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Research Article

Multivariate analysis of grain yield attributes and spot blotch incidence in wheat (*Triticum aestivum* L.) under sub-Himalayan agroclimatic condition

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Abstract

An Elite Spring Wheat Yield Trial (EWYT) was conducted with 50 diverse genotypes of Wheat (*Triticum aestivum* L.) and analyzed by multivariate analysis during 2018-19 *rabi* season. Correlation analysis revealed positive association of plant height, grains per spike, spike length, test weight and biomass with grain yield. Path analysis revealed the highest direct effect on grain yield/metre by biomass/metre (1.508) which was also positively associated with grain yield/metre (0.833). PCA analysis showed 11 principal components out of which five principal components (PC1 to PC5) exhibited eigen value greater than one. The correlation between AUDPC and physiological characters indicated that chlorophyll loss was associated with high spot blotch disease incidence at later stages of crop growth.

Keywords: Wheat, correlation, path analysis, PCA, spot blotch

INTRODUCTION

Wheat is one of the most grown crops in the world and nearly 600 million tonnes is produced across various continents like Asia, America, Europe, Africa and Australia. Wheat covers 17% of cropping area worldwide (Goyal *et al.*, 2020) and contributes 20% of the total protein in human nutrition (Goel *et al.*, 2018). It also acts as an important energy source to farm animals and can be processed for various other uses (Heuzé *et al.*, 2015). The rapid increase in world population created a demand for the products derived from wheat (Baboev *et*

al., 2014). India is the third largest wheat producer and has produced over 106 million metric tonnes during the year of 2022 (Statista, 2022).

Grain yield is a complex polygenic character which is influenced by environmental factors. It is very important to determine characters contributing to grain yield to enhance the breeding efficiency through meaningful selection criteria (Gashaw *et al.*, 2007). Yield contributing attributes (both direct and indirect) need genetic analysis

of breeding values along with magnitude of selection responses for proper utilization in breeding programme. It is, therefore, essential to have information on these aspects to resolve and quantify their mode of contribution to grain yield. On the other hand, many biotic factors such as yield reducing diseases influence the reduction in wheat grain yield (Wegulo *et al.*, 2009). Among many biotic factors, spot blotch [*Bipolaris sorokiniana* (Sacc.) Shoem] has affected wheat for past four decades in north India's Eastern Gangetic Plains (EGP) and it is estimated that it contributes to nearly 15-25% of crop loss (Poddar and Roy, 2022). Therefore, it is important to develop new wheat varieties to withstand the disease as well as for grain yield production.

Selection and variation are two important factors that helps breeders to develop resistant genotypes. Variability analysis such as association analysis, cause and effect relationship between grain yield and spot blotch disease and principal components were utilised by Wegulo *et al.* (2009), Meena *et al.* (2014), Tembo *et al.* (2018) and Gupt *et al.* (2021) Therefore, the objective of the present research is to evaluate spring wheat genotypes by estimating genetic parameters such as association, cause and effect relationship with grain yield along with spot blotch resistance and principal component analysis for spot blotch resistance in wheat.

MATERIALS AND METHODS

The experiment was conducted at Uttar Banga Krishi Vishwavidyalaya, Cooch Behar, West Bengal. The experimental material comprised of 50 diverse Elite Spring Wheat (*Triticum aestivum* L.) Yield Trial (ESWYT) genotypes (ESWYT1 to ESWTT50), which were evaluated during 2018-19 *rabi* season (Table 1). The evaluation of ESWTY wheat genotypes was done following randomized block design (RBD) with two replications under timely sown condition. The experimental plot consisted of six rows per plot of two metres length with 20 cm row to row spacing. During the crop cultivation, standard crop management practices were followed, and the plots were manually harvested. Observations such as plant height (cm), days to 50 % heading, grains/spike, awn length (cm), spike length (cm), tillers/metre, test weight (g), grain yield/metre (g) and biomass/metre (g) were recorded in each replicate. The data for plant height, grains/spike, awn length, spike length, tillers/metre, grain yield/metre and biomass/metre were recorded from five samples per replication whereas, the data for days to 50% heading was recorded on per plot basis.

Physiological parameters like chlorophyll index was recorded at four crop growth stages viz. 85 DAS, 92 DAS, 99 DAS and 106 DAS. Field scout CM 1000 chlorophyll metre was used to record the chlorophyll index values. The laser guided lights were used to aim the metre at target row sections and the value obtained was directly displayed and noted. Observations were recorded

between 10 a.m. and 2 p.m. with the sun to the back of the reader without shading the ambient light receiver. The readings for the CM 1000 metre were taken 3 to 5 feet from the canopy at either 45° or 90° angles of the metre in relation to the wheat canopy surface. The chlorophyll index value was considered only if the ambient light level was displayed greater than one, on a scale of zero to nine. Measurements are made in a circular area, approximately 13 to 35 square inches (at 3 to 5 feet from the canopy) including many plants and leaves.

The disease observations for spot blotch (*Bipolaris sorokiniana* (Sacc.) Shoem) was also done at four crop growth stages viz. 85 DAS, 92 DAS, 99 DAS and 106 DAS. Disease scoring was done by using a double-digit scale (00-99) developed as a modification of Saari and Prescott's severity scale (Saari and Prescott, 1975).

For each score, the percentage of disease severity was estimated based on the following formula:

$$\text{Severity (\%)} = (D1/9) \times (D2 /9) \times 100$$

Area under disease progress curve (AUDPC) was calculated by using the following formula suggested by Wilcoxson *et al.* (1975).

The AUDPC gives a quantitative measure of epidemic development and disease intensity (Reynolds and Neher, 1997)

On preliminary analysis of the data for the different characters, it was found that they were not following normal distribution. Hence, the data was subjected to Asinh transformation and subsequently the statistical analysis was done. Character wise replicated data was subjected to analysis of variance (ANOVA), correlation analysis (Pearson,1901), path coefficient analysis (Dewey and Lu,1959) and principal component analysis (PCA). The software used for statistical analysis were GENRES (1994), IRRI software - STAR (version 2.0.1, January 2014) and R-project version 3.5.

RESULTS AND DISCUSSION

The ANOVA for the nine characters revealed significant difference between the genotypes for all the characters (Table 2) revealing substantial variability among the wheat genotypes. Similarly, the two-way ANOVA for chlorophyll index (Table 3) and disease severity (%) [Table 4] also exhibited significant difference among the wheat genotypes.

The correlation analysis revealed that among the 10 yield attributing characters only five were positively and significantly associated with grain yield (Table 5). They were plant height, grains/spike, spike length, test weight and biomass/metre. Plant height was found to be positively associated with only chlorophyll index but not associated

Table 1. List of ESWYT wheat genotypes evaluated during 2018-2019

S. No.	Genotype	Pedigree
1	ESWYT1	Local check
2	ESWYT2	MUCUY
3	ESWYT3	KACHU/SAUAL/4/ATTILA*2/PBW65/PIHA/3/ATTILA/2*PASTOR
4	ESWYT4	CROC-/AE.SQUARROSA(205)//BORL95/3/ATTILA/2*PASTOR
5	ESWYT5	NELOKI/SOKOLL/EXCALIBUR
6	ESWYT6	SUP152/QUAIU #2//BECARD/QUAIU #1
7	ESWYT7	BORL14//BECARD/QUAIU #1
8	ESWYT8	KACHU//WBLL1*2//BRAMBLING/3/KACHU/KIRITAKI
9	ESWYT9	WBLL4/KUKUNA//WBLL1/3/WBLL1*2//BRAMBLING/4/BORL14
10	ESWYT10	SUP152/AKURI//SUP152/3/MUCUY
11	ESWYT11	PRL/2*PASTOR*2//MISR2, EGY/3/2*BECARD//IND643/2*WBLL1
12	ESWYT12	SUP152/BLOUK#1/3/PRL/2*PASTOR*2//VORB/4/SUP152/...
13	ESWYT13	BOLOTA//BECARD/QUAIU#1//2*BORL14
14	ESWYT14	SUP152/HUIRIVIS#1//2*BORL14
15	ESWYT15	KSW/SAUAL//SAUAL/3/TRCH/HUIRIVIS#1/5/UP2338*2/SHAMA
16	ESWYT16	BORL14*2/7/MUU/5/WBLL1*2/4/YACO/PBW65/3KAUZ*2/TRAP//...
17	ESWYT17	WBLL1/4/BOW/NKT//CBRD/3/CBRD/3/CBRD/5/WBLL1*2/TUKURU/6/...
18	ESWYT18	NADI//TRCH/HUIRIVIS#1/3/NADI
19	ESWYT19	KACHU//WBLL1*2//BRAMBLING/3/BAJ#1/AKURI/4/KACHU//...
20	ESWYT20	SUP152/BAJ#1/3/KIRITATI//ATTILA*2/PASTOR/5/...
21	ESWYT21	WBLL1*2//BRAMBLING//WBLL1*2//BRAMBLING/3/2*BORL14
22	ESWYT22	KIRITATI/WBLL1//2*BLOUK#1*2//BRAMBLING/3/2*BORL14
23	ESWYT23	KACHU#1/3/T.DICOCCON P194624/AE.SQUARROSA (409)//BCN/...
24	ESWYT24	BAJ #1/3/SUP152//WBLL1*2//BRAMBLING
25	ESWYT25	TACUPETO F2001/BRSMBLING//KACHU/8/REH/HARE//2*BCN//3/...
26	ESWYT 26	BORL14/4/BAJ #1/3/KIRITATI//ATTILA*2/PASTOR
27	ESWYT 27	MUTUS/ROLF07//MUCUY
28	ESWYT 28	MUTUS/AKURI/SUP152/BAJ #1
29	ESWYT 29	BAJ #/TECUE#1//MUTUS*2/TECUE#1
30	ESWYT 30	KINGBIRD #1//INQALAB 91*2/TUKURU/3/BECARD/FRNCLN
31	ESWYT 31	SUP152/BAJ #1/3/KACHU//WBLL1*2//BRAMBLING
32	ESWYT 32	WBLL4/KUKUNA//WBLL1/3/WBLL1*2//BRAMBLING/4/BECARD/FRNCL
33	ESWYT 33	BECARD/QUAIU #1//ONIX/KBIRD
34	ESWYT 34	KACHU/BECARD//WBLL1*2//BRAMBLING/3/FRNCLN*/TECUE#1
35	ESWYT 35	OASIS/SKAUZ//4*BCN*2/3/PASTOR/4/HEILO/5PAURAQ/6/...
36	ESWYT 36	CIR016/2*BORL14
37	ESWYT 37	BORL14*2/3/KBIRD//WBLL1*2//KURUKU
38	ESWYT 38	BPORL14*2//KFA/2*KACHU
39	ESWYT 39	BORL14*2//KFA/2*KACHU
40	ESWYT 40	BORL14*2//BECARD/QUAIU #1
41	ESWYT 41	CNO79//PF70354/MUS/3/PASOR/4/BAV92*2/5/HAR311/6/...
42	ESWYT 42	FIFTIS*2/3/ATTILA*2/PBW65*2//MURGA
43	ESWYT 43	SUP152/BLOUK #1*2/4/TUKURU//BAV92/RAYON*2/3/KIRITATI
44	ESWYT 44	NADI*2/3/MUTUS/AKURI #1//MUTUS
45	ESWYT 45	KACHU//WBLL1*2//BRAMBLING*2/3/KACHU/KIRITATI
46	ESWYT 46	KACHU//WBLL1*2/3/KACHU/KIRITATI
47	ESWYT 47	ONIX/KBIRD//BORL14/3/ONIX/KBIRD
48	ESWYT 48	STLN/MUNAL#1//2*BORL14
49	ESWYT 49	WBLL1*2//BRAMBLING//CHYAK*2/3/KINGBIRD #1//INQALAB 91*2/..
50	ESWYT 50	FRET2*2//BRAMBLING//BECARD/3/WBLL1*2//BRAMBLING*2/4/...

Table 2. Analysis of Variance (ANOVA) for the nine grain yield attributing characters in wheat during 2018-19

Sources of variation	df	Mean sum of squares								
		PH	DF	GPS	AL	SPL	TM	TGW	BM	GY
Replication	1	0.0001	0.00292	0.00053	0.00436	0.00084	1.11936	0.00058	0.056	0.017
Genotype	49	0.0057**	0.0018**	0.0359**	0.024**	0.014**	0.0431*	0.008**	0.059**	0.141**
Error	49	0.00023	0.0003	0.00128	0.00065	0.00027	0.02284	0.00007	0.018	0.0345
Total	99	0.00297	0.00111	0.01841	0.01231	0.00722	0.04398	0.00404	0.039	0.087

*Significant at 5% probability level, **Significant at 1% probability level; PH = Plant height, DF = Days to 50 % Heading, GPS = Grains/spike, AL = Awn length, SPL= Spike length, TM= Tillers/metre, TGW= 1000 grain weight, BM = Biomass/metre and GY= Grain yield/metre

Table 3. Two-way ANOVA for chlorophyll index value of 50 wheat genotypes

Source	df	MSS
Replication	1	1036.8
Genotype	49	1101.78**
GS	3	43884.2**
Genotype×GS	147	138.2
Error	199	150.5

**Significant at 1% probability level

Table 4. Two-way ANOVA for disease severity (%)

Source	df	MSS
Replication	1	4.41
Genotype	49	232.18**
GS	3	7662.17**
Genotype×GS	147	96.89**
Error	199	36.30

**Significant at 1% probability level

Table 5. Genotypic correlation between the 11 grain yield attributing characters and spot blotch incidence (AUDPC) in wheat

Characters	DF 50%	GPS	AL	SPL	TM	TGW	BM	CI	AUDPC	GY
PH	-0.044	0.388**	0.199	0.396**	-0.082	-0.038	0.471**	0.332**	-0.137	0.428**
DF 50%		0.175	-0.235	0.065	0.190	-0.241	-0.224	0.381**	-0.137	-0.153
GPS			0.215	0.559**	0.144	0.253*	0.515**	0.399**	0.146	0.534**
AL				0.294*	-0.034	0.035	0.159	-0.149	0.228	0.180
SPL					0.146	0.274*	0.205	0.102	0.066	0.277*
TM						-0.372	0.366**	-0.126	0.335**	0.072
TGW							0.161	0.018	0.162	0.277*
BM								0.325	0.118	0.835**
CI									-0.274	0.146
AUDPC										-0.022

*significant at 5% probability level, **significant at 1% probability level; ESWTY=Elite Selection Wheat Yield trail, C.V.%= Coefficient of variation, C.D.(5%)= Critical Difference, PH= Plant height (cm), DF 50%= Days to 50 % Heading, GPS= Grains per spike, AL = Awn length, SPL= Spike length (cm), TM= Tillers per metre, TGW= Test weight in (g), BM= Bio mass per metre (g), CI = Chlorophyll Index, AUDPC= Area under disease progress curve and GYMP= Grain yield (g)

with grain yield/metre. Grains per spike was positively associated with five characters namely, spike length, 1000 grain weight, biomass/metre and chlorophyll index and grain yield/metre. Awn length was positively associated with only spike length (0.294). Spike length was found to be positively associated with test weight (0.274 g) along with grain yield/metre (0.277). Tillers/metre was found to be positively associated with biomass/metre (0.366) and AUDPC (0.335), but not with grain yield/metre. The correlation of physiological character like chlorophyll index was lower and negative (-0.274) with AUDPC and was higher and positive (0.147) with grain yield/metre, suggesting their possible application in screening for spot blotch tolerant wheat genotypes (Rosyara *et al.*, 2010)

The path analysis (Table 6) revealed that the highest direct effect on grain yield/metre was exhibited by biomass/metre (1.508) which also exhibited positive correlation with grain yield/metre (0.836). This indicated that improvement in biomass/metre would lead to direct increment in grain yield/metre. Although plant height had low direct effect on grain yield/metre (-0.258) but it had positive association with grain yield/metre (0.427) due to its very high indirect effect via biomass/metre (0.710). Grains/spike showed very low direct effect on grain yield/metre (0.062) although it had positive association with grain yield/metre (0.532) due to its very high indirect effect via biomass/metre (0.776). The character spike length had a low direct effect on grain yield/metre (0.280) but significant association with grain yield/metre (0.277) due to its high indirect effect via biomass/metre (0.309). The character 1000 grain weight had a low and negative direct effect on grain yield/metre (-0.234) but a positive association with grain yield/metre (0.277), due to its higher indirect effect via tillers/metre (0.292) and biomass/metre (0.243). Similar observations were reported by Sharma *et al.* (2004) and Duveiller *et*

al. (2005) regarding the relationship of grain yield/metre and 1000 grain weight with spot blotch incidence and the variability in association of physiological characters of wheat genotypes, was attributed to the differences in biomass yield, harvest index, tillering capacity, kernels/spike and 1000 grain weight. Hence, emphasis may be laid on the characters biomass/metre, grains/spike, plant height, spike length and 1000 grain weight for the improvement of grain yield/metre, as these five characters were positively correlated with grain yield/metre and with higher direct effect or indirect effect via other characters. An interesting finding here was that the biomass/metre was directly influencing grain yield/metre (Devesh *et al.*, 2021) due to its high direct effect and also assisting other characters like plant height, grains/spike, spike length and test weight to neutralise their lower direct effects, which ultimately resulted in their positive association with grain yield/metre (Table 6). Hence, emphasis on biomass/metre needs to be laid for the wheat genotypes under present study for development of superior high yielding genotypes with tolerance to spot blotch. Further although non-significant, the correlation between biomass/metre and chlorophyll index (0.325) was higher than that between biomass/metre and AUDPC (0.118) indicating that greater chlorophyll index or chlorophyll content in the wheat genotypes reduced the effect of spot blotch infection on grain yield (Rosyara *et al.*, 2007). In certain crops like groundnut chlorophyll index declines abruptly at post flowering stage (Maheswari *et al.*, 2019). Hence wheat genotypes which have a stay green feature are more resistant to spot blotch. The residual effect of path analysis was 0.178 which was not substantially low which indicated that the present set of eleven characters are not sufficient to explain the total diversity of the fifty wheat genotypes. Some more characters needed to have been included to account for total diversity.

Table 6. Genotypic path coefficient analysis depicting the direct (diagonal) and indirect (off diagonal) effects of the characters on grain yield/metre in wheat

Characters	PH	DF 50%	GPS	AL	SPL	TM	TGW	BM	CI	AUDPC	Correlation with grain yield/metre
PH	-0.258	-0.019	0.024	-0.020	0.111	0.064	0.009	0.710	-0.199	0.006	0.428**
DF 50%	0.0113	0.436	0.011	0.023	0.018	-0.149	0.057	-0.338	-0.228	0.006	-0.153
GPS	-0.100	0.077	0.062	-0.021	0.157	-0.113	-0.059	0.776	-0.239	-0.006	0.534**
AL	-0.051	-0.103	0.013	-0.099	0.082	0.027	-0.008	0.240	0.089	-0.010	0.180
SPL	-0.102	0.028	0.034	-0.029	0.280	-0.115	-0.064	0.309	-0.061	-0.003	0.277*
TM	0.0211	0.083	0.009	0.003	0.041	-0.786	0.087	0.552	0.076	-0.014	0.072
TGW	0.010	-0.105	0.016	-0.004	0.077	0.292	-0.234	0.243	-0.011	-0.007	0.277*
BM	-0.122	-0.098	0.032	-0.016	0.057	-0.288	-0.038	1.508	-0.195	-0.005	0.835**
CI	-0.086	0.166	0.025	0.015	0.029	0.099	-0.004	0.490	-0.599	0.011	0.146
AUDPC	0.036	-0.060	0.009	-0.023	0.018	-0.264	-0.038	0.178	0.164	-0.042	-0.022

*Significant at 5% probability level, **Significant at 1% probability level; Residual Effect = 0.178; PH = Plant height, DF 50%= Days to 50 % Heading, GPS= Grains/spike, AL = Awn length, SPL= Spike length, TM = Tillers/metre, TGW = 1000 grain weight, BM = Bio mass/metre, CI = Chlorophyll Index, AUDPC = Area under disease progress curve, GY = Grain yield/metre

Table 7. Summary of the contribution of the principal components to variability

Components	Eigen Value	Percent of cumulative variance	Total variance
PC1	2.92	26.54	26.54
PC2	1.70	15.42	41.96
PC3	1.36	12.33	54.29
PC4	1.20	10.88	65.17
PC5	1.07	9.69	74.86
PC6	0.70	6.40	81.25
PC7	0.59	5.35	86.60
PC8	0.56	5.09	91.69
PC9	0.38	3.43	95.12
PC10	0.28	2.55	97.67
PC11	0.26	2.33	100.00

Principal components for spot blotch resistance in wheat genotypes were reported by Eisa *et al.* (2013), Meena *et al.* (2014), Nitish *et al.* (2014), Gupt *et al.* (2021), Bainsla *et al.* (2020) and Ahirwar *et al.* (2020). The ten characters were rearranged into 11 principal components among which the principal component 1 (PC 1), PC 2, PC 3, PC 4, and PC 5 expressed eigen value greater than one (eigen > 1). The first five PC's exhibiting the eigen value more than unity is also reported by Meena *et al.*, 2014. These principal components accounted for 74.86 % cumulative proportion of variance (Table 7). Among them PC 1 and PC 2 accounted for 26.54% and 15.42% variance individually, respectively. The results indicated

that effective contributing traits in PC1 and PC2 have the significant role in diversification of genotypes and selection may be possible based on these characters for future breeding programmes. Relationship among the contributing characters in PCA is graphically represented by the PCA-Variable plot (Fig. 1). The variable plots on the basis of the position of the characters, displayed positive association among the characters chlorophyll index, plant height, grains/spike, spike length, grain yield/metre and biomass/metre, while days to 50% heading showed negative association with grain yield/metre, 1000 grain weight, tillers/metre, awn length and AUDPC. Similar reports of correlation positive correlation between plant

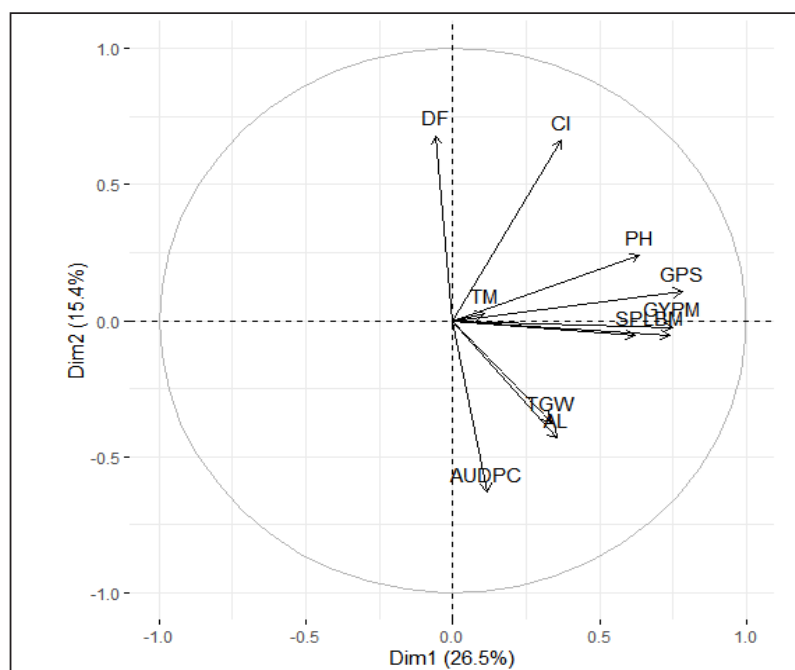


Fig. 1. Variable plots showing the relationship among the different characters

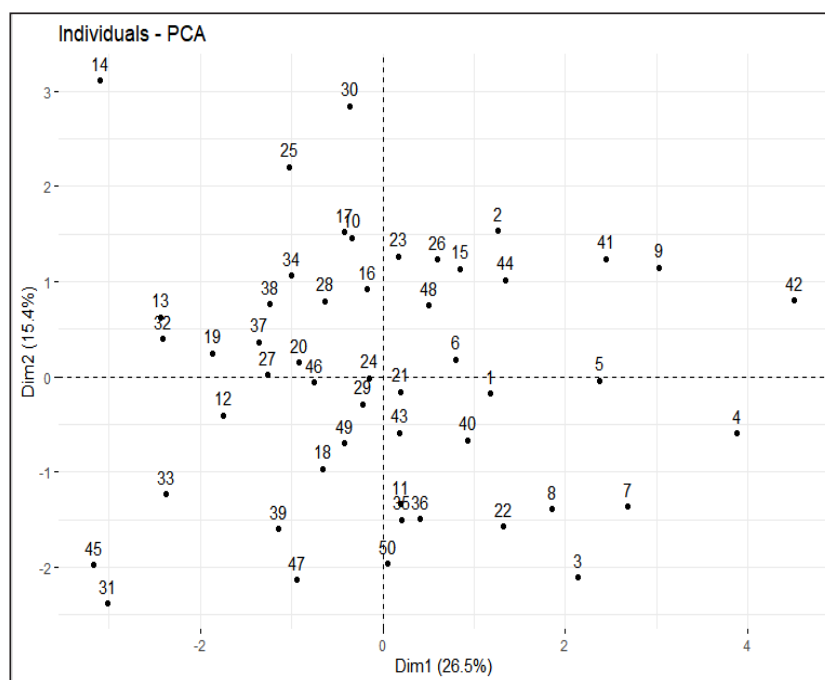


Fig. 2. Individual PCA plot showing the diversity of wheat genotypes based on the yield attributing characters and spot blotch incidence

height, grain yield and biomass was observed by Meena *et al.* (2014). Grouping of 1000 grain weight and AUDPC was reported by Gupt *et al.*, 2021. Similarly, negative association of days to 50% flowering with AUDPC is reported by Ahirwar *et al.* (2020). Individual PCA plot (Fig. 2) on the basis of uniform scattering and distribution of the genotypes, showed that the wheat population in the present study has sufficient divergence with respect to the characters under consideration and which may further be helpful for selection of diverse parents for future hybridization programmes. With respect to both the plots, ESWYT-30 has a high influence on days to 50% flowering, ESWYT 48, ESWYT 15 and ESWYT 2 have a moderate to high influence on chlorophyll index. Genotypes such as ESWYT 41, ESWYT 9, ESWYT 5 and ESWYT 6 were highly influenced by plant height, grains/spike, grain yield, biomass/metre, spike length and slightly influenced by tillers/metre.

The presence of variability among the wheat genotypes under present study can be utilized in the selection of parents for hybridization programme for the improvement of yield and disease resistance. Emphasis on biomass/metre would be rewarding. The correlation between AUDPC and physiological traits emphasized that loss of chlorophyll was associated with high spot blotch disease incidence at later stages of crop growth. Individual PCA plot showed that the wheat population under present study had sufficient divergence with respect to the characters under study. The genotypes ESWYT 41, ESWYT 9, ESWYT 5 and ESWYT 6 showed an association with

grain yield and its attributes along with spot blotch disease resistance and therefore, these genotypes can be utilized for future wheat breeding programme for higher grain yield and spot blotch resistance.

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