Path coefficient correlation and genetic divergence (*Triticum aestivum L.*) in bread wheat

Abstract

Genetic variation, heritability, genetic advance, correlation coefficient, path coefficient analysis and genetic divergence studied in wheat during rabi 2015-16 at oilseed farm of Chandra Shekhar Azad University of Agriculture &Technology, Kanpur (U.P). A collection of fifty wheat genotypes from different eco-geographic origin were evaluated for ten quantitative characters viz. days to 50 % flowering, days to reproductive phase, days to maturity, plant height (cm), number of reproductive tillers per plant, spike length (cm), number of grains per spike, grain weight per spike (gm.), test weight (gm.) and grain yield per plant (gm.).All the characters, under study showed considerable amount of variability, phenotypic coefficient of variability was higher than genotypic coefficient of variability.These traits exhibited higher variation for GCV and PCV across the environments. A persual of coeffiecient of variability indicates that PCV and GCV were quiet high for grain yield per plant. Moderate PCV and GCV were recorded in spike length and grain weight per spike and the lowest observed in days to maturityand days to 50% flowering.

A high estimate of heritability was found for grain yield per plant. Genetic advance confirms the heritability estimate. High genetic advance was observed for grain yield (30.16) and minimum in days to reproductive phase(2.27). Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for all the character combinations. Grain yield per plant showed highly positive association ship with plant height, spike length, grain weight per spike and number of grains per spike grain weight per spike. Genetic divergence was determined using D^2 and all the fifty genotypes were grouped into eight clusters. Maximum inter cluster distances were observed betweenVI and VIII followed by cluster VII and VIII and cluster V and VIII. Cluster VII retains highest rank in spike length and grains per spike. Cluster-V holds first rank in days to flowering and days to maturity.On the basis of genetic divergence , it is suggested that the crosses between VIII ,VII , VI and V may be effective components in hybridization.

Keywords: Variability, correlation coefficient, cluster, hybridization

Introduction

Wheat 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). Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). Wheat is cultivated over a wide range of climatic conditions and therefore understanding of genetics is of great value for genetics and plant breeding purposes. Wheat belongs to family

Poaceae(*Gramineae*) which includes major crop plants such as wheat (*Triticum spp.*), barley (*Hordeum vulgare*), oat (*Avenasativa*), rye (*Secale cereale*), maize (*Zea mays*) and rice (*Oryza sativa*). *Triticeae*is one of the tribes containing more than 15 genera and 300 species including wheat and barley. In 1918, Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. He separated wheat into three groups viz. diploids (2n=14), tetraploids (2n=28) and hexaploids (2n=42) chromosomes. Wheat is a**'King of cereals'** because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade.

Wheat is a cereal grain (botanically, a type of fruit called caryopsis) originally from the Levant region of the Near East but now cultivated world's wide. Wheat is a self-pollinated C3 plant with cleistogamous condition.The wheat is most successfully grown between the latitudes of 30° and 60°N and 27 and 40° **(S. Nuttonson, 1955)**, but it can be grown beyond these latitudes limitsfrom within the Arctic Circle to higher elevations near the equator. The optimum temperature for wheat growth is 25°C with minimum and maximum growth temperatures of 30°C to 40°C and 30°C to 32°C, respectively **(Briggle, 1980).** Wheat is adapted to a wide range of moisture conditions from xerophytic to lithoral. Cultivars of widely differing pedigree are grown under varied conditions of soil and climate andshow wide trait variation.

Wheat is world's most widely cultivated food crop.In India,it is the second important staple food crop after rice and it is used in several form to make flour for leavened, flat and steamed breads, biscuits, cookies, cakes, breakfast cereal, pasta, noodles, couscous and for fermentation to make beer other alcoholic beverages, and biofuel. The raised bread loaf is possible because wheat kernel contains gluten, a visco-elastic form of protein that traps minute bubbles of carbon dioxide when fermentation occurs in leavened dough, causing the dough to **(Hanson et al., 1982).** Wheat is a major diet component because of wheat plants agronomic adaptability, ease of grain storage and ease of converting grain into flour for making edible, palatable and satisfactory foods. Wheat is planted to a limited extent as a forage crop for livestock, although the straw is used as cattle feed.

The total production of wheat estimated at 96.76 million tons with coverage area of 259.37 lakh hectares is a new record.U.P is the leading state in wheat production. The major wheat producing states are Uttar Pradesh, Punjab, Haryana, Madhya Pradesh., Rajasthan, Bihar, Maharashtra, Gujarat, Karnataka, West Bengal, Uttaranchal, Himachal Pradesh and Jammu Kashmir. These states contribute about 99.5 per cent of total wheat production in the country. Remaining states namely Jharkhand, Assam, Chhattisgarh, Delhi and other North East states contribute only about 0.5 per cent of the total wheat production in the country.

Bread wheat belongs to family Gramineae and it is a hexaploid species with (2n = 42) having AABBDD with A, B and D genome).The species of bread wheat may be divided into diploid, tetraploid and hexaploid species with chromosome number 2n = 14(AA), 2n =14(BB), 2n = 28(AABB) and 2n = 42(AABBDD) respectively with basic chromosome number (x) = 7 **(Sleper and Poehlman,** 2006). Bread wheat (*Triticum aestivum*),Macaroni wheat(*Triticum durum*) and emmer wheat(*Triticum dicoccum*) occupy the place of prominence among the seven cultivated species of wheat grown in the world. Amongthese,first two occupies maximum acreage and production and have great significance for human and animal consumption.Bread and Macaroni wheat are widely cultivated under different agro climatic condition due to their versatile genotype which have wider adaptation in diverse agroecological condition.Nevertheless,the crop offer sizeableopportunities of quantum jump by accelerating its yield potential through genetic manipulation. These gains could be realized by utilizing vast and enormous magnitude of genetic variability available in these species. There are six classifications of wheat: 1) hard red winter 2) hard red spring 3) soft red winter 4) durum hard 5) Hard white and 6) soft white wheat.

Wheat growing in India is divided into six zones viz. The Indo-Genetic plainscomprising the North Western Plains Zone (NWPZ) and the North Eastern Plains Zone (NEPZ), forms the major wheat tract followed by the Central Zone (CZ), the Peninsular Zone (PZ), The Northern Hill Zone and the Southern Hill Zone. Wheat has versatile nature because it has high yield potential and can be grown easily in different agro-ecological conditions. Having such a yield potential, there is an imperative need to improve the quality of grains as a sizeable protein as well as quantity of wheat to cater the everincreasing demand of the population. Almost all the wheat varieties are low in protein content as well of essential amino acids such as lysine and tryptophan. Breeders can improve the nutritional value of this very important crop through the genetic manipulation.

The genetic divergence analysis using techniques Non-hierarchical Euclidean Cluster analysis, classify the genotypes into homogenous groups/clusters with similarity of genotypes for different characters within clusters while genotypes between two clusters are more divergent than the genotypes of the same clusters .Thus, suitable genotypes from diverse cluster can be It has been suggested that yield components have either a direct or an indirect effect on grain yield, or both. Therefore, it was essential to determine the effects of yield component on grain yield.

Materials and methods

The present investigation entitled was carried out during *rabi* 2015 - 16at oil seed farm of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.).Oil seeds farm is situated between 26.4607^o N latitude, 80.3334^o E longitude and at an altitude of 126 m above the mean sea level in about 3 km , away from CSA University of Agriculture and Technology, Kanpur. The climate of district Kanpur is humid subtropical and it has one of the lowest temperature in northern plains during the winter season and is one of the warmest during the summer season. Nearly 80% of total rainfall is received during the monsoon (up to September) with a few showers in the winter.The experimental materials of the study comprised of 50 germ plasm/varieties from Indian origin. These varieties/lines were procured from germplasm lines available in wheat Section, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture & Technology, Kanpur**.**A field experiment was conducted during *Rabi* season 2015-16 at oilseed farm crop Research Farm, CSAUAT, Kanpur. All the strains were sown in Randomized Complete Block Design with three replications.Each genotype was sown in two lines in 5.0 m long and 1.38 m broad plots and space planted at 23 x 5 cm between row to row and plant to plant distance respectively.Observations on yield and yield attributing characters were recorded. In each plot, five random plants were tagged to record these observations. By taking the average, the mean value for the treatment was computed. The characters adopted to are daysto flowering, days to maturity, plant height, spike length,number of productive tiller per plant, number of grains per sike, grain weight per spike, thousand grain weight and grain yield.

Result and discussion

The economic product i.e. grain yield analysis of variance showed significant differences among all the genotypes under study. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters indicating the effect of environment on these characters.Maximum genetic variation was recorded for plant height followed by grain per spike, number of grains per spike, days to reproductive phase and days to maturity.High heritability estimates were found for ten characters under study. High heritability was recorded for yield per plant (g) followed by grain weight per spike grain per spike plant height spike length. It was minimum for reproductive phase, reproductive tillers per plant followed by days to maturity. Studies on variability, heritability and genetic advance showed that plant height, days to maturity, number of grain per spike, grain weight per spike followed by days to reproductive phase, days to 50% flowering are having considerable importance to breeder for selection. Genotypic and phenotypic correlations for the above characters were determined. Observations revealed that the genotypic correlations wasmaximum for grain yield per plant (17.87 and 21.82) followed by grain weight per spike (16.49and 20.21). With almost all the characters the phenotypic correlations where as in the same direction in the present research. Grain yield per plant was positively correlated with plant height, spike length, productive tillers per plant, , number of grains per spike, grain weight per spike and 1000 grain weight at both genotypic and phenotypic levels.

Path coefficient analysis revealed that characters viz; Grain yield per plant was positively correlated with plant height, spike length, productive tillers per plant, , number of grains per spike, grain weight per spike and 1000 grain weight having positive correlations with grain yield per plant indicates that grain yield per plant can be improved by considering the above mentioned six characters. Mahalanobis D^2 statistics was used to calculation the genetic divergence in the present group of material. All the fifty genotypes were classified into eight clusters. Cluster II comprise the ten genotypes followed by cluster III comprises of nine genotypes, followed by cluster I and fourth both comprises of eight genotypes, cluster V comprises seven genotypes and cluster VIII having four genotype, cluster VI and cluster VII two genotype.Maximum inter-cluster distance was observed between cluster VI and cluster VIII , followed by cluster VII and cluster VIII , cluster V and cluster VIII, cluster IV and cluster VIII and lowest inter-cluster distance was observed between cluster III and cluster VIII followed by cluster I and cluster VIII, and cluster II and cluster VIII . For high yield cluster III are found desirable because cluster III holds first rank in grains weight per spike and yield per plant, cluster V hold first rank Days to flowering and days to maturity and cluster VII holds first rank in spike length and grain per spike.Plant height (46.78) had maximum contribution in the exixtance diversity of genotype followed by spike length (17.71), grain per spike (10.20), days to maturity (6.04), productive tillers per plant (5.55) while minimum contribution by grain weight per spike (3.76) and grain yield per plant (0.82).

Hence it is quite clear that these clusters are most desirable for breeding program me for creating the desired variability as well as for effective selections.

CONCLUSION

1. Studies of variation indicated that considerable amount of variation for yield per plant, plant height, followed by days to maturity and reproductive phase which could be utilized for breeding for improvement.
2. All traits showed high heritability except reproductive phase and reproductive tillers.
3. The higher genetic advance showed in yield per plant (30.16) and low in days reproductive phase (2.27).
4. Correlation and path analysis provide information about yeild components.Thus it help in selection of superior genotype from diverse genetic population.
5. Path coefficient analysis provide informaton about highly positive association ship of grain weight per spike, number of grains per spike, plant height, spike length. grain weight per spike indicated maximum emphasis should be given while making selection for improving yield.
6. The maximum inter cluster distance had been observed betweenVI and VIII followed by cluster VII and VIII and cluster V and VIII. Cluster-VII holds first rank in spike length and grains per spike. For the development of superior hybrids we have to make the crosses between the inbred of cluster VII & VIII. Plant height (46.78) had maximum contribution in the exixtance diversity of genotype followed by spike length number of grains per spike, days to maturity and productive tiller. Remaining traits had minimum or no contribution in divergence.

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Table 1: Genotypic, Phenotypic &Environmental coefficient of variation

S.no	**Character**	**GCV**	**PCV**
1	Days to flowering (50%)	2.91	3.54
2	Days to maturity	1.59	2.04
3	Plant height(cm	11.53	11.83
4	Spike length(cm)	11.60	12.78
5	Reproductive tillers per plant	6.14	8.26
6	Reproductive phase	2.52	5.77
7	Number of Grains per spike	13.71	15.81
8	Grain weight per spike(g)	16.49	20.21
9	Thousand grain weight(g)	11.25	15.48
10	Yield per plant(g)	17.87	21.82

Table 2: Inter and intra cluster distances (D2) among eight clusters in wheat:

	I Cluster	II Cluster	III Cluster	IV Cluster	V Cluster	VI Cluster	VII Cluster
I Cluster	26.116	36.678	37.624	59.606	43.696	110.392	90.679
II Cluster	36.678	23.149	48.959	43.199	41.139	90.100	115.841
III Cluster	37.624	48.959	23.134	57.404	79.728	157.021	114.476
IV Cluster	59.606	43.199	57.404	32.533	60.725	79.976	128.612
V Cluster	43.696	41.139	79.728	60.725	18.763	48.607	80.645
VI Cluster	110.392	90.100	157.021	79.976	48.607	20.842	123.818
VII Cluster	90.679	115.841	114.476	128.612	80.645	123.818	92.429
VIII Cluster	173.888	183.366	111.864	203.072	292.254	433.068	324.216

Table 3: Cluster mean for nine characters of fifty genotypes in wheat:

S.No.	Flowering Days	Maturity Days	Plant Hight cm	Spike Length cm	Tillers/ Spike	Grains/ Spike	Grain Weight/ Spike	Yield/ Plant	1000 Grain Weight
1	71.083	112.542	93.325	10.883	4.633	42.392	1.558	7.210	37.245
2	71.300	112.900	91.633	8.963	4.620	39.687	1.403	6.471	35.447
3	69.185	112.222	99.326	10.711	4.548	48.674	1.860	8.424	38.191
4	67.333	109.833	89.650	8.604	4.450	42.379	1.613	7.297	38.365
5	71.524	113.905	82.019	9.705	4.476	43.667	1.524	6.828	35.048
6	68.500	110.167	73.467	8.283	4.933	41.117	1.508	7.433	37.065
7	70.667	113.500	85.100	11.017	4.567	60.633	1.728	7.828	28.242
8	69.333	111.333	119.600	10.800	4.400	44.050	1.646	7.234	37.370
Mean	69.987	112.160	92.875	9.833	4.555	43.969	1.597	7.277	36.570
Treat MSS	16.079	12.240	718.698	6.696	0.087	142.154	0.158	2.922	31.954
Err MSS	2.939	2.498	16.405	0.512	0.102	23.398	0.068	1.810	20.231
F Ratio	**5.472**	**4.899**	**43.810**	**13.078**	0.852	**6.076**	2.321	1.615	1.579
Probability	0.000	0.000	0.000	0.000	0.552	0.000	0.043	0.158	0.168

Table No:4 Contribution of each character to genetic divergence in wheat genotype:

Source	**Time Ranked 1st**	**Contribution %**
Days to 50% Flowering	63	5.14
Days to Maturity	74	6.04
Plant height (cm)	573	46.78
Spike length (cm)	217	17.71
Reproductive Tillers/Plant	68	5.55
Grian /spike	125	10.20
Grain weight per Ear (gm.)	46	3.76
Test Weight(1000)	49	4.00
Grain yield per plant (gm.)	10	0.82

Cluster range

S No	**Characters**	**Range**	
		Min.	**Max.**
1	Days to 50% flowering	67.33	71.524
2	Days to maturity	109.83	113.90
3	Plant height(cm)	73.46	119.60
4	Spike Length(cm)	8.28	11.01
5	Reproductive Tillers/ plant	4.40	4.93

6	Test weight(1000)	28.24	38.36
7	Grain yield/Plant(gm.)	6.47	8.42
8	Grain weight/ par(gm.)	1.40	1.86
9	Grain/spike	39.68	60.63