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Research Article

Classification of wheat genotypes on the basis of morphological and physiological traits in combination with spot blotch resistance under terai sub-Himalayan region

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Abstract
The present study was carried out to evaluate variability among 50 diverse genotypes of wheat (*Triticum aestivum* L.*)* for yield attributes and biotic factor like spot blotch during 2018-19 *rabi* season. Observations were recorded for morpho-phenetic traits, physiological parameter and disease observations of spot blotch (*Bipolaris sorokiniana* (Sacc.) Shoem) was done at four crop growth stages viz. 85 DAS, 92 DAS, 99 DAS and 106 DAS. The mean value of chlorophyll index (CI) indicated gradual decline of CI with advancement in growth stages. Highest value of AUCIDC was shown by ESWYT-50 (128.33), while the lowest value was exhibited by ESWYT-25 (22.75). Mean value of disease severity in the different growth stages indicated gradual increase in disease severity along with advancement in growth stages. Correlation study among AUDPC, AUCIDC along with three morpho-phenotypic traits revealed significant and positive correlation between AUDPC and AUCIDC. The D^2 analysis distributed 50 wheat genotypes into six clusters. The genotypes having lower selection index values were ESWYT-36, ESWYT-40, ESWYT-22, ESWYT-35, ESWYT-18, ESWYT-10, and ESWYT-1, which were also distributed in different divergent clusters as per D^2 analysis. Thus, they could be used as spot blotch resistant genotypes with early flowering type along with high yield. All the traits exhibited low PCV and GCV values indicating the presence of common parents in the ancestry of the wheat genotypes.

Keywords: Wheat, chlorophyll index, selection index, variability, spot blotch disease

INTRODUCTION

India produces almost 15% of the world's wheat, making it the second-largest producer next to China. Wheat is cultivated in more than 30 million hectares in India, with a productivity of 3.5 t/ha and a total production of around 110 million tonnes. Since 1981, CIMMYT's (International Maize and wheat improvement centre) spring bread wheat breeding programme has included new elite lines intended for irrigated areas all around the world as part of

the elite spring wheat yield trial (ESWYT). The ESWYT are made up of the lines that did well with high and steady grain yields compared to checks in the fully irrigated trials in the chosen sites in South Asia and Obregon, Mexico, as well as lines that also had good to moderate drought and heat tolerance. It includes 50 lines that are dispersed globally each year and are aimed at irrigated wheat-growing regions with generally favourable temperatures during the main crop season, such as the north-western Gangetic Plains of South Asia, Egypt, north-western Mexico (Obregon), various spring wheat-growing regions of Turkey, Afghanistan, Iran, etc.

Although, West Bengal is not a major wheat growing state, the area under wheat is increasing day by day, despite several biotic and abiotic stresses which hamper its productivity. Among the major biotic stresses, spot blotch or foliar blight disease caused by *Bipolaris sorokiniana (Sacc.) Shoem* is a major disease which causes small dark brown lesions in the leaf which coagulates and extends very quickly in susceptible genotypes. The disease has a special significance in eastern Gangetic plains of South Asia that includes India, Nepal and Bangladesh (Sharma and Duveiller, 2004). The average yield losses due to spot blotch in India were reported to be 15.5 per cent (Dubin and Van Ginkel, 1991) and 17 per cent (Saari, 1998), even the grain yield losses ranging from 17.63-20 per cent under favourable conditions (Goel *et al.*, 2006). However, the yield loss may increase to 80% under heavy infestation (Joshi *et al.*, 2007). Terai region of West Bengal with a very high humidity along with shorter winter period is considered as a hot spot location for spot blotch (Kumar *et al.,* 2017). Sometimes, spot blotch is associated with leaf tip necrosis (LTN) as the LTN belongs to the same genomic region where the gene for spot blotch and leaf rust is present (Kumar *et al*., 2018). The resistance to spot blotch which is a "foliar fungal disease" is a must-have trait in all the wheat genotypes to be cultivated in North-Eastern Plain Zone ecology (Chattopadhyay *et al*., 2022). Breeding for resistance to this disease requires identification of donors. One of the solutions to this is the wheat breeding lines from CIMMYT, which have long been used as donor for enhancing resistance towards different diseases (Vasistha *et al*., 2017). Considering the above facts, the present investigation was undertaken with the objective to study the genetic divergence and variability in the ESWYT nursery wheat lines from CIMMYT, for quantitative traits related to grain yield and their classification on the basis of morphological and physiological traits along with biotic stress factor like resistance to spot blotch disease.

MATERIALS AND METHODS

The present study was conducted during the *rabi* season of 2018-19 at University Instructional Farm, Uttar Banga Krishi Vishwavidyalaya, Pundibari, Cooch Behar, West Bengal. The farm is situated at 26°19'86" N latitude, 89°23' 53" E longitude with an altitude of 43 m above the mean sea level. The experimental material comprised of 50 diverse ESWYT genotypes of wheat. The experiment was laid out in a randomized block design with two replications and morpho-phenetic data was recorded for the following nine traits *viz*., plant height (cm), days to 50% heading, grains per spike, awn length (cm), spike length (cm), tillers per metre, 1000 grain weight (g), biomass per metre (g) and grain yield per metre (g). The data was collected from five random samples selected from each plot in case of plant height, grains per spike, awn length and spike length, whereas tillers per metre, biomass per metre and grain yield per metre were recorded on per metre basis per replication. The days to heading was recorded on per plot basis per replication.

Physiological parameter 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 meter was used to record the chlorophyll index values. The laser guide lights were used to aim the meter 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 meter were taken 3 to 5 feet away from the canopy at either 45° or 90° angles of the meter in relation to the wheat canopy surface. The chlorophyll index value is considered only if the ambient light level is 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.

Area under Chlorophyll index decline curve (AUCIDC) was calculated as per following formula suggested by Rosyara *et al*. (2007):

$$AUCIDC = \Sigma\ 1/2\ (S_{i+1} – Si)\ d$$

Where,

S_i= Chlorophyll index value at the end of time 'i'

Si_{+1}= Chlorophyll index value at the end of time 'i+1'

d = Days interval between two observations

Disease observations for spot blotch was recorded 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). The first digit (D1) indicates disease progress in the canopy height from ground level; the second digit (D2) refers to measured severity based on diseased leaf area. Both D1 and D2 are scored on a scale of 1-9. Disease scoring was done at 65 DAS, 85 DAS, 95 DAS and 110 DAS. For each score, the percentage of disease severity is estimated based on the following formula:

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

To analyze the severity of the disease, Area Under

Disease Progress Curve (AUDPC) was calculated by using the following formula suggested by Wilcoxson *et al.* (1975). The AUDPC has no unit.

$$AUDPC = \sum 1/2 (X_i+1+X_i) d$$

where,

X_i+1 = Disease severity on 'i+1'th day

X_i = Disease severity on 'i'th day

d = Days interval between two observations

Genotypes were classified as resistant (R), moderately resistant (MR), moderately resistant to moderately susceptible (MR-MS), moderately susceptible (MS), moderately susceptible to susceptible (MS-S), susceptible (S), susceptible to highly susceptible (S-HS) and highly susceptible (HS) based on AUDPC value (Liatukas and Ruzgas , 2012). The AUDPC scale is as follows:

AUDPC value	Type of resistance
< 100.0	Resistant (R)
100.1-150.00	Moderately Resistant (MR)
150.1-200.00	MR-MS
200.1- 250.00	Moderately susceptible (MS)
250.1-300.00	MS-S
300.1-350.00	S
350.1-400.00	S-HS
> 400.00	Highly susceptible (HS)

To facilitate selection in the field condition, Selection Index (SI) was calculated as per the formula suggested by Duveiller and Sharma (2009):

SI = (AUDPC rank in ascending order) + (DHD rank in ascending order) + (TGW rank in descending order)

This index was calculated for each genotype, with entries with the lowest SI being more promising. This approach was shown to be effective in the selection process to identify improved progenies.

Heritability in broad sense (h_b^2) was computed as a ratio of genotypic variance to phenotypic variance (Allard, 1960). The expected genetic advance under selection for the different traits was estimated as suggested by Allard (1960). Genetic advance as percentage of mean for each trait was calculated as suggested by Johnson *et al.* (1955). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed following the method suggested by Burton and Devane (1953). The range of heritability and genetic advance as percentage of mean was classified as suggested by Johnson *et al.* (1955).

On preliminary analysis of data, it was found to be not following normal distribution. Hence the total data was subjected to arcsine transformation and subsequently the statistical analysis was done by using the softwares GENRES (1994), STAR (version 2.0.1, January 2014) and R-project version 3.5.

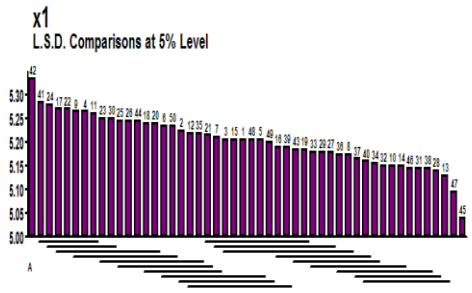
RESULTS AND DISCUSSION

The ANOVA for the 10 traits indicated significant differences between the genotypes for all the traits under study, which indicated that there was substantial variability among the wheat genotypes for those traits (**Table 1**). The mean values for the traits, indicated variability among the genotypes. The least square difference (LSD) comparison at 5% probability level gave a clear picture about the performance of the genotypes for the different traits (**Fig. 1**). The best performance for plant height was exhibited by the genotype ESWYT-42 (5.335) which differed significantly from all other genotypes. The result was in confirmation with the report of Hussain *et al.* (2012). Two genotypes namely ESWYT-14 (5.08) and ESWYT-30 (5.08) exhibited the highest days to heading which differed significantly from all other genotypes.

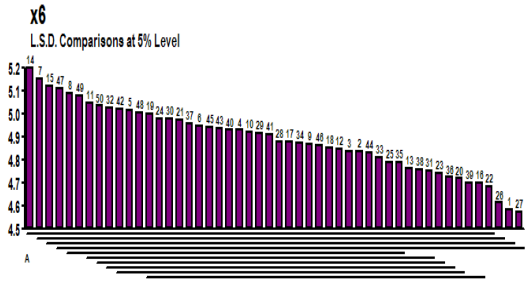
Table 1. Analysis of Variance for 9 traits in wheat (*Triticum aestivum* L.)

Traits	Sources of variation			
	Replication	Genotype	Error	Total
	df = 1	df = 49	df = 49	df = 99
Plant height (cm)	0.0001	0.0057**	0.00023	0.00297
Days to 50 % Heading	0.00292	0.0018**	0.0003	0.00111
Grains per spike	0.00053	0.0359**	0.00128	0.01841
Awn length (cm)	0.00436*	0.024**	0.00065	0.01231
Spike length (cm)	0.00084	0.014**	0.00027	0.00722
Tillers per meter	1.11936**	0.0431*	0.02284	0.04398
Test weight	0.00058**	0.008**	0.00007	0.00404
Biomass per metre (g)	0.056	0.059**	0.018	0.039
Grain yield per metre (g)	0.017	0.0141**	0.0345	0.087

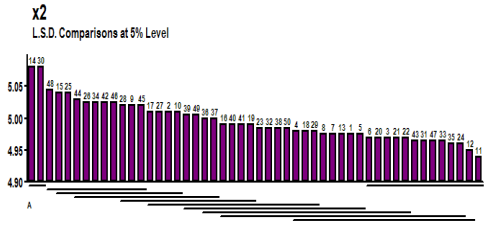
*Significant at 5% probability level, **Significant at 1% probability level; df = degrees of freedom



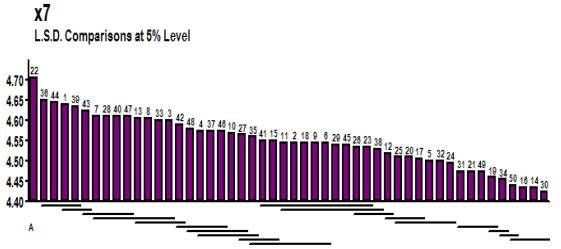
LSD comparison for Plant height



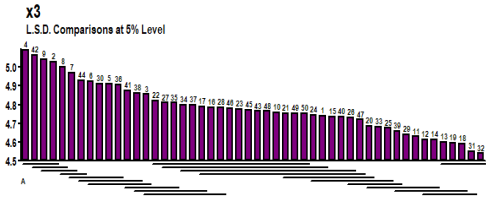
LSD comparison for Tillers per metre



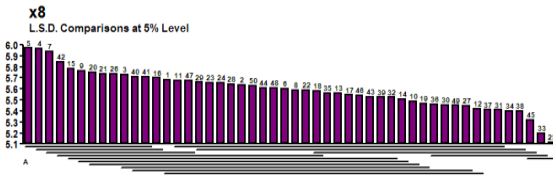
LSD comparison for Days to heading



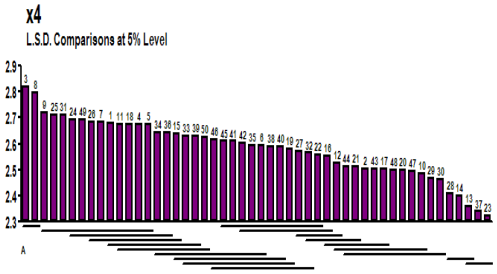
LSD comparison for Test weight



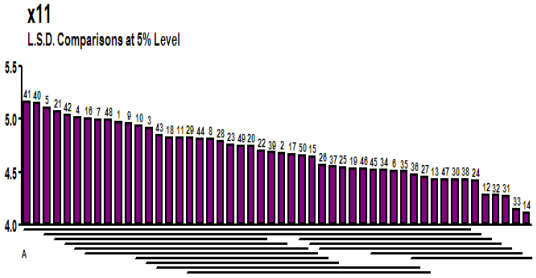
LSD comparison for Grains per spike



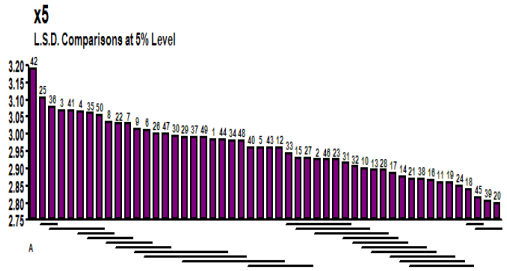
LSD comparison for Biomass per metre



LSD comparison for Awn length



LSD comparison for Grain yield per metre (g)



LSD comparison for Spike length

Fig. 1. The least square difference comparison of the performance of nine traits

The genotype ESWYT-11 (4.94) exhibited lowest days to heading. Similar diversity for days to maturity was reported by Anwar *et al.* (2009).

The genotypes exhibiting very high grains per spike were ESWYT-4 (5.090), ESWYT-42 (5.065), ESWYT-9 (5.04) and ESWYT-2 (5.03), which did not differ significantly from each other. These results are in conformity with Kashif and Khaliq (2006), who reported highest grains per spike and significant difference among the genotypes for grain weight per spike. Genotypes which showed high awn length were ESWYT-3 (2.82) and ESWYT-8 (2.795) which did not differ significantly from each other but differed significantly from all other genotypes. The genotype ESWYT-42 (3.19) exhibited the highest spike length and it differed significantly from all other genotypes. Similar results were reported by Anwar *et al.* (2009) and Hussain *et al.* (2012) who reported significant difference among genotypes for spike length. Nearly 47 genotypes [except ESWYT-26 (4.615), ESWYT-1 (4.585) and ESWYT-27 (4.575)] exhibited high performance for tillers per metre and they did not differ significantly from each other. The genotype ESWYT-22 (4.705) showed the highest test weight and it differed significantly from all other genotypes. Similar results were obtained by Anwar *et al.* (2009), Hussain *et al.* (2012) and Kalimullah *et al.* (2012), who found significant differences among wheat genotypes for 1000-grain weight. Twelve genotypes exhibited the highest biomass per metre and did not differ significantly from each other. Forty-four genotypes [except ESWYT-24 (4.42), ESWYT-12 (4.290), ESWYT-32 (94.28), ESWYT-31 (4.27), ESWYT-33 (4.115) and ESWYT-14 (4.1150)] exhibited high grain yield per metre and they did not differ significantly from each other. Highly significant differences among the wheat genotypes for high grain yield was reported by Kalimullah *et al.* (2012), Hussain *et al.* (2012) and Anwar *et al.* (2009).

Chlorophyll index (CI) studied at four different crop growth stages (85 DAS, 92 DAS, 99 DAS and 106 DAS) showed significant difference among the genotypes as well as growth stages. However, genotype × growth stage interaction was found non-significant (**Table 2**). The mean value of chlorophyll index indicated gradual decline of its value with advancement in growth stages (**Table 3**). This might be due to the gradual decay in chlorophyll pigmentation with the maturity of the crop. However, the rate of decrease in chlorophyll index value was found highly variable among the wheat genotypes in present study. In order to quantify the rate in decrease of CI value, Area Under Chlorophyll Index Decline Curve (AUCIDC) was estimated by formula suggested by Rosyara *et al.* (2007). Highest value of AUCIDC was exhibited by ESWYT-50 (128.33) while lowest value was shown by ESWYT-25 (22.75). Similar result was reported by Rosyara *et al.* (2010) where chlorophyll content decline was found significant among genotypes after anthesis in terms of AUSDC (Area Under SPAD Decline Curve) value where chlorophyll content was measured by SPAD reading.

Spot blotch scoring was done at four crop growth stages in double-digit scale (00-99) developed by Saari and Prescott (1975). Disease severity and AUDPC (Area Under Disease Progress Curve) was calculated as suggested by Wilcoxson *et al.* (1975). Analysis of variance revealed a highly significant effect of genotype as well as growth stages on disease severity (%)

Table 2. Two-way ANOVA of Chlorophyll index of 50 wheat genotypes

Source	df	MSS	
		Chlorophyll index	disease severity (%)
Replication	1	1036.8	4.41
Genotype	49	1101.78**	232.18**
GS	3	43884.2**	7662.17**
Genotype x GS	147	138.2	96.89**
Error	199	150.5	36.30

*Significant at 5% probability level, **Significant at 1% probability level

Table 3. Mean Chlorophyll index values of 50 wheat genotypes at different growth stages

DAS	Chlorophyll index		Disease severity (%)	
	Mean	Range	Mean	Range
85 DAS	109.46	85-151	4.27	0.00-9.88
92 DAS	95.12	68-147	10.02	1.85-25.93
99 DAS	77.0	42-111	18.51	5.56-40.12
106 DAS	61.46	20-98	23.96	6.17-56.17

Table 4. Genotypic mean value for disease severity (%) [DS (%)], AUDPC and AUCIDC

Genotype	DS (%)	AUDPC	AUCIDC	Resistance
ESWYT-1	8.33	179.32	52.50	MR-MS
ESWYT-2	16.51	347.84	70.58	S
ESWYT-3	19.29	429.94	71.75	HS
ESWYT-4	16.36	365.12	47.25	S-HS
ESWYT-5	14.35	272.22	71.17	MS-S
ESWYT-6	9.88	229.01	35.00	MS
ESWYT-7	12.65	257.10	49.58	MS-S
ESWYT-8	15.74	337.04	58.33	S
ESWYT-9	14.66	272.22	68.83	MS-S
ESWYT-10	10.34	216.05	33.25	MS
ESWYT-11	15.90	326.23	38.50	S
ESWYT-12	11.88	270.06	26.25	MS-S
ESWYT-13	5.25	114.51	51.33	MR
ESWYT-14	8.64	196.60	42.58	MR-MS
ESWYT-15	18.21	414.81	64.17	HS
ESWYT-16	9.10	200.93	72.92	MS
ESWYT-17	8.33	162.04	49.58	MR-MS
ESWYT-18	14.2	324.07	44.92	S
ESWYT-19	16.98	352.16	43.75	S-HS
ESWYT-20	7.10	164.20	46.08	MR
ESWYT-21	13.89	270.06	42.58	MS-S
ESWYT-22	18.67	427.78	70.58	HS
ESWYT-23	14.66	330.56	45.50	S
ESWYT-24	13.58	259.26	44.33	MS-S
ESWYT-25	3.86	86.42	22.75	R
ESWYT-26	8.8	187.96	34.42	MR-MS
ESWYT-27	11.42	235.49	46.67	MS
ESWYT-28	10.65	209.57	49.00	MS
ESWYT-29	16.36	360.8	72.33	S-HS
ESWYT-30	16.98	306.79	56.00	S
ESWYT-31	17.44	367.28	75.25	S-HS
ESWYT-32	9.10	196.6	29.75	MR-MS
ESWYT-33	10.96	270.06	56.00	MS-S
ESWYT-34	11.73	263.58	60.67	MS-S
ESWYT-35	19.29	391.05	71.75	S-HS
ESWYT-36	22.99	451.54	70.58	HS
ESWYT-37	10.96	226.85	65.91	MS
ESWYT-38	11.27	231.17	31.50	MS
ESWYT-39	22.84	518.52	75.25	HS
ESWYT-40	14.66	317.59	51.91	S
ESWYT-41	5.40	118.83	30.33	MR
ESWYT-42	16.51	330.56	91.00	S
ESWYT-43	14.2	300.31	49.58	S
ESWYT-44	10.49	231.17	49.58	MS
ESWYT-45	24.54	496.91	81.67	HS
ESWYT-46	18.67	350.00	47.83	S
ESWYT-47	26.08	505.56	72.92	HS
ESWYT-48	15.74	300.31	66.50	S
ESWYT-49	14.04	326.23	71.17	S
ESWYT-50	30.09	637.35	128.33	HS
S.Em (±)	2.13	41.03	9.15	
L.S.D. (P=0.05)	5.94	116.614	26.00	

(**Table 2**). Interaction between genotype and growth stages was also found significant. Mean value of severity among different growth stages indicated gradual increase in severity along with increase in growth stages (**Table 3**). This is obvious in spot blotch resistance where disease progresses rapidly with the advancement in maturity of crop especially in susceptible genotypes (Joshi *et al.,* 2007 and Duveiller *et al.,* 2005).

To identify the progress of disease along with growth stages, AUDPC value was calculated for each genotype and they were classified based on resistance reaction. Among the 50 genotypes eight genotypes were grouped as HS, five genotypes as S-HS, 12 genotypes as S, eight genotypes as MS-S, eight genotypes as MS, five genotypes as MR-MS, three as MR and one as R (**Table 4**). The only resistant (R) genotype found was ESWYT-25 with a AUDPC value of 86.42.

Correlation study among AUDPC, AUCIDC along with three morpho-phenotypic traits *viz.,* days to 50% heading (DF), test weight (TGW) and plant height (PH) revealed significant and positive correlation between AUDPC and AUCIDC (**Table 5**), which indicated that loss in chlorophyll was associated with high disease infestation at later stages of crop growth. Similar findings were reported by Rosyara *et al.* (2007), where resistant genotypes showed lower reduction in chlorophyll content than susceptible one.

Selection Index (SI) was calculated to facilitate selection in field condition and also a good concurrence was found between assessment of phenotypic resistance, yield components and earliness as per the formula suggested by Duveiller and Sharma **(**2009). The full SI values (**Table 7**) revealed that the genotypes having lower SI values were ESWYT-36, ESWYT-40, ESWYT-22, ESWYT-35, ESWYT-18, ESWYT-10, and ESWYT-1. Thus, they could be selected as resistant genotypes with early flowering type along with high yield. The genotype ESWYT-25 was found to be highly resistant (**Table 6**), but it had higher selection index which made it unsuitable to be selected for direct use, but it could be used as a disease resistance donor parent. Similar observations were recorded earlier by Kumari *et al.* (2018), when they identified a wheat germplasm accession line IC443669 to be specifically adapted to the present location of investigation at Cooch Behar district of West Bengal.

The arcsine transformed data for the eleven traits namely PH, DF, GPS, AL, SPL, TM, TGW, BM, CI, AUDPC and GYPM were used for further analysis for the estimation of genetic parameters, correlation study and path analysis. The values of coefficient of variation (CV), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) indicated very low variability among the wheat genotypes under the present study, probably due to the very close ancestry of the ESWYT genotypes (**Table 7**). All the PCV and GCV values observed to under low category as per the scale of Sivasubramanian and Madhavamenon (1973). For all the traits, it was found that PCV values were higher than GCV values but the difference between them was quite low, which indicated a lower environmental influence on the traits. Similar findings have been reported by Emmadishetty and Gurjar (2022). In case of broad sense heritability (h^2_b) most of the traits exhibited high heritability except tillers per metre (0.3073), biomass per metre (0.5425 g) and chlorophyll index (0.4788). Regarding genetic advance (GAM) as percentage of mean, nearly all the traits exhibited low values except AUDPC (10.543) which was moderate in nature. As most of the traits exhibited high heritability accompanied with low genetic advance, it could be concluded that non-additive gene action was preponderant and selection for such traits may not be rewarding. The exception was the AUDPC with high heritability and moderate genetic advance, which indicated that the heritability for this trait was due to additive gene effect and selection may be effective. Similar finding regarding significant contribution of additive gene effects to spot blotch resistance was reported by Goel *et al.* (2005), Sharma *et al.* (2003) and Khan *et al.* (2010).

The application of D^2-statistics is a time-tested method to measure the genetic divergence in wheat (Chandra, 1977; Jaradat, 1991; Lee and Kaltsikes,1973). When the wheat genotypes are to be treated as parents in a crossing programme, then genetic divergence along

Table 5. Correlation table among AUDPC, AUCIDC and morphological traits

	DF	TGW	PH	AUDPC	AUCIDC
DF	1.00				
TGW	-0.2	1.00			
PH	-0.019	-0.045	1.00		
AUDPC	-0.14	0.145	-0.15	1.00	
AUCIDC	0.018	0.029	-0.053	0.72**	1.00

**Significant at 1% probability level; DF = Days to heading, TGW = 1000 grain weight, PH = Plant height, AUDPC = Area under disease progress curve; AUCIDC = Area under Chlorophyll index decline curve

Table 6. Selection index (SI) of 50 wheat genotypes as per Duveiller and Sharma (2009)

Genotype	AUDPC rank* (X)	DF rank* (Y)	TGW rank** (Z)	SI (X+Y+Z)
ESWYT-1	25	11	3	**39**
ESWYT-2	13	12	28	53
ESWYT-3	41	24	14	79
ESWYT-4	17	35	19	71
ESWYT-5	20	31	39	90
ESWYT-6	1	33	25	59
ESWYT-7	26	43	9	78
ESWYT-8	14	47	12	73
ESWYT-9	32	3	27	62
ESWYT-10	16	6	20	**42**
ESWYT-11	28	20	29	77
ESWYT-12	10	21	35	66
ESWYT-13	37	22	11	70
ESWYT-14	6	1	49	56
ESWYT-15	38	5	23	66
ESWYT-16	44	7	48	99
ESWYT-17	27	8	40	75
ESWYT-18	7	13	25	**45**
ESWYT-19	24	29	46	99
ESWYT-20	34	4	36	74
ESWYT-21	12	18	43	73
ESWYT-22	21	23	1	**45**
ESWYT-23	33	32	33	98
ESWYT-24	9	38	41	88
ESWYT-25	5	50	37	92
ESWYT-26	48	16	32	96
ESWYT-27	43	19	21	83
ESWYT-28	30	40	8	78
ESWYT-29	40	41	30	111
ESWYT-30	18	36	50	104
ESWYT-31	11	37	44	92
ESWYT-32	49	39	38	126
ESWYT-33	23	49	32	104
ESWYT-34	42	2	45	89
ESWYT-35	8	10	22	**40**
ESWYT-36	2	17	2	**21**
ESWYT-37	46	27	17	90
ESWYT-38	19	28	34	81
ESWYT-39	29	45	5	79
ESWYT-40	4	9	9	**22**
ESWYT-41	31	26	24	81
ESWYT-42	35	34	15	84
ESWYT-43	15	42	6	63
ESWYT-44	22	46	3	71
ESWYT-45	3	44	30	77
ESWYT-46	36	15	18	69
ESWYT-47	45	25	7	77
ESWYT-48	47	48	16	111
ESWYT-49	39	14	42	95
ESWYT-50	50	30	47	127

*Rank in ascending order, **Rank in descending order; AUDPC Rank = Rank for area under disease progress curve; DF rank = Rank for days to heading; SI = Selection index.

Table 7. Genetic parameters for nine morpho-phenetic traits of wheat

S. No.	Trait	Mean	Range	CV	PCV	GCV	h^2_{bs}	GAM (%)
1	PH	90.98 (5.203)	104.3-77.3	0.291	1.0577	1.0137	0.9185	2.0013
2	DF	73.80 (4.995)	70-80	0.344	0.6623	0.5604	0.716	0.9769
3	GPS	60.24 (4.783)	35.8-45	0.747	2.8515	2.7499	0.93	5.4627
4	AL	6.62 (2.583)	3.5-4.9	0.991	4.3087	4.1932	0.9471	8.4066
5	SPL	9.60 (2.957)	8.2-12.3	0.555	2.8863	2.8316	0.9624	5.7223
6	TM	67.99 (4.891)	38.5-111	3.091	3.7149	2.0593	0.3073	2.3517
7	TGW	47.34 (4.549)	41.7-55.5	0.186	1.4023	1.3941	0.9883	2.8549
8	GY	56.58 (4.687)	26.83-94.0	3.962	6.3241	4.9309	0.6079	7.9199
9	BM	136.58 (5.591)	72.04-215.51	2.381	3.5184	2.5914	0.5425	3.9319

Values in parenthesis indicate the Arcsine transformed values; PH= Plant height (cm), DF 50%= Days to 50 % Heading, GPS= Grains per spike, AL = Awn length (cm), SPL= Spike length (cm), TM= Tillers per metre, TGW= Test weight (g), GY= Grain yield per metre (g), BM= Bio mass per metre (g). PCV= Phenotypic correlation Coefficient, GCV= Genotypic Correlation coefficient, h^2_{bs} = Heritability (broad sense) and GAM (%) = Genetic advance as percentage of mean.

with the parental performance can help in predicting the progeny performance (Cox and Murphy, 1990). Even in case of hybrid wheat breeding, information of genetic distance between heterotic groups is extremely important for which assessment of genetic diversity in the available wheat genotypic collection is very important (Boeven *et al.,* 2016). In the present study, the Chi-square test indicated that there was sufficient divergence in the wheat genotypes and hence D^2 analysis (Mahalanobis, 1936) was done. The 50 wheat genotypes were distributed into six clusters (**Table 8**). Cluster-I had the highest of 14 genotypes followed by cluster-V, cluster-II, cluster-III cluster-IV and cluster-VI which had 10, 9, 9, 7 and 1 genotypes, respectively. The distribution of genotypes into six different clusters on basis of D^2 analysis based on 11 traits indicated substantial genetic diversity present in the experimental material.

The average intra (diagonal) and inter (off-diagonal) cluster distance (**Table 9**) indicated that the maximum inter cluster distance was exhibited by the cluster-V and VI (855.65) followed by cluster-III and IV (742.92) which was closely followed by the inter cluster distance of cluster-I and VI (625.464), cluster IV and V (545.356) and cluster-II and V (508.761). This high inter cluster distance suggested that the wheat genotypes present in these clusters has a broad spectrum of genetic diversity and could be utilized in crossing programmes to isolate desirable transgressive segregants (Arya *et al.*, 2017). It was observed that Cluster-V and Cluster-VI revealed the maximum inter-cluster distance with all the other clusters, indicating the presence of high divergence in these groups. Cluster-V contained 10 genotypes whereas cluster-VI contained only one genotype (ESWYT-50) which was found to be highly susceptible to spot blotch (**Table 4**). For disease resistance, genotypes with low selection index are desirable. Therefore, ESWYT-36 (SI=21) with S-HS status is highly preferable to be crossed with any of the genotypes of other clusters. Similarly, ESWYT-1 (S.I = 39), ESWYT-10 (S.I = 42) and ESWYT-18 (S.I = 45) from cluster-I possess low S.I and MR-MS for disease. Also, all these genotypes come under the forty-four genotypes with high grain yield. Hence, crossing between ESWYT-36, ESWYT-1 and ESWYT-18 of cluster I, may be done to develop a high-yielding wheat genotype with moderate resistance to spot blotch disease. The genotype ESWYT-22 (SI=45) and ESWYT-40 (SI=22) from cluster III and ESWYT-35 (SI = 40) from cluster IV had a low SI with high grain yield but they were highly susceptible. The maximum intra cluster distance was exhibited by cluster-III (418.664) which was closely followed by cluster-V (396.483), indicating greater genetic divergence between the genotypes in these clusters. From the intra and inter cluster distance values, it was revealed that the genotypes from the most divergent clusters- V and VI would yield better genetic combination and would be rewarding in selection, when done appropriately for the specific traits.

The cluster mean for the 11 traits of the wheat genotypes are presented in **Table 10**. The difference in cluster means was exhibited by all the traits studied (Aashu *et al.,* 2022). The maximum contribution to genetic divergence was exhibited by 1000 grain weight (28.33%) which was closely followed by grain yield per metre (23.35%). Hence emphasis may be laid on these two traits for development of superior wheat genotypes. For the most divergent clusters-V and VI, it was observed that in cluster-V the value of test weight (4.59) was higher than the mean (4.549) whereas, the value for the test weight for cluster-VI (4.44) was lower than the mean (4.549). The grain yield per metre value for cluster-V (4.71) was higher than the mean value (4.687) and the grain yield per metre value for the cluster-VI (4.655) was lower than the mean value (4.687).

Table 8. Distribution of 50 wheat genotypes in different clusters

Cluster No.	Number of genotypes	Name of genotypes
I	14	ESWYT 1, ESWYT 2, ESWYT 3, ESWYT 4, ESWYT 5, ESWYT 6, ESWYT 7, ESWYT 8, ESWYT 9, ESWYT 10, ESWYT 11, ESWYT 13 and ESWYT 18
II	9	ESWYT 14, ESWYT 15, ESWYT 16, ESWYT 17, ESWYT 19, ESWYT 20, ESWYT 21, ESWYT 27 and ESWYT 46
III	9	ESWYT 22, ESWYT 23, ESWYT 24, ESWYT 25, ESWYT 26, ESWYT 28, ESWYT 29, ESWYT 40 and ESWYT 43
IV	7	ESWYT 30, ESWYT 31, ESWYT 32, ESWYT 33, ESWYT 34, ESWYT 35 and ESWYT 49
V	10	ESWYT 36, ESWYT 37, ESWYT 38, ESWYT 39, ESWYT 41, ESWYT 42, ESWYT 44, ESWYT 45, ESWYT 47 and ESWYT 48
VI	1	ESWYT 50

Table 9. Average intra (diagonal) and inter (off diagonal) cluster distance of 50 genotypes of wheat

Cluster No.	I	II	III	IV	V	VI
I	**324.131**	425.097	369.282	427.505	367.481	625.464
II		**217.793**	439.564	285.131	508.761	420.240
III			**418.664**	479.385	382.857	742.920
IV				**321.931**	545.356	315.062
V					**396.483**	855.650
VI						**0.000**

Table 10. Cluster mean for the traits of the wheat genotypes

Cluster No.	PH	DF	GPS	AL	SPL	TM	TGW	BM	CI	AUDPC	GYPM
I	5.214	4.979	4.84	2.634	2.968	4.908	4.568	5.686	5.155	6.276	4.806
II	5.198	5.009	4.728	2.542	2.882	4.893	4.501	5.608	5.11	6.188	4.641
III	5.217	4.993	4.741	2.55	2.968	4.831	4.574	5.588	5.154	6.213	4.736
IV	5.186	4.998	4.721	2.615	2.97	4.902	4.499	5.428	5.016	6.38	4.416
V	5.188	5.007	4.835	2.554	2.978	4.897	4.59	5.557	5.049	6.426	4.71
VI	5.235	4.985	4.755	2.625	3.055	5.035	4.44	5.63	4.735	7.145	4.655
Mean	**5.203**	**4.995**	**4.783**	**2.583**	**2.957**	**4.891**	**4.549**	**5.591**	**5.098**	**6.311**	**4.687**
Percentage contribution to Divergence	**2.6939**	**0.000**	**5.7959**	**10.0408**	**8.8163**	**0.000**	**28.3265**	**2.9388**	**12.4082**	**5.6327**	**23.3469**

ESWTY= Elite Selection Wheat Yield trail, PH= Plant height (cm), DF 50%= Days to 50 % Heading, GPS= Grains per spike, AL = Awn length, SPL= Spike length (cm), TM= Tillers per meter, TGW= 1000 grain weight (g), BM= Bio mass per meter (g), CI = Chlorophyll Index, AUDPC= Area under disease progress curve and GYMP= Grain Yield per Meter (g)

High variability was observed for the wheat genotypes to be utilized in the selection of parents for hybridization programme for the improvement of yield and disease resistance. Mean value of disease severity spread across different growth stages of plant growth, indicated gradual increase in severity along with increase in crop growth stages. This is mainly applicable in spot blotch resistance where the disease is found to progress with the advancement of maturity of the crop. Most of the traits exhibited high heritability with low genetic advance as percentage of mean indicating preponderance of non-additive gene action with AUDPC as the only exception, which was under additive gene control. The maximum contribution to genetic divergence was by test weight followed by grain yield per metre and so emphasis may be laid on these two traits for the development of superior yielding and spot blotch resistant wheat genotypes. The genotypes from the most divergent clusters V and VI would yield better genetic combination and would be rewarding in selection when done appropriately for the

specific traits. The highest direct effect on seed yield was exhibited by biomass per metre which indicated that an increment in this trait would result in increase in grain yield. The genotypes ESWYT-36, ESWYT-40, ESWYT-22, ESWYT-35, ESWYT-18, ESWYT-10 and ESWYT-1 with lower Selection Index (SI) values had greater genetic distance between them, due to which they were distributed in divergent clusters and can be selected as wheat genotypes resistant to spot blotch with higher yield and early flowering and can be used in crossing programmes accordingly.

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