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RESEARCH **P**APER

Genetic diversity studies in whaet (*Triticum aestivum* L.) based on cluster analysis

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The significant differences between 32 genotypes of wheat for all the characters were observed. Genotypes were grouped into six clusters with cluster I having maximum genotypes (18) followed by cluster III and clusters II, clusters IV and VI were monogenotypic. Maximum inter-cluster distance was recorded between cluster V and VI (860.24) and maximum intra-cluster distance was recorded in cluster III (130.18). Cluster III registered maximum cluster mean values for grain yield and important yield contributing characters like ear head length, spikelets per spike, tillers per running meter, grains per spike, 1000 grain weight, hectolitre weight and protein content. The highest contribution towards genetic diversity was contributed by plant height followed by protein content and 1000 grain weight. Therefore, for hybridization genotypes from cluster V and VI should be selected for obtaining desired recombinants in the segregating generations.

Key words : Genetic diversity, Clusters, Soybean

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INTRODUCTION

Genetic diversity of plants determines their potential for improved efficiency and hence, their use in plant breeding may result in enhanced food production.The use of modern plant breeding techniques resulted in plant uniformity, which is more efficient by means of different goals, however, much more research must be done to indicate the most optimized methods that can be used for the production of efficient plants. One of the important approaches to wheat breeding is hybridization and subsequent selection. Estimation of genetic diversity is a prerequisite for proper selection of suitable diverse parents for hybridization in order to obtain desired recombinants in the segregating generations. The D^2 analysis classifies the genotypes into homogenous groups/clusters with the little diversity within the cluster, while the diversity between two clusters is usually high. Diversity analysis helps in avoiding the duplicates in germplasm by getting first-hand information about the level of diversity present in genotypes based on morphological characters, aids in maintaining more collections and also gives fair amount of information about the diversity present in new cultivars developed from the already released commercial varieties. Therefore, the present study was carried out to measure the degree of diversification of genotypes and also the relative contribution of each component character to the total divergence.

RESEARCH METHODOLOGY

Thirty-two genotypes of bread wheat procured

from the Agriculture Research Station, Niphad were evaluated in the Randomized Block Design with three replications during *Rabi* 2011-12 at Post Graduate Research Farm, College of Agriculture, Kolhapur. Each genotype was dibbled in a 5 m long double row plot with plant-to-plant distance 5 cm and row-to-row distance 22.5 cm. Recommended agronomic package of practices were followed as and when required during the entire growth period to raise a good crop. Five competitive plants were randomly selected and tagged in each experimental plot in each replication for recording observations on eleven quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), ear head length (cm), spikelets per spike, tillers per running meter, grains per spike, 1000 grain weight (g), hectolitre weight (g), protein content (%), grain yield per plot (g) and grain yield (Qt/ha). Data from five plants of each genotype were averaged replication wise and mean data was subjected to analysis of variance followed by multivariate analysis (Mahalanobis, 1936) and contribution of different characters to total divergence was worked out as per Tocher's method (Rao, 1952). The genotypes were further grouped into clusters on the basis of Ward's minimum sum of squares.

RESEARCH FINDINGS AND ANALYSIS

The analysis of variance revealed highly significant differences among the genotypes for all the characters indicating the presence of sufficient amount of genetic variability among the genotypes under study. Thirty two genotypes were grouped into six clusters using Ward's minimum variance method (Table 1). Cluster I had the maximum number of genotypes (18) followed by cluster III (8), cluster V (3) and clusters II, IV and VI were solitary. Distribution of genotypes into various clusters showed no uniformity and those belonging to same place were distributed among various clusters, thus ruling out the association between geographical distribution of genotypes and genetic divergence. Similar result was also reported by Kumar *et al*. (2013) and Singh *et al*. (2014). Lack of correspondence between genetic diversity and geographical distribution imparted that forces other than geographic origin, such as genetic drift, free and frequent exchange of breeding material, variation and artificial selection, differential gene expression due to genotype-environment interaction were responsible for creation of genetic diversity (Singh *et al*., 1971). Genetic diversity among genotypes of common geographical origin could be due to heterogeneity, genetic architecture, past history of selection, development at traits and combining ability (Murthy and Arunachalam, 1966).

The estimates of intra and inter-cluster distances of varying magnitudes among genotypes represented by D^2 and D values have been given in Table 2. Inter-cluster D^2 values ranged from 105.67 to 860.24. Maximum inter-cluster distance was recorded between cluster V and VI (860.24) followed by between cluster III and VI (754.60), cluster III and V (707.02) and cluster I and VI indicating a wider genetic diversity between the genotypes of these clusters. The genotypes from these clusters could be used as parents in hybridization programme to develop desirable types because crosses between genetically diverse parents generates heterotic segregants and chances of getting transgressive segregants are maximum when genetically divergent parents are crossed (Zaman *et al*., 2005 and Kumar *et al*., 2014). Inter-cluster distance was found to be minimum between cluster II and III indicating close relationship and similarity for most of the characters of the genotypes in these clusters. Intra-cluster D^2

Table 1: Distribution of 32 wheat genotypes in different clusters on the basis of D^2statistic

Clusters	Number of genotypes	Name of the genotypes
I	18	Niphad-4, NI-5643, NIAW-1415, NIAW-1689, NIAW-1773, NIAW-1885, NIAW-1895, NIAW-1945, NIAW-1947, NIAW-1951, NIAW-2006, NIAW-2032, NIAW-2059, NIAW-2060, NIAW-2064, NIAW-2073, NIAW-2255, NIAW-2286.
II	1	NIAW-2030
III	8	HD-2189, NI-747-19, NIAW-1867, NIAW-1994, NIAW-2031, NIAW-34, NIAW-301, NIAW-917.
IV	1	KENFAD-39
V	3	NI-5439, NIAW-1923, NIAW-2075.
VI	1	NI-179.

values ranged from 0.00 to 130.18. Cluster III registered maximum intra-cluster distance (130.18) followed by cluster V (106.70) indicating considerable amount of diversity within these clusters. Low intra-cluster distance was recorded in the clusters II, IV and VI because these clusters are monogenotypic.

The cluster mean values revealed marked differences between the six clusters for twelve characters (Table 3). Cluster III recorded highest mean values for ear head length, spikelets per spike, tillers per running meter, grains per spike, 1000 grain weight, hectolitre weight, protein content, grain yield per plot and grain yield per hectare. Maximum mean values for days to 50 per cent flowering and days to maturity were observed in cluster IV and for plant height in cluster VI. Cluster V registered minimum mean values for days to maturity, plant height, ear head length, spikelets per spike, tillers per running meter, grains per spike, 1000 grain weight, hectolitre weight, grain yield per plot and grain yield per hectare. Minimum number of days to 50 per cent flowering and protein content was found in the cluster VI. Similar findings have been reported by Singh and Dwivedi (2002); Tsegaye *et al*. (2012) and Kumar *et al*. (2014) which reflected probability of getting better segregants and recombinants, if genotypes from these cluster are used in hybridization programme.

Greater emphasis should be given to the characters contributing maximum to the genetic divergence while deciding the clusters for further selection (Jagadev *et al*., 1991).The highest contribution to genetic divergence was exhibited by the character plant height (18.95%) followed by protein content (18.14%), 1000 grain weight (16.12%), grain yield per plot (9.06%), grain yield per hectare(8.86%) and tillers per running meter (6.85%). Whereas, days to maturity, grains per spike,days to 50 per cent flowering, ear head length, spikelets per spike and hectolitre weight contributed least towards divergence. Therefore, as considerable genetic divergence is found in the genotypes included in the present study, it offers the sufficient scope for genetic improvement in wheat through hybridization between the genotypes from divergent clusters.

Table 2 : Average intra and inter cluster (D^2)and D values for 32 genotypes in wheat

Cluster	I	II	III	IV	V	VI
I	102.21 (10.11)	154.50 (12.43)	248.06 (15.75)	210.25 (14.5)	284.59 (16.87)	607.62 (24.65)
II		0.00 (0.00)	105.67 (10.28)	118.81 (10.9)	529 (23)	393.62 (19.84)
III			130.18 (11.41)	291.04 (17.06)	707.02 (26.59)	754.60 (27.47)
IV				0.00 (0.00)	564.06 (23.75)	222.30 (14.91)
V					106.70 (10.33)	860.24 (29.33)
VI						0.00 (0.00)

Table 3 : Cluster means for 12 characters in soybean

Characters / Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Ear head length (cm)	Spikelet's / spike	Tillers / running meter	Grains / spike	1000-grain weight (g)	Hectoliter weight (g)	Protein content %	Grain yield/ Plot (g)	Grain yield (Qt/ha)
I	56.76	110.19	82.06	8.45	14.17	110.70	40.89	39.74	80.21	11.33	892.29	40.15
II	57.00	108.00	93.00	9.00	15.60	114.00	45.00	41.90	80.66	11.77	928.40	41.77
III	58.13	109.63	86.46	9.11	15.87	116.67	45.88	43.51	81.17	12.05	942.91	42.41
IV	63.00	119.00	92.20	8.80	15.00	113.00	44.00	41.40	81.15	10.81	902.00	40.59
V	57.33	107.33	79.89	7.74	12.52	103.67	35.33	34.28	78.50	11.34	796.93	35.86
VI	56.00	112.00	110.4	8.60	15.00	112.00	40.67	39.77	80.12	10.66	893.00	40.18
Mean	57.33	110.04	84.50	8.57	14.53	111.75	41.83	40.28	80.32	11.48	897.18	40.06
S.E.±	0.89	0.61	0.50	0.06	0.19	0.58	0.53	0.23	0.18	0.04	6.12	0.25
% contribution	4.03	5.44	18.95	3.22	2.16	6.85	5.24	16.12	2.01	18.14	9.06	8.86

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