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ASSESSMENT OF DIVERSITY FOR YIELD AND ITS COMPONENT TRAITS IN F_2 POPULATION OF WHEAT (*Triticum aestivum* L.) UNDER SALINITY CONDITIONS

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ABSTRACT

Genetic diversity analysis of yield and yield contributing traits in F_2 population of wheat cross 'Kharchia 65 x HD 2851' was estimated, based on D^2-statistics, for 100 selected phenotypically superior plants that were grouped into 13 clusters. Clustering pattern revealed that cluster II and IV were the largest ones with 14 genotypes. The highest inter-cluster distance was observed between clusters VII and VIII (11.67), followed by between clusters VII and X (10.85), VII and IX (9.88) and VII and XII (9.88). This indicates that plants included in these clusters possess wide genetic diversity. Further, cluster VIII exhibited high mean value for number of spikelets spike^{-1} (18.0), number of grains ear^{-1} (36.0), grain yield plant^{-1} (0.911 g) and biological yield plant^{-1} (4.342 g). Cluster I showed highest mean value for the number of grains spikelet^{-1} (3.0), moderate 1000-grain weight (32.95 g) and acceptable harvest index (34.6%). The clusters VII, I, II, III, XI and XII were outstanding on the basis of better cluster mean for most of the characters. The genotypes in these clusters should be selected and utilized to the advanced generation in a breeding program for improved salinity tolerance.

Key words: Cluster analysis, D^2-statistics, genetic diversity, salinity, wheat

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the one of the important cereal crops of the world along with rice and maize as a source of human food and a major commodity in international grain market. Wheat is the 2nd largest cereal grown in India after rice. The total area under wheat crop during 2015-16 was 30.23 million ha with the production of 93.5 million t and average productivity of 30.93 q ha^{-1} (IIW&BR, 2016). Wheat may be compared well with other cereals so far as nutritive values are concerned. It has good nutrition profile with 12.1% protein, 1.8% lipids, 1.8% ash, 2.0% reducing sugars, 6.7% pent sans, 59.2% starch, 70% total carbohydrates and provides 314 kcal 100 g^{-1} food (Lorenz and Kulp, 1991). It is also a good source of minerals and vitamins *viz*., calcium (37 mg 100 g^{-1}), iron (4.1 mg 100 g^{-1}), thiamine (0.45 mg 100 g^{-1}), riboflavin (0.13 mg 100 g^{-1}) and nicotinic acid (5.4 mg 100 mg^{-1}) [Lorenz and Kulp, 1991].

Wheat production and productivity directly influences human needs in developing countries and quality of life in developed countries (Dixon *et al*., 2009). Productivity of a crop mainly depends on the genetic efficiency of crop, soil type, environmental conditions and the ability of a crop to overcome biotic and abiotic stresses. If any of these is unfavourable, the crop productivity tends to decrease. Therefore, to increase crop productivity the emphasis should be given to these important aspects. To overcome climatic aberration, it is imperative to incorporate multiple stress-tolerant genes in crops to sustain crop production under changing climatic scenarios.

Salinity is one of the major abiotic stresses and yield limiting factor in irrigated and rain-fed agriculture cropping system, thereby reducing the plant growth and productivity worldwide as well as affecting about 7% of world's total land area. It causes undesirable effects on plant growth, development, physiological and biochemical changes, due to low osmotic potential of soil solution (osmotic stress), specific ion effects (salt stress), nutritional imbalance or a combination of these factors (Ashraf, 2004). In Asia, 21.5 million ha land area is affected by salinity causing an estimated 50% crop loss in fertile land (Nazar *et al.*, 2011). Increased salt tolerance in crops is widely recognized as an effective mean to overcome the limitations of crop production in salinized areas (Takeda *et al.*, 1995). For improving the salt stress tolerance of crop varieties by plant breeding, it is necessary to identify genotypes having tolerance to salt stress in all growth stages.

Genetic diversity serves as a way for populations to adapt for changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Genetic diversity plays an important role in the survival and adaptability of a species because when the environment changes, slight gene variations are necessary to produce changes in the species that enables it to adapt and survive. A species that possesses a large degree of genetic diversity among its population will have more variations from which to choose the fit alleles. One of the potent techniques for assessing genetic divergence is D^2 statistic proposed by Mahalanobis (1936). Genetic diversity is the basis of plant breeding produced due to inherent genetic differences in plant species and is of major interest to the plant breeder. This technique measures the forces of differentiation at two levels *viz*., intra- and inter-cluster that helps in the selection of genetically divergent parents for exploitation in hybridization programmes. Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. Therefore, the present study was aimed to evaluate the extent of genetic variation in F_2 population of wheat on the basis of agronomic traits so as to screen superior plants.

MATERIALS AND METHODS

The present study was conducted with 100 phenotypically superior F_2 plants of wheat (selected on the basis of phenotypic traits like grain yield plant^{-1}, tillers plant^{-1} and grains ear^{-1}) along with their parents to assess the degree of divergence among them. The F_1 seeds of 'Kharchia 65 x HD 2851' F_1 were procured from Wheat & Barley Section, Department of Genetics and Plant Breeding, CCSHAU, Hisar (India). Variety 'Kharchia 65' is salt tolerant and can grow and set seeds up to pH 9.4 but its seeds are red colour and the crop is susceptible to lodging. 'HD 2851' is early maturing variety (126-134 days) and on maturity attains a height of 80-90 cm. The variety is very good for bread making with protein content of 11-12%. The F_1 seeds were sown in pots in a net house during *rabi* 2013-2014 in the Research Area of the Department of Genetics & Plant Breeding, CCSHAU, Hisar. The recommended agronomic practices were followed for raising a good wheat crop (CCSHAU, 2014). Hoagland's nutrient solution was given to the plants growing in pots in net house 10 days after seed sowing. Four treatments of salt solution of 8 dS m^{-1} EC were given, two at sowing time and two 20 days after sowing. At maturity, the final soil EC was 12. The composition of Hoagland's nutrient solution were as follow: macronutrient stock solution A (g L^{-1}): $Ca(NO_3)_2$ - 364.09; KNO_3 - 221.3; $MgSO_4$ - 217.6 and KH_2PO_4 - 62.1, micronutrient stock solution B (g L^{-1}): $ZnSO_4$ - 0.097; H_3BO_3 - 1.26; Na_2MoO_4 - 0.4; $CuSO_4$ - 0.33 and $MnSO_4$ - 0.6; stock solution C (g L^{-1}): tartaric acid - 4.0 and $FeSO_4.7H_2O$ - 5.0. Separate stock solutions of solution A, B and C were prepared. Then, 62.5 mL each of solution A and B and 15 mL of solution C were mixed and diluted to 25 L. The different salts used to make salt solution included NaCl - 3.0686 (g L^{-1}); $CaCl_2.2H_2O$ -

0.965 (g L^{-1}); $MgCl_2.6H_2O$ - 0.76 (g L^{-1}) and $MgSo_4.7H_2O$ - 3.88 (g L^{-1}). Solution A (50 mL), solution B (12.5 mL) and solution C (3 mL) of Hoagland's solution were added to prepare a stock of salt solution to get 5 L salt solution of EC ~ 8 dS m^{-1}. The observations were recorded on individual plants of F_2 population with respect to 10 morphological characters *viz.,* plant height, number of tillers plant^{-1}, ear length, number of spikelets spike^{-1}, number of grains spikelet^{-1}, number of grains ear^{-1}, 1000 grain weight, grain yield plant^{-1}, biological yield plant^{-1} and harvest index. Mahalanobis (1936) D^2-statistic analysis was used for the estimation of genetic divergence among 49 genotypes used. The clustering of D^2 values was formed by using Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

One hundred phenotypically superior under salinity F_2 plants of wheat along with their parents were grouped into 13 clusters based on the relative magnitude of their D^2 values, in such a way that genotypes within each cluster had smaller D^2 value than between the clusters. The composition of clusters has been depicted in Table 1. The distribution pattern of genotypes showed that cluster II and IV had maximum number of genotypes (14), each followed cluster IX, 1, XI, XIII, III, VI and VI with 13, 12, 11, 10, 6, 6 and 4 genotypes, respectively. The remaining clusters had 3 genotypes each. Salt tolerant parent cv. 'Kharchia 65' was grouped in cluster I F_2 plants whereas cv. 'HD 2851' was grouped in cluster II F_2 plants on the basis of clustering approach. Genotypes within a cluster were less diverse among themselves. Both the parents fell in different clusters which clearly revealed that they are diverse. Kumar *et al.* (2009), Arya *et al.* (2017), Pandey *et al.* (2017) and Singh *et al.* (2017) also reported similar results. Prasad et *al.* (2015) classified 50 genotypes of wheat into 3 clusters with 11, 24 and 15 genotypes in I, II and III cluster, respectively. Singh *et al.* (2017) clustered 108 wheat genotypes in 4 groups for salinity and water logging tolerance. Singh *et al.* (2009) also classified 300 wheat genotypes in 7 clusters based on agronomic features and salt tolerance using non-hierarchical Euclidean cluster analysis. Because a breeding program mainly depends on the magnitude of genetic variability, morphological characterizations is an important step in the description and classification of crop germplasm Piyada *et al.* (2010).

Table 1: Clustering of 100 selected F_2 plants and their parent of wheat for intra-cluster distance

Clusters	F_2 population	Number of the entry
I	12	7, 279, 237, 421, 124, 128, 319, 246, 382, 390, 384 and Kharchia 65
II	14	53, 232, 239, 146, 361, 173, 230, 398, 295, 385, 190, 343, 207 and HD 2851
III	6	9, 81, 266, 399, 23 and 92
IV	14	8, 165, 270, 75, 272, 71, 115, 285, 269, 137, 290, 215, 287 and 441
V	3	172, 296 and 314
VI	6	22, 349, 233, 369, 274 and 448
VII	3	188, 444 and 405
VIII	3	29, 212 and 119
IX	13	58, 393, 169, 439, 13, 105, 67, 94, 103, 275, 134, 303 and 123
X	4	150, 186, 95 and 142
XI	11	56, 312, 104, 219, 181, 74, 135, 262, 261, 324 and 41
XII	3	223, 243 and 70
XIII	10	147, 289, 179, 383, 129, 310, 267, 403, 43 and 200

The inter-cluster distance was higher than intra-cluster, suggesting wide genetic diversity among F_2 plants (Table 2). The inter-cluster distance varied from 2.58 to 11.67. Maximum inter-cluster distance was observed between cluster VII and cluster VIII (11.67) followed by between cluster VII and X (10.85),

Table 2: Intra- and inter-clusters among 100 selected F_2 plants of wheat

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**1.69**	2.58	4.42	2.78	4.29	3.80	6.58	7.39	4.22	5.96	2.62	4.67	3.91
II		**2.47**	4.06	3.28	4.39	3.37	5.90	7.42	5.04	6.24	3.88	5.31	4.64
III			**3.61**	4.86	5.52	4.55	5.68	7.84	6.35	7.18	5.51	6.53	4.74
IV				**1.74**	3.09	3.21	8.01	5.96	2.93	4.02	2.68	4.22	3.44
V					**1.76**	3.59	8.86	3.95	3.80	3.66	4.28	4.07	4.29
VI						**2.01**	6.85	6.59	4.85	4.76	4.83	6.06	4.70
VII							**2.74**	11.67	9.88	10.85	8.44	9.88	8.44
VIII								**2.55**	5.64	4.65	6.82	5.22	6.28
IX									**2.28**	3.63	3.02	3.89	3.73
X										**1.58**	5.31	5.72	4.92
XI											**1.63**	3.63	3.56
XII												**2.69**	4.76
XIII													**2.77**

VII and IX (9.88) and VII and XII (9.88). However, minimum distance was observed between cluster I and II (2.58) indicating close relationship between these clusters would not provide good results. The greater distance between clusters indicates broad spectrum of divergence and may produce desirable transgressive segregants. This would be useful in wheat breeding programme for developing high yield potential varieties. When diversity was studied within the clusters based on intra-cluster D^2 values, it showed a range of 1.58 to 3.61. Cluster X had minimum intra-cluster value (1.58) indicating a minimum difference among the genotypes grouped in this cluster. The maximum intra-cluster D^2 value was observed for cluster III (3.61), followed by cluster XIII (2.77) and cluster VII (2.74) which revealed the existence of maximum differences among the genotypes that fall in these clusters. Similar findings were also reported by Singh *et al.* (2009), Naik *et al.* (2016), Singh and Kumar (2017) and Ali *et al.* (2017).

Since improvement in yield and other related characters is a basic objective in any breeding programme, therefore cluster means for seed yield plant^{-1} and its major components need to be considered for the selection of genotypes. The data revealed considerable differences among all the clusters for most of the characters studied (Table 3). The cluster means analyzed for 10 characters under study revealed that Cluster VII exhibited highest mean value plant height (89.23 cm), ear length (9.37 cm), number of spikelets spike^{-1} (18.0), number of grains ear^{-1} (36.0), grain yield plant^{-1}

Table 3: Mean values of different cluster for 10 traits in wheat

Characters / Clusters	Plant height (cm)	Tillers plant^{-1} (No.)	Ear length (cm)	Spikelets spike^{-1}	Grains spikelet^{-1}	Grains ear^{-1} (No)	1000-grain weight (g)	Grain yield plant^{-1} (g)	Biological yield plant^{-1} (g)	Harvest index (%)
I	66.4	1.02	5.86	9.42	3.00	18.00	32.9	0.588	1.711	34.6
II	62.4	1.00	6.87	11.59	2.79	21.93	25.9	0.565	1.911	29.7
III	61.7	2.17	7.10	12.67	2.67	23.83	23.2	0.529	2.201	26.0
IV	50.2	1.00	5.08	8.43	3.00	14.36	24.1	0.340	1.162	30.6
V	56.4	1.00	4.53	6.67	2.00	11.68	18.2	0.215	1.059	20.2
VI	63.7	1.00	6.50	10.67	3.00	17.68	14.9	0.257	1.761	14.4
VII	89.2	1.67	9.37	18.00	3.00	36.00	25.8	0.911	4.342	21.0
VIII	31.8	1.33	3.27	4.67	1.00	3.33	16.8	0.052	0.402	12.5
IX	40.9	1.00	4.35	5.92	3.00	5.46	32.9	0.179	0.563	31.7
1X	33.7	1.00	3.67	4.50	3.00	3.00	15.0	0.040	0.383	11.5
XI	52.2	1.00	4.68	7.18	3.00	15.54	38.1	0.476	1.152	41.4
XII	42.5	1.00	4.60	7.00	1.67	8.00	39.7	0.315	0.750	42.0
XIII	53.3	2.00	4.76	6.90	3.00	10.80	31.8	0.340	1.109	29.8
Mean	54.2	1.25	5.43	8.74	2.63	14.59	26.1	0.369	1.423	26.6

Table 4: Diverse and superior F_2 plants from different clusters

F_2 plants	Cluster	Characters
444, 405	VII	Plant height, ear length, spikelets spike-1, grains ear^{-1}, grain yield plant^{-1} and biological yield plant^{-1}
7, 128, 319	I	Plant height, tillers plant^{-1}, grains ear^{-1}, 1000 grain weight, grain yield plant^{-1} and biological yield plant^{-1} and harvest index
190, 207	II	Plant height, ear length, spikelet spike^{-1}, grains ear^{-1}, grain yield plant^{-1} and biological yield plant^{-1}
9, 23, 92	III	Tillers plant^{-1}, ear length, spikelet spike^{-1}, grains ear^{-1}, grain yield plant^{-1} and biological yield plant^{-1}
74, 104, 262	XI	1000-grain weight, grains ear^{-1} and harvest index
223, 243	XII	1000-grain weight and harvest index

(0.911 g) and biological yield plant^{-1} (4.342 g). Cluster I showed highest mean value for number of grains spikelet^{-1} (3.0), better 1000-grain weight (32.95 g) and harvest index (34.61%). However, maximum number of tillers plant^{-1} was observed in cluster III (2.17). Cluster XII revealed highest mean for 1000-grain weight and harvest index. Similar results have been reported by Shah *et al.* (2015), Tewari *et al.* (2015), Arya *et al.* (2017) and Kumar *et al.* (2017).

The cluster VII, I, II, III, XI and XII were ascertained outstanding on the basis of better cluster mean for most of the characters. Phenotypically superior genotypes, presented in Table 4, were selected from these clusters and character for which they perform well. The results demonstrated that there was a substantial genetic diversity between different progeny lines. The progeny lines identified from different clusters for various traits may be extended for further evaluation in next generation for the development of superior lines or varieties with desirable traits.

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