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Research Article

Analysis of Genetic Diversity among the Different Wheat (*Triticum aestivum* L.) Genotypes

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Abstract

Forty one wheat (*Triticum aestivum L.*)genotypes were studied for days to booting, days to heading, plant height at vegetative, plant height at maturity, days to 50% anthesis, days to 100% anthesis, flag leaf senescence, days to physiological maturity, peduncle length, effective tillers, spikelet's length, grain per spike, biomass ,harvest index, sterility percentage, thousand grain weight and grain yield in random complete block design at terai, Nepal with the objective to identify superior genotypes after clustering them based on their genetic diversity in performance. Result of multivariable analysis revealed that 41 wheat genotypes formed four clusters. Cluster 4 and 2 had highest value of effective tiller, spike length, grain per spike, thousand grain weight, biomass, harvest index ,grain yield and lowest value days to heading, days to booting ,days to anthesis and sterility percentage. Cluster 3 had high days to booting, days to heading, days to 50% and 100% anthesis, days to flag leaf senescence and low in plant height at maturity, thousand grain weight ,harvest index and grain yield. Considering of multivariable analysis and other agronomic performance wheat genotypes HD 1982 and Pitic 62 may be utilized as high yielding genotypes in Terai condition of Nepal.

Keywords: Wheat (*Triticum aestivum L.*), genetic divergence, multivariable analysis

Introduction

Wheat is hexaploid ($2n = 6x = 42$) cereal crop belong to family Poaceae (grasses) and genus *Triticum* (Bozzini, 1988). Wheat is the world's most favored staple food. It is nutritious, easy to store and transport and can be processed into various types of food. Wheat is considered a good source of protein, minerals, B-group of vitamins and dietary fiber (Shewry, 2007). It is an excellent health-building food and used for preparation in bread, biscuits, confectionary products and noodles. Wheat is also used as animal feed, for ethanol production and brewing of wheat beer. Wheat accounted nearly 55% of carbohydrate consumed worldwide (Gupta et al., 1999).

Wheat comes third in Nepal after rice and maize. It is a major winter cereal crop in Nepal and more than 80% of wheat is grown in rice-wheat cropping pattern. Wheat production and productivity is 18, 11,889 mt and 2.5 t ha^{-1} respectively (MoAC, 2015/16). Wheat grows well in temperature 15-18°C during grain filling period. Wheat doesn't remain untouched to this scenario. Projection of wheat demand by 60% by 2050 is accompanied with the present decrease in production by 20-30% due to induced temperature rise by (Rosegrant and Agcaoili 2010). Wheat production will suffer the effects of stagnating or decreasing on farm productivity and wrong choice of varieties on the part of the farmers. Cluster analysis is a group of multivariate analysis which enables grouping of individuals based on similarity or dissimilarity in traits. The resultant clusters of individuals perform high homogeneity between clusters.

On the other hand, many factors like climate change, hindrance in selection of good genotypes, improver knowledge are resulting in decrease in its production and productivity annually. Maintaining and increasing productivity of cereals like wheat being the most challenging issue in Nepal and probably in the world, the proposed study is of utmost importance. The research was carried out in identical environment, for all genotypes suggested for the selection of comparative better genotype based on the performance observed and records obtained during the field research.

Materials and Methods

The investigation was carried out RCBD design with three replications at agriculture college farm, institute of Agriculture and Animal Science (IAAS), Paklihawa, Rupendehi during December to March, 2015. This site contains sandy loam soil with acidic reaction. The research location is characteristic of tropical climate. The spacing of wheat in 22.5×8 cm and plot of size 2.4*0.22 sqm. Inter replication gap was 1 meter. The line sowing was done on 9 December 2014 by manually. Compost manure at the rate of 5 ton/ha and fertilizer was applied at the rate of 120:60:40 NPK kg ha^{-1}. Half dose of Nitrogen and full dose of P_2O_5 and K_2O were applied during the field preparation and remaining half dose of N was applied in equal amount as side dressing at 30 and 60 DAS. The artificial irrigation was given at CRI stage, grain filling stage and milking stage where as other requirement of water was fulfilled through natural precipitation. Two manual weeding were done after 30 and 60 days of sowing. Harvesting was done by serrated sickles when the grains were dried enough and had turned to straw colour. Each genotypes harvested were kept in different tagged bags. Harvested wheat was dried on sun for two days and was threshed by beating with sticks. The data were taken from five randomly selected plants per genotype per replication were used. Data of the following mentioned traits were recorded.

Physio-morphological traits

DTB-Days to booting, DTH-Days to heading, PHV-Plant height at vegetative, PHM-Plant height at maturity, NH-Days to 50% anthesis, ANF-Days to 100% anthesis, FLS-Flag leaf senescence, PM-Days to physiological maturity , PL-Peduncle length(cm),

Yield attributing traits

ET-Effective tillers, SL-Spikelet's length (cm), GPS-Grain per spike, BM-Biomass (ton/ha), GY-Grain yield (ton/ha), HI-Harvest index, ST-Sterility (%), TGW- Thousand grain weight (gm).

The plant materials were obtained from International Maize and Wheat Improvement Centre (CIMMYT). The list of 41 genotypes included in the study is presented in Table 1.

Table 1. List of the genotypes used for the experiment

Treatments	Genotypes	Treatments	Genotypes	Treatments	Genotypes
1	LR52	15	Nepal-251	29	WK-1204
2	LR64	16	Annapurna-1	30	Aditya
3	KalyanSona	17	Annapurna-2	31	NL-971
4	Pitic 62	18	Annapurna-3	32	Vijay
5	RR21	19	BL-1022	33	Gaura
6	NL 30	20	Bhrikuti	34	Dhaulagiri
7	HD1982	21	NL-1135	35	NL-1073
8	UP262	22	Annapurna 4	36	NL-1064
9	Lumbini	23	Achyut	37	BL-3623
10	Triveni	24	Rohini	38	BL-3629
11	Vinayak	25	Kanti	39	BL-3972
12	Siddartha	26	PasangLhamu	40	NL-1055
13	Vaskar	27	BL-1473	41	NL-1164
14	Nepal-297	28	Gautam		

Statistical analysis

Data entry and processing was carried out using Microsoft excel (MS- Excel, 2010.The collected data were subjected to multivariable analysis was done using statistical software packages of Minitab ver.14 (Mohammadi and Prasanna, 2003).

Result and Discussion

Cluster analysis

All the genotypes were clustered using days to booting, days to heading, days to anthesis (50% and 100%), length of flag leaf, days to flag leaf senescence, days to maturity, Plant height vegetative and maturity, peduncle length, number of effective tiller per plant, number of grains per spike, sterility percentage, weight of grains per spike, grain yield, 1000 grain weight, biomass yield and harvest index. The dendrogram of 41 genotypes was constructed in single linkage and Euclidean distance (Fig 1).Distance between different clusters centroids of wheat genotypes is presented in Table 2.

Table 2. Distances between different cluster centroids of wheat genotypes

	Cluster1	Cluster2	Cluster3	Cluster4
Cluster1	0.0000	29.2950	25.0020	21.1976
Cluster2		0.0000	40.0828	36.7247
Cluster3			0.0000	35.5311
Cluster4				0.0000

The critical examination of dendrogram revealed four clusters with 48.58 % similarity level in UPGMA clustering. The cluster one consisted of 38 genotypes, which represents 92% genotypes. It includes 38 genotype trements number 1, 2, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 and 41 as shown in Table 1.This cluster had almost intermediate quantitative traits as shown in Table 3.

Cluster 2 consisted of 1 genotype)Pitic 62) and this cluster had highest value of effective tiller, spike length, grain per spike, thousand grain weight, biomass, harvest index and grain yield. The cluster of this genotypes is suitable for cultivation due to high yield and yield attribution traits.

Cluster 3 had 1 genotype (Kalyansona) and this cluster had high days to booting, days to heading, days to 50% and 100% anthesis, days to flag leaf senescence and low in plant height at maturity, thousand grain weight and harvest index. These genotypes had inferior trait values for yield and yield attributing trait value under study condition.

The cluster 4 had 1 genotype (HD1982) and this cluster had high in plant height at vegetative, days to plant maturity, number of effective tillers, spikelet’s length and thousand grain weight, grain yield and lowest value in days to booting, heading, 50% anthesis, flag leaf senescence and sterility percentage. Since cluster of this genotypes HD1982 and cluster 2 genotypes Pitic 62 had superior trait values in terai condition and theses genotypes may be of interest to researchers. The distance between the clusters centroid was found highest between clusters 3 and 4 and lowest between clusters 1 and 4.

Table 3. Mean values of single linkage method clustering of wheat genotypes

S.N.	Variable	Cluster1	Cluster2	Cluster3	Cluster4	Grand centroid
1	No. of observation	38	1(Pitic62)	1(KS)	1(HD1982)	
2	DTB	69.184	68.333	77.333	58.333	69.098
3	DTH	73.851	75.000	82.333	63.333	73.829
4	PHV	43.523	44.427	43.220	47.453	43.634
5	PHMAT	72.440	66.100	59.753	65.173	71.798
6	ANTH(50)	78.044	80.000	86.333	72.000	78.146
7	Anth(100)	83.509	84.667	91.333	82.000	83.691
8	FLS	106.237	105.333	111.333	102.667	106.252
9	PMAT	116.781	115.000	117.667	118.000	116.789
10	EFFTILLER	3.947	4.000	3.667	4.667	3.959
11	PEDLEGN	16.909	15.300	19.067	13.133	16.830
12	SPIKELNTH	16.401	16.447	13.313	16.500	16.329
13	GRAINPERSPIKE	49.030	76.800	41.867	45.133	49.437
14	Sterility	9.563	3.995	1.684	1.498	9.038
15	HI	0.453	0.448	0.437	0.455	0.453
16	TGW	40.914	41.333	35.000	42.000	40.806
17	Biomass (T/ha)	5.883	6.808	3.606	7.563	5.891
18	Grain yield(T/ha)	2.666	3.089	1.566	3.485	2.670

Principal component analysis

Seventeen quantitative traits were constructed into six principal component among 17 traits which had eigen value greater than 1 exhibits almost all variability exist in components and eigen values, proportion of variance and coefficient of quantitative traits are presented in table no 4.The first six principal components revealed that 77.5 variability among 41 genotypes of wheat . Similarly 5, 4, 3, 2 and 1 principal component revealed 70.7, 63, 52.9, 40.7 and 24.2 % of cumulative variance respectively. The first principal component had days to heading, booting, and anthesis 50% and flag leaf senescence had positive loading. The first principal component explained phonological characters.

Second principal component had positive loading with effective tiller, spike length, grain per spike, thousand grain weights, biomass, harvest index and grain yield and negative loading days to 100 % antithesis.

Third principal component had positive loading with number of effective tillers and negative loading with peduncle, spikelet's length and thousand grain weights.

Fourth principal component had negative loading with sterility and plant height at maturity and positive loading with effective tiller, spike length, grain per spike, biomass, harvest index and negative loading with days to booting and heading.

Fifth principal components had negative loading with days to physiological maturity, thousand grain weight and sterility and positive loading with peduncle length, grain per spike and harvest index and sixth principal component had negative loading with sterility and grain per spike and positive loading with peduncle length, days to physiological maturity and harvest index.

The present research revealed that these genotype formed in cluster 4 and 2 in trail condition were the most suitable for cultivation under studied condition The finding PCA supported the result obtained by cluster analysis and PCA score plot was shown in Figure 2.

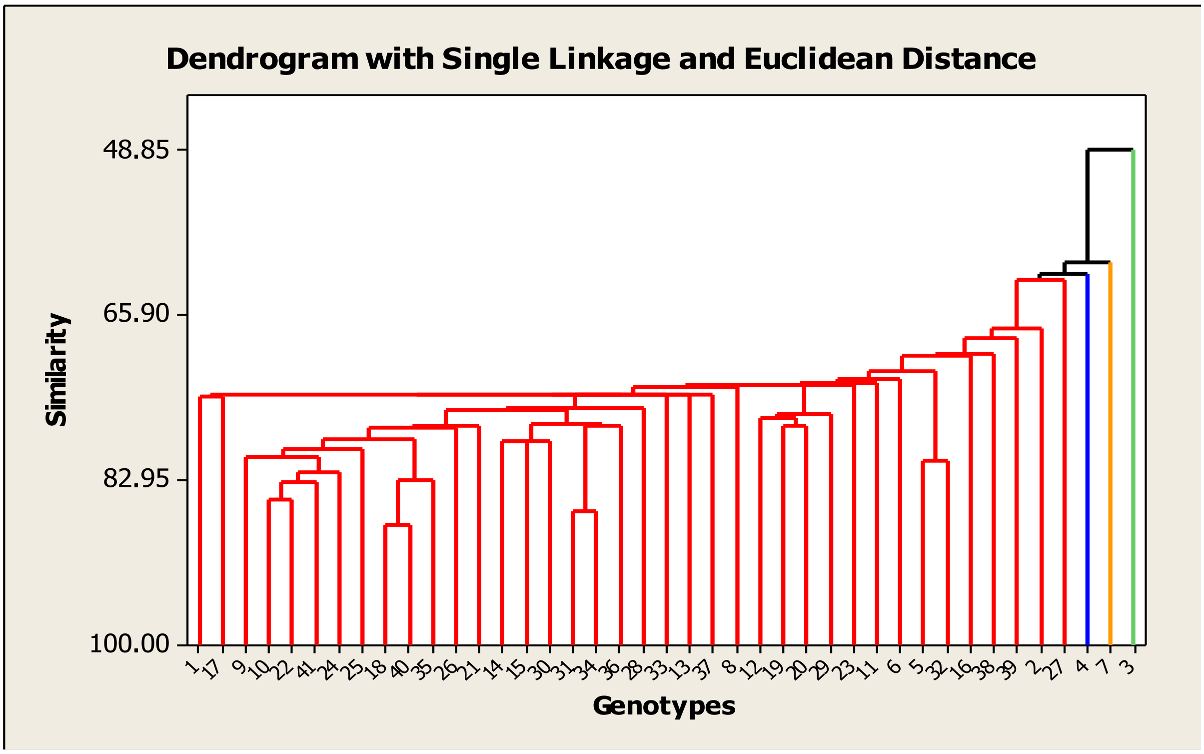

Figure 1. Dendrogram with Single linkage and euclidean distance of 41 genotypes of wheat

In present study there is sustainable genetic diversity in physio-morph and yield attributing trait of wheat. Cluster analysis revealed that genotypes formed four distinct clusters.The high yielding genotypes and low yielding genotypes formed different cluster.The member of cluster 2 and 4 were found most suitable to terai condition for cultivation. Ajmal et al., (2013) also reported cluster analysis help selection process more easy by genotypes which show better performance in yield attributing traits are grouped in one cluster from this study genotypes HD 1982 and Pitic 62 were found most suitable for cultivation in terai condition of Nepal which had high value for grain yiled and yield attribution traits.Similar to the findings by Ali et al. (2008) who reported that cluster analysis can be useful for finding high yielding wheat genotypes. In this study of principal component use to reduces of original variables into six principal component and information about each variable which support cluster analysis result. Kamara et al., (2003) also used principal component analysis to categorize traits of maize that accounted for most of the variance in the data. Similar to the findings about presence of a high genetic divergence among wheat genotypes reported by (Singh and Dwivedi 2002). Principal component analysis is usually used in plant sciences for the reduction of variables and grouping of genotypes. Therefore principal component analysis is a powerful tool to obtain parental lines for a successful breeding program (Akter et al., 2009).

Table 4. Coefficient, eigen values and variance for 17 quantitative traits of 41 genotypes of wheat

Variable	PC1	PC2	PC3	PC4	PC5	PC6
DTB	0.424	0.120	-0.032	-0.150	0.071	-0.129
DTH	0.415	0.146	-0.097	-0.096	0.210	-0.096
PHV	-0.241	0.121	-0.203	0.072	-0.170	0.240
PHMAT	-0.080	0.246	-0.185	-0.527	0.170	0.023
ANTH(50)	0.433	0.039	-0.084	0.045	0.049	0.122
Anth(100)	0.378	-0.113	0.026	0.210	-0.071	0.113
FLS	0.369	0.308	-0.137	0.017	-0.017	0.086
PMAT	0.171	0.197	-0.050	-0.035	-0.385	0.434
EFFTILLER	0.046	0.091	0.566	-0.184	-0.115	0.168
PEDLEGN	-0.115	0.003	-0.356	-0.285	0.387	0.328
SPIKELNTH	-0.123	0.208	-0.401	0.250	-0.204	-0.246
GRAINPERSPIKE	0.040	0.181	0.050	0.395	0.402	-0.397
Sterility	-0.002	-0.093	-0.105	-0.482	-0.046	-0.424
HI	-0.144	0.156	-0.018	0.233	0.510	0.369
TGW	-0.076	0.378	-0.313	0.102	-0.309	-0.083
Biomass (T/ha)	-0.104	0.488	0.293	-0.091	-0.054	-0.126
Grain yield(T/ha)	-0.138	0.493	0.282	-0.009	0.100	-0.012
Eigen value	4.1069	2.8165	2.0695	1.7114	1.3121	1.1551
Proportion	0.242	0.166	0.122	0.101	0.077	0.068
% of cumulative variance	24.2	40.7	52.9	63	70.7	77.5

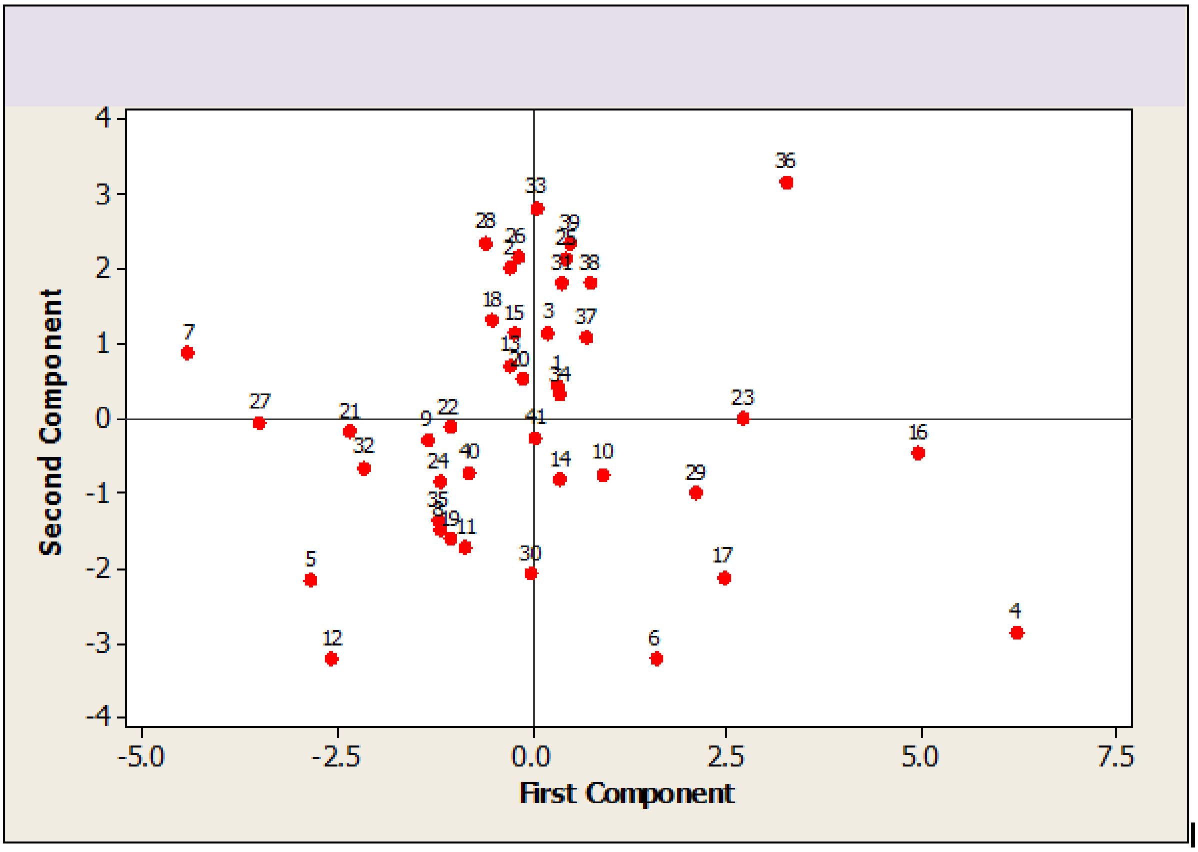

Figure 2. Principal component analysis using correlation matrix of forty-one wheat genotypes.

Conclusion

The genetic diversity was observed in days to booting, days to heading, plant height at vegetative, plant height at maturity, days to 50% anthesis, days to 100% anthesis, flag leaf senescence, days to physiological maturity, peduncle length, effective tillers, spikelet's length ,grain per spike, biomass ,harvest index, sterility ,thousand grain weight and grain yield in the tested wheat genotypes. The genotypes grouped into 4 and 2 cluster were good because of their desirable yield attributing traits. The presence of high level of diversity among the tested genotypes grouped into divergent clusters and supported by principal component indicated their suitability for further research can be done in this direction by selectiong superior genotypes.Theses genotypes could be very useful in developing commercial variety in terai condition of Nepal.

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