Website : www.asthafoundation.in
Frontiers in Crop Improvement
Vol 10 (1) : 65-70 (January-2022) Print ISSN : 2393-8234 Online ISSN : 2454-6011
Astha Foundation, Meerut (U.P.) India

Analysis of Genetic Variability and Variation Yield and its Component Trait in Wheat (*Triticum aestivum* L.)

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Abstract

A total of 52 wheat genotypes were to estimate the nature and magnitude of genetic variability and diversity in order to efficient utilization of genetics materials in a breeding programme. These wheat genotype were sown in randomized block design with three replications in the experimental field of Department of Genetics and plant breeding,Motherhood university Roorkee(U.K).Data was recorded for fourteen character*viz*days to 75% flowering, plant height, peduncle length, number of productive tillers per plant, days to maturity, spike length, number of spikelet's per spike, number of grains per spike, 1000-grain weight, biological yield per plant, grain yield per plant, harvest index, gluten and protein content were all recorded. For all of the charactersstudied, analysis of variance revealed substantial variations between genotypes. Grain yield per plant had the highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). These 52 genotypes were grouped into eight clusters. Cluster VI and Cluster V had the greatest inter-cluster distance. This suggests that the genotypes of these clusters distantly related. Peduncle length (3.64 percent) contributing. The most tothe overall genetic divergence, hence,this trait was a major driver of genetic diversity. On the basis of genetic divergence and cluster mean, it is concluded that good recombinants might be obtained by attempting crosses between genotypes of cluster VIII, VII, and IV. Thus, crosses between the genetically diverse genotypes of Cluster VIII (genotypes 1013, 2040, and 8056) and Cluster VII (genotypes 1036, GS1039 MUCUY, HD2733, 8028, 8050, 8054, 10001 and 10001) are expected to exhibit substantial heterosis and to produce new recombinants with desired features.

Key words : *Genetic variability, variation, yield, component trait, wheat.*

Introduction

Bread wheat *(Triticum aestivum* L.*),* one of the oldest cereal crops, is known as the "King of Cereals" because of its enormous production area, high productivity, and major role in the international food grain trade (1). It is the primary food source in South Asian countries and second most important cereal crop in India after rice (2). India's total wheat production has increased dramatically, from 12.26 million tonnes in 1964-65 to 103.6 million tonnes in 2018-19. According to a recent prediction from the United States Department of Agriculture (USDA), India's wheat production would reach a new high of 107.0 million tonnes in 2020-21 (3).

Bread wheat production in Southeast Asian countries, including India, continues to be hampered by factors such as rising temperatures, unexpected hailstorms, and erratic and unusual precipitation in February and March, exposing the crop to diseases and pests such as spot blotch or wheat foliar blight. West Bengal has been considered as a disease hotspot due to its moderate and short winters, humid environment, and late sowing due to kharif rice harvest delays and occasionally excessive soil moisture following harvest. The disease is aggravated by the region's warm and humid climate, which severely limits the development of intensive agricultural systems (4). Depending on the stage of infection, yield loss can range from 25 to 43 percent, with a nationwide yield loss of roughly 18–22 percent (2).

The ongoing development of the best available genotypes for further enhancement of their yield potential, either directly or through improvement of many parameters that contribute directly or indirectly to high yield, is a primary source of worry for a plant breeder. As a result, the breeding process should be such that it can incorporate positive alterations either through selection or hybridization of superior genotypes. In this context, knowing the nature and magnitude of genetic diversity is crucial before beginning any systematic crop breeding programme. The presence of significant genetic variation in the base material guarantees that targeted plant kinds have a better chance of developingan improved line (5). Genetic parameters such as heritability and genetic advance under selection are extremely valuable for anticipating genetic advancement in breeding

Received : December-2021; Revised : December-2021; Accepted : January-2021

Table-1 : Analysis of variance (ANOVA) for 14 characters in bread wheat.

Source of variation	DF	Days to 75% flowering	Plant height (cm)	Peduncle length	No. of productive tiller/plant	Days to maturity	Spike length (cm)	No. of spikelets/ spike
Replication	2	5.81	34.38	3.21	0.15	0.03	0.30	7.14
Treatment	51	11.39**	79.97**	13.57**	0.21**	10.98**	1.53**	3.67**
Error	102	2.60	1.77	1.72	0.06	1.92	0.11	0.45

Table-1 : Contd...

Source of variation	DF	No. of grains/ spike	1000 grain weight	Biological yield/plant (gm)	Grain yield/plant (gm)	Harvest index/plant (%)	Gluten content (%)	Protein content (%)
Replication	2	2.41	2.77	0.17	0.02	0.27	0.03	0.14
Treatment	51	399.77**	25.94**	74.09**	11.16**	0.60**	0.57**	0.86**
Error	102	1.10	0.19	0.39	0.06	0.15	0.05	0.06

Table-2 : Genetic parameters for 14 characters in wheat.

S. No.	Character crops	Coefficient of variation		Heritability (%) in broad sense	Genetics advance	GA as % mean
		GCV (%)	PCV (%)			
1.	Days to 75% flowering	1.94	2.67	53.02	2.57	2.91
2.	Plant height (cm)	5.76	5.96	93.64	10.18	11.49
3.	Peduncle length	5.92	7.09	69.65	3.42	10.18
4.	No. of productive tiller/plant	4.88	7.07	47.53	0.32	6.93
5.	Days to maturity	1.48	1.89	61.16	2.80	2.38
6.	Spike length (cm)	7.00	7.80	80.58	1.27	12.94
7.	No. of spikelets/spike	6.15	7.31	70.59	1.79	10.64
8.	No. of grains/spike	20.13	20.21	99.18	23.65	41.29
9.	1000 grain weight	7.29	7.37	97.80	5.97	14.85
10.	Biological yield/plant (gm)	21.41	21.58	98.42	10.13	43.76
11.	Grain yield/plant (gm)	21.14	21.30	98.46	3.93	43.21
12.	Harvest index/plant (%)	0.99	1.40	49.55	0.56	1.43
13.	Gluten content (%)	5.36	6.12	76.63	0.75	9.66
14.	Protein content (%)	4.28	4.74	81.66	0.96	7.97

programmes and creating effective breeding strategies (6). Any crop enhancement program's effectiveness is determined by the genetic diversity present in existing germplasm (7). As a result, a quantitative assessment of population genetic diversity usually aids a plant breeder in selecting appropriate parents for a breeding programme. The greater the genetic distance between parents, greater the chance of heterosis in progenies (8). With this in mind, the current present study used D^2 statistic to examine a collection of 52 wheat genotypes with the goal of analysing genetic variability, heritability, and genetic progress for yield and its component.

Materials and Methods

The experimental materialincluded 52 wheat varieties and grown in a randomized block design with three replications at the research farm of Motherhood University's. In November, 2018-2019 and November, 2019-2020, an experiment was done in a 5-row plot with a 5-meter length. The space between rows and plants was kept at 22.5 cm and 10 cm, respectively. To counteract the border effect, the border rows were also planted. For a good wheat crop and competitive crop stand, the prescribed agronomic procedures were followed. Days to 75 percent flowering, plant height (cm), peduncle length (cm), number of productive tillers per plant, days to maturity, spike length (cm), number of spikelet's per spike, number of grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (percent) were all recorded on five randomly selected competitive plants from each genotype in each replication.The treatment means for all character were used to compute the analysis of variance following the model proposed by (9). Using the procedure proposed by (10), the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated. The formula given by (11) was used to determine heritability in the broad sense (b) and genetic advanceas a percentage of the mean. The D^2

Table-3 : Clustering pattern of 52 wheat genotypes on the basis of D^2 cluster analysis.

Clusters	No of genotypes	Genotypes	Name of genotype
I	1	31	6013
II	5	3,6,27,35,50	1006,1022, 4032, 8010, 10014
III	7	14,15,17,28,42,43,45	1052, 2003, 2020, 4058, 9016, 9050, 9053
IV	8	1,2,5,8,18,24,26,38	1001,1003, 1019, CHIPAK 1033,2021, 3016, 4018, 8043
V	9	7,12,13,16,19,23,30,37,52	NADI 1026,1043,1051, 2019, 2027,3009, 5040, 8031, 10021
VI	11	9,10,22,36,39,40,46,47,48,49,51	1036, GS1039 MUCUY, HD2733,8028, 8050, 8054, 10001, 10006,
VII	8	11,21,25,29,32,33,34,44	1036, GS1039 MUCUY, HD2733,8028, 8050, 8054, 10001, 10006,
VIII	3	4,20,41	1013, 2040, 8056

Table-4 : Estimates of average inter and intra cluster distances for 8 clusters in wheat.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	1.004							
II	7.751	2.630						
III	10.628	4.448	2.949					
IV	7.512	3.149	4.548	2.645				
V	7.481	3.527	4.150	2.865	2.866			
VI	8.218	3.584	3.719	3.507	3.081	2.761		
VII	7.871	3.608	4.513	2.685	2.916	3.067	2.592	
VIII	7.693	3.693	4.380	3.647	3.449	3.834	4.192	2.245

Statistic analysis was used to estimate genetic divergence among forty-nine genotypes.

Results and Discussion

Genetic Variability : The results of the analysis of variance revealed for all the charactersinvestigatedthat there is significant variation available among the 52 wheat varieties used in this study. This revealed the presence of variability, which might be exploited in future breeding programs (12). The prevalence of such a wide range of diversity could be owing to the various sources of breeding materials usedand environmental influences. Table-2 lists the genetic parameters that were investigated.

For all traits tested, the magnitude of phenotypic coefficients of variation was often higher than genotypic coefficients of variation, indicating the environment had influence on the expression of characters under study. In most cases, the two results differ minimally, showing that environmental influences have less influenceso phenotypic selection for such characters would be effective as genotype contributed more than environment in the expression of these characters. PCV and GCV values were classed as high (>20%), medium (10-20%), and low (10%) by (13). In characters like productive tillers per plant, peduncle length, test weight, spikelet's per spike, flag leaf area, and spike weight, medium PCV and GCV were found. The medium PCV and GCV indicate that selection based on these qualities may be beneficial. (14, 15) also showed comparable result.

The biological yield per plant (21.58) had the highest PCV, followed by grain yield per plant (21.58). The number of grains per spike is 20.13. Spike length (7.80), 1000 grain weight (7.37), number of spikelet's/spike (7.31), and peduncle length (7.31) all had a low percentage of PCV (7.09) gluten content (6.12)) number of productive tillers/plant(7.07).Similar results were also reported by (16, 17, 18, 19).

Heritability is the proportion of variability passed down from parents to offspring (20). Strong heritability estimates were found for grain yield/plant. (12, 21, 22) reported similar results for number of productive tillers/plant, followed by grain yield/plant and harvest index. Low GCV and PCV scores suggested that the characters in the population under study had a low level of variability. Days to 75 percent flowering, days to maturity, tillers per plant, grain per spike, test weight, and grain yield per plant all had strong heritability. This demonstrates the presence of an additive gene effect, and selection can be done to improve these traits. Low heritable traits are being heavily influenced by environmental factors, and genetic improvement through phenotypic selection may be challenging in such situations. According to (23), a trait with a high heritability does not always imply a strong genetic advance. Butwhen heritability is combined with genetic advance then is

Table-5 : Cluster mean for 14 characters in wheat.

Characters		Days to 75%flowering	Plant height (cm)	Ped-uncle length	No. of productive tiller/plant	Days to maturity	Spike length (cm)	No. of spikelets/spike	No. of grains/spike	1000 grain weight	Biological yield/plant (gm)	Grain yield/plant (gm)	Harvest index/plant (%)	Gluten content (%)	Protein content (%)
I	Mean	86.33	83.75	30.73	4.13	120.00	10.68	17.27	95.40	40.37	37.83	15.10	39.92	7.20	11.73
II	Mean	90.93	87.24	31.39	4.17	116.53	10.36	17.03	54.48	41.00	23.61	9.25	39.19	8.15	11.54
III	Mean	88.95	88.57	34.64	3.85	117.38	10.05	16.26	38.77	38.93	12.83	5.01	39.02	7.71	12.05
IV	Mean	89.46	92.67	31.77	4.30	118.50	9.40	15.82	56.87	36.35	24.37	9.55	39.16	7.60	11.68
V	Mean	87.89	87.39	32.33	3.63	118.93	9.78	15.87	62.33	40.30	23.09	9.01	39.03	7.35	11.68
VI	Mean	89.42	83.99	33.89	4.21	119.91	9.78	17.70	52.70	40.32	21.14	8.25	39.05	7.44	12.46
VII	Mean	88.75	85.15	34.12	4.21	118.75	8.72	15.43	60.58	39.42	24.27	9.49	39.08	8.01	12.23
VII	Mean	90.00	88.57	33.38	3.80	115.78	10.98	16.04	61.09	37.72	23.09	9.03	39.22	7.19	12.70
Cobtribution % grain yield		1.73	2.04	3.64	0.24	0.69	0.50	0.90	2.83	2.16	1.53	0.64	0.14	0.02	0.46

rewarding as far as improvement in those traits is concerned (24). Hence estimation of heritability combined with genetic advance is more useful in understanding the type of gene action involved in the expression of a particular polygenic trait.

Grain yield, test weight, grains per spike, spikelet's per spike, spike weight, spike length, peduncle length, and flag leaf area all had high heritability as a percent of mean, indicating that additive gene action played a significant role in the expression of the characters and that selection may be effective. For days to heading and plant height, (5) found comparable results. For the traits like canopy temperature index, harvest index, spike length, grains per spike, test weight, grain yield per plant, tillers per plant, 1st inter-node length, weight of spike per plant, weight of grains per spike, biological yield, and plant height, (26) found high heritability and high genetic advance as percent of mean, indicating that these characters are governed by additive gene effects and one can go for phenotypic selection for these traits. Grain yield, grains per spike, spike length, peduncle length, test weight, spikelets per spike, flag leaf area, and spike weight all had high heritability values, indicating that these characters are governed by additive gene effects and that direct selection for these traits would be more effective for desired genetic traits.

Genetic Diversity : Based on D^2-statistics, fifty-two wheat genotypes were categorized into eight clusters, with genotypes inside a cluster having lower D^2 values than those between the clusters. The composition of clusters has been given in Table-3. Cluster VI has the highest number of genotypes (eleven), cluster V has the most genotypes (nine), cluster IV and VII have (eight), cluster III has (seven), cluster II has the most genotypes (five), and cluster VIII has the fewest genotypes (three).

The inter-cluster distance was found to be greater than the intra-cluster distance, indicating that genotypes had a lot of genetic variety (Table 4). Cluster III (2.9), Cluster V (2.8), Cluster VI (2.76), Cluster VI (2.64), Cluster IV (2.63), Cluster II (2.59), Cluster VII (2.24), and Cluster VIII (1.0) cluster I had the greatest intra cluster distance. The greatest inter cluster D^2-value revealed that cluster VII and VIII genotypes are not very closely associated, however the minimum inter cluster distance indicated that these clusters genotypes are quite closely related. Cluster I and V genotypes had the shortest inter-cluster distance, indicating that they are closely related.

Higher inter cluster distance indicated that the genotypes gathered in these clusters exhibited a wide range of genetic variation and might be used in future wheat breeding programmes to extract attractive transgressive segregantes for producing high yielding wheat varieties (27). Cluster III (2.94) had the smallest intra-cluster distance, followed by cluster V (2.86) and cluster VI (2.76), showing that the genotypes are uniform with little variation between them, and so selection will be ineffectual.

The cluster averages for the 14 characters under investigation (Table-5) revealed that Cluster VIII had the highest mean value for Days to 75 percent blooming, Cluster II had the highest mean (90.93), and Cluster VII had the best spike length (10.98). Cluster number IV had the highest mean for plant height (92.67), whereas cluster number I had the lowest mean for this parameter (83.75). Cluster number III had the highest mean for peduncle length (34.64), whereas cluster number I had the lowest mean for this feature (30.73). Cluster IV had the highest mean (4.30) and Cluster VI had the lowest mean (2.10) of productive tillers per plant (3.80). Cluster I had the highest average days to maturity (120.00) while cluster VII had the lowest average days to maturity (115.78). Cluster number VII had the highest mean spike length (10.98) and the lowest mean spike length (8.72). For this character, the highest mean value (17.27) was found in cluster number I and the lowest (15.43) was found in cluster number VII. Cluster number I had the greatest mean value (95.40) and cluster number III had the lowest (38.77) for number of grains per spike. Cluster number II (41.00) had the highest mean value for 1000-grain weight, whereas cluster number IV had the lowest mean value (36.35). Clusters IV and III had the highest (24.37) and lowest (12.83) mean values for biological yield per plant, respectively. Cluster number I (15.10) had the highest mean value for grain yield per plant, whereas cluster number IV had the lowest mean value (5.01). Cluster number I had the highest mean value (39.92%) and cluster number V had the lowest mean value (39.03%) for harvest index (percent). Gluten content had a maximum mean in cluster II (8.15) and a lowest mean in cluster VII (7.19) for this character. Cluster VII had the highest mean protein content (12.70) Cluster number II, on the other hand, reflected the character's lowest mean (11.54).

The findings were consistent with those of a previous study (28). According to the findings of this study, crossing genotypes from various clusters with good mean performance may aid in reaching high yield. Hybridization with more divergent parents can improve the chances of achieving greater heterosis and provide a wider range of genetic variability in the segregating generation. On the basis of divergence and cluster mean, it is possible to conclude that maximum heterosis and good recombinants might be obtained in varietal improvement crosses between genotypes of cluster VIII, VII, and IV.

Individual trait days to peduncle length provided the most deviation (3.64), followed by number of grains per spike (2.83), and plant height (2.83). (2.04). As a result, features including peduncle length, number of grains per spike, and plant height play a big role in genetic divergence.

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