EVALUATION OF GENETIC PARAMETERS AND DIVERGENCE IN WHEAT (TRITICUM SPECIES) GENOTYPES FOR YIELD AND YIELD CONTRIBUTING TRAITS

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Abstract - Studying genetic variability and divergence of quantitative traits and their contribution towards yield is prerequisite to meet the diversified goals of plant breeder for developing high yielding varieties with better quality, adaptability and resistivity. The present investigation was carried out to evaluate the genetic parameters and divergence in thirty genotypes of varieties in wheat Triticum aestivum L. and Triticum durumDesf. in agro-climatic conditions of Punjab. Analysis of variance showed highly significant differences among treatment for all the traits. High values of PCV were shown for number of productive tillers per plant (23.57), number of grains per plant (23.03) and grain yield per plant (g) (20.41), whereas moderate values of GCV were shown for number of productive tillers per plant (16.98), grain yield per plant (g) (13.63), number of grains per plant (13.00), biological yield per plant (g) (12.98), number of grains per spike (10.90) and spike length (cm) (10.21). The estimates of heritability recorded high for spike length (cm) (81.80), plant height (cm) (73.00) and peduncle length (cm) (70.50). High estimates of heritability coupled with moderate genetic advance as percent of mean was recorded for spike length (cm), plant height (cm) and peduncle length (cm). Therefore, a plant breeder should emphasize on these traits while practicing selection of high yielding wheat cultivars. Based on result of diversity, 30 genotypes were grouped into six clusters. Cluster I and cluster II had largest genotypes (09 each) followed by cluster IV (04). The inter-cluster distances were higher than intra-cluster distance, indicating wide genetic diversity among genotypes of different groups. The maximum intra- cluster distance was observed for cluster III (D^2=13.00) followed by cluster II (D^2=8.31). Cluster V and VI (D^2=66.56) showed maximum inter-cluster distance indicating that crossing between the varieties of these clusters will create wide spectrum of variability in wheat followed by cluster II and VI (D^2=56.97). Cluster VI exhibited highest mean value for biological yield per plant (g) (27.81), 1000- grain weight (g) (44.61), plant height (cm) (104.10), days to maturity (119.33) and number of productive tillers per plant (10.00). Further, cluster III had highest mean values for spike length (cm) (12.36), number of grains per plant (356.44) and grain yield per plant (g) (11.03), and lowest mean for days to maturity (116.73)i.e. early maturity genotypes were also found in this cluster. Thus, it may be suggested that crossing of genotypes from these clusters may be considered as donor parent for hybridization programme for creating desired variability as well as for effective selection criteria.

Keywords - Wheat, Variability, PCV, GCV, Heritability, Genetic advance and Divergence.

I. INTRODUCTION

Wheat of both the tetraploid (Triticum durumDesf.) and hexaploid (Triticum aestivum L.), a self-pollinated crop is an ancient origin of agriculture, belongs to the family Gramineae and important food grain crop of the world which ranks first among cereals. In order to meet the growing demand for a swiftly growing population of food in the country, wheat yield per unit area could increase to the extent through it could bring itself out from insufficiency to a self- sufficient status. Grain yield is the principle quantitative character of cereal crops. Selection for desirable genotypes for improvement should not only based on yield alone, therefore, the other yield components should also be considered. For a successful utilization breeding programme, the presence of genetic variability plays a vital role. It is therefore, knowledge on genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance are paramount importance to practice selection criteria. Further, it is widely accepted that the information on germplasm diversity and genetic relatedness among elite breeding materials are also fundamental elements in plant breeding (Ferdous et al. 2011). Divergence analysis is a useful tool in quantifying the degree of divergence between biological population of geographical level and to access in assessing relative contribution of different components to the total divergence both at intra and inter cluster levels (Amin et al. 2014). With this view, study of different genotypes were made with an attempt to generate information on variability and diversity among 30 wheat genotypes and the information thus obtained will be used to define suitable selection criteria for yield improvement in hybridization programme.

II. METHOD AND MATERIAL

The present investigation was conducted during Rabi season 2017-18 at Research Farm, G.K.S.M Government College, Tanda Urmar (Hoshiarpur), India. The material comprised of thirty genotypes of wheat viz. DL-153-2, DBW-71, PBW-154, RAJ-1972, PBW-590, WL-711, UP-2425, PBW-34, PBW-226, WL-2265, HD-2270, PDW-314, KalayanSona, PBW-65, HD-2204, DBW-90, HD-2687, WH-1080, HD-2285, RAJ-3077, WH-1105, GW-120, HD-3043, PBW-175, HD-2281, RAJ-2184, DPW-621-50, HD-

1941, PBW-299 andPBW-396 which were collected from Indian Institute of Wheat and Barley Research, Karnal and were grown in a Randomized Block Design (RBD) with three replications, keeping row to row distance of 22.5 centimetre with an appropriate plant to plant distance of 5 centimetre in each replication. Recommended agronomic package of practices was followed to raise a good and healthy crop. Five competitive plants of each genotype were randomly selected from each replication for recording the observations. The data were recorded from randomly selected plants from the field for twelve quantitative characters. Averages of the data from each replication in respect of different characters were used for various statistical analyses. Statistical analysis of the data was done with Windostat® ver. 9.2. Analysis of variance (ANOVA) estimated according to Panse and Sukhatme (1967).The analysis for divergence was done by following Mahalanobis (1936) D^2statistic. The varieties were grouped into number of clusters with D^2 being treated as the square of generalized distance, according to the method described by Tocher (Rao, 1952).

III. RESULT AND DISCUSSION

The present study was undertaken to evaluate the performance of wheat genotypes for various yields and its contributing traits.

Estimates of Genetic Parameters: The ANOVA indicated that there was a significant difference between all the traits studied, suggested adequate genetic variability among genotypes for all the traits. The presence of large amount of variability might be due to diverse source of material as well as environmental influence affecting the expression of the traits. The estimates of genetic variability parameters for all the traits were worked out and were presented in Table-1.The estimates of PCV were higher for number of productive tillers per plant (23.57), number of grains per plats (23.03) and grain yield per plant (g) (20.41). The remaining traits recorded moderate to low estimates of PCV, whereas moderate estimates of GCV were recorded for number of productive tillers per plant (16.98),grain yield per plant (g) (13.63), number of grains per plant (13.00), biological yield per plant (g) (12.98), number of grains per spike (10.90) and spike length (cm) (10.21). High PCV values and moderate GCV values indicated that there was variability existing among genotypes and there was a better opportunity for improvement in these traits through selection. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on phenotypes. Results of present study concur with that of Tambe et al. (2013), Kumar et al. (2013) and Tripathi et al. (2015). High heritability was observed by spike length (cm) (81.80) followed by plant height (cm) (73.00) and peduncle length (cm) (70.50). The remaining traits showed moderate heritability. The high genetic advance as percent of mean was recorded for number of productive tillers per plant (25.21) and all traits showed moderate heritability except days to maturity and number of spikelets per spike. Heritability estimates accompanied with genetic advance as percent of mean are more helpful in predicting the gain under selection than heritability estimates alone. High estimations of heritability value coupled with moderate genetic advance was observed for plant height (cm), spike length (cm) and peduncle length (cm) indicating that these characters were less influenced by environments but governed by both additive and non-additive gene actions. Therefore, these traits have higher contribution towards the total genetic divergence. Similar results were revealed by Verma et al. (2014) for most of the traits under study.

Divergence Analysis (D^2- Analysis): In hybridization programme, genetically diverse parent are selected to produce high heterotic effect which create a wide range of recombinant and variability. Therefore, knowledge of genetic diversity among the genotype is necessary. Based on Mahalanobis D^2 analysis using Tocher's method categorized the genotypes into six different clusters (Table 2) and Fig.1suggesting considerable amount of genetic diversity in the material. The cluster II and cluster VI both had the largest number of genotypes comprising 09 genotypes indicating overall homogeneity among them followed by cluster IV(04), cluster I and cluster III (03 each), whereas cluster V had lowest number of genotypes (02).Similar results were in close agreement with Dhakar et al. (2012). The inter-cluster distance was higher than intra-cluster distance were given in Table 3 indicating wide genetic diversity among genotypes. The magnitude of intra cluster distance measures the extent of genetic diversity between the genotypes of same cluster, while intra cluster distance gives a measure of genetic distance between two clusters. The highest inter-cluster distance was observed in cluster III (D^2=13.00) indicating more heterogeneity that is, genotypes involved in this cluster are more divergent among themselves and would produce more desirable breeding materials for achieving maximum genetic advance, whereas the lowest intra-cluster distance was in cluster V (D^2=0) and cluster VI (D^2=0) indicating close relationship and the narrower genetic variation within a cluster. Similar results are concordance with Singh et al.(2010). Further, the maximum inter- cluster distance was reported between cluster V and VI (D^2=66.56) followed by distance between cluster II and VI (D^2=56.97) and between cluster III and IV (D^2=54.82) indicating that genotypes involved in these clusters are more divergent and can be used to produce superior hybrids and transgressive segregants facilitating further selection and improvement. However, the minimum inter- cluster distance was observed minimum

between cluster I and II (D^2=14.55) indicated that there was a close relationship among the individuals included in these two clusters which would not provide good level of segregation. Similar results are evidenced by Kumar et al. (2013) and Singh et al. (2014). Increasing parental distance implies a greater number of constraining alleles at the desired loci, and then to the extent that these loci recombine in the F_2 and F_3 generations following a cross of distantly related parents, the greater will be the opportunities for successful selection for any character of yield interest (Gashaw et al. 2007).

The six clusters showed considerable differences in average mean value for 12 different traits under study (Table 4). Cluster I and cluster II had individuals of moderate mean values for almost all the traits studied except cluster II had highest mean value for number of spikelets per spike (21.46) and number of grains per spike (53.97). The cluster V had moderate mean values for days to maturity (117.67), productive tillers per plant (8.67), spike length (cm) (10.52), grains per spike (51.53), grains per plant (336.13) and biological yield per plant (%) (24.34), whereas, cluster V showed lowest mean values for the remaining traits. Individuals of cluster VI were late maturing (119.33), also they had maximum mean values for number productive tillers per plant (10.00), plant height (cm) (104.10), peduncle length (cm) (37.18), biological yield per plant (g) (27.81) and 1000- grain weight (g) (44.61), whereas, lowest mean for number of spikelets per spike (19.00), number of grains per spike (38.07) and number of grains per plant (276.47). Also, moderate mean values were recorded for other remaining traits of this cluster. The lowest cluster mean for days to maturity was observed for cluster III (116.73), which indicated that the genotypes of this cluster have early flowering than genotypes involved in other clusters. The genotypes having high mean performance for grain yield per plant (g) (11.03), number of grains per plant (356.44) and spike length (cm) (12.36) were found in cluster III. Therefore, selection will be effective for these traits from cluster III. The cluster IV had highest mean values for harvest index (%) (45.86), whereas lowest mean for number of productive tillers per plant (7.17), peduncle length (cm) (37.18), biological yield per plant (g) (21.08) and spike length (cm) (7.95). These results are in agreement with Kumar et al.(2014), Kumar et al.(2015), Uddin et al.(2015) and Sapi et al.(2017).The percent contribution of 12 characters towards total genetic divergence is listed in Table 5. The selection and choice of parents mainly depends upon contribution of characters towards divergence (Sapi et al. 2017). The utility of D^2 statistics is enhanced by its applicability to estimate the relative contribution of the various characters to genetic divergence. Plant height (cm) (ranked first 119 times out of 435 total numbers of combinations) contributed 27.36 percent to divergence of genotypes. This was followed by number of spikelets per spike (27.23%), spike length (cm) (19.31), 1000-grain weight (g) (7.13), peduncle length (cm) (4.14%), productive tillers per plant (3.22), number of grains per spike (2.99%), number of grains per plant (2.99%), biological yield per plant (g) (2.53), harvest index (%) (2.30), days to maturity (0.69%) and grain yield per plant (g) (0.23%). Similar results are in concordance with Lal et al. (2009), Khare et al. (2015), Rahman et al. (2015) and Arya et al. (2017).

CONCLUSION

The present research delivered considerable information which could be very useful in genetic improvement of wheat genotypes. The mean sum of square due to genotypes was significant for all the character studied. High values of PCV were shown for number of productive tillers per plant, number of grains per plant and grain yield per plant (g), whereas moderate values of GCV were shown for number of productive tillers per plant, grain yield per plant (g), number of grains per plant, biological yield per plant (g), number of grains per spike and spike length (cm). The estimates of heritability recorded high for spike length (cm), plant height (cm) and peduncle length (cm).High estimates of heritability coupled with moderate genetic advance as percent of mean was recorded for spike length (cm), plant height (cm) and peduncle length (cm). Therefore, a plant breeder should emphasize on these traits while practicing selection of high yielding wheat cultivars. Based on result of diversity, 30 genotypes were grouped into six clusters. Cluster I and cluster II had largest genotypes followed by cluster IV. The inter-cluster distances were higher than intra-cluster distance, indicating wide genetic diversity among genotypes of different groups. The maximum intra- cluster distance was observed for cluster III followed by cluster II. Cluster V and VI showed maximum inter-cluster distance indicating that crossing between the varieties of these clusters will create wide spectrum of variability in wheat followed by cluster II and VI. Cluster VI exhibited highest mean value for biological yield per plant (g), 1000- grain weight (g), plant height (cm), days to maturity and number of productive tillers per plant. Further, cluster III had highest mean values for spike length (cm), number of grains per plant and grain yield per plant (g), and lowest mean for days to maturity i.e early maturity genotypes were also found in this cluster. Thus, it may be recommended that crossing of genotypes from these clusters may be considered as donor parent to the remaining genotypes in other cluster can be utilized for further breeding program for improvement and promising segregates and recombinants.

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Table-1. Estimates of genetic parameters for various traits of 60 wheat genotypes

Parameters / Characters	σ^2_p	σ^2_g	PCV (%)	GCV (%)	h^2_{bs} (%)	GA	GA as % of Mean
Days to maturity	2.70	0.93	1.39	0.822	34.60	1.17	0.99
No. of productive tillers per plant	4.03	2.09	23.57	16.98	51.90	2.14	25.21
Plant height(cm)	58.85	42.93	8.33	7.12	73.00	11.53	12.53
Spike length(cm)	1.75	1.43	11.29	10.21	81.80	2.23	19.02
Peduncle length(cm)	9.61	6.77	9.41	7.90	70.50	4.50	13.67
No. of spikelets per spike	1.58	0.92	6.22	4.75	58.20	1.51	7.47
No. of grains per spike	69.39	25.98	17.81	10.90	37.40	6.42	13.74
No. of grains per plant	5895.11	1879.53	23.03	13.00	31.90	50.42	15.12
Biological yield per plant(g)	22.48	9.82	19.65	12.98	43.70	4.26	17.68
Grain yield per plant(g)	4.46	1.99	20.41	13.63	44.60	1.94	18.75
Harvest index (%)	5.29	2.14	5.29	3.42	41.70	1.95	4.55
1000-grain weight(g)	12.84	7.57	12.84	8.30	41.80	3.66	11.05

σ^2_p – phenotypic variance; σ^2_g – genotypic variance; PCV – Phenotypic coefficient of variance; GCV – Genotypic coefficient of variance; h^2_{bs} – heritability in broad sense; GA – Genetic advance (at 5% selection intensity i.e. K = 2.06)

2*Values in parenthesis are transformed values

Table 2: Distribution of 30 wheat genotypes in different clusters

CLUSTER	NO. OF GENOTYPES IN CLUSTER	GENOTYPES
I	03	DBW-71, PBW-590, DPW-621-50
II	09	PBW-226, HD-2270, KALYAN SONA, PBW-65, DBW-90,WH-1080, HD-2285, RAJ-3077, HD-2281
III	03	DL-153-2, WL-2265, PBW-175
IV	04	HD-2204, HD-2687, WH-1105, HD-1941
V	02	PBW-34, PBW-314
VI	09	PBW-154, RAJ-1972, WL-711, UP-2425, PBW-396, GW-120, HD-3043, RAJ-2184, PBW-299

Table 3: Intra- and inter-cluster distance (D^2-value) of clusters formed with 30 genotypes of wheat

CLUSTERS	CLUSTER I	CLUSTER II	CLUSTER III	CLUSTER IV	CLUSTER V	CLUSTER VI
CLUSTER I	**5.03**	14.55	15.10	30.41	21.89	25.23
CLUSTER II		**8.31**	21.29	52.79	21.88	56.97
CLUSTER III			**13.00**	54.82	44.65	32.61
CLUSTER IV				**6.46**	48.93	47.45
CLUSTER V					**0.00**	66.56
CLUSTER VI						**0.00**

Table 4: Mean values of the characters of the clusters

Characters / Clusters	Days to Maturity	Productive Tillers / Plant	Plant Height (cm)	Spike Length (cm)	Peduncle Length (cm)	Spikelets/ Spike	Grains/ Spike	Grains / Plant	Biological Yield / Plant (g)	Grain Yield / Plant (g)	harvest Index (%)	1000-Grain Weight (g)
I	118.07	7.87	91.20	11.65	32.28	19.58	46.00	315.68	23.67	10.17	42.79	33.65
II	117.44	7.63	87.08	12.08	31.01	21.46	53.97	328.18	22.20	9.62	43.32	32.29
III	116.73	9.62	95.79	12.36	34.34	20.57	45.13	356.44	25.75	11.03	42.70	31.90
IV	118.67	7.17	92.77	7.95	35.88	18.93	39.50	328.20	21.08	9.74	45.86	36.00
V	117.67	8.67	74.05	10.52	24.97	18.67	51.53	336.13	24.34	9.45	38.72	30.75
VI	119.33	10.00	104.10	11.85	37.18	19.00	38.07	276.47	27.81	10.96	39.76	44.61

Table 5:Percentcontribution of each characters towards the divergence in 30 genotypes of wheat

S.NO.	CHARACTERS	PERCENT CONTRIBUTION (%)	NUMBER OF TIMES APPEARING FIRST IN RANKING
1	Days to maturity	0.69	3
2	Productive tillers/ plant	3.22	14
3	Plant height (cm)	27.36	119
4	Spike length (cm)	19.31	84
5	Peducle length (cm)	4.14	18
6	Spikelets/ spike	27.13	118
7	Grains/ spike	2.99	13
8	Grains/ plant	2.99	13
9	Biological yield/ plant (g)	2.53	11
10	Grain yield/ plant (g)	0.23	1
11	Harvest index (%)	2.30	10
12	1000-Grain weight (g)	7.13	31

Research category: Evaluation of genetic parameters and divergence in wheat genotypes for yield and yield contributing characters

Abbreviations:

% : Percent
Cm : Centimetre
G : Gram
PCV: Phenotypic coefficient of variance
GCV: Genotypic coefficient of variance
Ver. : Version
et.al : Other authors
F_2 : 2nd Filal generation
F_3 : 3rd Filal generation
No. : Number
Fig. : Figure

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