GENETIC DIVERSITY OF NEWLY DEVELOPED LINES IN BREAD WHEAT (*Triticum aestivum* L.)

by

Mr. Mane Pravin Gorakh
(Reg. No. 019/045)

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

In partial fulfilment of the requirements for the degree

of

MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(GENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
POST GRADUATE INSTITUTE
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APPROVED BY

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2021

CANDIDATE’S DECLARATION

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

Place : MPKV, Rahuri (P.G. Mane)
Date : / /2021

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CERTIFICATE

This is to certify that the thesis entitled, "**GENETIC DIVERSITY OF NEWLY DEVELOPED LINES IN BREAD WHEAT (*Triticum aestivum* L.)**", submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra) in partial fulfilment of the requirement for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **AGRICULTURAL BOTANY (GENETICS AND PLANT BREEDING)**, embodies the result of a piece of bonafide research work carried out by **Mr. MANE PRAVIN GORAKH** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

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

Place : M.P.K.V., Rahuri
Date : / /2021

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Place : M.P.K.V., Rahuri **(P.N. Rasal)**
Date : / /2021

ACKNOWLEDGEMENTS

“Words provide wings to our ideas but not always can words express our feelings in words or languages.” No research work is possible alone, as it requires many minds and hands to beautify and to make it possible.

Everything has its own beauty, but not everyone can see without critical observation and great vision. Honestly no words would suffice to reveal the depth of my repeal and deep sense of gratitude to the Chairman of my Advisory Committee and Research Guide, ***Dr. U.G. Kachole****, Wheat Breeder, Agricultural Research Station, Niphad. Today I stand on door of this vision only due to my research guide. His valuable suggestions, intellectual guidance, constructive criticism, motivation, urge, zeal, support and constant encouragement throughout the course of this investigation, lead me towards successful completion of my research work.*

I wish to express my sincere thanks to ***Dr. P.N. Rasal****, Dean (F/A) and Associate Dean, PGI, MPKV, Rahuri for providing the research facilities.*

I accolade my highest respect to ***Dr. V.L. Amolic****, Head, Department of Agricultural Botany, MPKV, Rahuri for offering valuable guidance, help and constructive suggestions during my research work.*

I have immense pleasure in expressing my profound sense of gratitude to members of my Advisory Committee. I owe a special gratitude to ***Dr. S.S. Dodake****, Wheat Specialist, Agricultural Research Station, Niphad, for providing prompt guidance, constant inspiration and valuable help during the period of investigation and preparation of this thesis.*

I am very much thankful to ***Dr. R.S. Wagh,*** *Cotton Breeder, Cotton Improvement Project, Department of Agricultural Botany, MPKV, Rahuri for his valuable suggestions, guidance and help during the course of this investigation.*

I am also thankful to ***Dr. V.S. Wani****, Associate Professor, Department of Statistics, MPKV, Rahuri for his valuable help in statistical analysis.*

I am really thankful to ***Dr. G.C. Shinde,*** *Assistant Professor of Agricultural Botany, MPKV, Rahuri, for his support and valuable guidance during this course of investigation.*

It is my proud privilege to record my sincere thanks to Mr. Vijay Patil, Agriculture Assistant, Agricultural Research Station, Niphad, for his help during field observations and my research work. I am also thankful to Mr. Pritam Shinde and other staff members of Agricultural Research Station, Niphad, for their valuable help and encouragement throughout the course of study and research work.

I would like to express deep sense of gratitude and sincere thanks to my kindergarten teachers, primary school teachers, school teachers and teachers from New English School, Sangola and Sangola Vidyamandir Sangola, for cultivating my hopeful mind and growing the crop of ignition on barren land of my mind.

I express my cordial thanks to respected Assistant Professors of my UG college I. E. Sharad College of Agriculture, Jainapur, for valuable help in educational and life journey. Special thanks for Dr. S.C. Patil sir and Mr. Umesh Mohite sir for their valuable guidance to built my future.

The words are small trophies to express my feelings of affection and indebtedness to my dear friends Yashraj, Rahul, Pradeep, Atul, Viraj for their constant encouragement, kind help and close co-operation.

I whole heartedly express my thanks to my close associates, Pramod, Sushant, Pratap, Kiran, Akshay, Ananthu, Lekhan, Rupali, Ashwini and my seniors Deepak sir, Niranjan sir for their kind co-operation at various stages of my PG degree and memorable for me.

I am also thankful to my beloved friends Pravin, Rohit, Vivek, Jeevan, Anirudhha, Rohit, Ganesh, Rahul, Aniket and my juniors Ramesh, Anil, Sourabh, Avadhut, Rohan, Akshay, Abhishek and all for their constant support and help in my life.

It seems one used choicest of words to measure the boundless love and unlimited and unfold sacrifices of someone very close. However, I find no such measures adequate to quantify all that my parents, brother and sister have done for me. I will forever remain undebted to my beloved 'Tai' and 'Kaka', my brother Giridhar, my vahini Kajal, my sister Gita and Manju, for the sacrifice made by them to shape my career and whose long-cherished dreams are turning into reality in the form of this dissertation.

While travelling on this path of education, many hands pushed me forth. Learned hearts put me on the right track enlightenment by their knowledge and experience, I ever rest thanks to all of them.

I feel very lucky to admit here and offer my special thanks to this institute of excellence named 'Mahatma Phule Krishi Vidyapeeth, Rahuri.'

Last but not least I wish to thank all my friends and well-wishers who directly and indirectly encourage me at every step of life.

Place : M.P.K.V., Rahuri
Date : / /2021 (P.G. Mane)

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LIST OF ABBREVIATIONS

%	Percent
/	Per
∑	Summation of
$б^2$	Variance
b.s.	Broad sense
cm	Centimeters
C.D.	Critical difference
Cov.	Covariance
C.V.	Coefficient of variation
D.F.	Degrees of freedom
EC	Exotic collection
EMP	Error Mean Sum of Product
et al.	*et allia*(And other)
Fig.	Figure
g	Grams
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GCV	Genotypic Coefficient of Variation
GMP	Genotypic mean sum of products
h^2	Heritability
i.e.	*id est*(that is)
IC	Indigenous collection
kg	Kilogram (s)
M.S.S.	Mean sum of squares
m	Meters
mg	Milligrams
No.	Numbers
PCV	Phenotypic coefficient of variation
R.B.D.	Randomized Block Design
r	Correlation coefficient
S.E.	Standard Error
S.S.	Sum of Squares
Via.	By way of, by means of
Viz.	Videlicet (Namely)
Vs.	Versus

ABSTRACT

“GENETIC DIVERSITY OF NEWLY DEVELOPED LINES IN BREAD WHEAT (*Triticum aestivum* L).”

by

MR. MANE PRAVIN GORAKH

A candidate for the degree
of
MASTER OF SCIENCE (AGRICULTURE)
in
AGRICULTURE BOTANY
2021

Research Guide : **Dr. U. G. Kachole**
Department : **Agricultural Botany**
Major discipline : **Genetics and Plant Breeding**

The investigation on “Genetic diversity of newly developed lines in bread wheat *(Triticum aestivum* L*)*” was conducted on 50 genotypes of wheat to know the variability, interrelationship among yield and its components, their direct and indirect effects on seed yield and genetic divergence of various wheat genotypes.

Observations were recorded for days to 50 per cent flowering, days to maturity, plant height, spike length, number of spiklets per earhead, number of grains per earhead, 1000 grain weight and grain yield per plot.

Highest phenotypic coefficient of variation was exhibited by grain yield per plot (29.84%) followed by number of spikelets per earhead (13.39%), 1000 grain weight (13.06%), number of grains per earhead (10.97%), spike length (10.20%) and plant height (8.53%). Comparatively lower phenotypic coefficient of variation was observed for days to fifty percent flowering (7.12%) and days to maturity (4.62%).

For grain yield per plot, 1000 grain weight, number of spikelets per earhead, and number of grains per earhead, high heritability with high genetic advance as a percent of mean was observed, indicating that the heritability is due to additive gene effect and direct selection in early generations may be effective.

Grain yield per plot recorded significant positive correlation with number of grains per earhead, thousand grains weight, number of spikelets per earhead, spike length at both genotypic and phenotypic levels, so these characters could be improved through selection. Whereas, grain yield showed significant negative correlation with 50 percent flowering, days to maturity and plant height at genotypic as well as phenotypic levels.

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

The D^2 statistics showed that there was adequate diversity among the genotypes. On the basis of D^2 values of 50 genotypes studied were grouped into six clusters. On the basis of inter cluster distances, cluster mean and *per se* performance and divergence class observed in the present study, the genotypes *viz.,* NIAW-4293, NIAW-4390, NIAW-4299, NIAW-4354, NIAW-4320, NIAW-4345, NIAW-4434, NIAW-4289, NIAW-4393, NIAW-4324, NIAW-4461, NIAW-4394, NIAW-4348 and NIAW-4395 were distinct and diverse and can be classified as promising genotypes. These genotypes could be used in crossing programme to achieve desired segregates in wheat.

Pages 1 to 57

1. INTRODUCTION

Wheat is a grass that is widely farmed around the world for its nutritious and valuable grain. Wheat is the largest grain crop on this planet. Because of its vast acreage, excellent production and significant position in the world’s food grain trade, wheat has been dubbed the "King of Cereals".

Wheat was a popular farmed cereal in South Western Asia, where it originated. In Lebanon, Syria, Northern Israel, Iraq and Eastern Turkey, many wild *Triticum* species can be found. Wheat was farmed in prehistoric times in ancient Greece and Egypt. Bread and the use of the oven were invented by the early Egyptians and baking became one of the first large-scale food production industries. Wheat had reached England and Scandinavia by 3000 BC. It arrived in China a millennium later. DNA examination of materials from a granary dating to 1350 BC at Assiros in Greek Macedonia discovered the first recognized bread wheat (*Triticum aestivum*) with sufficient gluten for yeasted loaves.

Wheat species are widespread. Bread or common wheat (*Triticum aestivum*) is a hexaploid species that is the most frequently grown in the world, covering 90 per cent of the land surface. Another hexaploid species farmed in small amounts is spelt (*T. spelta*). The botanical name for spelt is *Triticum aestivum sub sp. spelta*, which is frequently regarded a subspecies of the closely related species of common wheat (*T. aestivum*). The only tetraploid variety of wheat utilised now is *T. durum*, which is also the second most extensively grown wheat. Emmer *(T. dicoccum)* is a tetraploid species that was once widely cultivated. Some species are diploid. *T. monococcum* is a diploid plant that comes in both wild and cultivated varieties.

Wheat provides 20 per cent of a person's total calorie intake (Anonymous, 2018-a). Wheat has a protein concentration of roughly 12 per cent, which is rather high when compared to other major cereals. Wheat contains 70 per cent carbohydrates, 2 per cent fiber, 2 per cent vitamins, 1-1.5 per cent fat and a variety of minerals (Anonymous, 2018-b). Wheat is a low-cost supply of amino acids, as well as a good source of P, Fe, Cu, Mn, Mg, Zn and vitamin B. Wheat protein has a high concentration of ‘niacine' and ‘thiamine'. The structural framework for the spongy cellular structure of bread, *chapati* and other baked items is provided by gluten, which accounts for 75 to 85 per cent of the protein in wheat.

Wheat is the most widely produced grain crop in the world, covering 215 million hectares. The overall area under wheat cultivation in India is 29.14 million hectares, with an annual yield of 99.8 million tonnes in 2018–19 and an average productivity of 3507 kg ha^{-1} (DAC & FW, 2018-19). It occupied an area of 8.00 lakh ha in Maharashtra, with a yield of 12.08 lakh tonnes and a productivity of 1508 kg ha^{-1} in 2017-18. (Anonymous 2018).

Wheat is a self-pollinated cool-season crop that thrives in climates with average temperatures of 18°C to 22°C and rainfall of 750-1600 mm. Wheat crops require roughly 40 ha cm of water. The chasmogamous state of the flowers is the primary cause of self pollination.

Yield is a complex character that is made up of a number of other characters and their interactions with the environment. Examining the structure of a yield entails determining the interrelationships between the numerous characters that contribute to the yield. In this case, genotypic and phenotypic correlation reflects the degree of relationship between different characters, assisting in the selection of yield and yield attributing characters at the same time. Path coefficient analysis also aids in the segmentation of correlation coefficients into direct and indirect impacts, as well as the assessment of each component character's relative contribution to the yield.

Wheat genotype collection and evaluation is a pre-requisite for every breeding programme that aims to maximise diversity. A quantitative assessment of genetic divergence among germplasm collections and the relative contributions of different variables to genetic divergence provide crucial and effective information to breeders in their hybridization programmes, resulting in genetic yield enhancement. The necessity for finding out genetic divergence among the genotypes is more pronounced because two important reasons i.e., 1. When genetically varied parents are used in a hybridization procedure, the heterotic effect is likely to be substantial. 2. In the segregating generation of crosses involving distantly related parents, a large range of variability could be expected.

Yield is a complicated trait that is controlled by multiple genes, making successful yield selection a difficult task. The effectiveness of selection can be improved by associating yield with its component qualities. Study of the relationship between yield-contributing characters and path coefficient analysis, which provides a comprehensive picture of the direct and indirect effects of characters on yield, which is important to breeders in crop development. Selection for the best genetic advance should be based on carefully calculated parameters. Unfavorable associations between desired traits under selection, on the other hand, may cause genetic slippage.

Genetic diversity refers to the variation that exists among the species genotypes. Mahalanobis (1936) proposed an excellent method known as "Mahalanobis D^2 statistics" or "D^2 methodology" that is extensively used to determine genetic diversity in germplasm.

This technique assesses the forces of differentiation at the intra-cluster and inter-cluster levels, assisting in the selection of genetically distinct parents for use in hybridization programs. The D^2 statistics also determines the proportion of each component character to the total divergence and quantifies the degree of diversification.

The nature and size of inter relationships between grain yield and its contributing components have been determined using correlation analysis. The correlation coefficient analysis determines the components features on which selection can be relied upon to achieve improvement by measuring the mutual link between distinct characters.

In plant breeding, genetic diversity is vital for exploiting heterosis or generating productive recombinants. In a breeding programme, choosing the right parents is crucial. As a result, understanding genetic diversity and relatedness in germplasm is a must for any crop improvement initiative. As a result, precise information on the nature and degree of genetic variation contained in wheat collections from the main agricultural areas will aid in the selection of parents for developing superior varieties. Diverse genotypes from existing germplasm should be selected and employed in future breeding programmes to improve the genetics of this crop. With following consideration in mind, an effort was made to analyse a set of wheat genotypes with the following goals in mind:

1. Genetic divergence study between different genotypes.

2. REVIEW OF LITERATURE

A thorough assessment of the literature is a necessary component of any scientific investigation. It is usually required to do a literature review in order to compare the current findings to those of past studies conducted by researchers.

2.1 Genetic Variability

Any effective breeding programme must start with a thorough examination of genetic variability in the available germplasm. Johannsen recognized a distinction between genotype and phenotype (1909). It is obvious from this that variability is caused by interactions between genotype and environment (Fisher, 1930). Using estimates of environmental variance from non-segregating populations, the overall variance was partitioned into genotypic and phenotypic variances (Charles and Smith, 1939). Burton (1952) and Panse and Sukhatme (1995) presented statistical methods for calculating the genetic component of variances.

Rebetzke *et al.* (1999) observed for plant height, there was a high heritability combined with a moderate genetic advance.

Majumder *et al.* (2008) studied twenty spring wheat varieties to find out genetic variability for grain yield and its components characters. They discovered that in all of the traits, both genotypic and phenotypic variants were extremely significant, with slightly higher phenotypic variability than typical. Similarly, the small discrepancies between the phenotypic and genotypic coefficients of variation suggested that the expression of these traits was not influenced by the environment. Plant height, grains per spike, 1000 grain weight, harvest index and grain yield all showed substantial heritability and genetic advance.

Yousaf Ali *et al.* (2008) reported plant height; number of productive tillers per plant, number of spikelets per spike, spike length, number of grains per spike, fertility per cent, 1000 grain weight and yield per plant are all examples of genetic variability in wheat. They discovered significant genotypic differences for all of the traits investigated, showing that each feature has a lot of diversity among genotypes. For yield per plant, number of productive tillers per plant and number of grains per spike, the estimations of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high. The remaining attributes had PCV and GCV values that were moderate to low.

Ajmal *et al.* (2009) observed plant height; number of tillers per plant, number of spikelets per spike, grains per spike and grain yield per plant were all significantly varied between genotypes. Plant height, tillers per plant, grains per spike and grain yield had strong wide sense heredity, but number of spikelets per spike had low broad sense heritability.

Kumar *et al*. (2009) evaluated for yield and other associated parameters, thirty genotypes of bread wheat were used. Plant height (cm), number of tillers per plant, spike length (cm), number of grains per spike, 1000 grain weight (g) and grain yield per plant (g) all had high PCV and GCV, however days to 50 per cent flowering and days to maturity had relatively low variability.

Monpara (2009) observed majority of the characteristics in wheat have a broad range of variance. All of the traits had a moderate genotypic coefficient of variation, with the exception of one, which had a low magnitude. Plant height, spike length and grains per spike all showed substantial heritability and genetic advance.

Subhashchandra *et al.* (2009) studied in tetraploid wheat, the variability parameters in the F_2 populations of 28 crosses produced by the Diallel Mating System. Yield per plant had the largest genotypic and phenotypic coefficient of variations, followed by productive tillers per plant. Plant height and sedimentation value had high heritability and moderate genetic advance as a per cent mean.

Yagdi and Sozen (2009) noticed broad-sense heritability estimates ranged from 0.72 per cent to 30.43 per cent. Among the traits, the test weight exhibited the highest heritability value (17.69%), followed by gluten content (10.12%) and protein content (5.38%), respectively.

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

Kahrizi *et al.* (2010) observed for the parameters plant height and number of tillers per plant, there was significant variance among genotypes. For plant height, heritability estimates were high.

Laghari *et al*. (2010) reported spike length, grain yield per plant and 1000-grain weight has modarate genotypic coefficients of variation. Grain yield per plant, 1000-grain weight, plant height and number of spikes per plant have high heritability estimates.

Kalim Ullah *et al.* (2011) observed for all of the characters studied, there were significant genotypic differences. Plant height, days to 50 per cent flowering, duration to physiological maturity (days), spikelets per spike and spike length (cm) all showed a significant amount of variance between genotypes.

Mohammed *et al.* (2011) revealed for the 12 attributes tested, there were extremely significant variances across 16 durum wheat genotypes, indicating the possibility of enhancing durum wheat for these qualities. Plant height and number of grains per spike had the largest phenotypic and genotypic coefficients of variation and genetic advance, according to the researchers. Plant height had the highest heredity of 98.3 per cent, while the number of spikelets per spike had the lowest heritability of 36.4 per cent. For test weight, there was a high heritability but not a high genetic advance.

Yadav *et al.* (2011) observed days to heading, days to maturity, plant height, tillers per plant, spike length, grains per ear, 1000-grain weight, biological yield per plant and grain yield per plant all showed significant genetic variability. Except for plant height and grains per ear, all of the traits had a high heritability.

Kalim Ullah *et al.* (2012) reported number of grains per spike, number of tillers per plant, 1000-grain weight, grain yield per plant and spike density genetic diversity in forty one bread wheat varieties. They discovered significant genotypic differences for all of the traits tested, showing that each feature has a high diversity among genotypes

Asaye *et al.* (2013) observed grain yield, 1000 grain weight and grains per spike had the highest genotypic coefficient of variation. Days to maturity and hectolitre weight, on the other hand, had the lowest genotypic coefficients of variation.

Awale *et al.* (2013) reported for the number of tillers per plant and grain production per plot, the phenotypic and genotypic coefficients of variation were both large. 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 all had high heritability. The amount of spikelets per spike had a moderate heritability.

Kumar *et al.* (2013) showed characters including days to 50 per cent flowering, days to maturity, plant height, tillers per plant, spike length, grains per spike, test weight and yield per plant have a high variance between genotypes.

Vir *et al.* (2013) observed grain yield per plant, 1000-grain weight, number of spikelets per spike, number of grains per spike, spike length, plant height and days to 50 per cent flowering all showed significant genotypic differences.

Khan (2013) showed highly significant differences among the genotypes for days to heading and plant height. Days to maturity, number of tillers per plant, spike length, spikelets per spike, grains per spike and grain yield per plant were low heritable.

Ashfaq *et al.* (2014) observed for plant height and grain yield per plant, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). 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 all had low PCV and GCV.

Sabaghnia *et al.* (2014) evaluated that there were substantial differences in plant height, spike length, spikelet number, grain number, number of days to flowering, 1000 grain weight and grain yield among 56 bread wheat varieties studied. Grain yield (25.61%), number of tillers per plant (22.06%) and number of grains per spike all had significant coefficients of variation (CV) (21.45%).

Yahaya (2014) observed high heritability with high genetic advance for total tillers per plant, spike length and number of grains per spike 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 coefficients variation for number of grains per spike, number of effective tillers, number of spikelets per spike, yield per plant and number of tillers per plant. Grain weight, spike length, number of spikelets per spike, days to bloom initiation and days to maturity were all moderate. The estimates of phenotypic and genotypic coefficients variation indicated that the material had enough variety.

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

Deoraj *et al.* (2016) reported there was a high variety in the F_2 of 21 crossings, 7 parents and 2 checks. GCV and PCV were highest for productive tillers per plant and spikelets per spike, whereas GCV and PCV were lowest for days to maturity and days to 50 per cent flowering. The high heritability was complemented with high magnitude of genetic advance in terms of per cent of mean for spike length, productive tillers per running metre, 1000 grain weight and grain yield per plant, implying additive genetic control in the expression of these traits.

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

Sohail *et al.* (2018) studied in 11 F_4 bread wheat *(Triticum aestivum* L.*)* genotypes, genetic variability, heritability and genetic advance were investigated. For the traits studied, statistically significant differences were discovered. Days to heading (3.90%) and spike length (8.13%), plant height (9.95%) had low expected genetic advance, while grain weight spike^{-1} (11.54%) and 1000 grain weight (13.41%) had moderate expected genetic advance and flag leaf area (24.72%) and grain yield plant^{-1} (20.45%) had high expected genetic advance.

2.2 Correlation and Path Analysis

Yield is a complicated trait that is influenced by a number of factors. The correlation coefficient is a useful estimate for determining the relationship between various characters and identifying characters that are of little or no significance in the selection process.

Robinson *et al.* (1949) observed that because selection frequently involves modifying two or more features at the same time, correlation values are potentially important.

Dewey and Lu (1959) used these correlation coefficients first time in plant for path analysis. He described the path analysis strategy in full, which was a novel approach to removing environmental variations.

Grafius (1964) has pointed out that it would be more informative if the structure of yield was presented by its components rather than by its overall performance. It is vital to investigate these yield components, their interrelationships with yield and their direct and indirect contributions in order to improve yield through breeding.

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

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

Ajmal *et al.* (2009) observed that the number of tillers demonstrated a substantial positive correlation with plant height. The number of tillers per plant had a negative correlation with the number of spikelets per spike, the weight of 1000 grain per spike and the number of grains per spike. The number of grains per spike and 1000 grain weight were both positively and significantly correlated with grain yield. They also suggested that these traits be given emphasis during selection of wheat genotypes for improving productivity.

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

Yagdi and Sozen (2009) observed significant positive correlation between the grain yield, plant height and spike length. Gluten content and grain number per spike, grain weight per spike and plant density, sedimentation and number of spikelet per spike and grain number per spike and protein content and grain number per spike were all found to have negative and significant correlation. Thus, indicated that generally the important agronomical characteristics were inversely correlated with the quality traits.

Bilgin *et al.* (2010) observed that protein content and grain yield have a significant and negative correlation coefficient.

Siahbidi *et al*. (2012) while studying in durum wheat genotypes, there was a positive correlation between the number of spikes and the quantity of grains per spike.

Awale *et al.* (2013) observed that grain yield per plot, number of tillers per plant and grains per spike all have a positive and extremely significant correlation. The number of tillers per plant and the number of grains per spike both contributed significantly to grain yield per plot and both characters should be prioritized in future bread wheat yield development efforts.

Zeeshan *et al.* (2013) revealed the number of spikelets per spike, the number of grains per spike and the weight of 1000 grain per spike all have a positive correlation with grain yield. They also proposed that future wheat yield development efforts should focus on the number of spikelets each spike, the number of grains per spike and the weight of 1000 grain per spike.

Yahaya (2014) observed grain yield per plant was high and effective tiller per plant was positively correlated. The length of the spike, the number of spikelets per spike and plant height all had a positive significant corelation with yield.

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

2.3 Genetic Diversity

Individuals' genetic variances in regard to certain morphological traits are referred to as genetic diversity. It can be used to evaluate the contribution of each character to overall divergence and hence aid in the selection of superior parents for hybridization programmes.

Mahalanobis (1936) explains the basics of D^2 statistics as a quantitative technique for evaluating population genetic divergence. Evolutionary forces cause variations in the frequency of various populations, resulting in genetic diversity.

Rao (1952) describes D^2 statistics could be used in plant breeding to determine genetic variability, according to the authors. Geographical distribution has little effect on genetic diversity, according to Moll *et al.* (1962).

Mahalanobis generalised distance computed by statistic is used to measure the degree of divergence between biological populations and to compute the relevant contribution of different components to the total divergence. In the realm of plant breeding, Nair and Mukharjee (1960) were the first to apply the D^2 statistic as a measure of genetic divergence for classification.

Lee and Kaltsikes (1973) investigated genetic divergence and it was discovered that there is no link between genetic divergence and geographic origin.

Jain *et al.* (1975) showed using the globe collection, researchers discovered spatial patterns of phenotypic variety in durum wheat and devised a programme to safeguard genetic resources by identifying and assessing inter variation and intra societies. Traits could be considered a function of variety because genetic diversity could be the outcome of geographical impact through evolution.

Kumar *et al.* (2009) showed that six clusters were formed from the thirty genotypes. Cluster VI has been discovered for choosing parents for incorporating grain yield per plant, tillers per plant and plant height, Cluster V for spike length, grains per spike and early maturity and Cluster III for 1000 grain weight, according to cluster means.

Jaiswal *et al.* (2010) divided three hundred indigenous germplasms of bread wheat into twenty-three clusters, each with a different mean value for the features under investigation. They also recommended that genotypes with desired values from different clusters could be used in a breeding programme to increase bread wheat yield and quality.

Hailegiorgis *et al.* (2011) revealed that the genotypes were divided into 22 separate clusters, revealing a significant range of variability across the genotypes studied. Genotypes in Clusters IX and XIII should be considered for direct use as parents in hybridization operations to generate high yielding wheat varieties based on cluster mean values. They also noticed that genotypes in Clusters III and XVI could be used to improve protein, early maturity and other desirable traits other than grain yield and concluded that genotype differentiation was due to the small contribution of a few characters rather than the cumulative effect of a number of characters. The information obtained can be used to plan crosses and maximize the use of genetic diversity and expression of heterosis.

Kumar *et al.* (2013) observed inter-cluster distance between K816 and HUW-533 mono-cluster genotypes from Cluster VI and VII is the greatest, followed by mono-cluster genotype K816 from Cluster VI with 3 genotypes from Cluster II, which has a high degree of genetic diversity and can be used in an inter-varietal hybridization programme.

Singh *et al.* (2014) grouped genotypes by using both Tocher's and Euclidian methods of divergence, thirteen wheat genotypes were divided into four groups. They also noticed that the genotypes and numbers of genotypes in each method's clusters were varied.

Verma *et al.* (2014) analyse the genetic diversity for yield and yield attributes, 108 bread wheat accessions from India and Australia were used. They discovered that these genotypes were divided into eleven clusters with a distribution pattern indicating that Cluster IV (26) had the most genotypes, followed by Cluster VI (22) and Cluster II (12). In most of the cases, the inter-cluster distance was greater than the intra-cluster distance, showing greater genetic diversity across accessions from different groups. Cluster VIII and IX had the greatest inter-cluster distance (113.94), followed by VIII and X (97.72), demonstrating the groups' broad diversity. Cluster X (13.96) had the highest intra-cluster distance, while Cluster VII had the smallest (00.00). Cluster X genotypes exhibited the highest mean grain yield, harvest index and spike weight values. 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) divided 65 wheat accessions into six groups. Cluster 1 and Cluster 4 have the most diversity. This high level of diversity explains why future breeding programmes will have superior parental selection.

Fikre *et al.* (2015) showed that nine clusters were formed from the 64 genotypes. Cluster I and IX exhibited the greatest inter cluster distance ($D^2 = 5112.1$), followed by Clusters III and IX ($D^2 = 4694.4$) and VIII and IX ($D^2 = 3871.9$), indicating that they were genetically more dissimilar from one another than any other cluster. Cluster I genotypes crossed with Cluster IX, Cluster III genotypes crossed with Cluster IX and Cluster VIII genotypes crossed with Cluster IX are likely to yield progenies with superior genetic recombination and segregation.

Getachew *et al.* (2017) evaluated for 11 characteristics, 49 bread wheat genotypes were tested. The 49 genotypes were divided into six clusters using average linkage cluster analysis. Cluster I and III had the highest inter-cluster distance, followed by Cluster II and IV and Cluster II and III, indicating that these clusters have more genetic diversity.

3. MATERIALS AND METHODS

The present investigation on "Genetic diversity of newly developed lines in bread Wheat (*Triticum aestivum* L.*)"* was conducted at Agriculture Research Station, Niphad-422 303, Dist- Nashik during *Rabi*, 2019-20. The materials and procedures used to conduct the genetic divergence research, as well as the experimental design and statistical approach used, are all described in this chapter.

3.1 Experimental Materials

The experimental material for the present investigation consisted of 50 genotypes of wheat (*Triticum aestivum* L.) collected from office of Wheat Specialist, Agricultural Research Station, Niphad (MPKV. Rahuri). The list of genotypes along with pedigree is given in Table 3.1.

3.2 Experimental Design

Ploughing and harrowing were used to bring a plot of soil chosen for the experiment to fine tilth. With two replications, the experiment was conducted in Randomized Block Design (RBD). Dibbling was used to sow the grains. Each entry was represented by two rows of 6.0 meters each with a 40-centimeter space between them.

The recommended dose of 90:60:40 NPK (kg/ha) was applied and the experiment was sown on 28th November 2019. All necessary recommended packages of practices were carried out to raise a good crop.

Table 3.1 List of Wheat Genotypes with Pedigree

Sr. No.	Genotypes	Pedigree
1	NIAW 4256	NIAW 1594 X PHS 1101
2	NIAW 4259	LOK 62 X NIAW 1698
3	NIAW 4261	RAJ 4176 X LOK 62
4	NIAW 4265	PHS 1101 X King Bird
5	NIAW 4267	NIAW 1885 X NIAW 1415
6	NIAW 4279	NIAW 1415 X DBW 17
7	NIAW 4282	NIAW 1994 X SRRSN 6123
8	NIAW 4289	DBW 17 X NIAW 1885
9	NIAW 4293	C 306 X SRRSN 6066
10	NIAW 4299	PUSA BAKER X LOK 54
11	NIAW 4308	AKAW 4627 X NIAW 1994
12	NIAW 4311	NI 9947 X LOK 1
13	NIAW 4315	NI 343 X NIAW 1994
14	NIAW 4320	HD 2932 X AKAW 4627

(Contd…)

Table 3.1 (contd…)

Sr. No.	Genotypes	Pedigree
15	NIAW 4324	NI 5643 X NIAW 1994
16	NIAW 4331	RAJ 4304 X NIAW 1994
17	NIAW 4340	NIAW 34 X RAJ 4304
18	NIAW 4343	NI 9947 X NIAW 1994
19	NIAW 4345	DBW 17 X NI 5643
20	NIAW 4348	NIAW 1415 X PUSA BAKER
21	NIAW 4351	NIAW 1885 X NIAW 1994
22	NIAW 4354	NIAW 1994 X FRANCOLIN #1
23	NIAW 4358	NIAW 1415 X NIAW 2268
24	NIAW 4368	NIAW 301 X FRANCOLIN # 1
25	NIAW 4372	NIAW 34 X NIAW 1994
26	NIAW 4379	NIAW 2030 X SRRSN 6115
27	NIAW 4380	MACS 6222 X SRRSN 6006
28	NIAW 4384	DBW 93 X MACS 6222
29	NIAW 4386	NIAW 1415 X (NI343) X NIAW 34)
30	NIAW 4387	(NIAW 1885 X SRRSN 6022)X SRRSN 6022
31	NIAW 4388	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
32	NIAW 4389	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
33	NIAW 4390	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
34	NIAW 4391	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)
35	NIAW 4392	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)
36	NIAW 4393	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)
37	NIAW 4394	(LOK 1 X HD2932) X (LOK 1) X NIAW 1994)
38	NIAW 4395	(LOK 1 X HD2932) X (LOK 1) X NIAW 1994)
39	NIAW 4396	(NIAW 34 X HD 2932) X (NIAW 1994 X NI 343)
40	NIAW 4399	(DBW 17 X NIAW 1415) X NIAW 1415
41	NIAW 4402	PYT TS 18
42	NIAW 4409	PYT TS 52
43	NIAW 4423	KUTZ*2/5/UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1
44	NIAW 4428	KACHU #1/KIRITATI//KACHU*2/3/BECARD/FRNCLN
45	NIAW 4431	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07/4/MUTUS*2/TECUE #1
46	NIAW 4434	KACHU #1/KIRITATI//KACHU*2/3/GRACK/CHYAK
47	NIAW 4459	FRET2/TUKURU//FRET2/3/MUNAL #1/4/SUP152/AKURI//SUP152
48	NIAW 4460	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PANDION//FILIN/2*PASTO R/3/BERKUT
49	NIAW 4461	19th KBSN 29
50	NIAW 4462	18th HTWSBYT 28

3.3 Recording of Observations

3.3.1 Sampling of Plants

From each treatment, five plants were chosen at random. The average of these five plants was calculated for statistical purposes and then employed in the genetic divergence analysis.

3.3.2 Observations Recorded

The number of observations recorded and the method used to make each observation is listed below.

3.3.2.1 Days to 50 per cent flowering

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

3.3.2.2 Days to maturity

Days to maturity were defined as the number of days required from the date of sowing to physiological maturity.

3.3.2.3 Plant height (cm)

On observational plants, plant height was measured at maturity from the ground level to the tip of the plant. It is measured in centimeters (cm).

3.3.2.4 Spike length (cm)

The average spike length of five plants on the main culm was measured in centimetres from the base of the spike to the top, omitting awns and average was worked out.

3.3.2.5 Number of spikelets per earhead

At maturity, the total number of spikelets on the main spike of five observational plants was counted and the average was recorded.

3.3.2.6 Number of grains per earhead

At harvest, the total quantity of grains in the main spike was counted and recorded.

3.3.2.7 1000 grain weight (g)

Each genotype's total weight of 1000 grain was measured and recorded in gram.

3.3.2.8 Grain yield per plot (g)

The total weight of grains gathered from each plot was measured in gram per plot.

3.4 Statistical Analysis

For statistical analysis, the mean values of five randomly selected observational plants for eight different characters were employed. For the presentation of data on distinct quantitative features, the following statistical parameters were calculated.

3.4.1 Assessment of Variability

The analysis of variance for distinct characters was carried out utilizing mean data from several sources, according to Panse and Sukhatme's technique (1995).

Table 3.2 Analysis of variance (ANOVA)

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

3.4.1.1 Estimation of mean and range

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

$$\overline{X} = \frac{1}{N} (\sum_{i=0}^{n} Xi)$$

Where,

$\overline{X}$ = Mean of character

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

N = Number of observations

The range was defined as the difference between the highest and lowest values from the mean of each character.

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

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

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

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

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

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

3.4.1.3 Estimation of components of variation

As shown below, the phenotypic and genotypic variances were estimated using the mean squares from the variance table (Johnson *et al.*, 1955-b).

Environmental variance (σ^2_e) = EMS

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

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications.

3.4.1.4 Estimation of coefficient of variation

Burton and Devane's formulas were used to calculate the genotypic and phenotypic coefficients of variation (1953).

3.4.1.4.2 Phenotypic coefficient of variation (PCV)

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

Where,

$\sigma^2 p$ = Phenotypic variance

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

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

In a broad sense, the heritability per cent was calculated using Burton's formula (1952).

h^2 (b.s.) = (V_g/V_p) x 100 or h^2(b.s.) = (σ^2_g / σ^2_p) x 100

Where,

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

σ^2_g : Genotypic variance

σ^2_p : Phenotypic variance

According to Johnson *et al.* (1955-a) values, the heritability estimates were classed as high, medium, or low

Low heritability = 5-10 per cent

Moderate heritability = 10-30 per cent

High heritability = 30-60 per cent

3.4.1.6 Estimation of genetic advance

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

$GA = K \times (\sigma^2_g / \sigma^2_p) \times \sigma_p$ or $GA = K \times h^2 \times \sigma_p$

Where,

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

σ^2_g = genotypic variance

σ^2_p = phenotypic variance

σ_p = phenotypic standard deviation

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

$\overline{X}$ = Mean of the character

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

Less than 10 per cent : Low

10-20 per cent : Moderate

More than 20 per cent : High

3.4.2 Correlation

The simple correlation coefficients were estimated in each of the populations separately to establish the degree of association of distinct features with grain yield and also among yield components in each of the generations. To test their significance, correlation coefficients were compared to Table ‘r' values at (n-2) d.f at the probability levels of 0.05 and 0.01. Simple correlations were computed by using the formula as given below.

$$r = \text{cov.xy} \div \sqrt{\text{vx.}}\,\text{vy}$$

Where,

Cov xy = Covariance between the characters x and y

V_x = Variance of the character x

V_y = Variance of the character y

3.4.3 Path Analysis

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

Path coefficient analysis is a standardized partial regression coefficient that divides a simple correlation into measurements of direct and indirect effects, i.e. it analyses the direct and indirect contributions of various independent characters on dependent characters. If ‘Y’ is dependent (causal) character and X_1, X_2, X_3 ------- are independent characters and some undefined factors designated by R, this relation can be represent by

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

Path analysis determines whether the association is due to their direct effect or their indirect effects viz., other component characters. The direct effects and indirect effects via other characters are divided in the correlation between cause (X_1) and effect (Y_1).

a) Direct effects

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

σ (r (x,y) = a + r (x_1, x_2) b + r (x_1, x_3) + (------)

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

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

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

b) Indirect effect

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

For each component character, direct and indirect effects of all possible combinations were determined.

c) Residual effect

The residual effect R was calculated as below

R = [1- ($Px_1y.rx_1y$)- ($Px_{2y}.rx_2y$) ……(Pxny.rxny)]1/2

Where,

Px_1y, Px_2y…. Pxny = Direct effects of respective character on grain yield

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

Path diagram

Path diagrams are line diagrams that are created using simple correlation coefficients among several characters in a study.

r_{ny}= Correlation coefficient

3.4.4 Genetic Diversity

3.4.4.1 D^2 analysis

The analysis of divergence was carried out by D^2 statistic of Mahalnobis (1936) as described by Rao (1952). To examine the significances among the genotypes, RBD was used to calculate analysis of variance for the different characters analyzed. Only the characters with significant differences were considered in further D^2 statistical analysis. The analysis of covariance for characters pairs, based on plot averages was carried out (Cochran and Cox, 1957).

3.4.4.2 Wilk’s criterion

After testing for differences between populations, Wilk's Δ criterion (Wilk, 1932) was used to estimate a simultaneous test of significance of difference in the mean values of a number of correlated variables with regard to the pooled effect of eight characters examined together.

$$\Delta = \frac{|E|}{|E + V|}$$

Where,

$|E|$ is the determinant of the experimental error sum of square and sum of products matrix and $|E + V|$ the determinant of experimental error sum of squares and sum of products, plus the population sum of squares and product matrix significance of Δ was estimated by X^2 as

$X^2pq = V = - m. \log e \Delta$

Where,

$m = n - ((p+q+1))/2$

$n = N_1 + \ldots\ldots + NK - 1$

= Total number of observations – 1

P = Number of significant characters

Q = K – 1 (d. f. of varieties)

K = Number of varieties/genotypes

3.4.4.3 Mahalanobis’s generalized distance

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

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

Where,

λi.j = Reciprocal matrix to the common dispersion matrix

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

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

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

The coefficients for the transformation were calculated by dividing the first row of the reduced matrix by the square root of the appropriate pivotal condensation element.

3.4.4.4 Determination of group constellation

Tocher's approach, as reported by Rao in 1952, was used to generate clusters. Because a cluster is not a well-defined term, no formal procedures can be established for locating them. The only criterion appears to be that any two groups belonging to the same cluster should have a smaller D^2 than those belonging to two distinct clusters on average. Starting with the two closely related groups, locate a third group that has the smaller D^2 from the two, as suggested by Tocher and reported by Rao (1952). In the same way, the fourth is picked to have the lowest D^2 value of the first three and so on. If the average D^2 of a group from those already listed appears to be high at any point. This group does not fit within the previous groups, hence it is moved outside of the previous cluster. The first cluster's group is then omitted and the remaining clusters are processed identically. Calculating the change in average D^2 within a cluster due to the addition of a new group is also useful. If the changes are significant, the newly added group must be considered separate from the cluster.

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

3.4.4.5.1 Average intra cluster D^2

The intra-cluster distances were calculated as

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

Where,

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

3.4.4.5.2 Average inter cluster D^2

The technique for estimating the inter-cluster distance began with measuring the distance between Clusters I and II, I and III, I and IV and so on. Similarly, the clusters were examined one by one and the distance between them was computed. After that, the average inter-cluster distance was computed as follows:

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

Where,

ni = Number of population in cluster i

nj = Number of population in cluster j

3.4.4.5.3 Average intra and inter cluster distance (D)

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

3.4.4.6 Cluster means

Individual character cluster means were determined using the mean performance of the genotypes in that cluster.

3.4.4.7 Contribution of individual characters towards divergence

In all of the combinations, the first rank was given to the character with the greatest mean difference. The percentage contribution was calculated by counting how many times each character appeared first in the rank in all possible combinations (Singh and Choudhary, 1977).

3.4.4.8 Cluster diagram

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

3.4.4.9 Genetic diversity as an index for desirable parents for hybridization

Following Arunachalam and Bandopadhay (1984), the probable limits to paternal divergence within which there were quite high probability of heterosis were computed. They suggested dividing parental divergence into four classes to account for the varying level of variation in parental divergence; the mean (M) and standard deviation (S) of divergence values were calculated. The following are the divergence classes:

DC_1 =D> or = M+S

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

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

DC_4 =D< (M-S)

When two parents with genetic divergence between (M-S) and (M+S), i.e. in the classes DC_2 and DC_3, are crossed, they are more likely to produce high frequency and magnitude of heterosis than a cross with parental divergence outside the limit [(M-S), (M+S)].

4. RESULTS AND DISSCUSSION

The present investigation entitled “Genetic diversity of newly developed lines in bread wheat (*Triticum aestivum* L.)” was undertaken with a view to study genetic diversity, correlation, heritability and genetic advance for 50 diverse genotypes of wheat. The observations were recorded on eight characters. The results obtained are presented in this chapter.

4.1 Mean Performance

Table 4.1 shows the average performance of 50 wheat genotypes for the eight characters studied.

4.1.1 Days to 50 per cent Flowering

The general mean for days to 50 per cent flowering was 67.37 days. The variation in days to 50 per cent flowering ranged between 59.50 (NIAW-4390) to 79.00 (NIAW-4391) days. Twenty-five genotypes were found to be early for 50 per cent flowering, while twenty-five genotypes were found to be late for 50 per cent flowering when compared with general mean. The genotypes NIAW-4390 (59.50 days), NIAW-4293 (60.00 days), NIAW-4320 and NIAW-4343 (60.50 days) were found significantly earlier for days to 50 per cent flowering. While, NIAW-4391 (79.00 days), NIAW-4423 and NIAW-4431 (76.00 days) are comparatively late in 50 per cent flowering than the general mean.

4.1.2 Days to Maturity

The general mean for number of days to maturity was 112.41 days. The days to maturity ranged from 103.50 (NIAW-4320) to 122.00 (NIAW-4394) days. Twenty three genotypes were found to be early and twenty seven genotypes were late to mature as compared to general mean. The genotype NIAW-4320 was significantly early for days to maturity (103.50 days) followed by NIAW-4289, NIAW-4293 and NIAW-4390 (104.00 days) over the general mean. While, genotypes NIAW-4394 (122.00 days), NIAW-4395 (121.50 days) and NIAW-4388 (121.00 days) were comparatively late in maturity.

4.1.3 Plant Height (cm)

The general mean for plant height was 96.51 cm. Plant height ranged from 83.2 cm (NIAW-4308) to 123.00 cm (NIAW-4279). Eighteen genotypes were taller than the general mean. The genotypes NIAW-4308 (83.20 cm), NIAW-4391 (84.00 cm) and NIAW-4320 (85.00 cm) were significantly dwarf, while the genotypes NIAW-4279 (123.00 cm), NIAW- 4379 (114.00 cm) were comparatively taller than general mean.

4.1.4 Spike Length (cm)

The general mean for spike length was 11.22 cm. The variation in spike length ranged from 8.95 cm (NIAW-4379) to 14.30 cm (NIAW-4395). Twenty five genotypes recorded longer spike length, while twenty five genotypes recorded shorter spike length than the general mean. The genotype NIAW-4395 (14.30 cm) showed significantly maximum spike length followed by NIAW-4390 (13.05 cm). While genotype NIAW-4379 (8.95 cm) recorded minimum spike length.

4.1.5 Number of Spikelets per Earhead

The general mean for number of spikelets per spike was 16.08. The variation in number of spikelets per earhead ranged from 13.50 (NIAW-4379) to 21.40 (NIAW-4393). Fifteen genotypes produced maximum number of spikelets, while other thirty five produced minimum number of spikelets per earhead than the general mean.

4.1.6 Number of Grains per Earhead

The values for number of grains per earhead ranged from 35.10 (NIAW-4396) to 58.40 (NIAW-4461) with population mean of 44.76. Nineteen genotypes recorded more number of grains per earhead than population mean. The genotype NIAW-4461 (58.40) recorded highest number of grains per earhead followed by NIAW-4434 (58.30).

4.1.7 1000 Grain Weight (g)

Estimates of 1000 grain weight ranged from 31.40 g (NIAW-4379) to 53.35 g (NIAW-4390) with the population mean 39.23 g. Twenty three genotypes had higher while twenty seven genotypes had lower 1000 grain weight than population mean.

4.1.8 Grain Yield per Plot (g)

The estimates for this economical character ranged from 479 g (NIAW-4379) to 1644 g (NIAW-4390) with population mean 924.22 g. Twenty four genotypes recorded higher values while twenty six genotypes recorded lower yield than the population mean. Highest grain yield was recorded by NIAW-4390 followed by NIAW-4293 (1481 g).

Table 4.1 Mean values of different yield contributing characters of wheat genotypes

Sr. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Spike length (cm)	No. of spikelets per earhead	No. of grains per earhead	1000 grain weight (g)	Grain yield per plot (g)
1	NIAW-4256	65.50	109.50	102.50	12.55	14.90	43.00	39.90	894.50
2	NIAW-4259	64.50	106.50	86.20	11.10	15.40	44.10	42.10	1003.00
3	NIAW-4261	65.00	108.00	91.75	10.85	15.20	45.50	41.10	952.00
4	NIAW-4265	71.50	117.50	105.50	12.85	14.00	40.15	34.10	607.50
5	NIAW-4267	68.00	113.50	103.00	11.45	14.50	41.80	39.40	769.00
6	NIAW-4279	72.00	119.50	123.00	10.85	13.70	39.30	32.60	527.50
7	NIAW-4282	68.50	114.50	93.95	11.50	14.60	42.00	37.70	783.50
8	NIAW-4289	60.50	104.00	91.95	10.80	16.00	45.70	45.30	1163.00
9	NIAW-4293	60.00	104.00	96.10	13.20	16.90	47.70	53.10	1481.00
10	NIAW-4299	61.50	105.50	95.10	12.20	15.90	45.95	45.10	1152.00
11	NIAW-4308	64.50	109.00	83.20	10.95	15.30	43.80	41.70	985.00
12	NIAW-4311	65.00	107.50	96.10	11.50	15.30	44.00	43.30	1015.00
13	NIAW-4315	68.50	115.50	96.40	11.60	14.30	40.80	35.50	675.00
14	NIAW-4320	60.50	103.50	85.00	10.30	16.50	47.10	48.80	1343.00
15	NIAW-4324	62.50	107.00	96.40	11.00	15.50	44.50	43.00	1051.50
16	NIAW-4331	68.00	112.50	102.00	12.55	14.60	41.80	37.60	781.00
17	NIAW-4340	69.00	114.50	97.40	11.35	14.40	41.10	36.60	727.50
18	NIAW-4343	67.00	109.50	94.70	11.85	14.70	42.10	38.60	827.00
19	NIAW-4345	63.00	107.50	105.50	11.45	15.50	44.50	42.70	1033.00
20	NIAW-4348	61.00	106.00	96.50	12.10	16.00	45.50	44.80	1141.00
21	NIAW-4351	70.00	115.50	111.50	10.05	14.40	41.40	36.30	712.00
22	NIAW-4354	61.50	105.50	95.00	12.10	15.90	45.30	44.70	1136.50
23	NIAW-4358	63.50	109.00	96.80	11.45	15.40	44.00	42.10	1000.00
24	NIAW-4368	70.50	114.00	95.20	9.85	14.30	40.90	35.70	684.50
25	NIAW-4372	70.00	115.50	96.70	9.90	14.30	40.90	35.70	685.00
26	NIAW-4379	74.50	118.00	114.00	8.95	13.50	38.60	31.40	479.00
27	NIAW4380	63.50	106.50	95.90	11.50	15.30	44.10	41.15	1007.00
28	NIAW-4384	64.50	109.00	85.20	10.85	14.80	42.80	39.40	876.00

(contd…)

Table 4.1 (contd…)

Sr. No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Spike length (cm)	No. of spikelets per earhead	No. of grains per earhead	1000 grain weight (g)	Grain yield per plot (g)
29	NIAW-4386	68.00	114.50	95.90	10.35	14.60	41.80	36.60	780.00
30	NIAW-4387	63.00	108.00	93.10	11.70	15.50	44.30	41.90	1045.00
31	NIAW-4388	64.00	121.00	91.00	11.55	15.90	36.10	35.00	544.00
32	NIAW-4389	68.00	111.00	93.80	12.40	14.10	44.80	32.05	811.00
33	NIAW-4390	59.50	104.00	95.20	13.05	16.80	47.30	53.35	1644.00
34	NIAW-4391	79.00	112.00	84.00	12.00	14.15	44.20	37.95	773.50
35	NIAW-4392	65.50	115.00	85.10	11.45	14.50	44.60	36.90	874.50
36	NIAW-4393	63.00	111.50	91.70	10.10	21.40	57.70	41.95	1392.00
37	NIAW-4394	68.00	122.00	102.00	12.70	19.70	50.10	38.10	1021.00
38	NIAW-4395	66.00	121.50	95.30	14.30	16.30	50.40	36.10	1043.50
39	NIAW-4396	69.00	119.50	112.00	11.20	15.70	35.10	37.00	513.00
40	NIAW-4399	71.00	115.50	105.50	10.05	17.90	42.90	36.10	702.00
41	NIAW-4402	66.00	116.50	85.80	10.15	17.70	42.60	32.95	644.00
41	NIAW-4402	66.00	116.50	85.80	10.15	17.70	42.60	32.95	644.00
42	NIAW-4409	73.00	111.00	85.60	10.95	19.50	49.80	38.90	1068.50
43	NIAW-4423	76.00	117.00	95.20	11.25	19.70	49.20	40.15	1055.00
44	NIAW-4428	73.00	114.00	100.60	9.15	18.90	47.10	33.00	891.00
45	NIAW-4431	76.00	114.00	103.50	11.05	19.30	47.50	32.00	910.50
46	NIAW-4434	75.00	117.50	96.00	10.40	21.30	58.30	38.10	1331.00
47	NIAW-4459	66.50	117.00	101.00	9.70	14.20	40.90	38.00	520.00
48	NIAW-4460	71.50	118.00	94.80	10.60	14.60	44.40	42.00	753.50
49	NIAW-4461	68.00	112.50	85.70	10.35	21.00	58.40	38.10	1338.00
50	NIAW-4462	75.50	119.50	100.30	9.65	19.90	52.10	35.90	1064.00
	Mean	67.37	112.41	96.51	11.22	16.08	44.76	39.23	924.22
	Range	59.50-79.00	103.50-122.00	83.20-123.00	8.95-14.30	13.50-21.40	35.10-58.40	31.40-53.35	479.00-1644.00
	S.E±	0.50	0.58	1.01	0.34	0.24	0.96	1.63	81.40
	C.D.at 5%	1.43	1.66	2.87	0.96	0.68	2.74	4.62	231.32
	C. V.	1.06	0.73	1.48	4.25	2.11	3.05	5.87	12.45

4.2 Analysis of Variance

The analysis of variance for eight characters is presented in Table 4.2. For all of the parameters studied, there were extremely significant variances between genotypes, revealing a large range of diversity in 50 wheat genotypes.

Table 4.2 Analysis of variance for eight characters in wheat

Sr. No.	Characters	Replications	Genotypes	Error
	DF	1	49	49
1	Days to 50% flowering	1.69	45.52**	0.51
2	Days to maturity	0.25	53.48**	0.68
3	Plant height (cm)	2.86	133.72**	2.03
4	Spike length (cm)	0.42	2.37**	0.23
5	No. of spikelets per earhead	3.57**	9.16**	0.11
6	No. of grains per earhead	47.33**	46.35**	1.86
7	1000 grain weight (g)	39.31	47.26**	5.29
8	Grain yield per plot (g)	221841.00	138891.47**	13250.33

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

For each of the eight traits tested, the analysis of variance indicated substantial variations across genotypes. This data revealed that a significant degree of diversity exists across all the characters and that selecting for these characters can result in significant improvements. However, the analysis of variance by itself is unable to explain all of the collection's inherent genetic variability. When the overall genetic diversity inherent in genotypes is separated from the phenotypic variance, this becomes clear (Grafius, 1964). As a result, the phenotypic and genotypic coefficients of variation, which represent the extent of variability for particular features, must be calculated.

4.2.1 Coefficient of Variation

Table 4.3 shows estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) as indicated by Sivasubramanian and Madhavamenon (1973).

For all of the characters studied, GCV estimates were lower than PCV. Phenotypic coefficients of variation had a larger magnitude than genotypic coefficients of variation. Grain yield per plot (29.84%) had the highest phenotypic coefficient of variation, followed by number of spikes per earhead (13.39%), 1000 grain weight (13.06%), number of grains per earhead (10.97%), spike length (10.20%) and plant height (8.53%). Comparatively days to maturity (4.62%) and days to 50 per cent flowering (7.12%) had lower phenotypic coefficients of variation.

The inherent genetic variability is expressed by the genotypic coefficient of variation. Highest genotypic coefficient of variation was exhibited by grain yield per plot (27.11%) followed by number of spike per earhead (13.23%), 1000 grain weight (11.67%), number of grains per earhead (10.53%), spike length (9.26%) and plant height (8.40%). Comparatively lower genotypic coefficient of variation was observed for days to maturity (4.57%) and days to 50 per cent flowering (7.04%).

4.2.2 Heritability % (b.s.)

Heritability in broad sense ranged from 79.86 to 97.78 per cent. Highest estimate of heritability was recorded for days to 50 per cent flowering (97.78%) followed by days to maturity (97.49%), number of spikelets per earhead (97.41%), plant height (97.00%). Comparatively lower estimate of heritability was recorded for 1000 grain weight (79.86%) followed by spike length (82.44%).

4.2.3 Genetic Advance

Estimates of genetic advance ranged from 1.74 to 469.20. Highest estimate of genetic advance was recorded for yield per plot (469.20) followed by plant height (16.46), days to maturity (10.45). Comparatively lower estimate of genetic advance was recorded for spike length (1.74) followed by number of spikelets per earhead (4.32).

4.2.4 Genetic Advance as a Per cent of Mean

Genetic advance as a per cent of mean was observed highest for grain yield per plot (50.76%) followed by number of spikelets per earhead (26.88%), 1000 grain weight (21.49%), number of grains per earhead (20.85%). Comparatively lower estimate of genetic advance as per cent of mean was recorded for days to maturity (9.29) followed by days to 50 per cent flowering (14.43).

Estimating the genotypic (heritable), phenotypic and environmental (non heritable) components of total variability is necessary because it aids in the selection of the best breeding approach. Using environmental variance, Johannsen (1909), Nilsson Elhe (1909) and East (1916) differentiated genetic variance from total variance. It is now a widely accepted pattern in all biometrical studies and it aids in determining the genuine breeding value of genotypes. The components of variation, such as genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as a per cent of mean, were computed in the current study in relation to grain yield per plot.

High estimates of genotypic and phenotypic coefficients of variation were found for the character grain yield per plot and medium estimates of genotypic and phenotypic coefficients of variation were found for the characters number of spikelets per earhead, 1000 grain weight and number of grains per earhead in the current study.

Similar results were obtained for grain yield per plant, number of tillers per plant and number of grains per spike by Yousaf Ali *et al.* (2008), Kumar *et al.* (2009) and Devi *et al.* (2014). Subhashchandra *et al.* (2009) for sedimentation value.

Whereas, for the characters spike length, plant height, days to 50 per cent flowering and days to maturity, low estimates of genotypic and phenotypic coefficients of variation were observed. Low estimates of GCV and PCV were reported by Kumar *et al*. (2009) for days to 50 per cent flowering and days to maturity; Mohammed *et al.* (2011) for days to maturity and 1000 grain weight; Asaye *et al.* (2013) for days to maturity; Ashfaq (2014) for days to heading, plant height and 1000 grain weight.

For all traits in this analysis, phenotypic coefficients of variance were greater than genotypic coefficients of variation. This could be due to an effect of the environment. Similar results were also reported by Majumder *et al.* (2008) and Ashfaq *et al.* (2014).

For all of the characters, the difference between GCV and PCV was quite small, indicating that the environment played a minor effect in their expression. The presence of great genetic variability indicates that they have a lot of room for improvement through hybridization and selection. These results are in conformity with results of Majumder *et al.* (2008).

Heritability is a good indicator of character transfer from parents to offspring. The proportion of total variability that is related to genetic factors is known as heritability. To put it another way, it's the genotypic variance divided by total variance. The genetic advance is a measure of genetic gain under selection, calculated as the average genotypic value of the parental population. Accordingly, Johnson *et al.* (1955-b) has suggested estimation of which the expected genetic advance under selection, mainly depends upon

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

High heritability with high genetic advance as a per cent of mean was observed for grain yield per plot, 1000 grain weight, number of spikelets per earhead and number of grains per earhead; high heritability with moderate genetic advance as a per cent of mean was observed for plant height, spike length, days to 50 per cent flowering.

Table 4.3 Estimation of variability parameters for different characters of wheat

Sr. No.	Characters	Mean	Range	Genotypic variance	Phenotypic variance	PCV (%)	GCV (%)	h^2 % (b.s.)	GA	GA as % mean
1	Days to 50% flowering	67.37	59.50 - 79.00	22.51	23.02	7.12	7.04	97.78	9.66	14.34
2	Days to maturity	112.41	103.50 -122.00	26.40	27.08	4.62	4.57	97.49	10.45	9.29
3	Plant height (cm)	96.51	83.20 - 123.00	65.84	67.87	8.53	8.41	97.00	16.46	17.05
4	Spike length (cm)	11.22	8.95 - 14.30	1.08	1.31	10.20	9.26	82.44	1.74	17.32
5	No. of spikelets per earhead	16.08	13.50 - 21.40	4.52	4.64	13.39	13.23	97.41	4.35	26.88
6	No. of grains per earhead	44.76	35.10 - 58.40	22.25	24.11	10.97	10.53	92.28	9.33	20.85
7	1000 grain weight(g)	39.23	31.40 - 53.10	20.99	26.27	13.06	11.67	79.86	8.43	21.49
8	Grain yield per plot(g)	924.22	479.00 -1644.00	62820.57	76070.90	29.84	27.11	82.58	469.20	50.76

These findings suggested that these characters are influenced by additive genetic variance; and high heritability with low genetic advance as a per cent of mean was observed for days to 50 per cent flowering. This finding suggested that thise character is influenced by non additive genetic variance. Rebetzke (1999) found high heritability with moderate genetic advance for plant height and Subhashchandra (2009) reported high heritability with moderate genetic advance for plant height and sedimentation value. In the case of days to maturity, Kumar *et al*. (2013) observed substantial heritability with low genetic advance.

When the estimates of genetic parameters such as genotypic coefficient of variation, heritability and genetic advance as a per cent of mean are added together, the grain yield per plot and number of grains per earhead, 1000 grain weight, number of spikelets per earhead and spike length become clear important characters.

4.3 Correlation

Table 4.4 shows the estimated correlation coefficients between grain yield and all other characters.

4.3.1 Phenotypic Correlation between Grain Yield per Plot and Other Characters

The grain yield (Table 4.4) showed strong significant and positive correlation with 1000 grain weight (0.759), number of grains per earhead (0.775), number of spikelets per earhead (0.568) and spike length (0.271). Grain yield showed significant negative correlation with days to maturity (-0.606), days to 50 per cent flowering (-0.457) and plant height (-0.417).

4.3.2 Genotypic Correlation between Grain Yield per Plot and Other Characters

The grain yield (Table 4.4) showed strong significant and positive correlation with number of grains per earhead (0.797), 1000 grain weight (0.746), number of spikelets per earhead (0.573), spike length (0.268). Grain yield showed significant negative correlation with days to maturity (-0.638), days to 50 per cent flowering (-0.478) and plant height (-0.446).

The yield contributing characters exhibited varying degrees of association among themselves. These are presented below;

4.3.3 Inter Relationship of Yield Components

4.3.3.1 Days to 50 per cent flowering

At both genotypic and phenotypic levels, days to 50 per cent flowering exhibited a highly significant positive correlation with days to maturity and plant height, whereas it showed a highly significant negative correlation with spike length and 1000 grain weight

4.3.3.2 Days to maturity

Plant height demonstrated a positive correlation with days to maturity at both the genotypic and phenotypic levels. At both the genotypic and phenotypic levels, it demonstrated a negative correlation with 1000 grain weight and spike length.

4.3.3.3 Plant height (cm)

At both the genotypic and phenotypic levels, plant height demonstrated a highly significant positive correlation with days to 50 per cent flowering and days to maturity. At the genotypic and phenotypic levels, it had a negative correlation with the number of grains per earhead, the weight of a 1000 grain and the number of spikelets per earhead.

4.3.3.4 Spike length (cm)

At both the genotypic and phenotypic levels, spike length had a highly significant positive correlation with 1000 grain weight. At the genotypic and phenotypic level, it demonstrated a negative correlation with days to 50 per cent flowering and days to maturity.

4.3.3.5 No. of spikelets per earhead

At both the phenotypic and genotypic levels, the number of spikelets per earhead demonstrated a highly significant positive correlation with the number of grains per earhead. At both the phenotypic and genotypic levels, it demonstrated a substantial negative correlation with plant height.

4.3.3.6 No. of grains per spike

At the genotypic and phenotypic levels, number of grains per earhead demonstrated a significantly positive correlation with 1000 grain weight and number of spikelets per earhead. At both the phenotypic and genotypic levels, it demonstrated a substantial negative correlation with plant height.

4.3.3.7 1000 grain weight (g)

At both the genotypic and phenotypic levels, test weight had a highly significant positive correlation with the number of grains per earhead and spike length. At the phenotypic and genotypic level, it demonstrated a substantial negative correlation with days to 50 per cent flowering, days to maturity and plant height.

Table 4.4 Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among grain yield and seven yield contributing characters in fifty genotypes

Characters	Days to 50% heading	Days to maturity	Plant height (cm)	Spike length (cm)	No. of spikelets per earhead	No. of grains per earhead	1000 grain weight (g)	Grain yield per plot (g)
Days to 50% flowering	**1.000**	0.673**	0.296**	-0.366**	0.166	0.025	-0.740**	-0.478**
Days to maturity	0.669**	**1.000**	0.402**	-0.211*	0.102	-0.132	-0.808**	-0.638**
Plant height (cm)	0.292**	0.395**	**1.000**	-0.076	-0.195*	-0.367**	-0.349**	-0.446**
Spike length (cm)	-0.351**	-0.197*	-0.076	**1.000**	-0.177	-0.066	0.345**	0.268**
No. of spikelets per earhead	0.161	0.100	-0.188*	-0.160	**1.000**	0.830**	0.058	0.573**
No. of grains per earhead	0.024	-0.129	-0.351**	0.006	0.824**	**1.000**	0.2637**	0.797**
1000 grain weight (g)	-0.701**	-0.763**	-0.328**	0.342**	0.077	0.260**	**1.000**	0.746**
Grain yield per plot (g)	-0.457**	-0.606**	-0.417**	0.271**	0.568**	0.775**	0.759**	**1.000**

***and ** significant at P= 5 and P = 1 level of significance, respectively**

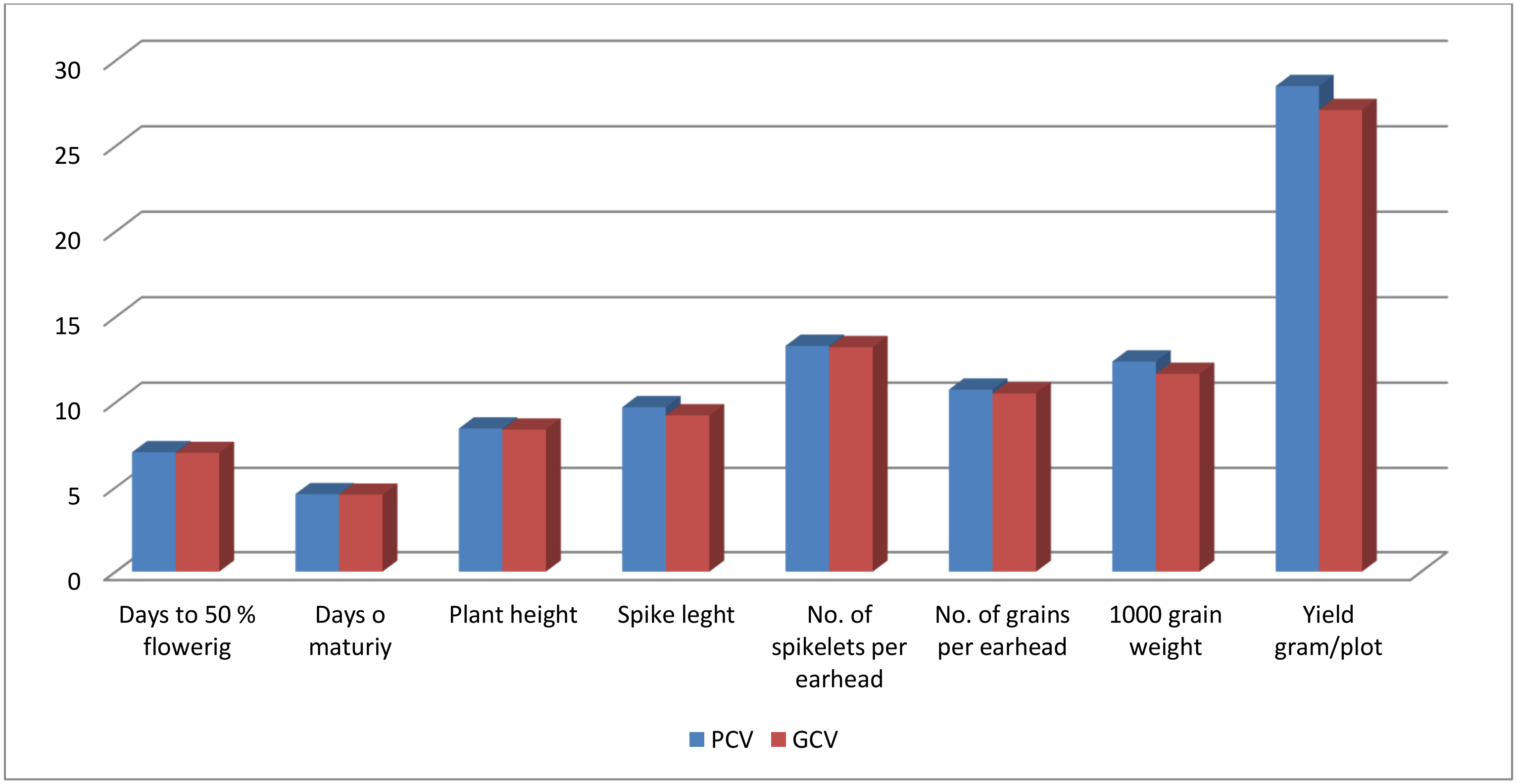


Fig. 1. Graphical comparison of GCV and PCV for eight characters studied in wheat

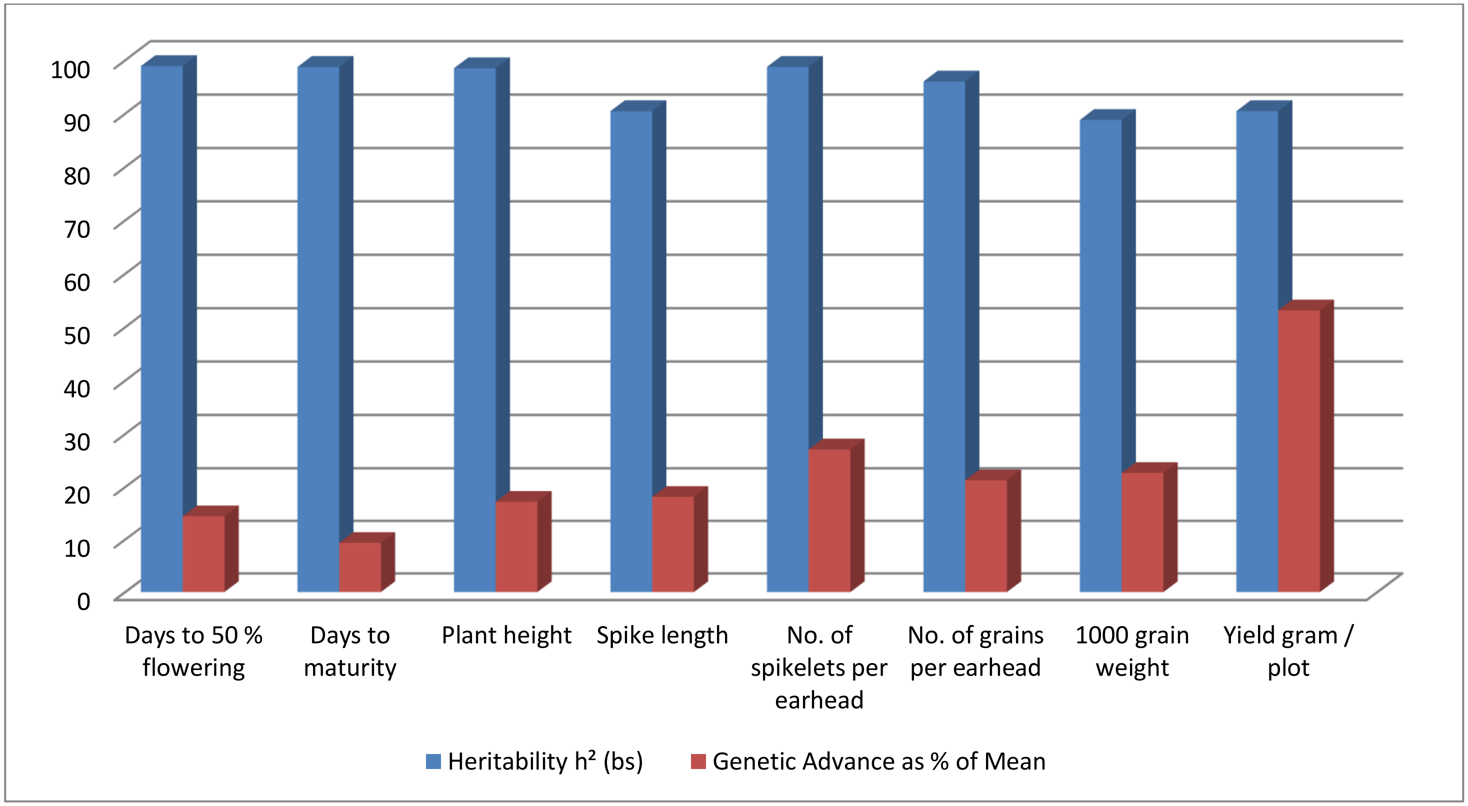


Fig. 2. Graphical comparison of heritability and expected genetic advance as percent of mean for eight characters in Wheat

Any plant's phenotype is the product of a complex interaction of several factors. As a result, the final yield is the sum of the impacts of a number of component characteristics, all of which are polygenically regulated quantitative characters. Correlation studies can be used to determine the impact of these features on yield. Correlation coefficient measures the magnitude and direction of association between two characters taken at a time.

The genetic origins of correlation through the pleiotrophic activity of genes, improvement brought about by selection through related characters and natural selection all contribute to the importance of the correlation coefficient between characters. The interaction between the economic features is extremely beneficial to a successful selection programme. When positive correlations are found, it is possible to improve two or more characters at the same time, whereas negative correlations indicate the necessity to compromise between desirable characters.

Genotypic and phenotypic correlation coefficients are used to determine the degree and direction of relationship between features. Characters with high heritability estimates have lower environmental correlations than genotypic correlations, according to the link between genotypic and phenotypic correlation. Because phenotypic correlation includes both genotypic and environmental correlations, highly heritable traits have higher genotypic correlations than phenotypic correlation when all correlations are in the same direction. When the heritability of two traits is low and the environmental correlation is strong, the phenotypic correlation is greater than the genotypic correlation.

The correlation analysis in this study indicated a pattern of relationship between distinct yield components and grain yield. At both the genotypic and phenotypic levels, Table 4.4 shows the correlation coefficient between the characteristics and grain yield per plot.

At both the genotypic and phenotypic levels, grain yield per plot had a significant positive correlation with 1000 grain weight, number of grains per earhead, spike length and number of spikelets per earhead, whereas characters like days to 50 per cent flowering, days to maturity and plant height had a negative correlation. Ajmal *et al.* (2009) observed that the number of grains per spike and 1000 grain weight were both positively and significantly linked with grain yield and Awale *et al.* (2013) observed that the number of grains per spike contributed significantly to grain yield per plot. Also Yahaya (2014) observed the length of the spike and the number of spikelets per spike both had a positive significant correlation with yield.

4.4 Path Coefficient Analysis

The direct and indirect contributions of each character to the grain yield per plot were determined using path coefficient analysis. Because the correlation coefficient is more essential, it was solely divided into direct and indirect effects, as shown in Table 4.5.

4.4.1 Grain Yield Vs. Days to 50 per cent Flowering

The character days to 50 per cent flowering showed negative direct effect (-0.117) on grain yield per plot and positive indirect effect on grain yield per plot *via,* plant height, number of grains per earhead, number of spikelets per earhead while negative indirect effects on grain yield per plot *via,* days to maturity, spike length, 1000 grain weight. The total genotypic correlation with grain yield per plot was -0.478.

4.4.2 Grain Yield Vs. Days to Maturity

The character days to maturity had negative direct effect (-0.317) on grain yield per plot. It had positive indirect effect on grain yield per plot *via,* plant height, number of spikelets per earhead and negative indirect effect on grain yield per plot *via,* days to 50 per cent flowering, spike length, number of grains per earhead, 1000 grain weight. The total genotypic correlation with grain yield per plot was -0.638.

4.4.3 Grain Yield Vs. Plant Height (cm)

The character plant height had positive direct effect (0.048) on grain yield per plot. It had positive indirect effect on grain yield per plot *via,* days to 50 per cent flowering and days to maturity and negative indirect effect on grain yield per plot *via,* spike length, number of grains per earhead, 1000 grain weight and number of spikelets per earhead. The total genotypic correlation with grain yield was -0.446.

4.4.4 Grain Yield Vs. Spike Length (cm)

The character spike length had positive direct effect (0.118) on grain yield. It had positive indirect effect *via,* days to 50 per cent flowering, days to maturity and 1000 grain weight and negative indirect effect *via,* plant height number of spikelets per earhead and number of grains per earhead on grain yield per plot. The total genotypic correlation with grain yield was 0.268.

4.4.5 Grain Yield Vs. Number of Spikelets per Earhead

The character number of spikelets per earhead had positive direct effect (0.143) on grain yield. It had positive indirect effect *via,* number of grains per earhead and 1000 grain weight and negative indirect effect *via,* days to 50 per cent flowering, days to maturity, plant height and spike length. The total genotypic correlation with grain yield was 0.573.

4.4.6 Grain Yield Vs. Number of Grains per Earhead

The character grains per earhead had positive direct effect (0.602) on grain yield. It had positive indirect effect *via,* days to 50 per cent flowering, 1000 grain weight, number of spikelets per earhead and negative indirect effect through days to maturity, plant height, spike length. The total genotypic correlation with grain yield was 0.797.

4.4.7 Grain Yield Vs. 1000 Grain Weight

The character test weight had positive direct effect (0.211) on grain yield. It had positive indirect effect *via,* spike length, number of grains per earhead, number of spikelets per earhead and negative indirect effect *via,* days to 50 per cent flowering, days to maturity and plant height on grain yield per plot. The total genotypic correlation with grain yield was 0.746.

The obtained correlation coefficient values can be used to explain the nature and extent of the relationship between two characters. Grain yield is an economic element that is dependent on various component characters that are interconnected. Correlation explains the true association that exists between component and dependent character (grain yield).

A minor adjustment in any component will eventually cause the complex to become unbalanced. As a result, a character's action must be determined, which is accomplished using path analysis, which yields two types of effects: direct and indirect effects of component characters on grain yield, which are not recorded by correlation studies.

The direct and indirect contributions of each character to the grain yield per plot were determined using path coefficient analysis. Because the correlation coefficient is more essential, it was solely divided into direct and indirect effects, as shown in Table 4.5.

Path coefficient analysis was performed at the genotypic level in this study, with grain yield per plot as the dependent character and all other characters that showed a significant association with grain yield as independent characters. The path analysis results are given in Table 4.5. The number of grains per earhead, the number of spikelets per earhead and the spike length all exhibited higher magnitude positive and direct effects on grain yield.

Number of grain per earhead had the highest positive direct effect on grain yield, followed by 1000 grain weight, number of spikelets per earhead and spike length, which is confermity with the findings of Zeeshan *et al*. (2013), who found that 1000 grain weight and number of grains per spike had a significant positive direct effect on grain yield. Due to its substantial direct, positive and indirect effects on the entire primary yield contributing characters on grain yield, direct selection for number of grains per earhead alone can result in a significant increase in grain production.

According to Ajmal *et al*. (2009), 1000 grain weight had a high direct effect on grain yield. As a result, 1000 grain weight can be considered during selection to improve grain wheat production. Awale *et al.* (2013) observed the number of grains per spike had a high direct effect on grain yield per plot. Also Yahaya (2014) observed length of the spike and the number of spikelets per spike had a high direct effect on grain yield.

Table 4.5 Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of component characters on grain yield in fifty genotypes

Character	Days to 50% heading	Days to maturity	Plant height (cm)	Spike length (cm)	No. of spikelets per earhead	No. of grains per earhead	1000 grain weight (g)	Grain yield per plot (g)
Days to 50% flowering	**-0.117**	-0.214	0.014	-0.043	0.024	0.015	-0.156	-0.478**
Days to maturity	-0.079	**-0.317**	0.019	-0.025	0.015	-0.079	-0.170	-0.638**
Plant height (cm)	-0.035	-0.128	**0.048**	-0.009	-0.028	-0.221	-0.074	-0.446**
Spike length (cm)	0.043	0.067	-0.004	**0.118**	-0.025	-0.004	0.072	0.268**
No. of spikelets per earhead	-0.019	-0.033	-0.009	-0.020	**0.143**	0.499	0.012	0.573**
No. of grains per earhead	-0.003	0.042	-0.018	-0.001	0.119	**0.602**	0.056	0.797**
1000 grain weight (g)	0.087	0.257	-0.017	0.041	0.008	0.159	**0.211**	0.746**

Residual effect= 0.110

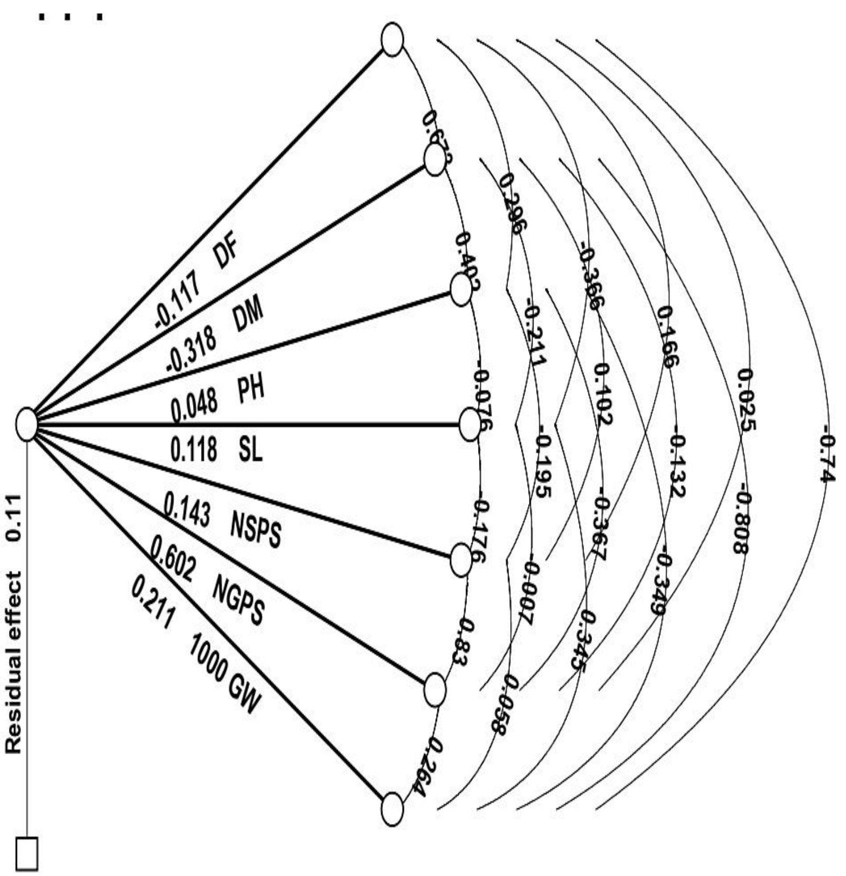


Fig.3. Genotypic Path Diagram for Grain Yield per Plot

4.5 Genetic Divergence

Estimation of genetic divergence by Mahalanobis D^2 statistics for 50 wheat genotypes with eight characters provided genetic divergence.

4.5.1 Cluster Formation

As mentioned by Rao (1952), the cluster creation was done using Tocher's approach. The 50 wheat genotypes under examination were divided into six clusters, with Cluster I containing the most genotypes (31 genotypes). Cluster III had eleven genotypes, while Cluster II had five. Clusters IV, V and VI each had one genotype (Table 4.6).

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

Clusters	No. of genotypes include	Name of genotypes	Origin
I	31	NIAW 4299	PUSA BAKER X LOK 54
		NIAW 4354	NIAW 1994 X FRANCOLIN #1
		NIAW 4348	NIAW 1415 X PUSA BAKER
		NIAW 4324	NI 5643 X NIAW 1994
		NIAW 4380	MACS 6222 X SRRSN 6006
		NIAW 4387	(NIAW 1885 X SRRSN 6022)X SRRSN 6022
		NIAW 4358	NIAW 1415 X NIAW 2268
		NIAW 4311	NI 9947 X LOK 1
		NIAW 4261	RAJ 4176 X LOK 62
		NIAW 4289	DBW 17 X NIAW 1885
		NIAW 4293	C 306 X SRRSN 6066
		NIAW 4390	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
		NIAW 4343	NI 9947 X NIAW 1994
		NIAW 4259	LOK 62 X NIAW 1698
		NIAW 4384	DBW 93 X MACS 6222
		NIAW 4308	AKAW 4627 X NIAW 1994
		NIAW 4320	HD 2932 X AKAW 4627
		NIAW 4345	DBW 17 X NI 5643
		NIAW 4256	NIAW 1594 X PHS 1101
		NIAW 4282	NIAW 1994 X SRRSN 6123
		NIAW 4386	NIAW 1415 X (NI343) X NIAW 34)
		NIAW 4389	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
		NIAW 4392	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)
		NIAW 4340	NIAW 34 X RAJ 4304
		NIAW 4315	NI 343 X NIAW 1994
		NIAW 4368	NIAW 301 X FRANCOLIN # 1
		NIAW 4331	RAJ 4304 X NIAW 1994
		NIAW 4372	NIAW 34 X NIAW 1994
		NIAW 4267	NIAW 1885 X NIAW 1415
		NIAW 4459	FRET2/TUKURU//FRET2/3/MUNAL #1/4/SUP152/AKURI//SUP152

(Contd…)

Table 4.6 (contd…)

Clusters	No. of genotypes include	Name of genotypes	Origin
		NIAW 4460	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PANDION//FILIN/2*PASTOR/3/BERKUT
II	5	NIAW 4351	NIAW 1885 X NIAW 1994
		NIAW 4379	NIAW 2030 X SRRSN 6115
		NIAW 4265	PHS 1101 X King Bird
		NIAW 4279	NIAW 1415 X DBW 17
		NIAW 4396	(NIAW 34 X HD 2932) X (NIAW 1994 X NI 343)
III	11	NIAW 4423	KUTZ*2/5/UP2338*2/VIVITSI/3/FRET2/TUKURU//FRET2/4/MISR 1
		NIAW 4462	18th HTWSBYT 28
		NIAW 4434	KACHU #1/KIRITATI//KACHU*2/3/GRACK/CHYAK
		NIAW 4428	KACHU #1/KIRITATI//KACHU*2/3/BECARD/FRNCLN
		NIAW 4431	PRL/2*PASTOR//PBW343*2/KUKUNA/3/ROLF07/4/MUTUS*2/TECUE #1
		NIAW 4409	PYT TS 52
		NIAW 4399	(DBW 17 X NIAW 1415) X NIAW 1415
		NIAW 4394	(LOK 1 X HD2932) X (LOK 1) X NIAW 1994)
		NIAW 4402	PYT TS 18
		NIAW 4461	19th KBSN 29
		NIAW 4393	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)
IV	1	NIAW 4395	(LOK 1 X HD2932) X (LOK 1) X NIAW 1994)
V	1	NIAW 4388	(AKAW 4627 X RAJ 4304) X (PUSA BEKER X SRRSN 6066)
VI	1	NIAW 4391	(C 306 X SRRSN 6022) X (AKAW 4627 X NI 9947)

Table 4.7 Average intra (diagonal) and inter (above diagonal) cluster D and D^2 (in bracket) values of six clusters formed from fifty genotypes of wheat

Clusters	I	II	III	IV	V	VI
I	12.26 (150.31)	23.83 (567.87)	31.90 (1017.61)	18.57 (344.84)	22.42 (502.66)	23.69 (561.22)
II		14.06 (197.68)	37.12 (1377.89)	22.91 (524.87)	26.88 (722.53)	30.86 (952.34)
III			16.75 (280.56)	30.72 (943.72)	25.42 (646.18)	30.66 (940.04)
IV				0.00 (00.00)	16.76 (180.90)	28.58 (816.82)
V					0.00 (00.00)	32.13 (1032.34)
VI						0.00 (00.00)

4.5.2 Intra and Inter Cluster Distance

D^2 statistics were used to calculate intra and inter cluster D^2 and D values. The intra and inter cluster distances were calculated using the mean D^2 values of cluster constituents. Table 4.7 shows the results.

The maximum inter cluster distance was observed between Cluster II and III (1377.89) followed by Cluster V and VI (1032.34), Cluster I and III (1017.61), Cluster II and VI (952.34), Cluster III and IV (943.72), Cluster III and VI (940.64), Cluster IV and VI (816.82).

The maximum Intra cluster divergence among the six clusters revealed that Cluster III had maximum intra cluster distance (280.56) followed by Cluster II (197.68) and Cluster I (150.31). The minimum intra cluster distance was observed for Cluster IV, V, VI (D =0).

4.5.3 Cluster Mean

Table 4.8 shows the cluster means for eight characters. It found that most of the traits have a broad range of variability.

4.5.3.1Days to 50 per cent flowering

Cluster V (64.00 days) was early for days to 50 per cent flowering followed by Cluster I (65.10 days), Cluster VI (66.00 days), however Cluster VI (79.00 days) had late flowering.

4.5.3.2 Days to maturity

Cluster I (109.84 days) was early for days to maturity followed by Cluster VI (112.00 days) and Cluster III (115.55 days). However, Cluster IV (121.50 days) and Cluster V (121.00 days) shown the late maturity.

4.5.3.3 Plant height (cm)

Cluster II (113.20 cm) recorded highest cluster mean for plant height followed by Cluster III (95.63 cm), Cluster IV (95.30 cm). Cluster VI (84.00 cm) was dwarf.

4.5.3.4 Spike length (cm)

Cluster IV (14.30 cm) recorded highest cluster mean for spike length followed by Cluster VI (12.00 cm), Cluster V (11.55 cm) and lowest mean in Cluster III (10.53 cm).

4.5.3.5 Number of spikelets per earhead

Cluster III (19.66) recorded highest cluster mean for number of spikelets per earhead followed by Cluster IV (16.30), V (15.90), Cluster I (15.16) and lowest number of spikelets per earhead observed in Cluster VI (14.15).

4.5.3.6 Number of grains per earhead

Cluster III (50.52) recorded highest cluster mean for grains per earhead followed by Cluster IV (50.40), Cluster VI (44.20) and lowest grains per earhead observed in Cluster V (36.10).

4.5.3.7 1000 grain weight (g)

Cluster I (41.16 g) recorded highest cluster mean for test weight followed by Cluster VI (37.95 g), Cluster III (36.84 g) and lowest cluster mean observed in Cluster V (35.00 g).

4.5.3.8 Grain yield per plot (g)

Cluster IV (1043.50 g) recorded highest cluster mean for grain yield per plot followed by Cluster III (1037.91 g), Cluster I (954.65 g) and lowest cluster mean observed in Cluster V (544.00 g).

The most important and hardest task for any hybridization programme is to choose elite genotypes with high *per se* performance for yield and yield contributing characters with appropriate genetic divergence among them. It would be possible to identify desirable genotypes based on the genetic variability, but it would be difficult to expect extraordinary results from their progeny unless we knew about their divergence.

D^2 statistics concept was created by Mahalanobis (1936) and it is an important tool for plant breeders. This method may be used to assess the degree of divergence between biological populations at the genotypic level, as well as the relative contributions of different components to the total divergence at both the intra and inter cluster levels. Rao (1952) was the first to suggest that this technique can be used to measure genetic diversity in plant breeding.

Genetic diversity is an important aspect in crop improvement programmes and it is a necessary pre-requisite for hybridization programmes to produce high-yielding progenies.

Plant breeders have used quantitative studies of genetic divergence among different characters to better understand racial affinities and evolutionary patterns in diverse cultivated plant species, as well as to choose the best parental combination in hybridization programmes. Incorporating divergent parents into a hybridization programme aids in the combination of desired genes, resulting in desirable recombinants. In the preliminary evaluation of genotypes under study, quantitative measurement of genetic diversity would be more beneficial.

Table 4.8 Mean performance of cluster for eight characters in fifty wheat genotypes

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Spike length (cm)	No. of spikelets per earhead	No. of grains per earhead	1000 grain weight (g)	Grain yield per plot (g)
Cluster I	65.10	109.84	94.76	11.39	15.16	43.78	41.16	954.65
Cluster II	71.40	118.00	113.20	10.78	14.26	38.91	34.28	567.80
Cluster III	71.32	115.55	95.63	10.53	19.66	50.52	36.84	1037.91
Cluster IV	66.00	121.50	95.30	14.30	16.30	50.40	36.10	1043.50
Cluster V	64.00	121.00	91.00	11.55	15.90	36.10	35.00	544.00
Cluster VI	79.00	112.00	84.00	12.00	14.15	44.20	37.95	773.50

Table 4.7 summarizes data on intra-cluster (diagonal) and inter-cluster (inter-cluster) distances across eight clusters, revealing that intra-cluster distance values ranged from 0.00 to 280.56. Because of the occurrence of varied accessions within distinct clusters, the largest level of heterosis is expected in cross combinations comprising the genotypes of the most divergent clusters, according to the inter-cluster distance data. As aggregates of traits measured, genotypes clustered into the same cluster are likely to differ little from one another. Crossing genotypes from the same cluster should not produce superior hybrids or desirable segregants, according to theory. However, there is a general theory that the greater the diversity between genotypes, the greater the heterosis (Falconer, 1981). As a result, it would be preferable to try crossings between genotypes from different clusters in order to obtain extremely heterotic hybrids. Furthermore, heterosis cannot be used in a crop that is largely self-fertilized. In the case of additive gene action, however, substantial heterosis may be useful in distinguishing superior segregants.

Those genotypes found in Clusters with the maximum inter-Cluster distance are clearly more genetically diverse. As a result, it would make sense to include genotypes from these clusters in future breeding programmes. The maximum inter-cluster distance was recorded between clusters II and III in this situation (1377.89). Cluster IV and V had the minimum inter-cluster distance (180.90). Cluster III has the maximum intra cluster distance (280.56), followed by Cluster II (197.68) and Cluster I (150.31).The least intra cluster distance was observed for cluster IV, V, VI (D =0).

An important part of any breeding for crop improvement effort is determining the level and pattern of genetic diversity. It has a wide range of uses, including: i) genetic variability analysis. ii) identifying various parental pairings to provide genetic variability for further selection and iii) introducing desirable genes from various germplasm into the genetic base. Cluster analysis' main goal is to put individual together based on their shared traits, such that individual with similar descriptions are mathematically grouped together. Variability and relationships among accessions can be studied using a variety of techniques based on total grain proteins, isozymes and various types of molecular marker profiles. However, in the description and classification of germplasms, morphological characterization is the initial step. It's also been suggested that the more different the parents, the better the chances of creating a wide range of variability in segregating populations (Arunachalam, 1981).

4.6 Genetic Divergence and Selection of Potent Parent

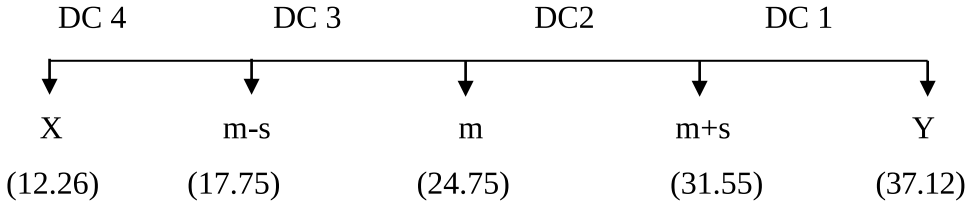
Selection of the best parent with high potential for economically essential traits is critical to the success of any crop improvement effort. Among the several ways for selecting parents, diversity-based selection has its own relevance, as diversity is a fundamental requirement for crop improvement. As a result, the diversity among different genotypes was investigated in this study, yielding valuable information that could be useful in the selection of a potent parent for hybridization.

Crosses between different parents yielded greater heterosis than crosses between closely related parents, according to Hays and Johanson (1939) and East and Hays (1942). Timothy (1963) stated that one of the factors for selecting parents for hybridization is genetic divergence, which can result in transgressive segregants in segregating generations. For the selection of parents, Bhatt (1970) advised the use of multivariate analysis. He also suggested that statistical distances between genotypes belonging to clusters separated by a large estimated statistical distance could be used arbitrarily as a guideline and that it would be logical to effect crosses between genotypes belonging to clusters separated by a large estimated statistical distance.

Following the technique proposed by Arunachalam and Bandopadhay (1984), an attempt was made to classify the cluster combination into four divergence classes in the current study. Table 4.7 shows the statistical distance (D^2) between clusters as an indicator of genetic diversity.

The mean of fifteen inter clusters and three intra-clusters was 24.75 and standard deviation 6.80. The minimum (X) and maximum (Y) values among these distances were 12.26 and 37.12, respectively. Thus, the divergence classes were as

Divergence Classes



On the light of discussion, the initial choice of parents should be made from cluster combinations in the DC 2 and DC 3 divergence classes. When crossing genotypes within a cluster, the genotypes *per se* performance for various traits such as earliness days to maturity, spike length, number of spikelets per earhead, number of grains per earhead, grain yield per plot and so on should be considered so that desirable transgressive segregants can be obtained after hybridization.

Table 4.9 Distribution of different clusters combinations into four divergence classes based on D^2 values between them. (Cluster Combinations)

Y (37.12)

DC 1 (I, III), (II, III), (V, VI)

m + s (31.55)

DC 2 (III, V), (II, V), (IV, VI), (III, VI), (III, IV), (II, VI)

m (24.75)

DC 3 (I, II), (I, VI), (II, IV), (I, V), (I, IV)

m – s (17.95)

DC 4 (IV,V)

X (12.26)

Source clusters are formed using the cluster means in Table 4.8 and are presented in Table 4.10. These source clusters provide the desired parents for hybridization programmes aimed at improving the characters listed against them.

Table 4.10 Characters improvement on the basis of source clusters

Sr. No.	Characters	Source Clusters
1.	Days to maturity (Early)	I, III, VI
2.	Spike length (Maximum)	IV, V, VI
3.	Number of spikelets per earhead (Maximum)	III, IV, V
4.	Number of grains per earhead (Maximum)	III, IV, VI
5.	Grain yield per plot (Maximum)	I, III, IV

Considering all of the aforementioned factors, the following genotypes in the current investigations deserve to be evaluated as potential parents for future cross-breeding programmes aimed at increasing grain yield and contributing characteristics.

Sr. No.	Genotypes	Sr. No.	Genotypes
1	NIAW-4293	8	NIAW-4289
2	NIAW-4390	9	NIAW-4393
3	NIAW-4299	10	NIAW-4324
4	NIAW-4354	11	NIAW-4461
5	NIAW-4320	12	NIAW-4394
6	NIAW-4345	13	NIAW-4348
7	NIAW-4434	14	NIAW-4395

Considering the inter-cluster distance, cluster means and *per se* performance of genotypes and divergence class, the above genotypes may be used in future breeding programmes to create a broad range of variability for various yield contributing characters, allowing for the development of superior genotypes in more than one character and the possibility of improving more than one character.

4.7 Per cent Contribution of Various Characters for Divergence

The per cent contribution of the eight characters studied towards the total divergence was presented in Table 4.11. It was revealed that days to 50 per cent flowering (26.04%) contributed highest for genetic divergence followed by plant height (23.92%), number of spikelets per earhead (17.71%), days to maturity (14.45%), 1000 grain weight (10.20%), yield per plot (3.59%), spike length (2.53%). However, the character number of grains per spike (1.55%) contributed least to genetic divergence.

Table 4.11 Per cent contribution of eight different characters of wheat genotype for divergence

Sr. No.	Source	Times ranked first	Contribution %
1	Days to 50% flowering	319	26.04
2	Days to maturity	177	14.45
3	Plant height (cm)	293	23.92
4	Spike length (cm)	31	2.53
5	No. of spikelets per earhead	217	17.71
6	No. of grains per earhead	19	1.55
7	1000 grain weight (g)	125	10.20
8	Grain yield per plot (g)	44	3.59
	Total	**-**	**100**

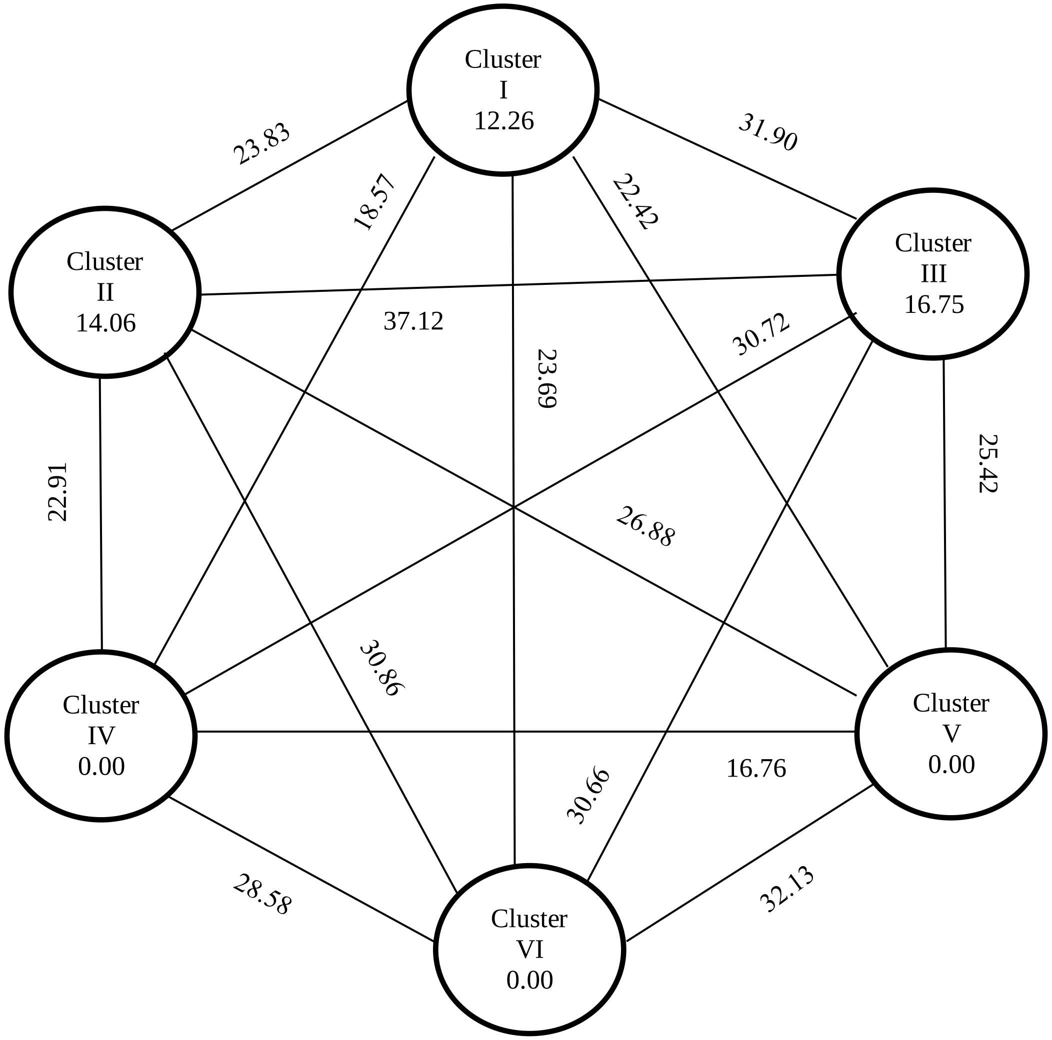


Fig. 4. Cluster diagram

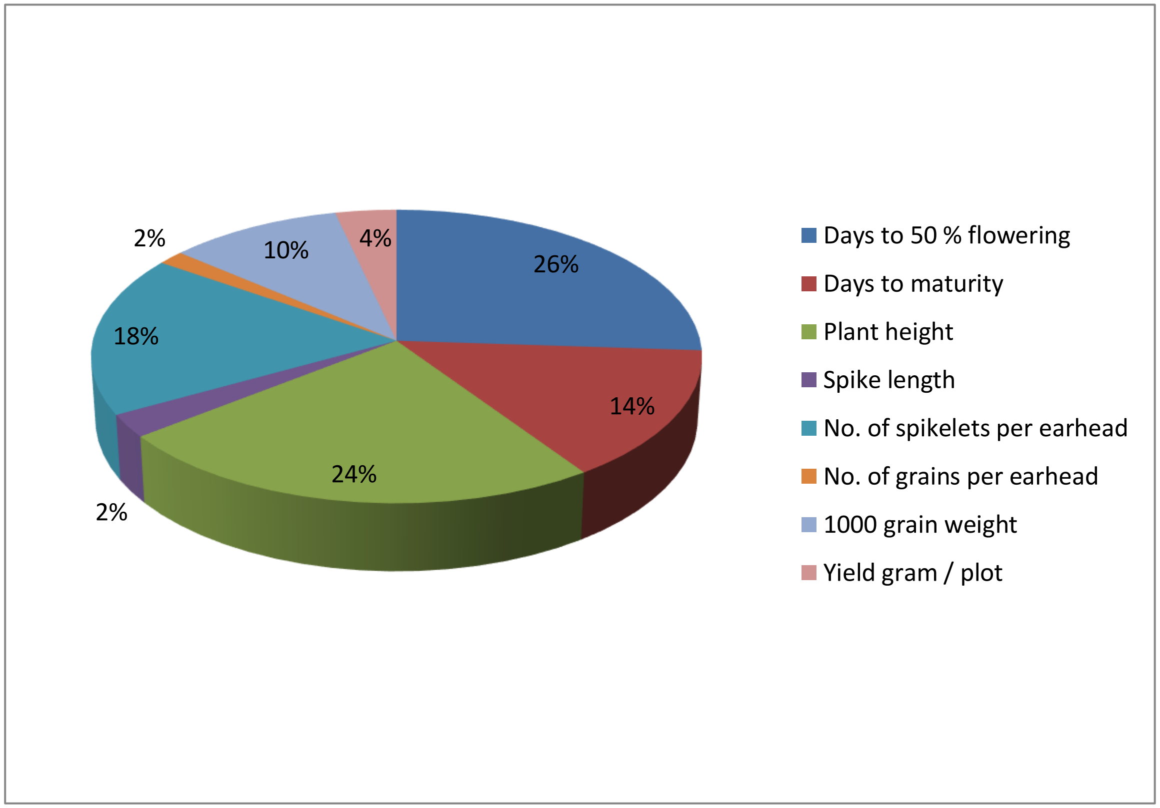


Fig. 5. Per cent contribution of eight characters in total diversity of Wheat

5. SUMMARY AND CONCLUSIONS

The present investigation entitled "Genetic diversity of newly developed lines in bread wheat (*Triticum aestivum* L.)" was undertaken with a view to study genetic diversity, correlation, heritability and genetic advance for 50 diverse genotypes of wheat. Eight characters were used to record the observations. During *rabi* 2019-20, the experiment was conducted using 50 genotypes in a Randomized Block Design with two replications. For a total of eight characters, observations were taken. Days to 50 per cent flowering, days to maturity, plant height, spike length, number of spikelets per earhead, number of grains per earhead, 1000 grain weight and grain yield per plot were the characteristics studied.

5.1 Variability, Heritability and Genetic Advance

For 50 genotypes, eight characters were analysed to determine genetic variability and variety. In the genotypes, there was a significant degree of variation. For all of the characters, the phenotypic coefficient of variation (PCV) was found to be marginally larger than the genotypic coefficient of variation (GCV), indicating that the phenotypic coefficient of variation dominates the expression of these features.

Highest phenotypic coefficient of variation was exhibited by grain yield per plot (29.84%), followed by number of spikes per earhead (13.39%), 1000 grain weight (13.06%) and number of grains per earhead (10.97%), spike length (10.20%) and plant height (8.53%). Comparatively days to maturity (4.62%) and days to 50 per cent flowering (7.12%) had lower phenotypic coefficients of variation.

Heritability in broad sense ranged from 79.86 to 97.78 per cent. Highest estimate of heritability was recorded for days to 50 per cent flowering (97.78%) followed by days to maturity (97.49%), number of spikelets per earhead (97.41%), plant height (97.00%). Comparatively lower estimate of heritability was recorded for 1000 grain weight (79.86%) followed by spike length (82.44%).

Estimates of genetic advance ranged from 1.74 to 469.20. Highest estimate of genetic advance was recorded for yield per plot (469.20) followed by plant height (16.46), days to maturity (10.45). Comparatively lower estimate of genetic advance was recorded for spike length (1.74) followed by number of spikelets per earhead (4.32).

Genetic advance as a per cent of mean was observed highest for grain yield per plot (50.76%) followed by number of spikelets per earhead (26.88%), 1000 grain weight (21.49%), number of grains per earhead (20.85%). Comparatively lower estimate of genetic advance as per cent of mean was recorded for days to maturity (9.29) followed by days to 50 per cent flowering (14.43).

1. High estimates of genotypic coefficient of variation among the genotypes indicates variability for the characters *viz,* grain yield per plot followed by number of spikelets per earhead, 1000 grain weight, number of grains per earhead, spike length, plant height, days to 50 per cent flowering and days to maturity.
2. The magnitude of PCV was more than GCV for all the characters.
3. For grain yield per plot, 1000 grain weight, number of spikelets per earhead and number of grains per earhead, high heritability with high genetic advance as a per cent of mean was observed, indicating that the heritability is due to additive gene effect and direct selection in early generations may be effective.

5.2 Correlation

Grain yield per plot recorded significant positive correlation with number of grains per earhead, 1000 grain weight, number of spikelets per earhead, spike length at both genotypic and phenotypic levels so these characters could be improved through selection. Whereas, grain yield showed significant negative correlation with 50 per cent flowering, days to maturity, plant height at genotypic as well as phenotypic levels.

5.3 Path Coefficient Analysis

Path coefficient analysis revealed that number of grains per earhead had highest direct effect on grain yield per plot followed by 1000 grain weight, number of spikelets per earhead and spike length. Therefore, emphasis should be given on these characters while making selection for desired improvement for grain yield of wheat. While, making selection for desired improvement in grain yield, emphasis should be given on characters *viz.*, number of grains per earhead, 1000 grain weight, number of spikelets per earhead and spike length as these characters showed significant positive association with grain yield.

5.4 Genetic Divergence

In the present investigation, the genotypes grouped into six clusters, by using Tocher's method as described by Rao (1952). Cluster I was with 31 genotypes emerged as the largest cluster. Cluster III was with 11 genotypes and cluster II with 5 genotypes were larger clusters. The clusters IV, V, VI were mono-genotypic.

The maximum inter cluster distance was observed between cluster II and III (1377.89) followed by cluster V and VI (1032.34), cluster I and III (1017.61), cluster II and VI (952.34), cluster III and IV (943.72),cluster III and VI (940.64) and cluster IV and

VI (816.82). It is desirable to select accessions from clusters having high inter-cluster distance. Cluster IV and V had the minimum inter-cluster distance (180.90).

Cluster III has the maximum intra cluster distance (280.56), followed by Cluster II (197.68) and Cluster I (150.31). The minimum intra cluster distance was observed for Cluster IV, V, VI (D =0).

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

1. There is substantial genetic diversity among the genotypes studied
2. The 50 genotypes were grouped into six clusters
3. No parallelism between genetic diversity and geographical distribution was observed
4. On the basis of inter cluster distances, cluster mean and *per se* performance and divergence class observed in the present study, the genotypes *viz.,* NIAW-4293, NIAW-4390, NIAW-4299, NIAW-4354, NIAW-4320, NIAW-4345, NIAW-4434, NIAW-4289, NIAW-4393, NIAW-4324, NIAW-4461, NIAW-4394, NIAW-4348 and NIAW-4395 were distinct and diverse and can be classified as promising genotypes. These genotypes could be used in crossing programme to achieve desired segregants in wheat.

6. LITERATURE CITED

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IN

AGRICULTURAL BOTANY

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2021

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