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ASSESSMENT OF GENETIC DIVERSITY OF BREAD WHEAT (*Triticum aestivum* L.) GENOTYPES THROUGH CLUSTER AND PRINCIPAL COMPONENT ANALYSIS

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Abstract

Genetic variation of plants decides their potential for enhancement of the efficiency and consequently their utilization in breeding, which eventually may lead to increased food production. Diversity assessment can be performed through various process. This study was conducted with the aim to assess the variability of advanced wheat lines and identification as well as selection of superior genotypes with the help of different multivariate technique. 50 genotypes obtained from CIMMYT were used for study. Field experiment was conducted in Alpha Lattice design. Observation were taken for days to booting, days to heading, days to maturity, days to flag leaf senescence, thousand kernel weight, grain filling duration, flag leaf area, SPAD reading, number of grains per spike, grain weight per spike, plant height and grin yield. The present study confirmed that bread wheat genotypes showed wide amount of variations for the character studied and it also suggested that ample opportunities for genetic improvement of bead wheat genotypes through selection of superior genotypes. Selection of genotypes from Cluster 2 (Gautam andSOKOLL/ 3/ PASTOR// HXL7573/ 2*BAU/5/ CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2) would lead to selection of the superior genotypes and these genotypes can be considered of breeding operations as well as for further study for developing superior wheat genotypes

Key words: cluster analysis, *Triticum aestivum*, PCA, selection, wheat

Introduction

Common wheat (*Triticum aestivum* L.) is considered as one of the most important cereals currently cultivated in most parts of the world (Mwale et al., 2016). It approximately forms more than 40% of the world's commonly consumed food and 95% of people in the developing countries eat wheat or maize in form of flour as a main food source (Akhtar et al., 2011; Coventry et al., 2011). Wheat is a cereal crop belonging to family Poaceae along with other important cereals like rice, wheat, maize, barley, oat and rye. Worldwide, it is grown on nearly 217 million hectares, with a production of 653 million tons (FAO Stat, 2013). It is a primary staple food crop for South Asia; it is grown on nearly 38 million hectares, with a production of 139.88 million tons (FAO Stat, 2013).

Genetic variation of plants decides their potential for enhancement of the efficiency

and consequently their utilization in breeding, which eventually may lead to increased food production. (Zadfar and Golabadi, 2013). By conserving the genetic diversity, farmers could achieve a greater improvement rate of desired traits such as pest resistance and high yields in the available wheat cultivars while maintaining land size (Mwale et al., 2016). Jain et al., (1975) investigated the geographical patterns of phenotypic diversity of durum wheat using the world collection and achieved a developed program for the protection of genetic resources to identify and assess inter variation and intra societies. Genetic diversity could be the result of geographical impact through the evolution and hence traits could be considered as a function of variety (Benadeki, 1992).

Diversity assessment can be performed through various process. Some suitable methods, cluster analysis, Principal Component Analysis (PCA), for genetic diversity identification, parental selection, finding the pathway to evolution of crops, center of origin and diversity, and study interaction between the environment are currently available and are very useful (Bhatt, 1970; Carves et al*.,* 1987; Eivazi et al., 2007; Mohammadi and Prasanna, 2003). Assessment of genetic diversity can be useful for the selection of the most efficient genotypes. Accordingly, if such efforts result to the detail study of diversity and exploration of process for production of plants with higher uniformity, which may guarantee the production of enough food for the world increasing population. (Khodadadi et al*.,* 2011).

Since, the selection for grain yield improvement can be effective if sufficient genetic variability exists in the breeding material (Ali et al*.,* 2008), this study will help in assessing and quantifying the diversity in different spring wheat lines which might have potential of yielding more. Thus, this study was conducted with the aim to assess the variability of advanced wheat lines and identification as well as selection of superior genotypes with the help of which those superior lines can be studied further for development of better varieties.

Materials and Methodology

The field experiment was conducted at the research farm of Agriculture and Forestry University, Faculty of Agriculture, Rampur, Chitwan, Nepal from November 2014 to April 2014, geographically located at $27^0$37' N Latitude and $84^0$25' E Longitude at an altitude of 228 meters above sea level. This site contains sandy loam soil with acidic reaction. The research location is characteristics of subtropical climate. The plant materials were obtained from CIMMYT. Among 50 genotypes used, Gautam was used as check variety. The list of genotypes included in the study is presented in Table 1.

Field experiment was conducted in Alpha Lattice design. Each replication comprised five blocks consisting of ten plots each. Each plot was 4 m in length 1.5 m wide. Each plot had 6 rows with spacing 25 cm between rows. Inter-block gap of 0.5 m was maintained. The dose of chemical fertilizers applied was 120:60:60 kg NPK per hectare. Irrigation was done at the three important stages; crown root initiation (CRI) stage, flowering stage and milking stage. The planting was done on 22nd November 2014.

Observation were taken for days to booting, days to heading, days to maturity, days to flag leaf senescence, thousand kernel weight, grain filling duration, flag leaf area, SPAD reading, number of grains per spike, grain weight per spike, plant height and grin yield.

Data entry and processing was carried our using Microsoft Office Excel 2007. Multivariate analysis was carried out through

Rstudio. Dendogram was constructed with the use of package dendextend.

Result and Discussion

Principal component analysis (PCA)

Twelve components could have been extracted from all the studied traits by the PCA analysis. The first four components that explained 76.24% (Table 2) of total variation were taken under study and for the clustering genotypes. The number of components were also determined with the help of the scree plot (Fig 1) and the variance plot (Fig 2). Through this technique, 12 variables were reduced to four principal variables with the help of the PCA. The four components could not take much variation as the studied traits were found to be spread in accordance to different components which is also demonstrated by the biplot (Fig 3).

The most effective trait in the first component were number of days to booting, days to heading, days to maturity, flag leaf duration and grain filling duration. Days to flag leaf senescence, days to maturity, number of grains per spike, grain weight per spike and grain yield were the major effective traits in the second component. The most effective traits in third component were number of grains per spike and plant height. Also, days to flag leaf senescence, grain weight per spike and plant height were the most effective trait governing fourth component (Table 3). These were the major effective traits that governed the variation in these four components. Chahal and Gosal (2002), stated that characters with largest absolute values closer to unity within the first PC influence the clustering more than those with lower absolute values closer to zero.

Cluster analysis

The clustering of the 50 genotypes under study based on the studied traits are presented in the dendrogram (Fig 4). Clustering was done through Ward's method. The critical examination of the dendrogram after the cluster analysis and PCA, revealed four clusters. Since, the analysis is based on quantitative traits, cluster was obtained based on similarity percentage and related characters. The mean value of all the traits studied of all the clusters formed are presented in Table 4.

Two wheat genotypes, genotype 1 and 50 were grouped in cluster 1 which represented the least 4% of total genotypes. This cluster represented the genotype having highest value of days to flag leaf senescence, flag leaf duration, grain filling duration, thousand kernel weight, flag leaf area, plant height and grain yield.

Cluster 2 included 15 wheat genotypes (2, 4, 5, 9, 11, 22, 24, 25, 26, 28, 29, 31, 32, 36 and 38). This group comprises 30% of total wheat genotypes which are kept under study. Cluster 2 had the highest value of days to booting, days to heading and lowest flag leaf area and yield in comparison to other clusters. This cluster had shown moderate value of plant height, number of grains per spike and days to maturity.

Cluster 3 had the most 23 genotypes (Genotype 3, 6, 7, 8, 12, 13, 14, 16, 18, 23, 27, 30, 33, 34, 35, 37, 39, 41, 44, 45, 46, 47 and 49) which represented 46% of the total study population. This cluster had moderate value of all the traits that were studied.

There were 10 genotypes (Genotype 10, 15, 17, 19, 20, 21, 40, 42, 43 and 48) in Cluster 4, which represented 20% of the genotype. The genotype of this cluster had the highest number of grains per spike. The genotypes also showed moderate performance in terms of grain yield, plant height and grain filling duration.

Thus, some distinct clusters were observed in the study in the multivariate analysis after

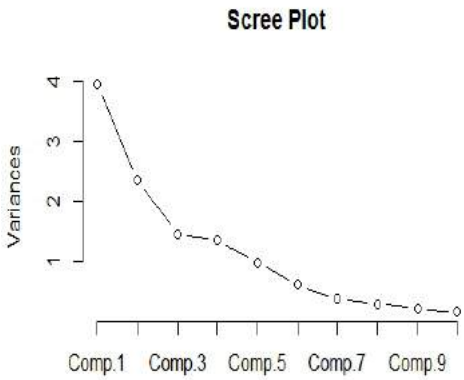

Figure 1. Scree plot for the determination of number of components in PCA.

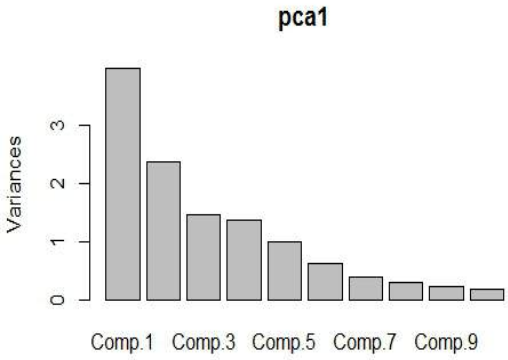

Figure 2. Plot showing the number of principal components and respective variances.

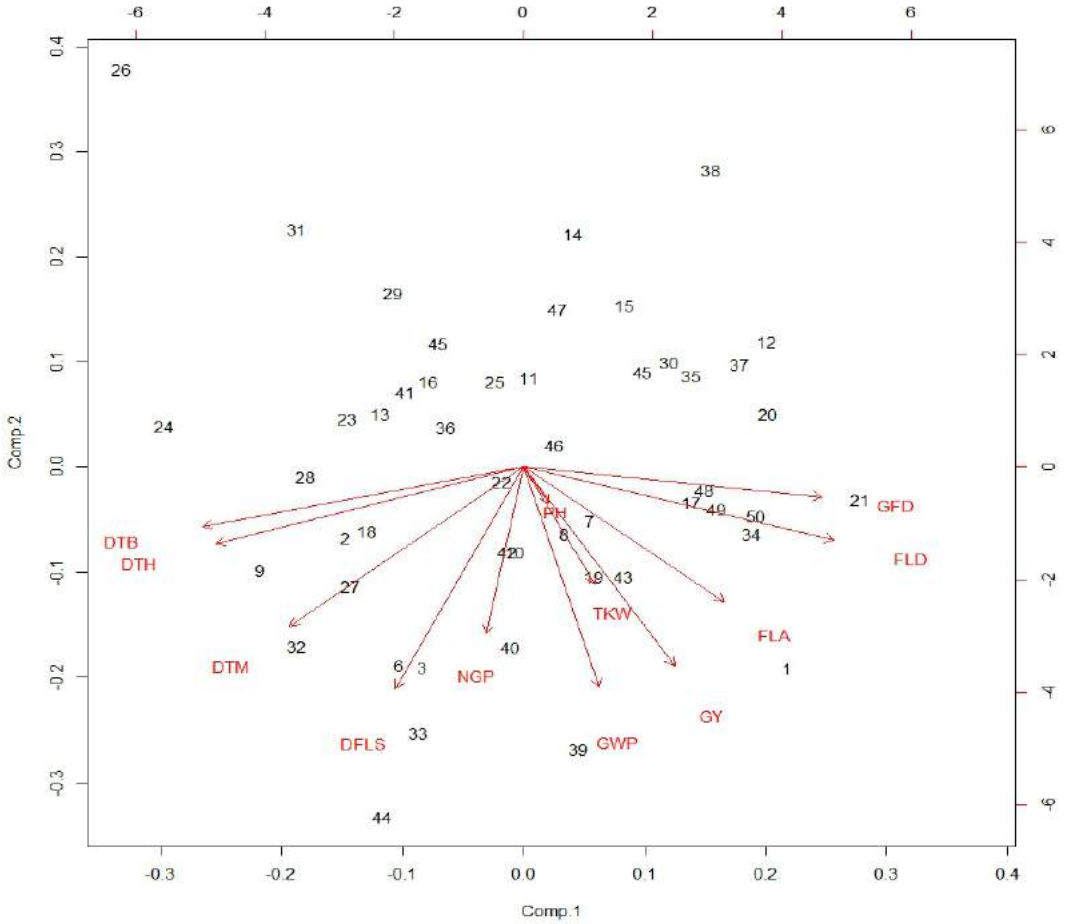

Figure 3. Biplot of all the studied traits of 50 wheat genotypes.

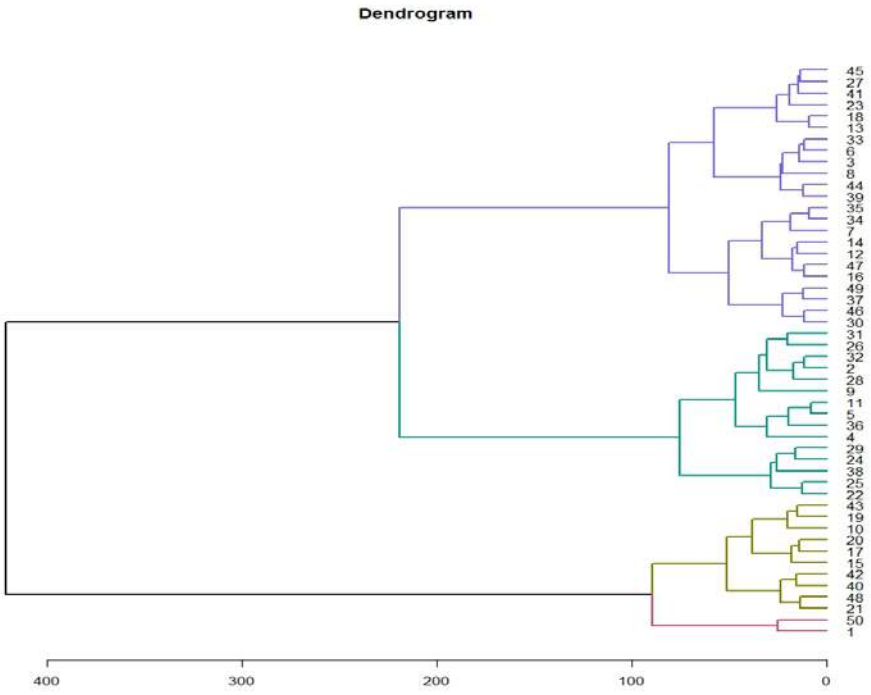

Figure 4. Dendogram of 50 genotypes for 12 studied variables using hierarchical cluster analysis (ward's method).

Table 1. List of the genotypes used for the experiment.

Entry No.	Genotype
1	GAUTAM
2	KACHU #1
3	QUAIU #1
4	BAJ #1
5	FRANCOLIN #1
6	KACHU/BECARD//WBLL1*2/BRAMBLING
7	QUAIU #1/SUP152
8	QUAIU #1/SUP152
9	KACHU//KIRITATI/2*TRCH
10	KIRITATI//HUW234+LR34/PRINIA/3/BAJ #1
11	ND643/2*WBLL1//VILLA JUAREZ F2009
12	SUP152/FRNCLN
13	BAJ #1/SUP152
14	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3 *CNO79//2*SERI
15	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/2*DANPHE #1
16	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/2*FRNCLN
17	BAJ #1/3/2*HUW234+LR34/PRINIA//PFAU/WEAVER
18	KISKADEE #1*2//KIRITATI/2*TRCH
19	MUTUS*2/HARIL #1
20	BAJ #1*2/TINKIO #1
21	BAJ #1*2//ND643/2*WBLL1

22	WBLL1*2/BRAMBLING*2//BAVIS
23	PRL/2*PASTOR//WHEAR/SOKOLL
24	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/4/WAXWING*2/KRONSTAD F2004
25	WHEAR/KIRITATI/3/C80.1/3*BATAVIA//2*WBLL1/4/BECARD
26	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/KIRITATI/2*TRCH/6/BAJ #1
27	FRET2*2/BRAMBLING//KIRITATI/2*TRCH/3/FRET2/TUKURU//FRET2
28	KACHU*2/SUP152
29	DANPHE/PAURAQUE #1//MUNAL #1
30	KIRITATI//2*PRL/2*PASTOR/3/CHONTE/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
31	KIRITATI//HUW234+LR34/PRINIA/3/CHONTE/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
32	KIRITATI//HUW234+LR34/PRINIA/3/FRANCOLIN #1/4/BAJ #1
33	MUTUS//KIRITATI/2*TRCH/3/WHEAR/KRONSTAD F2004
34	ND643/2*WBLL1//2*KACHU
35	PAURAQ/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/6/PAURAQUE #1
36	PAURAQ/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/PAURAQUE #1
37	FRANCOLIN #1*2//ND643/2*WBLL1
38	FRANCOLIN #1/CHONTE//FRNCLN
39	BAJ #1*2/KISKADEE #1
40	WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1*2/4/KIRITATI/2*TRCH
41	TAM200/PASTOR//TOBA97/3/FRNCLN/4/WHEAR//2*PRL/2*PASTOR
42	TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/VORB/8/MILAN/KAUZ//DHARWAR DRY/3/BAV92
43	FALCIN/AE.SQUARROSA (312)/3/THB/CEP7780//SHA4/LIRA/4/FRET2/5/DANPHE #1/11/CROC_1/AE.SQUARROSA (213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA
44	BAVIS/NAVJ07
45	CROC_1/AE.SQUARROSA (213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA/11/ATTILA*2/PBW65
46	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1/5/DANPHE #1
47	BAVIS/3/ATTILA/BAV92//PASTOR/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2
48	BABAX/LR42//BABAX/3/ER2000/4/PAURAQUE #1
49	VEE/MJI//2*TUI/3/PASTOR/4/BERKUT/5/BAVIS
50	SOKOLL/3/PASTOR//HXL7573/2*BAU/5/CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2

Table 2. Eigen analysis of the Correlation Matrix.

	Comp.1	Comp.2	Comp.3	Comp.4	Comp.5	Comp.6
Standard deviation	1.990348	1.535779	1.212858	1.165205	0.998895	0.790714
Proportion of Variance	0.330124	0.196551	0.122585	0.113142	0.083149	0.052102
Cumulative Proportion	0.330124	0.526675	0.649261	0.762403	0.845552	0.897654
	Comp.7	**Comp.8**	**Comp.9**	**Comp.10**	**Comp.11**	**Comp.12**
Standard deviation	0.629812	0.556996	0.473683	0.42085	0.320398	0.130749
Proportion of Variance	0.033055	0.025854	0.018698	0.01476	0.008555	0.001425
Cumulative Proportion	0.93071	0.956563	0.975261	0.990021	0.998575	1

Table 3. PCA analysis of 16 studied traits in wheat genotypes.

	Comp.1	Comp.2	Comp.3	Comp.4
Days to booting	-0.441	-0.121	-	0.129
Days to heading	-0.423	-0.157	0.217	-
Days to flag leaf senescence	-0.176	-0.453	-	-0.454
Days to maturity	-0.322	-0.326	0.235	-0.311
Flag leaf duration	0.426	-0.15	-	-0.27
Grain filling duration	0.41	-	0.154	-0.291
Thousand kernel weight	-	-0.239	0.205	-
Flag leaf area	0.275	-0.275	0.157	-
Number of grains per spike	-	-0.341	-0.636	-
Grain weight per spike	0.104	-0.45	-0.173	0.466
Plant height	-	-	0.602	0.493
Grain yield	0.207	-0.407	-	0.22

Table 4. Mean value of all the studied traits of the clusters formed after cluster analysis.

Variable	Cluster 1	Cluster2	Cluster3	Cluster4	Grand centroid
Days to booting	61.75	67.777	66.483	64.12	66.209
Days to heading	68.26	72.871	71.672	69.5	71.461
Days to flag leaf senescence	115.04	113.737	114.773	113.558	114.23
Days to maturity	121.03	121.411	121.14	120.513	121.092
Flag leaf duration	60	50.693	54.895	57.307	54.321
Grain filling duration	46.24	39.835	41.916	43.394	41.76
Thousand kernel weight (gm)	55.08	46.3	43.76	42.564	44.736
Flag leaf area (cm^2)	157.49	66.962	92.752	121.327	93.319
Number of grains per spike	45.365	50.926	52.616	55.062	52.308
Grain weight per spike (gm)	2.37	2.204	2.334	2.431	2.316
Plant height (cm)	104.735	101.529	103.596	103.679	103.038
Grain yield (t/ha)	5.865	4.971	5.719	5.714	5.499

the study of PCA. Similar works have been done by Maqbool et al., 2010 and Sajjad et al., 2011 for grouping of germplasm by principal component analysis (Degewione and Alamerew, 2013).

Hence, the PCA and cluster analysis showed the variation in different traits as well as in the different genotypes under study.

Conclusion

The present study confirmed that bread wheat genotypes showed wide amount of variations for the character studied and it also suggested that ample opportunities for genetic improvement of bead wheat genotypes through selection directly from wheat genotypes and conservation of the germplasm for future utilization. Selection of genotypes from Cluster 2 (Gautam

andSOKOLL/3/PASTOR//HXL7573/2*BAU/5/CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2)would lead to selection of the superior genotypes. Also cluster 4 can be considered worthwhile for selection due to its high yield, higher flag leaf area, grain weight per spike, flag leaf duration and lower days to maturity. These genotypes can be considered of breeding operations as well as for further study for developing superior wheat genotypes. These wheat genotypes need to be crossed and selected to develop high yielding pure line variety.

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