GENETIC DIVERSITY ANALYSIS FOR VARIOUS MORPHOLOGICAL AND QUALITY TRAITS IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

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Abstract

The present investigation was carried out during *rabi* 2017-18 at Faculty of Agriculture, Wadura with 96 genotypes from CIMMYT to assess the genetic diversity for various yield traits and quality trait *viz*; number of tillers plant[-1], ear length (cm), number of seeds spike[-1], 1000-seed weight (g), plant height (cm), grain yield plant[-1] (g), protein content (%), spikelets spike[-1] and days to 75% flowering. The cluster analysis grouped 96 genotypes in 8 clusters which revealed that the Cluster I contained the highest number of genotypes (66) followed by Cluster III (23), Cluster VII (2) and other clusters were mono-genotypic. Among all clusters cluster-V and cluster-VIII showed the maximum cluster mean values for maximum number of traits, suggesting that these traits were superior over other traits and genotypes falling in this clusters would be selected directly on the basis of these traits and could be used in hybridization programme. The maximum contribution towards divergence was by grain yield plant[-1], followed by 1000 seed weight (g), seeds spike[-1], ear length (cm), spikelets spike[-1], plant height (cm), days to 75% flowering therefore may be used as selection parameters.

Keywords : *Triticum aestivum*, morphological traits, spikelets, bread wheat.

Introduction

Wheat (*Triticum aestivum* L.) is the most important cereal crop for the majority of world's populations. It is the most important staple food of about two billion people (36% of the world population). To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons and hence, there is an immediate need to increase wheat production to achieve this target (Sharma *et al*., 2011). This can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergence. The main objective of any plant breeding programme is to develop cultivars of high yield potential with acceptable quality. The knowledge of genetic variability for yield and its contributing components helps in the improvement of grain yield and planning of effective breeding programme. The creation and utilization of genetic diversity is essential to overcome the problems of narrow genetic base and also to generating precise information on the nature and degree of genetic diversity in selecting the parents for targeted hybridization. It is important that variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. However the genetic diversity of selected genotype is not always based on factors such as geographic diversity place of release of ploidy level. Hence, characterization of genotypes should be based on statistical procedure such as D^2 statistics and on hierarchical euclidean cluster analysis. These procedures characterize genetic divergence using the criterion of similarity or dissimilarity based on the aggregate effect of a number of agronomically important characters. For effective utilization of germplasm in crop improvement programmes substaintial knowledge of full genetic potential and their availability with desired traits is needed. Therefore proper evaluation of available germplasm is important for proper utilization.

Materials and Methods

The investigation was carried out at research fields of Faculty of Agriculture, Wadura, Sopore, SKUAST Kashmir. The 96 genotypes were obtained from CYMMIT, Mexico. The research location is characteristic of temperate climate. Seeds of each genotype were hand dibbled. Row to row spacing was 22 cm and plant to plant spacing was 10cm. Recommended dose of 120 Kg/ha N, 60 Kg/ha P_2O_5 and 40 Kg/ha K_2O was applied. Entire dose of P_2O_5 and K_2O along with ½ dose of N was applied as basal dose and remaining dose of nitrogen was applied 30 days after sowing as top dressing. Two hand weeding were carried out in April and May. The standard agronomic practices were adopted for normal crop growth. Data was recorded from randomly selected plants. Observation were recorded from randomly selected three plants in a row for number of tillers plant[-1], ear length (cm), number of seeds spike[-1], 1000-seed weight (g), plant height (cm), grain yield plant[-1] (g), protein content (%), spikelets spike[-1] and days to 75% flowering. The genetic diversity was done through cluster analysis using D2 statistics suggested by Mahalanobis (1936) and they were grouped into five clusters based on D2 value using Tochers method suggested by Rao, (1952) using software window stat version 9.1.

Table 1 : List of Genotypes used.

S. No	Genotype	S.No	Genotypes	S.No	Genotypes
1	Gs 2012	19	GS1028	37	GS 9015
2	Gs 6013	20	GS 3056	38	GS 5058
3	Gs 5057	21	GS 6030	39	GS 9037
4	Gs 9005	22	GS 2005	40	GS 8053
5	Gs 9049	23	GS 9046	41	GS 10030
6	Gs 9052	24	GS 10046	42	GS 4010
7	Gs 10051	25	GS 70058	43	ESWYT 17
8	Gs 6001	26	GS 9001	44	GS 8049
9	Gs 7045	27	GS 7055	45	GS 9018
10	Gs 7049	28	GS 9009	46	GS 8036
11	SAWYT-12	29	GS 6048	47	GS 7060
12	GS 4036	30	GS 9057	48	GS 9060
13	GS 9010	31	GS 8005	49	GS 1016
14	GS 10056	32	GS 9042	50	SAWYT 28
15	GS 6037	33	GS 6018	51	GS 4015
16	GS 10015	34	SAWYT 6	52	GS 5028
17	GS 10010	35	HTWYT 31	53	ESWYT 13
18	SAWYT 19	36	GS 9016	54	ESWYT 6
55	GS 10024	62	GS 10044	69	SAWYT 31
56	GS 20506	63	GS 7003	70	GS 2036
57	GS 3001	64	GS 5050	71	GS 6014
58	GS 3025	65	GS 10042	72	GS 8029
59	GS 4041	66	ESWYT 24	73	GS 8022
60	GS 3027	67	GS 5057	74	GS 1043
61	Gs 3034	68	GS 3034	75	GS 7007
76	GS 3043	78	GS 6010	80	GS 7014
77	GS 1040	79	GS 7042	81	ESWYT 38
82	GS 9027	83	GS 3006	84	GS 4006
85	GS 8032	86	GS 10053	87	GS 5050
88	GS 2014	91	ESWYT 46	94	GS 1029
89	GS 2044	92	GS 8040	95	GS 10055
90	SAWYT 5	93	GS 7024	96	GS 8056

Results and Discussion

The results of genetic diversity among 35 diverse wheat genotypes for various morphological and quality traits are presented in Table 2. Based on the results of genetic diversity, 96 genotypes were grouped into eight clusters with maximum number of genotypes (66) in cluster-I followed by cluster-III (23), cluster-VII (2) whereas clusters- II, IV, V, VI and VIII were mono-genotypic. The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh *et al.*(2014), Verma *et al.* (2014), Tewari *et al.*(2015), Kumar *et al.*(2016) and Vora *et al.*(2017) in wheat. Similarly, Degewione and Alamerew (2013) grouped 26 bread wheat genotypes into six clusters. Shashikala (2006) grouped 169 wheat genotypes into 12 clusters where 28 genotypes were present in cluster-II and VIII, IX, X, XI and XII were mono-genotypic. The inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes. The inter-cluster distance was found to be highest between cluster-VI and cluster-VIII (548.81), followed by cluster-IV and-VIII (438.22), cluster-V and-VIII (425.15), cluster-VII and VIII (417.29 and cluster-I and VIII (272.36). The least inter-cluster distance was found between cluster-IV and V (26.24).The inter-cluster values that indicated close relationship were to be considered that hybridization among the genotypes of these clusters would not provide good levels of segregation It is well recognized that greater the distance between clusters, wider the genetic diversity would be between the genotypes. Similar findings were also reported by Singh *et al.* (2014), Verma *et al.* (2014) and Rahim *et al.* (2010). Therefore, highly divergent genotypes would produce a broad spectrum of segregation in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants of high magnitude of heterosis. This information would be very useful in planning wheat breeding programme, particularly, for improving grain yield in wheat crop.

Cluster means revealed that substantial variability existed for morphological, quality and yield traits. Highest cluster means for days to flowering, seeds spike^{-1}, 1000 seed weight and protein content were recorded for cluster-V containing single genotype (SAWYT 12). Similarly cluster means for number of tillers plant^{-1}, ear length, plant height, and grain yield plant^{-1} were recorded highest for cluster-VIII comprising single genotype (ESWYT46). Highest mean for spikelets spike^{1} was recorded for cluster-VII (GS2012, GS 10051). However, rest of the clusters showed no desirable cluster means for any of the trait. Among all clusters, cluster-V and cluster-VIII showed the maximum cluster mean values for maximum number of traits, suggesting that these traits were superior over other traits and genotypes falling in these clusters would be selected directly on the basis of these traits and could be used in hybridization programme. Similar

results were obtained by Singh *et al.* (2017) who reported that nine (9) genotypes in cluster-IV were responsible for high cluster mean for days to 75% flowering, days to maturity, plant height, spike length, number of spikelets spike[-1], number of grains spike[-1], 1000 grain weight, biological yield and grain yield.

The per cent contribution of different characters towards divergence revealed that maximum contribution was by grain yield plant[-1] followed by 1000 seed weight, seeds spike[-1], ear length, spikes spikelet[-1], plant height, days to 75%

flowering, number of tillers plant[-1] and protein content. The present findings are supported with earlier reports of Singhal and Upadhyay (1977), Sethi *et al.* (1992), Shoran and Tandon (1995), Nimbalkar *et al.* (2002), Chapla *et al.* (2008), Kolakar *et al.* (2014) and Kumar *et al.* (2014). The contribution of grain yield plant[-1] in divergence had also been reported by Rahman *et al.* (2015), Khare *et al.* (2015), Lal *et al.* (2009), Salavati *et al.* (2008) and Jishan and Zhu (2008), 1000 grain weight and number of spikelet spike[-1] by Dobariya *et al.* (2006)

Table 2 : Distribution of different Wheat (*Triticum aestivum* L.) genotypes into clusters based on D^2 statistics

Cluster	Number of genotypes in the cluster	Genotype number
I	66	Gs 5057, Gs 9005, Gs 6013, ESWYT 13, GS 6014, GS 2036 GS 8036, GS 5058, GS 8053, 8022, 20506, 4041, 7045, 10044, 4036, 1029, 1040, 9057, 9060, 9018, 7014,7049,8029, 9049, 3034, SAWYT 5, 9015, 5028, ESWYT17, ESWYT24, 2005, 10015,5057,5050, 8005, 9016, 9010, 6001, 10056, 3006, 10046,10055, 3034, 6037,1028, 1043, 1016, 3060,8049,4010, 3027, 2044, 6048, 2014, SAWYT19, 5050, 7055, 4015, 7003, 10042, 8040, 9037,3001, ESWYT6, 10024,HTWYT31
II	1	GS 10010
III	23	Gs10030, 7060, 6010, 8032, 4006, 3025, 7042, 9009, 8056, 70058, 6018, 9042, 6030, SAWYT28, 9001, 3056, 9046,7007, ESWYT38, 7042, 9027, SAWYT31, 10053
IV	1	GS 9052
V	1	SAWYT 12
VI	1	SAWYT 6
VII	2	GS 2012, 10051
VIII	1	ESWYT 46

Table 3 : Cluster means for different traits in different clusters of Wheat (*Triticum aestivum* L.) genotypes

Clusters	No. of tillers[-] plant	Ear length (cm)	Seeds spike[-1]	1000 seed weight (g)	Plant height (cm)	Grain yield plant[-1] (g)	Protein content (%)	Spikelets spike[-1]	Days to flowering
Cluster 1	9.14	8.06	31.43	46.42	100.86	15.02	12.18	14.79	158.84
Cluster 2	8.00	7.67	29.22	44.00	107.00	21.17	11.01	14.11	162.00
Cluster3	8.93	8.11	31.08	48.86	101.32	24.06	12.33	14.54	161.35
Cluster 4	12.00	9.07	30.11	48.33	100.17	8.52	10.73	14.89	158.00
Cluster 5	11.67	8.37	34.00	52.67	99.00	9.83	13.14	15.00	154.33
Cluster 6	6.67	8.10	26.00	47.33	89.67	7.13	12.98	13.33	156.00
Cluster 7	10.83	8.53	32.00	51.00	78.65	10.32	12.10	16.00	158.00
Cluster 8	12.00	10.77	31.00	47.00	111.00	33.27	11.17	15.00	160.67

Table 4 : Average inter-cluster (above diagonal) and intra-cluster (diagonal) D^2 values among different Wheat (*Triticum aestivum* L.) genotypes

Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster7	Cluster 8
1	**31.30**	47.58	86.52	51.91	48.66	77.37	64.84	272.36
2		**0.00**	28.99	115.38	126.23	167.12	131.18	130.81
3			**28.33**	187.78	170.27	234.05	163.97	96.25
4				**0.00**	26.24	32.89	47.75	438.22
5					**0.00**	35.15	41.15	425.15
6						**0.00**	47.05	548.81
7							**18.00**	417.29
8								**0.00**

Table 5 : Per cent contribution of individual traits towards total divergence in wheat (*Triticum aestivum* L.)

Traits	Number of times appearing first in ranking	Per cent contribution towards total divergence
Number of tillers plant[-1]	291	6.24
Ear length (cm)	575	12.34
Seeds spike[-1]	580	12.46
1000 seed weight (g)	587	12.61
Plant height (cm)	450	9.66
Grain yield plant[-1] (g)	1005	21.61
Protein content (%)	281	6.04
Spikes spikelet[-1]	542	11.63
Days to flowering	345	7.41

Conclusion

The traits which have sufficient variability suggested that hybridization programme involving these diverse genotypes may lead to transgressive segregants and thus an overall genetic improvement in wheat crop. Maximum inter-cluster distance exhibited between cluster VI and VIII indicating maximum genetic divergence for genotypes falling in these two clusters followed by cluster-IV and VIII, cluster-V and VIII, cluster-VII and VIII and cluster-I and VIII. Divergence study, suggested that genotypes belonging to clusters-VI and VIII may be used as suitable parents in the future hybridization programme both of which were mono-genotypic. Cluster mean for different traits showed that among all clusters, cluster-VIII and cluster-V showed maximum cluster mean values for maximum number of traits, suggesting that these traits were superior over other traits and genotypes falling in these cluster would be selected directly on the basis of these traits and could be used in hybridization programme.

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