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Cluster analysis of Elite spring wheat (*Triticum aestivum* L.) genotypes based on yield and yield attributing traits under irrigated condition

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Abstract

The present study comprises the observation of thirty bread wheat genotypes developed by Nepal Agriculture Research Council and International Maize and Wheat Improvement Centre. This study was conducted with the objective to study the clusters of those wheat lines and the specific characters of the clusters, relationship among various clusters and their performance regarding different phenological, agro-morphological, grain yield and its components and others traits. The experiment was conducted in Alpha-lattice design with thirty wheat genotypes as treatments with three replications. Observations were recorded for days to booting, days to heading, days to maturity, days to flag leaf senescence, flag leaf duration, plant height, spike length, grains per spike, thousand kernel weights, biomass yield, grain yield and hectoliter weight and SPAD reading of the flag leaf. Four clusters of wheat genotypes were formed in a dendrogram by using euclidean distance and average linkage method. Cluster analysis revealed the grouping of four genotypes in one cluster that had better performance in yield and its attributes like; 1000-grain weight, plant height, grain filling duration and hectolitre weight. The observation of first cluster and the association therein of high value for the positively correlated yield attributing traits and high value of yield itself hint that selection of varieties from the first cluster can be worthwhile. So, these genotypes may be exploited for their direct release or as parents in hybridization programmes to develop high yielding wheat varieties

Key words: CIMMYT, Cluster analysis, Elite spring wheat, NARC, Wheat.

Introduction

Wheat (*Triticum aestivum* L.) is a cereal crop which belongs to the grass family (Class Liliopsida, Family Poaceae). It belongs to the tribe Triticeae (McFadden & Sears, 1946). On world basis, wheat ranks first in terms of acreage and production while it ranks third in Nepal after rice and maize in terms of production but in terms of consumption it ranks second. The area under cultivation, production

and productivity was 762373 hectares, 1975625 metric ton and 2591 kg/ha respectively (MoAD, 2014/15). Wheat occupies 22.57% of the total area under cereal production and contributes 21.32% of total cereal production in Nepal (MoAD, 2014/15). Thus, wheat is a major crop in the world as well as in Nepal.

Cluster analysis is one of the multivariate techniques whose main objective is to group individuals or objects based on characteristics they possess, so that individuals with similar description are mathematically gathered into the same cluster. The clusters formed should show higher homogeneity within clusters and heterogeneity between clusters. Thus, if the classification is successful, individuals within a cluster come closer when plotted geometrically and different clusters are plotted apart (Hair et al., 1995). Hierarchical clustering methods are generally used in analysis of genetic diversity in crop species. These methods proceed either by a series of successive mergers or by a series of successive divisions of group of individuals, which is also known as 'agglomerative hierarchical' method, starts with a single individual. Thus, initially there are as many clusters as individuals (Mohammadi & Prasanna, 2003). The most similar individuals are first grouped and these initial groups are merged according to their similarities. Among various agglomerative hierarchal methods, the UPGMA (Unweighted Paired Group Method using Arithmetic averages) (Panchen, 1992) is most commonly used clustering algorithm, followed by the Ward's minimum variance method (Ward, 1963).

The study comprises the observation of different wheat lines developed by National Agriculture Research Council (NARC) of Nepal, different elite lines of spring wheat developed by International Maize and Wheat Improvement Centre (CIMMYT) and also different harvest plus lines developed by CIMMYT. This study was conducted with the objective to study the clusters of those wheat lines and the specific characters of the clusters, relationship among various clusters and their performance regarding different phenological, agro-morphological, grain yield and its components and others traits. The objective is also to identify the superior cluster and the superior wheat lines which can be further used in national as well as international breeding programs as promising parents as well as making different breeding strategies. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase (Islam, 2004; Raut et al., 2017). Through understanding the interrelationships existed between yield and its contributing components and understanding the diversity in the performance in different genotypes, we can improve the efficiency of crop breeding programmes (Mohammadi et al., 2003; Raut et al., 2017).

Material and Methods

The study was carried at the research farm of Agriculture and Forestry University, Rampur, Chitwan, Nepal, from November 2015 to June 2016. The GPS location of the site was 27.647680N latitude and 84.347500E longitude and it was at an altitude of 171 meters above sea level. Thirty bread wheat genotypes listed in Table 1 were used as planting material. They were obtained from the Agriculture Botany Division, Nepal Agriculture Research Council, Khumaltar, Nepal which included twenty three elite lines selected from 35th Elite Spring Wheat Yield Trial (ESWYT), five bio-fortified harvest plus lines from 5th Harvest Plus Yield Trial (HPYT) developed from CIMMYT, Mexico and two Nepalese commercial cultivars, namely

Vijay and Gautam. The experiment was conducted in Alpha-lattice design with thirty wheat genotypes as treatments with three replications. Each replication consisted of 5 blocks and six plots were formed in each block. Each plot was 2 m in length and 2 m in width. Each plot consisted of 8 rows with a spacing of 25 cm between rows and continuous sowing was done in each row. The planting was done in 4th December 2015. The chemical fertilizers were applied at the rate of 120:60:60 kg NPK per hectare. First irrigation was done at the crown root initiation (CRI) stage (Zadoks' growth stage Z1.3, Z2.1) second at the time of booting stage (Zadoks' growth stage) and third at grain filling stage.

Observations were recorded for days to booting, days to heading, days to maturity, days to flag leaf senescence, flag leaf duration, plant height, spike length, grains per spike, thousand kernel weights, biomass yield, grain yield and hectoliter weight and SPAD reading of the flag leaf. Data entry and processing was carried out using Microsoft Office Excel 2007. Cluster analysis was done with the help of Minitab 17.

Results and Discussions

Genotypes were grouped into various clusters on the basis of their performance which is displayed in a dendrogram (Figure 1). The dendrogram for thirty wheat genotypes on the basis of their morpho-physiological and yield and yield attributing traits was constructed based on the similarity percentage and related characters. Four clusters of wheat genotypes were formed in a dendrogram by using euclidean distance and average linkage method. ESWYT 120 and ESWYT 145 (similarity = 98.68%) and ESWYT 115 and ESWYT 143 (similarity = 98.44%) were most closely related genotypes while Vijay and HPYT 403 were most distantly related (similarity = 42.73%).

Cluster 1 consisted of four genotypes namely; Vijay, CHIBIA// PRLII/ CM65531/ 3/ FISCAL/ 4/ DANPHE #1/ 5/ CHIBIA// PRLII/ CM65531/ 3/ SKAUZ/ BAV92, Gautam and BLOUK#1/4/ WHEAR/ KUKUNA/3/ C80.1/ 3*BATAVIA// 2*WBLL1/5/MUNAL #1. It was observed that high value traits like grain yield, thousand kernel weight, biomass yield, hectoliter weight, plant height, spike length, flag leaf and grain filling duration were associated with genotypes of this cluster.

Cluster 2 consisted of eight genotypes. They were ESWYT 104, ESWYT 139, ESWYT 148, ESWYT 115, ESWYT 143, ESWYT 106, ESWYT 111 and ESWYT 129. It was observed that number of grains per spike and AUSRC values were associated with genotypes of this cluster.

Cluster 3 consisted of ten genotypes; ESWYT 105, ESWYT 120, ESWYT 145, ESWYT 123, ESWYT 109, HPYT 402, HPYT 438, ESWYT 110, ESWYT 119 and HPYT 420. The genotypes belonging to this cluster had average performance for almost all traits.

Cluster 4 consisted of eight genotypes; ESWYT 112, HPYT 414, ESWYT 147, ESWYT 114, ESWYT 121, ESWYT 118, ESWYT 140 and HPYT 403. Genotypes belonging to this cluster had least values of grain yield, biomass yield, thousand kernel weight, hectoliter weight and plant height.

Cluster analysis revealed the grouping of four genotypes in one cluster that had better performance in yield and its attributes like; 1000-grain weight, plant height, grain filling duration and hectolitre weight. Khodadadi et al., (2011) and Ajmal et al., (2013) also reported same kind of results, that genotypes which show better performance in yield attributing traits are grouped in one cluster. The observation of first cluster and the association therein of high value for the positively correlated yield attributing traits and high value

Table 1. List of wheat genotypes grown for the field experiment, 2015/2016.

| Trt.	Genotypes	Cross/Pedigree
1	Vijay	Vijay
2	Gautam	Gautam
3	ESWYT 104	MISR 1
4	ESWYT 105	MUNAL #1
5	ESWYT 106	BECARD #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ
6	ESWYT 109	KACHU//KIRITATI/2*TRCH
7	ESWYT 110	KACHU/CHONTE
8	ESWYT 111	KIRITATI//HUW234+LR34/PRINIA/3/BAJ #1
9	ESWYT 112	MUTUS//ND643/2*WBLL1
10	ESWYT 114	ND643/2*WBLL1//KACHU
11	ESWYT 115	SUP152/QUAIU #2
12	ESWYT 118	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/CNO79//PF70354/MUS/3/PASTOR/4/BAV92/6/ND643/2*WBLL1
13	ESWYT 119	BAJ #1/KISKADEE #1
14	ESWYT 120	CHEWINK #1/MUTUS
15	ESWYT 121	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/2*MUNAL
16	ESWYT 123	QUAIU #1/2*SUP152
17	ESWYT 129	CHYAK1*2/3/HUW234+LR34/PRINIA//PFAU/WEAVER
18	ESWYT 138	BLOUK #1/4/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/MUNAL #1
19	ESWYT 139	BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47/4/ND643/2*WBLL1/5/BABAX/LR42//BABAX*2/3/PAVON 7S3, +LR47
20	ESWYT 140	QUAIU #1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/6/BECARD
21	ESWYT 141	CHIBIA//PRLII/CM65531/3/FISCAL/4/DANPHE #1/5/CHIBIA//PRLII/CM65531/3/SKAUZ/BAV92
22	ESWYT 143	KACHU*2/CHONTE
23	ESWYT 145	ND643/2*WBLL1//2*KACHU
24	ESWYT 147	FRANCOLIN #1*2//ND643/2*WBLL1
25	ESWYT 148	BECARD//KIRITATI/2*TRCH/3/BECARD
26	HPYT 402	BAJ #1
27	HPYT 403	KACHU #1
28	HPYT 414	FRANCOLIN #1/7/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES/5/T.SPELTA PI348599/6/REH/ HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213)//PGO/4/HUITES
29	HPYT 420	NELOKI/3/IWA 8600211//2*PBW343*2/KUKUNA
30	HPYT 438	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU#1/6/TOBA97/PASTOR/3/T.DICOCCON PI94624/AE.SQUARROSA(409)//BCN/4/BL 1496/MILAN//PI 610750

Table 2. Cluster centroids of different traits observed on thirty wheat genotypes at Rampur, Chitwan (2015/16).

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Grand centroid
DH	80.58	80.96	81.10	81.88	81.20
DM	116.50	114.58	115.93	114.21	115.19
FLD	39.25	36.67	36.17	34.63	36.30
GFD	34.67	30.33	31.90	29.13	31.11
PH	93.01	85.56	87.19	82.25	86.21
SL	10.39	9.71	9.85	9.68	9.84
NGPS	43.83	45.21	45.40	42.71	44.42
TKW	44.05	36.61	37.45	33.92	37.16
GY	3140.00	2048.75	2379.50	1460.84	2147.72
BY	8436.67	5731.25	6908.50	4444.58	6141.28
Kg/hL	78.33	73.77	76.47	72.44	74.92
AUSRC	581.38	593.83	602.71	579.41	591.29
DH=Days to Heading, DM= Days to Maturity, FLD= Flag Leaf Duration, GFD= Grain Filling Duration, PH= Plant Height, SL= Spike Length, NGPS= Number of Grains per Spike, TKW= Thousand Kernel Weight, GY= Grain Yield, BY= Biological Yield, Kg/hL= Hectolitre weight, AUSRC= Area under SPAD Retreat Curve					

Table 3. Distances between cluster centroids of wheat genotypes grown at Rampur, Chitwan (2015/16).

	Cluster1	Cluster2	Cluster3	Cluster4
Cluster1		2917.26	1707.11	4330.89
Cluster2			1222.87	1414.71
Cluster3				2629.72
Cluster4				

Figure 1. UPGMA clustering of thirty wheat genotypes grown at Rampur, Chitwan (2015/16).
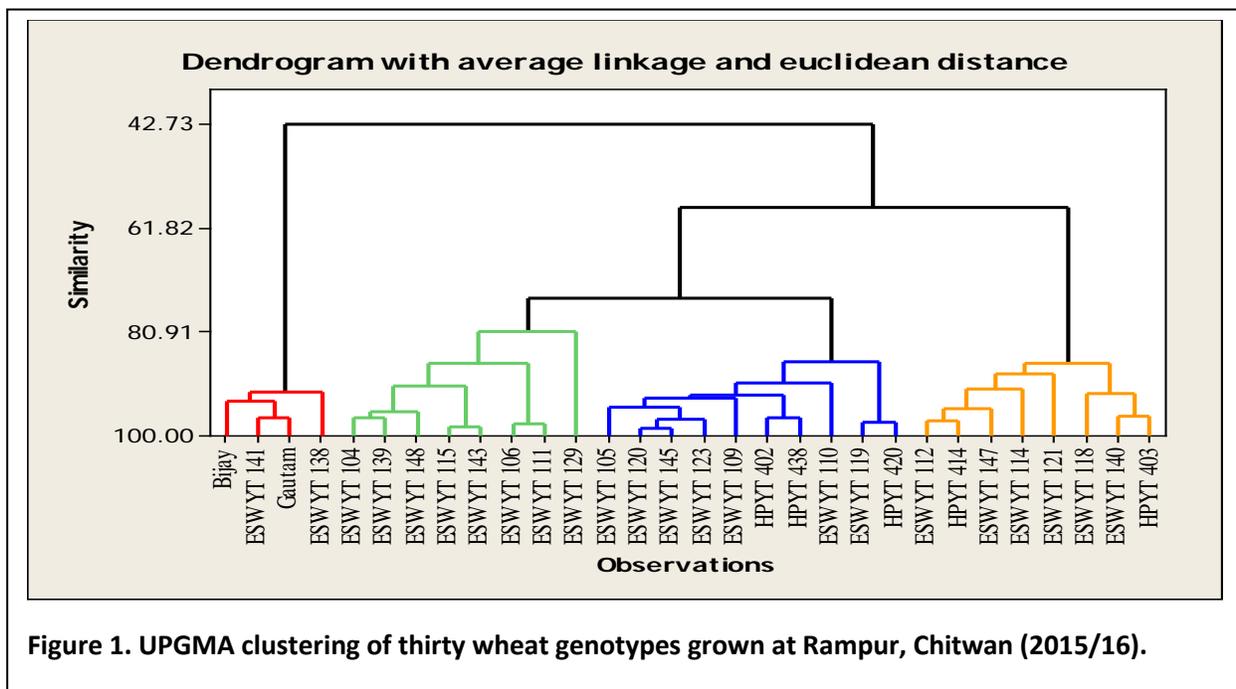
of yield itself hint that selection of varieties from the first cluster can be worthwhile. The distribution pattern among all genotypes into different clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits. Genotypes of Cluster 1 had shown best performance than others on grain yield, thousand kernel weight, biomass yield, hectoliter weight, plant height, spike length, flag leaf and grain filling duration. So, these genotypes may be exploited for their direct release or as parents in hybridization programmes to develop high yielding wheat varieties.

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