"ASSESSMENT OF GENETIC DIVERGENCE IN WHEAT (*Triticum aestivum* L.)"

A thesis submitted to the

Mahatma Phule Krishi Vidyapeeth, Rahuri- 413 722
Dist. Ahmednagar, Maharashtra, India

By

Mr. BANKAR MAHESH BAPURAO

(Reg. No. 14/037)

in partial fulfillment 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,
MAHATMA PHULE KRISHI VIDYAPEETH
RAHURI- 413 722
MAHARASHTRA, INDIA

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Approved by

Dr. D. V. Kusalkar
(Chairman and Research Guide)

Dr. A. P. Padhye
(Committee Member)

Dr. D. A. Gadekar
(Committee Member)

Dr. R. S. Wagh
(Committee Member)

Dr. V. S. Wani
(Committee Member)

CANDIDATE'S DECLARATION

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

Place : Rahuri **(M.B.Bankar)**

Dated : / /2016

Dr. D. V. Kusalkar,
Professor of Agril. Botany,
PGI, MPKV Rahuri.
Maharashtra State, India.

CERTIFICATE

This is to certify that the thesis entitled, **“ASSESSMENT OF GENETIC DIVERGENCE IN WHEAT (*Triticum aestivum* L.)”** submitted to the faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra in partial fulfillment of the requirements for the award of degree of **MASTER OF SCIENCE (Agriculture)** in **Agricultural Botany (Genetics and Plant Breeding)** embodies the results of a piece of *bonafide* research work carried out by **Mr. Bankar Mahesh Bapurao** under my guidance and supervision, and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and the help received during the course of this investigation have been duly acknowledged.

Place : Rahuri
Date : / /2016

(D.V.KUSALKAR)
Research Guide

Dr. B. R. Ulmek,
Associate Dean,
PGI, MPKV Rahuri,
Maharashtra State, India.

CERTIFICATE

This is to certify that the thesis entitled, **"ASSESSMENT OF GENETIC DIVERGENCE IN WHEAT (*Triticum aestivum* L.)"** submitted to the faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar, Maharashtra, in partial fulfillment of the requirements for the award of degree of **MASTER OF SCIENCE (Agriculture)** in **Agricultural Botany (Genetics and Plant Breeding)** embodies the results of a piece of *bonafide* research work carried out by **Mr. Bankar Mahesh Bapurao** under the guidance and supervision of **Dr. D.V.Kusalkar**, Professor of Agril. Botany, PGI, MPKV Rahuri and that no part of this thesis has been submitted for any other degree or diploma.

Place : Rahuri **(B. R. ULMEK)**
Date : / /2016 Associate Dean

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Place: Rahuri *(M.B.Bankar)*

Date : / /2016

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LIST OF ABBREVIATIONS

-	:	minus
%	:	Percentage
σ^2_e	:	Environmental variance
σ^2_g	:	Genotypic variance
σ^2_p	:	Phenotypic variance
/	:	Per
+	:	Plus
<	:	Less than
=	:	Equal to
>	:	Greater than
C.D	:	Critical difference
C.V	:	Coefficient of variance
cm	:	Centimeters
D	:	Divergence
et al.	:	etc all (and others)
g	:	Gram
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
h^2 (b.s)	:	Heritability in broad sense
i.e	:	That is
No.	:	Number
PCV	:	Phenotypic coefficient of variation
Per se	:	Actual
R	:	Residual effect
S.E.	:	Standard error
via	:	through
viz.,	:	Videlicet (namely)
$\overline{X}$	:	General mean
Y	:	Yield

ABSTRACT

“ASSESSMENT OF GENETIC DIVERGENCE IN WHEAT
(*Triticum aestivum* L.)”.

By

BANKAR MAHESH BAPURAO
A Candidate for the degree
of
MASTER OF SCIENCE (AGRICULTURE)
In
Agricultural Botany
(Genetics and Plant breeding)

Research Guide	:	**Dr. D.V.Kusalkar**
Department	:	**Agricultural Botany**
Major field	:	**Genetics and Plant Breeding**

The present investigation “Assessment of genetic divergence in wheat (*Triticum aestivum* L.)” was undertaken to study the extent of genetic variability, heritability (broad sense), genetic advance, correlation and genetic divergence in 36 genotypes of wheat. The material was evaluated in randomized block design with two replications during Rabi-2014 at Post Graduate Research Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri.

Observations were recorded on ten characters *viz.*, days to 50 per cent flowering, days to maturity, spiklets per spike (no.),tillers per running meter(no.),plant height (cm),ear head length (cm), grains per ear head (no), grain yield per plant (g)1000 grain weight (g),and protein content (%).

Significant treatment mean sum of squares for all characters studied were observed. The trait grain yield per plant showed maximum GCV and PCV than other traits followed by grains per spike and spikelets per spike.

Environmental influence was less on expression of these characters as evident by narrow gap between genotypic and phenotypic coefficient of variation.

All characters showed high heritability except for days to maturity and thousand grain weight. The character days to 50% flowering showed high broad sense heritability with low genetic advance.

Grain yield per plant exhibited significant and positive correlation with tillers per running meter, grain per spike, ear head length, spiklets per spike and 1000 grain weight.

Substantial amount of genetic diversity was observed among 36 genotypes of wheat. All 36 genotypes were grouped into 7 clusters. Cluster II and IV were the largest among all clusters with 9 genotypes in each followed by cluster III (7 genotypes), cluster I (6 genotypes), Cluster VII (3 genotypes) while cluster V and VI contained solitary genotype each. The inter cluster distance (D) was ranged between 5.64 (cluster V and VI) and 10.50 (cluster VI and VII).

On the basis of inter cluster means and performance observed in the present study, genotypes AJINKYATARA, PHS-0622 and LOK BOLD were found to the superior genotypes for further improvement of yield.

1. INTRODUCTION

Wheat is a type of grass grown all over the world for its highly nutritious and useful grain. It is one of the annual or biennial grass having erect flower spikes and light brown grains. It is the world's largest cereal crop. 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.

Wheat was an important cultivated cereal in South-western Asia, which is 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 early Egyptians were developers of bread and the use of the oven and developed baking into one of the first large-scale food production industries." By 3000 BC, wheat had reached England and Scandinavia. A millennium later it reached China. The first identifiable bread wheat (*Triticum aestivum*) with sufficient gluten for yeaste breads has been identified using DNA analysis in samples from a granary dating to 1350 BC at Assiros in Greek Macedonia.

Wheat species are common wheat or bread wheat (*T. aestivum*) is a hexaploid species that is the most widely cultivated in the world which covers 90 per cent area. Spelt (*T. spelta*) is another hexaploid species cultivated in limited quantities. Spelt is sometimes considered a subspecies of the closely related species of common wheat (*T. aestivum*), in which its botanical name is considered to be *Triticum aestivum* sub sp. *spelta*. Tetraploid species durum (*T. durum*) is the only tetraploid form of wheat widely used today, and the second most widely cultivated wheat. Emmer (*T. dicoccum*) is tetraploid species, cultivated in ancient times but no longer in widespread use. Diploid Species Einkorn (*T. monococcum*) is a diploid species with wild and cultivated variants. Domesticated at the same time as emmer wheat, but never reached the same importance.

Wheat is self pollinated, cool season crop, which requires average temperature of 18^0C to 22^0C, and grows successfully in the areas receiving rainfall 750-1600 mm. Water requirement of wheat crop is about 40 ha cm. The self pollination is mainly due to chasmogamous condition of flowers. Wheat crop required 100 to 130 days between planting and harvest, depending upon climate, seed type and soil conditions.

Wheat is the world's most favored staple food. Wheat provides more nourishment for humans than any other food source. Wheat crop having more nutritional value, In 100 gm of hard red winter wheat contain about 12.6 gm of protein, 1.5 gm of total fat, 71 gm of carbohydrate (by difference), 12.2 gm of dietary fiber and 3.2 mg of iron (17% of the daily requirement); the same weight of hard red spring wheat contains about 15.4 grams of protein, 1.9 grams of total fat, 68 grams of carbohydrate (by difference), 12.2 grams of dietary fiber, and 3.6 mg of iron (20% of the daily requirement). Wheat protein is easily digested by nearly 99% of human population. Wheat also contains a diversity of minerals, vitamins and fats (lipids). With a small amount of animal or legume protein added, a wheat-based meal is highly nutritious.

Wheat is the second most important food crop after rice in terms of both area and production, India contributes 12 per cent to the world wheat pool. in India, During 2013-14 area under wheat cultivation was 30.59 m ha with the annual production of 95.91 m tones with an average productivity of 30.75 q/ha. In Maharashtra it occupied an area of 10.97 lakh ha with production of 16.02 lakh tonnes with an average productivity of 14.60 q/ha. Major wheat producing states are Punjab, Haryana, Uttar Pradesh, Bihar and Rajasthan which are located in the Indo-Gangetic Plains and accounts for 85 per cent of total wheat production in the India.

Genetic diversity serves as a way for populations to adapt for changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment. Genetic diversity plays a very important role in survival and adaptability of a species because when the environment changes, slight gene variations are necessary to produce changes in the species that enables it to adapt and survive. A species that has a large degree of genetic diversity among its population will have more variations from which to choose the most fit alleles.

A method used by Mahalanobis (1936) known as 'Mahalanobis' D^2 statistics is widely used to know genetic diversity in the available genotypes. The genetic diversity which is the basis of plant breeding produced due to inherent genetic differences in the plant species and is of major interest to the plant breeder. The D^2 statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. It helps to measure the force of differentiation at intra cluster and inter cluster levels and helps in selection of genetically divergent parents for their exploitation in hybridization programme. 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.

Yield is complex character which is controlled by poly genes thus, the effective selection for yield is a complex process. Association between yield and its component characters themselves can improve the efficiency of selection, Study of correlation between yield contributing characters and path coefficient analysis which give the total idea of direct and indirect effect of characters on yield which is useful to breeder in crop improvement programmes. Selection for an optimum genetic advance should be based on judiciously computed parameters. However, unfavourable association between desired characters under selection may result in genetic slippage.

Improvement in crop is based on selection of superior parents which generated superior traits to its progenies. More variation within species are useful for selection of parents. In the present investigation diverse genotypes of wheat were evaluated. On the basis of this study, superior genotypes can be investigated and can be used in crop improvement programmes.

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, 36 released and unique genotypes were used for assessing the diversity considering yield as one of the important selection criterion.

Effort has been made in the present study to evaluate a set of wheat genotypes with the following objectives.

- To study the genetic variability for yield and yield contributing characters in the wheat.
- To group the genotypes into different clusters.
- To study the correlation of yield with yield contributing characters.

2. REVIEW OF LITERATURE

Success of any breeding programme depends on the availability of variation and selection practice. The selection of elite genotypes requires the knowledge of quantitative traits. Being very vast literature is available on genetic diversity; heritability and correlation in wheat, the specific references related to wheat are included and reviewed under the following sub heads of genetic variability, heritability, genetic advance, correlation and genetic diversity.

2.1 Genetic variability and heritability

Johanssen (1909) demonstrated the distinction between genotype and phenotype and Nilsson-Ehle (1908) and East (1916) gave the concept of multiple factor hypothesis and proved that quantitative characters are inherited according to Mendel's laws. From these discoveries, it becomes clear that variability is resulted from the joint action of genotype and environment (Fisher, 1930). Charles and Smith (1939) and Power *et al.* (1950) partitioned genetic variance from total variance by use of estimate of environmental variance from the non-segregating population. This work made possible to use genotypic coefficient of variation (GCV) as a relative magnitude of genetic diversity present in the material and helps to compare the genetic variability present in different characters. Hutchinson (1940) provided means to compare genetic variability present in population for various traits. The statistical method to compare the genetic component of variance were given by Frankel (1947), Burton (1952) and Panse and Sukhatme (1995).

Camargo *et al.* (2000) stated that the objective of the present work was to estimate the variance and the narrow-sense heritability values for grain yield, spike length, rachis internode length and height of wheat plants (*Triticum aestivum* L.), as well as the environmental, phenotypic and genetic correlations between these characteristics. The narrow sense heritability values for plant height (0.608-0.861), spike length (0.406-0.667), rachis internode length (0.545-0.781) and grain yield (0.421-0.550) indicated that the great part of the verified genetic variability in the hybrid populations for these traits were due to additive gene action.

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 is able to maintain variability for selection of improved genotypes. High heritability estimates coupled with high genetic advance were observed 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. Selection based on number of grains per ear and biological yield may be effective for improvement in durum grain yield under normal and rainfed conditions.

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

Patil and Jain (2002) studied the nature and magnitude of variation of yield and yield components in sixteen wheat genotypes. High heritability was observed for all the characters except spikelets spike^{-1} and number of grains spike^{-1}.

Ashraf *et al.* (2002) conducted experiment to analyse the phenotypic and genotypic variation, heritability, genetic advance, correlation coefficient and path coefficient for yield and yield components in wheat under rainfed conditions. High heritability estimates coupled with high genetic advance were observed for spike length, 1000 grain weight and flag leaf area. They revealed that these characters were controlled by additive gene action and improvement may be expected by direct selection.

Wegrzyn *et al.* (2002) determined the heritability and inter relationships of traits such as grain yield, 1000 grain weight, days to heading and plant height. In winter wheat It was noted that all the traits except grain yield under study showed the highest heritability coefficients.

Munawar *et al.* (2003) reported significant differences among the genotypes in terms of number of days to 50 per cent heading, plant height, number of spikelet's spike^{-1}, grain yield and 100 kernel weight.

Singh *et al.* (2003) studied genetic variation in 45 wheat accessions, including five checks for days to flowering, days to maturity, flag leaf area, plant height, number of grains spike^{-1}, weight of grains spike^{-1}, spike length, 1000 grain weight and grain yield. Number of grains spike^{-1} recorded the highest genotypic and phenotypic coefficients of variation. The number of grains spike^{-1} exhibited maximum direct effect on grain yield, followed by spike length and 1000 grain weight.

Novoselovic *et al.* (2004) the objective of this study was to estimate gene effects and genetic variability for some quantitative traits of two winter wheat crosses (Soissons Zitarka and Soissons Sana) by generation mean analysis. Only complementary type epistasis was observed. The estimated values of narrow-sense heritability (h^2n) varied for plant height (54-81 %), number of heads plant^{-1} (9-76 %), number of grains spike^{-1} (11-99.8 %), grain weight spike^{-1} (23-73 %), grain yield plant^{-1} (21-78 %) and single grain weight (49.7-72 %). The adequacy of certain modes of inheritance as well as the importance and significance of gene effects and genetic components of variance for analyzed traits was dependent upon the particular cross combination and experimental site.

Singh and Supriya Kumari (2006) revealed that the estimate of genetic advance, genetic advances as per cent of mean, heritability and genetic coefficient of variability were higher for flag leaf area, number of effective tillers plant^{-1}, number grains spike^{-1} and grain yield plant^{-1} indicating the presence of additive gene action and importance of individual plant selection for the improvement of these traits.

Yousaf Ali *et al.* (2008) estimated variability parameters, correlations and path coefficients for eight metric traits i.e., plant height, number of productive tillers plant^{-1}, number of spikelet's spike^{-1}, spike length, number of grains spike^{-1}, fertility per cent, 1000 grain weight and yield plant^{-1}. Significant genotypic differences were observed 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. Moderate heritability was observed for number of productive tillers per plant and fertility per cent. High heritability estimates were recorded for plant height, number of spikelet's spike^{-1}, spike length, number of grains spike^{-1}, 1000 grain weight and yield plant^{-1}. These traits also indicated high genetic advance (except fertility %).

Ali *et al.* (2008) observed significant genotypic differences for all the traits studied in wheat indicating that there was 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 plant^{-1}, number of productive tillers plant^{-1} and number of grains spike^{-1}. While remaining traits recorded moderate to low PCV and GCV estimates. Moderate heritability was observed for number of productive tillers plant^{-1} and fertility percent. High heritability estimates were recorded for plant height, number of spikelets spike^{-1}, spike length, number of grains spike^{-1}, 1000 grain weight and yield plant^{-1}. These traits also indicated high genetic advance except fertility per cent.

Majumder *et al.* (2008) studied twenty spring wheat varieties to find out genetic variability and genetic association for grain yield and its component characters. 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 spike^{-1}, 100 grain weight, harvest index and grain yield.

Binod Kumar (2009) evaluated thirty genotypes of bread wheat *(Triticum aestivum* L.) for yield and other characters *viz.*, plant height, effective tillers plant^{-1}, grain yield plant^{-1}, spike length, grains spike^{-1} and 1000 grain weight exhibited high variability. The remaining traits showed moderate to low variability.

B. Subhashchandra *et al.* (2009) conducted an experiment to study the variability parameters, correlations and path coefficients for nine metric traits in the F_2 populations of 28 crosses derived through diallel mating system in tetraploid wheat. Significant genotypic differences were observed for all the traits studied indicating considerable amount of variation generated in the segregating population for each character. The highest genotypic and phenotypic coefficient of variation was observed for yield plant^{-1} followed by productive tillers plant^{-1}. Similarly, high heritability and genetic advance were also observed for these traits along with spike length and days to 50 per cent flowering indicating the scope for their improvement through simple selection.

Tazeen *et al.* (2009) conducted research with the objective to evaluate the genetic variability for quantitative traits and the direct and indirect contributions of important yield components towards grain yield as well as to identify the characters of at most importance that may be used as selection criteria in a wheat breeding program. The experimental material consisted of seeds of 95 synthetic elites of wheat. Agronomic characters were recorded including days to heading, flowering, anthesis, physiological maturity, grain filling period, plant height, biomass, number of spikes plant^{-1}, number of spikelet's spike^{-1}, spike length, grain yield, 1000 grain weight and harvest index. According to the obtained results, heritability among the traits, phenotypic correlation and their path coefficients were estimated. Harvest index exhibited highest heritability value of 83.31 per cent while 1000 grain weight showed minimum value of 42.32 per cent.

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 days to maturity, vegetative period and grain filling period for which the low magnitude was noted. High heritability coupled with high genetic advances was observed for days to emergence, plant height, spike length, grains spike^{-1} however, low heritability along with moderate genetic advance was observed for grain yield plant^{-1} which indicated that direct selection for grain yield may not be effective. Therefore, these characters should be considered as important components for grain yield and emphasis should be given to these traits in selection programme.

Kotal *et al.* (2010) observed highly significant differences and adequate genetic variability were observed among the genotypes for all the ten selected characters. In this context, it was found that numbers of effective tillers plant^{-1} and grain yield plant^{-1} were characterized by high GCV, high heritability and high genetic advance and would be effective for selection.

Danail Kahrizi *et al.* (2010) observed that the analysis of variance showed a significantly variation among genotypes for the characters plant height, number of tillers^{-1}, peduncle length, flag length, leaf dry weight, stem dry weight, spike dry weight, spike height, leaf area ratio and net assimilation rate. Heritability estimates were high for plant height, peduncle length, leaf dry weight, stem dry weight and net assimilation rate.

Kamboj (2010) studied twelve wheat genotypes under salinity conditions and grain yield plot^{-1} and harvest index recorded the highest phenotypic and genotypic variations. Also high heritability was recorded for grain yield plot^{-1} thus suggesting direct selection for yield would be effective under saline conditions.

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. Plant height and number of kernels spike^{-1} showed the highest phenotypic and genotypic coefficients of variations and genetic advance, whereas, days to maturity and test weight had the lowest values. Plant height exhibited highest heritability value of 98.3 per cent while number of spikelet's spike^{-1} showed minimum value of 36.4 per cent.

Kalim Ullah *et al.* (2011) observed significant genotypic differences for all measured traits, indicating a considerable amount of variation among genotypes. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highly significant ($P=0.05$) for spike length, days to 50 per cent flowering and plant height. High heritability estimates were recorded for plant height, days to 50 per cent flowering, days to heading, spikelet's spike^{-1} and spike length. Plant height, days to physiological maturity and spikelet's spike^{-1} also indicate high expected genetic advance. Based on the Euclidian dissimilarity distance, cluster analysis separated the wheat genotypes into four groups and nine different clusters.

Asaye *et al.* (2013) observed highest genotypic coefficient of variation for grain yield, thousand 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 eight characters, days to 50% flowering, days to maturity, plant height, tillers per plant, spike length, grains per spike, test 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% 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.

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 and reported significant differences among measured traits i.e. plant height, spike length, spikelet number, grain number, number of days to flowering, thousand 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) Studied genetic variability and correlation coefficients for some quantitative character in Bread wheat and 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 percent of mean (GAM).

2.2 Correlation studies

The yield is complex character dependent on many attributes of plants. The correlation studies helps in understanding the association between the traits. The chief genetic cause of correlation is pleiotropy and linkage (Falconer, 1981), because of which it becomes difficult to get the actual idea about positive or negative effect of genes. The path coefficient analysis is the solution to such problems as it measures the direct as well as indirect effect of various traits on yield.

Robinson *et al.* (1951) observed that the correlation values are of potential importance since selection is usually concerned with changing two or more traits simultaneously. Learner (1958) found them useful in construction of selection indices and predicting correlated response. 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.

Shrivastava *et al.* (1980) in their studies in rainfed wheat reported that the number of ears meter^{-1} and weight of grains ears^{-1} made the important contribution to grain yield and the effect of 1000 grain weight was negative and low.

Falcinelli *et al.* (1983) observed significant and negative association between days to 50 per cent heading and 1000 grain weight. While, positive significant association between plant height and 1000 grain weight was also observed.

Deshmukh *et al.* (1990) observed that the days to 50 per cent flowering had a positive and significant correlation with grain yield under rainfed condition but under irrigated conditions it was negative and non significant and also reported the significant positive correlation between grain yield and weight of 1000 kernels in durum wheat.

Camargo *et al.* (2000) estimate the variance, heterosis and heterobeltiosis, and the narrow-sense heritability values for grain yield, spike length, rachis internode length and height of wheat plants (*Triticum aestivum* L.), as well as the environmental, phenotypic and genetic correlations between these characteristics. The phenotypic correlations between plant height with grain yield and between spike length and rachis internode length were positive and significant to all crosses and showing associations between these characters; however the obtained results suggest that large F_2 populations will be required to ensure the frequency of desired recombinants, showing semi dwarf plants with high yield potential.

Chaudhari *et al.* (2000) computed correlation and path coefficients for plant height, flag leaf area, grains spike^{-1}, 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) worked out the variability, correlation and path analysis for ten characters from the study of fifty genotypes of bread wheat collected from India and Mexico under irrigated conditions. Spikes plant^{-1}, grains spike^{-1}, plant height and harvest index showed significant positive correlation with grain yield, whereas, spikes plant^{-1} and grains spikes^{-1} showed high positive direct effect on grain yield.

Budak and Yildirim (2002) observed that grain yield had positive significant correlations with days to heading and plant height for Kunduru where these correlations were negative for Ege 88. It was further revealed that protein contents had negative significant correlations with days to heading, plant height and grain yield.

Patil and Jain (2002) studied the nature and magnitude of variation for yield and yield components in sixteen wheat genotypes. High heritability was observed for all the characters except spikelet's spike^{-1} and number of grains spike^{-1}. They observed that grain yield had positive and highly significant correlation with number of tillers plant^{-1} and number of grains spike^{-1}, whereas it exhibited negative and non-significant correlation with days to heading, days to maturity, plant height and 1000 grain weight. The number of grains spike^{-1} had the highest positive and direct effect on grain yield, while a negative direct effect on yield was observed with the number of spikelet's spike^{-1}.

Wegrzyn *et al.* (2002) determined the heritability and inter relationships of traits such as grain yield, 1000 grain weight, days to heading and plant height. Genotypic correlation values exceeded phenotypic correlations. The highest positive correlation was observed in grain yield and 1000 grain weight. On the other hand, the correlation between yield and number of days to heading was observed to be negative.

Ansari (2002) studied the inter-relationship among grain yield and its components in bread wheat varieties. The association of grain yield with spike length, grain weight plant^{-1} and 100 grain weight was positive and significant, whereas it was significantly negative with plant height.

Ashraf *et al.* (2002) conducted experiment to analyse the phenotypic and genotypic variation, heritability, genetic advance, correlation coefficients and path coefficient for yield and yield components in wheat under rainfed conditions.

Golabady and Arzani (2003) evaluated 300 genotypes of durum wheat for the level of genetic variation. They recorded the data on days to heading, days to maturity, plant height, spike length, grain weight spike^{-1}, number of grains spike^{-1}, number of spikes in^{-2}, 1000 grain weight and grain yield. They observed considerable genetic variations for the traits studied. Grain yield was found to be positively and significantly correlated with days to heading, days to maturity, number of grains spike^{-1} and grain weight spike^{-1}.

Jamali *el al.* (2003) evaluated wheat lines for number of days to heading, plant height, number of grains spike^{-1}, main spike yield, grain weight, number of grains spikelet^{-1} and plot yield. The results of correlation analysis suggested that the number of grains spike^{-1} and spikelets^{-1} were positively and significantly correlated with main spike grain yield in all the genotypes. Combined correlation results indicated that grain weight was negatively correlated with days to heading, number of spikelet's and number of grains spike^{-1} however, positively correlated with plant height.

Lad *et al.* (2003) carried out experiment for estimate correlation and path coefficient in 24 diverse genotypes of wheat. The phenotypic and genotypic coefficients of variation were higher for yield plant^{-1}, productive tillers, grains spike^{-1} and grain weight spike^{-1}. The grain yield exhibited highly significant and positive correlation with productive tillers plant^{-1}, spikelets spike^{-1}, grains spike^{-1} and grain weight spike^{-1} at both genotypic and phenotypic levels.

Singh *et al.* (2003) conducted the experiment to estimate correlation in 50 genotypes of bread wheat. They revealed positive and significant correlation between effective tillers plant^{-1}, biological yield plant^{-1} and harvest index with grain yield plant^{-1}. However, days to heading had negative significant correlation with 1000 grain weight.

Singh *et al.* (2007) reported phenotypic and genotypic variation, heritability, genetic advance, correlation coefficients and path analysis for yield and yield contributing traits under three sowing conditions *viz.*, timely sown, late sown and very late sown. Harvest, index, biological yield meter^{-1}, canopy temperature depression, number of spikelet's spike^{-1} , ear length and number of grains spike^{-1} had direct positive effect on yield both at genotypic and phenotypic levels across the three environments.

Ali *et al.* (2008) revealed that, seventy local and exotic wheat genotypes were evaluated for variability parameters, correlations and path coefficients for eight metric traits i.e., plant height, number of productive tillers plant^{-1}, number of spikelet's spike^{-1}, spike length, number of grains spike^{-1}, fertility per cent, 1000 grain weight and yield plant^{-1}. Grain yield per plant showed highly significant positive correlation with number of productive tillers plant^{-1}, number of spiklets spike^{-1} and number of grains spike^{-1} and significant positive correlation with spike length.

Majumder *et al.* (2008) revealed that, twenty spring wheat varieties were studied to find out genetic variability and genetic association for grain yield and its component characters. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Spikes plant^{-1}, grains spike^{-1}, spike length, 100 grain weight and harvest index were the most important characters which possessed positive association with grain yield.

Anwar *et al.* (2009) revealed that grain yield plant^{-1} was positively and significantly correlated with number of tillers plant^{-1} and days to maturity at genotypic level but non-significantly correlated at phenotypic level. Days to maturity had positive genotypic correlation with grain yield plant^{-1}, number of tillers plant^{-1} and 1000-grain weight. Days to maturity and tillers plant^{-1} had positive direct effect on grain yield plant^{-1} also. Therefore, more days to maturity and more tillers plant^{-1} would be important selection criteria for improving grain yield plant^{-1} in the breeding material studied.

Anwar *et al.* (2009) observed significant genotypic differences among the genotypes. Correlation coefficients were computed for grain yield plant^{-1}, tillers plant^{-1}, spikelet's spike^{-1}, 1000 grain weight, spike length, days to heading, days to maturity and plant height from the F_1 crosses developed from four lines and three testers including their parents. The results revealed that grain yield plant^{-1} was positively and significantly correlated with number of tillers plant^{-1} and days to maturity at genotypic level but non-significantly correlated at phenotypic level. Days to maturity had positive genotypic correlation with grain yield plant^{-1}, number of tillers plant^{-1} and 1000 grain weight. Days to maturity and tillers plant^{-1} had positive direct effect on grain yield plant^{-1} also. Therefore, more days to maturity and more tillers plant^{-1} would be important selection criteria for improved grain yield plant^{-1} in the breeding material studied.

B. Subhashchandra *et al.* (2009) conducted an experiment to study the variability parameters, correlations and path coefficients for nine metric traits in the F_2 populations of 28 crosses derived through diallel mating system in tetraploid wheat. Positive and significant correlation of yield plant^{-1} with spike length and productive tillers plant^{-1} was observed, while days to 80 per cent maturity showed negative and significant association with spike length, plant height and protein content

Tazeen Mohsi *et al.* (2009) conducted research with the objective to evaluate the genetic variability for quantitative traits and the direct and indirect contributions of important yield components towards grain yield as well as to identify the characters of at most importance that may be used as selection criteria in a wheat breeding program. The experimental material consisted of seeds of 95 synthetic elites of wheat. Agronomic characters were recorded including days to heading, flowering, anthesis, physiological maturity, grain filling period, plant height, biomass, number of spikes plant^{-1}, number of spikelet's spike^{-1}, spike length, grain yield, 1000 grain weight and harvest index. Grain yield correlated positively with flag leaf area, plant height, biomass, number of spikes, spike length, number of spikelets spike^{-1}, number of grains spike^{-1}, 1000 grain weight and harvest index.

Kangarc *et al.* (2010) concluded that the seed yield showed positive and significant correlation with effective tillers plant^{-1}, grains spike^{-1}, spike length and 1000 grain weight both at genotypic and phenotypic level. Seed yield plant^{-1} showed positive direct effect of effective tillers plant^{-1}, plant height, 1000 grain weight and days to maturity. Thus, these characters may be effective as selection indices during breeding programme for improving wheat yield.

Kotal *et al.* (2010) studied the correlation and path coefficient analysis which revealed the importance of number of effective tillers plant^{-1}, number of spiklets panicle^{-1}, number of grains panicle^{-1} and harvest index for improving grain yield plant^{-1} as they had positive direct effects on yield and these traits were also significantly and positively correlated with grain yield plant^{-1}. So, for increasing grain yield plant^{-1}, a wheat genotype should have more number of effective tillers plant^{-1}, more number of spikelet's per panicle, more number of grains panicle^{-1} and high harvest index. In this regard the importance of large panicle length and more 1000 grain weight should not be under mined for yield improvement.

Oguz Bilgin *et al. (*2010) carried out study to estimate variation, heritability and correlation for milling characteristics of 25 durum wheat genotypes under rainfed conditions in three environment of north Turkey. Protein content showed positive significant correlation with wet gluten content (0.708), semolina colour (0.492) and vitreous grain (0.445) negative significant relationship of protein content were determined with 1000 grain weight (-0.539), and ash content (-0.446). Viterous grain was positively correlated with semolina colour (0.392) and both traits showed significant correlation with wet gluten content (0.338-0.462) and protein content (0.445-0.432) respectively. The significant and negative correlation coefficient (-0.288) was observed between protein content and grain yield.

Waquar Ul Haq (2010) concluded that the analysis of variance showed highly significant differences among the genotypes for all the traits. The correlation coefficient indicated that spike length, number of spikes plant^{-1}, number of spikelet's spike^{-1}, number of grains spike^{-1}, number of tillers per square m$^{2-1,}$ and 1000 grain weight were significantly and positively correlated with grain yield plant^{-1}, while days to heading, days to maturity and plant height showed non significant correlation with grain yield plant^{-1}.

Khan *et al.* (2010) concluded that estimates of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for all the character combinations. Seed yield was significantly and positively associated with number of spikelet's plant^{-1}, followed by number of effective tillers and 100 seed weight at both phenotypic and genotypic levels. Seed yield showed a significant negative association with number of seeds spikelet^{-1}. Among the significant inter-relationships, the association of days to 75 per cent spike emergence with days to maturity and 100 seed weight were significant and positive, but were negative and significantly associated with number of seeds spikelet^{-1} and number of grains spike^{-1}. Similarly, the associations of spike length with number of seeds spikelet^{-1} and number of spikelet's plant^{-1} and number of effective tillers were negative and significant. The association of number of spikelet's plant^{-1} with number of effective tillers was also positive and highly significant.

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 should 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) Studied correlation and path analysis in advance lines of Wheat, they observed that plant height exhibited positive correlation with hectoliter weight and tiller per plant showed positive correlation with yield per plant.

Khan *et al.* (2015) reported that correlation analysis exhibited significant positive genotypic and phenotypic association of grain yield with plant height, tillers m^{-2}, spike length and biological yield. Moreover, significant positive association of grain yield was observed with grains $spike_{-}^{1}$ and harvest index at phenotypic level only. Strong association of these traits with grain yield suggested that these traits could be safely used as selection criterion for further improvement in yield of wheat.

2.3. Genetic diversity

Genetic diversity is the genetic differences as observed between the genetic stocks with respect to individual trait or an array of traits. It is the result of inherent genetic variations present in the germplasm. The knowledge of nature and degree of genetic divergence is useful in selecting the desirable parents for breeding programme. Different workers in various crops have successfully utilized the selection criteria based on genetic divergence.

Mahalanobis (1936) described D^2 statistics as a tool for quantitative estimates of genetic divergence between the populations. Rao (1952) suggested more flexible method, which would replace the measurement on large number of characters, all of which contribute in some degree towards discrimination relatively few measurements.

Mahalanobis originally developed the concept of D^2 statistics in 1928. Rao (1952) suggested the application of this technique for assessment of genetic diversity in plant breeding.

Moll *et al.* (1962) reported no relationship between geographical distribution and genetic diversity and its reflection in expression of heterosis.

Allard (1961) concluded that genetic diversity and productivity are complexly related, while divergence stability appeared to be more simply related.

Murthy and Arunachalam (1966) studied on different crops and revealed that geographical distribution and genetic diversity could not be directly related in any of the crops.

Singh *et al.* (1996) grouped 24 genotypes of wheat into six clusters using Mahalnobis D^2 analysis. Cluster-I had 19 genotypes, while clusters II, VI each had a single genotype. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied. Maximum and minimum generalized distances were observed between clusters II and IV and between I and IV, respectively. Days to 50 per cent flowering, plant height, spikelet's ear^{-1}, biological yield plant^{-1} and 1000 grain weight contributed maximum to the total genetic divergence. The genotypes in clusters II and IV and those in II and V can be used as parents in hybridization programmes to develop high yielding wheat varieties.

Gartan *et al.* (2003) studied genetic divergence for quantitative characters in 68 bread wheat genotypes. The genotype grouped into 6 clusters. The greatest genetic distance was observed between clusters V and VI. Cluster-I had the highest mean value for grain yield and spike length and the second highest mean values for number of tillers and early maturity. Cluster-VI also recorded the greatest 100 seed weights.

Singh *et al.* (2005) studied genetic divergence for 12 characters in 24 wheat genotypes. Mahalanobis D^2 analysis grouped the genotypes into 6 clusters, with cluster-I comprising genotypes and other clusters consisting one genotype each. Maximum generalized distance was observed in between cluster-II and IV. Whereas minimum generalized distance was observed between cluster-I and IV, days to 50 per cent flowering, plant height, spikelet's ear^{-1}, biological yield plant^{-1} and 1000 grain weight had the highest contribution towards the total genetic divergence.

Arega Gashaw *et al.* (2007) studied genetic divergence based on multivariate analysis using Mahalanobis D^2 statistics which grouped the durum wheat genotypes into 10 clusters. The highest inter cluster distance was between cluster-II and cluster-III. The presence of significant genetic variability among the evaluated durum wheat genotypes suggested for hybridization.

Jaiswal *et al.* (2010) was assess genetic diversity for yield, yield contributing traits and quality traits in three hundred indigenous germplasm of bread wheat. The germplasm along with 4 checks were evaluated on the basis of dissimilarity coefficient, these genotypes were grouped into twenty three clusters each having certain mean value for characters under study. The genotypes bearing desired value from different clusters can be used in breeding program for improvement of yield as well as quality characters.

Kalim Ullah *et al.* (2011) was evaluated forty one wheat genotypes for genetic diversity regarding different metric traits, that is plant height, days to 50 per cent flowering, time to reach physiological maturity, spikelet's spike^{-1} and spike length. Significant genotypic differences were observed for all measured traits, indicating a considerable amount of variation among genotypes. Based on the Euclidian dissimilarity distance, cluster analysis separated the wheat genotypes into four groups and nine different clusters.

Hafida Zarkti *et al.* (2012) indicated that the evaluated germplasm comprises of useful variation for future breeding activities. Furthermore, the cluster analysis based on microsatellite data showed the closest correlation with the groupings of particular genotypes based on agro-morphological characters. The authors results suggest that the characterization based on agro morphological traits and genotypic markers will be a useful tool to the breeders to choose genotypes with appropriate diversity.

Kumar *et al.* (2013) observed inter-mating of K-816 and HUW-533 mono-cluster genotypes from cluster VI and VII showing maximum inter-cluster distance between them followed by mono- cluster genotype K-816 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 grouped 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 1 and cluster 4. 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 (D2=5112.1) followed by that between clusters III and IX (D2=4694.4) and VIII and IX (D2=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.

3. MATERIALS AND METHODS

The present investigation on "Assessment of Genetic divergence in wheat (*Triticum aestivum L.*)" was conducted at Post Graduate Research farm, PGI, MPKV, Rahuri. The details of the material used and methods followed are described in this chapter.

3.1 Material

The experimental material for the present investigation consisted of 30 genotypes and 6 checks (HD-2189, MACS-2496, NIAW-9947, NIAW-301, NIAW-34 and LOK-1) of bread wheat (*Triticum aestivum* L.) procured from the Agriculture Research Station, Niphad, Dist-Nashik were used for the present study. The list of genotypes is given in table 3.1

Table 3.1 Genotypes included in the studies

Sr. No.	Genotype	Pedigree
1	Ajinkyatara	-
2	AKAW 4210-6	DF-99-186 (Selection from 3rd SSN 1999-2000)
3	C-306	REGENT1974/3*CHZ//*C591/3/P19/C281
4	DBW-17	CMH79A.95/3*CNO79//RAJ3777
5	DBW-51	HD1963/HD1931
6	EXOTIC-21	
7	FLW-1	HD-4672/PDW-233[4281]; UP-2338/CENTURK
8	FLW-8	HI-1077/(THATCHER-Lr19)RL-6040
9	GUINEA-3	
10	H-961	CMH83.2517-1B-1Y-3B-0Y-2Y-OB
11	HALNA	HD 1982/K816
12	HD-2189	HD1963/HD1931
13	HI-1500	HW2002*2//STREMPALLI/PNC5
14	JOBNER	
15	KINGBIRD	TAM200/TUI/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
16	LOKBOLD	
17	LOK-54	LOK1/J.24/SONALIKA"S"//HW2006/RW2358/HW

		2002
18	MACS-2496	SERI”S”
19	MACS-6222	HD2189*2/MACS2496
20	MP-3097	C-306//RG11-4/CPAN 1882
21	NIAW-9947	MRL”S”/BUL”S” CM 61959-3M-4Y-1M-1Y-1M-OY
22	NIAW-1275	DL 218-6 / NIAW 600
23	NIAW-1342	CMH-771-917-BOW/HW 2008
24	NIAW-2300	HD 2781 / RAJ 4037
25	NIAW-301	SERI 2/3/MRS /JUP/HORK ‘S’
26	NIAW-34	CNO79/PRL”S”
27	NIAW-917	BOOMER33/PLATA8
28	PBW-343	ND/VG9144//KAL//BB/3/YACO’S’/4/VEE#5’S’
29	PHS-622	VS 1065 / PBW 343
30	PHS-830	LONG 94 444 / WH 542
31	LOK-1	S308/S331
32	RAJ-4083	PBW343/UP2442/WR258/UP2425
33	UP-2783	HW2017/CHOI XM95
34	WH-736	CMH81.137/CMH81.580
35	WSM-55	EDUIT51/DWR192
36	HD-2998	RL 6010/6*YR70//3*SERI82

3.2 Methods

3.2. Experimental design

The experiment was laid out in randomized block design. The field was divided into two homogeneous replications. Thirty genotypes along with Six checks were randomly planted in two replications. Each entry was represented by a double row of 2.8 m length spaced at 20 cm between the rows.

3.2.1. Sowing and cultural practices

A uniform piece of land was selected and brought to the fine tilth by ploughing and harrowing. A basal dose of 60 kg N, 60 kg P_2O_5, 40 kg K_2O per ha was applied at the time of sowing. Seeds were directly sown by dibbling. The spacing of 20 cm between the rows was kept. The remaining dose of 60 kg N was applied one month after sowing. The cultural practices like plant protection and weeding were followed as and when required during the crop growth period.

3.3 Observations recorded

Five plants were selected at random from each genotype in each replication. The randomly selected plants were tagged for recording observations on various morphological characters. At the time of harvest, these five selected plants were harvested separately. The following observations were recorded on five plants from each genotype at different growth stages of crop and average values per plant were worked out.

3.3.1 Morphological characters

i) Days to 50 percent flowering

The number of days required from the date of sowing to the date on which the 50 per cent of the population in a strain exhibited 50 per cent anthesis in the main earhead was recorded as days to 50 per cent flowering.

ii) Days to maturity

When the grains in spiklets become hard and easily removed from the glumes, that observation was recorded as maturity. The date of maturity recorded and number of days from sowing were counted as days required for maturity.

iii) Plant height (cm)

The plant height was measured in centimeters from ground level to the top of the main tillers and sub tillers at the time of harvest and mean for each treatment per worked out.

iv) No. of tillers per running meter

The tillers bearing spikes in one meter row length were counted at maturity and mean number of tillers per plant worked out for each treatment per replication.

v) Ear head length (cm)

The length of peduncle was measured from first top internode to the base of spike of main as well as sub tillers and average was worked out for each treatment per replication.

vi) No. of spiklets per spike

Total number of spiklets per spike of main and sub tillers were counted and mean number of spiklets per spike worked out for each treatment.

vii) Number of grains per spike

Total number of grains obtained from the spike of main tillers as well as sub tillers were counted and average number of grains recorded.

viii) Thousand grain weight (g)

One thousand grains from bulk sample randomly counted from each treatment per replication and weight of grains were taken in grams.

ix) Grain yield (g/plant)

Total dry weight of grains harvested from all tillers of plant were taken as grain yield per plant and expressed in grams.

3.3.2 Bio-chemical characters:

The analysis of protein was carried out by following standard biochemical procedure.

Estimation of Protein:

Seed sample from selected plant were grinded in a grinder and 0.2 g of grinded sample was analysed in laboratory for protein content. Per cent crude protein of the wheat sample was estimated by determining total nitrogen content of seeds by adopting Micro-Kjeldhal distillation method and per cent protein was calculated by using following formula.

$$\text{Protein } \% = \text{Nitrogen } \% \times 6.25$$

The per cent protein in seeds was calculated by multiplying per cent nitrogen in sample by 6.25 representing the common factor for material used.

3.4 Statistical Analysis

The mean values of five randomly selected observational plants for ten different traits were used for statistical analysis. The following statistical measures parameters were worked out for presentation of the data in different quantitative attributes.

3.4.1 Analysis of variance (ANOVA)

The analysis of variance was done as suggested by Panse and Sukhatme (1995) in following form

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

Where,

r = Number of replications,

t = Number of treatments,

e = Error

3.4.2 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

$\sum X_i$ = Sum total of characters

n = Number of observations

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

3.4.3 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.

3.4.4 Estimation of components of variation

The phenotypic and genotypic variances were calculated by utilizing the respective means square values from the variance table (Johnson *et al.,* 1955).

i. Environmental variance $(\sigma^2 e) = \mathrm{MSe}$

ii. Genotypic variance $(\sigma^2\, g) = \frac{(\mathrm{MSt} - \mathrm{MSe})}{\mathrm{r}}$

iii. Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \sigma^2 e$

Where, MSt = Treatment mean sum of square
MSe = Error mean sum of square
r = Number of replications

3.4.5 Estimation of coefficient of variation

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

i) Phenotypic coefficient of variation (PCV)

$$\mathrm{PCV\%} = \overline{\sigma^2 \mathrm{p}}\ \ \mathrm{X\ x\ 100}$$

Where,

σ^2p = Phenotypic variance

X = General mean of character

ii) Genotypic coefficient of variation (GCV)

$$\mathrm{GCV\%} = \overline{\sigma^2 \mathrm{g}}\ \ \mathrm{X \ x \ 100}$$

Where,

σ²g = Genotypic variance

X = General mean of character.

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

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

$$\mathrm{h^2\ \ b.s\ \ = (V_g\ \ V_p)x100\ \ or\ \ h^2\ \ b.s\ \ = (\sigma^2 g\ \ \sigma^2\ p)x100}$$

Where,

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

σ^2g =Genotypic variance

σ^2p= Phenotypic variance

The high, medium and low heritability estimates were classified on the basis of values given by Robinson (1966).

Low heritability = 5-10 percent.

Moderate heritability = 10-30 percent.

High heritability = 30-60 percent.

3.4.7 Estimation of genetic advance

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

$$\mathrm{GA = K\,x\ \ \sigma^2 g\ \ \sigma^2 p\ \ x\,\sigma p\ \ \ or\ \ \ GA = K\,x\,h^2\,x\,\sigma p}$$

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

σ^2g = genotypic variance

σ^2p = phenotypic variance

σ p = phenotypic standard deviation

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

X = Mean of the character

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

Less than 10 percent : Low
10 – 20 percent : Moderate
More than 20 percent : High

3.4.8 Estimation of Correlation coefficient

Analysis of co-variance was carried out by taking two characters at a time. The plot error was used as environment co-variance. The phenotypic and genotypic co-variance were derived as detail below:

Sr. No.	Source of Variation	Degree of Freedom	Mean product
1	Replication	(r-1)	
2	Treatment	(t-1)	MPt
3	Error	(r-1)(t-1)	MPe
	Total	(rt-1)	

Where,

r = no. of replications,
t = no. of treatments,
MPt = Treatment sum of product,
MPe = Error sum of product.

To understand the association among the characters, genotypic and phenotypic correlation coefficients were worked out by adopting method described by Singh and Chaudhari (1977).

a. Environmental co-varience

$$(\text{cov.e } x.y) = \text{MPe}$$

b. Genotypic co-variance

$$(\text{cov.g } x.y = \text{MPt-MPe}/r)$$

c. Phenotypic co-variance

$$(\mathrm{cov.px.y}) = (\mathrm{cov.e\ x.y}) + (\mathrm{cov.g\ x.y})$$

The appropriate variances and co-variances were used for calculating phenotypic, genotypic and environmental correlation coefficients (Johnson *et al.,* 1955).

3.4.8.1 Phenotypic correlation coefficient (r_p)

$$\mathrm{r_p\ x.y} = (\mathrm{cov.}_\mathrm{p}\ \mathrm{x.y}) \quad \overline{(\sigma^2\mathrm{p}_1).(\sigma^2\mathrm{p}_2)}$$

Where,

r_p $_{x.y}$ = phenotypic correlation between character x and y

$(cov._p\ x.y)$= phenotypic co-variance between character x and y

p_1 and $\sigma^2\mathrm{p}_2$= phenotypic variance of character x and y, respectively.

3.4.8.2 Genotypic correlation coefficient (r_g)

$$\mathrm{r_g\ x.y} = (\mathrm{cov.}_\mathrm{g}\ \mathrm{x.y}) \quad \overline{(\sigma^2\mathrm{g}_1).(\sigma^2\mathrm{g}_2)}$$

Where,

rg $_{x.y}$= genotypic correlation between character x and y

$(cov._g\ x.y)$= genotypic co-variance between character x and y

$\sigma^2\mathrm{g}_1$ and $\sigma^2\mathrm{g}_2$= genotypic variance of character x and y, respectively.

The significance of the phenotypic and genotypic correlation coefficient were tested by 't' test.

$$\mathrm{t} = \mathrm{r} \quad \overline{(\mathrm{n}-2) \quad (1-\mathrm{r}^2)}$$

Where,

r = Correlation coefficients

n = Total number of observations

The calculated 't' value was tested with table 't' value for respective (n-2) degrees of freedom for significance.

3.4.9 Mahalanobis generalized distance

The generalized distance between two population is defined by Mahalanobis (1936) as $D^2=\sum\sum \lambda i.j.\ di.\ dj$

Where,

$\lambda i.j$=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^2values 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 Chaudhari, 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.

3.4.10 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.

3.4.11 Average intra and inter cluster D^2 and D values

3.4.11.1 Average intra cluster D^2

The intra-cluster distances were calculated as

$$D^2 = \quad Di^2 \quad n$$

Where,

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

3.4.11.2 Average inter cluster D^2

The procedure followed for calculating the inter-cluster 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

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

Where,

ni = number of population in cluster i

nj = number of population in cluster j

3.4.11.3 Average intra and inter cluster distance (D)

$$D = \quad \overline{D^2}$$

3.4.11.4 Cluster means

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

3.4.11.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of $d_i = Yj_i - Yk_{j.}$ 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 Chaudhari, 1977).

3.4.11.6 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.

4. EXPERIMENTAL RESULTS

A study of the genetic variations is the first important step to breed for the high yield and quality as well as for disease resistance. The results obtained in the present investigation on "Assessment of Genetic Divergence in wheat (*Triticum aestivum L.*)" are described in this chapter.

4.1. Analysis of Variance

The analysis of variance for ten characters is presented in Table 4.1. It is revealed that there were highly significant differences among the genotypes for all the characters under study, showing wide range of variation in 36 genotypes of wheat.

4.2. Mean performance

The data on mean performance for ten characters of 36 genotypes of wheat is presented in Table 4.2.

4.2.1. Days to 50 percent flowering

The population mean for these characters was 56.34 days. The genotype EXOTIC-21 (50.50 days) was the earliest for 50 per cent flowering followed by WSM-55 (51.50 days) and RAJ-4083 (52.00 days). The check variety MACS-2496 (64.00 days) was late for 50 per cent flowering followed by UP-2783 (62.50 days), LOK-1 and PBW-343 (both showing 62.00 days). Out of 36 genotypes twenty genotypes (55.55%) were earlier in 50 per cent flowering than population mean.

4.2.2. Days to maturity

The population mean for this character was 108.41 days. The AJINKYATARA, HALNA, check variety NIAW-9947 and WSM-55 (102.00 days) all were matured early followed by RAJ-4083 (103.00 days) and check variety NIAW-34 (103.50 days). The check variety LOK-1 (118.00 days) and MACS-2496 (117.00 days) with genotype PBW-343 (116.50 days) were showing comparatively late maturity. From the thirty six genotypes studies eighteen genotypes (50.00%) were matured early than population mean (108.41 days).

4.2.3. Plant height (cm)

NIAW-1275 (92.69 cm) was tallest genotype among all genotypes, followed by check variety NIAW-301 (92.00 cm), PHS-830 (88.38 cm) and LOK-54 (88.13 cm). The genotype C-306 was dwarfest with only 73.36 cm height followed by check variety LOK-1 (74.31 cm), AKAW-4210-6 (75.41 cm) and H-961 (75.45 cm). Among the thirty six genotypes seventeen genotypes (47.22%) were taller than population mean (81.87cm).

4.2.4. Number of tillers per running meter

The variations for number of tillers per running meter were ranged from 96.50 (LOK-1) to 124.50 (PHS-0622) with population mean 110.48. Twenty one genotypes (58.33 %) showed more number of tillers per running meter than population mean. The genotype PHS-0622 (124.50) showed highest number of tillers per running meter followed by NIAW-1342 (122.50), DBW-17 (120.50) and GUINEA-3 (119.00). The check variety LOK-1 (96.50) having less number of tillers per running meter followed by WH-736 (97.50), JOBNER-828 (99.50) and NIAW-1275 (100.50).

4.2.5. Ear head length (cm)

The variation for ear head length was ranged between 7.62 cm (LOK-1) to 10.59 cm (PHS-0622) with population mean 8.64 cm. fifteen genotypes (41.66 %) produced highest ear head length than the population mean. The genotype PHS-0622 showed highest ear head length (10.59cm) followed by LOK-54 (9.84 cm) and DBW-17 (9.52 cm). The check variety LOK-1 (7.62 cm) showed lowest ear head length followed by KING BIRD (7.65 cm) and FLW-1 (7.67 cm).

4.2.6 No. of spiklets per spike

The variation for spiklets per spike was ranged between 13.00 (HALNA) to 18.20 (MACS-6222) with population mean 15.36. Fifteen genotypes (41.66 %) were showed more number of spiklets per spike than population mean. Genotype MACS-6222 (18.20) having more number of spiklets followed by PHS-0622 (17.90), LOK-54 and FLW-8 (both showing 17.60 spiklets per spike).The Genotypes HALNA, PBW-343 and check variety NIAW-9947 (13.00) showed less number of spiklets per spike.

4.2.7. Grains per spike (No.)

The variation for grains per spike ranged from 36.45 (LOK BOLD) to 58.60 (PHS-0622) with population mean of 45.75. Eighteen genotypes (50.00%) showed more number of grains per spike than population mean. The genotype PHS-0622 (58.60) showed highest number of grains per spike followed by

AJINKYATARA (55.00), MACS-6222 (53.80) and GUINEA-3 (52.60). Genotype LOK BOLD (36.45) having less number of grains per spiklets followed by PBW-343 (38.35) and RAJ-4083 (39.10).

4.2.8. Thousand Grain weight (gm)

The variation for thousand grain weight ranged from 38.54 gm (MACS-2496) to 55.50 gm (MP-3097) with the population mean 45.56 gm. Sixteen genotypes (44.44%) having highest thousand grain weight than population mean. Genotype MP-3097 (55.50 gm) recorded highest thousand grain weight followed by LOK BOLD (55.00 gm), AKAW-4210-6 (54.20 gm) and WSM-55 (51.78 gm). The check variety MACS-2496 (38.54 gm) showed less thousand grain weight followed by JOBNER-828 (39.97 gm) and LOK-1 (40.05 gm).

4.2.9 Grain yield per plant (gm)

The variation for grain yield per plant ranged from 9.14 gm. (NIAW-1275) to 23.14 gm (PHS-0622) with mean of 14.63 gm. Seventeen genotypes (47.22%) showed more grain yield per plant than the population mean. The genotype PHS-0622 (23.14 gm) recorded highest grain yield per plant among all genotypes followed by DBW-17 (20.88 gm.), GUINEA-3 (20.78 gm.) and NIAW-1342 (20.08 gm). The genotype NIAW-1275 (9.14 gm) recorded less grain yield followed by check variety LOK-1 (9.16 gm) and LOK BOLD (10.48 gm).

4.2.10 Protein content (%)

The variation for protein content ranged from 10.22 per cent (LOK-1) to 12.65 per cent (NIAW-301) with means 11.47

per cent. Seventeen genotypes (47.22%) recorded more protein content than the population mean. The check variety NIAW-301 (12.65%) showed more protein content than the other genotypes followed by WH-736 (12.40%) and NIAW-917 (12.39%). The check variety LOK-1 (10.22%) showed less protein content followed by JOBNER-828 (10.31%), C-306 (10.58%) and NIAW-1342 (10.80%).

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 summarized in Table 4.4. The important findings are discussed below

4.3.1 Coefficient of variation

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. The grain yield per plant (27.90) exhibited highest phenotypic coefficient of variation and the remaining characters expressed low phenotypic coefficient of variation viz. thousand grain weight (13.29), number of grains per spike (11.67), number of spiklets per spike (11.21), earhead length (9.02), number of tillers per running meter (7.88), plant height (6.38), days to 50 per cent flowering (5.83), protein content (5.70) and days to maturity (5.24).

The inherent genetic variability is expressed by the genotypic coefficient of variation. The character wise genotype coefficient of variation were *viz*. grain yield per plant (22.50) number of grains per spike (10.70), number of spiklets per spike (8.30), thousand grain weight (7.02), earhead length (6.96), plant height (6.05), days to 50 per cent flowering (5.60), protein content (5.32), number of tillers per running meter (4.98) and days to maturity (3.12).

4.3.2 Heritability (b.s.)

Heritability in broad sense ranged from 52.82 per cent for thousand grain weight to 96.20 per cent for days to 50 per cent flowering. High values were recorded for days to 50 per cent flowering (96.2%), plant height (94.83%), protein content (93.41%), number of grains per spike (89.91%), grain yield per plant (80.64%), ear head length (77.15%), no. of spiklets per spike (74.02%), number of tillers per running meter (63.19%), days to maturity (59.54%) and thousand grain weight (52.82%). All the characters showed high heritability except days to maturity and thousand grain weight.

4.3.3. Genetic advance

The highest magnitude of genetic advance was observed for the character plant height (5.63) followed by number of grains per spike (5.45), number of tillers per running meter (4.84), days to 50 per cent flowering (4.54), grain yield per plant (4.23), days to maturity (3.68) and thousand grain weight (3.37). The lowest magnitude of genetic advance was observed for the character ear head length (1.76) followed by protein content (1.96) and number of spikelets per spike (3.20).

4.3.4 Genetic advance as percent of mean

Genetic advance as per cent mean was observed highest in the character grain yield per plant (28.94) followed by protein content (27.10), number of spiklets per spike (20.83) and earhead length (20.47). The lowest magnitude of genetic advance as per cent mean was observed for days to maturity (3.40) followed by number of tillers per meter (4.38), plant height (6.68), thousand grain weight (7.42), days to 50 per cent flowering (8.06) and number of grains per spike (11.32).

4.4. Correlation

The table 4.5 represents the correlation coefficient between the characters with grain yield at both genotypic and phenotypic levels. The genotypic correlation is very important and it is described under following headings.

4.4.1. Genotypic correlation coefficient

Days to 50 per cent flowering

Days to 50 per cent flowering recorded positive and highly significant correlation with days to maturity (0.7718). while, positive but non significant correlation was noticed with protein content (0.1762), ear head length (0.0272) and plant height (0.0049). Days to 50 per cent flowering negatively and non significantly correlated with thousand grain weight (-0.3867), grain yield per plant (-0.2136), number of tillers per running meter (-0.1875), grains per spike (0.1825) and spikelets per spike (-0.1707).

Days to maturity

Days to maturity recorded negative and non significant correlation with all characters.

Plant height

Plant height recorded positive and highly significant correlation with protein content (0.3663), spiklets per spike (0.3470) and ear head length (0.3241). while positively but non significantly correlated with tillers per running meter (0.2171), grain yield per plant (0.1512), thousand grain weight (0.0762), grains per spike (0.0396).

Tillers per running meter

Tillers per running meter recorded positive and highly significant correlation with grain yield per plant (0.9562), grains per spike (0.7433), ear head length (0.5442) and number of spiklets per spike (0.5371), also it was positively but non significantly correlated with thousand grain weight (0.2044) and protein content (0.1175).

Ear head length

Ear head length recorded positive and highly significant correlation with grains per spike (0.6585), number of spiklets per spike (0.6146), grain yield per plant (0.6205) while positively but non significantly correlated with protein content (0.2247) and thousand grain weight (0.0471).

Spikelet's per spike

Spiklets per spike having positive and high significantly correlated with grains per spike (0.7278) and grain yield per plant (0.5587) also it was positively but non significantly correlated with protein content (0.1050) and thousand grain weight (0.0271).

Grains per spike

Grains per spike having positive and highly significant correlation with grain yield per plant (0.7717). also it was positively but non significantly correlated with thousand grain weight (0.1318) and protein content (0.0977).

Thousand Grain weight

Thousand grain weights recorded positive and significant correlation with grain yield per plant (0.2392), but negative non significant correlation protein content (-0.1172).

Protein content

Protein content recorded positive but non significant correlation with grain yield per plant (0.1125).

4.4.2 Phenotypic correlation coefficient

Days to maturity

Days to maturity having positive and highly significant correlation with days to 50 per cent flowering (0.7592).

Plant height

Plant height having positively and non significantly correlated with 50 per cent flowering (0.0051) while negatively and non significantly correlated with days to maturity (-0.0788).

Tillers per running meter

Tillers per running meter having positive and non significant correlation with plant height (0.2130). while negatively and non significantly correlated with 50 per cent flowering (-0.1956) and days to maturity (-0.2767).

Ear head length

The character ear head length having positive and highly significant correlation with tillers per running meter (0.5357) and plant height (0.3235) whereas positively but non significantly correlated with days to 50 per cent flowering (0.0278) and negatively correlated with days to maturity (-0.0015).

Spiklets per spike

The spiklets per spike having positive and highly significant correlation with ear head length (0.6096), tillers per running meter (0.5255) and plant height (0.3444) while negatively and non significantly correlated with days to 50 per cent flowering (-0.1676) and days to maturity (-0.0817).

Grains per spike

The grains per spike having positive and highly significant correlation with ear head length (0.6567), spikelets per spike (0.7224) and tillers per running meter (0.7311). Whereas positive and significantly correlated with days to and plant height (0.0398). The grains per spike were negative and non significantly correlated with days to maturity (-0.2538) and 50 per cent flowering (-0.1819).

Thousand grain weight

The thousand grain weight having positive and non significant correlation to ear head length (0.0446), spikelet’s per spike (0.0244), tillers per running meter (0.1849), grain per spike

(0.1260) and plant height (0.0726), whereas negative and non significantly correlated with days to 50 per cent flowering (-0.3571) and days to maturity (-0.3061).

Protein content

Protein content having positive and high significant correlation with plant height (0.3658). while positive and non significantly correlated with ear head length (0.2239), days to 50 per cent flowering (0.1757), spiklets per spike (0.1053), tillers per running meter (0.1161) and grains per spike (0.0975), whereas negative and non significantly correlated with days to maturity (-0.0412) and thousand grain weight (-0.1120).

4.5 Genetic Divergence

Estimation by Mahalanobis D^2 statistics for 36 genotypes with 10 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 36 genotypes under investigation were grouped into 7 clusters in which cluster II and IV was with 9 genotypes each emerged as the largest cluster. Cluster III was with 7 genotypes, cluster I with 6 genotypes and cluster VII with 3 genotypes were other larger clusters. The clusters V and VI contained 1 genotype each (Table 4.6).

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 4.7.

The maximum intra-cluster distance was observed for cluster VII (7.58) followed by IV (7.04) and II (6.33). The least intra cluster distance was observed for cluster V and VI (D =0).

The maximum inter cluster distance was observed between cluster VI and VII (10.50) and was followed by distance between cluster V and VII (10.14). The least inter cluster distance was observed between cluster V and VI (5.64), followed by I and IV (7.40) and cluster I and II (7.46).

Cluster I-

Cluster I had the largest distance from cluster V (D^2 =72.73), followed by cluster VII (D^2 =70.75), cluster VI (D^2 =65.19), cluster III (D^2 =61.79), cluster II (D^2 =55.77) and cluster IV (D^2 =54.83).

Cluster II-

The distance between cluster II and cluster VI was highest (82.50), followed by cluster V (80.54), cluster VII (61.63). Cluster II was closer to IV (59.03).

Cluster III-

The highest distance was observed between cluster III and cluster IV (76.68), followed by cluster VI (71.09) and cluster VII (65.47).

Cluster-IV

Cluster IV was distantly placed from cluster VII (89.81), while cluster IV was closer to cluster VI (65.86).

Cluster-V

Cluster V was distantly placed from cluster VII (102.82) while cluster V was closer to cluster VI (31.82).

Cluster-VI

Cluster V was distantly placed from cluster VII (110.33).

4.7 Cluster means

Cluster means for ten characters are presented in table 4.8. It revealed a wide range of variability for most of the characters.

4.7.1 Days to 50 per cent flowering

Cluster V (54.00 days) was early for days to 50 percent flowering followed by cluster II (54.44 days), cluster VII (55.83days) and cluster VI (56.00 days). However cluster IV (58.50 days) had late flowering.

4.7.2. Days to maturity

Cluster VII (105.83 days) the genotypes in this cluster shown early maturity followed by cluster II (106.72 days) and cluster V (107.00 days). However, the cluster IV (111.06 days) shown the late maturity followed by cluster I (109.08 days).

4.7.3 Plant height

The genotypes having high magnitude for plant height are grouped into cluster V (92.69 cm) followed by cluster III (88.15 cm) and cluster VI (87.75 cm). While, genotypes grouped into cluster I (78.34 cm) were dwarf followed by cluster IV (79.62 cm).

4.7.4 Tillers per running meter

Cluster mean for this character was maximum for cluster VII (117.50) followed by cluster II (114.78). While, minimum tillers per running meter were in cluster V and VI (100.50) followed by cluster IV (105.72).

4.7.5 Ear head length

The length of ear head ranged from 7.98 cm (cluster VI) to 9.62 cm (cluster VII). Cluster VII recorded highest cluster mean for this trait followed by cluster III (9.25 cm), cluster V (8.59 cm). While, cluster VI (7.98cm) exhibit lowest value followed by cluster IV (8.28 cm).

4.7.6 Spiklets per spike

Genotypes having more number of spikelet's per spike grouped into cluster III (16.67) where as cluster VI (13.50) having genotypes with less number of spikelet's per spike.

4.7.7 Grains per spike

The genotypes having more number of grains per spike were grouped into cluster VII (54.73), followed by cluster II (48.58) and cluster III (48.15). Whereas the genotypes having less number of grains per spike are grouped into cluster VI (36.45), followed by cluster V (40.40) and cluster IV (40.49).

4.7.8 Thousand grain weight

Range for this character varied from 43.29gm (cluster IV) to 55.00 gm (cluster VI). Cluster VI (55.00 gm) was having the group of genotypes containing highest thousand grain weight, followed by the cluster II (47.54 gm). Whereas the cluster IV (43.29 gm) were containing the genotypes with less thousand grain weights, followed by cluster I (43.80 gm).

4.7.9 Grain yield per plant

Considerable variability for grain yield per plant was observed with cluster mean. The cluster VII showed the highest mean (19.22 gm) followed by cluster II (16.49 gm) for this trait. Whereas, cluster V containing genotypes having less grain yield (9.14 gm) per plant.

4.7.10 Protein content

The highest cluster mean recorded for this trait in cluster I (12.02%) followed by cluster III (11.96%) and cluster VI (11.84 %). Whereas, the lowest cluster mean value was recorded for this trait in cluster II (11.02%), followed by cluster IV (11.03%).

4.8 Per cent contribution of various characters for divergence.

The per cent contribution of the 10 characters studied towards the total divergence was presented in Table 4.9. It was revealed that the grains per spike contributed highest (36.03 %) for divergence followed by plant height (25.71%), grain yield per plant (17.49%), protein content (10.33%) and ear head length (5.87%). Whereas, the per cent contribution for divergence was very less from days to 50 per cent flowering (0.16%), tillers per running meter (0.32), spiklets per spike (1.75%) and days to maturity (2.38%).

5.DISCUSSION

Variability and genetic diversity are the basic factors required for the success of any breeding programme and selection of elite genotypes. Many statistical methods are available to assess the available variability. Genotypic and phenotypic coefficient of variation allows evaluating the extent of variability present in the material under study, whereas the heritability suggested the relative role of genetic factors in expression of phenotypes (Falconer, 1981). It also acts as an index of inheritance of particular character to its offspring. However, knowledge of the heritability alone does not help in selecting genotypes for breeding programme. Heritability along with genetic advance will help to fix the possible genetic control for any particular character. All the variability parameters help to select the breeding method, where as the association analysis and path coefficient analysis explains the nature of dependency of yield and yield contributing characters on each other. The D^2 statistics suggested by Mahalanobis (1936) and clustering (Rao, 1952) guides to select the genetically diverse genotypes for hybridization programme.

In the present investigation, attempts were made to study the variability for 10 different morphological and biochemical characters among 36 genotypes, the correlation between the dependent and independent variables along with genetic diversity among all genotypes. The results on various aspects are discussed in this chapter under the following sub headings.

5.1 Genetic variability
5.2 Heritability and genetic advance
5.3 Correlation
5.4 Genetic divergence

5.1 Genetic variability

Considerable amount of variability was observed for all ten characters studied. The variability observed for grain yield per plant ranged between 9.14 gm to 23.14 gm with a mean of 14.63 gm. Along with yield, other yield contributing characters also showed good amount of variability *viz.*, days to 50 per cent flowering (50.50 to 64.00 days), days to maturity (102.00 to 118.00 days), plant height (73.3 to 92.69cm), ear head length (7.62 to 10.59 cm), number of spiklets per spike (13.00 to 18.20), number of tillers per running meter (96.5 to 124.5), number of grains per spike (36.45 to 58.60), thousand grain weight (38.54 to 55.5 gm) and protein content (10.22 to 12.65 %). Among 36 genotypes EXOTIC-21 and WSM-55 for days to 50 per cent flowering, AJINKYATARA and HALANA for days to maturity, C-306 and check variety LOK-1 for plant height, PHS-0622 and LOK-54 for ear head length, MACS-6222 and PHS-0622 for spiklets per spike, PHS-0622, NIAW-1342 and DBW-17 for tillers per running meter, PHS-0622 and AJINKYATARA for grains per spike, MP-3097 and LOK BOLD for thousand grain weight, check variety NIAW-301, WH-736 and NIAW-917 for protein content were found to be superior and recorded the highest performance for the respective characters.

While, comparing the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), it was observed that PCV estimates were magnitudinally higher than GCV for all characters indicating the influence of environment on these traits. The estimates of GCV and PCV were low magnitude in respect of days to maturity, days to 50 per cent flowering, tillers per running meter, protein content, plant height, earhead length, thousand grain weight, spiklets per spike, grains per spike and grain yield per plant. These results were in conformity with the findings of Chaturvedi and Gupta (1995) for characters days to 50 per cent flowering and plant height. Jay Shoran (1995) for days to maturity, Singh *et al.* (1996) for thousand grain weight and Singh *et al.* (2001) for number spiklets per spike.

5.2 Heritability and genetic advance

Heritability decides the resemblance of progeny with their parents (Falconer, 1981). While, genetic advance provides knowledge about expected gain for a particular characters after selection. In general, in self–pollinated crops, characters with high heritability possess high genetic advance, but when phenotypic variation in the population is low, genetic advance also tends to be low and vice–versa. This shows the variation and heritability are very much important for any breeding programme.

When heritability is moderate to high with larger magnitude of expected genetic advance for a particular character, it is said to be governed by additive gene action.

However, if high heritability with low genetic advance or low heritability with low genetic advance is observed for any given character, non-additive gene action may be suspected to be involved in the expression of the trait.

While evaluating 36 wheat genotypes high heritability was observed for all characters except thousand grain weight and days to maturity. Days to 50 per cent flowering recorded the maximum (96.2%) heritability followed by Plant height (94.83%), protein content (93.41%), grains per spike (89.91%), grain yield per plant (80.64%), ear head length (77.15%), spikelet's per spike (74.02%), tillers per running meter (63.19%), days to maturity (59.54%) and thousand grain weight (52.82%). These results were confirmed by the earlier findings of as Dixit (1990) for the plant height and days to maturity, Mandal *et al.* (1991) for the characters spike length, Mahmood and Shahid (1991) for the characters spiklets per spike and thousand grain weight and Kamboj *et al.* (2000) for grains per spike and Jitendrakumar and Lutra (1995) for days to 50 per cent flowering.

In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, protein content, ear head length, spiklets per spike. whereas, high heritability and moderate genetic advance as per cent of mean were obtained for no. of grains per spike. These results suggested the additive genetic variance for expression of these traits. High heritability coupled with high genetic advance were confirmed earlier by the Ozkan *et al.* (1997) for grains per spike and Rebetzke (1999) for plant height.

Whereas, high heritability coupled with low genetic advance was confirmed earlier by the findings of Jitendrakumar and Lutra (1995) for days to 50 per cent flowering.

5.3 Correlation

The information about relationship between the yield and yield components facilitate the choice of suitable breeding methods to be applied and selecting the parents for hybridization to improve the crop. The phenotypic and genotypic correlations have their own importance in breeding programme. The phenotypic correlation coefficient helps in determining selection index, whereas, genotypic correlation coefficient provides a close measure of association between characters and gives an indication of characters which may be useful for overall improvement of the crop. They may also help to identify characters that have little or no importance in the selection programme.

In the present investigation, it was observed that the genotypic correlation coefficient were higher in magnitude than their corresponding phenotypic correlation coefficient for all the characters. The traits ear head length, spikelet's per spike, tillers per running meter and grains per spike were positively and highly significantly correlated with grain yield per plant at both phenotypic and genotypic level and these results were in conformity with Khan and Bejwa (1999) for spiklets per spike, Jat and Dhakar (2003) for tillers per meter. Whereas, thousand grain weight was positively and significantly correlated with grain yield per plant similar results were obtained by Naik (2000).

Protein content and plant height were positively and non significantly correlated with grain yield per plant at both phenotypic and genotypic level. Days to 50 per cent flowering and days to maturity were negatively and non significantly correlated with grain yield per plant.

5.4. Genetic divergence

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 extra ordinary 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.

5.4.1 Clusters, intra and inter-cluster distance and mean performance

The basic concept behind the formation of clusters is to get intra and inter cluster distance. This acts as an index for selection of parents with diverse origin. The intra and inter cluster values are means derived from D^2 values of cluster elements. The crossing between the genotypes in different clusters with high inter cluster D^2 values will prove to be more correct approach to get desirable results.

Total 7 clusters were formed by using the Tocher's method as described by Rao (1952) from 36 genotypes. The distribution of genotypes into clusters is presented in Table 4.6. Cluster II and IV were largest with 9 genotypes followed by cluster III (7 genotypes), cluster I (6 genotypes), cluster VII (3 genotypes) While cluster V, VI were monogenotypic. In present investigation on grouping of genotypes into seven clusters suggested the presence of substantial amount of genetic diversity in the material under investigation.

The maximum intra-cluster distance was observed for luster VII (7.58) followed by IV (7.04) and II (6.33) suggesting that the genotypes present in these clusters might have different genetic architecture (Table 4.7).

Maximum inter cluster distance was observed between clusters VI and VII (10.50) and was followed by distance between clusters V and VII (10.14) indicating wide divergence among these clusters. It also suggested that genotypes present in one cluster differ entirely from those present in other cluster. The minimum inter cluster distance was found between clusters V and VI (5.64), indicating that genetic constitution of the genotypes in one cluster had close proximity with the genotypes in other clusters of the pair.

Based on the mean performance of the clusters for 10 characters (Table 4.8) it was observed that the cluster VII exhibited the magnitudinally higher grain yield per plant than all clusters. Cluster V having genotypes which were early in flowering and cluster VII was early in maturity. According to mean performance it shows that cluster III and cluster II were performing well for most of the characters studied.

Table no. 5.4. Promising parents for hybridization

Sr. no.	Characters	Cluster Source	Superior genotypes
1	Earliness to flowering	**V, II**	NIAW-1275, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GIANI-3, MACS-6222.
2	Earliness to maturity	**VII, II, V**	AJINKYATARA, HI-1500, PHS-0622, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GIANI-3, MACS-6222, NI-1275.
3	Plant height	**I, IV**	H-961, HD-2998, NIAW-917, WH-736, NIAW-2300, KINGBIRD, HALANA, RAJ-4083, NI-9947, JOBNER-828, MACS-2496, UP-2783, PBW-343, C-306, LOK-1.
4	Tillers per running meter	**VII, II**	AJINKYATARA, HI-1500, PHS-0622, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GIANI-3, MACS-6222.
5	Ear head length	**VII, III**	AJINKYATARA, HI-1500, PHS-0622, HD-2189, MP-3097, PHS-830, DBW-17, NIAW-301, NIAW-34, LOK-54.

6	Spiklets per spike	**III, VII**	HD-2189, MP-3097, PHS-830, DBW-17, NIAW-301, NIAW-34, LOK-54, AJINKYATARA, HI-1500, PHS-0622.
7	Grains per spike	**VII, II**	AJINKYATARA, HI-1500, PHS-0622, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GUINEA-3, MACS-6222.
8	Thousand grain weight	**VI, II**	LOK BOLD, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GIANI-3, MACS-6222.
9	Grain yield per plant	**VII, II**	AJINKYATARA, HI-1500, PHS-0622, FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GIANI-3, MACS-6222.
10	Protein content	**I, III**	H-961, HD-2998, NIAW-917, WH-736, NIAW-2300, KINGBIRD, HD-2189, MP-3097, PHS-830, DBW-17, NIAW-301, NIAW-34, LOK-54.

On the basis of cluster means and performance observed in the present study, the hybridization programme is suggested which involves the genotypes, so that the better recombinants may be obtained in the segregating generation.

The D^2 analysis thus proved to be a very useful technique in isolating diverse groups from the germplasm under study. On the basis of cluster means and performance observed in the present study the three genotypes *viz.* LOK BOLD, AJINKYATARA and PHS-0622 were found to be superior and can be used as a potent parent for improvement of wheat.

5.1 Salient features of three promising wheat entries

Sr. no.	Genotypes	Seed yield per plant	Spiklets per spike	Grains per spike	Thousand grain weight	Earhead length	Protein content
1	LOK BOLD	10.48	13.50	36.45	55.00	7.98	11.83
2	AJINKYATARA	15.27	15.00	55.00	42.71	9.11	11.79
3	PHS-0622	23.14	17.90	58.60	47.70	10.59	11.21

5.4.2. Relative contribution of various characters for divergence.

The per cent contribution of the ten characters studied towards the total divergent was presented in Table 4.9. It revealed that grains per spike contribute highest (36.03 %) for divergence followed by plant height (25.71%), grain yield per plant (17.49%), protein content (10.33%) and ear head length (5.87%) as main characters contributing to the genetic divergence in present material. Whereas days to 50 per cent flowering (0.16%), tillers per running meter (0.32%), spikelets per spike (1.75%), days to maturity (2.38%) contributed least toward divergence.

6. SUMMARY AND CONCLUSIONS

The present investigation "Variability, correlation and D^2 in wheat" was conducted with a view to estimate and analyse the variability, to determine correlation between yield and yield components. The experiment possesses thirty six genotypes and accordingly trial was conducted. The experiment was conducted during *Rabi* 2014-2015 using Randomized Block design with two replications. Observations were recorded on five randomly selected plants in each treatment for ten different characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, ear head length, spikelet's per spike, tillers per running meter, grains per spike, thousand grain weight, protein content, and grain yield per plant.

A. Variability and genetic parameters

Ten characters were studied to estimate genetic variability and genetic parameter in the genotypes. Sufficient 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.

The grain yield per plant trait showed maximum GCV and PCV than other traits followed by grains per spike and spiklets per spike. The least GCV and PCV were recorded for days to maturity followed by tillers per running meter and protein content. Environmental influence was less on expression of these characters as it was evident by narrow gap between genotypic and phenotypic coefficient of variation.

In present study all characters showed high heritability except days to maturity and thousand grain weight. The estimates of heritability (b.s.) exhibited the range from 52.82 to 96.02 per cent. The maximum heritability observed for days to 50% flowering (96.2%) followed by plant height (94.83%) and protein content (93.41%). The range of genetic advance was between 1.76 to 5.63.

The expected genetic advance expressed as percentage over mean exhibited high magnitude for traits grain yield per plant (28.94), protein content (27.10), spiklets per spike (20.83) and ear head length (20.47). On the contrary low estimates were found for days to maturity (3.40), tillers per running meter (4.38), plant height (6.68), thousand grain weight (7.42) and days to 50 per cent flowering (8.06).

High heritability coupled with high genetic advance as percent of mean was observed for grain yield per plant, no. of spikelets per spike and earhead length suggesting additive gene action in these traits and scope for selection for these characters indicated additive gene action in the inheritance of these characters.

In present study, genotypic correlation in general was higher than the corresponding phenotypic correlation. Grain yield per plant was highly significant and positively correlated with tillers per running meter, ear head length, spiklets per spike and grains per spike and significantly and positively correlated with thousand grain weight. While studying the association among component characters, plant height significantly correlated with ear head length, spiklets per spike and protein content. The character tillers per running meter was significantly correlated with ear head length, spiklets per spike and grains per spike. The character ear head length was significantly correlated with spiklets per spike and grains per spike. The character spiklets per spike was significantly correlated with grains per spike. The character grains per spike was correlated with thousand grain weight and protein content while, the character thousand grain weight with protein content. These results suggest inter dependency of these characters on each other and simultaneous association between them.

B. Genetic divergence

In the present investigation, The genotypes grouped into seven clusters, following Tochers method as described by Rao (1952). Cluster II and IV was largest with 9 genotypes in each followed by cluster III (7 genotypes), cluster I (6 genotypes), cluster VII (3 genotypes), while cluster V and VI were monogenotypic. There was no parallelism between genetic diversity and geographical distribution.

The maximum intra-cluster distance was observed for cluster VII (7.58) followed by IV (7.04), II (6.33) suggesting that the genotypes present in these cluster might have different genetical architecture and might originated from different genetic pool. The maximum inter cluster distance was observed between cluster VI and VII (10.50) and was followed by distance between cluster V and VII (10.04) indicating wide divergence among these clusters. This suggested that genotypes present in one cluster differ entirely from those present in another cluster. The minimum inter cluster distance was found between clusters V and VI (5.64), 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 also with high grain yield as parents in the recombination breeding programmes.

Out of ten characters studied, grains per spike contribute highest (36.03 %) for divergence followed by plant height (25.71%), grain yield per plant (17.49%), protein content (10.33%) and ear head length (5.87%) as main characters contributing to the genetic divergence in present material. Whereas days to 50 per cent flowering (0.16%), tillers per running meter (0.32%), spikelets per spike (1.75%), days to maturity (2.38%) contributed least toward divergence.

The D^2 analysis thus proved to be a very useful technique in isolating diverse groups from the germplasm under study. On the basis of cluster means and performance observed in the present study the seven genotypes *viz.* LOK BOLD, AJINKYATARA and PHS-0622 were found to be superior and can be used as a potent parent for improvement of wheat.

Sr. no.	**Character**	**Source of cluster**	**Name of genotype**
1	Thousand grain weight.	VI	LOK BOLD
2	Grain yield per plant, Spikelets per spike, Grains per spike, Tillers per running meter, Earhead length.	VII	PHS-0622
3	Grains per spike, Days to maturity.	VII	AJINKYATARA

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8. VITA

Mr. BANKAR MAHESH BAPURAO

A candidate for the degree of

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(GENETICS AND PLANT BREEDING)
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Title of thesis	:	“Assessment of Genetic divergence in wheat (*Triticum aestivum* L.)”
Major field	:	Genetics and Plant Breeding

Biographical information

Personal	:	Born on 29th Aug 1992 at Mirajgoan, Tal Karjat, Dist. Ahmednagar (M.S.), Son of Sau. Sindhu B. Bankar and Shri. Bapurao N. Bankar.
Educational	:	Passed S.S.C. from Shri Bhairavnath Vidyalaya Nimbavi, Tal- Shrigonda, Dist-Ahmednagar, in 2008 with first class.
	:	Passed H.S.C. from Shri. Chhatrapati Shivaji Mahavidyalaya Shrigonda, Dist-Ahmednagar, in 2010 with first class.
	:	Received Bachelor of Science (Agriculture) degree with first class with distinction in 2014 from College of Agriculture, Kolhapur.
Address	:	A/P- Erandoli, Tal- Shrigonda, Dist : Ahmednagar 413703
E-mail	:	mahibankar92@gmail.com

Table 4.1 Analysis of variance for 10 characters in wheat

Sr. No.	**Characters**	**Mean Sum of Square**		
		Replication (1)	**Genotypes (35)**	**Error (35)**
1	Days to 50% flowering	0.125	20.794**	0.1821
2	Days to maturity	0.222	40.928**	0.1936
3	Plant height (cm)	0.044	50.179**	0.0307
4	No. of tillers/running meter (No.)	0.347	93.471**	1.3757
5	Ear head length (cm)	0.004	0.915**	0.0012
6	No. of spikelet's /spike	0.056	4.497**	0.0237
7	No. of grains / spike	0.036	52.41**	0.0421
8	1000 grain weight (g)	2.595	34.44**	1.4694
9	Grain yield/plant (g)	0.022	26.96**	0.0044
10	Protein content (%)	-	0.7524**	0.0005

*,** significant at 5% and 1% probability respectively.

Values in parenthesis indicate degrees of freedom.

Table 4.2 Mean performance of 36 genotypes for 10 characters in wheat

Sr. No.	Genotypes	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Tillers / running meter (No.)	Ear head length (cm)	No. of Spikelets /spike (No.)	Grains/ spike (No.)	Thousand grain weight (g)	Grain yield/plant (g)	Protein %
1	**AJINKYATARA**	58.00	102.00	76.65	109.50	9.11	15.00	55.00	42.71	15.27	11.79
2	**AKAW-4210-6**	53.50	109.00	75.41	112.50	8.52	14.10	46.99	54.20	16.36	10.94
3	**C-306**	59.00	115.00	73.36	113.50	8.21	14.59	41.80	45.19	12.63	10.58
4	**DBW-17**	56.50	105.00	86.98	120.50	9.52	16.50	52.35	50.50	20.88	12.01
5	**DBW-51**	58.50	110.00	80.70	111.00	8.55	15.60	49.95	46.04	14.12	11.23
6	**EXOTIC-21**	50.50	105.00	80.75	111.50	8.55	17.30	45.90	46.58	14.73	10.80
7	**FLW-1**	54.00	108.50	83.17	112.00	7.67	15.10	45.75	43.18	14.51	10.98
8	**FLW-8**	57.00	104.00	85.65	115.50	8.59	17.60	47.40	46.30	17.66	11.17
9	**GUINEA-3**	55.00	105.00	76.93	119.00	8.71	15.10	52.60	48.97	20.78	11.13
10	**H-961**	56.00	109.00	75.45	108.50	8.63	14.60	43.90	45.44	15.62	12.25
11	**HALNA**	55.00	102.00	76.62	104.00	8.56	13.00	40.50	48.15	12.52	10.90
12	**HD-2189**	56.00	107.00	86.70	111.00	9.19	17.20	46.30	43.16	12.06	12.23
13	**HI-1500**	54.50	106.00	77.49	118.50	9.16	16.20	50.60	44.10	19.26	12.16
14	**JOBNER-828**	57.00	113.00	83.11	99.50	8.83	14.90	40.80	39.97	13.10	10.31
15	**KINGBIRD**	53.50	106.50	80.35	110.50	7.65	15.10	45.50	42.29	11.66	11.46
16	**LOK BOLD**	56.00	108.50	87.75	100.50	7.98	13.50	36.45	55.00	10.48	11.83
17	**LOK-54**	58.50	113.00	88.13	113.50	9.84	17.60	52.00	44.46	11.85	11.36
18	**MACS-2496**	64.00	117.00	80.90	112.50	8.55	14.00	41.00	38.54	14.10	11.60

Sr. No.	Genotypes	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Tillers / Running meter (No.)	Ear head length (cm)	No. of spiklets /spike (No.)	Grains/ spike (No.)	Thousand grain weight (g)	Grain yield/plant (g)	Protein %
19	**MACS-6222**	54.50	105.00	80.46	115.50	9.21	18.20	53.80	43.03	17.46	11.30
20	**MP-3097**	57.00	109.50	86.69	109.50	9.23	16.40	47.10	55.50	13.18	11.73
21	**NIAW-9947**	53.00	102.00	83.39	109.50	8.01	13.00	40.50	41.21	13.84	11.35
22	**NIAW-1275**	54.00	107.00	92.69	100.50	8.59	15.00	40.40	46.27	9.14	11.72
23	**NIAW-1342**	56.00	112.00	79.04	122.50	9.14	16.40	49.00	47.80	20.08	10.80
24	**NIAW-2300**	55.50	107.50	77.44	107.50	8.83	15.40	45.30	47.05	13.39	11.37
25	**NIAW-301**	59.50	112.00	92.00	116.00	9.02	17.40	47.10	42.80	18.09	12.65
26	**NIAW-34**	57.00	103.50	88.15	113.50	8.54	14.20	43.00	43.65	16.18	11.97
27	**NIAW-917**	58.00	108.50	80.19	108.50	8.35	15.00	43.35	43.00	15.08	12.39
28	**PBW-343**	62.00	116.50	83.67	106.50	9.22	13.00	38.35	40.60	14.73	11.90
29	**PHS-0622**	55.00	109.00	85.03	124.50	10.59	17.90	58.60	47.70	23.14	11.21
30	**PHS-830**	53.00	105.00	88.38	117.50	9.40	17.40	49.20	44.25	19.35	11.79
31	**LOK-1**	62.00	118.00	74.31	96.50	7.62	14.50	39.20	40.05	9.16	10.22
32	**RAJ-4083**	52.00	103.00	77.52	105.00	7.71	13.80	39.10	48.29	8.46	10.88
33	**UP-2783**	62.50	113.00	83.70	115.00	7.78	13.60	43.20	47.63	10.51	11.51
34	**WH-736**	60.50	115.00	78.43	97.50	7.91	15.50	44.50	42.035	13.58	12.40
35	**WSM-55**	51.50	102.00	82.09	113.50	7.70	15.00	45.80	51.78	10.74	10.84
36	**HD-2998**	53.50	108.00	78.17	106.00	8.46	14.30	45.00	42.65	15.30	12.25
	Mean	**56.34**	**108.41**	**81.87**	**110.48**	**8.64**	**15.36**	**45.75**	**45.56**	**14.63**	**11.47**
	S.E.	**0.3018**	**0.3112**	**0.1241**	**0.8294**	**0.0251**	**0.1090**	**0.1451**	**0.8572**	**0.0474**	**0.0169**
	C.D. at 5%	**0.8664**	**0.8934**	**0.3563**	**2.3812**	**0.0722**	**0.3130**	**0.4166**	**2.4609**	**0.1359**	**0.0486**

Table 4.3 Genotypes showing High and Low performance for 10 characters in wheat

Sr.no.	Name of character	Range	Genotype showing high performance	Genotype showing low performance
1	Days to 50% flowering	50.5-64.0	EXOTIC-21	MACS-2496
2	Days to maturity	102.0-118.0	AJINKYATARA, HALANA, NI-9947	LOK-1
3	Plant height (cm)	73.3-92.69	C-306	NIAW-1275
4	No. of tillers/running meter (No.)	96.5-124.5	PHS-0622	LOK-1
5	Ear head length (cm)	7.62-10.59	PHS-0622	LOK-1
6	No. of spikelet's /spike	13.00-18.20	MACS-6222	NIAW-9947, PBW-343
7	No. of grains / spike	36.45-58.60	PHS-0622	LOK BOLD
8	1000 grain weight (g)	38.54-55.5	MP-3097	MACS-2496
9	Grain yield/plant (g)	9.14-23.14	PHS-0622	RAJ-4083
10	Protein content (%)	10.22-12.65	NIAW-301	LOK-1

Table 4.4 Genetic variability in 36 genotypes of wheat

Sr. NO.	Characters	General mean	Range	GCV	PCV	Heritability % (bs)	Genetic advance	G.A. as % of mean
1	**Days to 50% flowering (No.)**	56.34	50.5-64.0	5.60	5.83	96.20	4.54	8.06
2	**Days to maturity (No.)**	108.41	102.0-118.0	3.12	5.24	59.54	3.68	3.40
3	**Plant height (cm)**	81.87	73.3-92.69	6.05	6.38	94.83	5.63	6.68
4	**No. of tillers per running meter (No.)**	110.48	96.5-124.5	4.98	7.88	63.19	4.84	4.38
5	**Ear head length (cm)**	8.64	7.62-10.59	6.96	9.02	77.15	1.76	20.47
6	**No. of spikelet's/spike (No.)**	15.36	13.00-18.20	8.30	11.21	74.02	3.20	20.83
7	**No. of grains/spike (No.)**	45.75	36.45-58.60	10.70	11.67	89.91	5.45	11.92
8	**Thousand grain weight (g)**	45.56	38.54-55.5	7.02	13.29	52.82	3.37	7.42
9	**Grain yield/plant (g)**	14.63	9.14-23.14	22.50	27.90	80.64	4.23	28.94
10	**Protein %**	11.47	10.22-12.65	5.32	5.70	93.41	1.96	27.10

GCV= Genotypic coefficient of variation b.s. = Broad sense

PCV= Phenotypic coefficient of variation G.A.= Genetic advance

Table 4.5: Genotypic (above diagonal) & Phenotypic (below diagonal) correlation of 10 characters in Wheat

Sr. No.	**Characters**	**Days to 50% Flowering**	**Days to maturity**	**Plant height**	**Tillers/ running meter**	**Ear head length**	**Spikelet's Per spike**	**Grains per spike**	**Thousand grain weight**	**Protein%**	**Grain yield/ plant**
1	**Days to 50% flowering**	**1.00**	0.7718**	0.0049	-0.1875	0.0272	-0.1707	-0.1825	-0.3867	0.1762	-0.2136
2	**Days to maturity**	0.7592**	**1.00**	-0.0794	-0.2814	-0.0017	-0.0846	-0.2554	-0.3208	-0.0415	-0.2542
3	**Plant height**	0.0051	-0.0788	**1.00**	0.2171	0.3241**	0.3470**	0.0396	0.0762	0.3663**	0.1512
4	**Tillers/running meter**	-0.1956	-0.2767	0.2130	**1.00**	0.5442**	0.5371**	0.7433**	0.2044	0.1175	0.9562**
5	**Ear head length (cm)**	0.0278	-0.0015	0.3235**	0.5357**	**1.00**	0.6146**	0.6585**	0.0471	0.2247	0.6205**
6	**Spikelet's/spike**	-0.1676	-0.0817	0.3444**	0.5255**	0.6096**	**1.00**	0.7278**	0.0271	0.1050	0.5587**
7	**Grains/spike**	-0.1819	-0.2538	0.0398	0.7311**	0.6567**	0.7224**	**1.00**	0.1318	0.0977	0.7717**
8	**Thousand grain weigh**	-0.3571	-0.3061	0.0726	0.1849	0.0446	0.0244	0.1260	**1.00**	-0.1172	0.2392*
9	**Protein %**	0.1757	-0.0412	0.3658**	0.1161	0.2239	0.1053	0.0975	-0.1120	**1.00**	0.1125
10	**Grain yield/plant**	-0.2134	-0.2521	0.1504	0.9441**	0.6192**	0.5543**	0.7699**	0.2276	0.1123	**1.00**

*,** significant at 5% and 1% probability

Table 4.6 Distribution of 36 genotypes of wheat in to different clusters

Clusters	Number of genotypes included	Genotypes
I	06	H-961, HD-2998, NIAW-917, WH-736, NIAW-2300, KINGBIRD.
II	09	FLW-1, WSM-55, FLW-8, EXOTIC-21, DBW-51, AKAW-4210-6, NIAW-1342, GUINEA-3, MACS-6222.
III	07	HD-2189, MP-3097, PHS-830, DBW-17, NIAW-301, NIAW-34, LOK-54.
IV	09	HALANA, RAJ-4083, NIAW-9947, JOBNER-828, MACS-2496, UP-2783, PBW-343, C-306, LOK-1.
V	01	NIAW-1275.
VI	01	LOK BOLD.
VII	03	AJINKYATARA, HI-1500, PHS-0622.

Table 4.7 Average intra and inter cluster D^2 and D values of seven clusters formed from thirty six genotypes in wheat.

Cluster	I	II	III	IV	V	VI	VII
I	**32.24** **(5.67)**	55.77 (7.46)	61.79 (7.86)	54.83 (7.40)	72.73 (8.52)	65.19 (8.07)	70.75 (8.41)
II		**40.12** **(6.33)**	59.77 (7.73)	59.03 (7.68)	80.54 (8.97)	82.50 (9.08)	61.63 (7.85)
III			**38.17** **(6.17)**	76.68 (8.75)	56.74 (7.53)	71.09 (8.43)	65.47 (8.09)
IV				**49.70** **(7.04)**	75.96 (8.71)	65.86 (8.11)	89.81 (9.47)
V					**0.00** **(0.00)**	31.82 (5.64)	102.82 (10.14)
VI						**0.00** **(0.00)**	110.33 (10.50)
VII							**57.58** **(7.58)**

Table No. 4.8. Mean performance of cluster for 10 characters in 36 wheat genotypes

Characters Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Tillers per running meter	Ear head length (cm)	Spikelet's per spike	Grains per spike	Thousand grain weight (gm)	Grain yield/ plant (gm)	Protein content %
I	56.17	109.08	78.34	106.42	8.31	14.98	44.59	43.80	14.10	12.02
II	54.44	106.72	80.47	114.78	8.52	16.04	48.58	47.54	16.49	11.02
III	56.79	107.93	88.15	114.43	9.25	16.67	48.15	46.33	15.94	11.96
IV	58.50	111.06	79.62	105.72	8.28	13.82	40.49	43.29	12.11	11.03
V	54.00	107.00	92.69	100.50	8.59	15.00	40.40	46.28	9.14	11.72
VI	56.00	108.50	87.75	100.50	7.98	13.50	36.45	55.00	10.48	11.84
VII	55.83	105.83	79.72	117.50	9.62	16.37	54.73	44.84	19.22	11.72

Table 4.9 Per cent contribution of 10 characters for divergence in wheat

Sr. No.	Characters	No. of times Appeared 1st in ranking	Per cent contribution
1	**Days to 50 per cent flowering**	01	0.16
2	**Days to maturity**	15	2.38
3	**Plant height**	162	25.71
4	**No. of tillers per running meter**	02	0.32
5	**Ear head length(cm)**	37	5.87
6	**No. of spikelets per spike**	11	1.75
7	**Grains per spike**	227	36.03
8	**Thousand grain weight**	-	-
9	**Grain yield/plant**	110	17.49
10	**Protein content**	65	10.33
	Total	630	100

Fig. 4: A cluster diagram showing interrelationship between 7 clusters.(Not to the scale)