture and breeding programmes. Plant Pathol., **33**: 279-300.

Bishnoi S. K., He X., Phuke R. M., Kashyap P. L., Alakonya A., Chhokar V., Singh R. P. and Singh P. K. 2020. Karnal bunt: A re-emerging old foe of wheat. Front. Plant Sci., **11**: 569057.

Das A., Parihar A. K., Saxena D., Singh D., Singha K. D., Kushwaha K. P. S., Chand R., Bal R. S., Chandra S. and Gupta S. 2019. Deciphering genotype-by-environment interaction for targeting test environments and rust resistant genotypes in field pea (*Pisum sativum* L.). Front. Plant Sci., **10**: 825.

Draz I. S. and Abd El-Kreem T. H. 2021. Partial resistance to powdery mildew and leaf rust of wheat in Egyptian and CIMMYT genotypes. Egypt. J. Agric. Res., **99**(1): 61-76.

Draz I. S., Esmail S. M., El-Halim M. A., Abou-Zeid, El-Moniem Essa, T. A. 2019. Powdery mildew susceptibility of spring wheat cultivars as a major constraint on grain yield. Annals Agri. Sci., **64**: 39-45.

Draz I. S., Abou-Elseoud M. S., Abd-Elmageed M. K., Abd-Ellatif A. O., El-Bebany A. F. 2015. Screening of wheat genotypes for leaf rust resistance along with grain yield. Annals Agri. Sci., **60**(1): 29-39.

El Jarroudi M., Lahlali R., Kouadio L., Denis A., Belleflamme A., El Jarroudi M., Boulif M., Mahyou H. and Tychon B. 2020. Weather-based predictive modeling of wheat stripe rust infection in Morocco. Agronomy, **10**: 280.

Elbasyoni I. S., El-Orabey W. M., Morsy S., Baenziger P. S., Al Ajlouni Z. and Dowikat I. 2019. Evaluation of a global spring wheat panel for stripe rust: Resistance loci validation and novel resources identification. PLoS ONE, **14**(11): e0222755.

El-Orabey W. M., Ashmawy M. A., Shahin A. A. and Ahmed M. I. 2020. Screening of CIMMYT wheat genotypes against yellow rust in Egypt. Int. J. Phytopathol., **9**(01): 51-70.

Emara H. M., Omar A. F., El-Shamy M. M. and Mohamed M. E. 2016. Identification of *Pm24*, *Pm35* and *Pm37* in thirteen Egyptian bread wheat cultivars using SSR markers. Ciência e Agrotecnologia, **40**(3): 279-287.

Emebiri L., Singh S., Tan M., Singh P. K., Fuentes-Dávila G. and Ogbonnaya F. 2020. Unravelling the complex genetics of Karnal bunt (*Tilletia indica*) resistance in common wheat (*Triticum aestivum*) by genetic linkage and genome-wide association analyses. Scientific Rep., **10**: 5999

Figlan S., Ntushelo K., Mwadzingeni L., Terefe T., Tsilo T. J. and Shimelis H. 2020. Breeding wheat for durable leaf rust resistance in southern Africa: variability, distribution, current control strategies, challenges and future prospects. Front. Plant Sci., **11**: 549.

Fuentes-Dávila G., Rajaram S. and Singh G. 1995. Inheritance of resistance to Karnal bunt (*Tilletia indica* Mitra) in bread wheat (*Triticum aestivum* L.). Plant Breed., **114**: 250-252.

Gupta V., Kumar R. S., Kumar S., Mishra C. N., Tiwari V. and Sharma I.

2016. Evaluation and identification of resistance to powdery mildew in Indian wheat varieties under artificially created epiphytotic. J. Appl. Nat. Sci., **8**: 565-569

HaiRong Z., Peng W., Ning Z., Yu Z. W. and Yong C. Q. 2011. Identification and analysis of resistance to powdery mildew and rust in some wheat germplasm resources. J. Triticeae Cr., **29**: 925-929.

Han J., Liu Y., Hou C., Li J., Wang J., Zhang Q., Yang Q., Chen X. and Wu J. 2020. A 1Ns disomic addition from psathyrostachys huashanica keng confers resistance to powdery mildew in wheat. Agronomy, **10**(2): 312.

Herrera-Foessel S. A., Singh R. P., Lillemo M., Huerta-Espino J., Bhavani S., Singh S., Lan C., Calvo-Salazar V. and Lagudah E. S. 2014. *Lr67/Yr46* confers adult plant resistance to stem rust and powdery mildew in wheat. Theor. Appl. Genet., **127**: 781-789.

Jamil S., Shahzad R., Ahmad S., Fatima R., Zahid R., Anwar M., Iqbal M. Z. and Wang X. 2020. Role of genetics, genomics, and breeding approaches to combat stripe rust of wheat. Front. Nutr., **7**: 580715.

Kochumadhavan M., Tomar S. M. S. and Nambisan P. N. N. 1980. Sources of rust resistance in wheat. Indian J. Gen. Plant Breed., **40**(3): 610-618.

Lillemo M., Skinnes H. and Brown J. K. M. 2010. Race specific resistance to powdery mildew in Scandinavian wheat cultivars, breeding lines and introduced genotypes with partial resistance. Plant Breed., **129**(3): 297-303.

Ma H. and Singh R. P. 1996. Expression of adult plant resistant to stripe rust at different growth stages of wheat. Pl. Dis., **80**: 375-379.

Mayee and Datar. 1986. Pathometery and crop growth stages book. p. 31.

McIntosh R.A. , Dubcovsky J., Rogers W.J. , Morris C.F. and Xia X.C. 2017. Catalogue of gene symbols for wheat **(**Suppl.), https://shigen.nig.ac.jp/wheat/komugi/genes/macgene/supplement2017.pdf .

Mehari M., Tesfay M., Yirga H., Mesele A., Abebe T., Workineh A. and Amare B. 2015. GGE biplot analysis of genotype-by-environment interaction and grain yield stability of bread wheat genotypes in South Tigray, Ethiopia. Commun. Biomet. Crop Sci., **10**(1): 17-26.

Morgounov, A., Tufan, H. A., Sharma, R., Akin, B., Bagci, A., Braun, H. J., et al. 2012. Global incidence of wheat rusts and powdery mildew during 1969-2010 and durability of resistance of winter wheat variety Bezostaya 1. Eur. J. Plant Pathol., **132**: 323–340. doi: 10.1007/s10658-011-9879-y.

Muhammad F., Anjum M. and Atiq-ur-Rehman R. 2014. Screening of wheat commercial varieties for resistance against powdery mildew (*Blumeria graminis* f.sp. *tritici*) at Kaghan Valley, Pakistan. Pak. J. Phytopath., **26**: 7-13.

Nass H. A., Pedersen W. L., Mackenzie D. R. and Nelson R. R. 1981. The residual effect of some "defeated" powdery mildew resistance genes in isolines of chancellor winter wheat. Phytopathol., **71**: 1315-1318.

Niu Z., Chao S., Cai X., Whetten R. B., Breiland M., Cowger C., Chen X., Friebe B., Gill B. S., Rasmussen J. B., Klindworth D. L. and Xu S. S. 2018. Molecular and cytogenetic characterization of six wheat-*Aegilops markgrafii* disomic addition lines and their resistance to rusts and powdery mildew. Front. Plant Sci., **9**: 1616.

Pacheco A., Vargas M., Alvarado G., Rodriguez F., Crossa J. and Burgueño J. 2015. Gea-R (Genotype X Environment Analysis with R for Windows) Version 2.0. Mexico: CIMMYT.

Parihar A. K., Basandrai A. K., Saxena D. R., Kushwaha K. P. S., Chandra S., Sharma K., Singha K. D., Singh D., Lal H. C. and Gupta S. 2017. Biplot evaluation of test environments and identification of lentil genotypes with durable resistance to fusarium wilt in India. Crop Past. Sci., **68**: 1024-1030.

Parihar A. K., Basandrai A. K., Kushwaha K. P. S., Chandra S., Singha K. D., Bal R. S., Saxena D., Singh D. and Gupta S. 2018. Targeting test environments and rust-resistant genotypes in lentils (*Lens culinaris*L.) by using heritability-adjusted biplot analysis. Crop Past. Sci., **69**: 1113-1125.

Parks R., Carbone I., Murphy J. P., Marshall D. and Cowger C. 2008. Virulence structure of the Eastern US wheat powdery mildew population. Plant Dis., **92**: 1074-1082.

Parlevliet J. E. 1985. Resistance of the non-race-specific type. In: Roelfs AP, Bushnell WR (eds) The cereal rusts, vol. II, Diseases, distribution, epidemiology, and control. Academic Press, Inc., ORL, FL, pp 501-525.

Peterson R. F., Campbell A. B. and Hannah A. E. 1948. A diagrammatic scale for rust intensity on leaves and stems of cereals. Can. J.. Res., **26**: 496-500.

R Core Team. 2021. R: A language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing. Retrieved from https://www.R-project.org/.

Rani R., Singh R. and Yadav N. R. 2019. Evaluating stripe rust resistance in Indian wheat genotypes and breeding lines using molecular markers. Comptes Rendus Biologies, **342**: 154-174.

Roelfs A. P., Singh R. P. and Saari E. E. 1992. Rust diseases of wheat: Concepts and methods of diseases management. CIMMYT, Mexico, DF. pp. 81.

Sankar S. M., Singh S. P., Prakash G., Satyavathi C. T., Soumya S. L., Yadav Y., Sharma L. D., Rao A. R., Singh N. and Srivastava R. K. 2021. Deciphering genotype-by- environment interaction for target environmental delineation and identification of stable resistant sources against foliar blast disease of pearl millet. Front. Plant Sci., **12**: 656158.

Shaner G. and Finney R. E. 1977. The effect of nitrogen fertilization on the expression of slow-mildewing resistance in Knox wheat. Phytopath., **67**: 1051-1056.

Sharma S. C., Parkash V., Basandrai A. K. and Aulakh K. S. 1991. Residual resistance in wheat to *Erysiphe graminis* f. sp . *tritici*. Pl. Dis. Res., **6**: 70-74.

Sharma I., Bains N. S. and Nanda G. S. 2005. Additive genes at nine loci govern Karnal bunt resistance in a set of common wheat cultivars. Euphytica, **142**: 301-307.

Shrestha R. and Mahto B. N. 2021. Screening of wheat (*Triticum aestivum* L.) genotypes for rust-resistance and assessment on prevalence and distribution of the rust diseases in wheat production fields. J. Agri. Nat. Res., **4**(2): 186-200.

Singh H., Grewal T. S., Pannu P. P. S. and Dhaliwal H. S. 1999. Genetic of resistance to Karnal bunt disease of wheat. Euphytica, **105**: 125-131.

Singh S. and Pannu P. P. S. 2014. Influence of weather factors on occurrence and progress of powdery mildew of wheat in the screen house. Plant Dis. Res., **30**: 50-55.

Singh S.P., Hurni S., Ruinelli M. Brunner S., Sanchez J.,Martin P., Krukowski D., Peditto G., Buchmann H., Zbinden G. and Keller B. 2018. Evolutionary divergence of the

rye *Pm17* and *Pm8* resistance genes reveals ancient diversity. Plant Mol. Biol., 98: 249-260.

Smith H. C. and Blair I. J. D. 1950. Wheat powdery mildew investigations. J. Appl. Biol., **37**: 570-583.

Sood T., Basandrai D., Basandrai A. K., Sohu V. S., Rana V., Mehta A., Sharma B. K., Mavi G. S., Kaur J. and Bains N. S. 2020. Stable sources of resistance to yellow rust and powdery mildew in Indian and exotic wheat germplasm. J. Cereal Res., **12**(1): 23-28.

Todorovska E., Christov N., Slavov S., Christova P. and Vassilev D. 2009. Biotic stress resistance in wheat–breeding and genomic selection implications. Biotechnol. Biotechnological Equip., **23**: 1410-1413.

Vander Plank J. E. 1963. Plant Diseases: Epidemics and Control. Academic Press, Inc. pp 249.

Vikas V. K., Kumar S., Archak Set al. 2020. Screening of 19,460 genotypes of wheat species for resistance to powdery mildew and identification of potential candidate using FIGS approach. Crop Sci., **60**(6): csc2.20196.

Wan A. M., Chen X. M. and He Z. H. 2004. Wheat stripe rust in China. Aust. J. Agric. Res., **58**: 605-619.

Xu H. X., Yi Y. J., Ma P. T., Qie Y. M., Fu X. Y., Xu Y. F. et al. 2015. Molecular tagging of a new broad-spectrum powdery mildew resistance allele *Pm2c* in Chinese wheat landrace Niaomai. Theor. Appl. Genet., **128**: 2077–2084.

Yan W. 1999. 'Methodology of cultivar evaluation based on yield trial data with special reference to winter wheat in Ontario.' (University of Guelph: Ontario, Canada).

Yan W. and Kang M. S. 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. boca raton, FL: CRC Press.

Yan W. and Tinker N. A. 2006. Biplot analysis of multi-environment trial data: principles and applications. Canadian J. Pl. Sci., **86**: 623-645.

Yan W., Kang M. S., Ma B., Woods S. and Cornelius P. L. 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Sci., **47**: 643-653.

Yang L., Zhang X., Zhang X., Wang J., Luo M., Yang M., Wang H., Xiang L., Zeng F., Yu D., Fu D. and Rosewarne G. M. 2017. Identification and evaluation of resistance to powdery mildew and yellow rust in a wheat mapping population. PLoS ONE, **12**(5): e0177905.

Yang M. J., Huang K.Y. and Han Q. D. 2016. Research progresses on wheat powdery mildew and its resistance. Mol. Plant Breed., **14**: 1244-1254.

Zhang D., Zhu K., Dong Y., Liang Y., Li G., Fang T.,Guo G.,Wu Q.,Wu J.,Xie Y., Chen Y.. Lu P., Li M., Zhang H., Wang Z., Zhang Y., Sun Q. and Liu Z. 2019. Wheat powdery mildew resistance gene *Pm64* derived from wild emmer (*Triticum turgidum* var. *dicoccoides*) is tightly linked in repulsion with stripe rust resistance gene *Yr5*. Crop J. https://doi.org/10.1016/j.cj.2019.03.0.

Zhao F., Li Y., Yang B. and Yuan H. 2018. Powdery mildew disease resistance and marker-assisted screening at the *Pm60* locus in wild diploid wheat *Triticum urartu*. Plant Mol. Biol., **98**: 249-260.

Supplementary Table S1. Reaction to powdery mildew at seedling stage and terminal disease severity (%) of powdery mildew and yellow rust at adult plant stage in powdery mildew, leaf rust, loose smut differential lines and promising wheat genotypes at CSKHPKV Palampur (*Rabi* 2016-17 and 2017-18), RWRC Malan (*Rabi* 2016-17), HAREC Kukumseri (Summer 2016), and PAU, Research Station, Keylong (Summer 2017)

S. N.	Genotype/cultivation	Reaction to powdery mildew at								
		Seedling stage at Malan	Terminal disease severity at adult plant stage (%) at					Terminal yellow rust severity at (%)		
		(0-4)	Palampur (2016-17)	Palampur (2017-18)	Malan (2016-17)	Kukumseri (2016)	Mean	Malan (2016-17)	Kukumseri (2016)	Keylong (2017)	Mean
1	CROC_1/*Ae. squarrosa*(662)	3	0	20	0	0	5.00	0	40	40	26.67
2	68.111/RGB-U//WARD/3/FGO/4 /RABI/5/*Ae. squarrosa*(905)	3	0	10	0	0	2.50	0	50	60	36.67
3	CROC_1/*Ae. squarrosa*(362)	3	15	25	30	11.25	20.31	0	20	80	33.33
4	Amigo (*Pm17*)	0	15	30	0	6.5	12.88	5	80	50	45.00
5	Kavkaz (*Pm8*)	3	15	10	20	4.75	12.44	10	10	30	16.67
6	Maris dove (*Pm2,Mld*)	0	0	0	0	0	0	10	3	0	4.33
7	Soissons (*Pm3g*)	2	20	30	10	15	18.75	20	10	80	36.67
8	Chancellor (*Pm 10,15*)	3	40	10	35	57.5	35.63	20	30	80	43.33
9	Near iso-genic (*Pm1*) Axminister X Cc^8	0	15	10	0	3.25	7.06	30	45	70	48.33
10	Near iso-genic (*Pm2*)Ulka X Cc^8	1	10	0	0	0	2.50	30	60	90	60.00
11	Near iso-genic (*Pm3a*)Asosan X Cc^8	0	15	20	0	7.75	10.69	30	60	80	56.67
12	Near iso-genic (*Pm3b*)Chul X Cc^8	1	20	20	30	16.5	21.63	30	70	80	60.00
13	Near iso-genic (*Pm3c*)Sonara X Cc^8	2	0	10	40	1	12.75	30	65	0	31.67
14	Near iso-genic (*Pm4*)Khapli X Cc^8	3	5	10	20	1	9.00	30	70	80	60.00
15	Citr 14125 (HopexCc^8) *pm5*	4	0	25	10	1	9.00	30	70	80	60.00
16	Wembley (*Pm12*)	2	5	20	30	20	18.75	40	60	40	46.67
17	NC96BGTA5 (*Pm25*)	2	5	25	10	0	10.00	40	30	80	50.00
18	CItR 15888Michigen Amber X Cc^8 (*Pm3f*)	2	5	20	20	2	11.75	40	40	0	26.67
19	IWP 94 (*Lr23*)	2	15	15	10	42.5	20.63	0	20	0	6.67
20	Kharchia local	3	15	NG	20	57.5	30.83	0	20	0	6.67
21	Ra 3765	3	20	50	30	25	31.25	0	10	0	3.33
22	HD 2189	4	10	30	20	25.5	21.38	3	5	0	2.67
23	AGRA LOCAL	3	5	30	50	35	30.00	10	20	30	20.00
24	*Lr*14 A	4	10	NG	50	30	30.00	5	20	20	15.00
25	*Lr* 24	3	25	50	20	32.5	31.88	30	30	40	33.33
26	*Lr* 18	3	20	50	20	32.5	30.63	0	40	80	40.00
27	*Lr* 13	3	30	40	25	22.5	29.38	0	10	80	30.00

S. N.	Genotype/cultivation	Reaction to powdery mildew at								
		Seedling stage at Malan	Terminal disease severity at adult plant stage (%) at					Terminal yellow rust severity at (%)			
		(0-4)	Palampur (2016-17)	Palampur (2017-18)	Malan (2016-17)	Kukumseri (2016)	Mean	Malan (2016-17)	Kukumseri (2016)	Keylong (2017)	Mean
28	*Lr* 17	3	25	30	50	25	32.50	10	20	0	10.00
29	*Lr* 15	3	30	40	30	22	30.50	0	40	0	13.33
30	*Lr* 10	3	10	30	40	20	25.00	0	30	0	10.00
31	*Lr* 19	4	7	25	20	22.75	18.69	0	40	0	13.33
32	Thew (*Lr20*)	4	20	10	30	25	21.25	0	5	0	1.67
33	HP 1633 (*Lr9a*)	3	20	40	50	20	32.50	0	10	0	3.33
34	*TD 1* (Mindum)	2	30	40	30	23.75	30.94	0	3	0	1.00
35	*TD 2*(*Renfrew*)	4	40	50	40	20	37.50	0	5	0	1.67
36	*TD 4* (*Kota*)	2	45	50	50	17.5	40.63	0	20	0	6.67
37	*TD 5* (*Little Club*)	2	55	40	50	25	42.50	0	20	30	16.67
38	*TD 6*(*Pl69282*)	2	35	40	50	17.5	35.63	0	30	0	10.00
39	*TD 7*(*Reward*)	3	40	40	30	14.5	31.13	0	40	0	13.33
40	*TD 8*(*Karma*)	2	30	40	20	14.5	26.13	0	60	0	20.00
41	*TD 9*(*Little bobs*)	3	25	40	45	28.75	34.69	0	40	0	13.33
42	*TD 10*(*Red bobs*)	3	15	NG	30	25	23.33	0	50	0	16.67
43	*TD 11*(*Pentad*)	4	20	40	30	50	35.00	0	50	0	16.67
44	*TD 12*(*Thatcher x Regent*)	2	30	30	30	26.25	29.06	0	60	60	40.00
45	*TD 13* (*PI298554 CI7795*)	3	5	35	30	18.75	22.19	0	40	60	33.33
46	*TD 14*(*Sonop*)	3	35	35	40	19.25	32.31	0	60	0	20.00
47	*TD 15*(*H44 x Marguis*)	3	40	30	30	22.5	30.63	0	60	0	20.00
48	*TD 16*(*Morroqui 588*)	3	35	25	30	18.75	27.19	0	70	0	23.33
49	TD 17(Marquillo*Waratah)	3	10	15	40	12.75	19.44	0	70	0	23.33
50	*TD 18*(*CT439*)	3	20	15	30	23.75	22.19	0	40	0	13.33
51	*TD 19*(*Wakooma*)	2	15	25	30	15.5	21.38	0	40	0	13.33
52	TD 20 (WL 711)	2	25	30	30	12.75	24.44	0	60	0	20.00
53	UP 2382	2	30	30	30	21.25	27.81	0	30	0	10.00
54	PBW 343	3	20	25	40	48.75	33.44	NG	20	40	20.00
55	WL 6975	3	5	20	20	24.25	17.31	10	30	0	13.33
56	CAPAN 3045	3	15	25	20	16.5	19.13	2	30	0	10.67
57	HD 30	3	20	25	20	23.75	22.19	0	30	0	10.00

S. N.	Genotype/cultivation	Reaction to powdery mildew at								
		Seedling stage at Malan	Terminal disease severity at adult plant stage (%) at					Terminal yellow rust severity at (%)			
		(0-4)	Palampur (2016-17)	Palampur (2017-18)	Malan (2016-17)	Kukumseri (2016)	Mean	Malan (2016-17)	Kukumseri (2016)	Keylong (2017)	Mean
58	SHANGAI	3	30	30	40	17.25	29.31	0	10	0	3.33
59	PBW 233	3	20	25	30	19.25	23.56	0	30	0	10.00
60	TL 1210	4	40	20	30	13	25.75	3	10	0	4.33
61	Rye	0	0	0	0	0	0.00	0	0	0	0.00
62	ALDAN	3	20	25	0	14	14.75	0	2	0	0.67
63	CMM 77308	2	5	25	15	14	14.75	0	2	0	0.67
64	H 56771	1	20	25	15	19.25	19.81	0	2	0	0.67
65	HD 29	3	15	20	20	28.25	20.81	0	10	0	3.33
66	HP 1531	3	10	25	20	15.25	17.56	0	40	0	13.33
67	W 485	4	10	25	30	10.25	18.81	10	20	30	20.00
68	HD 2932	4	15	25	30	6.75	19.19	40	3	40	27.67
69	SAW 71	3	20	13	10	16.75	14.93	0	30	0	10.00
70	SAW 74	4	15	7	20	16.75	14.68	0	0	0	0.00
71	Lehmi (check)	3	25	30	40	70	41.25	80	70	60	70.00
	Mean		19.04	26.57	25.56	19.54	22.62	8.42	32.68	22.39	21.16

NG= no germination

Supplementary Table S2. Area under disease progress curve (AUDPC), relative area under disease progress curve (rAUDPC) and infection rate 'r' in some powdery mildew, leaf rust, loose smut differentials lines, and promising wheat genotypes at CSKHPKV Palampur (*rabi* 2016-17 and 2017-18), RWRC Malan (*Rabi* 2016-17) and HAREC Kukumseri (Summer 2016)

S. N.	Genotypes	AUDPC					rAUDPC					Infection rate				
		Palampur 2016-17		Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean
1	CROC_1/*Ae. squarrosa*(662)	0	120	0	0	30	0	16	0	0	4	0	0.06	0	0	0.02
2	68.111/RGB-U//WARD/3/FGO/4/RABI/5/*Ae. squarrosa*(905)	0	82.5	0	0	20.63	0	11	0	0	2.75	0	0.05	0	0	0.01
3	CROC_1/*Ae. squarrosa*(362)	189	487.5	1440	335.63	613.03	29.03	65	62.15	14.44	42.66	0.07	0.03	0.03	0.06	0.05
4	Amigo (*Pm17*)	378	562.5	0	221.25	290.44	58.06	75	0	9.52	35.65	0.03	0.05	0	0.04	0.03
5	Kavkaz (*Pm8*)	437.5	97.5	787.5	136.88	364.85	67.2	13	33.99	5.89	30.02	0.01	0.05	0.03	0.04	0.03
6	Maris dove (*Pm2,Mld*)	490	NG	0	0	122.5	75.27	NG	0	0	18.82	0.02		0	0	0.01
7	Soissons (*Pm3g*)	402.5	382.5	499.5	465	437.38	61.83	51	21.56	20	38.6	0.04	0.08	0.05	0.05	0.06
8	Chancellor (*Pm 10,15*)	1597.5	382.5	1552.5	2193.75	1431.56	68.95	51	67	94.35	70.33	0.06	0.05	0.04	0.03	0.05
9	Near iso-genic (*Pm1*) Axminister X Cc^8	343	307.5	0	69.38	179.97	52.69	41	0	2.98	24.17	0.02	0.05	0	0.04	0.03
10	Near iso-genic (*Pm2*) Ulka X Cc^8	311.5	0	0	0	77.88	47.85	0	0	0	11.96	0.03	0	0	0	0.01
11	Near iso-genic (*Pm3a*)Asosan X Cc^8	399	195	0	208.13	200.53	61.29	26	0	8.95	24.06	0.03	0.06	0	0.05	0.04
12	Near iso-genic (*Pm3b*) Chul X Cc^8	465.5	375	1102.5	450	598.25	71.51	50	47.58	19.35	47.11	0.04	0.03	0.05	0.04	0.04
13	Near iso-genic (*Pm3c*) Sonara X Cc^8	0	412.5	1273.5	37.5	430.88	0	55	54.96	1.61	27.89	0	0.02	0.07	0.02	0.03
14	Near iso-genic (*Pm4*) Khapli X Cc^8	112	337.5	742.5	37.5	307.38	17.2	45	32.05	1.61	23.97	0.04	0.02	0.03	0.02	0.03
15	Citr 14125	0	172.5	553.5	37.5	190.88	0	23	23.89	1.61	12.13	0	0.07	0.03	0.02	0.03
16	Wembley (*Pm12*)	56	420	1021.5	618.75	529.06	8.6	56	44.09	26.61	33.83	0.04	0.06	0.04	0.03	0.04
17	NC96BGTA5 (*Pm25*)	56	382.5	364.5	0	200.75	8.6	51	15.73	0	18.83	0.04	0.07	0.05	0	0.04
18	CItR 15888 Michigen Amber X Cc^8 (*Pm3f*)	56	345	553.5	52.5	251.75	8.6	46	23.89	2.26	20.19	0.04	0.06	0.05	0.02	0.04
19	IWP 94 (*Lr23*)	357	637.5	418.5	1593.75	751.69	54.84	85	18.06	68.55	56.61	0.04	0.01	0.05	0.02	0.03
20	Kharchia Local	420	NG	1012.5	2193.75	906.56	64.52	NG	43.7	94.35	50.64	0.02	NG	0.03	0.03	0.02
21	Ra 3765	560	1087.5	1440	975	1015.63	86.02	145	62.15	41.94	83.78	0.02	0.04	0.03	0.02	0.03
22	HD 2189	136.5	750	1093.5	986.25	741.56	20.97	100	47.19	42.42	52.65	0.06	0.03	0.05	0.02	0.04
23	Agra Local	84	900	1935	1293.75	1053.19	12.9	120	83.51	55.65	68.02	0.04	0.03	0.03	0.02	0.03
24	*Lr*14 A	304.5	NG	2430	1200	983.63	46.77	NG	104.88	51.61	50.82	0.03	NG	0.05	0.02	0.03
25	*Lr* 24	483	975	1575	1256.25	1072.31	74.19	130	67.98	54.03	81.55	0.04	0.03	0.02	0.02	0.03
26	*Lr* 18	472.5	900	1305	1143.75	955.31	72.58	120	56.32	49.19	74.52	0.03	0.05	0.02	0.02	0.03
27	*Lr* 13	444.5	900	1417.5	663.75	856.44	68.28	120	61.18	28.55	69.5	0.06	0.02	0.02	0.05	0.04

S. N.	Genotypes	AUDPC					rAUDPC					Infection rate				
		Palampur 2016-17		Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean
28	*Lr* 17	542.5	750	2340	858.75	1122.81	83.33	100	100.99	36.94	80.32	0.03	0.03	0.05	0.03	0.03
29	*Lr* 15	630	900	1620	975	1031.25	96.77	120	69.92	41.94	82.16	0.03	0.02	0.03	0.02	0.03
30	*Lr* 10	353.5	637.5	1552.5	915	864.63	54.3	85	67	39.35	61.41	0.01	0.02	0.06	0.02	0.03
31	*Lr* 19	217	487.5	1363.5	924.38	748.09	33.33	65	58.85	39.76	49.24	0.05	0.04	0.05	0.02	0.04
32	Thew (*Lr20*)	525	450	1350	765	772.5	80.65	60	58.27	32.9	57.96	0.02	0	0.03	0.03	0.02
33	HP 1633 (*Lr9a*)	717.5	675	2160	825	1094.38	110.22	90	93.22	35.48	82.23	0.01	0.04	0.05	0.02	0.03
34	*TD 1* (Mindum)	945	937.5	1440	909.38	1057.97	145.16	125	62.15	39.11	92.86	0.01	0.02	0.03	0.02	0.02
35	*TD 2*(*Renfrew*)	1400	1012.5	2385	806.25	1400.94	215.05	135	102.93	34.68	121.92	0.01	0.02	0.04	0.02	0.02
36	*TD 4* (*Kota*)	1680	1050	1822.5	708.75	1315.31	258.06	140	78.66	30.48	126.8	0.01	0.03	0.04	0.02	0.03
37	*TD 5* (*Little Club*)	1697.5	1012.5	2430	1012.5	1538.13	260.75	135	104.88	43.55	136.05	0.02	0.02	0.05	0.02	0.03
38	*TD 6* (*Pl69282*)	1277.5	937.5	2070	768.75	1263.44	196.24	125	89.34	33.06	110.91	0.02	0.03	0.05	0.01	0.03
39	*TD 7*(*Reward*)	1312.5	862.5	1822.5	738.75	1184.06	201.61	115	78.66	31.77	106.76	0.02	0.03	0.02	0.01	0.02
40	*TD 8* (*Karma*)	1102.5	937.5	1485	701.25	1056.56	169.35	125	64.09	30.16	97.15	0.01	0.02	0.02	0.01	0.01
41	*TD 9*(*Little bobs*)	840	937.5	2340	1265.63	1345.78	129.03	125	100.99	54.44	102.37	0.02	0.02	0.03	0.02	0.02
42	*TD 10* (*Red bobs*)	469	NG	1642.5	682.5	698.5	72.04	NG	70.89	29.35	43.07	0.03	NG	0.02	0.04	0.02
43	*TD 11*(*Pentad*)	700	900	1710	2100	1352.5	107.53	120	73.8	90.32	97.91	0.02	0.02	0.03	0.02	0.02
44	*TD 12* (*Thatcher x Regent*)	1085	862.5	1530	871.88	1087.34	166.67	115	66.03	37.5	96.3	0.01	0.01	0.03	0.03	0.02
45	*TD 13* (*Pl298554 Cl7795*)	56	862.5	1498.5	736.88	788.47	8.6	115	64.67	31.69	54.99	0.04	0.02	0.06	0.02	0.03
46	*TD 14* (*Sonop*)	1102.5	862.5	1890	500.63	1088.91	169.35	115	81.57	21.53	96.86	0.02	0.02	0.02	0.05	0.03
47	*TD 15* (*H44 x Marguis*)	1067.5	787.5	1710	881.25	1111.56	163.98	105	73.8	37.9	95.17	0.03	0.02	0.03	0.02	0.02
48	*TD 16* (*Morroqui 588*)	574	712.5	1530	646.88	865.84	88.17	95	66.03	27.82	69.26	0.06	0.01	0.03	0.03	0.03
49	TD 17(Marquillo*Waratah)	346.5	562.5	1395	478.13	695.53	53.23	75	60.21	20.56	52.25	0.02	-0.01	0.04	0.03	0.02
50	*TD 18* (*CT439*)	549.5	562.5	1440	909.38	865.34	84.41	75	62.15	39.11	65.17	0.03	-0.01	0.03	0.02	0.02
51	*TD 19* (*Wakooma*)	647.5	562.5	1665	517.5	848.13	99.46	75	71.86	22.26	67.15	0.01	0.01	0.01	0.04	0.02
52	TD 20 (WL 711)	546	750	1462.5	406.88	791.35	83.87	100	63.12	17.5	66.12	0.08	0.03	0.02	0.06	0.05
53	UP 2382	311.5	862.5	1440	706.88	830.22	47.85	115	62.15	30.4	63.85	0.09	0.01	0.03	0.05	0.04
54	PBW 343	525	637.5	1215	1696.88	1018.6	80.65	85	52.44	72.98	72.77	0.02	0.04	0.04	0.04	0.04
55	WL 6975	84	525	1125	950.63	671.16	12.9	70	48.55	40.89	43.09	0.04	0.02	0.02	0.02	0.02
56	CAPAN 3045	357	637.5	967.5	600	640.5	54.84	85	41.76	25.81	51.85	0.04	0.04	0.03	0.03	0.04
57	HD 30	206.5	675	1395	928.13	801.16	31.72	90	60.21	39.92	55.46	0.08	0.02	0.02	0.02	0.04
58	SHANGAI	276.5	787.5	1485	729.38	819.6	42.47	105	64.09	31.37	60.73	0.09	0.02	0.04	0.02	0.04
59	PBW 233	206.5	637.5	1462.5	673.13	744.91	31.72	85	63.12	28.95	52.2	0.08	0.04	0.02	0.03	0.04
60	TL 1210	416.5	675	1732.5	480	826	63.98	90	74.77	20.65	62.35	0.1	0.02	0.02	0.03	0.04
61	Rye	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

S. N.	Genotypes	AUDPC					rAUDPC					Infection rate				
		Palampur 2016-17		Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean	Palampur 2016-17	Palampur 2017-18	Malan 2016-17	Kukum Seri 2016	Mean
62	ALDAN	486.5	487.5	0	476.25	362.56	74.73	65	0	20.48	40.05	0.04	0.04	0	0.04	0.03
63	CMM 77308	84	607.5	765	521.25	494.44	12.9	81	33.02	22.42	37.34	0.04	0.08	0.03	0.03	0.04
64	H 56771	451.5	607.5	540	669.38	567.1	69.35	81	23.31	28.79	50.61	0.04	0.08	0.03	0.03	0.04
65	HD 29	469	600	1021.5	924.38	753.72	72.04	80	44.09	39.76	58.97	0.03	0.03	0.03	0.03	0.03
66	HP 1531	346.5	607.5	1215	613.13	695.53	53.23	81	52.44	26.37	53.26	0.02	0.08	0.02	0.03	0.04
67	W 485	255.5	637.5	1552.5	425.63	717.78	39.25	85	67	18.31	52.39	0.02	0.04	0.02	0.02	0.03
68	HD 2932	378	787.5	1822.5	316.88	826.22	58.06	105	78.66	13.63	63.84	0.03	0.04	0.02	0.03	0.03
69	SAW 71	514.5	450	832.5	568.13	591.28	79.03	60	35.93	24.44	49.85	0.03	0.03	0.02	0.03	0.03
70	SAW 74	378	412.5	1012.5	519.38	580.6	58.06	55	43.7	22.34	44.78	0.03	0.02	0.03	0.04	0.03
71	Lehmi (check)	651	750	2317.5	2325	1510.88	100	100	100.02	96.7	99.18	0.08	0.03	0.03	0.03	0.04

NG= no germination