

# Characterization of Genetic Diversity to Ecological Stripe Rust Resistance in Bread Wheat (*Triticum aestivum* L.)

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**Abstract.** Wheat is the most commonly cultivated crop in the world and is a staple diet for many people. The current study was carried out in the field to evaluate the 51 genotypes based on morphological and physiological traits under artificial inoculation by stripe rust spore suspension and to determine the genetic diversity among these genotypes. Correlation analysis and principal component analysis showed Plant Height correlates highly and positively with chlorophyll content index, grain per spike, grain filling period, peduncle length, spike length and negatively correlated with spikelet per spike. Spike length (SL) was significantly correlated to plant height (PH), grain filling period, peduncle length and negatively associated with grain weight per spike and thousand grain weight. Chlorophyll content index had significant and positive association with grain filling period, plant height, peduncle length, spikelet per spike and spike length. Flag leaf area is significantly and positively associated with grain filling period. Yellow rust severity data collected from genotypes indicated that highly susceptible genotype was G27 (40S). Out of 51 genotypes, 19 genotypes were completely resistant (37.25%), three genotypes were moderately resistant with 10MR score (5.88%), one genotype was moderately resistant with 20MR score (1.96%), sixteen genotypes were moderately resistant with 5MR (31.37%), two genotypes were moderately susceptible in each MS10 (3.92%), MS20 (3.92%), MS40 (3.92%) score, one genotype was susceptible with 40S score (1.96%). Results of scatter biplot diagram showed that lines representing plant height and thousand grain weight were long depicting more variation among these traits as these were further away from origin. Traits under study like plant height, chlorophyll content index, grain per spike, thousand grain weight, grain filling period, peduncle length, and spike length had positive relation as depicted by correlation analysis. Lines 16, 22, 37, 27 and 51 were far away from other lines thus showed that these were highly diverse in respect to studied parameters.

**Keywords:** Genetic diversity, yellow rust, Wheat, Morpho-physiological diversity, Resistance.

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## 1 Introduction

In terms of importance, wheat is the most important crop because of its processing properties. Soft, hard and durum are the three types of wheat. It is impossible to categorize wheat quality in a straight forward manner (from flour to bread, pasta, or cookies) because wheat quality depends greatly on its producers (from farmers to those who process the grains). Wheat is widely believed to be the first crop domesticated by humans on Earth (Sootaher et al. 2020). Even though it is grown in diverse settings, it is a major grain crop in temperate regions around the world, just as rice is in tropical areas. Twenty percent of the world's calories come from wheat grain, 59% carbohydrates, 11.3 % protein, 13.2% fibers, 1.8 fats, 12.6 % water, and 1.7 minerals (Wiese 1987).

As an inexpensive source of energy, wheat is also rich in minerals and calories as well as a good source of fibre and vitamins. The majority of wheat grown in the world is hexaploid ( $2n = 6x = 42$ ), according to current research. There were 2520 million tons of grains produced globally in 2013-14, with wheat contributing 715 million tons. A major food crop, it accounts for one-sixth (17%) of all wheat acreage worldwide, providing food for over half of the world's population as well as one-fifth of the total food calories and protein consumed by humans (Singh et al. 2016).

Almost everywhere in the world, wheat (*Triticum aestivum* L.) has been widely produced as a major food crop. Known as the "king" of cereals, it is a staple food crop that is grown worldwide. Like rice in the tropics, it is a major grain crop in temperate climates (Fahad et al. 2017). Climatic changes, water shortages, and a deteriorating eco environment have all had a significant impact on wheat cultivation. While wheat demand continues to rise as a result of an increasing population, existing varieties and advance lines are being intensified to meet this growing demand. As a result, we need to choose wheat strains that have the desired features quickly and efficiently. The problem has been solved to a certain extent by modern procedures, but most of them are reported to be expensive, time-consuming, or unethical. There is a continued reliance upon traditional breeding and selection processes to produce crop varieties with desirable characteristics (Ahmar et al. 2020). (Tilman et al. 2011) stated that we need a 50% increase in crop production by the year 2050 to meet this goal, but present rates of yield increase are insufficient. Identifying ways to boost crop yield, such as genetically improving cultivars and improving agronomic practices, is consequently vital and urgently needed (Hawkesford et al. 2013).

Due to increasing population pressure, it is necessary to produce more wheat in order to assure food security around the globe (Ali et al. 2015a). Wheat crop is primarily affected by different rust diseases like leaf/brown rust, stripe/yellow rust and stem/black rust. The pathogen of stripe rust prevails in the regions with mild temperature and humid weather conditions. The production losses caused by stripe rust vary according to the severity of infection, resistance level of cultivar and geographical variation (Huerta-Espino et al. 2011). However, the severity of disease depends upon the response (resistance or susceptibility) of the cultivars. Growth and yield parameters of the wheat are badly affected by rusts (Jabran et al. 2021). For stripe rust management, numerous approaches have been employed. Development of resistant cultivars is the most eco-friendly and durable approach to tackle the rust diseases. The field based evaluation of resistance is a big challenge for the breeders in developing countries. Cluster analysis, correlation and principal component have been largely employed for the assessment of diversity of various traits in different crop plants (Ali et al. 2009). These parameters divide the data sets into various homogenous clusters which are primarily deviating from the other clusters. These types of analyses could be very helpful for grouping of disease responses of wheat cultivars. The current research was designed to study the genetic diversity for disease resistance and yield contributing characters in 51 genotypes under field conditions in Bahawalpur. Current study was planned to fulfill

following objectives; Quantify and characterize the morphological and physiological traits associated with stripe rust resistance in bread wheat. Evaluate the genetic diversity in wheat germplasm for stripe rust resistance using morpho-physiological markers. Identify and select superior genotypes for stripe rust resistance in wheat based on morpho-physiological traits.

## 2 Materials and Methods

Current experiment was performed to access the genetic diversity to stripe rust resistance in wheat on morpho-physiological bases. Experiment was conducted on 2021-2022 wheat season in field research area of the Department of Plant Breeding and Genetics (PBG), Faculty of Agriculture and Environment, The Islamia university of Bahawalpur located at latitude 29° 24' and longitude 71° 47'. Temperature on average ranges from 21°C to 11°C with average humidity at 57% in early period of crop growth with increasing temperature as crop matures. Fifty-one genotypes used in this experiment were acquired from Regional Agriculture Research Institute Bahawalpur (Table 1). Sowing of the experiment was done in month of November 2021. Each entry had 2 lines with 2 meters length each. Row to Row distance was one ft. Morocco highly susceptible wheat genotype was used as check and spreader and was sown after every 10 genotypes. Recommended amount of fertilizer was applied. Artificial inoculation was performed using knapsack when plants were at tillering stage. Suspension was prepared in double distilled water with 300 milligram (mg) spores per 1 liter of water. By utilizing Modified Cobb's scale (Peterson et al. 1948) the genotypes were scored at 15-day interval beginning from first appearance of symptoms till the disease ceased to develop. Disease severity (%) was calculated (Roelfs et al. 1992). Ten plants in each line were tagged for data recording. Data were recorded for Grain Filling Period, Chlorophyll Content, Flag Leaf Area, Plant Height, Peduncle Length, Spike Length, Spikelet per spike, Grains per Spike, Thousand Grain Weight and Grain Weight per Spike.

Correlation was performed using Software Statistix 8.1.

$$r = \frac{n(\sum xy) - (\sum x)(\sum y)}{\sqrt{[n \sum x^2 - (\sum x)^2][n \sum y^2 - (\sum y)^2]}}$$

Principal component analysis (PCA) was done on the data using software Past4 project to obtain PC1 and PC2 which further used to construct Biplot diagrams.

Cluster analysis is a data-processing statistical approach. It operates by categorizing items into groups, or clusters, on the basis of their relatedness. Two dendrograms were built using Software IBM SPSS 26.

**Table 1.** Parentage/Pedigree of bread wheat genotypes under study

Code	Parentage/Pedigree
G1	FRANCOLIN #1/3/IWA 8600211//2*PBW343*2/KUKUNA/4/KACHU/3/IWA 8600211//2*PBW343*2/KUKUNA
G2	DANPHE#1*2/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//SHA4/CHIL/6/WBLL1/3/STAR//KAUZ/STAR/4/BAV92/RAYON/5/TRAP#1/BOW/3/VEE/PJN//2* TUI/4/BAV92/RAYON/7/MUCUY
G3	FRNCLN*2/7/CMH83.1020/HUITES/6/CMH79A.955/4/AGA/3/4*SN64/CNO67//I NIA66/5/NAC/8/WBLL1*2/KURUKU//HEILO/9/WBLL1*2/KURUKU//HEILO/10 /KACHU #1/T.SPELTA PI348764//2*KACHU/4/2*ATTILA*2//CHIL/BUC*2/3/KUKUNA

Continuation of table 1.

G4	HGO94.7.1.12/2*QUAIU#1//QUAI#2/5/KIRITATI/4/2*BAV92//IRENA/KAUZ/3/HUITES/6/MUCUY/7/KIRITATI/2*WBLL1/5/FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI/6/BECARD #1
G5	COAH90.26.31/4/2*BL2064//SW895124*2/FASAN/3/TILHI/5/UP2338*2/KKTS*2//YANAC/6/MUTUS/AKURI/7/PBW343*2/KUKUNA*2//FRTL/PIFED/3/KFA/2*KACHU
G6	MAYIL/5/PFAU/WEAVER*2/4/BOW/NKT//CBRD/3/CBRD/6/KINDE*2/SOLALA/3/UP2338*2/KKTS*2//YANAC/4/UP2338*2/SHAMA//2*BAJ #1
G7	SHAKTI//MUTUS*2/MUU/3/MUCUY
G8	MANKU/3/PAURAQ/SOLALA//PAURAUQUE#1/8/PSN/BOW//SERI/3/MILAN/4/ATTILA/5/KAUZ*2/CHEN//BCN/3/MILAN/6/WBLL1*2/SHAMA/7/IWA 8600211//2*PBW343*2/KUKUNA
G9	MANKU/3/PAURAQ/SOLALA//PAURAUQUE#1/8/PSN/BOW//SERI/3/MILAN/4/ATTILA/5/KAUZ*2/CHEN//BCN/3/MILAN/6/WBLL1*2/SHAMA/7/IWA 8600211//2*PBW343*2/KUKUNA
G10	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA 8600211//2*PBW343*2/KUKUNA/6/BORL14/7/BOKOTA
G11	BOKOTA//KFA/2*KACHU
G12	BORL14*2/FITIS
G13	Jauhar-16/ISBWYT-16
G14	CNDO/R143//ENTE/MEXI 2/3/AEGILOPS SQUARROSA (TAUS)/4/WEAVER/5/2*JANZ/6/SKAUZ/BAV92/7/2*KUTZ
G15	KUTZ*2//KFA/2*KACHU
G16	PAKHW*2/DEMAI 4*2/3/ATTILA*2/PBW65*2//MURGA
G17	BAV92/SERI+Aas-11//F1-E-12
G18	MUTUS/ROLF07*2//KACHU/KINDE
G19	MUNAL#1/NARC-11
G20	BORL14*2/FITIS
G21	TUKURU//BAV92/RAYON/3/FRNCLN/4/KSW/SAUAL//SAUAL/5/TUKURU//BAV92/RAYON/3/FRNCLN
G22	MUCUY*2/BORL14
G23	SB-75/PUNJNAD-01
G24	PFAU/SERI.1B//AMAD/3/WAXWING/4/AKURI/5/PFAU/---/6/Lasani-08
G25	FRET2*2/SHAMA//KIRITATI/2*TRCH/3/KFA/2*KACHU/4/FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA
G26	CHEN/AE.SQ//2*OPTA/3/FINSI+YSB-1/4/2511
G27	Morroco
G28	MUU/KBIRD//2*KACHU/KIRITATI
G29	BORL14*2/FITIS
G30	WBLL1*2/SHAMA//KACHU/3/SUP152*2/TECUE #1/4/WBLL1/KUKUNA//TACUPETO F2001/3/BAJ #1
G31	BECARD/FRNCLN*2//BORL14
G32	OASIS/5*BORL95/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI/6/KACHU/BECARD//WBLL1*2/BRAMBLING/7/KACHU/BECARD//WBLL1*2/BRAMBLING
G33	KUTZ//KFA/2*KACHU
G34	CMSS11Y01084T-099TOPM-099Y-099M-099NJ-099NJ-19WGY-...
G35	PBW343*2/KUKUNA*2//FRTL/PIFED/3/KFA/2*KACHU CMSS11B00190S-099M-099NJ-099NJ-20WGY-0B
G36	KACHU#1/YUNMAI 47//KACHU/5/SAUAL/3/C80.1/... CMSS11B00786T-099TOPY-099M-0SY-31M-0WGY

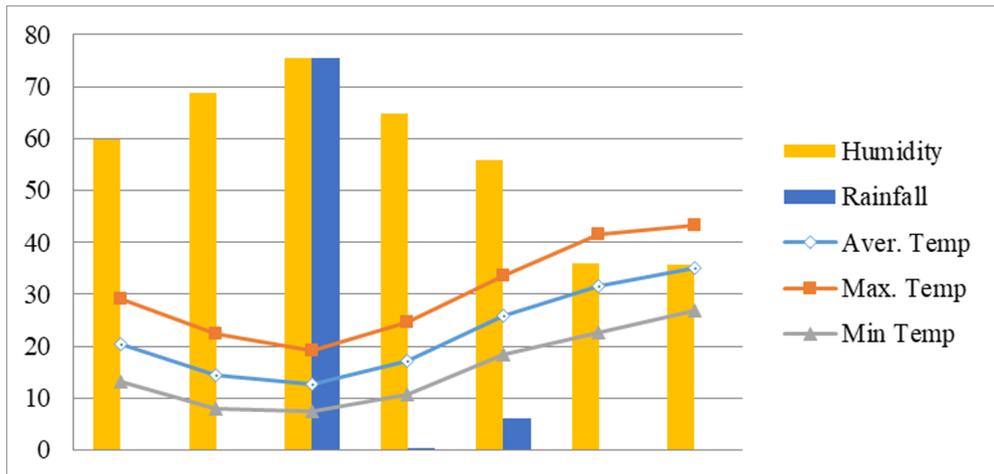
**Continuation of table 1.**

G37	KFA/2*KACHU/3/PBW343*2/KUKUNA*2//FRTL/PIFED/... CMSS11B00954T-099TOPY-099M-0SY-27M-0WGY
G38	KACHU#1/YUNMAI47//KACHU/5/SAUAL/3/C80.1/... CMSS11Y00191S-099Y-099M-099NJ-099NJ-11WGY-0B
G39	THELIN/2*WBLL1/5/KAUZ//ALTAR 84/AOS/3/KAUZ/4/... CMSS11Y01218T-099TOPM-099Y-099M-099NJ-099NJ-6WGY-0B
G40	MUNAL*2/WESTONIA CMSS08Y00833T-099TOPM-099Y-099M-099NJ-099NJ-14WGY-0B
G41	WHEAR/SOKOLL/8/BOW/VEE/5/ND/VG9144//KAL/BB/3/YACO/4/... CMSA11Y00467S-099Y-099M-099NJ-099NJ-12WGY-
G42	SHI4414/CROW/4/NIF/3/SOTY//NAD/CHR/5/FRAME/6/SUNCO/2*PASTOR/7/WBLL1*2/BRAMBLING/4/BABAX/LR42//BABAX*2/3/SHAMA/8/KACHU/BECARD//WBLL1*2/BRAMBLING
G43	NADI/3/PBW343*2/KUKUNA*2//FRTL/PIFED/4/NADI CMSS11B00908T-099TOPY-099M-099NJ-099NJ-32WGY-0B
G44	NADI CMSS06B00734T-099TOPY-099ZTM-099Y-099M-13WGY-0B
G45	ALTAR 84/AE.SQUARROSA (221)//3*BORL95/3/URES/JUN//KAU CMSS12B00768T-099TOPY-099M-0SY-14M-0WGY
G46	WBLL1*2/SHAMA//BAJ#1*2/3/KACHU#1/KIRITATI//KACHU CMSS12B00720T-099TOPY-099M-0SY-11M-0WGY
G47	MUU/KBIRD//KACHU/KIRITATI
G48	NR-399/8203
G49	TWS12411/NR-99
G50	TWS12495/NR-99
G51	BOKOTA//KFA/2*KACHU CMSS12Y00163S-099Y-099M-0SY-73M-0WGY

### 3 Results

#### 3.1 Meteorological data for the wheat growing seasons (Nov, 2021 to May 2022).

Meteorological data from November, 2021 to May, 2022 (Figure 1) shows mean monthly values of temperature, relative humidity and rainfall.

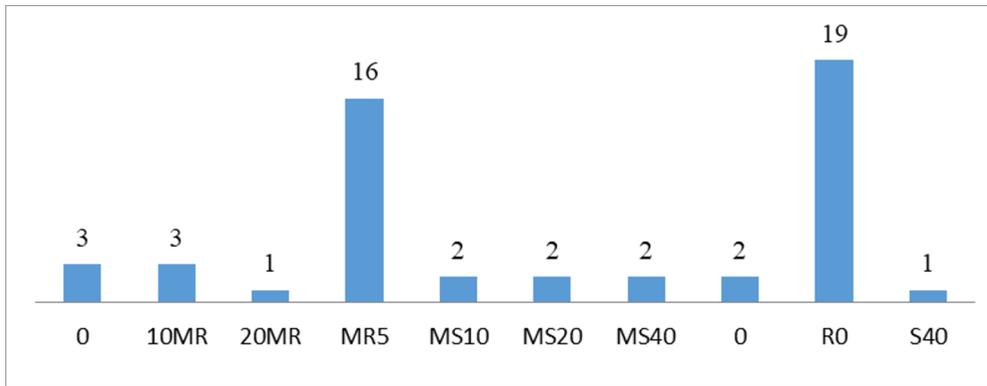


**Fig. 1.** Meteorological data for the wheat growing seasons (Nov, 2021 to May 2022).

Mean values of maximum temperature during 2021 growing season were recorded as 29 °C and 22.3°C in the months of November and December, respectively. Whereas in 2022 mean values; 19.1 °C, 24.7 °C, 33.7 °C, 41.6 °C and 43.2 of maximum temperature were found in the months of January to May respectively. Maximum relative humidity was recorded in January-22 (75.6 %) and December-21 (68.9 %). Total rainfall during growing period was 81.78 mm. Maximum rainfall (75.43) was recorded in January, 2022.

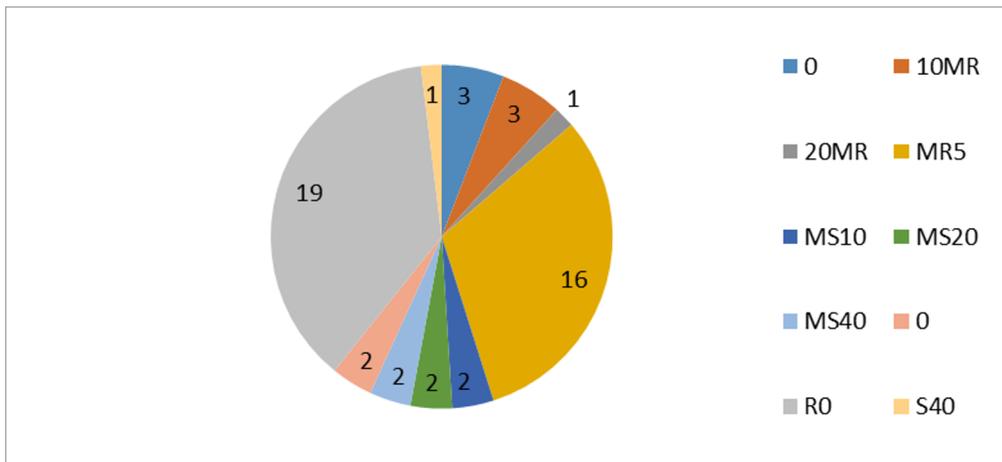
### 3.2 Disease severity

Stripe rust severity data collected from genotypes indicated that highly susceptible genotype was G27 (Morocco) (40S). Out of 51, 19 genotypes were completely resistant genotypes (Figure 2).



**Fig. 2.** Count of severity.

Out of 51 genotypes, 19 genotypes were completely resistant (37.25%), three genotypes were moderately resistant with 10MR score (5.88%), one genotype was moderately resistant with 20MR score (1.96%), sixteen genotypes were moderately resistant with 5MR (31.37%), two genotypes were moderately susceptible in each MS10 (3.92%), MS20 (3.92%), MS40 (3.92%) score, one genotype was susceptible with 40S score (1.96%); (Figure 2 and 3).



**Fig. 3.** Pie chart of 51 genotypes to stripe rust disease response.

### 3.3 Mean values of all traits in studied genotypes

Plant height varied from maximum in resistant variety G37 (103.5 cm) to minimum in resistant cultivar G17 (68.4 cm). Maximum mean value of spike length was witnessed in line G10 (15.3 cm) while G27 had the shortest spike recorded (10.5 cm). Flag leaf area was from 19.5 cm<sup>2</sup> in G26 to 9.45 cm<sup>2</sup> in G43. Thousand grain weight (TGW) was observed maximum in G29 at 43.9 grams and minimum in G34 at 22.2 grams. Peduncle length varied from 36 cm in G50 to 22 in G10. G34 had the highest number of spikelet's (25) while G5 had the lowest number of spikelet's (17). Grain filling period varied from maximum in G47 (25) to minimum in cultivar G14 (20). Maximum mean value of chlorophyll content index was recorded in G1 (32.45) while G20 had the minimum value measured (15.75). Grains per spike varied greatly from 46 in G51 to 31 in G47. Grain weight per spike (GW/S) was observed maximum in G51 at 1.8 grams and minimum in G1 at 0.8 grams (Table 2).

**Table 2.** Mean values of all traits under study.

Genotype	GFP	C.CNT	FLA	PH	PL	SL	S/S	G/S	TGW	GW/S
G1	22	32.45	22.42	83	32.7	14	18	32	25	0.8
G2	23	28.13	22.14	81.1	34.4	14.7	23	44	31.8	1.4
G3	23	23.31	22.42	88	32	14.4	20	40	35	1.4
G4	23	24.71	15.9	87.2	29	12.5	23	33	30.3	1
G5	22	17.99	21.18	78.2	23.1	11.8	17	39	30.7	1.2
G6	23	26.12	16.5	85.5	28.7	11	21	44	36.3	1.6
G7	21	29.09	23.1	73.1	23	13.3	25	0	0	0
G8	22	30.96	14.4	72.4	27.4	12.5	23	0	0	0
G9	22	26.29	16.04	74	28.8	15	21	0	0	0
G10	22	31.94	12.25	74.9	22	15.3	24	0	0	0
G11	22	25.21	22.14	82	27	13.3	24	37	32.4	1.2
G12	21	15.93	18.72	72.4	29.1	13.5	24	0	0	0
G13	21	17.27	18.52	83	32.4	14	22	41	29.2	1.2
G14	20	25.26	16.87	78.4	32.4	13.5	20	0	0	0
G15	21	24.85	13.5	70	23.6	14.6	22	0	0	0
G16	19	27.75	14.5	76.5	25.1	12.3	0	0	0	0
G17	21	22.4	13.2	68.4	25.9	12.6	22	0	0	0
G18	23	31.37	15	76.5	25.1	12.3	23	45	31.1	1.4
G19	24	25.19	23.49	72.2	32.7	12.7	21	0	0	0
G20	21	15.75	24.66	69.5	26.9	14	21	0	0	0
G21	20	32.2	19.31	71.9	31.2	12	21	0	0	0
G22	23	17.52	13.05	69	33.5	13	21	0	0	0
G23	23	24.23	15.9	84.5	29.6	11.5	25	39	30.7	1.2
G24	22	32.3	25.5	83.4	30.2	12	21	41	39	1.6
G25	23	25.9	17.1	73	29.6	12.8	21	45	35.5	1.6
G26	24	24.66	19.5	79	25.3	11.1	21	43	32.5	1.4
G27	23	24.44	16.99	76	33	10.5	17	46	34.7	1.6
G28	22	25.54	10.32	78.6	24	12	23	32	25	0.8
G29	21	23.77	12.72	71.1	22.4	11	20	41	43.9	1.8
G30	22	23.18	17.43	70.1	31.4	11.7	19	40	25	1
G31	23	29.81	18.78	74	29.4	11.5	24	39	35.8	1.4
G32	22	25.5	25.42	81.4	28.3	12	23	0	0	0
G33	22	24.2	15.25	77	27.1	12.6	21	33	30.3	1
G34	22	19.8	15.9	82.2	24	15	25	36	22.2	0.8
G35	23	22.2	10.8	71	26	11.9	21	43	32.5	1.4
G36	21	15.9	19.5	79.2	30.8	11.9	21	33	24.2	0.8
G37	22	23.8	24.37	103.5	34	13	21	40	25	1

Continuation of table 2.

Genotype	GFP	C.CNT	FLA	PH	PL	SL	S/S	G/S	TGW	GW/S
G38	24	31.5	18.72	83	29.9	12.1	19	41	24.3	1
G39	21	20.1	16.92	78.6	24.4	13	23	36	27.7	1
G40	22	17.2	23.94	81	27	14	21	39	25.6	1
G41	23	28.01	20.25	75.4	29.6	11.9	23	36	27.7	1
G42	21	24.01	18	81.4	25.3	11.2	19	34	23.5	0.8
G43	23	19.21	9.45	84.7	34.6	15	21	43	32.5	1.4
G44	24	29.21	12.82	72.2	25.2	12.8	24	36	33.3	1.2
G45	22	26.3	11.75	0	0	0	23	0	0	0
G46	21	28.01	11.75	75.4	27.5	12.5	24	41	29.2	1.2
G47	25	30.21	17.43	76.4	31.3	11.5	18	31	31.2	1
G48	24	26.1	15.45	79.4	28.8	11.8	22	41	39	1.6
G49	21	24.61	15.1	78.6	33	12.1	22	37	27	1
G50	23	30.31	13.95	82.1	36	15	21	39	30.7	1.2
G51	24	22.12	13.95	86.1	35.4	10.5	21	46	39.1	1.8

GFP: Grain Filling Period, CC: Chlorophyll Content, FLA: Flag Leaf Area, PH: Plant Height, PL: Peduncle Length, SL: Spike Length, S/S: Spikelet per spike, G/S: Grains per Spike, TGW: Thousand Grain Weight, GW/S: Grain Weight per Spike

### 3.4 Correlation analysis

Plant Height correlates highly and positively with chlorophyll content index, grain per spike, grain filling period, peduncle length, spike length and negatively correlated with spikelet per spike. Spike length (SL) was significantly correlated to plant height (PH), grain filling period, peduncle length and negatively associated with grain weight per spike and thousand grain weight. Chlorophyll content index had significant and positive association with grain filling period, plant height, peduncle length, spikelet per spike and spike length. Flag leaf area is significantly and positively associated with grain filling period. Grain per spike has the significant and positive correlation with grain filling period, grain weight per spike, plant height and thousand grain weight per spike as exhibited in Table 3.

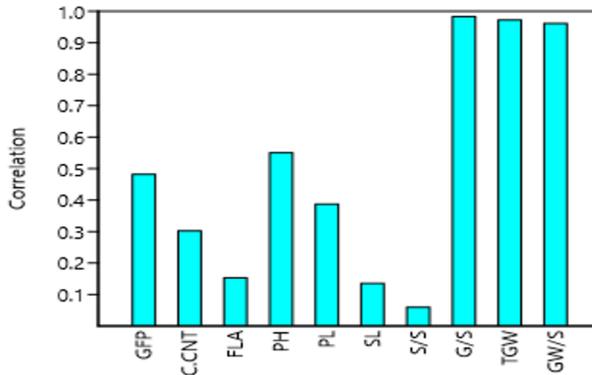
Table 3. Correlation analysis (Pearson) of morpho-physiological traits under study.

	CC	FLA	G/S	GFP	GW/S	PH	PL	S/S	SL
FLA	0.251	1							
G/S	0.199	0.116	1						
GFP	0.744**	0.372*	0.374*	1					
GW/S	0.216	0.097	0.963**	0.369	1				
PH	0.448*	0.211	0.415**	0.621**	0.368	1			
PL	0.427*	0.137	0.269	0.608**	0.257	0.763**	1		
S/S	0.425*	0.248	0.052	0.514**	0.045	-0.063	-0.083	1	
SL	0.395*	0.056	0.015	0.540**	-0.032	0.719**	0.619**	0.044	1
TGW	0.225	0.090	0.969**	0.376*	0.985**	0.385	0.244	0.053	-0.018

CC: Chlorophyll Content Index, FLA: Flag Leaf Area, G/S: Grains per Spike, GFP: Grain Filling Period, GW/S: Grain Weight per Spike, PH: Plant Height, PL: Peduncle Length, S/S: Spikelet per spike, SL: Spike Length, TGW: Thousand Grain Weight

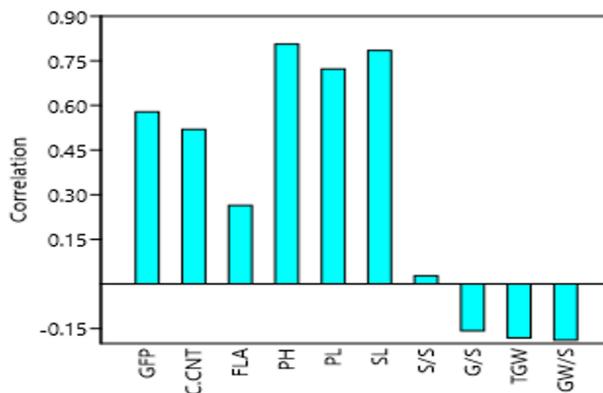
### 3.5 Principal Component Analysis

**Principal Component 1 (PC1).** Factor loading 1 gives maximum positive load for grain weight per spike, thousand grain weight, grain per spike, plant height, chlorophyll content index and grain filling period. This PC analysis can be effective for grain per spike displaying positive correlation of grain per spike with grain filling period, grain weight per spike, plant height and thousand grain weight per spike (Figure 4).



**Fig. 4.** Factor loading (PC1) for traits under study.

**Principal Component 2 (PC2).** Factor loading 2 depicts maximum positive load of traits like spike length, peduncle length, plant height, and chlorophyll content index while negative load was contributed by grain weight per spike, thousand grain weight and grain per spike. The PC analysis can be effective estimation for plant height having significantly positive association with chlorophyll content index, grain per spike, grain filling period, peduncle length, spike length (Figure 5).

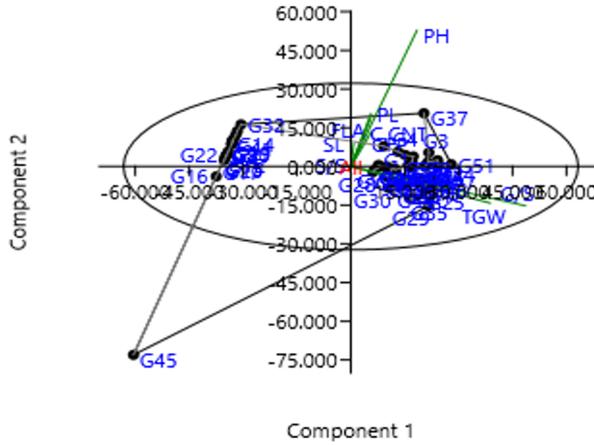


**Fig. 5.** Factor loading (PC2) for traits under study.

### 3.6 Biplot and dendograms construction

These two PC were used to construct a scatter biplot diagram (Figure 6). Lines expressing plant height and thousand grain weight were long depicting more variation among these traits as these were further away from origin. Traits under study like plant height, chlorophyll

content index, grain per spike, grain filling period, peduncle length, spike length had positive relation as depicted by correlation analysis.



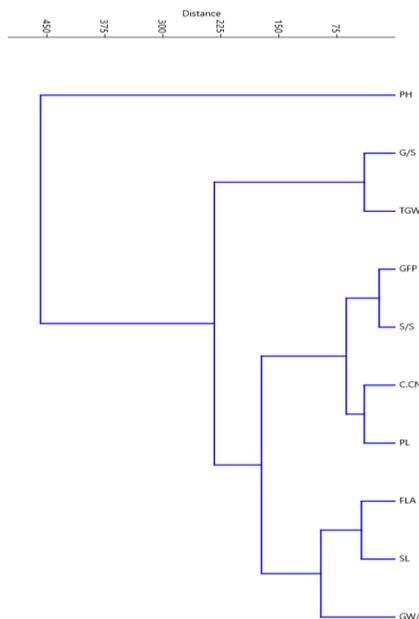
**Fig. 6** Biplot diagram.

Lines 16, 22, 37, 51 and 27 were far away from other lines thus showed their high diversity in terms of studies attributes.

### 3.7 Dendrogram based on morph-physiological parameters

Figure 7 showed different clusters at linkage distance of 450. Plant height was present Cluster 1 and other parameters were in the separate Clusters.

Dendrogram Using ward Linkage Rescaled Distance Cluster Combine



**Fig. 7.** Cluster Analysis of studied parameters.

Traits like grain per spike and thousand grain weight were present within same Cluster depicting positive association. Likewise, grain filling period & spikelet per spike, chlorophyll content index and peduncle length, flag leaf area and spike length were present in same Cluster signifying close connection.



**Fig. 8.** Average linkage distance among 51 Genotypes.

## 4 Discussion

Wheat is repeatedly exposed to numerous biotic challenges due to the constantly changing climate, such as rust diseases, which are a severe problem for wheat in the current climate change scenario. Under real-world circumstances, these pressures have the potential to affect yield characteristics (Taiwo and Akinjogunla 2006). The breeding of resistant cultivars is the ideal strategy for preventing rust disease (Martínez-Carrasco et al. 2005). According to (Ahmad et al. 2006), yield losses might vary depending on the type of disease, and other factors such late seeding can affect plant height. When the illness severity of the most susceptible variety, Morocco, reached 80–100% in the current investigation, the disease data were noted. Out of 51 genotypes, 19 genotypes were completely resistant (37.25%), three genotypes were moderately resistant with 10MR score (5.88%), one genotype was moderately resistant with 20MR score (1.96%), sixteen genotypes were moderately resistant with 5MR (31.37%), two genotypes were moderately susceptible in each MS10 (3.92%), MS20 (3.92%), MS40 (3.92%) score, one genotype was susceptible with 40S score (1.96%). The level of rust represents the sum of all resistance elements throughout the course of the epidemic (Parlevliet and Van Ommeren 1975). In line with the outcomes of (Bastiaans et al. 2001) and (Lopez et al. 2002), which showed higher chlorophyll contents in control plants as compared to diseased plants, this showed that chlorophyll was severely reduced by the prevalence of rust. According to (Ali et al. 2009) and (Ali et al. 2009), the analysis of correlation coefficients allows for the simultaneous selection of desirable features and the production of ideal plant types. Without association studies, it can be challenging to choose resistant plants for breeding programs (Toker and Ilhan Cagiran 2004). Because we discovered certain statistically significant correlations between the attributes in the diseased condition that weren't present in the controlled situations, the disease had an impact on the correlation coefficients in the current investigation, and vice versa. (Ibrahim 2019) noted that while spike-length (SL) was positively significant correlated to grain yield on the genotypic level, not the phenotypic level, flag leaf area (FL), number of spikelets (NOS), grain per spike, and 1000 grain weight (GW) were all positively significant related to grain yield on both phenotypic and genotypic levels. By dividing the overall variance into its characters, it would be possible to study the genetic variability among the genetic resources. Additionally,

enabling the selection of acceptable germplasm in various crop-enhancement techniques for specific plant traits (Sneath 1973); (Pecetti and Damania 1996). Principal component (PC) analysis shortens the difficult data by converting set of observed correlated variables into a short number of variables known as principal components. It is a simple method for choosing genotypes with desirable traits to improve crop yield (Awan et al. 2015); (Ali et al. 2015b). In current experiment; factor loading and PCA shows contribution of traits in over all data set. Similar findings were observed by (Ali et al. 2011), who found that the first few principal components contributed more heavily based on various plant characteristics.

Fifty one wheat genotypes were divided into 3 clusters in the current study method of clustering, according to the morpho-physiological characteristics under disease and control conditions. Based on similarities between the means of the studied traits; cluster analysis placed related genotypes in a single cluster (Ali et al. 2015a).

## 5 Conclusion

Out of 51 studied genotypes, 19 were resistant. These genotypes were shown to be dispersed as depicted through biplot and tree diagrams, indicating diversity. The identified resistant sources could be a used in future wheat breeding programs for developing disease-free cultivars.

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