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Genetic Divergence Analysis for Grain Yield, Its Components and Quality Traits under Normal and Heat Stress Environments in Bread Wheat

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ABSTRACT

The genetic divergence among 75 genotypes of bread wheat was assessed for 12 grain yield, its components and quality traits of bread wheat under normal and heat stress environment. Significant genotypic differences were observed for all the characters under both environments. Based on Euclidean cluster analysis,75 genotypes were grouped into 9 clusters under both normal and heat stress environment. Cluster VIII was the largest cluster consisting of 15 genotypes followed by cluster III (12 genotypes) in normal environment while heat stress environment most of genotypes were grouped in cluster V (13 genotypes) and in cluster VII (12 genotypes). The genotypes of cluster VII, VIII and IX were identified as diverse as well as having higher mean values for most of the yield traits in both environments. Hybridization involving genotype of cluster VII and IX in timely sown conditions and clusters VII and VIII in late sown conditions is advocated in order to achieve high yielding segregants based on high performance for grain yield and quality traits and genetic divergence. The genotypes viz. PBW175, DBW88, HD2967, WH1105, WH542 and WH711 were found high yielding and divergent in timely sown conditions while genotypes WH542, WH1142, DBW88, DBW90, WH1124 and WH1021 were found high yielding and heat stress tolerant in late sown conditions.

Key words: *Genetic divergence, Cluster, Grain Yield, Heat stress.*

INTRODUCTION

Wheat is the most important food crop in India and is a staple food of millions of people especially in northern and north-western part of the country. Total production of wheat worldwide during 2017 was 754.31 million tonnes whereas India contributed 97.4 million tonnes, 6% higher than 2015-16. To meet the demands of ever growing population increasing the wheat productivity is very crucial and it can be achieved by continuous breeding efforts towards development of improved cultivars. The success of any hybridization programme depends upon selection of genetically diverse parents for crossing as well as collection of exotic and indigenous germplasm.

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If the parents are identified on the basis of divergence analysis, the resulting recombinants through hybridization can be more heterotic with the more chances of achieving high yielding segregants. Thus, the assessment of genetic diversity for different traits in the germplasm is essential for the identification of suitable parents in the hybridization programme. In the present study, the genotypes were subjected to Euclidean cluster analysis (Spark, 1973) to cluster the genotypes in different groups based on genetic divergence.

MATERIAL AND METHODS

The experimental material consisted of a random sample of 75 from wheat germplasm maintained by the Wheat and Barley Section, Deptartment of Genetics & Plant Breeding, CCS HAU, Hisar. Seventy five genotypes of wheat were grown in randomized block design (RBD) with three replications at Hisar location with two dates of sowing as 15th Nov. 2015 as timely sown (Normal environment) and 20th Dec. 2015 as late sown (Heat stress environment). Each entry was accommodated in paired row of 3 meter length with spacing of 30 cm between row to row and 10 cm between plant to plant in each replication. Five competitive plants of each genotype in each replication and in each environment were randomly selected, tagged. The terminal plants of each plot were excluded to minimize the border effect. Observations were recorded for different characters days to 50% heading, days to maturity, plant height (cm), number of effective tillers per meter, number of grains per ear, 1000 grain weight (g), biological yield per plot(g), grain yield per plot (g), harvest index (%), protein (%), sedimentation value (ml) and canopy temperature.

RESULTS AND DISCUSSION

Analysis of variance

All the characters studied showed significant variation in respect of the genotypes under the present investigation.There was also significant differences exist at genotypic level under normal and heat stress environments indicating sufficient scope for further improvement in these traits.Cluster analysis was done by using data of normal and heat stress environment and analyzed results are presented in table 1,2,3 and 4.

Cluster analysis

Divergence analysis of 75 bread wheat genotypes was carried out by Euclidean cluster analysis[7], and results with respect to normal and heat stress environments are presented in table 2,3 and 4.

On the basis of relative magnitude of distances genotypes were grouped into 9 cluster (Table 2). Further, cluster pattern revealed that in normal environment cluster VIII was the largest cluster consisting of 15 genotypes which was followed by cluster III (12 genotypes), cluster IV (11 genotypes), cluster I,VI (6 genotypes each) and cluster V, IX (5 genotypes each) and cluster VII which was the smallest cluster (3 genotypes). Under heat stress environment among the nine clusters, cluster V was the largest cluster consisting of 13 genotypes which was followed by cluster VII (12 genotypes), cluster IV (10 genotypes), cluster VIII (8 genotypes), cluster III (7 genotypes) and cluster II, VI (5 genotypes each) and cluster IX which was the smallest cluster (4 genotypes). The clustering pattern indicates that there was little association of genetic divergence with ecogeographical distribution of genotypes, as genotypes with different ecogeographical origins were grouped into same cluster, thus, suggesting that geographical diversity does not necessarily represent genetic diversity. These results are in agreement with the findings of Dwivedi and Pawar[1], and Goel et al.[2], Verma et al.[8], and Kumar *et al*., However, to some extent the genotypes related by their place of origin have shown tendency to group in the same cluster which maybe because of dependence upon the directional selection pressure that leads to well evolved homeostatic mechanism that would favour consistency of the associated character and thus resulting in indiscriminate clustering as reasoned by Dwivedi and Pawar[1].

The magnitude of intra-cluster distances measures the extent of genetic diversity between the genotypes of the same cluster. Inter-cluster distance is a measure of genetic distance between two cluster. The genotypes within the cluster had much smaller distance than the genotypes belonging to different clusters. In normal environment (Table 3) maximum intra cluster distance was shown by cluster V (4.356) which was followed by cluster I (4.205), cluster VII (3.879), cluster VI (3.764), cluster II (3.495), cluster III (3.474) and cluster IV (3.412), cluster VIII (3.265) and cluster IX (3.265). Maximum intercluster distance was between cluster II and cluster IX (8.057), followed by cluster II and cluster VII (7.664), followed by cluster I and cluster VII (7.399). This shows that genotypes in cluster II and IX were more divergent than other clusters, these genotypes may be used to produce the superior hybrids and transgressive segregants. The minimum inter-cluster distance was shown by cluster IV with cluster VIII (3.889). This implies that cluster IV was less divergent. The genotypes in cluster II and IX exhibited maximum divergence and indicated that the genotypes KBRL13, HD30 (cluster II) and genotypes HD2967, PBW343, WH1105, WH542, and WH711 (cluster IX) may be used to produce superior hybrids based on maximum divergence distance shown by genotypes.

Under heat stress environment the maximum intra cluster distance was shown by cluster VII (3.968) which was followed by cluster I (3.921), cluster V (3.719), cluster VII(3.685), cluster IV (3.47), cluster VIII (3.369) and cluster II (3.348), cluster IX (3.343) and cluster III (3.256). In general intra-cluster distances were relatively lower than inter-cluster distances showing that genotypes included within a cluster were genetically closer to each other than the genotypes included in different clusters. The minimum inter-cluster distance was shown by cluster IV and cluster V (4.062). This implies that cluster IV was less divergent. Maximum intercluster distance was shown by cluster II and Cluster IX (7.764), followed by Cluster III and Cluster IX (7.666), followed by Cluster VI and Cluster IX (7.666). The genotypes in cluster II and IX exhibited maximum divergence and indicated that the genotypes KBRL13,KBRL22 (cluster II) and genotypes WH1124, DBW90 and HD3059 (cluster VIII) may be used to produce superior hybrids based on maximum divergence distance shown by genotypes. Similar results have been reported by Kumar *et al*. and Divya *et al*.

The genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selections other than ecological and geographical diversification. In other words, genetic divergence has been found related with several genetic and non-genetic phenomena/conditions like ecogeographical distribution of genotypes, extent of heterosis, combining ability, genotype x environment interaction, ancestry and components of genetic variation. Therefore, selection of parents for hybridization to get more heterotic F_1's and desirable transgressive segregants should be properly based on genetic diversity rather than on geographic diversity. However, caution should be taken in selecting very divergent genotypes that have better combining ability and such crosses should give results proportionate to heterotic response. Therefore, a hybridization programme may be initiated involving the genotypes belonging to diverse clusters with high mean values for almost all the component characters**.** The involvement of genotypes belonging to clusters VII and IX in timely sown conditions and VII and VIII in late sown conditions for hybridization should be preferred to obtain transgressive segregants for grain yield based on performance for yield and quality traits and genetic divergence.

Cluster means of different clusters for various characters

The cluster means for different traits were reflections of genetic differences prevalent among the clusters. The cluster showed difference with each other for one or more traits. In normal environment cluster I was comprised of genotypes which were having highest cluster mean value for protein (%), cluster III had high mean value for plant height (105.53 cm), biological yield per plot (2109.81g) and sedimentation value (53.47 ml). The cluster V can be exploited for characters like low sedimentation value (32.13 ml) and low canopy temperature (post-anthesis 7 days and post-anthesis 21 days) (20.09, 28.13) can be used for breeding for heat tolerance for terminal heat stress affecting grain yield adversely. Cluster VII had lowest mean value for days to 50 % heading (76.89) and days to maturity (127.78) while cluster VII genotypes had highest cluster mean value for 1000-grain weight (g) (44.25), cluster IX exhibited the highest mean values for days to 50% heading (95.00), days to maturity (144.13), number of effective tillers per meter (138.27), number of grains per ear (55.60), grain yield per plot (g) (925.0) and harvest index (44.79) while cluster IX revealed the lowest mean value for plant height(88.13cm) these traits values are desirable for improving grain yield accompanied by reduced plant height. The genotypes from these clusters could be chosen for use in particular breeding programme for crop improvement.

In heat stress environment cluster I was comprises of genotypes which are having highest cluster mean value for plant height (cm) (99.52). cluster II had highest mean value for days to 50% heading (84.47) and sedimentation value (ml) (53.60), cluster VI had lowest mean value for plant height (cm) (81.47) and low sedimentation value(ml) (33.95), cluster VII had highest mean value for days to maturity (132.89) and harvest index (42.60). The cluster VIII can be exploited for characters like lowest mean value for days to 50% heading (76.75) while cluster VIII genotypes had highest cluster mean value for number of effective tillers per meter (126.13), number of grains per ear (54.17) and protein % (12.77), cluster IX exhibited the lowest mean values for days to maturity (125.0), 1000 grain weight (g) (44.28), grain yield per plot (g) (776.0) while cluster IX revealed the lowest mean value for canopy temperature (post-anthesis 7 days and post-anthesis 21 days) (23.03, 27.11 respectively). Genotypes from these clusters with appropriate combination of yield and its attributing traits can be used in breeding programmes.

On the basis of mean performance of the genotypes within the clusters, genetically diverse genotypes i.e. PBW175, DBW88, HD2967, WH1105, WH542 and WH711 were found high yielding and divergent in normal environment while genotypes WH542, WH1142, DBW88, HD3059,DBW90, WH1124 and WH1021 were found high yielding and divergent in heat stress environment and were selected for further use in hybridization programme for yield improvement in bread wheat.

Table 1: Mean squares obtained from ANOVA for 12 characters in normal and heat stress environment

Sources of variation	**d.f.**	Days to 50% heading	Days to maturity	Plant height (cm	Number of Effective tillers per meter	Number of grains per ear	1000 grain weight (g)	Biological yield per plot(g)	Grain yield per plot (g)	Harvest index (%)	Protein (%)	Sedimentation value (ml)	Canopy Temperature ^{o}C (post-anthesis 7 days)	Canopy Temperature ^{o}C (post-anthesis 21 days)
Replication (Normal)	**2**	4.14	10.33*	8.59	46.21	2.68	1.88	1343.22	910.09	0.61	0.03	1.81	1.86	1.40
Replication (Heat stress)	**2**	5.68	3.90	11.66	22.64	0.22	0.67	6265.56	769.14	9.98	0.24	0.04	0.26	2.51
Genotype (Normal)	**74**	45.76*	54.56*	146.97*	268.51*	49.38*	17.74*	59091.76*	20714.00*	45.42*	2.47*	203.19*	10.40*	8.97*
Genotype (Heat stress)	**74**	29.12*	45.68*	213.25*	183.88*	41.43*	21.82*	99034.20*	25146.62*	53.85*	2.02*	173.30*	4.51*	13.48*
Error (Normal)	**148**	2.07	3.96	17.84	35.12	5.86	1.19	6316.56	851.41	4.69	0.08	4.32	0.90	0.80
Error (Heat stress)	**148**	2.61	4.63	14.17	20.33	5.90	1.33	3647.47	804.97	4.34	0.13	4.70	0.47	0.89

Table 2: Classification of genotypes into different clusters in normal and heat stress environment

Cluster	**Environment**	**No. of genotypes**	**Name of varieties**	**D^2 value**
I	(Normal)	6	CH-8, KBRL22, Atlas66, Aus15854, Stem6117,WH595	4.21
I	(Heat stress)	11	CH-8,CH-6, Atlas66, HPYT424, HPYT423, HPYT472, HPYT414, C306, VeeryS,WH1184, Kharchia local	3.92
II	(Normal)	8	CH-2, KBRL13, HD30, DWR GP-39, CH-9, Stem 6017, HPYT413, HPYT415	3.50
II	(Heat stress)	5	CH-2, DWR GP-39, CH-9, KBRL13,KBRL22	3.35
III	(Normal)	12	CH-6, Kharchia local, Raj3765, HPYT424, HPYT414, HPYT427 , HPYT423, HPYT404 ,HPYT428 , C306, HPYT472, WH712	3.47
III	(Heat stress)	7	WH1164, HPYT415,WHD943, HPYT404, HPYT413, HPYT468, HPYT427	3.26
IV	(Normal)	11	DBW 90, HD29,HPYT 468, HD3059, WH1025, WH1098, KRL210, Stem 6168, WH 1124, Raj MR-1, Stem6216	3.41
IV	(Heat stress)	10	Tobari, HD29, PBW644, RajMR-1, KRL210, Stem6168, Stem6117, HPYT416, HPYT44,WH157	3.50
V	(Normal)	5	HPYT 416, WH157, NapHal Sel, HPYT447,WH1021	4.36
V	(Heat stress)	13	WH896,WH283,CH-7,WHD948,DBW17, Stem 6081,WHD943, WH1138,WH1098,WH1129, WH1080,HD2329,WH147	3.72
VI	(Normal)	10	WHD948, Stem6081, WH896,WH283, WH1080, WH1129, WH1164, , Tobari, VeeryS, P5-3	3.76
VI	(Heat stress)	5	P 5-3, WH595,PBW550,Aus15854,NapHal Sel	3.69
VII	(Normal)	3	DBW71, DBW88, PBW175	3.9
VII	(Heat stress)	12	WH712,HD3086,HD2967,WH1179,WH1063,WH1164,WH1025, PBW343,WH1105,WH1142, WH542,WH711	3.97
VIII	(Normal)	15	WH1063, WHD943, HD3086, HD2329, WH1142, WH147, WH1184, WH730, WH 1138, WH1179, PBW550, DBW17, PBW644, CH-7, DPW621-50	3.26
VIII	(Heat stress)	8	DBW 90, DPW621-50, DBW71, WH1124,HD3059, Raj3765, DBW88, HPYT428	3.70
IX	(Normal)	5	HD2967, PBW343, WH1105, WH542, WH711	3.27
IX	(Heat stress)	4	PBW175, HD30, WH1021,WH730	3.43

Table 3: Intra (diagonal) and inter cluster D^2 (average) values in normal and heat stress environment

Cluster	**Environment**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
1	(Normal)	4.205	4.786	5.047	5.013	6.104	5.377	7.399	5.506	7.246
1	(Heat stress)	3.921	4.768	4.749	4.939	4.813	6.18	5.11	5.918	6.53
2	(Normal)		3.495	5.53	5.229	6.599	5.097	7.664	6.305	8.057
2	(Heat stress)		3.348	4.241	4.677	4.68	5.227	6.017	6.602	7.764
3	(Normal)			3.474	4.391	5.108	5.144	6.526	4.516	5.966
3	(Heat stress)			3.256	4.382	4.599	4.819	5.815	5.598	6.889
4	(Normal)				3.412	4.898	4.368	5.577	3.889	5.26
4	(Heat stress)				3.497	4.062	4.579	4.887	4.978	5.41
5	(Normal)					4.356	5.328	6.602	4.621	5.932
5	(Heat stress)					3.719	4.567	4.897	5.687	6.34
6	(Normal)						3.764	6.27	4.583	5.659
6	(Heat stress)						3.685	6.545	6.643	7.666
7	(Normal)							3.879	6.224	7.25
7	(Heat stress)							3.968	4.724	5.18
8	(Normal)								3.265	4.055
8	(Heat stress)								3.369	4.447
9	(Normal)									3.265
9	(Heat stress)									3.343

Table 4: Mean performance of clusters for 12 characters in normal and heat stress environment

Cluster		Days to 50% heading	Days to maturity	Plant height (cm)	Number of Effective tillers per meter	Number of grains per ear	1000 grain weight (g)	Biological yield per plot(g)	Grain yield per plot (g)	Harvest index (%)	Protein (%)	Sedimentation value (ml)	Canopy Temperature °C (post-anthesis 7 days)	Canopy Temperature°C (post-anthesis 21 days)
1	(Normal)	91.44	138.56	100.11	115.11	49.72	38.47	1933.33	672.11	34.94	13.96	44.83	24.26	30.72
1	(Heat stress)	84.18	133.61	99.52	116.11	49.61	42.29	1821.94	614.21	33.71	12.56	49.79	26.06	33.05
2	(Normal)	91.21	136.54	98.67	113.21	45.96	38.42	1748.75	620.58	35.73	12.03	52.63	24.65	32.73
2	(Heat stress)	84.47	132.33	92.27	107.97	49.73	36.68	1620.27	558.00	34.72	11.15	53.60	26.20	33.77
3	(Normal)	92.56	137.92	105.53	127.72	51.00	42.45	2109.81	729.53	34.65	12.44	53.47	22.12	30.68
3	(Heat stress)	80.86	125.81	94.43	119.41	46.38	39.15	1586.29	556.48	35.21	11.89	51.62	26.18	34.20
4	(Normal)	89.09	136.88	98.42	125.12	53.49	39.74	1939.70	774.55	40.02	11.90	48.06	22.68	29.66
4	(Heat stress)	81.87	127.60	91.27	112.53	50.13	39.89	1633.50	638.67	39.23	11.71	38.83	25.11	31.67
5	(Normal)	92.40	137.60	99.93	129.97	49.27	42.53	1975.20	726.07	36.80	11.65	32.13	20.09	28.13
5	(Heat stress)	83.62	131.00	85.46	111.28	49.39	42.01	1511.69	609.28	40.55	12.27	44.67	25.95	32.68
6	(Normal)	92.53	137.23	93.70	132.20	49.40	41.95	1810.10	747.40	41.30	12.13	41.67	24.15	31.72
6	(Heat stress)	80.67	128.40	81.47	110.10	47.67	37.91	1338.80	514.20	38.75	12.35	33.95	25.63	34.46
7	(Normal)	76.89	127.78	98.22	136.00	52.78	44.25	1931.56	811.67	42.11	12.58	44.67	21.49	30.02
7	(Heat stress)	84.06	132.89	91.22	125.93	54.11	42.73	1733.25	738.03	42.60	12.37	46.03	25.12	31.59
8	(Normal)	93.51	140.16	96.76	131.22	54.73	41.60	1956.73	801.47	41.03	12.58	45.20	20.95	29.12
8	(Heat stress)	76.75	126.50	92.54	126.13	54.17	40.31	1796.33	761.79	42.47	12.77	49.46	24.26	31.41
9	(Normal)	95.00	144.13	88.13	138.27	55.60	42.39	2067.33	925.00	44.79	12.33	46.33	20.42	29.38
9	(Heat stress)	80.08	125.00	98.42	122.63	53.25	44.28	1833.17	776.00	42.44	12.70	41.08	23.03	27.11

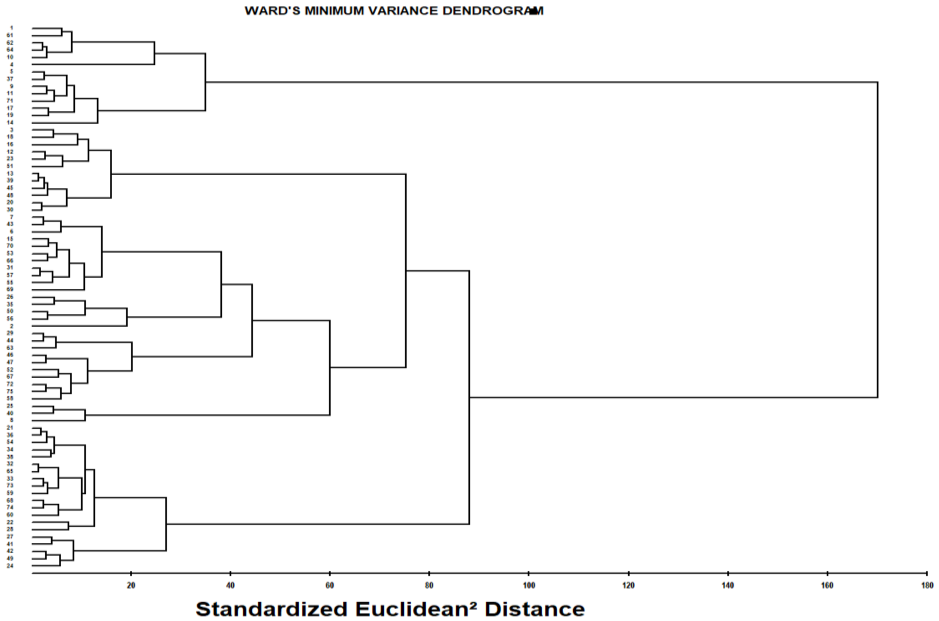

Fig. 1: Dendrogram of 75 bread wheat genotypes based on Euclidean distance in normal environment

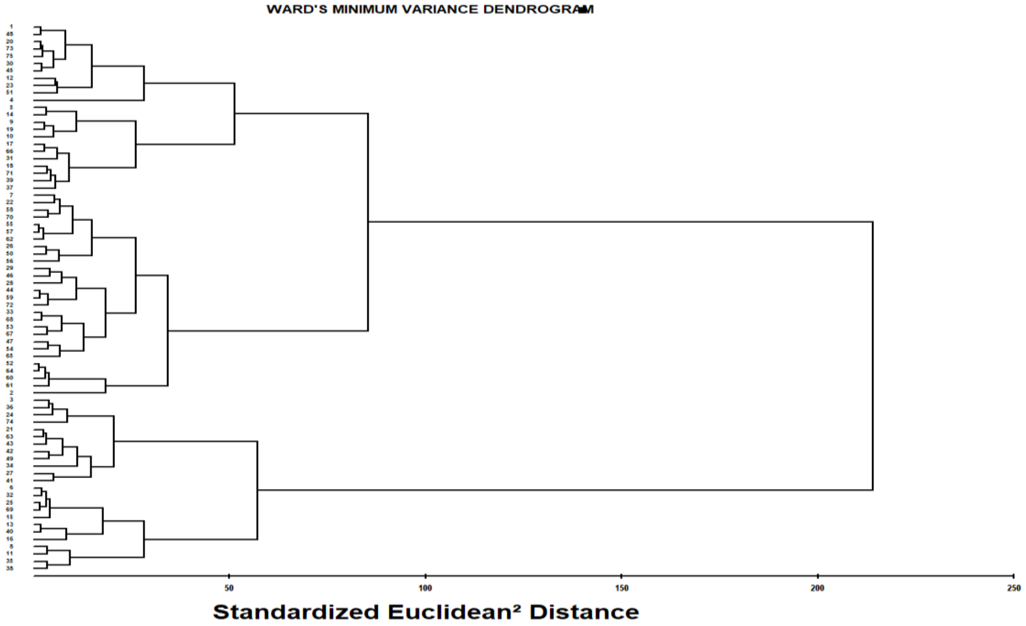

Fig. 2: Dendrogram of 75 bread wheat genotypes based on Euclidean distance in heat stress environment

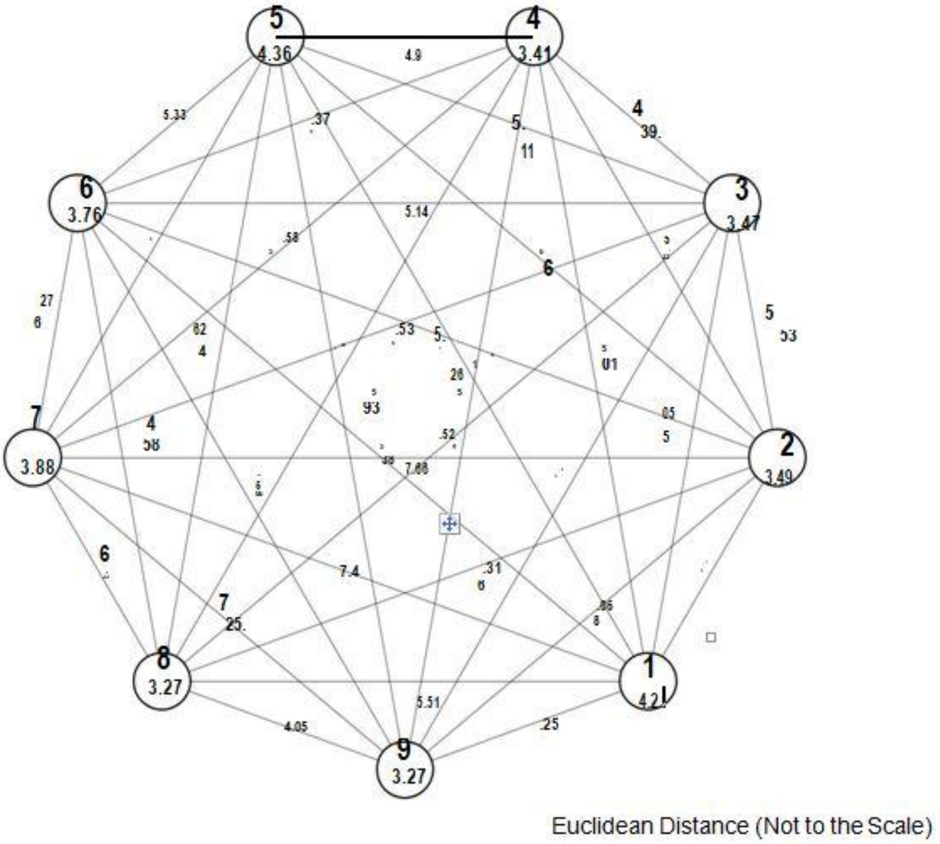

Fig. 3: Intra-inter Euclidean distance between 9 clusters of bread wheat genotypes

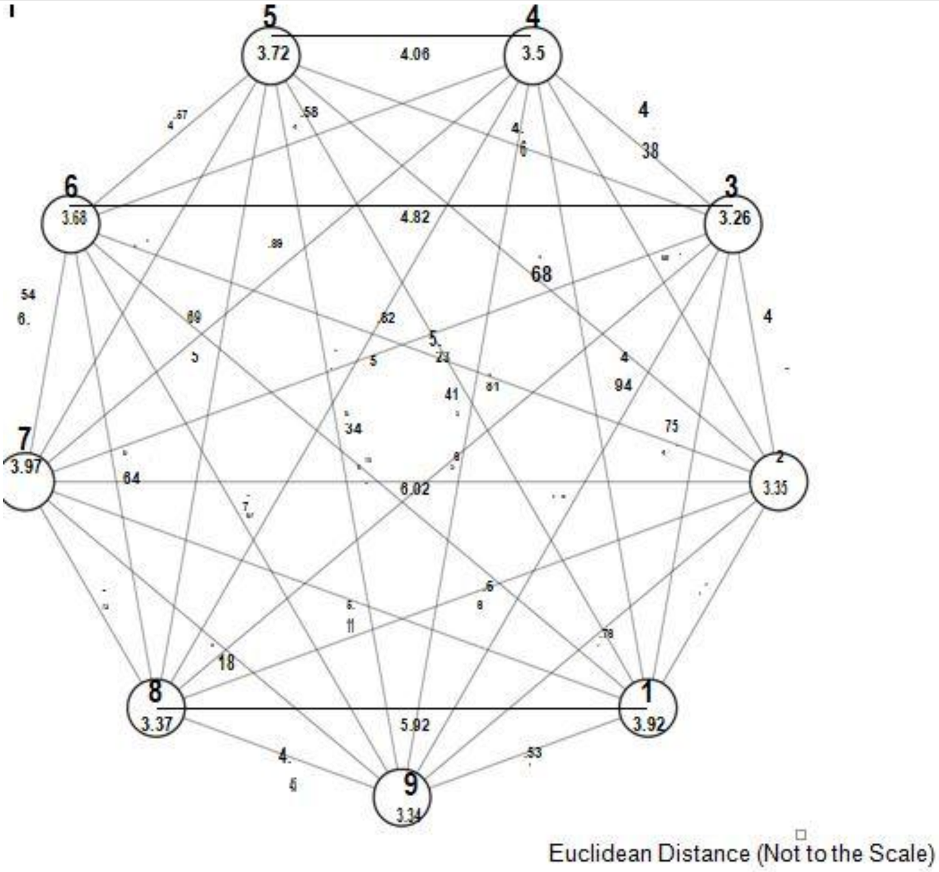

Fig. 4: Intra-inter Euclidean distance between 9 clusters of bread wheat genotypes

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