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Genetic evaluation of spring wheat (*Triticum aestivum* L.) genotypes for yield and spot blotch resistance in Eastern Gangetic Plains of India

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An experiment was conducted to evaluate 49 spring wheat (*Triticum aestivum* L.) genotypes of diverse origin by estimating genetic parameters viz. variability, character association, path coefficient, cluster and principle component analysis (PCA) for yield and spot blotch disease resistance during 2011 -2012 and 2012 - 2013. Highest phenotypic coefficient of variation (PCV) was observed for area under disease progress curve (AUDPC) (29.15%), plot yield (12.94%) and 1000-kernel weight (11.63%). The highest plot yield (g) was observed in genotypes WH1132 and WH 1131. Grain yield per plot (g) was significantly and positively associated with the 1000-kernel weight (g) (0.82*) and grain per spike (number) (0.79*). Path-coefficient analysis expressed that the maximum positive direct effect on yield showed by grain per spike (number) observed via 1000-kernel weight (g) and days to 75% flowering (days) while negative direct effects showed by 1000-kernel weight (g), AUDPC, days to maturity (days) and plant height (cm). All the 49 spring wheat genotypes were grouped into six distinct clusters. The genotypes of cluster II represented higher yield and disease resistance potential. Out of the major four principal components (PCs), three principal components (PC1, PC2 and PC3) accounted for 79.86% with proportionate values of 45.90, 18.73 and 15.23%, respectively. The third principal component has high positive component value for the days to 75% flowering, the plant height, the AUDPC and the 1000-kernel weight. The breeding objective of the present experiment is to identify genetically diverse wheat genotypes for developing high yielding and disease resistant variety for Eastern Gangetic Plains of India.

Key words: AUDPC, cluster analysis, dendrogram, genetic advance, yield, PCA and PCV.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the largest grown and second prominent produced cereal crops worldwide after maize (*Zea mays* L.) with 697.8 million tonnes every year (Anonymous, 2013; Velu and Singh, 2013). Global food production might be increase at least 70% by 2050 when global population may likely to reach 9 billion

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Abbreviations: AUDPC, Area under disease progress curve; **PCA,** principle component analysis.

(Anonymous, 2008). In India, wheat production and productivity was 92.46 million tonnes and 3.12 t/ha, respectively, in 2012 to 2013 which reveal decline trend in comparison with previous year (Anonymous, 2013). Several biotic and abiotic stresses such as spot blotch, leaf rust, terminal heat stress and drought stress have adverse impact on wheat productivity in the eastern regions of South Asia especially Eastern Gangetic Plains of India (Joshi et al., 2007). However, spot blotch is most serious constrain for the wheat production caused by *Cochliobolus sativus* (Ito and Kurib.) Drechsler ex Dastur [anamorph: *Bipolaris sorokiniana* (Sacc.) Shoem results substantial yield loss (Joshi et al., 2007). Present resistance potential against spot blotch disease in high yielded wheat genotypes especially in warmer humid regions of South Asia is still unsatisfactory and need enormous research (Sharma and Duveiller, 2006; Joshi et al., 2007; Meena et al., 2014). Significant negative correlations were observed between spot blotch resistance and some of yield components such as grain yield, 1000-kernel weight, biomass yield, harvest index and grain fill duration (Sharma et al., 1997a).

Under the climate changing scenario, it is a major threat to breeders to sustain food availability for growing population (Kumar et al., 2011). Estimation of heritability and genetic advance is prerequisite for a breeder which helps in understanding the magnitude, nature and interaction of genotype and environmental variation for particular traits. Character association reveals cause of relationship between two variables (Meena et al., 2014). The information obtained by path coefficient analysis helps in indirect selection for genetic improvement of yield because direct selection is not effective for low heritable trait like yield. The cluster analysis and PCA are the basic genetic diversity analysis tools with some relative differences with each other. Primary purpose of cluster analysis is to group individuals based on the characteristics so that individuals with similar characteristics are mathematically collected into the same cluster (Hair et al., 1995; Meena et al., 2014). Determination of optimal and acceptable clusters is another important aspect in cluster analysis. PCA is basically used to sort out the data to establish association between two or more characters by linear transformation of the original variables into a new group of uncorrelated variables regarded as principal components (PCs) (Wiley, 1981). The main objective of present experiment was to acquire information relevant to genetic variability for each trait, heritability, genetic advance, character association, path analysis and genetic diversity. Based on the information, we can propose promising genotypes for further research programmes.

MATERIALS AND METHODS

The present experiment was conducted at the Bihar Agricultural College (BAC) farm, Sabour, Bhagalpur (Bihar), India during Rabi 2011 to 2012 and 2012 to 2013 utilizing 49 genotypes (Table 1) in simple lattice design with two replications. The experimental site was situated at N 25° 15'and 84° 4' E at the 45.75 m above sea level. Soil pH ranged from 6.5 to 7.5, and the average rainfall in this area is about 1150 mm and average relative humidity is 70% as per meteorological data provided by agro-meteorological observatory, BAC Sabour. Most of the precipitation is usually received during the South-West monsoon season. The 49 spring wheat genotypes were grown under simple lattice design (7 x 7). Gross plot size of each treatment (genotype) was 6.0 m row length and six rows at 23 cm apart (6.0 x 1.38 m). Net plot size of each treatment was 6.0 m row length and four rows excluding border row (6.0 x 0.92 m). Observations were recorded for seven quantitative traits viz. days to 75% flowering (days), days to maturity (days), plant height (cm), 1000-kernel weight. (g), grain per spike (number), area under disease progress curve (AUDPC value) and plot yield (g) through random sampling method. Recommended agronomic package and practices were applied to raise a good crop.

Area under disease progress curve (AUDPC)

Spot blotch disease was induced by inoculating a pure culture of the locally most aggressive isolate of *B. sorokiniana* following the method of Chaurasia et al. (1999). Spot blotch disease was recorded at different growth stages viz. GS 69 (anthesis complete), GS73 (early milk) and GS 77 (late milk) **(**Zadoks et al., 1974). Disease severity (%) was recorded at different stages to calculate the AUDPC. The AUDPC (Van der Plank, 1963; Roelfs et al., 1992) was calculated using the following formula as:

$$\mathrm{AUDPC} = \sum_{i=1}^{n} \left[\left\{ \frac{Y_i + Y_{(i+1)}}{2} \right\} (t_{(i+1)} - t_i) \right]$$

Where, Yi is the disease level at time ti and t (i+1) - ti the time (days) between two disease scores and n is the number of dates on which spot blotch was recorded.

Statistical and biometrical analysis

Data of 10 plants of each treatment were averaged and pooled mean data was used for statistical analysis. Phenotypic and genotypic coefficients of variability were calculated as per method proposed by Burton (1952). Test of significance was estimated using F ratio value at 5% level of statistically significance. Genetic variability including mean, range, variance, CV, heritability (Burton and Devane, 1953) and genetic advance (by Johnson et al., 1955) were calculated. All these analyses were

Table 1. Used 49 wheat genotypes with their pedigree and sources.

Genotype	Pedigree	Source
Amber 28	WG5669/2/MACS2496/BOW	KSPL,Jalna (M.H)
WCW 2009-06	PBW 343/WH 147	SVBPUA&T, Merrut (U.P)
HUW 660	WAXWING*2//INQALAB91*2/KUKUNA	B.H.U, Varanasi (U.P.)
NW 5074	PRL/2 *PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI	NDUA&T., Faizabad(U.P.)
DBW 96	OASIS/SKAUZ//4*BCN/3/2*PASTOR	DWR,Karnal (Haryana)
RAJ 4287	HD3091/Raj3077//Raj3765/UP2338	SK ,RAU,Jaipur (Rajasthan)
UP 2837	HD 2590/3/PBW 343/UP 1109/UP 2425-10B	GBPUAT, Pantnagar
WH 1133	BABAX/LR 42//BABAX *2/3/VIVITSI	CCSHAU,Hisar (Haryana)
PBW 676	DBW 16/DBW 18	PAU , Ludhiana
PBW 679	PBW 51/HP 1744	“
UP 2834	PBW 503/HPW 89	“
PBW 343	ND/VG1944//KAL//BB/3/YACO'S'/4/VEE#5'S'	“
HD 3104	HD 2329/HDK 10	IARI, New Delhi
HD 3107	HD 2877/DL 388	“
RAJ 4285	Raj4037/HUW570	SK ,RAU,Jaipur (Rajasthan)
WH 1131	MUNIA/CHTO//AMSEL	CCSHAU,Hisar (Haryana)
K 1101	HD 2733/HD 2285	CSAUAT, Kanpur,(U.P.)
HD 2733	ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA	IARI, New Delhi
DBW 98	PBW65/2*PASTOR//PBW550	DWR,Karnal (Haryana)
HD 3105	WAXWING*2VIVITSI	IARI, New Delhi
HP 1941	FRAME//MILAN/KAUZ/3/PASTOR	IARI, R.S., Pusa (Bihar)
RAJ 4289	PBW283/B8//Raj3077/NW2044	SK ,RAU,Jaipur (Rajasthan)
WH 1134	PRL/2*PASTER	CCSHAU,Hisar (Haryana)
HUW 661	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1	B.H.U, Varanasi (U.P.)
DBW 112	INQUALAB/30thIBWSN116//HUW593	DWR,Karnal (Haryana)
DBW 17	CMH79A.95/3*CNO79//RAJ3777	“
NW 5077	PFAU/SERI.1B//AMAD/3/WAXWING	NDUA&T, Faizabad(U.P.)
RAJ 4286	W32/Raj3765//B8	SK ,RAU,Jaipur (Rajasthan)
UP 2835	CROC.1/Ae. 58(205)BORL95/3/2*MILAN/4/KO123	GBPUAT, Pantnagar
WH 1132	PBW 65/2*PASTER	CCSHAU,Hisar (Haryana)
UP 2838	CHOIXM95/4/NL 962/3/TRACHA-2//CMH.76-252/PVN'S	GBPUAT, Pantnagar
PBW 677	PFAU/MILAN/5/CHEN/A. squa//BCN/3/VEE#7/BOW/4/PAST	PAU , Ludhiana
HD 3108	WHEAR//2*PRL/2*PASTOR	IARI, New Delhi
TL 2984	NGSN23/JNIT141//TL551/M78-9224	PAU , Ludhiana
WH 1135	HD 29/2*WEAVER	CCSHAU,Hisar (Haryana)
DBW 99	HD2168/HJA70581//HD2590	DWR,Karnal (Haryana)
K 1102	PBW 343/Raj 3765	CSAUAT, Kanpur,(U.P.)
PBW 680	PBW 343/Tc+Lr37//PBW 343	PAU , Ludhiana
DBW 95	K9908/PBW534	DWR,Karnal (Haryana)
HP 1942	TOBA97/PASTOR	IARI, R.S., Pusa (Bihar)
K 307	K 8321/UP2003	CSAUAT, Kanpur,(U.P.)
JAUW 596	HD2687/Ae. Crassa//HD2687	SKAUST,Jammu (J &K)
DBW 97	KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES	DWR,Karnal (Haryana)
HD 3106	PRL/2*PASTER/4/CHOIX/STAR/3/HE.1/3/CNO79//2*SERI	IARI, New Delhi
PBW 678	INQ 91*3/TUKURU//DBW 18	PAU , Ludhiana
UP 2836	UP 2425/ZANDER 33/PHR 1010	GBPUAT, Pantnagar
RAJ 4288	Raj4048/Raj3777//Lok1	SK ,RAU,Jaipur (Rajasthan)
HP 1943	WAXWING*2/VIVITSI	IARI, R.S. Pusa (Bihar)
NW 5079	BABAX/LR 42//BABAX *2/3/PAVON 753+LR 47	NDUA&T, Faizabad(U.P.)

Table 2. Genetic variability, heritability and genetic advance for examined traits in 49 wheat genotypes.

Trait	Mean	Range	Vp	Vg	PCV (%)	GCV (%)	H^2 (B.S. %)	Genetic advance	GAPM (%)
DF	76.91	68.25 - 85.25	26.88	10.46	6.74	4.21	38.91	4.156	5.404
PH	97.88	84.75 - 111.25	57.34	24.61	7.74	5.10	42.92	6.696	6.841
TGW	39.49	33.50 - 45.00	5.43	1.26	11.63	5.61	23.24	1.115	2.825
GPS	42.39	35.00- 49.00	15.59	8.81	9.32	7.00	56.47	4.594	10.837
DM	123.15	118.75 – 126.75	5.55	1.18	1.91	0.88	21.17	1.027	0.834
AUDPC	377.14	210 - 620	16439.52	9355.56	29.15	21.99	56.91	150.312	39.855
PY	2067.68	1767.50 - 2447.50	71611.69	22104.96	12.94	7.19	30.87	170.163	8.230

Vp = Phenotypic variance, Vg = genotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, H^2 (b.s.) = heritability in broad sense, GAPM = genetic advance in per cent of mean, DF = days to 75% flowering, PH = plant height; TGW = 1000-kernel weight, GPS = grain per spike, DM = days to maturity, area under disease progress curve (AUDPC) and PY = Plot Yield.

al., 1955) were calculated. All these analyses were performed by SPAR 2.0 (Statistical software). Genetic advance as per cent of mean is the improvement in the mean of selected family over the base population (Johnson et al., 1955). Correlation coefficient analysis was calculated by Robinson et al. (1951). The significance of correlation coefficient was tested with the help of 'r' value at n-2 degree of freedom at 5% level of significance where 'n' is number of treatments. Path coefficient analysis was accessed by Dewey and Lu (1959) using SPAR 2.0 (Statistical software). The correlation coefficient analysis and genetic diversity analysis using cluster and PCA were calculated using statistical software of STATISTICA version 10.0.

RESULTS AND DISCUSSION

In the present experiment, 49 spring wheat (*T. aestivum* L.) genotypes were analyzed for genetic studies viz., the genetic variability, the character association, the cluster analysis and principal component analysis (PCA) for examined yield components (days to 75% flowering, days to maturity, plant height, 1000-kernel weight, grain per spike and plot yield) and spot blotch resistance. It was found that the PCV was slightly higher than the GCV for all studied character revealing the environmental effects on the expression of characters. Highest PCV value was observed for the AUDPC value (29.15%), plot yield (g) (12.94%) and 1000-kernel weight (g) (11.63%) as similar reported by (Ali et al., 2008) (Table 2). It expressed the presence of maximum genetic variability among cultivars. Heritability (B.S.) value was found the highest for character AUDPC (56.91%) followed by grain per spike (grain number) (56.47%) and plant height (cm) (42.92%). Highest heritability value along with maximum genetic advance as per cent of mean was observed for the AUDPC (56.91 and 39.85%) followed by grain per spike (56.47 and 10.83%) and plant height (42.92 and 6.84%) (Table 2), and it indicated the presence of additive genetic effects for expression of these characters; selection considering these characters would be effective. The best 10 genotypes based on mean performance of promising traits in desirable direction, are represented in Table 3. The genotypes TL 2984 and UP 2838 were showed lesser days to 75% flowering (68.25 and 69.75 days). The genotype WH 1134 was exhibited by the lowest AUDPC value (210) indicating resistant parent in consonance with (Sharma et al., 1997b) (Table 3). Low yield level indicates high susceptibility to spot blotch disease (Phadnawis et al., 2002). Highest 1000-kernel weight (g) was observed in HUW 661 and HD 3104 (45.00 g), and the highest grain per spike were found in the TL 2984 (49.00) (Table 3).

Similarly, the highest plot yield was recorded in WH1132 and WH 1131 (Table 3). It shows wide differences among the experimental material in terms of yield components and spot blotch resistant. Grain yield per plot (g) was significantly and positively associated with 1000-kernel weight (g) (0.82*) and grain per spike (0.79*) (Table 4). It suggests that the characters should be included for genetic improvement for spring wheat genotypes.

Negatively significant correlation (-0.689*) was observed between the yield (g) and the AUDPC value indicate that spot blotch is the major constraint for wheat production in Eastern Gangetic Plains of India representing major role of environment for the disease incidence (Table 4) as similar reported by (Gilchrist and Pfeiffer, 1991; Meena et al., 2014) AUDPC value showed negative and significant association with 1000-kernel weight (g) (-0.599*) and grain per spike (grain number) (-0.524*) (Table 4). Path-coefficient analysis exhibited that the maximum positive direct effect on yield showed by grain per spike (grain number) observed via the 1000-kernel weight (g) and days to 75% flowering (days) while negative direct effects showed by the 1000-kernel weight (g), the AUDPC (unit), the days to maturity (days) and the plant height (cm) (Table 5). Thus, path analysis suggest that grain per spike (unit), days to 75% flowering (days), 1000-kernel weight (g), the AUDPC value and the plant

Table 3. Best ten genotypes considering promising characters.

Trait	1	2	3	4	5	6	7	8	9	10
DF **(early)**	**TL 2984 (68.25)**	UP 2838 (69.75)	**WCW2009-06 (70.00)**	HD 3104 (70.50)	HUW 661 (71.75)	RAJ 4285 (72.00)	PBW 678 (72.00)	UP 2836 (72.00)	RAJ 4289 (72.25)	DBW 95 (73.50)
PH **(dwarf)**	RAJ 4286 (84.75)	HD 3108 (87.00)	DBW 17 (87.75)	K 1101 (88.75)	NW 5074 (90.25)	UP 2836 (91.00)	PBW 678 (91.50)	DBW 97 (91.75)	NW 5079 (91.75)	PBW 676 (92.00)
TGW **(high)**	**HUW 661 (45.00)**	**HD 3104 (45.00)**	DBW 99 (45.00)	PBW 676 (44.00)	WH 1132 (44.00)	**TL 2984 (44.00)**	HP 1943 (43.75)	UP 2836 (43.50)	HD 2733 (43.00)	DBW 112 (43.00)
GPS **(high)**	**TL 2984 (49.00)**	HD 2733 (48.00)	PBW 677 (48.00)	WH 1132 (47.50)	PBW 676 (47.00)	**WCW 2009-06 (47.00)**	HUW 661 (46.00)	HD 3106 (46.00)	WH 1131 (46.00)	HD 3104 (45.00)
DM **(early)**	HP 1942 (118.75)	**WH 1132 (119.75)**	**WH 1131 (120.75)**	HP 1943 (121.00)	NW 5079 (121.25)	UP 2834 (121.50)	PBW 677 (121.75)	K 1102 (121.75)	WH 1133 (121.75)	DBW 98 (122.00)
AUDPC **(low)**	WH 1134 (210.00)	**WCW 2009-06 (240.00)**	DBW 112 (240.00)	K 1101 (250.00)	**WH 1131 (260.00)**	HUW 661 (260.00)	WH 1132 (265.00)	HD 2733 (270.00)	DBW 98 (280.00)	UP 2836 (290.00)
PY **(high)**	**WH 1132 (2447.50)**	**WH 1131 (2402.50)**	**HD 3104 (2392.50)**	**HUW 661 (2372.50)**	PBW 676 (2362.50)	**TL 2984 (2360.00)**	**WCW 2009-06 (2330.00)**	HD 2733 (2320.00)	DBW 17 (2260.00)	UP 2836 (2255.00)

*Bold genotypes are better for several characters. DF: Days to 75% Flowering, PH = plant height; TGW= 1000-kernel weight, GPS = Grain per spike, DM = Days to maturity, Area under disease progress curve (AUDPC value) and PY = Plot Yield.

Table 4. Character association among seven characters in 49 wheat genotypes.

Trait	DF	PH	TGW	GPS	DM	AUDPC	PY
DF	1.000	0.041	-0.019	-0.133	0.253	0.053	-0.057
PH		1.000	0.180	0.105	-0.321*	0.077	0.081
TGW			1.000	0.781*	-0.127	-0.599*	0.822*
GPS				1.000	-0.179	-0.524*	0.790*
DM					1.000	0.156	-0.287*
AUDPC						1.000	-0.689*
PY							1.000

*Statistically significant at 5% level. DF = Days to 75% flowering, PH = plant height; TGW = 1000-kernel weight, GPS = grain per spike, DM = days to maturity, AUDPC = area under disease progress curve, PY = plot yield.

height (cm) may serve as effective selection variables for further wheat improvement programmes.

Genetic divergence analysis

All the 49 spring wheats were grouped into six distinct clusters through STATISTICA V.10 software (Table 6, Figure 1). Based on Euclidean genetic distance, paired entry (DBW96 and WH1132), (DBW96 and WH 1131) and (RAJ4287 and WH1131) were found extremely diverse while paired entry (HUW660 and DBW 98), (PBW679 and RAJ4288) exhibited extremely closest genetic relationship. In cluster I, only one entry Amber 28 found which represent poor yield potential. Seven genotypes are categories under cluster II.

The mean performance of the cluster genotypes for 1000-kernel weight (43.43 g), grain per spike (46.93 grain) and plot yield (2375.0 g) are above the mean of all genotypes and for the AUDPC value below the grand mean representing higher yield and disease resistance potential (Table 7).

Cluster III has 28 genotypes accounting for 57.14% of total genotypes having poor yield and resistance potential in consonance with (Atta et al., 2008; Khan et al., (2010).

Table 5. Direct and indirect effect of six characters on plot yield as independent variable.

Trait	DF	PH	TGW	GPS	DM	AUDPC	Correlation With PY
DF	**0.0300**	0.0008	-0.0039	-0.0041	0.0063	-0.0062	-0.057
PH	-0.0015	**-0.055**	-0.0093	-0.0068	0.0244	0.0032	0.081
TGW	0.0609	-0.083	**-0.4901**	-0.5331	0.0905	-0.0099	**0.822**
GPS	-0.2208	0.2026	1.7583	**1.6165**	-0.4547	0.1098	**0.790**
DM	-0.0192	0.0408	0.0169	0.0257	**-0.0914**	0.0374	**-0.287**
AUDPC	0.0489	0.0137	-0.0048	-0.0161	0.0969	**-0.2369**	**-0.689**

Residual effects = 0.415. DF = days to 75% flowering, PH = plant height; TGW = 1000-kernel weight, GPS = grain per spike, DM = days to maturity, AUDPC = area under disease progress curve, PY = plot yield.

Table 6. Clustering pattern of genotypes based on dendrogram (cluster analysis tree chart).

Clusters	No. of genotypes	Genotypes
Cluster I	1	Amber 28
Cluster II	7	WCW2009-06, HD2733, HD3104, TL2984, WH1131, HUW661 and WH1132
Cluster III	28	HUW660, DBW98, HP1943, K1101, DBW112, UP2837, JAUW596, K1102, PBW680, WH1134, NW5074, UP2835, NW5077, DBW 97, PBW679, NW5079, RAJ4288, K307, DBW95, HD3106, HP1941, RAJ4286, RAJ 4289, RAJ4285, UP2838, HD3108, WH1135 and PBW678,
Cluster IV	8	WH1133, HP1942, DBW99, HD3107, HD3105, PBW677, DBW17 and UP2836
Cluster V	2	DBW96 and RAJ4287
Cluster VI	3	PBW676, UP2834 and PBW343

The cluster IV has eight genotypes accounting for 16.32% of total genotypes. The mean performance of the cluster genotypes for the plant height (cm), 1000-kernel weight (g), grain–per spike (grain number) and plot yield (g) was higher than grand mean value and for the AUDPC value lower than the grand mean value representing better yield and resistant potential.

The cluster V has two genotypes representing poor yield potential while the cluster VI with three genotypes exhibited better yield and resistant potential because mean performance of the cluster genotypes for the plant height (cm), the 1000-kernel weight (g), the grain per spike (grain number) and the plot yield (g) was higher than grand mean value and for the AUDPC lower than the mean value (Table 7).

Principal components analysis (PCA)

It is generally used for data reduction to ascertain the relationship between two or more characters by linear transformation of the original variables into a new group of uncorrelated variables regarded as PCs. Four major PCs (PC1 to PC4) from the original data explained 89.13% of the total variation (Table 8) as similar reported by Hailegiorgis et al. (2011) and Meena et al. (2014). Out of the major four PCs, three principal components (PC1, PC2 and PC3) accounted with proportionate values of 45.90, 18.73 and 15.23%, respectively and contributed 79.86% of the cumulative variation having Eigen value more than one (Table 8). Two dimensional depictions of 49 wheat genotypes on PC axis 1 and 2 represented the existence of extreme genetic diversity among present wheat genotypes set (Figure 2).

The first principal component has high positive component value for AUDPC value, days to 75% flowering (days) and days to maturity (days). PC1 has negative component value for 1000-kernel weight (g), grain per spike (grain number) and plot yield (g) as similar reported by Khodadadi et al. (2011) and Meena et al. (2014).

The second PC has high positive component value for days to maturity (days), days to 75% flowering (days) and 1000-kernel weight (g) and high negative component value for plant height and AUDPC (Table 8). These characters having either high positive or negative component value reveals tremendous genetic diversity, and might be play significant role during clustering. The third PC has high positive component value for days to 75% flowering (days), plant height (cm), AUDPC value and 1000-kernel weight (g) (Table 8) as similar reported by Hailegiorgis et al. (2011).

The depiction of component traits on PC1 and PC2 represented that 1000-kernel weight and grain per spike (grain number) are positively related with grain yield (unit) and negative relation exhibited by the AUDPC value (Figure 3).

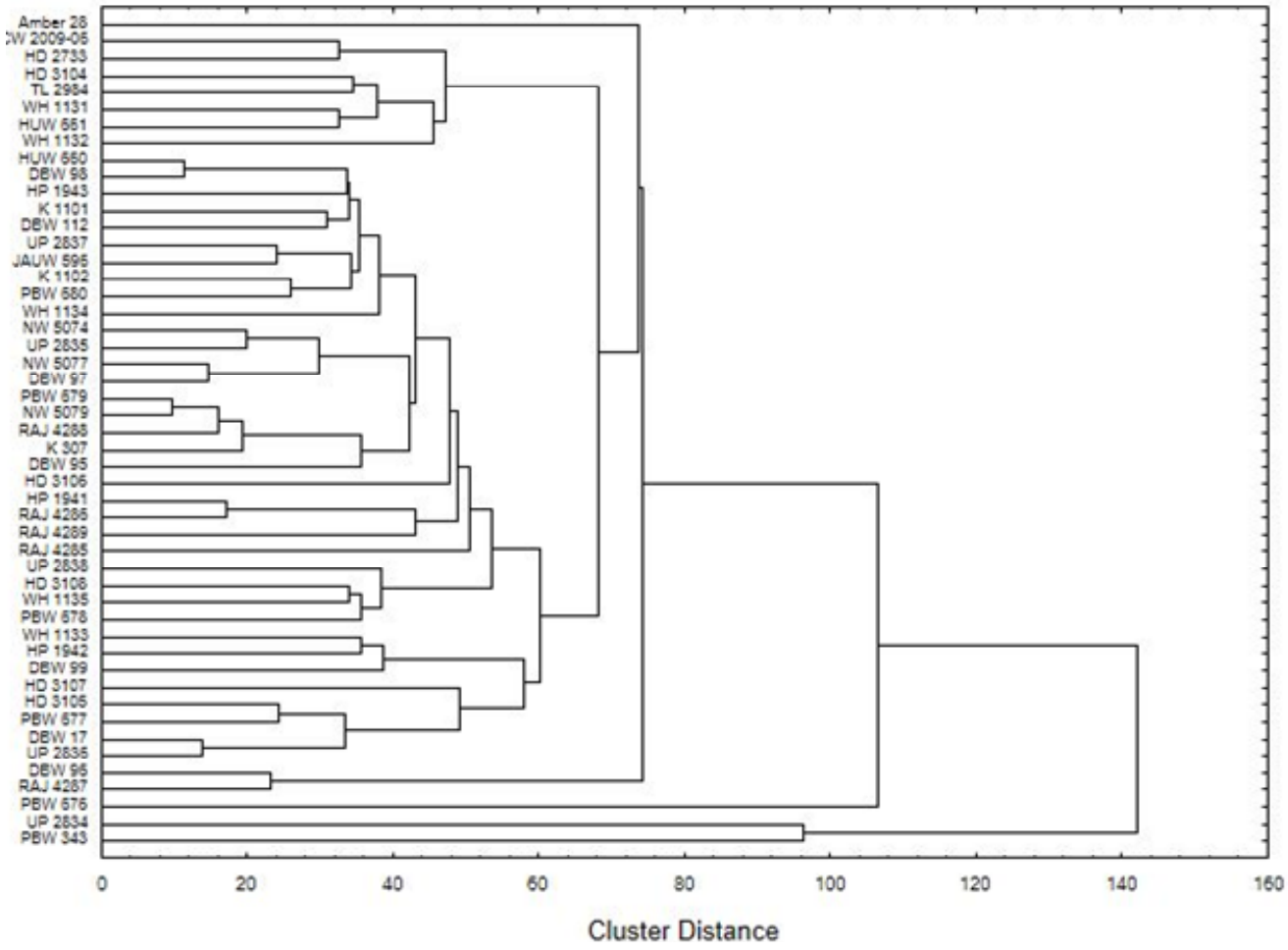

Figure 1. Dendrogram depicting genetic diversity among 49 wheat genotypes.

Table 7. The mean performance of each cluster parent (above number) and its deviation from grand mean (below number).

	DF	PH	TGW	GPS	DM	AUDPC	PY
Cluster1	74.50	97.75	33.50	42.00	123.25	570.00	1848.75
	-2.41	-0.13	-5.98	-0.39	0.10	192.86	-218.93
Cluster2	73.29	97.61	43.43	46.93	122.21	270.71	2375.00
	-3.62	-0.28	3.94	4.54	-0.94	-106.43	307.32
Cluster3	76.90	97.04	38.19	40.95	123.34	376.79	1971.34
	-0.01	-0.84	-1.30	-1.44	0.19	-0.36	-96.34
Cluster4	79.64	100.64	41.43	43.86	122.54	340.71	2203.21
	2.73	2.76	1.94	1.47	-0.62	-36.43	135.54
Cluster5	80.50	99.13	35.50	38.50	125.88	600.00	1772.50
	3.59	1.24	-3.98	-3.89	2.72	222.86	-295.18
Cluster6	79.08	101.42	41.17	43.67	123.00	530.00	2140.83
	2.18	3.53	1.68	1.28	-0.15	152.86	73.15

Table 8. Principal components analysis (PCA) for seven examined characters in 49 wheat genotypes.

Trait	PC1	PC2	PC3	PC4
Eigen value	3.213	1.311	1.066	0.649
Cumulative	3.213	4.524	5.590	6.239
% Total variation	45.903	18.730	15.230	9.270
Cumulative	45.903	64.633	79.862	89.133
Days to 75% flowering	0.077	0.382	0.778	0.438
Plant height	-0.095	-0.587	0.591	-0.344
1000-kernel weight	-0.502	0.108	0.143	-0.237
Grain per spike	-0.490	0.060	-0.008	-0.292
Days to maturity	0.189	0.666	0.091	-0.623
AUDPC value	0.427	-0.211	0.128	-0.392
Plot Yield	-0.524	0.071	0.015	0.082

DF = Days to 75% flowering, PH = plant height; TGW = 1000-kernel weight, GPS = grain per spike, DM = days to maturity, AUDPC = area under disease progress curve, PY = plot yield.

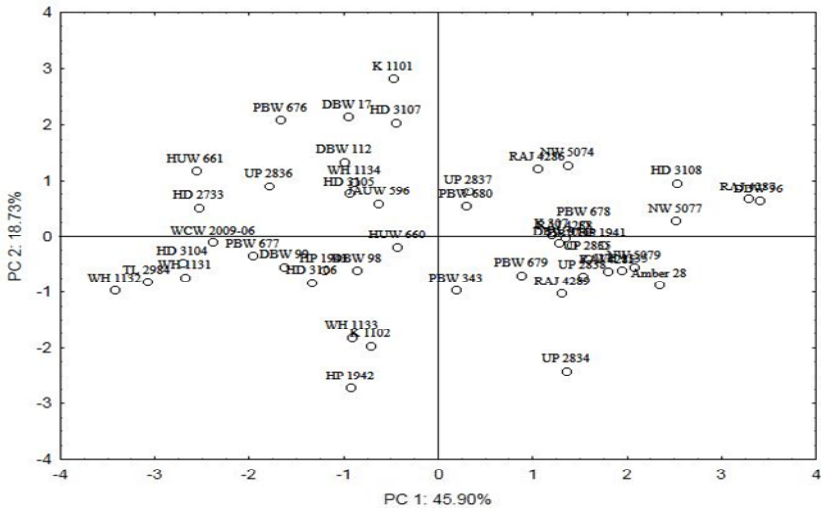

Figure 2. Scatter plot: Two dimensional depictions of 49 wheat genotypes on PC1 and PC2 axis.

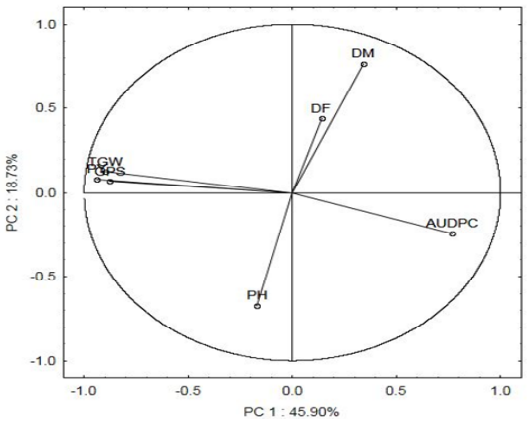

Figure 3. Scattered diagram based on first two principal components representing contribution of the examined characters. DF = Days to 75% flowering, PH = plant height; TGW= 1000-kernel weight, GPS = grain per spike, DM = days to maturity, AUDPC = area under disease progress curve and PY = Plot Yield.

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