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Genetic diversity for morpho-physiological and seed vigour traits in wheat (*Triticum aestivum* L.)

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ABSTRACT: Estimation of genetic diversity present in gene pools is an important segment for breeding programs in crops. The present study was carried out to analyse genetic diversity based on morpho-physiological and seed vigour traits using 60 genotypes of bread wheat during *Rabi* 2016-17. The data were recorded for yield, days to 50% heading, days to anthesis, grain growth rate (at 14, 21, 28 days), plant height, number of effective tillers, flag leaf length, width and area, spike length, spikelets per spike, number of grains per spike, 1000 grain weight, harvest index, germination, seed density, seedling length and dry weight, vigour index-I, vigour index-II along with dehydrogenase activity in seeds. Based on the cluster analysis using Ward's Algorithm and Squared Euclidean Distances, genotypes were assigned into 8 clusters. The intra-cluster distance ranged from 4.942 (II) to 7.191 (VIII), and inter-cluster distance ranged from 6.035 (between II and VI) to 9.507 (between III and VIII). These values were higher than any corresponding intra-cluster values. The cluster V was the largest cluster consisting of 12 genotypes followed by cluster VI (10 genotypes), II (8 genotypes), cluster IV (8 genotypes), cluster VII (7 genotypes), cluster I (6 genotypes), cluster III (5 genotypes) and cluster VIII (4 genotypes). Cluster III showed maximum genetic divergence with cluster VIII. The cluster possessing the maximum genetic distance can be used in the hybridization program as it is expected that more heterotic F_1 and more promising segregants will be produced in the segregating population. Therefore, more emphasis should be given on cluster III (P-13714, P-13717, P-13710, P-13718, and P-13743) followed by IV for selecting parents from available germplasm clusters to produce new recombinants with desired traits.

Key words: Cluster analysis, genetic distance, genetic diversity, vigour index, wheat

Wheat (*Triticum aestivum* L.) is the most important cereal crop and staple food for nearly 35% of the world population. It covers 32 per cent of the world's total acreage under cereal crops. India has the largest area under wheat cultivation and the second-largest producer after China in the world. In India, it is the second most important food crop after rice, both in terms of area and production (Anonymous, 2019-20). Due to its wider adaptability, it can be grown under different agro-climatic conditions even at very high elevations of mean sea level. The global and national challenges in terms of the burgeoning population, climate change along with diminishing factor productivity demand for efficient climate-resilient wheat cultivars of higher productive traits. So, there is an urgent need to increase the production of food grain to combat these adverse situations *vis-a-vis* to ensure food security at the national scale. To accomplish this purpose, the genotypes with suitable plant type are needed to be selected from a diverse gene pool for their future use as parents in hybridization programme. Effective selection programme depends on the availability of existing genetic variability in the breeding material for studying genetic divergence in crop plants. Genetic diversity is the basis for launching an efficient breeding programme that aimed for the improvement of wheat productivity. Wheat breeding through hybridization also requires the selection of diverse genotypes, irrespective of the product either a pure line or a hybrid (Prasad *et al*., 2000; Zeb *et al*., 2009). Characterization of genetic diversity and genetic relatedness is a fundamental element in crop improvement strategies (Zhu *et al*., 2000). Various methods are available for analysis of genetic diversity in germplasm accessions, breeding lines and segregating populations (Van Hintum and Elings, 1991). These methods could be based on pedigree, morphological, agronomic performance, biochemical and molecular (DNA-based) data (Mohammadi and Prasanna, 2003; Cox *et al*., 1985; Bernad *et al*., 1998; Salem *et al*., 2008). Morphological traits (plant height, number of effective tillers, flag leaf length, width and area, spike length, spikelets per spike, number of grains per spike) can be used to evaluate genetic diversity but generally influenced by environmental factors (Mahmood *et al*., 2011). The knowledge about germplasm diversity and genetic relationships among wheat breeding materials can be explored for making crop improvement strategies (Mohammadi and Prasanna, 2003; Arya *et al.,* 2017; Sansaloni *et al.,* 2020). The main objective of this study was to capture the potential genetic diversity among wheat genotypes by using cluster analysis, so that it could help to select parents for evolving superior varieties.

MATERIALS AND METHODS

The seed materials comprised of 60 bread wheat genotypes (received from Department of Genetics and Plant Breeding, CCS HAU, Hisar) which were grown in a randomized block design (RBD) with three replications during *Rabi* 2016-17 at Research Area of the Department of Genetics and Plant Breeding, CCS HAU, Hisar. Each plot consisted of three rows of 6-meter length and row to row distance was kept 20 cm in each replication. The recommended package of practices was followed for raising crop. All the cultural crop practices were kept constant. Weeds were removed manually as and when required. The data were recorded on randomly selected plants from each genotype in each replication for days to 50% heading, days to anthesis, grain growth rate (mg/gr/day) at14, 21 and 28 days, plant height (cm), number of effective tillers/meter row length, flag leaf length (cm), flag leaf width (cm), flag leaf area (cm^2), spike length (cm), spikelets per spike, number of grains per spike, 1000-grain weight (g), grain yield per plot (g), biological yield/plot (g), harvest index (%), germination (%), seed density (g/cc), seedling length (cm), seedling dry weight (mg), vigour index-I, vigour index-II and dehydrogenase activity (OD/g/ml).

Using the standard software, Euclidean cluster analysis according to Ward's Minimum Variance Method developed by Ward (1963) was performed to separate the genotypes into distinct groups and clusters. The cluster mean of a particular character is calculated by the summation of mean values of genotypes included in a cluster, divided by number of genotypes in the same cluster.

RESULTS AND DISCUSSION

Genetic diversity existing within and between groups of genotypes is important and particularly useful in proper choice of parents for realising higher heterosis and obtaining useful recombinants (Chapla *et al*., 2008). Morpho-physiological characters have been successfully used for estimation of genetic diversity and cultivar developments since they provide a simple way to quantify the genetic variation (Fufa *et al*., 2005). The analysis of variance revealed highly significant differences among the genotypes for all the characters, indicating a wide range of variability existing for all the traits studied for further selection and improvement. Based on relative magnitude of distances, 60 wheat genotypes were grouped into eight clusters as shown in the dendrogram (Fig.1) in such a way that the genotypes within the cluster had much smaller distance than those belonging to two different clusters.

The data of cluster pattern revealed that cluster V is the largest one with 12 genotypes, followed by cluster VI with

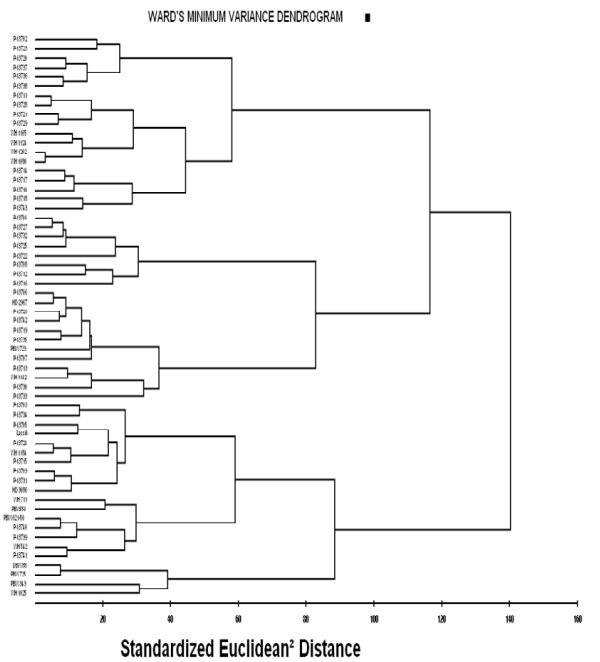

Fig 1: Dendrogram showing the genetic relationship among 60 genotypes of wheat based on Euclidean distance

10 genotypes, cluster II and IV each with 8 genotypes, cluster VII with 7 genotypes, cluster I with 6 genotypes, and clusters III and VIII with 5 and 4 genotypes, respectively (Table 1). The observations of the present study are supported by Arya *et al.* (2017), Dutamo *et al*. (2015), Imran *et al*. (2016), and Sheykhi *et al*. (2014). Phougat *et al*. (2016) grouped based on Euclidean cluster analysis 94 durum genotypes into 8 distinct clusters. Cluster VI was the biggest with 19 genotypes while cluster II was the smallest with 3 genotypes only.

Table 1: Clustering pattern of 60 bread wheat genotypes

Cluster	No. of genotypes	Genotypes
I	6	P-13702, P-13723, P-13720, P-13736, P-13737, P-13738
II	8	P-13711, P-13721, P-13728, P-13729, WH 1105, WH 1124, WH 1202, WH 1080
III	5	P-13714, P-13717, P-13710, P-13718, P-13743
IV	8	P-13704, P-13708, P-13712, P-13716, P-13722, P-13725, P-13727, P-13732
V	12	P-13706, P-13707, P-13713, P-13719, P-13726, P-13730, P-13733, P-13735, WH 1142, PBW 723, HD 2967, P-13742
VI	10	P-13703, P-13705, P-13709, P-13715, P-13724, P-13731, P-13734, WH 1184, Lassik, HD 3086
VII	7	WH 711, PBW 550, PBW 621-50, WH 542, P-13739, P-13740, P-13741
VIII	4	DBW 88, PBW 725, PBW 343, WH 1025

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 (Table 2). Intra cluster distance was maximum for cluster VIII (7.191) and minimum for cluster II (4.942). Cluster III and VIII showed maximum inter-cluster distance *i.e.* 9.507 and it was minimum in case cluster II and VI *i.e.,* 6.035 (Table 2). The higher inter-cluster distances exhibited the presence of more diversity among the genotypes involving these clusters.

Table 2: Average intra (diagonal) and inter (above diagonal) cluster distance values among grouped 60 genotypes of wheat

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**5.527**	6.169	6.901	7.981	6.812	6.605	7.125	9.368
II		**4.942**	6.146	6.994	6.579	6.035	6.531	8.343
III			**5.622**	6.984	6.415	6.710	8.331	9.507
IV				**5.727**	6.774	6.663	8.448	9.094
V					**5.581**	6.345	7.310	8.099
VI						**5.400**	6.533	8.159
VII							**5.959**	7.788
VIII								**7.191**

Values obtained in Table 2 were higher than any corresponding intra cluster values (Fig 2). In the present investigation genotypes of cluster III showed maximum genetic divergence with cluster VIII. Cluster III showed maximum genetic divergence with cluster VIII. If the cluster possessing maximum genetic distance could be involved in hybridization programme, it is expected that more hetrotic F_1's and most promising segregants in the segregating generations could be produced (Phougat *et al*., 2016). Therefore, more emphasis should be given on cluster III and IV for selecting germplasm as parents for crossing with the germplasm of cluster, which may produce new recombinants with desired traits which could be

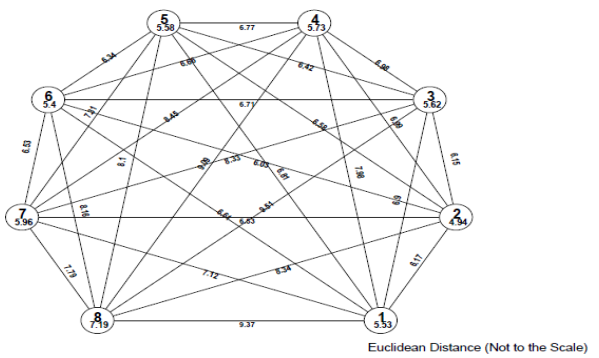

Fig 2: Intra and inter Euclidean distance between 8 clusters of wheat genotypes

Table 3: Mean values of 8 clusters for morpho-physiological traits in wheat

Cluster	DH	DA	GGR14	GGR21	GGR28	PH	T/M	FLL	FLB	FLA	SL	S/S	G/S	TGW	BY	GY	HI
I	88.83	97.56	2.06	2.10	1.88	107.84	124.56	31.61	2.12	50.13	12.17	20.35	55.61	39.72	2130.56	6244.44	34.22
II	89.33	98.17	2.04	2.07	1.86	109.91	98.33	31.13	2.13	49.77	11.97	19.64	62.02	42.34	1741.67	5039.58	34.48
III	90.00	98.73	2.60	2.60	2.21	113.06	102.07	31.54	2.18	51.52	12.55	19.65	60.07	43.30	1983.33	5706.67	34.98
IV	90.63	99.25	2.25	2.24	1.92	111.79	120.71	30.20	2.15	48.66	12.88	20.50	63.70	43.47	2212.50	6420.83	34.38
V	94.64	103.11	2.52	2.32	1.92	113.09	119.94	29.86	2.19	49.04	12.17	20.54	60.83	39.13	1970.83	5997.22	33.14
VI	90.23	99.27	2.23	2.16	1.89	110.53	114.90	29.10	2.01	43.94	11.47	19.11	56.83	41.30	2011.67	5985.00	33.90
VII	92.67	100.95	1.97	2.00	1.70	101.93	112.62	28.36	2.01	42.69	11.54	19.67	61.10	38.49	1595.24	4776.19	33.40
VIII	97.08	106.17	2.35	2.06	1.59	109.94	112.50	29.20	2.05	44.87	12.08	20.25	53.11	36.89	1104.17	4066.67	27.14
Mean	91.63	100.33	2.26	2.20	1.88	110.03	113.94	30.05	2.11	47.53	12.07	19.96	59.64	40.68	1894.72	5653.33	33.50

DH: Days to 50% heading; DA: Days to anthesis; GGR14, 21, 28: Grain growth rate at 14, 21 and 28 days (mg/gr/day); PH: Plant height (cm); T/M : Number tillers per meter; FLL: Flag leaf length (cm); FLB : Flag leaf width (cm); FLA : Flag leaf area (cm^2); SL: Spike length (cm); S/S : Spikelets per spike; G/S : Grains per spike; TGW: 1000 grain weight; BY: Biological yield (g); GY: Grain yield (g); HI: Harvest index (%)

Table 4: Mean values of 8 clusters for seed vigour parameters in wheat

Cluster	G%	SD	SL	SDW	V-I	V-II	DHA
Cluster 1	90.83	1.04	21.10	10.37	1915.32	941.11	0.31
Cluster 2	94.50	1.17	22.04	11.14	2084.28	1052.77	0.29
Cluster 3	95.00	1.06	22.48	11.16	2139.70	1058.05	0.31
Cluster 4	96.75	1.13	25.56	12.70	2468.44	1228.83	0.37
Cluster 5	94.50	1.03	22.03	11.66	2085.15	1101.14	0.35
Cluster 6	94.83	1.05	23.20	11.69	2201.75	1107.20	0.33
Cluster 7	91.05	1.11	21.77	11.38	1983.96	1035.54	0.31
Cluster 8	93.42	1.26	25.11	11.86	2347.06	1109.05	0.35
Mean	94.06	1.09	22.82	11.54	2148.79	1086.00	0.33

G: Germination%; SL: Seedling length (cm); SD: Seed dry weight (g x 10^{-3}); V-I: Vigour index –I; V-II: Vigour index-II; Sd: Seed density (g/cc); DHA: dehydrogenase activity test (OD/g)

exploited in crop improvement. Diverse genotypes selected from different clusters are crossed in diallel mating scheme and desirable segregents are selected among the segregating generations. Phougat *et al*. (2016) revealed Cluster II, V and VI had genotypes with highest cluster mean values for traits- tiller number per meter and 1000-grain weight. Kumar *et al*. (2009) could group 30 genotypes of wheat into 6 clusters based on observation on 6 characters. Yadav *et al*. (2014), Kumar *et al*. (2015), Shyam *et al*. (2018) observed diversity with high range of values of inter and intra cluster distance among wheat genotypes.

Cluster mean and general mean values of different clusters have been presented in Table 3 and 4. The genetic differences between the clusters were reflected by the cluster mean. The cluster differed from each other for one or more characters. There is significant genetic diversity among tested genotypes that shows the presence of excellent opportunity to bring about the improvement through wide hybridization by crossing genotypes indifferent clusters. Cluster I was comprised of early genotypes with cluster mean of 88.83 for days to 50% heading and 97.56 for days to anthesis and had highest cluster mean value of 31.61 cm for flag leaf length. Cluster III had highest cluster mean value for flag leaf area (51.52 cm^2), harvest index (34.98%), grain growth rate at 14, 21 and 28 days (2.60, 2.60 and 2.21 mg/gr/day respectively) and second highest for spike length (12.55 cm), 1000 grain weight (43.47 g), flag leaf length (31.54 cm), flag leaf breadth (2.18 cm) and germination (95%). The highest grain yield (2212.50 g), biological yield (6420.83 g), number of tillers per meter (120.71), spike length (12.88 cm), grain per spike (63.70), 1000 grain weight (43.47 g), germination (96.75%), seedling length (25.56 cm), seedling dry weight (12.70 mg), vigour index-I (2468.44), vigour index-II (1228.83) and dehydrogenase activity (0.37 OD/g) was observed for cluster IV. Cluster V consisted of taller (113.09 cm) genotypes with highest mean value for spikelets per spike (20.54), flag leaf breadth (2.19 cm), and second highest mean value for number of tillers per meter, grain growth rate at 14,21 and 28 days. Cluster VIII had highest mean value for seed density (1.26 g/cc), days to 50% heading (97.08) and days to anthesis (106.17). Results are in general agreement with Shahryari *et al*. (2011), Aharizad *et al*. (2012), Ajmal *et al*. (2013).Comparative evaluation of cluster means suggested that for improving specific characters the genotype should be taken from cluster having high mean value for that character. Cluster IV had the highest mean value for important yield components. Therefore, cluster IV and V were considered most desirable for selecting genotypes. Also similar findings were reported by Dutamo *et al*. (2015), Imran *et al*. (2016) and Sheykhi *et al*. (2014).

The results, thus, obtained in the present study would provide some guidelines in selection of parents and in the prediction of possible merits for genetic recombination and would also be of value in formulating model plant type for selection in segregating generations. Further genotypes could be selected from the diverse clusters and crossed in biparental mating scheme to develop desirable progenies.

CONCLUSION

Using Wards minimum method, 60 genotypes were grouped into 8 clusters. The intra-cluster distance was recorded as the highest for cluster VIII (7.191) which indicates the existence of maximum variability within this cluster. The lowest intra-cluster distance value was recorded for cluster II. Inter-cluster distance was maximum between cluster III and VIII which indicates that the genotypes included in these clusters are genetically diverse. The genotypes with high values of any clusters are diverse and can be used in crossing programme for further selection through pedigree method of breeding. So, it is desirable to select genotypes from the clusters having a high inter-cluster distance in the recombination breeding programmes. The cluster means for the parameters studied in wheat genotypes revealed considerable differences among all the clusters.

REFERENCES

Aharizad, S., Sabzi, M., Mohammadi, S.A. and Khodadadi, E. (2012). Multivariate analysis of genetic diversity in wheat (*Triticum aestivum* L.) recombinant inbred lines using agronomic traits. *Annals Biological Research,* 3(5): 2118-2126.

Ajmal, S.U., Minhas, N.M., Hamdani, A., Shakir, A., Zubair, M. and Ahmad, Z. (2013). Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) germplasm. *Pakistan Journal of Botany,* 45(5): 1643-1648.

Anonymous (2019-20). Project Director Report, IIWBR, Karnal 1p.

Arya, V.K., Singh, J., Kumar, L., Kumar, R., Kumar, P. and Chand, P. (2017). Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Research,* 51(2): 128-134.

Bernad, R.L., Cremeens, C.R., Cooper, R.L., Colins, F.L., Krober, O.A., Athow, K.L., Laviolette, F.A., Cobe, C.J. and Belson, R.L. (1998). Evaluation of the USDA Soybean germplasm collection; maturity group 000 to IV. Technical bulletin-United State Department of Agriculture, 1844p.

Chapla, J.N., Dobaria, K.L., Khanpara, M.D., Jivani, L.L. and Kacchadia, V.H. (2008). Genetic divergence in bread wheat. *National Journal of Plant Improvement,* 10(2): 97-102.

Cox, T.S., Lookhart, G.L.,Walker, D., Harrell, E.L.G., Albers, L.D. and Rodgers, M.D. (1985). Genetic relationships among hard red winter wheat cultivars as evaluated by pedigree analysis and gliadin polyacrylamide-gel electrophoretic patterns. *Crop Science,* 25: 1058-1063.

Dutamo, D.D., Alamerew, S., Eticha, F. and Assefa, E. (2015). Genetic Variability in Bread Wheat (*Triticum aestivum* L.) Germplasm for yield and yield component traits. *Journal of Biology, Agriculture and Healthcare,* 5(17): 2224-3208.

Fufa, H., Baenizger, P.S., Beecher, B.S., Dweikat, I., Graybosch, R.A. and Eskridge, K.M. (2005). Comparison of phenotypic and molecular-based classifications of hard red winter wheat cultivars. *Euphytica,* 145: 133-146.

Imran, J., Shahid, I.A., Hafiz, M.A. and Aurangzeb, R. (2016). Assessment of genetic diversity in wheat synthetic double haploids for yield and drought related traits through factor and cluster analyses. *Plant Gene and Trait,* 7(3): 1-9.

Kumar, B., Lal, G.M., Ruchi and Upadhyay, A. (2009). Genetic variability, diversity and association of quantitative traits with grain yield in bread wheat. *Asian Journal of Agricultural Research,* 1(1): 4-6.

Kumar, R., Prasad, B.K., Singh, M.K., Singh, G. and Verma, A. (2015). Genetic divergence analysis for morpho-physiological traits, under timely and late sown condition in bread wheat (*Triticum aestivum* L.). *Journal of Wheat Research,* 7(1): 27-30.

Mahmood, T., Siddiqua, A., Rasheed, A. and Nazar, N. (2011). Evaluation of genetic diversity in different Pakistani wheat land races. *Pakistan Journal of Botany,* 43(2): 1233-1239.

Mohammadi, S.A. and Prasanna, B.M. (2003). Analysis of genetic diversity in crop plant salient statistical tools and consideration. Review and interpretation. *Crop Science,* 43: 1235-1248.

Phougat, D., Godara, A., Sethi, S.K. and Sheokand, R.N. (2016). Genetic diversity and association studies for grain yield and its attributing traits in tetraploid wheat (*T. turgidum* subsps. durum). *The Bioscan,* 11(3): 2007-2011.

Prasad, P.V.V., Pisipati, S.R., Bukovnik, U. and Fritz, A.K. (2000). Impact of night time temperature on physiology and growth of wheat. *Crop Science,* 48: 2372–2380.

Salem, K.F.M., El-Zanaty, A.M. and Esmail, R.M. (2008). Assessing wheat (*Triticum aestivum* L.) genetic diversity using morphological characters and microsatellite markers. *World Journal of Agricultural Sciences,* 4(5): 538-544.

Sansaloni, C., Franco, J., Santos, B., Percival-Alwyn, L., Singh, S., Petroli, C. and Kilian, B. (2020). Diversity analysis of 80,000 wheat accessions reveals consequences and opportunities of selection footprints. *Nature communications*, 11(1): 1-12.

Shahryari,R., Mahfoozi, B., Mollasadeghi, V. and Khayatnezhad, M. (2011). Genetic diversity in bread wheat for phenological and morphological traits under terminal drought stress condition. *Advances in Environmental Biology,* 5(1): 169-172.

Sheykhi, A., Pirdashti, H., Abbasian, A. and Niknejhad, Y. (2014). Segregation of some wheat (*Triticum aestivum* L.) genotypes using cluster analysis procedure. *International Journal of Farming and Allied Sciences,* 3(2): 225-229.

Shyam, C., Chandrakar, P.K., Rastogi, N. K. and Banjare, U. (2018). Evaluation of genetic divergence analysis in wheat for yield and its component characters. *International Journal of Agriculture, Environment and Biotechnology,* 11(6): 829-834.

Van Hintum, T.J. and Elings, A. (1991). Assessment of

glutenin and phenotypic diversity of Syrian durum wheat landraces in relation to their geographical origin. *Euphytica,* 55: 209–215.

Ward, H.J. (1963). Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association,* 58: 236-244.

Yadav, S.K., Singh, A.K., Baghel, S.S., Jarman, M. and Singh, A.K. (2014). Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. *Journal of Wheat Research,* 6(1): 154-159.

Zeb, B., Khan, I.A., Ali, S., Bacha, S., Mumtaz, S. and Swati, Z.A. (2009). Study on genetic diversity in Pakistani wheat varieties using simple sequence repeat (SSR) markers. *African Journal of Biotechnology,* 8(17): 4016-4019.

Zhu, Y., Chen, H., Fan, W., Wanf, Y., Li, Y., Chen, J., Yang, S., Hu, L., Leung, H., Mew, T.W., Teng, P.S., Wang, Z. and Mundit, C.C. (2000). Genetic diversity and disease control in rice. *Nature,* 406: 718-722.

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