GENETIC DIVERGENCE ANALYSIS IN SPRING WHEAT
(T. AESTIVUM L.)

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ABSTRACT

Genetic divergence in 51 genotypes of spring wheat (40 advanced lines and 11 standard checks) was assessed using D^2 analysis. Clustering was done using three different Tocher's values, i.e. 1060, 500 and 300 and genotypes were grouped into 7, 9 and 10 different clusters, respectively. Linkage dendrogram and minimum spanning tree exhibited confirmity with the clustering pattern of D^2 statistic at Tocher's values 500 and 300. Protein content exhibited maximum contribution towards total divergence followed by phenol colour reaction and peduncle length.

Key words: Genetic divergence, Tocher's value, minimum spanning tree, linkage dendrogram, *T. aestivum*.

Wheat is the most important grain crop of the world as a source of human food. To determine genetic diversity, Mahalanobis D^2 statistic has already been used as a very powerful tool [1–6], as it gives the inherent genetic diversity perpetuated in lines. Besides, linkage dendrogram and minimum spanning tree also provide visual idea about clustering and variability present in the population [7–9]. Information is lacking on linkage dendrogram, minimum spanning tree and assessment of effect of parentage (ancestory) on clustering pattern of D^2 analysis. Therefore, the main objective of the present investigation was to study all these parameters in spring wheat.

MATERIALS AND METHODS

Fifty one diverse lines (Table 1) of spring wheat (40 advanced lines and 11 standard checks) were sown in RBD with 3 replications at the research farm of Chandra Shekhar Azad

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University of Agriculture and Technology, Kanpur during Rabi 1988–89. Each genotype was grown in three rows of 3 m length, spaced at 30 cm. The intrarow spacing was 15 cm. Five plants from each genotype replication wise were randomly taken and observations recorded for days to reproductive phase, number of awns per spike, length of peduncle, leaf senescence synchrony of maturity, length of main spike, grains per spike, grain weight per spike, 1000-grain weight, biological yield, grain yield, harvest index, phenol colour reaction, seed hardness, tillers per plant, plant height and protein percentage.

Mahalanobis' D^2 statistic was used to assess divergence. Group constellation was done on the basis of minimum generalized distances using Tocher's method as described by [10]. Clustering was done on three Tocher's values, i.e. 1060 as high 500 as medium and 300 as low. Linkage dendrogram and minimum spanning tree was constructed by using the method suggested by [11] and these formed on the basis of linkage order and r value.

RESULTS AND DISCUSSION

Variance analysis indicated significant differences among the lines for all the traits except tillers per plant. Based on Tocher value 1060 lines were grouped into seven clusters (Table 1) whereas, on Tocher values of 500 and 300, the genotypes were grouped into nine and ten clusters, respectively. At Tocher's value 1060 the biggest cluster was cluster I with 33 entries. Most of these genotypes were grouped into two different clusters at Tocher value 500. At Tocher value 300 the clustering pattern was similar to that of Tocher value of 500 with the exception that strain number 20 and 33 which were grouped in cluster V at Tocher's value 500 made an independent cluster VI at Tocher value 300 raising the total cluster to ten from nine. The striking feature which was common for all the three Tocher's values was that the strains namely 49, 51 and 23 each formed an independent cluster at all the Tocher values consisting of only one genotype each. The parentage of the genotypes did not influence the grouping of genotypes at Tocher values 500 and 300. However, at Tocher value 1060 almost all the check varieties were grouped in single cluster I excluding check DSN 72 (Table 1). DSN 72 framed last cluster in all the three cases. However, these checks grouped into cluster I, II, IV and V at Tocher value 500. On the other hand when Tocher value was reduced to 300, check varieties distributed into clusters I, II, IV and VI.

The highest magnitude of genetic distance was observed between the clusters consisting of ZC 13-26 and DSN 72 at all the three Tocher's value, i.e. 1060 (cluster VI and VII, 131.02), 500 (cluster VIII and IX, 131.02) and 300 (cluster IX and X, 131.02). Intra cluster D values ranged from 0.00 to 24.63 at Tocher value 1060, 0.00 to 16.89 at Tocher value 500 and 0.0 to 16.20 at Tocher value 300. On lowest D values, clusters indicated low variability as compared to the varieties included in cluster showing maximum divergence within the group. Protein content had maximum contribution towards total divergence (70.43%) followed by phenol

Table 1. Composition of clusters based on D^2 statistics in spring wheat (Tocher's value = 1060)

Cluster	Genotypes falling in the cluster	Total strains
I	HTON-10, HTON-BW-16, HD 2329, ZC-27-88, K-78, ZC-29-91, HTON-BW-6, K-8709, ZC-8-13, ZC-35-108, K 8743, HTON-8, K-72, ZC-36-148, ZC-24-71, ZC-12-25, ZC-15-28, Raj 3077, ZC-20-43, ZC-38-152, ZC-2-1, Sonalika, ZC-21-46, SC-31-97, HUW-234, ZC-28-89, HTON-BW-9, ZC-3-2, ZC-17-35 K 8703, ZC-25-73, K 8020, ZC-10-20	33
II	ZC-18-36, ZC-6-11, HTON-BW-15, ZC-5-9, ZC-30-96	5
III	ZC-16-30, ZC-19-38, ZC-26-85, ZC-32-99, ZC-34-106, ZC-22-53, ZC-4-3	7
IV	HTON-BW-13, HTON-BW-17, HTON-BW-22	3
V	HTON-BW-19	1
VI	ZC-13-26	1
VII	DSN 72	1

colour reaction (25.49%) and peduncle length (1.18%). These characters had very high variance ratio as compared to other characters. The cluster mean are presented in Table 2 for Tocher's value 1060.

Table 2. Intracluster character means in spring wheat (Tocher's value = 1060)

Character	Cluster means						
	I	II	III	IV	V	VI	VII
Reproductive phase (days)	49.9	49.6	49.7	49.0	47.3	50.7	51.0
Awns/spike	58.1	53.9	57.4	53.5	65.5	53.3	57.6
Peduncle length (cm)	13.1	13.9	13.3	15.0	13.8	8.7	18.4
Senescence of leaf (days)	6.2	6.5	5.9	5.3	2.7	6.3	8.0
Synchrony of maturity (days)	3.6	4.1	3.9	3.9	7.7	3.7	1.3
Spike length (cm)	10.2	9.9	10.4	6.8	7.3	9.8	10.9
Grains/spike	54.6	48.3	58.2	45.4	45.1	51.8	54.5
Grain weight/spike	1.9	1.8	2.2	1.8	2.0	1.9	1.9
1000-grain weight (g)	35.8	38.6	38.1	43.4	37.5	37.8	37.1
Biological yield/plant (g)	36.6	31.5	36.2	28.8	34.1	31.2	31.3
Economic yield/plant (g)	14.7	11.8	15.2	10.7	12.6	12.4	12.3
Harvest index (%)	40.4	37.3	41.5	37.0	35.8	40.9	39.2
Phenol colour reaction	3.1	3.4	2.7	1.0	1.0	4.0	4.0
Protein content (%)	12.3	14.8	9.7	14.7	11.3	7.6	17.1
Seed hardness	8.7	8.2	8.1	12.5	11.0	9.2	8.5
Tillers/plant	9.2	8.5	9.3	6.6	7.6	8.5	9.4
Plant height (cm)	84.5	87.4	86.0	80.0	79.2	83.7	78.6

Distribution of lines in different clusters based on minimum spanning tree were quite close to clustering pattern of Tocher's method at 500 and 300 values. However, clustering pattern did not show any relationship with spanning tree at Tocher's value 1060. Minimum spanning tree indicated that the strains namely 12, 25, 24, 31, 33 and 20 formed a separate cluster, which was also confirmed by cluster V at Tocher's value 500. The strains 14, 15, 28, 32, 41 and 44 and 47 included in the same cluster in D^2 statistic formed different twigs of the spanning tree. Strain ZC 17-35 acted as a bridge in joining both the twigs of spanning tree. Strain 4, 8, 18, 21, 22, 27, 29, 34, 35, 39, 40, 42, 45, 46 and 48 occurring in a single cluster in D^2 statistics, also formed different branches of spanning tree. As indicated earlier the main contributor towards total divergence were protein content and phenol colour reaction.

Table 3. Mean of the three most important contributing traits toward total divergence of wheat genotypes

Genotype	Peduncle length (cm)	Phenol colour reaction	Protein per-centage	Genotype	Peduncle length (cm)	Phenol colour reaction	Protein per-centage
HTON-10	13.6	4.0	13.5	ZC-12-25	16.6	2.0	12.2
ZC-18-36	15.6	4.0	14.7	ZC-15-28	13.2	4.0	12.4
HTON-BW-16	13.3	4.0	13.6	RAJ-3077	14.0	2.0	12.2
HD-2329	14.0	3.0	11.1	ZC-20-43	11.9	4.0	13.6
ZC-16-30	12.9	2.0	9.8	ZC-5-9	12.8	2.0	14.7
ZC-27-88	11.0	3.3	13.6	ZC-38-152	12.0	4.0	11.2
K-78	18.2	4.0	13.5	ZC-2-1	18.4	2.0	13.5
ZC-29-91	11.7	3.0	12.0	Sonalika	16.2	2.0	11.2
HTON-BW-6	14.4	3.0	13.6	ZC-21-46	13.1	3.0	12.3
K-8709	15.4	3.0	13.6	ZC-30-96	12.0	4.0	14.7
ZC-8-13	19.3	4.0	13.5	ZC-31-97	11.4	4.0	12.4
HTON-BW-13	13.9	1.0	14.6	ZC-34-106	12.8	2.0	10.1
ZC-19-38	22.1	4.0	9.8	HUW-234	14.0	2.0	11.3
ZC-35-100	10.9	4.0	11.2	ZC-28-89	14.5	2.0	12.4
K-8743	11.5	4.0	12.3	HTON-BW-9	14.5	4.0	11.3
ZC-6-11	11.5	4.0	14.7	ZC-3-2	11.6	3.0	11.2
ZC-26-85	11.0	4.0	9.8	ZC-22-53	13.1	2.0	9.9
HTON-B	13.6	2.0	12.3	ZC-17-35	10.9	4.0	12.2
ZC-32-99	10.0	3.0	9.7	K-8703	11.8	2.0	12.5
K-72	12.7	2.0	13.6	ZC-25-73	12.4	3.0	11.2
ZC-36-148	14.8	2.0	11.2	K-8020	8.1	4.0	12.4
ZC-24-71	8.1	3.0	11.2	ZC-10-20	10.7	3.0	11.4
DSN-72	18.4	4.0	17.1	HTON-BW-19	13.8	1.0	11.3
HTON-BW-17	14.9	1.0	14.8	ZC-4-3	11.2	2.0	8.9
HTON-BW-22	16.1	1.0	14.6	ZC-13-26	8.7	4.0	7.6
HTON-BW-15	14.7	3.0	14.9				

Genotypes 4, 22, 42, 46 and 48 had about 11.00% protein content with 3.00 phenol grade. Wheat lines viz. 18, 21, 27, 29, 34, 39, 40 and 45 having 12% protein and phenol colour grade 2.00 and lines 8 and 35 with 3 phenol grade were included in the same branch of spanning tree (Table 3). Tocher's method was not able to differentiate between these genotypes as included in a single cluster. While minimum spanning tree method was able to differentiate these lines in two separate branches of the tree.

Wheat lines HTON-BW-19, ZC 13-26 and DSN 72 formed distinct clusters, in both Tocher's and minimum spanning tree methods. Spanning tree and Tocher's method indicated that the strains 1, 2, 3, 6, 7, 9, 10, 11, 16, 26, 30 and 36 formed a single cluster. Similarly strains 5, 19, 38, 43 and 50 on one hand and strains 13 and 17 on the other hand formed two separate clusters and these results are corroborated to each other in both the method. Minimum spanning tree and linkage dendrogram was formed on the basis of

Table 4. Average linkage between different genotypes in wheat

Genotype pair	Linkage order	r_c	Genotype pair	Linkage order	r_c
18—40	8.06	1.00	48—22	53.73	0.63
16—36	9.61	1.00	20—33	55.24	0.64
4—46	12.46	1.00	39—21	58.94	0.65
1—3	13.33	1.00	29—45	62.70	0.71
7—11	16.32	1.00	43—38	75.88	0.74
5—43	18.09	1.00	13—17	94.99	0.76
15—28	18.80	1.00	45—21	139.66	0.86
40—27	19.87	0.96	30—6	174.54	0.84
27—29	20.23	0.80	22—41	183.63	0.86
12—25	20.48	0.79	2—26	184.41	0.86
37—47	22.92	0.77	35—21	185.51	0.83
14—32	24.07	0.77	38—19	186.59	0.83
28—47	24.37	0.70	21—44	213.69	0.72
42—48	25.61	0.69	19—50	240.07	0.72
34—39	27.14	0.69	24—31	270.06	0.70
47—44	28.16	0.71	41—44	293.27	0.59
8—35	29.98	0.70	6—26	331.35	0.56
25—24	31.04	0.70	31—33	453.20	0.54
9—10	31.11	0.70	44—50	566.80	0.70
46—48	33.30	0.68	50—17	616.23	0.68
32—41	33.53	0.68	17—49	754.50	0.65
10—6	37.45	0.70	26—49	1288.09	0.56
3—11	39.94	0.74	49—33	1777.16	0.52
11—30	41.79	0.69	33—23	2480.63	0.58
36—2	44.22	0.68	23—51	6630.01	0.59

average linkage (Table 4), however, r values were also taken into consideration in the formation of spanning tree. Linkage dendrogram also gave the almost similar indication as indicated by minimum spanning tree.

On the basis of genetic divergence and minimum spanning tree, protein content, phenol colour reaction and peduncle length; diversity seen in the lines are expected to give better results as they exhibited greater diversity and high performance. This study also provide the opportunity to select diverse parents for better recombinants for various characters and utilization of such diverse lines of wheat in breeding seems appropriate in achieving better and quicker gains.

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