

RESEARCH ARTICLE

Delineation of genetic diversity in the advance breeding lines developed through systematic breeding in wheat (*Triticum aestivum* L.)

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Abstract

An experiment was conducted at CCS HAU, Regional Research Station, Bawal (Haryana) during *rabi* 2013-14 with 46 bread wheat advance lines which were developed through systematic breeding to assess the genetic diversity for yield and its traits. The lines were grouped into eight distinct clusters and distribution pattern indicated that maximum number of lines were grouped into the clusters I and V with 8 genotypes each followed by cluster VII with 7 genotypes. The inter-cluster distance in most of the cases was higher than the intra-cluster distance, indicating wider genetic diversity among the advance lines of different groups. Genotypes grouped into cluster III showed maximum intra cluster diversity whereas highest inter cluster diversity was exhibited by clusters II and V followed by cluster II and IV, showing wide diversity among the groups. The genotypes P 12714, PBW 343, P12186, P 12876, P 12864 proved to be promising for one or more different characters. From cluster mean performance, the advanced lines in cluster III, IV and I deserve consideration for their direct use as parents in hybridization programmes to obtain high heterotic response and thus better segregants for high grain yield in bread wheat.

Keywords: Wheat, genetic diversity, cluster, grain yield, breeding line

Introduction

Wheat attains unique prominent position in agriculture and economic perspective of our country because of being second most important food crop after rice. In India, the area under wheat is around 29.55 million hectares with the production and productivity of 101.20 million tons and 3424 kg ha⁻¹, respectively. Haryana state has achieved a productivity level of 4.64 tons ha⁻¹ on 2.51 million hectares (ICAR-IIWBR, 2019). Our country has witnessed spectacular growth in production and productivity, which has made country not only self sufficient but also for exporting surplus wheat. There is need to further increase in production to fulfill requirement of exploding population, maintenance of adequate buffer stock and to meet out demand for processing industries.

The presence of genetic diversity among the genotypes is a prerequisite and paramount important for successful wheat breeding programme. It is true that the more diverse plants, the greater chance of obtaining high heterotic combinations in segregating generations during genetic improvement.

Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. This study was therefore, conducted to identify genetically divergent bread wheat advanced lines developed through systematic breeding and tested earlier for high yield potential along with well adapted varieties in the region to access the genetic diversity which could be subsequently utilized in the wheat improvement.

Materials and methods

The experimental material consisted of 46 bread wheat advanced breeding lines including six national checks/popular varieties namely HD 3086, WH 1105, PBW 343, HD 2967, DBW 17 and DBW 88 were evaluated in randomized block design with three replications at CCS HAU, Regional Research Station, Bawal (Haryana) during *rabi* 2013-14. These genotypes were received from Wheat and Barley Section of Department of Genetics and Plant Breeding, CCS HAU. These genotypes were selected from advanced breeding material developed during previous year for high seed yield and tested previously. Each genotype was grown in six rows with a plot size of 5 x 1.20 m². Recommended agronomic practices were followed to raise a good crop growth. The observations on ten quantitative traits viz., plant height (cm), ear length (cm), number of tillers per meter row, number of grains per spike, days to heading, days to maturity, 1000-grain weight (g), harvest index (%), biological yield (kg/plot) and grain yield (kg/plot) were recorded at appropriate crop growth stage. Five randomly selected competitive plants in each replication were recorded for all the traits under study except of days to heading, days to maturity, biological yield and grain yield which were recorded on plot basis. Harvest index was

calculated as per formula given by Donald and Humblin (1976).

Analysis of variance to test the significance for each character was carried out as per methodology given by Panse and Sukhatme (1967). To quantify genetic divergence between any two genotypes or group of genotypes, Mahalanobis' D² statistics (1936) as described by Rao (1952) was used and the genotypes were grouped into different clusters on the basis of Ward's minimum variance method (Spark, 1973).

Results and discussion

Diversity study will help breeder to choose particular material as per need in his crossing programme. Based on the clustering pattern the specificity and usefulness of the genotype will be decided. In the present study the mean sums of squares due to genotypes were significant thereby revealing sufficient amount of genetic variation among the lines for all the traits studied. It also indicates the genetic lineage differentiation among the lines.

The cluster analysis assigned 46 genotypes into eight distinct clusters (Table 1 and Fig. 1). Clustering pattern revealed that the clusters I and V were the largest one with 8 lines each followed by clusters VII, IV, VIII, III and VI with 7, 6, 6, 5 and 5, respectively. Minimum numbers of lines were recorded in cluster II comprised of one only. Significant amount of variability can be inferred from the pattern of group constellation. The grouping of genotypes and their possible classification for use in hybridization programme as donors for yield traits are very clear and based on present study might give transgressive segregants for desired traits. Earlier studies have also reported substantial genetic divergence in wheat materials (Ajmal *et al.*, 2013; Aharizad *et al.*, 2012; Ahmad *et al.*, 2014; Hailegiorgis *et al.*, 2011; Khodadadi *et al.*, 2014; Kumar *et al.*, 2013).

The estimates of intra-and inter-cluster distances (Table 2 and Fig. 2) revealed that the genotypes present in a cluster had little genetic divergence from each other with respect to aggregate effect of 10 characters under study, while much more genetic diversity was observed between the lines belonging to different clusters. The intra cluster distance in cluster III was maximum (3.828) followed cluster IV (3.470) and VIII (3.467) suggesting that the genotypes in these clusters were relatively more diverse among themselves. The highest inter-cluster distance was observed between clusters II and V followed by clusters II and IV while it was minimum between cluster V and VI (3.716). Ferdous *et al.*, (2011) studied genetic divergence in wheat genotypes and also reported smaller D^2 values for genotypes belonging to same group than between those belonging to different clusters.

The eight clusters showed considerable differences in mean values for different characters under study (Table 3). Cluster I consisted of 8 lines and had characteristic feature of high 1000-grain weight and moderately high number of tillers per meter row and biological yield with lowest number of grains per spike. The genetic distance between

these genotypes was 3.095. Cluster II, comprised of one genotype, exhibited minimum number of days to head and maturity, shortest plant height and had lowest cluster means value for number of tillers per meter row, 1000-grain weight, biological yield as well as grain yield. Cluster III had 5 genotypes including national check WH 1105 having characteristics of highest number of grains per spike, moderately high 1000-grain weight, biological yield and harvest index with highest grain yield. Maximum genetic distance (3.828) was observed between genotypes of this cluster. Cluster IV, contained 6 genotypes including PBW 343, HD 2967 and DBW 17, recorded with highest cluster mean for harvest index with second highest for grain yield. The genetic distance value of these genotypes was 3.470. Eight lines constituted cluster V and characterized by moderately high number of tillers per meter row, ear length, 1000-grain weight, harvest index and grain yield with maximum number of days to head. The genetic distance between these lines of cluster was 3.133. Cluster VI which consisted of 5 lines, exhibited longest ear length with maximum biological yield.

Table 1: Clustering pattern of different advanced lines

Cluster No.	Genotypes	No. of genotypes
I	P 12013 (1), P 12502 (12), P 12294 (42), P 12336 (3), HD 3086 (19), P 12465 (8), P 12804 (35), P 12186 (4)	8
II	P 12503 (11)	1
III	WH 1105 (6), P 12864 (34), P 12714 (14), P 12207 (29), P 12876 (41)	5
IV	P 12725 (18), PBW 343 (27), HD 2967 (24), DBW 17 (44), P 12811 (9), P 12505 (43)	6
V	P 12755 (2), P 12272 (37), P 12730 (32), P 12783 (38), P 13020 (16), P 12252 (45), P 12715 (28), P 12713 (31)	8
VI	P 12778 (17), P 13049 (22), P 12182 (25), P 12729 (33), P 12790 (26)	5
VII	P 12946 (5), P 12329 (20), P 12865 (7), P 12908 (10), P 12399 (30), P 12368 (46), P 12499 (23)	7
VIII	P 12302 (21), P 12768 (39), P 11970 (13), P 12385 (36), P 13042 (40), DBW 88 (15)	6

Values in parenthesis indicates the serial number of genotypes

Figure 1: Clustering of wheat advanced lines by Ward's minimum variance method

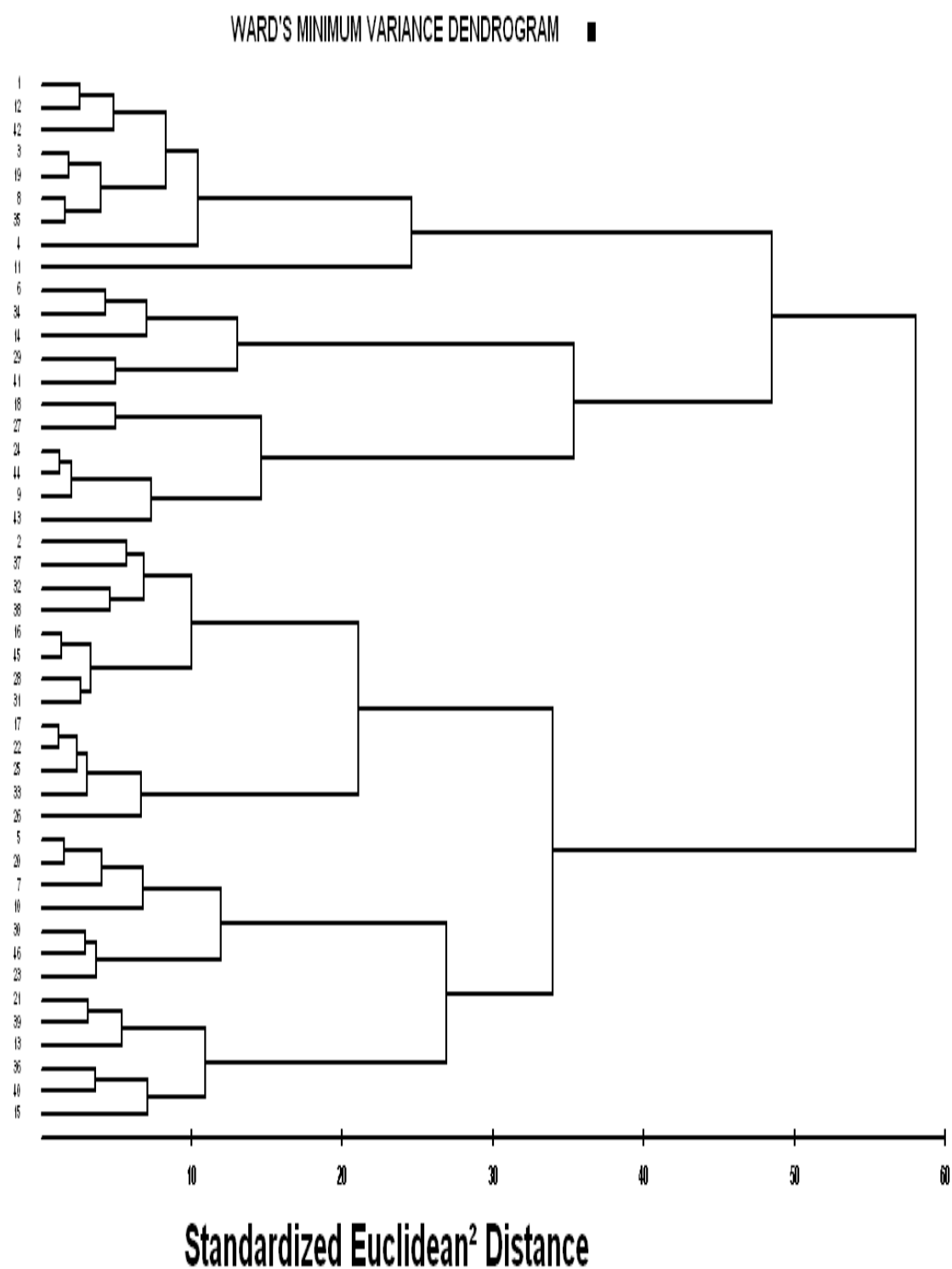


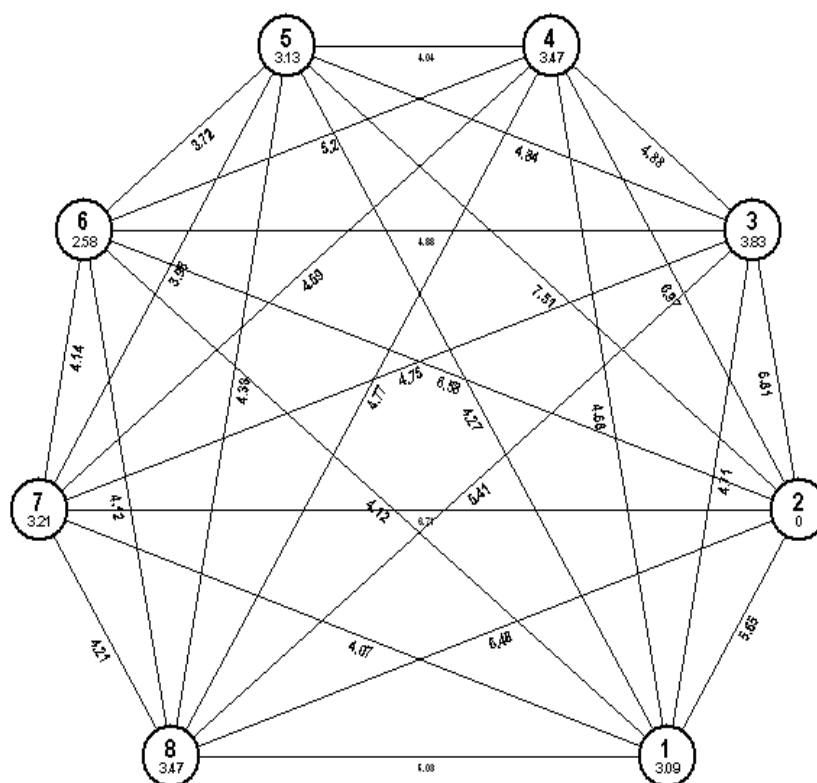
Table 2: Estimates of intra-and inter-cluster distances

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	3.095	5.645	4.708	4.682	4.267	4.124	4.067	5.031
II		0.000	6.809	6.973	7.506	6.578	6.713	6.478
III			3.828	4.882	4.842	4.876	4.751	5.406
IV				3.470	4.042	5.200	5.585	4.771
V					3.133	3.716	3.982	4.379
VI						2.580	4.144	4.122
VII							3.211	4.213
VIII								3.467

Diagonal: Intra-cluster distances

Off-diagonal: Inter-cluster distances

Figure 2: Euclidean Distances in wheat genotypes



Cluster VII had 7 genotypes was responsible for highest plant height and maximum number of tillers per meter row. The genotypes of this cluster showed genetic distance of 3.211. The six genotypes that constituted cluster VIII was characterized by maximum number of days to mature with shortest spikes and showed moderately high mean performance for number of grains per spike with genetic distance of 3.467. Several earlier researchers reported genetically distant parents for hybridization through diversity study (Singh *et al.*, 2014; Verma *et al.*, 2013, Verma *et al.*, 2014). Khodadadi *et al.* (2011) also showed the presence of high genetic divergence among wheat genotypes based on cluster and principal component analyses for breeding strategies. Out of 10 traits studied, contribution of number of grains per spike towards divergence was maximum (31.11%) followed by days to heading (30.82%), 1000-grain weight

(15.17%) and ear length (8.02%), whereas the remaining traits days to maturity (4.25%), plant height (3.77%), grain yield (3.57%), biological yield (1.35%), number of tillers (1.26%) and harvest index (0.68%) contributed very little to diversity (Table 4) and supported by results of Kumar *et al.*, (2009). Most diverse and superior genotypes with desirable traits from different clusters are represented in Table 5. PBW 343 and P 12714 performed good for number of grains per spike, 1000 grain weight, harvest index and grain yield; P 12186 for number of tillers per meter row; P 12876 and P 12864 for number of grains per spike, biological yield and grain yield, hence, these genotypes may be used in future hybridization program for wheat improvement similar results were reported by Ali *et al.*, (2008) in wheat.

Table 3: Average performance of different clusters for yield and its contributing traits

Characters	Cluster number							
	I	II	III	IV	V	VI	VII	VIII
Days to heading	96.71	91.67	96.67	99.89	101.75	99.80	99.48	101.50
Days to maturity	136.58	133.33	137.80	140.06	140.21	139.73	138.29	140.50
Plant height (cm)	97.54	87.00	101.67	94.89	101.83	100.80	105.19	100.17
No. of tillers per meter row	125.67	89.33	90.27	105.72	117.08	109.67	126.57	101.72
Ear length (cm)	11.49	11.03	12.10	10.97	12.41	12.81	11.02	10.69
No. of grains per spike	42.64	44.33	59.21	45.28	42.73	43.50	49.40	50.83
1000-grain weight (g)	39.16	33.17	38.06	37.49	38.29	36.45	34.14	35.18
Biological yield (kg/plot)	6.19	5.37	6.28	5.42	5.88	6.66	6.00	5.73
Harvest index (%)	35.64	31.23	39.25	43.64	38.46	30.86	36.96	33.00
Grain yield (kg/plot)	2.20	1.67	2.44	2.35	2.24	2.04	2.20	1.88

Table 4: Contribution of different characters towards divergence

Sr. No.	Source	Times ranked 1 st	Contribution towards divergence (%)
1	Days to heading	319	30.82
2	Days to maturity	44	4.25
3	Plant height (cm)	39	3.77
4	No. of tillers per meter row	13	1.26
5	Ear length (cm)	83	8.02
6	No. of grains per spike	322	31.11
7	1000-grain wt. (g)	157	15.17
8	Grain yield (kg/plot)	37	3.57
9	Biological yield (kg/plot)	14	1.35
10	Harvest index (%)	7	0.68

Table 5: Diverse and superior genotypes with desirable traits selected from different clusters

Sr. No.	Characters	Desirable genotypes
1	Days to heading (Early)	P 12503, P 12294
2	Days to maturity (Early)	P 12503, HD 3086
3	Plant height (Medium Dwarf)	P 12013, P 12725, PBW 343, P 12783, P 12294
4	No. of tillers per meter row	P 12186
5	Ear length (cm)	P 12876
6	No. of grains per spike	P 12714, PBW 343, P 12207, P 12864, P 12876
7	1000-grain wt. (g)	P 12714, PBW 343, P 12864
8	Biological yield (kg/plot)	P 12186, P 12864, P 12876
9	Harvest index (%)	P 12714, P 12725, PBW 343, P 12505
10	Grain yield (kg/plot)	P 12186, P 12714, PBW 343, P 12864, P 12876, P 12505

Conclusion

Clustering pattern of advanced breeding lines developed through systematic efforts for high yielding nature provided considerable useful information which could be utilized in genetic improvement of bread wheat. The lines grouped into cluster III showed maximum intra cluster diversity while cluster II and V, followed by clusters II and IV exhibited highest inter cluster diversity. Number of grains per spike contributed maximum towards divergence

followed by days to heading, 1000-grain weight and ear length. The genotypes P 12714, PBW 343, P12186, P 12876, P 12864 proved to be promising for one or more different characters which could be utilized in wheat improvement for trait specific breeding programme. The lines in cluster III, IV and I deserve consideration for their direct use as parents in hybridization programmes to obtain high heterotic response and thus better segregants for high grain yield in bread wheat.

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