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GENETIC DIVERGENCE ANALYSIS IN RELATION TO WHEAT (*TRITICUM AESTIVUM* L.) BREEDING PROGRAMME UNDER HEAT STRESS ENVIRONMENT

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ABSTRACT

The present investigation in the study of exotic and indigenous lines of bread wheat, showing wide spectrum of variation for various characters, were evaluated in reclaimed salt affected soil under timely sown and irrigated conditions during *Rabi*, 2024-25. The experiment was conducted at the main Experiment Station of LNCTU, Bhopal. The characters studied were flag leaf area, days to maturity, spike length, reproductive tillers per plant, grains per spike, 1000-grain weight, biological yield per plant, harvest index, and grain yield per plant flag leaf angle and leaf blight. The wide range of variation for different characters and comparison of means of germplasm lines using least significant differences indicated existence of very high degree of variability for all the characters in the exotic and indigenous wheat lines. In this context, the highest inter-cluster distance was observed between cluster VI and cluster XII followed by cluster VI and cluster VII, Thus, crosses between promising lines belonging to cluster pair having higher inter cluster distances may be attempted for isolating transgressive segregants as these cluster pair were also separated by high inter-cluster distances. The genotypes having high mean performance for grain yield per plant and several other yield components were found to be concentrated in cluster IV and VI which merit showed due consideration for selection of parents. The lines from these two clusters may be taken for hybridization with the promising lines of other clusters which had higher inter-cluster distances from these two clusters.

Keywords : Wheat crop, Non-hierarchical Euclidean cluster analysis, inter cluster distance.

Introduction

Heat stress is a major challenge for wheat crops, affecting growth, yield and quality. The rising temperatures are impact wheat productivity and suggest strategies for improving heat tolerance, including genetic and agronomic approaches. Heat stress in wheat is the global challenge the effects of heat stress on wheat, particularly during the reproductive phase, and highlights adaptation mechanisms and breeding strategies for heat tolerance. Impacts, tolerance, adaptation, and mitigation of heat stress on wheat is provides a detailed overview of wheat's physiological and biochemical responses to

heat stress and explores breeding and molecular approaches to enhance heat tolerance. Heat stress occurs when wheat is exposed to high temperatures, especially during critical growth stages like flowering and grain filling (Abdelrahman *et al.*, 2020). Physiological effects are reduced photosynthesis high temperatures disrupt the photosynthetic process, reducing the plant's ability to produce energy. Accelerated growth is wheat matures faster under heat stress, but this often leads to lower biomass accumulation and reduced grain yield. Stomatal closure is the plant closes its stomata to conserve water,

leading to reduced CO₂ intake and slower growth (Fukuda *et al.*, 2018).

Impact on yield and grain quality maller grains are the heat stress shortens the grain-filling period, resulting in smaller, less developed grains. Lower Protein Content are the high temperatures can impact protein synthesis, reducing wheat quality for milling and baking. Reduced pollination is the heat can impair pollen viability and fertilization, leading to lower seed production. Biochemical changes oxidative stress is the heat stress increases reactive oxygen species (ROS), which damage cellular structures. Altered hormone levels are the stress hormones like abscisic acid increase, influencing plant responses to heat. Enzyme dysfunction is the key enzymes involved in metabolic processes may become inactive or less efficient under high temperatures. Adaptive mechanisms heat shock proteins (HSPs) are the proteins help wheat cope with heat damage by stabilizing cellular structures. Antioxidant production is the plants boost their antioxidant defences to counteract oxidative stress (Bernfur *et al.*, 2017). Morphological changes are some wheat varieties develop traits like thicker leaves or deeper roots to with stand heat. Management strategies heat-tolerant varieties are the breeding programs focus on developing wheat with enhanced heat resistance. Optimized irrigation is the maintaining soil moisture helps counteract heat-induced dehydration. Photosynthesis pathway disruption high temperatures damage the photosystem-II (PS-II) complex, reducing electron transport efficiency. Rubisco enzyme is the activity declines, limiting CO₂ fixation and decreasing overall photosynthetic efficiency. Higher the photorespiration leads to energy loss, further weakening the plant (Kumar *et al.*, 2016). Oxidative stress and antioxidant defence heat stress leads to excessive production of reactive oxygen species (ROS) like superoxide radicals and hydrogen peroxide (Sun and Guo, 2016). The plant activates the antioxidant defence system, including is the superoxide dismutase (SOD), converts superoxide radicals into hydrogen peroxide. Catalase (CAT) breaks down hydrogen peroxide into water and oxygen.

Materials and Methods

The experimental material consists total of 140 exotic and indigenous germplasm lines and 3-check varieties *viz.*, KRL-210, NW-2036, NW-1067. These germplasms were procured from genetic stock available in wheat station, Department of Genetics and Plant Breeding, LNCTU, Bhopal. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The checks used in experiment are well adopted varieties of the

region. The experiment was conducted to evaluate 140 germplasm lines along with three checks under heat stress following Augmented Block Design. The entire experimental field the test genotypes which were not replicated while remaining 3 were allocated to checks *i.e.* KRL-210, NW-2036, NW-1067 which were replicated. Each plot will consist of two rows of 3 m length, following inter and intra row spacing of 25 cm and 5 cm, respectively. Recommended cultural practices were applied to raise a good crop. Non-hierarchical Euclidean cluster analysis according to (Beale, 1969 and Spark, 1973), numerical method is the following data are provided as input to the algorithm like matrix of observations, number of clusters, initial cluster centres. Initially each observation is allocated to its closest cluster centre. The means of the clusters are then calculated and are taken to be the new cluster centres. At the same time, the sum of squared deviations of the observations from their respective cluster centres is computed. The observations are then checked in turn to see if a move to a different cluster centre results in a decrease in the total sum of squares. It is clearly an improvement to reassign an observation from cluster k to cluster I if it is nearer the centre of the latter. That is if

$$d_I^2 < d_k^2$$

Where, d_i is the distances from the centre of cluster i . However, a more effective criterion involves reassigning the observation if the squared deviation from the centre of cluster I is less than that from the centre of cluster k, even when the cluster centres are simultaneously repositioned. That is when:

$$\frac{n_I}{n_I + 1} d_I^2 < \frac{n_k}{n_k - 1} d_k^2$$

Where, n_i is the number of observations in cluster i

The usual method of use entails calling the subroutine repeatedly, starting from a specified number of clusters and decreasing (or increasing) by one cluster at a time until a predetermined lower (or upper) number of clusters is reached. In the reference, Beale gives a criterion for merging pairs of clusters which may be used in this way. A pseudo-F-test is also given, allowing comparison of "significance" of different solutions. Since the reference may not be readily accessible, the essential formulae are given below.

- (a) The criterion for choosing two clusters to be merged is that the increase in the sum of squares of deviations shall be minimized. That is to say, clusters k and I are chosen such that

$$n_k n_I d_{kl} (n_k + n_I)$$

is a minimum where did is the distance between the cluster centres.

(b) The pseudo-F-statistic is computed as

$$\frac{R_{(c_1)} - R_{(c_2)}}{R_{(c_2)}} / \left\{ \frac{N - c_1}{N - c_2} \left(\frac{c_2}{c_1} \right)^{2/n} - 1 \right\}$$

With $n(C_2 - C_1)$ and $n(N - C_2)$ degrees of freedom, where $R(c)$ denotes the residual sum of squares when the N observations are divided into c clusters. This statistic is computed for all $c_1 < c_2 \leq c_{\max}$ and if, for a given c_1 it is significant for any C_2 it is deduced that the representation in terms of C_1 is not entirely adequate.

Results and Discussion

The non-hierarchical Euclidean cluster analysis was employed to study the genetic divergence existing among wheat germplasm collections on the basis of governed by several genes. The pseudo-F-test revealed that 12 cluster arrangements were most appropriate for grouping the 140 genotypes. Therefore, the 140 genotypes were accepted to be grouped into 12 non-overlapping clusters. The distribution of 140 wheat lines in 12 clusters is presented in Table-1. The highest numbers of genotype were presented in cluster II which contained 21 entries followed by cluster VII. Both cluster I and XII contained 15 entries each. Cluster III was constituted by 14 entries. Cluster IV, XI, IX, X, VIII, and V possessed 12, 11, 10, 9, 8 and 6 entries respectively. Only cluster VI contained 4 genotype which was very least number of entries.

The estimates of intra-and inter-cluster distances for 12 clusters are presented in Table-2. The highest intra-cluster distance was observed in case of cluster V (80.23), followed by cluster VI (77.54). The lowest intra-cluster value was recorded for cluster X (42.70), followed by cluster VII (43.15). The maximum inter-cluster distance was found between cluster VI and XII (1493.98), followed by cluster VI and VII (1016.52) had exhibit very high inter-cluster distance from remaining 10 clusters. The minimum inter-cluster distance was found between cluster VII and VIII (73.73) followed by cluster VII and IX (75.27).

The cluster means, for 11 characters are presented in Table-3. The highest cluster mean for flag leaf area was found in case of cluster X (21.43 cm²), followed by cluster VIII (21.10 cm²) and cluster VII (20.30). The lowest cluster mean for flag leaf area was recorded in case of cluster II (17.34), followed by cluster IX (17.38) and cluster XII (17.45). The genotype of cluster V was responsible for highest cluster mean for days to maturity (124.27 days), followed by entries of cluster XI (122.23 days) and cluster X (124.21 days). The

genotypes with early maturity were concentrated in cluster XII (122.50 days), followed by cluster IV (122.60 days) and cluster VII (122.77 days). The highest cluster mean for peduncle length was recorded for cluster IV (30.06 cm), followed by cluster VIII (29.19 cm) and cluster V (29.02 cm). The lowest cluster mean for peduncle length was found in case of cluster VI (25.19 cm), followed by cluster III (26.49 cm) and cluster IX (25.26 cm) while, remaining cluster had moderate means for peduncle length. The highest cluster mean for plant height was recorded in case of cluster VIII (84.33 cm) followed by cluster IV (83.8 cm). The lowest cluster mean for plant height was found in case of cluster VI (74.97 cm), followed by cluster III (78.52 cm) while remaining clusters had moderate means for plant height. The highest cluster mean for spike length in case of cluster IV (9.71 cm), followed by cluster X (9.23 cm) and cluster XI (9.19 cm). The lowest cluster mean for spike length was exhibited by cluster XII (8.17 cm), followed by cluster V (8.18 cm) and cluster VI (8.38 cm). The highest cluster mean for grains per spike was recorded for cluster IV (40.25), followed by cluster I (39.39) and cluster XI (39.21). The lowest cluster mean for grains per spike in case of cluster VIII (37.29), followed by cluster V (37.43) and cluster II (37.44). The remaining clusters were characterized by medium means for grains per spike. The highest and lowest cluster means for reproductive tillers per plant were observed for cluster VI (4.29) and cluster VII (3.33), respectively. The second highest and second lowest means for tillers per plant were recorded for cluster IV (4.05) and cluster XII (3.50), respectively. The genotypes of cluster XI (39.84 g) were responsible for highest cluster mean for 1000-grain weight, followed by the genotypes cluster X (39.78 g). Cluster VIII (37.88 g) resulted in lowest cluster mean for 1000-grain weight followed by the genotypes of cluster I (38.11g). Cluster IV (21.98 g), followed by cluster VI (21.63 g) showed highest cluster mean for biological yield per plant. Thus, the genotypes with higher biomass production ability appeared to be present in the two clusters mentioned above. The lowest mean for biological yield per plant was recorded for cluster XII (17.68g). The highest cluster mean for grain yield per plant was observed in case of cluster IV (7.51 g) which indicated that lines having higher grain yield were concentrated in this cluster. The cluster means for grain yield were also of higher order in case of cluster VI (7.48 g) and cluster III (6.93 g). The genotypes with very low grain yield were found to be grouped in cluster VII (5.93 g) followed by cluster XII (6.03 g) and cluster V (6.20 g). The highest cluster mean for harvest-index was observed in case of cluster IX (38.34%), followed by

cluster III (37.55%). The lowest mean for harvest-index was exhibited by cluster IV (36.36%), followed by cluster VII (36.59%). Remaining clusters were characterized by moderate means for harvest-index.

Conclusion

The non-hierarchical Euclidean cluster analysis successfully grouped 140 wheat genotypes into 12 distinct clusters, revealing substantial genetic divergence governed by multiple genes. Cluster distribution showed that Cluster II had the highest

number of entries (21), while Cluster VI contained the least (4), indicating varying levels of genetic diversity among clusters. Maximum intra-cluster divergence was in Cluster V (80.23), suggesting high heterogeneity within this group. Cluster VI exhibited the greatest genetic distance from Cluster XII (1493.98), indicating strong divergence and potential for hybridization to exploit heterosis. Minimum inter-cluster distance was between Cluster VII and VIII (73.73), reflecting close genetic similarity.

Table 1: Clustering pattern of 140 wheat genotypes on the basis of non-hierarchical euclidean cluster analysis of 11 characters.

Cluster No.	No. of genotypes	Name of genotypes
I	15	IBWSN-1023, KRL-210, IBWSN-1119, SAWSN-3052, ESWYT-131, IBWSN-1175-II, ESWYT-136, EC-663946, SAWSN-3082, EC-664193, IBWSN-1107, HRWSN-2026, SAWSN-3107, CSISADRYT-5217, ESWYT-130.
II	21	IBWSN-1121, IBWSN-1166, SAMNYT-411, KRL-302, SAWSN-3097, CSISADRYT-6764, IBWSN-1152, CSISADRYT-5218, ESWYT-118, CSISADRYT-5212, SAWSN-3011, EC-663954, EC-664196, EC-664244, IC-524282, IC-524284, EC-664236, SAWSN-3027, SAWSN-3069, ESRN-51, IBWSN-1158.
III	14	IBWSN-1113, EC-634300-88, KRL-301, KRL-312, EGPYT-7, KRL-315, CSISADRYT-6767, EC-664009, SATYN-60, IC-553917, SATYN-26, EC-663961, KRL-306, DSBWYT-407.
IV	12	IBWSN-1151, EC-634300-106, EC-634300-103, EC-634300-81, SATYN-45, IBWSN-1150, IBWSN-1038-II, IBWSN-1057, SATYN-37, SATYN-35, SATYN-38, IC-546933.
V	6	IBWSN-1173, EGPYT-11, SATYN-46, SATYN-53, DSBWYT-420, IBWSN-1175-I.
VI	4	EC-634300-69, EC-634300-99, EC-634300-64, EC-634300-110.
VII	18	IBWSN-1034, HRWYT-206, EC-664229, EBWYT-511, EC-664208, EC-664200, IBWSN-1112, SAWSN-3004, IBWSN-1038-I, IBWSN-1170, ESRN-11, NW-1067, IBWSN-1039, EC-634300-76, GW-2008-156, GW-2007-87, GW-2007-92, EC-664189.
VIII	8	ESWYT-110, EC-634300-95, RAJ-4211, NW-5029, GW-2008-157, NW-2036, IBWSN-1087, EC-664215.
IX	10	IC-524288, WH-1083, ESRN-15, KRL-307, KRL-322, ESRN-3, DSBWYT-422, KRL-305, KRL-299, GW-2008-153.
X	9	IBWSN-1164, KRL-309, EC-634300-82, KRL-323, IBWSN-1146, IBWSN-1167, IBWSN-1169, EGPSN-51, IBWSN-1065.
XI	11	ESWYT-119, IBWSN-1021, SATYN-23, WH-1097, EBWYT-509, KRL-300, IC-549914, EC-414149, KRL-303, KRL-304, IBWSN-1137.
XII	15	IBWSN-1063, KRL-324, EC-664199, IBWSN-1103, EC-634300-133, EC-664227, LBP-2009-24, KRL-316, GW-2008-159, GW-2006-17, GW-2007-96, EC-634300-94, EC-634300-63, RWP-2009-12, GW-2007-80.

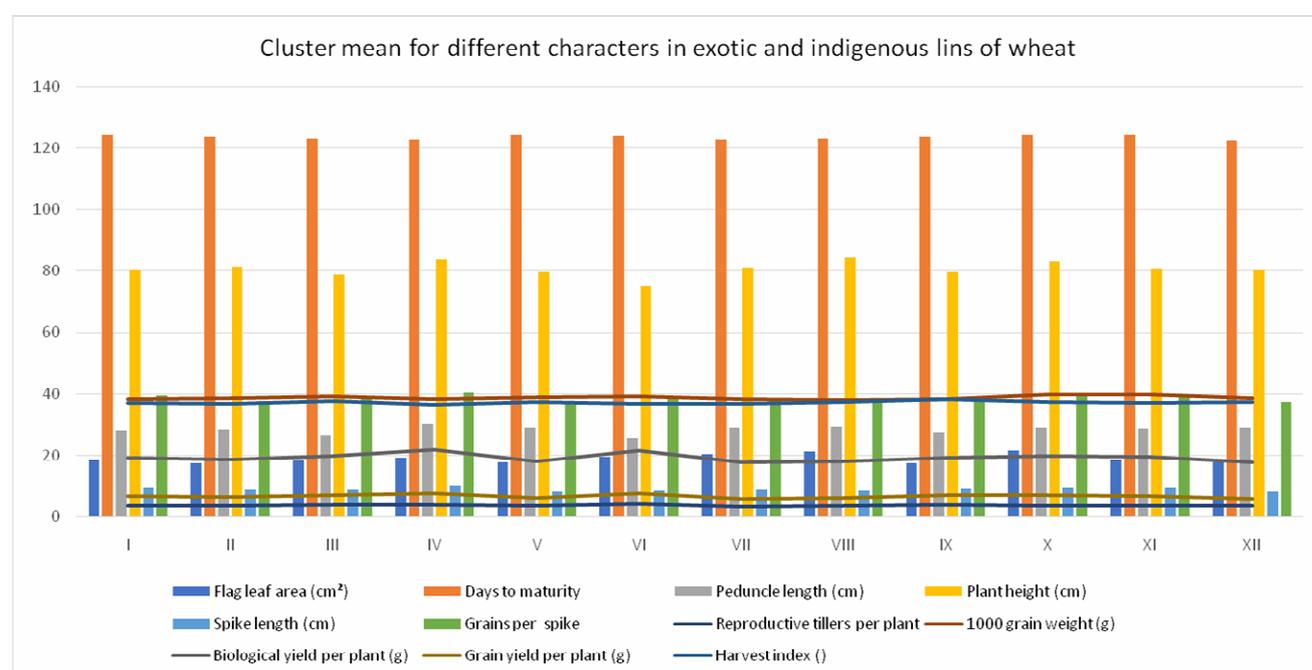
Table 2: Estimates of average intra and inter-cluster distances for 12 clusters in exotic and indigenous lines of wheat

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	49.23	106.69	205.92	183.61	415.96	782.29	142.45	80.45	198.06	98.72	199.17	243.82
II		63.50	128.71	126.18	201.96	474.75	219.81	152.11	206.60	135.24	259.86	404.76
III			60.76	83.04	191.79	491.35	172.98	179.26	112.19	140.56	164.77	379.94
IV				50.50	209.11	439.07	203.83	206.52	175.43	110.70	152.54	441.51
V					80.23	186.98	533.04	471.67	404.53	376.29	517.99	856.86
VI						77.54	1016.52	919.95	872.92	755.25	942.83	1493.98
VII							43.15	73.73	75.27	109.10	81.56	108.73
VIII								44.94	109.69	118.13	146.21	135.20
IX									47.99	130.15	102.83	172.36
X										42.70	96.23	238.90
XI											52.55	198.17
XII												66.42

Bold figures indicate intra-cluster distances

Table 3: Cluster means for different characters in exotic and indigenous lines of wheat.

Cluster number	Flag leaf area (cm ²)	Days to maturity	Peduncle length (cm)	Plant height (cm)	Spike length (cm)	Grains per spike	Reproductive tillers per plant	1000 grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index ()
I	18.49	124.17	28.00	80.26	9.17	39.40	3.65	38.11	19.25	6.59	36.89
II	17.34	123.72	28.32	81.46	8.72	37.44	3.65	38.54	18.75	6.36	36.66
III	18.16	123.13	26.49	78.52	8.65	38.26	3.89	39.11	19.81	6.93	37.55
IV	19.12	122.60	30.06	83.81	9.72	40.26	4.05	38.34	21.98	7.51	36.36
V	17.66	124.27	29.02	79.62	8.19	37.43	3.59	38.88	18.12	6.20	37.36
VI	19.32	124.02	25.20	74.97	8.38	38.09	4.30	39.29	21.63	7.48	36.80
VII	20.30	122.77	28.83	80.62	8.69	38.33	3.34	38.36	17.76	5.93	36.59
VIII	21.10	123.15	29.20	84.33	8.40	37.29	3.71	37.88	18.11	6.22	37.20
IX	17.39	123.67	27.28	79.58	8.97	39.00	3.91	38.22	19.28	6.89	38.34
X	21.43	124.21	28.95	83.20	9.24	38.95	3.60	39.78	19.98	6.92	37.20
XI	18.39	124.23	28.53	80.52	9.19	39.21	3.56	39.85	19.48	6.69	37.07
XII	17.47	122.50	28.90	80.16	8.17	37.22	3.51	38.47	17.68	6.03	37.20

**Fig. 1:** Cluster means for different characters in exotic and indigenous lines of wheat

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