ASSESSMENT OF GENETIC VARIABILITY FOR BIOCHEMICAL AND YIELD ATTRIBUTES IN WHEAT(*Triticum aestivum* L.)

by

Mr. Dagade Sachin Kantilal
Reg. No. 017/046

A Thesis submitted to the
MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI - 413 722, DIST. AHMEDNAGAR,
MAHARASHTRA, INDIA

in partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY

POST GRADUATE INSTITUTE,
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2019

CANDIDATE'S DECLARATION

I hereby declare that this thesis or part
there of has not been submitted
by me or other person to any
other University or Institute
for Degree or
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CERTIFICATE

This is to certify that the thesis entitled **"ASSESSMENT OF GENETIC VARIABILITY FOR BIOCHEMICAL AND YIELD ATRIBUTES IN WHEAT (*Triticum aestivum* L.)",** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist.- Ahmednagar, Maharashtra (India), in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING),** embodies results of piece of bonafide research work carried out by **Mr. DAGADE SACHIN KANTILAL** under my guidance and supervision and that no part of the thesis has been submitted to any other degree or diploma.

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Place : MPKV, Rahuri (S. K. Dagade)

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LIST OF ABBREVIATIONS

b.s.	: Broad sense
C.D.	: Critical difference
cm	: Centimeter
C.V.	: Coefficient of variation
Cov,	: Covariance
d.f.	: Degrees of freedom
et al.,	: And others (et alia)
Fig	: Figure
G	: Gramme (s)
GA	: Genetic advance
GCV	: Genotypic coefficients of variation
ha	: Hectare
h^2	: Heritability
i.e.	: That is (id est)
MSS	: Mean sum of squares
No.	: Number
PCV	: Phenotypic coefficient of variation
RBD	: Randomized Block Design
r	: Correlation coefficient
S.E.	: Standard Error
S.S.	: Sum of squares
Via	: By the way of, by means of
Viz.	: Videlicet (Namely)
Vs	: Versus
Σ	: Summation
%	: Percent

ABSTRACT

"ASSESSMENT OF GENETIC VARIABILITY FOR BIOCHEMICAL AND YIELD ATTRIBUTES IN WHEAT (*Triticum aestivum* L)."

by

Mr. DAGADE SACHIN KANTILAL

A candidate for the degree
of
MASTER OF SCIENCE (AGRICULTURE)
in
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2019

Research Guide	:	**Dr. S. S. Dodake**
Department	:	**Agricultural Botany**
Major discipline	:	**Genetics and Plant Breeding**

The present investigation entitled "Assessment of genetic variability for biochemical and yield attributes in wheat (*Triticum aestivum* L.)" was carried out to study the nature and extent of genetic diversity and to estimate the correlation coefficient among the different yield and yield attributing characters. Thirty genotypes of wheat were evaluated at Botany section, Post graduates institute, Mahatma Phule Krishi Vidyapeeth, Rahuri during *Rabi* 2017-18 in a Randomized Block Design with two replications.

The observations were recorded for the characters *viz;* days to 50 per cent flowering, days to maturity, plant height (cm), earhead length, number of spikelets, number of grains per earhead, 1000 grains weight (g), grain yield (q/ha), protein content (%), sedimentation value (ml), grain appearance score, yellow berry percentage, iron content (mg/100g) and zinc content (mg/100g).

The data revealed that, sufficient variability was present among the genotypes under study. Phenotypic coefficient of variation estimates was slightly higher than genotypic coefficient of variation. High estimates of heritability (b.s.) was observed for all the characters studied except number of spikelets per spike. High heritability accompanied with high genetic advance as percent mean was observed in case of grain yield and number of grains per spike, where as high heritability coupled with moderate genetic advance as per cent of mean was observed for grain appearance score followed by yellow berry percentage, 1000 grains weight, number of spikelets, plant height, earhead length, sedimentation value, days to 50 per cent flowering, protein content and Fe content indicating an additive gene action in the inheritance of these traits and scope for direct selection of these characters in early generations.

Abstract contd….. **Mr. Sachin K. Dagade**

Correlation study revealed that, grain yield showed strong significant and positive correlation with 1000 grains weight, number of grains per spike, spike length, number of spikelets per spike and protein content. While 50 per cent flowering showing non-significant positive correlation with grain yield, Grain yield showed significant negative correlation with days to maturity, protein, Zn content and Fe content.

Wheat genotypes were evaluated for fourteen yield and yield contributing characters to study the genetic diversity among the genotypes using Mahalnobis D^2 statistic. The analysis of data revealed the significant difference among the genotypes for all the characters. D^2 values between all possible pairs of thirty genotypes ranged from 141.37 to 944.33. Based on genetic distance (D^2 value), thirty genotypes were grouped into eight clusters indicating wider genetic diversity in the germplasm collections of wheat from different geographical origin. Out of eight clusters formed, cluster II was the largest with thirteen genotypes followed by cluster I with nine genotypes, cluster III with three genotypes and clusters IV,V, VI,VII, VIII were monogenotypic. The clustering pattern indicated the absence of relationship between genetic diversity and geographical origin of genotypes. The maximum inter-cluster distance was observed between cluster III and VII (D^2 =944.33), while lowest divergence was noticed between cluster VIII and VI (D^2 = 141.37). Whereas, maximum intra cluster distance was observed for cluster III (D^2= 135.48). Among the fourteen characters studied, grains per spike contributed highest (28.97 %) towards genetic divergence followed by number of spikelets (25.75 %), days to 50 per cent flowering (10.97 %), days to maturity (8.51 %), iron content (6.67 %), grain yield (6.44), thousand grain weight (5.29 %) and spike length (4.60 %).

Based on inter cluster distance and *per se* performance of genotypes, NIAW-3170, Netravati, HD-2932, NIAW-3390, NIAW-3386, NIAW-3354, NIAW-3553, Phule Samadhan, NIAW-3592, MACS-6222, NI-345, AKAW-4627, NIAW-3575, NIAW-3270, NIAW-3559 and NIAW-3525 were found distinct, diverse and can be classified as promising genotypes. Intercrossing among them can lead to upgrade genetic base in the base population and opportunities for obtaining the high heterotic effects and also to recover desirable transgressive segregants and wide spectrum of variability in subsequent generations.

Pages 1 to 79

1. INTRODUCTION

Wheat is the world's largest cereal crop of the *Graminae* (*Poaceae*) family. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade.

According to the earliest historic records, wheat was an important cultivated cereal in South-Western Asia, its geographical centre of origin. Many wild species of *Triticum* are found in Lebanon, Syria, Northern Israel, Iraq and Eastern Turkey. Wheat was cultivated in ancient Greece and Egypt in pre-historic times. The central Asia, Near East, Mediterranean and Ethiopian regions are the world's most important centers of diversity of wheat and its related species (Kundu and Nagarajan, 1996, Perrino and Porcedu, 1990). Hindukush area is the centre of diversity of hexaploid wheat (Kundu and Nagarajan, 1996). The majority of the cultivated wheat varieties belongs to three main species of the genus *Triticum*. These are the hexaploid, *T. aestivum* L. (bread wheat), the tetraploid, *T. durum* and the diploid, *T. dicocom*. Globally, *T. aestivum* wheat is the most important species which covers 90 per cent of the area. Second popular wheat being durum wheat which covers about 9 per cent while, *T. dicoccum* wheat cover less than one per cent of the total area.

The world acreage under wheat crop is 221.12 million ha with production of 736.1 million-tonnes with an average yield of 3160 kg ha^{-1} (Anonymous, 2018). India contributes 12 per cent of the world wheat production. In India, wheat is the second most important crop after rice occupying 30.72 million ha. With production of 3072 kg ha^{-1} (Anonymous, 2018). Uttar Pradesh, Madhya Pradesh and Punjab are the important states from the point of both area and production.

Wheat cultivation in Maharashtra is unique wherein all three cultivated species *viz., Triticum durum, Triticum aestivum*, and *Triticum dicoccum* are grown in typical hot tropical climate, characterized by the prevalence of high temperature during the crop growth. The area under wheat is about 1.07 million ha with annual production of 1.60 million tones (2017-18). The productivity is very low (1558 kg ha^{-1}) as compared to national average of 3072 kg ha^{-1}. This is mainly due to the fact that a small part of the crop period experiences the cool climate during the crop season. Very often the crop is exposed to terminal heat stress causing potential yield loss.

Wheat compares well with other cereals in nutritive value. It has good nutrition profile with average 12.1 per cent protein, 1.8 per cent lipids, 1.8 per cent ash, 2.0 per cent reducing sugars, 6.7 per cent pentosans, 59.2 per cent starch, 70 per cent total carbohydrates and provides 314K cal/100 g of food. It is also a good source of minerals and vitamins *viz.*, calcium (37 mg/100 g), iron (4.1 mg/100 g), thiamine (0.45 mg/100 g), riboflavin (0.13 mg/100 g) and nicotinic acid (5.4 mg/100 mg) (Lorenz and Kulp, 1991). Unlike other cereals, wheat contains a high amount of gluten, the protein that provides the elasticity necessary for excellent bread making. Hard wheat is high in protein (10-17 %) and yields a flour rich in gluten, making it particularly suitable for yeast breads. The low-protein (6 - 10 %) softer type yields flour lower in gluten and therefore, better suited for tender baked products, such as biscuits, pastries and cakes. *T. durum* wheat, although high in gluten, is not suitable for baking, but suitable for semolina, the basis for excellent pasta, such as spaghetti and macaroni preparation.

Yield being a complex character is a function of several component characters and their interaction with environment. Probing of structure of yield involves assessment of mutual relationship among various characters contributing to the yield. In this regard, genotypic and phenotypic correlation reveals the degree of association between different characters and thus aid in selection to improve the yield and yield attributing characters simultaneously. Further, path coefficient analysis helps in partitioning of correlation coefficients into direct and indirect effects and in the assessment of relative contribution of each component character to the yield.

Collection and evaluation of genotypes is a pre-requisite for any breeding programme, which provides better scope for exploiting diversity. A quantitative assessment of the genetic divergence among the collection of germplasm and their relative contribution of different traits towards the genetic divergence provide essential and effective information to breeder in his hybridization programme and thereby genetic improvement of yield. The necessity for finding out genetic divergence among the genotypes is more pronounced because of two reasons i.e.,

1. Genetically diverse parents if included in the hybridization programme are likely to produce high heterotic effect.
2. A wide spectrum of variability could be expected in the segregating generation of crosses involving distantly related parents.

Genetic diversity is variability available among the different genotypes of a species. A effective method suggested by Mahalanobis (1936) known as “Mahalanobis D^2 statistics” or “D^2 technique” is widely used to know genetic diversity in the germplasm. This technique measures the forces of differentiation at intra cluster and inter levels, which helps in the selection of genetically divergent parents for their exploitation in hybridization programme. The D^2 statistics also measures the degree of diversification and determines the relative proportion of each component character to the total divergence.

Correlation analysis has been widely used to determine the nature and magnitude of inter relationships between grain yield and it’s contributing components. The correlation coefficient analysis measures mutual relationship between various characters and determine the components traits on which selection can be relied upon to effect the improvement.

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of paramount importance in breeding programme. So, the knowledge of genetic diversity and relatedness in the germplasm is a pre- requisite for crop improvement programme. Reduction in the genetic variability makes the crops increasingly vulnerable to diseases and adverse climatic changes so precise information on the nature and degree of genetic diversity present in wheat collections from its principal areas of cultivation would help to select parents for evolving superior varieties. For the genetic amelioration of this crop, diverse genotypes from the existing germplasm should be selected and used in further breeding programme.

In the present study, 30 promising genotypes were used for assessing the diversity considering yield as one of the important selection criterion. Keeping these things in the view, an effort has been made to evaluate a set of wheat genotypes with the following objectives,

1. Genetic studies on quality parameters in wheat.
2. Genetic studies on yield and yield attributing traits in wheat.

2. REVIEW OF LITERATURE

A comprehensive review of literature is an essential part of any scientific investigation. Review of literature is always necessary to compare the present findings with the previous studies undertaken by research workers

2.1 Genetic variability

Exploration of genetic variability in the available germplasm is a pre-requisite for any successful breeding programme. Distinction between genotype and phenotype was noticed by Johannsen (1909). From this, it is clear that interaction between genotype and environment is responsible for variability (Fisher, 1930). The total variance was partitioned into genotypic and phenotypic variances by using estimates of environmental variance from non- segregating population (Charles and Smith, 1939). The statistical methods to calculate the genetic component of variances was given by Burton (1952), Panse and Sukhatme (1995).

Randhawa *et al.* (1975) observed high heritability coupled with high genetic advance as percentage of mean for characters like number of effective tiller per plant, number of grains per spike, spike length, number of spikelets per spike and yield per plant. It indicated the presence of additive gene action for expression of these characters.

Spagnoletti-Zeuli and Qualset (1987) reported that genetic variability among genotypes can be based on qualitative and quantitative traits.

Dixit (1990) reported moderate GCV for days to 50 per cent flowering and high heritability for plant height and days to maturity.

Tesfaye *et al*. (1991) evaluated 1223 entries of durum wheat accessions in Ethiopia for agro-morphological characters and reported a high degree of variation in their accessions.

Subhash *et al*. (1993) reported the highest GCV and PCV values for yield per plant followed by productive tillers per plant.

Chaturvedi and Gupta (1995) reported low genotypic and phenotypic coefficient of variation for days to 50 per cent flowering and plant height.

Jitendra Kumar and Lutra (1995) observed moderate GCV and PCV for days to 50 per cent flowering and days to maturity. Moderate PCV and GCV for number of grains per spike was reported by Jagashoran (1995).

Rebetzke *et al.* (1999) reported high heritability coupled with moderate genetic advance for plant height.

Gupta and Verma (2000) estimated the range of phenotypic and genotypic coefficients of variation, heritability and genetic advance under normal and rainfed conditions for eight quantitative traits in sixty progenies derived through selfing and intermating in durum wheat cross Shwa 's' x V44. The biparental mating was able to maintain variability for selection of improved genotypes. High heritability estimates coupled with high genetic advance for number of grains per ear, grain yield and biological yield per plant under both the environments. Medium to low heritability estimates were recorded for days to ear length, plant height, tiller number per plant, 1000 grain weight and harvest index under both the environments.

Kamboj *et al.* (2000) reported high heritability values for number of grains per spike, 1000 grain weight and grain yield per plot.

Bergale *et al*. (2001) observed variability for ten characters with fifty genotypes of bread wheat collected from India and Mexico under irrigated conditions and reported variability was high for traits, spikes per plant and grain yield per plant, which could be exploited in selection of superior genotypes. They also observed less influence of environment for characters viz., days to 50 per cent flowering, days to maturity and plant height. Grain yield recorded the highest GCV but showed the lowest heritability and genetic advance.

Ashraf *et al.* (2002) observed high heritability coupled with high genetic advance was for spike length and 1000 grain weight. They revealed that these characters were controlled by additive gene action and improvement may be expected by direct selection.

Bered *et al*. (2002) reported that the characterization of genetic variability and an estimate of the genetic relationship among varieties were essential to any breeding program. They evaluated genetic variability in different ways, including the Coefficient of Parentage (COP), which estimates the probability of two alleles in two different individuals being identical by descent. They also evaluated the degree of genetic relationship among 53 wheat genotypes, and identified the ancestor genotypes which contributed the most to the current wheat germplasm, as a prediction of the width of the genetic base of wheat.

Patil and Jain (2002) studied the nature and magnitude of variation of yield and yield components and observed high heritability for days to heading, days to maturity, plant height, 1000 grain weight, number of tillers per plant except number of spikelets per spike and number of grains per spike.

Wegrzyn *et al.* (2002) determined the heritability and interrelationships of traits such as grain yield, 1000 grain weight, days to heading and plant height. They noted that all the traits *viz.*, days to heading, days to maturity, number of grains per spike, number of spikelets per spike, number of tillers per plant, plant height and 1000 grain weight except grain yield showed the highest heritability.

Sharma and Garg (2002) observed high heritability accompanied with high genetic advance in case of plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits.

Sachan and Singh (2003) reported high heritability estimates for grain yield, number of spikelets per spike, number of seeds per spike, plant height, 100-seed weight and number of tillers per plant.

Kumar *et al*. (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelets per spike and 1000-grain weight in wheat.

Lad *et al.* (2003) observed that phenotypic and genotypic coefficients of variation were higher for yield per plant, productive tillers per plant, grains per spike and grain weight per spike.

Munawar *et al.* (2003) reported significant differences among the genotypes for days to 50 per cent heading, plant height, number of spikelets per spike, grain yield and 1000 kernel weight.

Singh *et al.* (2003) recorded the highest genotypic and phenotypic coefficient of variation for number of grains per spike.

Jagshoran and Mishra (2005) observed differences between the GCV and PCV were relatively very small which indicated that large amount of variation was contributed by genetic component and less by environmental influence.

Yadav *et al.* (2006) observed highest GCV and PCV for number of grains per ear followed by tiller number per plant, grain yield per plant and 1000-grain weight. The estimates of heritability were very high for grain yield per plant, 1000-grain weight, hectolitre weight, days to heading, protein content, plant height, sedimentation value and number of grains per ear except tiller number per plant and grain yield per plant. They also noticed that high estimates of heritability for hectolitre weight, days to heading, protein content, plant height, 1000-grain weight and sedimentation value were not associated with high values of genetic advance. High estimate of heritability coupled with highest genetic advance was observed for number of grains per ear.

Majumder *et al.* (2008) studied twenty spring wheat varieties to find out genetic variability and genetic association for grain yield and its components characters. They revealed that both genotypic and phenotypic variances were highly significant in all the traits with little higher phenotypic variations as usual. Similarly, the low differences between the phenotypic and genotypic coefficients of variations indicated low environmental influence on the expression of these characters. High heritability coupled with high genetic advance was obtained with plant height, grains per spike, 1000 grain weight, harvest index and grain yield.

Kaur *et al.* (2008) observed that analysis of variance showed highly significant difference for days to heading, days to maturity, ear length, number of tillers per running metre and grain yield. The maximum range of variability in percentage was observed for tillers per running metre followed by grain yield, sedimentation value, biological yield, number of spikelets per ear, number of grains per ear, 1000-grain weight, ear length, plant height, protein content, hectolitre weight, days to heading and days to maturity. They revealed that an estimate of the phenotypic coefficient of variation shows high values for grain yield, number of tillers per running meter and number of grains per ear moderate coefficients of variation for sedimentation value, biological yield, 1000-grain weight, ear length and protein content and low phenotypic coefficient of variation for plant height, days to heading, hectolitre weight and days to maturity.

Yousaf Ali *et al*. (2008) reported genetic variability in wheat (*Triticum aestivum)* germplasm for eight metric traits i.e., plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility per cent, 1000 grain weight and yield per plant. They observed significant genotypic difference for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for yield per plant, number of productive tillers per plant and number of grains per spike. The remaining traits recorded moderate to low PCV and GCV estimates. High heritability accompanied with high genetic advance was observed in case of plant height, number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, 1000 grain weight and yield per plant.

Ajmal *et al.* (2009) observed genotypes were significantly different for plant height, number of tillers per plant, number of spikelets per spike, grains per spike and grain yield per plant. The magnitude of broad sense heritability of plant height, tillers per plant, grains per spike and grain yield was high and was low in case of number of spikelets per spike. Fairly high estimates of heritability and genetic advance for plant height, number of tillers, and grains per spike suggested that selection for these traits could be practiced more effectively.

Kumar *et al*. (2009) evaluated thirty genotypes of bread wheat for yield and other related characters for variability. They observed high PCV and GCV for numbers of plant height (cm), number of tillers per plant, spike length (cm), number of grains per spike, 1000 grain weight (g) and grain yield per plant (g), whereas, days to 50 per cent flowering and days to maturity showed relatively low variability.

Monpara (2009) observed the wide range of variation for most of the characters in wheat. The genotypic coefficient of variation was moderate for all the characters except for which the low magnitude was noted. High heritability coupled with high genetic advance was observed for plant height, spike length, grains per spike. However, low heritability along with moderate genetic advance was observed for grain yield per plant, which indicated that direct selection for grain yield may not be effective.

Subhashchandra *et al.* (2009) studied the variability parameters in the F_2 populations of 28 crosses derived through Diallel Mating System in tetraploid wheat. The highest genotypic and phenotypic coefficient of variation was observed for yield per plant followed by productive tillers per plant. The moderate GCV and PCV were observed in case of days to 50 per cent flowering, days to maturity, spike length, protein content, plant height, sedimentation value. The high heritability with high genetic advance was observed for yield per plant, productive tillers per plant, spike length, protein content, days to maturity and days to 50 per cent flowering. High heritability with moderate genetic advance as per cent mean was observed for plant height and sedimentation value.

Yagdi and Sozen (2009) noticed values of broad-sense heritability between 0.72 and 30.43 per cent. Sedimentation had the lowest heritability value, whereas spike length had the highest. Heritability values determined were 6.35, 9.38, 6.13, 9.45 and 3.12 per cent for plant height, number of spikelet per spike, seed number per spike, 1000 kernel weight and grain yield, respectively. The 1000 grain weight had the highest heritability value (17.69 %) among the quality traits, followed by gluten content and protein content with 10.12 and 5.38 per cent, respectively.

Badole *et al.* (2010) observed that genotypes exhibited significant variation for all the characters *viz.*, plant height, days to heading, flowering, maturity, tiller number per plant, length of spike, number of spikes per plant, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, protein content, yield per plant and grain weight per meter square. The estimate of PCV in all the traits studied was greater than those of the GCV.

Chandra *et al.* (2010) reported high heritability estimates for grain yield per plant, number of seeds per spike, plant height, 1000 seed weight and number of tillers per plant.

Kahrizi *et al.* (2010) observed significant variation among genotypes for the characters i.e. plant height and number of tillers per plant. Heritability estimates were high for plant height.

Kotal *et al*. (2010) reported highly significant differences and adequate genetic variability among the genotypes and found that numbers of effective tillers per plant and grain yield per plant were characterized by high GCV, high heritability and high genetic advance and would be effective for selection.

Laghari *et al*. (2010) reported low genotypic coefficient of variation for spike length, grain yield per plant and 1000- grain weight whereas high heritability estimates was noticed for grain yield per plant, 1000-grain weight, plant height and number of spikes per plant.

Kalim Ullah *et al.* (2011) observed significant genotypic differences for all measured traits *viz.,* plant height, days to 50 per cent flowering, time to reach physiological maturity (days), spikelets per spike and spike length (cm), indicating a considerable amount of variation among genotypes. They also reported, estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highly significant for spike length, days to 50 per cent flowering and plant height.

Mohammed *et al.* (2011) revealed highly significant differences among 16 durum wheat genotypes for 12 traits studied, suggesting the possibility of improving durum wheat for these traits. They also reported, plant height and number of kernels per spike showed the highest phenotypic and genotypic coefficients of variations and genetic advance. Whereas, days to maturity and 1000 grain weight had the lowest values. Plant height exhibited highest heritability value of 98.3 per cent while number of spikelets per spike showed minimum value of 36.4 per cent. High heritability was observed for 1000 grain weight with low genetic advance.

Yadav *et al.* (2011) observed sufficient genetic variability for all ten character *viz.* days to heading, days to maturity, plant height, tillers per plant, spike length, grains per ear, 1000-grain weight, biological yield per plant and grain yield per plant. All the characters exhibited high heritability except plant height and grains per ear. Tillers per plant and grain yield per plant had high heritability coupled with high genetic advance, thereby indicating selection for these characters would be effective.

Kalim Ullah *et al*. (2012) reported genetic variability in forty one bread wheat genotypes for number of grains per spike, number of tillers per plant, 1000-grain weight, grain yield per plant and spike density. They observed, significant genotypic differences for all the traits studied indicating considerable amount of variation among genotypes for each character. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant and number of tillers per plant.

Asaye *et al.* (2013) observed highest genotypic coefficient of variation for grain yield, 1000 grain weight and kernels per spike. While, the lowest genotypic coefficient of variations were observed for days to maturity and hectolitre weight.

Awale *et al.* (2013) reported high phenotypic coefficient of variation and genotypic coefficient of variation for number of tillers per plant and grain yield per plot. High heritability recorded for days to heading, grain yield per plot, days to maturity, plant height, number of tillers per plant, number of grain per spike and 1000 grain weight. Moderate heritability were recorded for number spikelets per spike.

Kumar *et al.* (2013) showed the considerable amount of variation among genotypes for characters, days to 50 per cent flowering, days to maturity, plant height, tillers per plant, spike length, grains per spike, 1000 grain weight and yield per plant. The estimates of GCV and PCV were moderate for biological yield per plant, number of effective tillers per plant. High heritability for days to 50 per cent flowering and days to maturity coupled with low genetic advance indicates non additive gene effects.

Vir *et al.* (2013) observed significant genotypic difference for seed yield per plant, 1000-seed weight, number of spikelets per spike, number of seeds per spike, spike length, plant height and days to 50 per cent flowering.

Khan (2013) showed highly significant differences among the genotypes for days to heading and plant height. Plant height and days to heading were highly heritable with heritability values of 0.72 and 0.54, respectively, while days to maturity, number of tillers per plant, spike length, spikelets per spike, grains per spike and grain yield per plant were low heritable with heritability values of 0, 0, 0.19, 0.37, 0.16, and 0.16, respectively.

Ashfaq *et al.* (2014) observed values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for plant height and grain yield per plant. Low PCV and GCV were observed for days to heading, plant height, number of tillers per plant, number of spikelets per spike, spike length, 1000 grain weight and grain yield per plant.

Sabaghnia *et al.* (2014) evaluated genetic variability among 56 bread wheat genotypes and reported significant differences among measured traits i.e. plant height, spike length, spikelet number, grain number, number of days to 50 per cent flowering, 1000 seed weight and grain yield. The coefficient of variation (CV) was high for grain yield (25.61 %), number of tillers per plant (22.06 %) and number of grains per spike (21.45 %).

Yahaya (2014) observed high heritability for spike length and plant height and moderate heritability with high genetic advance for total tillers per plant, spike length and number of grains per spike.

Devi *et al.* (2014) observed highest phenotypic and genotypic coefficient variation for number of grain per spike, number of effective tillers, number of spikelets per spike, yield per plant and number of tiller per plant. While, it was recorded moderate for kernel weight, spike length, number of spikelet per spike, days to flower initiation, days to maturity. The estimates of phenotypic and genotypic coefficient variation suggested that sufficient variation present in the material.

Fikre *et al.* (2015) observed moderate PCV and GCV were recorded for 1000 kernel weight, grain yield, number of grains per spike and number of productive tiller. High heritability values were observed for days to heading, days to maturity, grain filling period, 1000 kernel weight, number of spikelets per spike, spike length and plant height. Among the characters, 1000 kernel weight showed high values of genetic gain whereas days to maturity, grain yield, productive tillers and number of grains per plant had moderate values of genetic advance as per cent of mean (GAM).

Deoraj *et al.* (2016) reported presence of considerable amount of variability in F_2's of 21 crosses, 7 parents and 2 checks. The magnitude of GCV and PCV were high for productive tillers per plant and spikelets per spike; whereas, days to maturity and days to 50 per cent flowering exhibited least GCV and PCV. The high heritability was accompanied with high genetic advance as per cent of mean for length of spike, productive tillers per running meter, 1000 grain weight and grain yield per plant indicating additive genetic control in the expression of these characters.

Pandey *et al.* (2016) screened 150 bread wheat genotypes for nutrient concentrations and grain protein content. Several fold variations among genotypes existed for almost all the elements. Three major components of principal component analysis (PCA) revealed 60.8 per cent variation among the genotypes. Nutrient variables segregated into two groups, one group containing all the macroelements except sulphur; and another cluster containing proteins and all the microelements except Zn and Mn.

Velu *et al.* (2017) studied genotypic variation in 100 advanced breeding lines developed for Indian peninsular zone by measuring phytic acid (PA), inorganic phosphate (IP), iron and zinc content in seeds and hundred kernel weight (HKW). Advanced breeding lines under investigation exhibited wide variation for the characters studied. The PA content ranged from 4.97 to 15.02 mg/g (mean of 9.58 mg/g). Iron and zinc content was in the range of 0.042 to 0.098 mg/g and 0.017 to 0.029 mg/g respectively. Iron content showed very high genotypic coefficient of variation and heritability (bs) as compared to zinc content and other traits. Low heritability of IP content indicated the environmental influence on the trait.

Chimdesa *et al.* (2017) conducted experiment with 21 released varieties and 4 promising lines using Randomized Complete Block Design where genotypes were replicated three times and 14 characters were recorded. Results of the analysis of variance revealed that genotypes differed significantly for all characters studied. Genotypic coefficient of variation (GCV) ranged from 4.59 (days to maturity) to 13.76 per cent (grain yield per hectare), while phenotypic coefficient of variation (PCV) ranged between 5.03 (days to maturity) to 20.85 per cent (grain yield per hectare). Heritability in broad sense and genetic advance as per cent of mean (GAM) ranged from 33.33 per cent (Tillers per plant) to 84.67 per cent (peduncle length) and 8.66 per cent (days to maturity) to 18.74 per cent (grain yield per hectare), respectively. Grain yield per hectare was positively correlated with biological yield per plot and harvest index, but was negatively correlated with peduncle length both at genotypic and phenotypic level.

Sohail *et al.* (2018) studied genetic variability, heritability and genetic advance in 11 F_4 bread wheat (*Triticum aestivum* L.) genotypes. The statistically significant differences were detected for the investigated traits. The high magnitude of heritability (0.62 %) was noted for all parameters except spike length (0.57 %) which was moderate. Low expected genetic advance was recorded for days to heading (3.90 %) and spike length (8.13 %), moderate expected genetic advance was observed for plant height (9.95 %), grain weight spike^{-1} (11.54 %) and 1000 grain weight (13.41 %), while high expected genetic advance was noted for flag leaf area (24.72 %), grain yield plant^{-1} (20.45 %), biological yield plant^{-1} (23.64 %) and harvest index (24.00 %).

Bilgrami *et al.* (2018) examined the concentrations of zinc, iron, and phytic acid, as well as its mole ratio to zinc in various wheat species. The concentrations of phytic acid and its mole ratio to zinc were 0.61 to 1.55 g kg^{-1} dry weight and 1.88 to 4.17 for autumn, and 0.97 to 2.02 g kg^{-1} dry weight and 2.10 to 4.05 for spring planting. Given that the concentration of Fe and Zn in all the studied genotypes is relatively high and due to the existence of other desirable agronomic traits, this study believes that it could possibly enhance the applicability of some of these genotypes for breeding purposes.

2.2 Correlation and Path analysis

Yield is complex character which depends on many component characters. Correlation coefficient is useful estimates to ascertain the association between various characters and identifying such characters which are of little or no importance in the the selection programme.

Robinson *et al.* (1949) observed that the correlation values are of potential importance since selection is usually concerned with changing two or more traits simultaneously.

Dewey and Lu (1959) used these correlation coefficients first time in plant for path analysis by following Wright (1921). He gave the detailed procedure for path analysis which was quite a different technique in eliminating the environmental variances.

Grafius (1964) has pointed out that it would be more meaningful if the structure of yield were provided through its components rather than *per se* performance. For improving yield through breeding, it is necessary to study these yield components, their interrelationship with yield and their direct and indirect contributions.

Kibite and Evans (1984) revealed that correlations between grain yield and protein content were negative and highly significant.

Deshmukh *et al.* (1990) observed that days to 50 per cent flowering had positive and significant correlation with grain yield and also reported the significant positive correlation between grain yield and 1000 grain weight.

Hadjichristodoulov (1990) reported the positive correlation between plant height and 1000 grain weight.

Dokuyucu and Akkaya (1999) reported positive direct effect of number of grains per spike and its positive association with grain yield in the Turkish wheat genotypes.

Choudhary *et al.* (2000) computed correlation and path coefficients for plant height, flag leaf area, grains per spike, 100 grain weight and grain yield in ten bread wheat genotypes. Maximum positive indirect effects of plant height, flag leaf area, 100 grain weight on grain yield were observed. They proposed that traits having positive direct effects on grain yield must be considered as suitable selection criteria for evolving high yielding genotypes.

Bergale *et al.* (2001) observed that spikes per plant, grains per spike, plant height showed significant positive correlation with grain yield.

Mondal and Khajuria (2001) indicated the positive correlation between grain yields and yield components traits in wheat such as number spikes per plant.

Korkut *et al.* (2001) reported grain yield was significantly and positively correlated with 1000-grain weight and the number of spikes per square meter.

Patil and Jain (2002) observed that grain yield had positive and highly significant correlation with number of tillers per plant and number of grains per spike. Whereas it exhibited negative and non-significant correlation with days to heading, days to maturity, plant height and 1000 grain weight.

Wegrzyn *et al.* (2002) observed highest positive correlation between grain yield and 1000 grain weight and negative correlation between grain yield and days to heading.

Lad *et al.* (2003) observed grain yield had highly significant and positive correlation with productive tillers per plant, spikelets per spike, grains per spike and grain weight per spike.

Singh *et al.* (2003) revealed that positive and significant correlation between effective tillers per plant, biological yield per plant and harvest index with grain yield per plant. However, days to heading had negative significant correlation with 1000 grain weight.

Kashif and Khaliq (2004) indicated the positive correlation between grain yield and grains number per spike.

Singh *et al.* (2006) observed significant correlation between grain yield and days to maturity, plant height, ear length, spikelets per ear, tillers per meter and grain per ear indicated scope for improving grain yield through simultaneous selection.

Sinha *et al*. (2006) reported positive and non significant genotypic correlation of 1000 grain weight with yield per plant under irrigated timely sown wheat.

Yadav *et al.* (2006) reported that tiller number per plant and hectolitre weight showed the highest positive correlation with grain yield.

Gashaw *et al*. (2007) showed that plant height and 1000 kernels weight had significant positive correlation with grain yield.

Ali *et al.* (2008) carried out experiment to study seventy local and exotic wheat genotypes, they evaluated for variability parameters, correlations and path coefficients for eight metric traits i.e., plant height, number of productive tillers per plant, number of spikelet's per spike, spike length, number of grains per spike, fertility per cent, 1000 grain weight and yield per plant. Path coefficient analysis revealed that number of productive tillers per plant and number of grains per spike had the highest direct effect on grain yield per plant.

Yousaf Ali *et al*. (2008) showed that grain yield per plant had highly significant positive correlation with number of productive tillers per plant, number of spikelets per spike and number of grains per spike and spike length.

Ajmal *et al.* (2009) observed that plant height had significantly positive correlation with number of tillers. Tillers per plant displayed negative relationship with spikelets per spike and 1000 grain weight and number of grains per spike. Grain yield was positively and significantly correlated with number of grains per spike and 1000 grain weight. They also suggested that these traits be given emphasis during selection of wheat genotypes for improving productivity.

Subhashchandra *et al.* (2009) observed that positive and significant correlation of yield per plant with spike length and productive tillers per plant, while days to 50 per cent maturity showed negative and significant association with spike length, plant height and protein content.

Yagdi and Sozen (2009) observed significant positive correlation between the seed yield, plant height and spike length. The negative and significant correlations determined between gluten content and seed number per spike, seed weight per spike and plant density, as well as between the sedimentation and number of spikelet per spike and seed number per spike and between protein content and seed number per spike. Thus, indicated that generally the important agronomical characteristics were inversely correlated with the quality traits.

Bilgin *et al.* (2010) observed significant and negative correlation coefficient was observed between protein content and grain yield.

Khan *et al*. (2010) confirmed the negative and non- significant correlation of spike length and grain yield per plant.

Siahbidi *et al*. (2012) while studying correlation between traits in durum wheat genotypes showed positive association between number of spikes and grain number per spike.

Awale *et al.* (2013) observed that positive and highly significant association between grain yield per plot, number of tillers per plant and grains per spike. The number of tillers per plant and grains per spike which showed significant contribution towards grain yield per plot and these traits may be given emphasis for future bread wheat yield improvement program.

Zeeshan *et al.* (2013) revealed positive correlation number of spikelets per spike, number of grains per spike and 1000 grain weight with grain yield. They also, suggested that number of spikelets per spike, number of grains per spike and 1000 grain weight should be given emphasis for future wheat yield improvement programs.

Yahaya (2014) observed grain yield per plant was high and positively correlated with effective tiller per plant. A positive significant correlation of yield was observed with length of spike, spikelets per spike and plant height.

Singh *et al.* (2015) observed plant height exhibited positive correlation with hectolitre weight and tiller per plant showed positive correlation with yield per plant.

2.3 Genetic diversity

Genetic diversity is nothing but the genetic differences exhibited by the individuals with respect to various morphological characters. It is useful in assessing the combination of each character towards the total divergence and thereby helping in selecting the superior parents for hybridization programme.

Mahalanobis (1936) describes the concepts of D^2 statistics at a quantitative tool for estimating genetic divergence between the population. Genetic divergence is the result of changes in the frequency of different population due to evolutionary forces.

Rao (1952) suggested the application of D^2 statistics to plant breeding for the assessment of genetic variability. Moll *et al.* (1962) found that the genetic diversity is not affected due to geographical distribution.

Estimation of the degree of the divergence between biological population and computation of relevant contribution of different components to the total divergence is done completely by Mahalanobis generalized distance estimated by statistic. Nair and Mukharjee (1960) were the pioneers to use D^2 statistic as measure of genetic divergence in the field of plant breeding for classification.

Lee and Kaltsikes (1973) studied genetic divergence and revealed no association between genetic divergence and geographic origin.

Jain *et al*. (1975) investigated the geographical patterns of phenotypic diversity of durum wheat using the world collection and achieved a developed program for the protection of genetic resources to identify and assess inter variation and intra societies. Genetic diversity could be the result of geographical impact through evolution and hence traits could be considered as a function of variety.

Vojdani *et al*. (1993) carried multivariate cluster analysis to categorize geographical sites as well as the eco- geographical sub-populations, based on plant characters. No specific pattern of variation among the regions was found due to eco-geographical variation.

Redhu *et al*. (1995) studied genetic diversity for nine quantitative characters in 121 indigenous and exotic varieties of wheat. They observed that varieties were grouped into 27 clusters. Cluster means for different characters indicated the existence of large variability for plant height, number of grains per ear, 1000 grain weight and grain yield per plant. They also reported that, grouping of varieties in different clusters were not related to their geographical origin.

Fang *et al*. (1996) noticed that 120 genotypes of durum wheat into five groups based on maturity date, plant height, spike length, number of seed per spike, 1000-seed weight, and spike seed yield.

Walia and Garg (1996) conducted cluster analysis in 405 pure breeding lines for grain yield and its associated traits. They observed 13 different clusters and the clustering pattern of the genotypes belonging to the same country revealed their distribution in more than one cluster showing non-parallelism between geographic and genetic diversity. Members of cluster IV and IX were highly diverse from each other and cluster VI had high mean values for grain yield, biological yield, number of tillers/unit area and harvest index.

Kim and Ward (1997) reported that COP analysis can be applied for estimation of genetic diversity among cultivars and parental germplasm. They also predicting breeding behavior of the progeny of crosses and summarizing regional crop diversity, identifying parents that have contributed to yield improvements, and searching trends in genetic diversity over time and space.

Al-Ajlouni and Jaradat (1997) indicated that regions that have similar geographical and climatic similarity exhibit the same distribution patterns. The results suggested that Jordanian land races were rich sources of genetic variation and could be used in the reconstruction of a gene pool of germplasm for durum wheat improvement.

Sharma *et al*. (1998) studied genetic divergence in 51 genotypes of spring wheat and clustering was done using three different Tocher's values, *i.e*., 1060, 500 and 300. They observed that genotypes were grouped into 7, 9 and 10 different clusters respectively. Linkage dendrogram and minimum spanning tree exhibited confirmity with the clustering pattern of D^2 statistic at Tocher's values 500 and300.

Dotlacil *et al*. (2000) reported 120 accessions of European winter wheat land races and obsolete cultivars were grouped into eight clusters and noticed that clustering has decreased the variability of cultivars within the clusters in most of evaluated characters, it was difficult to find a simple linkage between the geographic origin of cultivars and their appearance in particular clusters.

Bergale *et al*. (2001) studied genetic divergence among fifty bread wheat and observed the cultivars were grouped into 11 clusters and reported presences of genotypes of different geographical origin in a single cluster suggest the possibility of existence of ancestral relationship among the cultivars. They also reported that plant height had the greatest contribution to genetic divergence.

Nimbalkar *et al*. (2002) revealed that 24 genotypes were grouped into 12 clusters and observed highest and lowest intra cluster distance was observed in cluster III and I respectively. The inter cluster distance was highest between cluster VII and cluster XII. They observed that, number of grains per spike, 1000-grain weight, grain weight per spike and number of productive tillers contributed considerably to the genetic divergence.

Dwivedi *et al*. (2002) studied the genetic divergence among 72 lines of bread wheat by using Mahalanobis D^2 analysis. Based on D^2 values the genotypes were grouped into 8 clusters with cluster-I having highest number of genotypes and cluster-VIII with lowest number of genotypes. The genotypes of cluster-I, III, IV were indented as diverse and had higher mean values for most important yield component traits.

Gashaw *et al.* (2007) studied genetic divergence based on multivariate analysis using Mahalanobi's D^2 statistics which grouped the durum wheat genotypes into 10 clusters. The highest inter cluster distance was between cluster-II and cluster-III.

Kumar *et al.* (2009) revealed that the thirty genotypes were grouped into six clusters. Further, they also reported that on the basis of cluster means, cluster VI has been identified for selecting parents for incorporating grain yield per plant, tillers per plant and plant height, cluster V for spike length, grains per spike and early maturity and cluster III for 1000 grain weight.

Jaiswal *et al.* (2010) grouped three hundred indigenous germplasm of bread wheat into twenty three clusters each having certain mean value for characters under study. They also suggested that genotypes bearing desired value from different clusters can be used in breeding program for improvement of yield as well as quality characters of bread wheat.

Hailegiorgis *et al.* (2011) revealed that genotypes were grouped into 22 different clusters and reported the presence of wide diversity among the tested genotypes. From cluster mean values, genotypes in IX and XIII deserve consideration for their direct use as parent in hybridization programs to develop high yielding wheat varieties. They also noticed that genotypes in cluster III and XVI may be used for improvement of protein, early maturity and other desirable characters other than grain yield and suggested that differentiation of genotypes into different clusters was because of the small contribution of few characters rather than the cumulative effect of a number of characters. The information obtained can be used to plan crosses and maximize the use of genetic diversity and expression of heterosis.

Kumar *et al.* (2013) observed inter-mating of K816 and HUW-533 mono-cluster genotypes from cluster VI and VII showing maximum inter-cluster distance between them followed by mono- cluster genotype K816 from cluster VI with 3 genotypes from cluster II exhibiting high degree of genetic diversity and can be utilized through inter-varietal hybridization programme.

Singh *et al.* (2014) grouped thirteen wheat genotypes into four clusters by both Tocher's and Euclidian methods of divergence. They also observed that clusters of both methods were different on the basis of the genotypes and their numbers present in the cluster.

Verma *et al.* (2014) evaluated 108 bread wheat accessions from India and Australia to assess the genetic diversity for yield and yield traits. They noticed that these genotypes into eleven clusters and distribution pattern indicating that maximum number of genotypes grouped into the cluster IV (26) followed by cluster VI (22) and cluster II (12). The inter-cluster distance in most of the cases was higher than the intra-cluster distance, indicating wider genetic diversity among the accessions of different groups. The highest inter-cluster distance was observed between cluster VIII and IX (113.94) followed by VIII and X (97.72), showing wide diversity among the groups. The highest intra- cluster distance was observed for the cluster X (13.96) and the lowest for the cluster VII (00.00). Genotypes of cluster X had highest mean value for grain yield, harvest index and spike weight. The genotypes in these clusters *i.e.* Perenjori, KRL 261 and KRL 283 from cluster X, and Gutha from cluster IX may be used as potential donors for hybridization programme to develop genotypes with high grain yields.

Salman *et al.* (2014) classified 65 wheat accessions into 6 different clusters. Maximum diversity was found in cluster I and cluster IV. This maximum diversity explains the better parental selection for future breeding programme.

Fikre *et al.* (2015) showed that the 64 genotypes were clustered into nine clusters. Maximum inter cluster distance was observed between cluster I and IX (D^2=5112.1) followed by that between clusters III and IX (D^2=4694.4) and VIII and IX (D^2=3871.9) which had shown they were genetically more divergent from each other than any other clusters. Crosses between genotypes selected from cluster I with cluster IX, cluster III with cluster IX and cluster VIII with cluster IX are expected to produce relatively better genetic recombination and segregation in their progenies.

Getachew *et al.* (2017) evaluated 49 bread wheat genotypes for 11 traits. Average linkage cluster analysis classified the 49 genotypes into six clusters. Higher inter-cluster distance was exhibited between cluster I and III followed by cluster II and IV and cluster II and III indicating wider genetic diversity among these clusters. Thus, future crossing program between members of cluster I with cluster III, and cluster II with III and IV could possibly result in heterosis in the F_1, and great deal of variability in the F_2 generations.

3. MATERIALS AND METHODS

The present investigation on "Assessment of genetic variability for biochemical and yield attributes in Wheat (*Triticum aestivum* L.)" was conducted at Post graduate institute Farm, Post graduate institute, Mahatma Phule Krishi Vidyapeeth, Rahuri, Tal. Rahuri, Dist. Ahmednagar during *Rabi,* 2017-18. The details of materials and methods used to carry out the genetic divergence studies, experimental design adopted and statistical procedure followed are described in this chapter.

3.1 Experimental Materials

The experimental material for the present investigation consisted of 30 genotypes of wheat (*Triticum aestivum* L.) collected from Agricultural Research Station, Niphad (M.P.K.V. Rahuri). The list of genotypes along with pedigree is given in Table 1.

3.2 Experimental Design

A piece of land selected for experiment was brought to fine tilth by ploughing followed by harrowing. The experiment was conducted in Randomized Block Design (RBD) with two replications. The seeds were sown by dibbling. Each entry was represented by two rows of 2.5 meter length with spacing of 20 cm between the rows.

The recommended dose of 120:60:40 NPK (kg/ha) was applied and the experiment which sown on 21st November 2017. All other recommended package of practices were carried out to raise a good crop.

Table 1. List of Wheat Genotypes with Pedigree

Sr. No	Genotype	Pedigree
1	NIAW-3170	SKOLL/ROLF07
2	NIAW-3354	FRET2*/BRAMBLING//MESIA/3/BECARD
3	NIAW-3390	BECARD/CHYAK
4	NIAW-3386	BECARD/QUAIU#I
5	NIAW-3523	WBLLI*2/KURUKU//HEIIO
6	NIAW-3525	CS/TH.SC//3*PVN/3/MIRIO/BUC/4/URES/JUN//KAUZ///5/HUIT/7/CS/TH.C
7	NIAW-3270	NIAW 917 X NIAW 1415
8	MACS-6478	CS/TH.SC//3*VN/3/MIRLO/BUC/4/MILAN/5/TILHI

Table 1 contd….

Sr. No	Genotype	Pedigree
9	MACS-6222	HD 2189*2/MACS 2496
10	HD-2932	KAUZ/STAR//HD2643
11	AKAW-4627	WH-147/SUNSTAR*6/C-80-1
12	NI-345	Mondhya 417-5/HOFED I
13	NIAW-3581	LOK 54 X KING BIRD
14	NIAW-3624	DL 1022 X NIAW 1415
15	NIAW-3643	RAJ 4083 X NIAW 1275
16	NIAW-3553	AKAW 4210-6 X NIAW 1594
17	NIAW-3562	MACS 6348 X LOK 62
18	NIAW-3584	RAJ 4083 X NIAW 1594
19	NIAW-3592	(LOK 62 X RAJ 4083)X(HD 2987)X(LOK 1)
20	NIAW-3636	AKAW 4210-6 X RAJ 4083
21	NIAW-3559	NIAW 1621 X NIAW 1594
22	NIAW-3575	LOK 62 X VW 514
23	NIAW-3578	LOK 62 X NIAW 1621
24	NIAW-3583	RAJ 4083 X LOK 63
25	NIAW-3633	AKAW 4210-6 X MACS 3040
26	NIAW-34	CNO 79 / PRL “S”
27	Samadhan	NIAW 34/PBW435
28	Trimbak	SERI 82/3/MRS/JUP/HORK ‘S’
29	Tapovan	GW 244 / Bob White
30	Netravati	GW 9506/PRL/PRL

3.3 Recording of Observations

3.3.1 Sampling of Plants

Five plants were selected randomly from each treatment. The average from these five plants was worked out for the statistical computation and further used for the genetic divergence study.

3.3.2 Observations recorded

The details of observations recorded and the technique adopted to record each of the observations have been given below.

3.3.2.1 Days to 50 per cent flowering

The number of days required from the date of sowing to the date on which 50 per cent of the plants in each genotype flowered were recorded.

3.3.2.2 Days to maturity

Number of days required from the date of sowing to physiological maturity was considered as days to maturity.

3.3.2.3 Plant height (cm)

Plant height was measured at maturity from ground level to the tip of the plant on observational plants. It was expressed in centimetres (cm).

3.3.2.4 Earhead length (cm)

The average earhead length of five plants on the main culm from the base of the earhead to the top excluding awns was recorded in centimetre.

3.3.2.5 Number of spikelets per earhead

Total number of spikelets on main spike of all five plants were counted at the time of maturity and average was recorded.

3.3.2.6 Number of grains per earhead

Total number of grains in the main spike were counted at the time of harvest and recorded.

3.3.2.7 1000 grains weight (g)

Total weight of 1000 grains in each genotype was taken and weight was recorded in grams.

3.3.2.8 Grain yield (q/ha)

Total weight of grains harvested from each rows was taken separately and multiplied by hectare factor and calculated as quintal per hectare.

3.3.2.9 Protein content (%)

Total nitrogen was estimated by Kjedhal's method as suggested by Jackson (1967) and this was multiplied by factor 6.25 as suggested by Piper (1950) to calculate protein content in grain.

3.3.2.10 Sedimentation value (ml)

Sedimentation value was estimated by Zenley test.

3.3.2.11 Yellow berry percentage

Incidence of yellow berry was recorded by observing yellow spots on the grains kernels on percentage basis. About 200-300 wheat grains were randomly with drawn and placed on a very clean white filter paper and observed for yellow spots and the results were expressed on per cent basis.

3.3.2.12 Grain appearance score

The colour, size, luster, shape, boldness and shriveling of wheat grains were judged with the score out of 10. Maximum weightage was given to amber, bold, hard, lustrous and non shriveled grains. The mean of three independent observations was taken into consideration for the expression of results.

3.3.2.13 Estimation of iron and zinc (mg/100 g)

Iron and zinc contents were determined by Atomic Absorption Spectrophotometry (AAS). One gram of finely powdered wheat seeds were taken in 100 ml conical flask and 20 ml of mixture of concentrated nitric acid and perchloric acid (5:1) was added and kept overnight. Next day, the samples were digested on hotplate at 200^0C. Samples were then allowed to cool and volumes were made up to 50 ml using glass distilled water. The diluted samples were filtered through Whatman No. 42 filter paper and filtrate was used for the estimation of iron and zinc using atomic absorption spectrophotometer.

Quality analysis *viz.,* sedimentation value, yellow berry percentage, protein content, zinc content, iron content was done at Food Science Laboratory, Post Graduate Institute, MPKV, Rahuri.

3.4 Statistical analysis

The mean values of five randomly selected observational plants for fourteen different characters were used for statistical analysis. The following statistical parameters were calculated for presentation of data on different quantitative characters.

3.4.1 Assessment of Variability

The analysis of variance for different characters was carried out using the mean data into different sources by following the method given by Panse and Sukhatme (1995).

Analysis of variance (ANOVA)

Source of variation	DF	MSS	Expected mean square
Replication	(r-1)	RMS	$\sigma^2 e + t\,\sigma^2 r$
Treatment	(t-1)	TMS	$\sigma^2 e + r\,\sigma^2 r$
Error	(r-1) (t-1)	EMS	$\sigma^2 e$
Total	(rt-1)	———	

Where,

r = Number of replications,

t = Number of treatments,

e = Error

3.4.1.1 Estimation of mean and range

The mean values for each character were worked out by the following formula

$$\bar{X} = \frac{1}{N} \left(\sum_{i=1}^{n} X_i\right)$$

Where,

$\bar{X}$ = Mean of character

$\sum X_i$ = Total of all the observations for character

N = Number of observations

The difference between the highest and the lowest values, from mean of each character were recorded as range.

3.4.1.2 Estimation of standard error of mean, standard error of difference and critical difference

i. The S.E. of mean difference was calculated as

S.E. of mean [SEm] = $\sqrt{\sigma^2 e/r}$

ii. The standard error of difference between two means was calculated as

S.E. of difference [SE (d)] = SEm x $\sqrt{2}$

iii. The critical difference between any two means was calculated as C.D. = SE (d) x 't' at error d.f.

3.4.1.3 Estimation of components of variation

The phenotypic and genotypic variances were calculated by using the respective mean squares from variance table (Johnson *et al.* 1955 a) as below.

Environmental variance $(\sigma^2{}_e)$ = EMS

$$\text{Genotypic variance } (\sigma^2{}_g) = \frac{\text{GMS-EMS}}{r}$$

Phenotypic variance $(\sigma^2{}_p) = \sigma^2{}_g + \sigma^2{}_e$

Where,

GMS= Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications.

3.4.1.4 Estimation of coefficient of variation

The genotypic and phenotypic coefficient of variation were calculated by the formulae as suggested by Burton and Devane (1953).

3.4.1.4.1 Phenotypic coefficient of variation (PCV)

$$\text{PCV (\%)} = \sqrt{\sigma^2 p} \,/\, \bar{X} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{X}$ = General mean of character

3.4.1.5 Estimation of heritability percentage (h^2 b.s.)

Heritability percentage in broad sense was estimated as per the formula given by Burton (1952).

$$h^2 \text{ (b.s.)} = (Vg/Vp) \times 100 \text{ or } h^2\text{(b.s.)} = (\sigma^2 g/\sigma^2 p) \times 100$$

Where,

h^2(b.s.) = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Johnson *et al.* (1955a).

Low heritability = 5-10 %

Moderate heritability = 10-30 %

High heritability = 30-60 %

3.4.1.6 Estimation of genetic advance

Genetic advance was calculated by the formula given by Johnson *et al.* (1955a).

$GA = K \times (\sigma^2 g / \sigma^2 p) \times \sigma p$ or $GA = K \times h^2 \times \sigma p$

Where,

K = Selection differential which is 2.06 at 5 per cent selection intensity

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σ p = Phenotypic standard deviation

h^2(b.s) = Heritability broad sense

The range of genetic advance as per cent of mean was classified by Johnson *et al.* (1955a).

$GAM = GA \times 100 / \bar{X}$

Where,

G = Genetic advance

$\bar{X}$ = Grand mean of characters

< 10 % : Low

10-20 % : Moderate

> 20 % : High

3.4.2 Correlation

In all the generations, the simple correlation coefficients were calculated to determine the degree of association of different characters with grain yield and also among yield components in each of the populations separately. Correlation coefficients were compared against Table 'r' values at (n-2) d.f at the probability levels of 0.05 and 0.01 to test their significance. Simple correlations were computed by using the formula as given below.

$$r = \frac{cov.x\ y}{\sqrt{vx.vy}}$$

Where,

Cov xy = Covariance between the characters x and y

Vx = Variance of the character x

Vy = Variance of the character y

Test of significance for as $t = r / \sqrt{(1-r^2)} \times \sqrt{X^2}$

3.4.3 Path analysis

Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959).

Path coefficient analysis is simply standardized partial regression coefficient which split the simple correlation into the measures of direct and indirect effects i.e. it measures the direct and indirect contribution of various independent (effects) characters on different characters. If 'Y' is dependent (causal) characters by X_1, X_2, X_3 ------- independent characters and some undefined factors designated by R, this relation can be represent by

$$Y = X_1 + X_2 + X_3 + \text{-----} + R$$

Path analysis reveals whether the association is due to their direct effect or is a consequence of their indirect effects *viz.*, other component characters. Correlation between cause (X_1) and effect (Y_1) is partitioned into the direct effects and indirect effects via other characters.

a. Direct effects

Path coefficient is ratio of standard deviation of the effect due given cause to the standard deviation of effect i.e. ($\sigma X_1/y$). This gives the direct effect of cause on yield.

$$\sigma(\ r\ (x,y) = a + r\ (x_1, x_2)\ b + r\ (x_1, x_3)\ (\text{------})$$

Here, $r\ (x, y)$ = correlation coefficient between cause (x_1) and yield (effect) a, b, c are path coefficient (direct effects) of causal characters x_1, x_2, x_3 respectively.

$r\ (x_1, x_2)$ = Correlation coefficient between cause x_1 and x_2

$r\ (x_1, x_3)$ = Correlation coefficient between cause x_1 and x_3 .

b. Indirect effect

Indirect effect of x_1 via x_2 on $y = r\ (x_1, x_2)\ b$

Similarly, direct and indirect effects of all possible combinations were calculated for all component characters.

c. Residual effect

The residual effect R was calculated as below

$R = [1- (Px_1y.rx_1y)- (Px_2y.rx_2y) ......(Pxny.rxny)]1/2$

Where,

$Px_1y, Px_2y.... Pxny$ = Direct effects of respective character on seed yield

$rx_1y,rx_2y....rxny$ = correlation coefficient between respective characters and yield

Path diagram

A line diagram which is constructed with the help of simple correlation coefficients among various characters included in study is referred to as path diagram

r ny= Correlation coefficient

3.4.4 Genetic diversity

3.4.4.1 D^2 analysis

The analysis of divergence was carried out by D^2 statistic of Mahalnobis (1936) as described by Rao (1952). Analysis of variance for the individual characters studied was worked out as per RBD to test the significances among the genotypes. The characters exhibiting significant differences were only used for further analysis of D^2 statistic. The analysis of covariance for characters pairs, based on plot averages was carried out (Cochran and Cox, 1957).

3.4.4.2 Mahalanobis generalized distance

The generalized distance between two population is defined by Mahalanobis (1936) as

$D^2=\Sigma\Sigma\ \lambda i.j.\ di.\ dj$

Where,

λi.j = Reciprocal matrix to the common dispersion matrix

d i = Difference between the mean values of two populations for i^{th} character

d j = Difference between the mean values of two populations for j^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study, since it requires the inversion of a tenth order determinant and then the evaluation of 10 (10+1)/2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with Such transformed variables reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977).

The coefficients for the transformation were obtained by dividing the first row of reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.4.3 Determination of group constellation

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not a well defined term. The only criteria appears to be that any two groups belonging to same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. A simple device suggested by K.D. Tocher described by Rao (1952) is to start with the two closely associated groups and find a third group which has the smaller D^2 from the two. Similarly the fourth is chosen to have the smaller D^2value from the first three and so on. If at any stage the average $D^2$of group from those already listed appears to be high, then this group does not fit in the former groups and is therefore, taken outside the former cluster. The group of first cluster is then omitted and rest are treated similarly. It is also useful to calculate the change in average D^2within a cluster due to inclusion of an additional group. If the changes are appreciable, then the newly added group has to be considered as outside the cluster.

3.4.4.4 Average intra and enter cluster D^2 and D values

3.4.4.4.1 Average intra cluster D^2

The intra-cluster distances were calculated as

$$D^2 = \sum Di^2/n$$

Where,

Di is sum of distances between all possible combinations (n) of the population included in a cluster.

3.4.4.4.2 Average inter cluster D^2

The procedure followed for calculating the intercluster distance was first to measure the distance between cluster I and II, between I and III and between I and IV and so on. Likewise, the clusters were taken one by one and the distance from other clusters were calculated. The average inter-cluster distance were then calculated as

$$D^2 = \frac{\sum \text{distance between the population of cluster I and j}}{ni.nj}$$

Where,

ni = Number of population in cluster i

nj = Number of population in cluster j

3.4.4.4.3 Average intra and inter cluster distance (D)

$$D = \sqrt{D^2}$$

3.4.4.5 Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

3.4.4.6 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of The first rank was given to highest mean difference. The percentage contribution was calculated on the basis of number of times a character appeared first in the rank in all combinations (Singh and Chaudhary, 1977).

3.4.4.7 Cluster diagram

In D^2 analysis a line diagram is constructed with the help of D^2 or D values, which known as cluster diagram.

3.4.4.8 Genetic diversity as an index for desirable parents for hybridization

The possible limits to the parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyay (1984). They advised to delineate the divergence among parents into 4 divergence classes to take into account the variable magnitude of variation in parental divergence; the mean (M) and standard deviation (S) of values of divergence were calculated. The divergence classes were defined as follows,

DC_1 =D> or = M+S

DC_2 =D< (M+S) and > or = M

DC_3 =D> or = (M-S) and < M

DC_4 =D< (M-S)

They postulated that two parents whose genetic divergence falls between (M-S) and (M+S), i.e. in the classes DC_2 and DC_3 when crossed have higher chances of producing high frequency and magnitude of heterosis, when compared to a cross whose parental divergence falls outside the limit [(M-S),(M+S)].

4. RESULTS AND DISSCUSSION

The present investigation entitled "Assessment of genetic variability and biochemical attributes in wheat (*Triticum aestivum* L.)" was undertaken with a view to study genetic diversity, correlation, genetic variability, heritability and genetic advance for 30 diverse genotypes of wheat. The observations were recorded on fourteen characters. The results obtained are presented in this chapter.

4.1 Mean performance

The mean performance of 30 genotypes of wheat, for twelve characters studied are presented in Table 2.

4.1.1 Days to 50 per cent flowering

The general mean for days to 50 per cent flowering was 60.66 days. The variation in days to 50 per cent flowering ranged between 56.50 (NIAW-3525) to 69.50 (NIAW-3390) days. Nineteen genotypes were found to be early flowering, while eleven genotypes were late flowering when compared with general mean. The genotypes NIAW-3525 (56.50 days), AKAW-4623(57.00 days) were found significantly earlier for days to 50 per cent flowering. While, NIAW-3390 (69.50 days) and NIAW-917(68.50 days) were comparatively late in days to 50 per cent flowering than the general mean.

4.1.2 Days to maturity

The general mean for number of days to maturity was 105.40 days. The days to maturity ranged from 97.50 (NIAW-3170) to 115.50 (NIAW-1415) days. Fourteen genotypes were found to be early and sixteen genotypes were late as compared to general mean. The genotype NIAW-3170 was significantly early for days to maturity (97.50 days) followed by NIAW-3523 (98.50), NIAW-3624 (98.00) and NIAW-3643 (98 days) over the general mean. While, genotypes Netravati (115.50 days), Phule Samadhan (112.50 days) were comparatively late in maturity.

4.1.3 Plant height (cm)

The general mean for plant height was 82.34 cm. Plant height ranged from 72.25 cm (NIAW-3553) to 96.50 cm (NIAW-3583). Fifteen genotypes were taller than the general mean. The genotypes NIAW-3553 (72.25 cm), NIAW-3584 (74.65cm) and

NIAW-3636, NIAW-3575 (74.45 cm) were significantly dwarf, while the genotypes NIAW-3583 (96.50cm), NIAW- 301 (94.70 cm) were comparatively taller than general mean.

4.1.4 Earhead length (cm)

The general mean for earhead length was 10.67 cm. The variation in earhead length ranged from 9.26 cm (AKAW-4627) to 12.70 cm (NIAW-3553). Twelve genotypes showed long earhead length, while eighteen genotypes showed short earhead length than the general mean. The genotype NIAW-3553 (12.70 cm) showed significantly maximum earhead length followed by NIAW-3636 (12.10cm), NIAW-3354 (11.72 cm). While, genotype AKAW-4627 (9.26 cm) recorded minimum earhead length.

4.1.5 Number of spikelets per earhead

The general mean for number of spikelets per earhead was 14.03. The variation in number of spikelets per earhead ranged from 10.50 (NIAW-3583) to 17.50 (Netravati). Thirteen genotypes produced maximum number of spikelets, while other seventeen produced minimum number of spikelets per earhead than the general mean.

4.1.6 Grains per spike (No.)

The values for grains per spike ranged from 35.50 (NIAW-3624) to 52.50 (NIAW-3636) with population mean of 43.95. Eight genotypes showed more number of grains per spike than population mean. The genotype NIAW-3636 (52.50) showed highest number of grains per spike followed by NIAW-3643 (51.50), NIAW-3553 (51.00).

4.1.7 1000 grain weight (g)

Estimates of 1000 grain weight ranged from 39.60 g (Tapovan) to 51.50 g (HD-2932) with the population mean 45.92 g. Maximum 1000 grain weight was recorded by HD-2932 (51.5 g) while minimum was observed for Tapovan (39.60 g). Sixteen genotypes (53.33 %) had higher 1000 grain weight than population mean for the character.

4.1.8 Grain yield quintal per ha

The estimates for this economical character ranged from 41.33 q (NIAW-3583) to 68.31q (NIAW-3636) with population mean 56.47**.** Sixteen genotypes recorded higher values for grain yield than the population mean. Highest grain yield was recorded by NIAW-3583 followed by NI- 345 (68.28q) and Netravati (67.80 q).

4.1.9 Protein content (%)

The values for protein content ranged from 10.25 per cent (NIAW-3578) to 13.63 per cent (NIAW-3170) with mean protein content of 11.79 per cent. Thirteen genotypes recorded more protein content than the mean protein content of population. The genotype NIAW-3170 (13.63 %) recorded highest protein content, followed Phule samadhan (12.86 %) and NIAW-3354 (12.85 %). The genotype NIAW-3578 (10.25 %) showed lower protein content.

4.1.10 Zn content of grains (mg/100 g)

The values for Zn content ranged from 3.81 mg/100 g (NIAW-3584) to 4.54 mg/100 g (NIAW-3170) with mean Zn content of 4.15 mg/100 g. Fourteen genotypes (6 recorded more Zn content than the mean Zn content of population. The genotype NIAW 3170 (4.54 mg/100 g) recorded highest zinc content.

4.1.11 Fe content of grain (mg/100 g)

The values for Fe content of grain ranged from 2.60 mg/100 g (NIAW-3592) to 3.28 mg/100 g (NIAW-3575) with mean Fe content of 2.92 mg/100 g. Fourteen genotypes recorded more Fe content than the mean Fe content of population. The genotype NIAW-3575 (3.28 mg/100 g) recorded highest Fe content.

4.1.12 Sedimentation value (ml)

The general mean for sedimentation value was 49.38 ml. The variation in sedimentation value ranged from 45.50 ml (NIAW-3633, NIAW-3170) to 57.50 ml (NI-345). Thirteen genotypes showed maximum sedimentation value and seventeen genotypes produced minimum sedimentation value than the general mean. The genotype NI-345 (57.50), MACS-6478 (55.50), Netravati (52.50) and NIAW-3523 (51.00) was found to be significantly superior for sedimentation value.

4.1.13 Yellow berry percentage

Yellow berry percentage of genotypes ranged from 6.25 per cent (NI-345) to 9.40 per cent (HD-3932) with mean content of 7.56 per cent. Fifteen genotypes recorded lower yellow berry percentage than the population mean. The genotype NI-345 (6.25 %) showiest lower Yellow berry percentage.

Table 2. Mean values of different yield contributing characters of wheat genotypes

Sr. No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height (cm)	Earhead length (cm)	No. of spikelets	Grains/ spike	1000 grains weight(g)	Yield q/ha	Protein content (%)	Zinc (mg/100 g)	Iron (mg/100 g)	Sedimentation value(ml)	Yellow berry (%)	Grain appearance score
1	NIAW-3170	60.50	97.50	91.75	10.55	13.50	36.50	43.40	54.33	13.63	4.54	3.17	45.50	6.75	4.60
2	NIAW-3354	60.50	102.50	83.65	10.75	13.50	40.50	43.00	53.66	12.86	4.48	2.89	47.50	8.05	5.05
3	NIAW-3390	69.50	109.50	83.20	11.72	14.50	50.00	47.50	65.33	12.15	4.49	3.07	45.00	7.25	5.10
4	NIAW-3386	61.50	101.50	83.40	11.39	14.00	45.50	47.00	61.00	12.16	4.00	3.08	47.50	7.75	5.65
5	NIAW-3523	57.50	98.50	86.40	10.60	14.00	40.50	48.50	58.00	12.05	4.24	3.26	51.00	7.25	4.60
6	NIAW-3525	56.50	99.50	85.50	10.80	14.50	40.50	45.15	52.50	11.76	4.39	2.77	50.00	8.30	4.55
7	NIAW-3270	63.50	108.50	85.00	10.39	12.50	39.00	46.85	52.60	12.00	4.01	2.67	50.50	8.38	4.60
8	MACS-6478	63.50	110.50	77.25	10.85	14.50	40.50	44.50	52.33	11.37	4.08	2.96	55.50	7.87	5.65
9	MACS-6222	61.50	107.50	77.15	10.44	14.00	42.50	42.50	53.33	12.74	3.90	2.96	47.50	7.92	5.25
10	HD-2932	57.50	109.50	80.60	11.80	15.00	49.50	51.50	66.91	11.75	3.93	2.68	47.00	9.40	5.85
11	AKAW-4627	57.00	102.50	82.25	9.26	13.50	38.50	41.95	48.00	10.95	4.48	2.80	48.00	8.30	5.35
12	NI-345	59.50	100.50	85.50	11.28	13.50	50.00	50.10	68.28	12.70	4.22	2.88	57.50	6.25	5.55
13	NIAW-3581	57.50	102.50	89.60	10.10	15.50	42.50	48.25	56.33	11.70	4.29	2.84	55.50	7.25	6.00
14	NIAW-3624	58.50	98.00	82.14	9.50	13.00	35.50	40.50	44.16	10.95	4.13	2.99	49.50	7.05	5.75
15	NIAW-3643	58.00	98.00	83.10	10.60	14.50	51.50	49.15	63.33	11.66	3.98	2.71	45.50	7.80	5.50
16	NIAW-3553	57.50	103.50	72.25	12.70	16.00	51.00	50.50	66.00	10.85	3.89	2.90	47.50	6.55	6.10
17	NIAW-3562	58.50	106.50	75.95	10.50	14.50	50.00	49.20	64.33	12.07	4.38	3.08	48.50	7.45	5.65
18	NIAW-3584	67.00	107.50	74.65	10.65	15.50	50.50	49.00	61.00	11.15	3.81	2.72	53.50	9.25	5.15
19	NIAW-3592	59.50	99.00	77.45	10.21	13.50	48.00	48.65	63.33	12.04	3.89	2.60	47.50	8.20	5.35
20	NIAW-3636	63.50	108.50	74.45	12.10	15.00	52.50	50.05	68.31	11.53	4.13	2.81	53.50	6.90	5.30
21	NIAW-3559	61.00	110.00	78.95	9.95	11.50	40.50	40.75	41.67	11.25	4.17	3.08	48.50	7.60	5.60
22	NIAW-3575	59.00	104.00	74.45	11.25	14.50	48.00	49.00	61.17	12.01	3.98	3.28	51.00	7.25	4.25
23	NIAW-3578	60.50	100.50	75.80	11.40	14.50	47.00	48.25	60.67	10.25	4.08	3.01	47.50	8.08	4.45
24	NIAW-3583	60.50	111.50	96.50	9.46	10.50	39.50	41.50	41.33	10.75	4.14	2.79	46.50	8.15	4.55
25	NIAW-3633	59.00	109.00	83.80	9.85	12.50	45.50	42.25	51.82	11.02	4.27	2.84	45.50	7.90	4.85
26	NIAW-34	58.50	105.50	76.00	10.70	15.50	41.00	42.25	49.66	11.75	3.89	3.11	51.00	6.60	5.85
27	Phule Samadhan	57.50	112.50	89.14	10.35	12.50	38.50	45.00	53.00	12.86	4.39	2.94	51.50	6.65	5.75
28	Trimbak	63.50	110.50	94.70	10.25	13.50	37.50	41.50	45.00	11.75	4.30	2.91	47.50	6.70	5.50
29	Tapovan	68.50	111.50	89.10	9.55	14.00	37.00	39.60	49.17	11.77	4.02	3.07	46.50	7.35	6.10
30	Netravati	63.50	115.50	80.79	11.35	17.50	49.00	50.50	67.80	12.35	4.16	3.07	52.50	6.80	5.80
	Mean	**60.66**	**105.40**	**82.34**	**10.67**	**14.03**	**43.95**	**45.92**	**56.47**	**11.79**	**4.15**	**2.92**	**49.38**	**7.56**	**5.31**
	Range	**56.50-69.50**	**97.50-115.50**	**72.25-96.50**	**9.26-12.70**	**10.50-17.50**	**35.50-52.50**	**39.60-51.50**	**41.33-68.31**	**10.25-13.63**	**3.81-4.54**	**2.60-3.28**	**45.50-51.50**	**6.25-9.40**	**4.25-6.10**
	S.E±	**0.49**	**0.96**	**1.80**	**0.23**	**0.65**	**0.69**	**0.77**	**1.76**	**0.24**	**0.06**	**0.05**	**0.66**	**0.27**	**0.12**
	C.D.at 5%	**1.44**	**2.79**	**5.22**	**0.68**	**1.88**	**2.01**	**2.23**	**5.10**	**0.70**	**0.18**	**0.15**	**1.91**	**0.79**	**0.35**
	C.V.(%)	**1.16**	**1.29**	**3.10**	**3.15**	**6.56**	**2.24**	**2.38**	**4.42**	**2.93**	**2.12**	**2.57**	**1.89**	**5.16**	**3.29**

4.1.14 Grain appearance score

Grain appearance score of genotypes ranged from 4.25 (NIAW-3575) to 6.10 (Tapovan, NIAW-3553) with mean content of 5.31. Fourteen genotypes recorded higher grain appearance score than the population mean. The genotype NIAW-3553 and Tapovan (6.10) showed highest score.

4.2 Analysis of Variance

The analysis of variance for 14 characters is presented in Table 3. It is revealed that there were highly significant differences among the genotypes for all the characters under study, showing wide range of variation in 30 genotypes of wheat.

Table 3. Analysis of variance for 14 characters in wheat

Sr. No.	Character	Mean Sum of Square		
		Replication (1)	Genotypes (29)	Error (29)
1.	Days to 50 % flowering	9.600**	22.873**	0.4965
2.	Days to maturity	1.666	52.772**	1.8735
3.	Plant height (cm)	7.675	78.569**	6.5383
4.	Earhead length (cm)	0.3634	1.316**	0.1134
5.	Number of spikelets	2.400	3.756**	0.8482
6.	Number of grains per spike	7.530**	57.150**	0.9706
7.	1000 grains weight (g)	9.520*	26.560**	1.1984
8.	Yield (q/ha)	23.051	133.246**	6.2329
9.	Protein content %	0.0756	1.073**	0.1199
10.	Zinc content (mg/100 g)	0.0072	0.088**	0.0077
11.	Iron content (mg/100 g)	0.00007	0.0619**	0.0057
12.	Sedimentation value (ml)	0.0166	21.609**	0.8787
13.	Yellow berry (%)	0.4050	1.192**	0.1524
14.	Grain appearance score	0.0806	0.578**	0.0306

*, ** Significant at 5 % and 1 % probability respectively

The analysis of variance revealed significant differences among the genotypes for all the fourteen characters studied. This information suggests that considerable amount of variation persists for all the characters and considerable improvement can be achieved by selection for these characters. However, the analysis of variance by itself is inconclusive in explaining all the inherent genotype variability in the collection. This is evident by partitioning the total genetic variability inherent in the genotypes from the phenotypic variance (Grafius, 1964). Thus, it is necessary to work out the phenotypic and genotypic coefficients of variation, which indicate the extent of variability existing for various traits.

4.3 Genetic variability

The parameters of genetic variability *viz.*, mean, range, PCV, GCV, heritability (b.s.), genetic advance and genetic advance as per cent of mean are summarised in Table 4. The important findings are presented below.

4.3.1 Coefficient of variation

Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were classified as suggested by Sivasubramanian and Madhavamenon (1973) and are presented in Table 4.

The estimates of GCV were lower than PCV for all the characters under study. The magnitude, phenotypic coefficients of variation were greater than genotypic coefficients of variation. Highest phenotypic coefficient of variation was exhibited by grain yield (14.78) followed by grains per spike (12.26), yellow berry percentage (10.83), number of spikelets (10.81), grain appearance score (10.39), 1000 grain weight (8.11), plant height (7.922) and earhead length (7.920). Comparatively lower Phenotypic coefficient of variation was observed for sedimentation value (6.79), protein content (6.55), Fe content (6.27), days to 50 per cent flowering (5.63), Zn content (5.27) and days to maturity (4.959).

The inherent genetic variability is expressed by the genotypic coefficient of variation. Highest values for genotypic coefficient of variation was observed for grain yield (14.11) followed by grains per spike (12.05), grain appearance score (9.85), yellow berry percentage (9.53), number of spikelets (8.59), 1000 grain weight (7.75), plant height (7.28) and earhead length (7.26). Comparatively lower genotypic coefficient of variation was observed for sedimentation value (6.52), protein content (5.85), Fe content (5.72), days to 50 per cent flowering (5.51), Zn content (4.83) and days to maturity (4.78).

4.3.2 Heritability % (b.s.)

Heritability in broad sense ranged from 63.20 to 96.70 per cent. Highest estimate of heritability was recorded for number of grains per spike (96.70) followed by days to 50 per cent flowering (95.8), days to maturity (93.10), sedimentation value (92.20),

Table 4. Estimation of variability parameters for different characters of wheat

Sr. No	Characters	Mean	Range	σ^2 g	σ^2p	GCV %	PCV %	h^2 % (bs)	GA	GA as % mean
1	Days to 50% flowering	60.66	56.5-69	11.189	11.685	5.51	5.63	95.80	6.74	11.114
2	Days to maturity	105.40	97.5-115.5	25.449	27.323	4.786	4.959	93.10	10.03	9.516
3	Plant height (cm)	82.34	72.25-96.5	36.016	42.554	7.288	7.922	84.60	11.37	13.811
4	Earhead length (cm)	10.67	9.26-12.70	0.602	0.715	7.26	7.92	84.10	1.466	13.72
5	Yield (q/ha)	56.47	41.33-68.31	63.507	69.74	14.11	14.78	91.10	15.66	27.73
6	Number of grains per spike	43.95	36.50-52.50	28.09	29.06	12.05	12.26	96.70	10.73	24.42
7	1000 grains weight (g)	45.92	39.60-51.50	12.68	13.87	7.75	8.11	91.40	7.01	15.26
8	Number of spiklets/earhead	14.03	10.50-17.50	1.45	2.302	8.59	10.81	63.20	1.97	14.06
9	Protein content (%)	11.79	10.25-13.62	0.477	0.597	5.85	6.55	79.90	1.27	10.78
10	Zinc content (mg/100 g)	4.15	3.81-4.48	0.040	0.048	4.83	5.27	83.90	0.37	9.11
11	Iron content (mg/100 g)	2.92	2.67-3.26	0.028	0.034	5.72	6.27	83.10	0.31	10.75
12	Sedimentation value (ml)	49.38	45.50-51.50	10.366	11.244	6.52	6.79	92.20	6.36	12.89
13	Yellow berry (%)	7.56	6.25-9.40	0.520	0.673	9.53	10.83	77.30	1.30	17.26
14	Grain appearance score	5.31	4.25-6.10	0.274	0.304	9.85	10.39	89.90	1.02	19.24

1000 grains weight (91.40), grain yield (91.70), grain appearance score (89.90), plant height (84.60), earhead length (84.10), Zn content (83.90), Fe content (83.10), protein content (79.90), yellow berry percentage (77.30) and number of spikelets (63.20).

4.3.3 Genetic advance

Estimates of genetic advance ranged from 0.31 to 15.66. Highest estimate of genetic advance was recorded for grain yield (15.66) followed by plant height (11.37), number of grains per spike (10.73), days to maturity (10.03), 1000 grains weight (7.01), days to 50 per cent flowering (6.74), sedimentation value (6.36), number of spikelets (1.97), earhead length (1.46), yellow berry per cent (1.30), protein content (1.27), grain appearance score (1.02), Zn content (0.37), Fe content (0.31).

4.3.4 Genetic advance as a per cent of mean

Genetic advance as a per cent of mean (Table 5) was observed highest for grain yield (27.78 %) followed by number of grains (24.42 %), grain appearance score (19.24 %), yellow berry percentage (17.26 %), 1000 grains weight (15.26 %), number of spikelets (14.06 %), plant height (13.81 %), earhead length (13.72 %), sedimentation value (12.89 %), flowering (11.11 %), protein content (10.78 %), Fe content (10.75 %), days to maturity (9.51 %) and Zn content (9.11 %).

The estimation of genotypic (heritable), phenotypic and environmental (non heritable) component of total variability are required, as it helps in choice of desired breeding technique. Johannsen (1909), Nilsson Elhe (1909) and East (1916) separated genetic variance from total variance by using environmental variance. Now, it is an accepted pattern in all the biometrical studies, it helps in arriving at precise conclusion about the true breeding value of genotypes. Thus, in the present study, the components of variation such as genotypic and phenotypic coefficient of variations, heritability, predicted genetic advance and genetic advance as a per cent of mean were computed in respect of grain yield and it's components together with protein content, sedimentation value and zinc content.

In the present investigation, medium estimates of genotypic and phenotypic coefficients of variation were observed for the characters *viz.*, grain yield followed by grains per spike, yellow berry percentage, number of spikelets, grain appearance score, 1000 grains weight, plant height and earhead length.

Similar results were obtained for grain yield per plant, number of tillers per plant and number of grains per earhead by Subhash *et al*. (1993), Lad *et al.* (2003), Singh *et al.* (2003), Yadav *et al.* (2006), Yousaf Ali *et al*. (2008), Kumar *et al.* (2009) and Devi *et al.* (2014).

Whereas, low estimates of genotypic and phenotypic coefficients of variation were observed for the characters sedimentation value, protein content, Fe content, days to 50 per cent flowering, Zn content and days to maturity. Low estimates of GCV and PCV were reported by Chaturvedi and Gupta (1995) for days to 50 per cent flowering and plant height; Kumar *et al*. (2009) for days to 50 per cent flowering and days to maturity; Mohammed *et al.* (2011) for days to maturity and 1000 grains weight; Asaye *et al.* (2013) for days to maturity; Ashfaq (2014) for days to heading, plant height and 1000 grains weight.

In the present study phenotypic coefficients of variation was more than genotypic coefficients of variation for all the traits. This might be due to environmental effect. Similar results were also reported by Majumder *et al.* (2008), Badole *et al.* (2010) and Ashfaq *et al.* (2014).

However, the differences between GCV and PCV was very low for all the characters indicating less role of environment in the expression of these characters. The presence of high genetic variability is an indication of good scope for their improvement through hybridization followed by selection. These results are in conformity with results of Jagshoran and Mishra (2005) and Majumder *et al.* (2008).

The heritability is a good index of transmission of characters from parent to their off springs. Heritability specified the proportion of total variability i.e. due to genetic factor. In other words, it is the ratio of genotypic variance to total variance. The genetic advance is a measure of genetic gain under selection; which is mean genotypic value over parental population. Accordingly, Johnson *et al.* (1955) has suggested estimation of which the expected genetic advance under selection, mainly depends upon

1. Magnitude of genetic variability present in the base population.
2. Heritability of characters which are under consideration
3. Selection intensity on population or the plant selected

High heritability with moderate genetic advance as a per cent of mean was observed for grains per spike, plant height, earhead length, days to 50 per cent flowering and high heritability with low genetic advance as per cent of mean were observed for days to maturity and protein content. These results suggested the non additive genetic variance in expression of these traits. High heritability coupled with moderate genetic advance was reported earlier by Rebetzke (1999) for plant height; Subhashchandran (2009) for plant height and sedimentation value. Whereas, high heritability with low genetic advance was also reported by kumar *et al.* (2013) for days to maturity.

Thus, considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance as a per cent of mean together, it is evident that the number of tillers per meter, grain yield, sedimentation value and number of grains per earhead were found as the most important characters. Hybridization followed by selection in subsequent generations for these characters would pave the way for improvement of these characters in wheat.

4.4 Correlation

The correlation coefficients estimated between grain yield with all other characters are presented in Table 5.

4.4.1 Phenotypical correlation between grain yield and its components

The grain yield (Table 5) showed strong significant and positive correlation with 1000 grains weight (0.9186), number of grains per spike (0.8678), earhead length (0.7805), number of spikelets per earhead (0.6576), protein (0.2058), While days to 50 per cent flowering (0.0366) showing nonsignificant positive correlation with grain yield. Grain yield showed significant negative correlation with days to maturity (-0.1326), Zn content (-0.1664) and non- significant negative correlation with Fe content (-0.0521).

4.4.2 Genotypical correlation between grain yield and its components

The grain yield (Table 5) showed strong significant and positive correlation with 1000 grain weight (0.9249), number of grains per spike (0.8740), earhead length (0.7807), number of spikelets per earhead (0.6612), protein (0.2295), While days to 50 per cent flowering (0.0494)showing nonsignificant positive correlation with grain yield. Grain yield showed significant negative correlation with days to maturity (-0.1276), Zn content (-0.2124) and non- significant negative correlation with Fe content (-0.0884).

Table 5. **Estimates of genotypic correlation (below diagonal) and phenotypic correlation (above diagonal) for different quantitative and nutritional characters of wheat**

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Plant height(cm)	Earhead length (cm)	Number of spikelets	Grains / spike	1000 grains weight (g)	Protein (%)	Zinc (mg/100 g)	Iron (mg/100 g)	Yield (q/ha)
1.	Days to 50 % flowering	**1.000**	0.483**	0.022	0.068	0.074	0.064	-0.109	0.055	-0.0952	0.083	0.036
2.	Days to maturity	0.524**	**1.000**	0.068	-0.017	-0.027	0.0004	-0.143	-0.075	-0.078	-0.015	-0.132
3.	Plant height (cm)	0.014	0.052	**1.000**	-0.519**	-0.529**	-0.590**	-0.439**	0.242	0.451***	-0.030	-0.489
4.	Earhead length (cm)	0.084	0.0008	-0.470**	**1.000**	0.626**	0.689**	0.739**	0.101	-0.185	0.080	0.780
5.	Number of spikelets	0.106	0.0006	-0.455**	0.583**	**1.000**	0.518**	0.595**	0.040	-0.187	0.100	0.657
6.	Grains / spike	0.071	0.004	-0.594**	0.696**	0.537**	**1.000**	0.821***	-0.096	-0.313*	-0.179	0.867
7.	1000 grain weight (g)	-0.101	-0.136	-0.401**	0.726**	0.596**	0.826**	**1.000**	0.073	-0.219	-0.140	0.918
8.	Protein (%)	0.043	-0.040	0.277**	0.107	0.064	-0.109	0.078	**1.000**	0.314*	0.246	0.205
9.	Zinc (mg/100 g)	-0.199	-0.066	0.565**	-0.260*	-0.334*	-0.368**	-0.278	0.341**	**1.000**	0.192	-0.166
10.	Iron (mg/100 g)	0.097	0.0006	-0.036	0.094	0.129	-0.209	-0.182	0.267*	0.224	**1.000**	-0.052
11.	Yield (q/ha)	0.049	-0.127	-0.447**	0.780**	0.661**	0.874**	0.924**	0.229	-0.212	-0.088	

4.4.2 Inter relationship of yield components

4.4.2.1 Days to 50 per cent flowering

Days to 50 per cent flowering had showed highly significant positive correlation with days to maturity at both genotypic and phenotypic levels and it showed highly negative correlation with 1000 grains weight at genotypic and phenotypic level.

4.4.2.2 Days to maturity

Days to maturity had positive correlation with plant height, grains per spike at both genotypic and phenotypic levels. It had negative correlation with 1000 grains weight, earhead length, protein content at both genotypic and phenotypic levels.

4.4.2.3 Plant height (cm)

Plant height had highly significant positive correlation with zinc content and protein content at both genotypic and phenotypic levels. It had negative correlation with earhead length, grains per spike, 1000 grains weight, number of spikelets per earhead at genotypic and phenotypic level.

4.4.2.4 Earhead length (cm)

Earhead length had highly significant positive correlation with 1000 grains weight, grains per spike, number of spikelets, days to 50 per cent flowering at both genotypic and phenotypic levels. It had negative correlation with plant height at genotypic and phenotypic level.

4.4.2.5 Grains per spike

Grains per spike had highly significant positive correlation with 1000 grains weight, earhead length, number of spikelets per earhead at genotypic and phenotypic levels. It had significant negative correlation with plant height, zinc content at phenotypic and genotypic level.

4.4.2.6 1000 grains weight (g)

1000 grains weight had highly significant positive correlation with grains per spike, earhead length, number of spikelets at genotypic and phenotypic levels. It had significant negative correlation with plant height at phenotypic and genotypic level.

4.4.2.7 Number of spikelets

Number of spikelets had highly significant positive correlation with earhead length, 1000 grains weight, grains per spike at phenotypic levels. It had highly significant positive correlation with 1000 grains weight, earhead length, 1000 grains weight, grains per spike at genotypic levels It had significant negative correlation with plant height and zinc content at phenotypic and genotypic level.

4.4.2.8 Protein content (%)

Protein content had highly significant positive correlation with zinc content at phenotypic levels. It had significant positive correlation with zinc content, plant height, iron content at genotypic level. It had negative correlation with grains per spike, days to maturity at genotypic and phenotypic level.

4.4.2.9 Zinc content (mg/100 g)

Zinc content had highly significant positive correlation with plant height, protein content at phenotypic and genotypic levels. It had significant negative correlation with grains per spike, number of spikelets, 1000 grains weight, plant height at genotypic level.

4.4.2.10 Iron content (mg/100 g)

Iron content had positive correlation with plant height, protein content, zinc content, 1000 grains weight, days to 50 per cent flowering at phenotypic levels. It had significant positive correlation with protein content at genotypic level. It had negative correlation with 1000 grains weight, grains per spike, plant height at genotypic and phenotypic level.

The phenotype of any plant is the result of interaction of large number of factors. Therefore, the final yield is the sum total of the effects of several component characters which are polygenically controlled the quantitative characters. The influence of these characters on yield can be known through the correlation studies. Correlation coefficient measures the magnitude and direction of association between two characters taken at a time.

Correlation coefficient between characters assumes its importance due to genetic causes of correlation through the pleiotrophic action of genes, improvement brought about by selection through related characters and natural selection. The interrelationship among the economic characters is of immense help in effective selection programme. Simultaneous improvement in two or more characters is possible when positive correlations were observed, whereas negative associations indicate the need to compromise between desirable characters.

The degree and direction of association among characters is measured by genotypic and phenotypic correlation coefficients. The relationship between genotypic and phenotypic correlation indicates that the characters having high heritability estimates have lower environmental correlations than the genotypic correlations. When all the correlations are in same direction, highly heritable characters possess high genotypic correlations than phenotypic correlation because phenotypic correlation includes both genotypic and environmental correlations. If heritability of two characters is low coupled with a higher environmental correlation, then phenotypic correlation exceeds genotypic correlation.

In the present study, the correlation analysis revealed the association pattern of different yield components with grain yield (Table 5) represents the correlation coefficient between the characters with seed yield at both genotypic and phenotypic levels.

It was observed that, seed yield per plot had significant positive correlation with 1000 grains weight, grains per spike, earhead length, number of spikelets, protein content, days to 50 per cent flowering at both genotypic and phenotypic levels while character like days to maturity, plant height, zinc content, iron content negatively correlated at both the levels.

4.5 Path coefficient analysis

Path coefficient analysis was carried out to find out the direct and indirect contribution of each character towards the grain yield per hectare. The correlation coefficient being more important, were only partitioned into direct and indirect effects which are presented in Table 6.

4.5.1 Grain yield Vs. days to 50 per cent flowering

The character days to 50 per cent flowering showed positive direct effect (0.108) on seed yield and positive indirect effect on earhead length, grains per spike, number of spikelets per earhead, protein content while negative indirect effects on days to maturity, plant height 1000 grains weight, zinc content, iron content. The total genotypic correlation with seed yield was 0.0494.

Table 6. Direct and indirect effect of different quantitative and nutritional characters on grain yield of wheat

Sr. No.	Characters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Earhead length (cm)	Number of spikelets	Grains / spike	1000 grains weight (g)	Protein (%)	Zinc (mg/100 g)	Iron (mg/100 g)	Yield (q/ha)
1.	Days to 50 % flowering	**0.108**	-0.057	-0.0005	0.0074	0.0134	0.0287	-0.0446	0.0087	-0.0105	-0.0034	0.0494
2.	Days to maturity	0.056	**-0.110**	-0.002	0.0001	0.0001	0.0017	-0.059	-0.008	-0.005	0.000	-0.127
3.	Plant height (cm)	0.001	-0.005	**-0.037**	-0.041	-0.057	-0.238	-0.175	0.056	0.049	0.001	-0.447
4.	Earhead length (cm)	0.009	-0.0001	0.017	**0.088**	0.073	0.279	0.317	0.021	-0.022	-0.0033	0.780
5.	Number of spikelets	0.011	-0.0001	0.017	0.051	**0.125**	0.215	0.260	0.013	-0.029	-0.004	0.661
6.	Grains/spike	0.007	-0.0005	0.022	0.061	0.067	**0.401**	0.361	-0.022	-0.032	0.007	0.874
7.	1000 grains weight (g)	-0.011	0.015	0.150	0.064	0.074	0.331	**0.437**	0.015	-0.024	0.006	0.924
8.	Protein (%)	0.0046	0.0045	-0.010	0.009	0.008	-0.044	0.034	**0.202**	0.029	-0.009	0.229
9.	Zinc (mg/100 g)	-0.012	0.007	-0.021	-0.022	-0.042	-0.147	0.121	0.069	**0.087**	-0.007	-0.212
10.	Iron (mg/100 g)	0.010	-0.0001	0.001	0.008	0.016	-0.084	-0.080	0.054	0.019	**-0.034**	-0.034

4.5.2 Grain yield Vs. Days to maturity

The character days to maturity had negative direct effect (-0.110) on seed yield. It had positive indirect effect through days to 50 per cent flowering, earhead length, grains per spike, number of spikelets per earhead and negative indirect effect through plant height, 1000 grains weight, protein content, zinc content. The total genotypic correlation with seed yield was -0.1276.

4.5.3 Grain yield Vs. Plant height

The character plant height had negative direct effect (-0.0372) on seed yield. It had positive indirect effect through days to 50 per cent flowering, protein, zinc, iron content and negative indirect effect through days to maturity, earhead length, grains per spike, 1000 grains weight, number of spikelets. The total genotypic correlation with seed yield was -0.4474.

4.5.4 Grain yield Vs. Earhead length

The character earhead length had positive direct effect (0.0881) on seed yield. It had positive indirect effect through days to 50 per cent flowering, plant height, grains per spike, 1000 grains weight, number of spikelets, protein content and negative indirect effect through days to maturity, zinc content, iron content. The total genotypic correlation with seed yield was 0.7807.

4.5.5 Grain yield Vs. Grains per spike

The character grains per spike had positive direct effect (0.4013) on seed yield. It had positive indirect effect through days to 50 per cent flowering, plant height, earhead length, 1000 grains weight, number of spikelets, iron content and negative indirect effect through days to maturity, zinc content, protein content. The total genotypic correlation with seed yield was 0.8740.

4.5.6 Grain yield Vs. 1000 grains weight

The character 1000 grains weight had positive direct effect (0.4375) on seed yield. It had positive indirect effect through days to maturity, plant height, earhead length, grains per spike, number of spikelets, protein content, iron content and negative indirect effect through days to 50 per cent flowering and zinc content. The total genotypic correlation with seed yield was 0.9249.

4.5.7 Grain yield Vs. Number of spikelets

The character number of spikelets had positive direct effect (0.1257) on seed yield. It had positive indirect effect through days to 50 per cent flowering, plant height, earhead length, grains per spike, 1000 grains weight, protein content and negative indirect effect through days to maturity, zinc content, iron content. The total genotypic correlation with seed yield was 0.6612.

4.5.8 Grain yield Vs. Protein content

The character protein content had positive direct effect (0.2023) on seed yield. It had positive indirect effect through days to 50 per cent flowering, days to maturity, earhead length, 1000 grains weight, number of spikelets, zinc content and negative indirect effect through plant height, grains per spike, iron content. The total genotypic correlation with seed yield was 0.2295.

4.5.9 Grain yield Vs. Zinc content

The character zinc content had positive direct effect (0.0876) on seed yield. It had positive indirect effect through days to maturity, protein content and negative indirect effect through days to 50 per cent flowering, plant height, earhead length, grains per spike, 1000 grains weight, number of spikelets, iron content. The total genotypic correlation with seed yield was -0.2124.

4.5.10 Grain yield Vs. iron content

The character iron content had negative direct effect (-0.0346) on seed yield. It had positive indirect effect through days to 50 per cent flowering, plant height, earhead length, number of spikelets, protein content, zinc content and negative indirect effect through days to maturity, grain per spike and 1000 grains weight. The total genotypic correlation with grain yield was -0.0884.

The computed correlation coefficient values are useful in explaining the nature and extent of association existing between pairs of characters. The economic character like grain yield is dependent on several component characters which are mutually related. Correlation explains the true association existing between the component characters with dependent character (grain yield).

Slight change in any component will ultimately disturb the complex. Hence, a character has to be analyzed for its action which is done through path analysis where the two types of actions namely direct effect of component characters on seed yield are obtained which cannot be recorded by the correlation studies.

Path coefficient analysis was carried out to find out the direct and indirect contribution of each character towards the grain yield per plot. The correlation coefficient being more important, were only partitioned into direct and indirect effects which are presented in Table 6.

In the present study, Path coefficient analysis was carried out at genotypic level taking grain yield as dependent character and all the characters which exhibited significant association with grain yield were considered as independent characters. The results of path analysis are summarized in the Table 6 depicting that 1000 grains weight, grains per spike, protein content, number of spikelets had higher magnitude of positive and direct effects on grain yield. 50 per cent flowering, earhead length, zinc content had showed low but positive direct effect on grain yield.

Highest positive direct effect was exerted by 1000 grain weight on grain yield followed by grains per spike, protein content, number of spikelets, days to 50 per cent flowering, earhead length which is in conformity with the reports of Deshmukh *et al*. (1990) and Zeeshan *et al*. (2013) wherein they observed appreciable positive direct effect of 1000 grains weight. Direct selection for 1000 grains weight alone can bring about considerable improvement in the grain yield due to its high direct effect, positive and indirect effects through all the major yield contributing characters on seed yield.

Positive direct effect of seed weight on yield per plant was noticed and this was supplemented by positive indirect effects through stem girth, length of inflorescence, days to maturity. Ajmal *et al.* (2009) reported high direct effect of 1000 grains weight on grain yield. Hence, 1000 grains weight can also be considered during selection for improving yield in grain wheat.

4.6 Genetic Divergence

Estimation of genetic divergence by Mahalanobis D^2 statistics for 30 wheat genotypes with eleven characters provided genetic divergence.

4.6.1 Cluster formation

The cluster formation was done as per Tocher's method, as described by Rao (1952). The 30 genotypes of wheat under investigation were grouped into eight clusters in which cluster II was with thirteen genotypes emerged as the largest cluster. Cluster I was with nine genotypes, cluster III with three genotypes. The clusters IV, V, VI, VII, VIII contained 1 genotype each (Table 7).

Table 7. Distribution of 30 genotypes of wheat in to different clusters

Cluster	Number of genotypes included	Genotypes
I	9	NIAW-3386, NIAW-3578, NIAW-3553, NIAW-3575, NIAW-3633, HD-2932, NIAW-3562, NIAW-3636, NIAW-345
II	13	NIAW-3354, NIAW-3525, AKAW-4627, NIAW-3624, NIAW-3523, NIAW-1994 (Phule Samadhan), NIAW-3583, NIAW-3581, NIAW-301(Trimbak), MACS-6478,NIAW-3270, MACS-6222, NIAW-34
III	3	NIAW-3643, NIAW-3592, NIAW-3584
IV	1	NIAW- 3559
V	1	NIAW- 917 (Tapovan)
VI	1	NIAW- 3390
VII	1	NIAW- 3170
VIII	1	NIAW- 1415 (Netravati)

4.6.2 Intra and inter cluster distance

The intra and inter cluster D^2 and D values were worked out by D^2 statistics. The mean D^2 values of cluster elements were used as measures of intra and inter cluster distance. They are presented in Table 8.

The maximum inter cluster distance was observed between cluster III and VII (944.33) followed by cluster III and V (792.98), cluster VI and VII (685.91), cluster I and VII (583.22), cluster II and III (543.34), cluster VII and VIII (498.18).

The maximum Intra cluster divergence among the eight clusters revealed that cluster III had maximum intra cluster distance (135.48) followed by cluster II (134.32) and cluster I (100.60). The least intra cluster distance was observed for cluster IV, V, VI, VII, VIII (D =0).

Table 8. Average intra (diagonal) and inter (above diagonal) cluster D and D^2 (in bracket)values of 8 clusters formed from 30 genotypes of wheat

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**10.03 (100.60)**	17.69 (312.93)	13.20 (174.24)	16.08 (258.56)	23.13 (534.99)	14.02 (196.56)	24.15 (583.22)	14.02 (196.56)
II		**11.59 (134.32)**	23.31 (543.34)	14.31 (204.77)	14.70 (216.09)	21.21 (449.86)	13.96 (194.88)	16.42 (269.61)
III			**11.64 (135.48)**	21.62 (467.42)	28.16 (792.98)	17.10 (292.41)	30.73 (944.33)	17.15 (294.12)
IV				**0.00 (0.00)**	17.99 (323.64)	19.76 (390.45)	21.65 (468.72)	17.46 (304.85)
V					**0.00 (0.00)**	20.95 (438.90)	15.10 (228.01)	16.23 (263.41)
VI						**0.00 (0.00)**	26.19 (685.91)	11.89 (141.37)
VII							**0.00 (0.00)**	22.32 (498.18)
VIII								**0.00 (0.00)**

4.6.3 Cluster mean

Cluster means for eleven characters are presented in Table 9. It revealed a wide range of variability for most of the characters.

4.6.3.1 Days to 50 per cent flowering

Cluster I (59.61 days) was early for days to 50 per cent flowering followed by cluster II (59.69 days), cluster VII (60.50 days), however cluster VI (69.50 days) had late flowering.

4.6.3.2 Days to maturity

Cluster VII (97.50 days) was early for days to maturity followed by cluster III (101.50 days) and cluster II (105.38). However, However cluster VIII (115.50 days) shown the late maturity.

4.6.3.3 Plant height (cm)

Cluster VII (91.75 cm) recorded highest cluster mean for plant height followed by cluster V (89.10 cm), cluster II (85.02 cm) and cluster III (78.40) is dwarf.

4.6.3.4 Earhead length (cm)

Cluster VI (11.36) recorded highest cluster mean for earhead length followed by cluster I (11.36), cluster VIII (11.35) and lowest cluster mean V (9.55).

Table 9. Mean performance of cluster for 11 characters in 30 wheat genotypes

Characters / Clusters	Days to 50 % flowering	Days to maturity	Plant height (cm)	Earhead length (cm)	Yield (q/ha)	Grains / spike	1000 grains weight (g)	Number of spikelets	Protein content (%)	Zinc content (mg/100 g)	Iron content (mg/100 g)
I	59.61	104.83	78.47	11.36	63.16	48.78	48.65	14.39	11.59	4.10	2.95
II	59.69	105.38	85.02	10.27	50.76	39.73	43.96	13.62	11.81	4.21	2.91
III	61.50	101.50	78.40	10.49	62.55	50.00	48.93	14.50	11.62	3.89	2.67
IV	61.00	110.00	78.95	9.95	41.67	40.50	40.75	11.50	11.25	4.17	3.08
V	68.50	111.50	89.10	9.55	49.17	37.00	39.60	14.00	11.77	4.02	3.07
VI	69.50	109.50	83.20	11.72	65.33	50.00	47.50	14.50	12.15	4.49	3.07
VII	60.50	97.50	91.75	10.55	54.33	36.50	43.40	13.50	13.63	4.54	3.17
VIII	63.50	115.50	80.79	11.35	67.80	49.00	50.50	17.50	12.35	4.16	3.07

4.6.3.5 Grain yield (q/ha)

Cluster VIII (67.80) recorded highest cluster mean for yield per hectare followed by cluster VI (65.33), cluster I (63.16) and lowest cluster mean was observed in cluster IV (41.67).

4.6.3.6 Grains per spike

Cluster III and VIII (50.00) recorded highest cluster mean for grains per spike followed by cluster VIII (49.00), cluster I (48.78) and lowest cluster mean was observed in cluster VII (36.50).

4.6.3.7 1000 grains weight (gm)

Cluster VIII (50.50) recorded highest cluster mean for 1000 grains weight followed by cluster III (48.93), cluster I (48.65) and lowest cluster mean was observed in cluster V (39.60).

4.6.3.8 Number of spikelets

Cluster VIII (13.63) recorded highest cluster mean for number of spikelets followed by cluster VI and III (14.50), cluster V (14.00) and lowest cluster mean was observed in cluster IV (11.50).

4.6.3.9 Protein content

Cluster VII (67.80) recorded highest cluster mean for protein content followed by cluster VIII (12.35), cluster VI 12.15) and lowest cluster mean was observed in cluster IV (11.25).

4.6.3.10 Zinc content

Cluster VII (4.54) recorded highest cluster mean for zinc content followed by cluster VI (4.49), cluster II (4.21) and lowest cluster mean was observed in cluster III (3.89).

4.6.3.11 Iron content

Cluster VII (3.17) recorded highest cluster mean for zinc content followed by cluster IV (3.08), cluster V,VI,VIII (3.07) and lowest cluster mean was observed in cluster III (2.67).

Selection of elite genotypes with high *per se* performance for yield and yield contributing components with suitable genetic divergence among them is the most important and difficult job for starting any hybridization programme. It would be possible to identify desirable genotypes from the genetic variability estimated, but it is difficult to expect any extraordinary results from their progeny unless we have knowledge about divergence between them.

Mahalanobis (1936) developed the concept of D^2 statistics, which act as an important tool for plant breeders. The degree of divergence between biological population at genotypic level and the relative contribution of different components to the total divergence at both intra and inter cluster levels can be evaluated by this method. Rao (1952) first time suggested the application of this technique for the assessment of genetic diversity in plant breeding.

In the crop improvement programme genetic diversity is an important factor which is an essential pre-requisite for hybridization programme for obtaining high yielding progenies.

Quantitative measurements of genetic divergence among individual character have enabled to plant breeders for understand the racial affinities and evolutionary pattern in various species of cultivated plants as well as in making decision for the selection of best parental combination in hybridization programme. Inclusion of divergent parents in hybridization programme serves the purpose of combining desirable genes, so as to obtain desirable recombinants. Quantitative measurement of genetic diversity would be more useful in preliminary evaluation of genotypes under study.

The summarized information on intra-cluster (diagonal) and inter cluster distances among eight clusters is presented in the Table 8, which revealed that the intra- cluster distance value ranged from 0.00 to 135.48. The results of the intra-cluster distance indicated that, the presence of diverse accessions within different clusters, there by maximum amount of heterosis is expected in cross combination involving the genotypes of the most divergent clusters. Genotypes grouped into the same cluster presumably diverge little from one another as aggregates of characters measured. Theoretically, crossing of genotypes belonging to the same cluster is not expected to yield superior hybrids or desirable segregants. However, a general notion in theory exists that the larger is the divergence between the genotypes, higher will be the heterosis (Falconer, 1981). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses. Further, heterosis cannot be exploited in a highly self-fertilized crop. However, high heterosis might prove potential in isolating superior segregants in case of additive type of gene action.

Those genotypes included in Clusters with maximum inter-Cluster distance are obviously genetically more divergent. Hence, it would be logical to incorporate genotypes from these clusters in further breeding programmes. In this context,maximum inter cluster distance was observed between cluster III and VII (944.33). The minimum inter-cluster distance (141.37) was observed between cluster VII and VIII, indicating close genetic association between the genotypes of these two clusters. The maximum Intra cluster divergence among the eight clusters revealed that cluster III had maximum intra cluster distance (135.48) followed by cluster II (134.32) and cluster I (100.60). The least intra cluster distance was observed for cluster IV, V, VI, VII, VIII (D =0).

Assessment of the level and pattern of genetic diversity is an important component of breeding for crop improvement programme. It has diverse applications *viz.*, i) analysis of genetic variability ii) identification of diverse parental combinations to create genetic variability for further selection and iii) introgression of desirable genes from diverse germplasm into the available genetic base. The primary purpose of cluster analysis is to group individuals based on the characteristics they possess, so that individuals with similar description are mathematically gathered into the same cluster. There are various tools available for studying variability and the relationship among accessions based on their total seed proteins, isozymes and various types of molecular marker profiles. However, morphological characterization is the first step in the description and classifications of the germplasms. It has also been postulated that the more diverse parents, the greater are the chances of achieving the broad spectrum of variability in segregating populations.

4.7 Genetic divergence and selection of potent parent

Success of any crop improvement programme involves selection of best parent having high potential for the economically important characters. Among different approaches for selection of parents, selection based on diversity has its own significance, as diversity is a basic need of crop improvement. Therefore, in the present investigation diversity among different genotypes was studied, which yielded valuable information that could be useful in selection of potent parent for hybridization.

Hays and Johansson (1939) and East and Hays (1942) obtained great heterosis from crosses between diverse parent than those between closely related ones. Timothy (1963) reported that genetic divergence is one of the criteria for selecting the parents for hybridization; which may produce transgressive segregants in segregating generations. Bhatt (1970) advocated the use of multivariate analysis for the selection of parents. He also stated that statistical distance of all possible cluster combination may be considered arbitrarily as a guideline and suggested that it would be logical to effect crosses between genotypes belonging to cluster separated by high estimated statistical distance.

In the present study, an attempt was made to classify the cluster combination into four divergence classes by following the above procedure suggested by Arunachalam and Bandyopadhyay (1984). The statistical distance (D^2) given in Table 8, represents the index of genetic diversity among the clusters.

The mean of fourteen clusters and three intra-clusters was 18.18 and standard deviation 5.12. The minimum (X) and maximum (Y) values among these distances were 10.03 and 30.73, respectively. Thus, the divergence classes were as

Divergence Classes

	DC 4		DC 3		DC 2		DC 1	
↓		↓		↓		↓		↓
X		m-s		m		m+s		Y
(10.03)		(13.06)		(18.18)		(23.30)		(30.73)

On the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC2 and DC3. While crossing among the genotypes of a cluster, the *per se* performance of the genotypes for different traits such as earliness days to maturity, earhead length, number of spikelets per earhead, number of grains per earhead, grain yield per hectare, protein content, zinc content and iron content etc. should be taken into account, so that desirable transgressive segregants would be obtained after hybridization.

Table 10. Distribution of different clusters combinations into four divergence classes based on D^2 values between them. (Cluster Combinations)

DC 1 → Y (30, 70)
(I, VII), (II, III), (III, V), (III, VII), (VI, VII

DC 2 → m + s (23.30)
(I, V), (II, VI), (III, IV), (IV, VI), (IV, VII), (V, VI), (VII, VIII)

DC 3 → m (18.18)
(I, II), (I, III), (I, IV), (I, VI), (I, VIII), (II, IV), (II, V), (II, VII), (II, VIII), (III, IV), (III, VIII), (IV, V), (IV, VIII), (V, VIII), (V, VIII)

DC 4 → m-s (13.06)
(VI, VIII)

→ X (8.75)

Considering the cluster means presented in Table 9 source clusters are formed and are presented in Table 11. These source clusters provides desired parents for hybridization programmes for improvement in the characters shown against them are listed.

Table 11. Characters improvement on the basis of source clusters

Sr. No.	Characters	Source Clusters
1	Days to maturity (Early)	I, II,IV
2	Earhead length (Maximum)	I, VI, VIII
3	Number of spikelets per earhead (Maximum)	II, III, VIII
4	Number of grains per earhead (Maximum)	I, III, VIII
5	Grain yield per hectare (Maximum)	I, III, VI VIII
6	Protein content	II, VII, VIII
7	Zinc content	II, VII, VIII
8	Iron content	I, II, IV, VII

Keeping in view all the above aspects, the following genotypes in the present studies, deserve to be considered as potent parents for future crossing programme for improvement of grain yield and yield contributing characters.

Sr. No.	Genotypes	Sr. No.	Genotypes
1	NIAW-3170	8	NIAW-3553
2	Netravati	9	NIAW-34
3	HD-2932	10	Phule Samadhan
4	NIAW-3636	11	NIAW-3592
5	NIAW-3390	12	MACS-6222
6	NIAW-3386	13	NI-345
7	NIAW-3354	14	NIAW-3525

Considering the inter-cluster distance, cluster means and *per se* performance of genotypes and divergence class, the above genotypes may be utilized in future breeding programme for creating maximum spectrum of variability for different yield contributing characters which will facilitate to develop superior genotypes with respect to more than one characters and also possible to improve more than one character simultaneously.

Table 12. Tentative suggested crossing programme

Sr. No.	Characters to be improved	Cluster combination with inter cluster distance	Possible crosses
1.	Earliness days to maturity	I x II (17.69)	NIAW-3170 X NIAW-3270
		I x IV (16.08)	HD-2932 x NIAW-3559
2.	Earhead length	I x VI (14.02)	NIAW-3633 X NIAW-3390
		I x VIII (14.02)	NIAW-3553 X Netravti
3.	Number of spikelets	VIII x II (16.42)	Netravati x NIAW-3583
		I x III (13.20)	HD-2932 X NIAW-3592
4.	Number of grains per earhead	III x VIII (17.15)	NIAW-3592 X Netravati
		I x III (13.20)	NIAW-3553 X NIAW-3592
5.	Grain yield per hectare	I x VI (14.02)	HD-2932 X NIAW-3390
		VIII x I (14.02)	Netravati x NIAW-3633
		I x III (13.20)	NI-345 X NIAW-3584
6.	Protein content	II x VIII (16.42)	Phule samadhan X Netravati
		II x VII (13.96)	AKA-4627 x NIAW-3170
7.	Zinc content	VII x II (13.96)	NIAW-3170 x Phule Samadhan
		VIII x II (16.42)	Netravati x Phule Samadhan
8.	Iron content	IV x VII (21.65)	NIAW-3559 X NIAW-3170
		I x II (17.69)	NIAW-3575 X NIAW-3270

4.8 Per cent contribution of various characters for divergence

4.8.1 Per cent contribution of quantitative characters for divergence

The per cent contribution of the eight characters studied towards the total divergence is presented in Table 13. It was revealed that grains per spike (28.97 %) contributed highest for genetic divergence followed by number of spikelets (25.75 %), days to 50 per cent flowering (10.57), days to maturity (8.51), yield (6.44), 1000 grains weight (5.29), earhead length (4.60) However, the characters *viz.*, plant height (0.46) contributed least to genetic divergence.

4.8.2 Per cent contribution of nutritional characters for divergence

The per cent contribution of the three nutritional characters studied towards the total divergence was presented in Table 13. It was revealed that, iron (6.67 %) contributed highest for genetic divergence followed by zinc (1.84 %), protein (0.92 %).

Table 13. Per cent contribution of 11 characters for divergence in wheat

Sr. No.	Characters	Number of times appeared 1st in ranking	Per cent contribution
1.	Days to 50 % flowering	46	10.57
2.	Days to maturity	37	8.51
3.	Plant height (cm)	2	0.46
4.	Earhead length (cm)	20	4.60
5.	Yield (q/ha)	28	6.44
6.	Grains per spike	126	28.97
7.	1000 grains weight (g)	23	5.29
8.	Number of spikelets	112	25.75
9.	Protein content (%)	4	0.92
10.	Zinc content (mg/100 g)	8	1.82
11.	Iron content (mg/100 g)	29	6.67
	Total		**100.00**

5. SUMMARY AND CONCLUSIONS

The present investigation "Assessment of genetic variability for biochemical and yield attributes in wheat (*Triticum aestivum* L.)" was conducted with a view to estimate the genetic variability, genetic diversity and correlation for yield and yield contributing traits. The experiment was conducted during *Rabi* 2017-18 with thirty genotypes in Randomized Block Design with two replications. Observations were recorded for 8 morphological characters in field and for six characters in laboratory. The characters were days to 50 per cent flowering, days to maturity, plant height, earhead length, grain yield, number of grains per spike, 1000 grains weight, number of spikelets, protein content, Fe content, Zn content, sedimentation value and yellow berry percentage.

5.1 Variability, Heritability and Genetic advance

Fourteen characters were studied to estimate genetic variability and diversity for thirty genotypes. Considerable amount of variability was observed in the genotypes. Phenotypic coefficient of variation (PCV) was found to be marginally higher than the genotypic coefficient of variation (GCV) for all the characters, indicating the dominance of phenotypic coefficient of variation for expression of these traits.

Highest phenotypic coefficient of variation was exhibited by grain yield (14.78) followed by grains per spike (12.26), yellow berry percentage (10.83), number of spikelets (10.81), grain appearance score (10.39), 1000 grain weight (8.11), plant height (7.922) and earhead length (7.920).Comparatively lower Phenotypic coefficient of variation was observed for sedimentation value (6.79), protein content (6.55), Fe content (6.27), days to 50 per cent flowering (5.63), Zn content (5.27) and Days to maturity (4.959).

Heritability in broad sense ranged from 63.20 to 96.70 per cent. Highest estimate of heritability was recorded for number of grains per spike (96.70) followed by days to 50 per cent flowering (95.8), days to maturity (93.10), sedimentation value(92.20), 1000 grains weight (91.40), grain yield (91.70), grain appearance score (89.90), plant height (84.60), earhead length (84.10), Zn content (83.90), Fe content (83.10), protein content (79.90), yellow berry percentage (77.30) and number of spikelets (63.20).

Estimates of genetic advance ranged from 0.31 to 15.66. Highest estimate of Genetic advance was recorded for grain yield (15.66) followed by plant height (11.37), number of grains per spike (10.73), Days to maturity(10.03), 1000 grains weight (7.01), days to 50 per cent flowering (6.74), sedimentation value (6.36), number of spikelets (1.97), earhead length (1.46), yellow berry per cent (1.30), protein content (1.27), grain appearance score (1.02), Zn content (0.37) and Fe content (0.31).

Genetic advance as a per cent of mean was observed highest for grain yield (27.78 %) followed by number of grains (24.42 %), grain appearance score (19.24 %), yellow berry percentage (17.26 %), 1000 grains weight (15.26 %), number of spikelets (14.06 %), plant height (13.81 %), earhead length (13.72 %), sedimentation value (12.89 %), 50% flowering (11.11 %), protein content (10.78 %), Fe content (10.75 %), days to maturity (9.51 %) and Zn content (9.11 %).

1. High estimates of genotypic coefficient of variation among the genotypes indicates variability for the characters *viz.,* grain yield followed by grains per spike, yellow berry percentage, number of spikelets, grain appearance score, 1000 grain weight, plant height and earhead length.
2. The magnitude of PCV was more than GCV for all the characters.
3. High heritability coupled with high genetic advance was observed for the traits *viz.*, for grain yield and number of grains per spike were as high heritability along with moderate GAM was observed for number of grain appearance score and yellow berry percentage indicating that the heritability is due to additive gene effect and direct selection in early generations may be effective.

5.2 Correlation

Grain yield per plot recorded significant positive correlation with 1000 grains weight, number of grains per spike, earhead length, number of spikelets per earhead at both genotypic and phenotypic levels so these characters could be improved through selection. Whereas, grain yield showed non significant positive correlation with protein and days to 50 per cent flowering at genotypic as well as phenotypic level indicating that this variation due to by chance and grain yield is depend on this characters. While the character zinc, days to maturity, iron showed negative and non-significant correlation with grain yield at phenotypic level.

5.3 Path coefficient analysis

Path coefficient analysis revealed that 1000 grain weight had highest direct effect on grain yield per hectare followed by grains per spike, protein content, number of spikelets, days to 50 per cent flowering and earhead length therefore emphasis should be given on these characters while making selection for desired improvement for seed yield of wheat. While making selection for desired improvement in grain yield, emphasis may be given on characters *viz.,* 1000 grains weight, grains per spike, protein content, number of spikelets, days to 50 per cent flowering as these characters showed significant positive association with grain yield.

5.4 Genetic divergence

In the present investigation, the genotypes grouped into eight clusters, using Tocher's method as described by Rao (1952). Cluster II was with 13 genotypes each emerged as the largest cluster. Cluster I was with 9 genotypes, cluster III with 3 genotypes were larger clusters. The clusters IV, V, VI, VII, VIII were mono-genotypic.

The maximum inter cluster distance was observed between cluster III and VII (944.33) followed by cluster III and V (792.98), cluster VI and VII (685.91), cluster I and VII (583.22), cluster II and III (543.34), cluster VII and VIII (498.18) indicating that genetic constitution of the genotypes in one cluster had close proximity with the genotypes in other clusters of the pair. It is desirable to select accessions from clusters having high inter-cluster distance and

The maximum Intra cluster divergence among the eight clusters revealed that cluster III had maximum intra cluster distance (135.48) followed by cluster II (134.32) and cluster I (100.60) suggesting that the genotypes present in these cluster might have different genetic architecture and might have originated from different genetic pool, indicating wide divergence among these clusters.

On the basis of divergence classes (DC) crosses of genotypes from different clusters can be formulated for next programme and this was grouped on that crosses present between different clusters and separated by moderate genetic distance would give yield with heterotic effect of F_1 and transgressive seggregants in advance generation.

The D^2 analysis thus proved to be a very useful technique in isolating diverse groups from the genotypes under study.

1. There is substantial genetic diversity among the genotypes studied.
2. The thirty genotypes were grouped into eight clusters.
3. No parallelism between genetic diversity and geographical distribution was observed.
4. On the basis of inter cluster distances, cluster mean and *per se* performance and divergence class observed in the present study, the genotypes *viz.,* NIAW-3170, Netravati, HD-2932, NIAW-3390, NIAW-3386, NIAW-3354, NIAW-3553, Phule Samadhan, NIAW-3592, MACS-6222, NI-345, AKAW-4627, NIAW-3575, NIAW-3270, NIAW-3559 and NIAW-3525 were distinct and diverse and could be classified as promising genotypes. These genotypes may be used in crossing programme to achieve desired segregants in wheat.

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7. VITAE

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IN

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(GENETICS AND PLANT BREEDING)

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