

Genetic Analysis for Yield, its Components and Quality Characters in Wheat

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the Degree of**

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In

AGRICULTURE

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2018

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*This is to certify that the thesis entitled “**Genetic Analysis for Yield, its Components and Quality Characters in Wheat**” submitted in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE (Genetics and Plant Breeding)** of Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur is a record of the bonafide research work carried out by **Mr. LAVKESH CHOUDHARY** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instructions.*

All the assistance and help received during the course of the investigation has been acknowledged by him.

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List of abbreviations

d. f.	-	Degree of freedom
Fig.	-	Figure
GA	-	Genetic advance
GCV	-	Genotypic coefficient of variation
Max	-	Maximum
Mha	-	Million hectare
Min	-	Minimum
MSS	-	Mean sums of squares
PCV	-	Phenotypic coefficient of variation
STNT		Station Trial
S. No.	-	Serial number
SD	-	Standard deviation
SE	-	standard error
SS	-	Sums of squares
SV	-	Sources of variations

List of Symbols

	et al.,	-	And Others
	Cm	-	Centimeter
	©	-	Copyright
	°C	-	Degrees Celsius
	e.g.	-	For example
	G	-	Gram
	Ha	-	Hectare
	$h^2(b)$	-	Heritability in broad sense
	Hrs	-	Hours
	Max.	-	Maximum
	ml	-	Milliliter
	Min.	-	Minimum
	<i>viz.</i> ,	-	Namely
	/	-	Oblique
	%	-	Percentage
	±	-	Plus or Minus
	σ	-	Sigma
	$\sqrt{\quad}$	-	Square root
	Σ	-	Summation
	i.e.,	-	That is
	v/v	-	Volume by volume

INTRODUCTION

Wheat belongs to the genus “Triticum” of Poaceae family. There are 17 different species, out of which only 3 species are cultivated throughout the world. These are *Triticum aestivum* (bread wheat), *Triticum durum* (macaroni wheat) and *Triticum dicoccum* (emmer wheat) with polyploidy levels viz. hexaploid ($2n=6x=42$), tetraploid ($2n=4x=28$) and diploid ($2n=2x=14$) respectively. Wheat is grown under wide range of climatic conditions but adapted to cool and dry environment, between 30° and 60° N and 27° and 40° E latitudes. In India it is mostly grown in plains, in the Northern hilly region of Himalayas and Nilgiris and Palani hills of southern India. Especially *Triticum aestivum* is widely cultivated in temperate regions, with many varieties for its commercially important edible grain.

Wheat yields are greatly affected by irregularities of monsoon, distribution pattern of rainfall and winter temperature. Global warming creates problem in the form of drought and heat stress during wheat production. There is immense need to increase production and productivity/unit area of wheat to meet increasing food demand of fastly growing population. Wheat ranks second in world crop production and is a staple food for over 41% of the world's population in more than 40 countries, So It is known as “King of cereals”. The major wheat producing countries in the world are Russia, China, India, US, Canada, France, Argentina and Australia.

Wheat is the second important grain crop after rice in our country. India is the world's second largest wheat producer, behind China and ahead of the USA with a production of 93.50 million tonnes, (FAO, 2016). During *rabi* (2016-17) wheat production has reached an all-time record of 97.44 million tonnes with an average National productivity of 3172 kg/ha. In Madhya Pradesh area, production and productivity of wheat is 5.94 million hectare, 17.78 million tonnes and 2993 kg/ha.respectively (Anonymous, 2017).

The wheat inflorescence is a spike bearing sessile spikelets arranged alternatively on a zig-zag rachis. Three florets develop in each spikelet and bear grains. The grains may be white, red (brown) and amber. It may be hard, semi hard and soft in texture. Size of the grain or caryopsis may be large as in

durum or very small as in short wheat (*Triticum sphaerococcum*). An average nutritive composition of wheat is protein-12.17%, fatty acid-22.5 mg, gluten-8% and carbohydrate-71.2%.

Grain yield in wheat is a complex character governed by polygenes and is dependent on its components for genetic improvement of grain yield, quality and other characters in wheat, there is a need to examine the nature of genetic variability for the yield related attributes and quality traits. Estimation of Genotypic Coefficient of Variation (GCV%) and Phenotypic Coefficient of Variation (PCV%) helps to choose the potential genotype and heritability along with genetic advance would be more useful tool in predicting the resultant effect of selection of best genotypes for yield (Kumar *et al.* 2014).

However it is difficult for variety to be identified by the expression of the single morphological character, therefore use of different morphological features in a sequential fashion is useful and convenient to distinguish the variety (Singhal and Prakash 1992). Thus for the improvement of grain yield , knowledge of genetic variability of characters of economic importance, association relationship of yield and yield components are of utmost importance, which will help in planning of the future breeding programme. Besides these, the extent of divergence and relative contribution of different components to total divergence helps in the identification of diverse parents for hybridization and improvement of yield in wheat.

Breeding/identification of high yielding wheat lines of good quality associated with resistance to major biotic and abiotic factors is the prime objective of wheat improvement. Knowledge of pattern of existing genetic variability, trend of character association, identification of promising traits and extent of genetic divergence will definitely help researcher to identify important characters and development of high yielding wheat lines.

In order to increase the efficacy of germplasm the information on genetic basis of variation for economically important attributes is a pre-requisite for any breeding programme. Improvement in the desirable characters relies mainly upon identification of genetically superior and suitable genotypes. Selection of

progeny and its breeding depend upon the genetic variability in a population (Ajmal *et al.* 2009).

Keeping these in view, the present investigation has been conducted with the following objectives.

1. To estimate parameters of genetic variability
2. To find out characters association, direct and indirect effects
3. To estimate extent of genetic divergence (D^2) analysis
4. To identify suitable genotypes using principal component analysis

REVIEW OF LITERATURE

The success of any plant improvement programme mainly depends on the selection of material and its skillful management. It is only possible when we possess knowledge of previous work done in the concerned field. In wheat substantial contribution has been made to the literature regarding its genetics and breeding in the recent years. The literature pertaining to the various aspects of the present study has been reviewed under the following heads:

- 2.1 Parameters of genetic variability
 - 2.1.1 Coefficient of variation
 - 2.1.2 Heritability and genetic advance
- 2.2 Correlation coefficient analysis
- 2.3 Path coefficient analysis
- 2.4 Genetic divergence
- 2.5 Principal component analysis

2.1 Parameters of genetic variability

2.1.1 Coefficient of variation

Genetic variability in a population is important for biodiversity, because without variability, it becomes difficult for a population to adapt environmental changes. Hence, variability is the most key aspect of any research for a breeder, amount of which determining the extent of sources of selection. Various parameter of genetic variability are mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense habitability and genetic advance.

The idea of partitioning of variance was given by Fisher (1918), further many workers also suggested various techniques for estimation of components of variation.

Bisht and Gahalain (2009) reported high coefficient of variability for almost all the characters except for days to 75% spike emergence, plant height, days to maturity and number of spikelets/spike.

Mohibullah *et al.* (2011) statistically found high genetic diversity for all the traits.

Tsegaye *et al.* (2012)) revealed that the analysis of variance for traits showed significant ($P < 0.01$) differences among the genotypes and also observed the values of phenotypic coefficient of variation for most of the characters were closer than the corresponding genotypic coefficient variation values showing little environment effect on the expression of these characters.

Bhushan *et al.* (2013) revealed that the treatments were highly significant for all the characters. They reported high magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for grain yield, biological yield, productive tillers /plant and plant height.

Rajpoot *et al.* (2013) reported wide range of genetic variability among genotypes for days to 50% heading, plant height, length of ear, number of spikelets /spike, days to maturity, number of seeds /spike, test weight and grain yield/plant and also found that the phenotypic variances were higher than the genotypic variances.

Singh and Upadhyay (2013) reported significant differences among all the characters except, number of effective tillers/r plant and ear length. They observed that the phenotypic variance value for most of the characters was closer to the corresponding genotypic variance value showing little environment effect on the expression of these characters.

Rajdeep *et al.* (2014) reported significant differences among all the characters *viz.*, days to 50 % flowering, days to maturity, plant height, number of spikelets per spike, productive tillers per plant, ear length, number of grains per spike, 1000 grain weight, and biological yield per plant, grain yield per plant, harvest index and gluten content. A broad range of variation was observed for

plant height and biological yield/plant, number of grains /spike and test weight and found the phenotypic variance value for most of the characters was closer to the corresponding genotypic variance value showing little environment effect on the expression of these characters.

Kaddem *et al.* (2014) reported that the bread wheat genotypes were different significantly for all characters except for flag leaf width, indicating existence of sufficient genetic variability within different genotypes. They reported high estimates of phenotypic coefficient of variation for grain yield, but moderate for harvest index, biological yield, number of tillers /plant, test weight and spike length. Moderate genotypic coefficient of variation was recorded for test weight, number of tillers /plant, grain yield and spike length.

Kumar *et al.* (2014) reported highest GCV and PCV for grain yield/plant followed by biological yield and harvest index.

Desheva and Kyosev (2015) reported that the GCV values were lower than PCV values for all the traits.

Ghuttai *et al.* (2015) reported significant genotypic differences for all the traits studied except grain yield. F5 wheat population PS-05 x PS-04 showed maximum mean values for plant height (96.5 to 128.6 cm), AUP-4006 x PS-4 for 1000-grain weight (68.9 g), PS-05 x Ghaznavi for biological yield (6322 to 11978 kg ha).

Singh *et al.* (2015) studied 30 promising genotypes of bread wheat and recorded least PCV and GCV for starch content whereas, yield/plant and sedimentation value exhibited high values of PCV and GCV.

Ali and Abdulla (2016) reported maximum PCV and GCV for grain yield/plant followed by biological yield/plant and straw yield/plant.

Mecha *et al.* (2016) studied sixty four wheat genotypes and observed substantial genetic variability for all characters. High GCV and PCV for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot,

biomass yield per plot and harvest index. Low GCV and PCV for days to maturity, spike length and number of spikelets per spike.

Rahman *et al.* (2016) studied twelve wheat genotypes and observed high GCV and PCV for heading days (HD), plant/ m² (PPM), spikelets per spike (SPS) and 1000 grains weight (TGW). Grain yield had positive and highly significant association with heading days, maturity days and 1000 grains weight at both genotypic and phenotypic levels.

Tiwari *et al.* (2016) reported higher magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for grain yield/plant, biological yield/plant, ear weight, tillers/plant, harvest index, grains/ear and 1000-grain weight respectively.

Yaqoob M. (2016) studied twenty four wheat lines and observed substantial genetic variability for all the traits except number of grains/spike. The highest estimates of GCV (17.28) and PCV (26.41) were recorded for grain yield and number of tillers/plant respectively.

Arya *et al.* (2017) found highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for grain yield per plant in forty nine genotypes of wheat.

Chethana *et al.* (2017) reported high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the characters except for days to fifty percent heading, spike length and number of spikelets per spike.

Chimdesa *et al.* (2017) studied twenty five wheat genotype and observed substantial genetic variability for all the traits. Genotypic coefficient of variation (GCV) ranged from 4.59 (days to maturity) to 13.76% (grain yield per hectare), while phenotypic coefficient of variation (PCV) ranged between 5.03 (days to maturity) to 20.85% (grain yield per hectare).

Kabir *et al.* (2017) studied ten wheat (*Triticum aestivum* L.) genotypes and observed analysis of variance highly significant for all traits studied. High GCV and PCV for grain weight yield per plot and low for days to maturity.

Kumar *et al.* (2017) studied wheat population including 48 F1's + 48 F2's + 16 parents and observed substantial genetic variability for all the 10 characters. High GCV and PCV (>20%) were recorded for grain yield per plant and biological yield per plant only in F1 generation. Whereas, in F2 generation moderate estimates (10-20%) of PCV and GCV observed for grain yield per plant and biological yield per plant, whereas number of effective tillers per plant and plant height in both F1 and F2 generations exhibited moderate PCV and GCV.

Kumar A *et al.* (2017) observed highly significant differences for all the yield and its contributing traits, indicating the presence of high genetic variability. The phenotypic and genotypic co-efficient of variation (PCV and GCV) was high for grain yield per plant followed no of productive tiller per plant and moderate for plant height, spike length and thousand grain weight. High heritability coupled with high Genetic advance was found for the traits viz., plant height, no of productive tiller per plant, spike length, thousand grain weight and grain yield per plant indicating presence of substantial amount of variability for these traits which is key of practicing selection in any breeding programme.

Phougat *et al.* (2017) studied 44 diverse genotypes of bread wheat and reported highest genotypic and phenotypic coefficient of variation for harvest index (%), biological yield/plant (g), number of tillers/plant and grain yield/plant.

Sharaan *et al.* (2017) observed highly significant differences for all the yield and its contributing traits, indicating the presence of high genetic variability. The coefficients of variation were high for no. fertile tillers plant-1 (NFT), grains spike-1 (GS), grains weight spike-1 (GWS), grain yield plant-1 (GYP), spikes m-2 (NSM), grain yield (GY), and harvest index (HI). In addition, moderate values were recorded for heading date (HD) and spike length (SL) in the all seasons, and low for days to physiological maturity (DPM) in all seasons.

Sabit *et al.* (2017) studied nineteen wheat genotypes and observed substantial genetic variability for all the seventeen traits. High genotypic coefficient of variation (GCV) was observed for biological yield per plant, followed by seed yield per plant, grain filling periods, thousand grains weight, no. of grain

per spike, peduncle length, number of productive tiller per plant, plant height, and flag leaf width. Whereas, maximum phenotypic coefficient of variation (PCV) was exhibited for biological yield per plant, followed by grain yield per plant, grain filling periods, number of productive tiller per plant, thousand grains weight, main spike weight, no of grains per spike peduncle length, flag leaf width, flag leaf length, number of grains per spike, spike length and plant height.

2.1.2 Heritability and genetic advance

Tsegaye *et al.* (2012) reported high heritability coupled with high genetic advance as percent of mean for 1000-grain weight, spike length and number of spikelets/spike suggesting selection for these traits would give good response.

Bhushan *et al.* (2013) reported high heritability for all the characters except for grain filling period and test weight. High heritability coupled with high genetic advance as percent of means was recorded for plant height, harvest index, biological yield and grain yield that indicates predominance of additive gene action in the inheritance of these traits.

Mishra and Shukla (2013) reported high heritability coupled with high genetic advance for characters *viz.*, number of tillers/plant, protein content, sedimentation value, wet gluten content, biological yield/plant and grains/spike. While, high heritability coupled with low genetic advance reported for days to 50% heading and days to maturity.

Singh and Upadhyay (2013) reported high heritability coupled with high genetic advance as percent of mean for grain yield /ha, plant height at maturity, number of grains /spike and days to maturity suggesting selection for these traits would be very effective.

Kumar *et al.* (2014) reported that biological yield/plant exhibited highest heritability followed by test weight and flag leaf length. High genetic advance was reported for plant height, biological yield/plant, moderate by harvest index, test weight and low genetic advance was observed for flag leaf width, days to 50% flowering, spike length and flag leaf length. Characters such as plant height,

1000 seed weight and harvest index showed high heritability coupled with high genetic advance therefore, these characters should be given top priority during selection in wheat.

Rajdeep *et al.* (2014) reported that the estimated value of broad sense heritability was found between 45% (productive tillers /plant,) and 95 % (gluten content). Heritability values were determined as 92, 92, 89, 85, 84, 71, 68 % and 67 %, for plant height, days to maturity, test weight, days to 50 % flowering, ear length with awn, harvest index %, number of grains/spike, and grain yield/plant respectively. High heritability coupled with high genetic advance as percent over mean was observed for plant height, test weight, number of grains /spike and days to maturity suggesting selection for these traits would give good responses.

Desheva and Kyosev (2015) reported high heritability and high genetic advance combined for plant height and spike.

Ghuttai *et al.* (2015) reported high heritability for plant height, grains /spike, 1000-grain weight and biological yield. However, low heritability was recorded for flag leaf area, spike length and harvest index.

Mecha *et al.* (2016) studied heritability and genetic advance in sixty four genotypes of wheat and observed high heritability for all the characters. Genetic advance was highest for plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index.

Yaqoob M. (2016) studied twenty four wheat lines and observed heritability estimates were high for grain yield (99.83%) and days to 50 percent heading (84.73%) and moderate for plant height (45.79%). High heritability accompanied by high genetic advance was recorded for grain yield indicating the presence of additive genes effect for this trait

Rahman *et al.* (2016) studied twelve wheat genotypes and observed substantial genetic variability for all the 13 characters. Heading days (HD), plant/

m² (PPM), spikelets per spike (SPS) and 1000 grains weight (TGW) exhibited high heritability coupled with a moderate genetic advance.

Chethana *et al.* (2017) reported that high heritability and genetic advance were recorded for all the characters except days to fifty percent flowering, awn length, spike length, number of spikelet's per spike, thousand grain weight and seed yield per plant.

Chimdesa *et al.* (2017) observed that heritability in broad sense and genetic advance as percent of mean (GAM) ranged from 33.33% (Tillers per plant) to 84.67% (Peduncle length) and 8.66% (Days to maturity) to 18.74% (grain yield per hectare), respectively.

Kabir *et al.* (2017) studied ten wheat (*Triticum aestivum L.*) genotypes and observed high heritability coupled with high genetic advance for traits like yield per hectare, total grain yield per plot, straw weight per plot and harvest index indicated these traits were under additive gene control and simple selection is effective for improvement of these traits.

Kumar *et al.* (2017) studied wheat population including 48 F1's + 48 F2's + 16 parents and observed high heritability for plant height followed by 1000 grain weight, days to maturity and grain yield per plant in both F1 and F2 generation. Genetic advance as per cent of mean were high for grain yield per plant, biological yield per plant, plant height in both F1 and F2, whereas, number of effective tillers per plant in F1 only.

Sabit *et al.* (2017) studied nineteen wheat genotypes and observed high heritability for no of grains per spike, Plant height, thousand grains weight, biological yield, grain filling periods, days to 50% heading, days to 50%

flowering, peduncle length, spike length and seed yield per plant. High genetic advance was recorded for plant height.

Shah *et al.* (2017) studied eleven genotypes of wheat and observed highly significant differences for all the yield and its contributing traits. High magnitude of heritability (>0.62) was noted for all parameters except spike length (0.57) which was moderate. Low expected genetic advance was recorded for days to heading (3.90%) and spike length (8.13%), moderate expected genetic advance was observed for plant height (9.95%), grain weight spike-1 (11.54%) and 1000 grain weight (13.41%), while high expected genetic advance was noted for flag leaf area (24.72%), grain yield plant-1 (20.45%), biological yield plant-1 (23.64%) and harvest index (24%).

Sharaan *et al.* (2017) observed high heritability greater than 80% for all studied traits whereas genetic advance as a percentage of mean (GAM %) ranged from 12.22 (SS) to 77.00 (GY) in the 1st season and from 15.42 & 12.69 (DPM) to 112.07 & 68.35 (GYP) in 2nd and 3rd seasons.

2.2 Correlation coefficient analysis

Majumder *et al.* (2008) revealed that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Spikes/plant, grains /spike, spike length, 100grain weight and harvest index were the most important characters which possessed positive association with grain yield.

Rajpoot *et al.* (2013) reported high positive and significant correlation of yield /plant with number of tillers /plant, number of seed /ear and test weight.

Gelalcha and Hanchinal (2013) reported that the twelve elite bread wheat genotypes comprising six lines (females) and six testers (males) were crossed in an L × T fashion to study correlation between yield and yield components. The genotypic as well as phenotypic correlation between grain yield and other yield components such as number of tillers /plant, number of spikes /square meter,

number of grains/spike, total biomass /plant, harvest index and 1000 kernel weight were positive and highly significant.

Fellahi *et al.* (2013) reported that the grain yield was positively correlated with biological yield, straw yield and number of spikes/plant.

Khan *et al.* (2013) revealed positive significant correlation of grain yield with plant height, spikes/m², and 1000-grain weight. Days to heading and days maturity showed considerable negative correlation with grain yield.

Kaddem *et al.* (2014) reported highly significant positive correlation of grain yield with harvest index, plant height, biological yield and test weight at both genotypic as well as phenotypic levels. These traits should be given emphasis for future bread wheat yield improvement programme.

Rajdeep *et al.* (2014) reported that the grain yield/plant exhibited highly significant and positive correlation with biological yield/plant, test weight, productive tillers /plant, and number of grains/spike, number of spikelets /spike, spike length, plant height, and significant and positive correlation with harvest-index. It is suggested that these characters can be considered as selection criteria in improving the grain yield.

Suleiman *et al.* (2014) observed that seed yield per plant exhibited the highest significant positive genotypic correlation with number of tillers per row-meter, number of grains per spike and 1000- grains weight.

Rajpoot *et al.* (2015) recorded grain yield/plant had high positive and significant correlation with number of tillers/plant, number of grains/spike and test weight.

Poor *et al.* (2015) studied 18 genotypes of wheat and observed that seed yield per plant had significant and positive correlation with 1000-grain weight, grain weight per spike, total spike weight and number of grains per spike.

Chimdesa *et al.* (2017) studied grain yield per hectare was positively correlated with biological yield per plot and harvest index, but negatively correlated with peduncle length both at genotypic and phenotypic levels.

Phougat *et al.* (2017) reported positive and significant correlation of grain yield/plant with harvest index (%), biological yield/plant (g) and number of tillers /plant.

Sabit *et al.* (2017) reported that seed yield exhibited positive significant correlation with biological yield, main spike weight, spikelets/spike at genotypic level, while biological yield per plant showed positive significant association at both genotypic and phenotypic levels.

Shah *et al.* (2017) showed that the grain yield was found positively and strongly correlated with days to heading, plant height, flag leaf area, spike length, grain weight spike-1, 1000-grain weight, grain yield plant-1, biological yield plant-1 and harvest index.

Ahmed *et al.* (2018) studied 308 wheat genotypes and observed substantial genetic variability for all the 15 traits. Correlation was calculated among all the traits. Out of the total 105 paired combinations of all the 15 traits, only 72 combinations were significant (36 positive and 36 negative). The values of significant positive correlation varied from 0.11 (GPC-Fe) to 0.99 (DTH-DTA) and values of significant negative correlation ranged from -0.11 (TNPP-GYPP) to -0.724 (DTAGYPP) respectively.

2.3 Path coefficient analysis

Singh and Dwivedi (2002) studied path coefficient in wheat at the genotypic and phenotypic level and showed that all characters except biological yield/plant and harvest index/plant had small positive or negative effect on grain yield/plant but biological yield/plant had maximum direct effect on grain yield/plant followed by harvest index.

Singh *et al.* (2003) reported that biological yield/plant, number of grains/spike, 1000-grain weight and number of effective tillers/plant had positive and higher direct effect on grain yield/plant.

Majumder *et al.* (2008) revealed that number of grains/spike and 1000grain weight had positive direct effect on harvest index, days to maturity and spikes/plant had positive indirect effect on grain yield/plant.

Tsegaye *et al.* (2012) reported that biological yield (0.679) and harvest index (0.48) had direct contribution towards grain yield. It is suggested that these characters can be considered as selection criteria in improving the grain yield of durum wheat genotypes.

Khan *et al.* (2013) revealed that the maturity days, spikes/m², and 1000-grain weight had significant positive direct effects on grain yield. Grains/spike had direct positive effect but in low magnitude. The indirect effect of head days and plant height on grain yield was found mainly through maturity days and 1000-grain weight.

Rajpoot *et al.* (2013) reported maximum direct contribution towards yield /plant for length of ear followed by test weight (g). Hence, emphasis should be given to select these traits to increase the production and productivity of wheat.

Fellahi *et al.* (2013) reported that the biological yield and harvest index should be considered as the main yield components because these traits showed positive direct effects towards increasing grain yield with the values of + 1.051 and + 0.364, respectively.

Gelalcha and Hanchinal (2013) reported that biomass, harvest index, days to flowering and plant height imparted significant direct influence on grain yield. The remaining traits affected grain yield rather indirectly, mainly through impact on total biomass production.

Bhushan *et al.* (2013) showed that harvest index had highest direct positive effect on grain yield followed by biological yield, productive tillers /plant, spikelets/spike and test weight thereby indicated that these were main contributors to the grain yield.

Suleiman *et al.* (2014) studied path coefficient analysis and observed most of the evaluated traits exhibited positive direct effects on grain yield except plant

height and days to 50% heading where it was negative in both seasons, leaf area index and days to maturity were negative in the second season only. The number of tillers per row- meter, number of grains per spike and 1000- grain weight could be used as selection criteria for increasing grain yield.

Tiwari *et al.* (2016) carried out path analysis and found that biological yield had highest direct positive effect on grain yield followed by harvest index, 1000-grain weight, tillers/plant and ear weight.

Chimdesa *et al.* (2017) studied path coefficient and reported that days to maturity, number of productive tillers, and biological yield per plot, harvest index, and spike length had positive direct effect, while days to heading and grain filling period, had high negative direct effect at both genotypic and phenotypic levels.

Phougat *et al.* (2017) observed biological yield/plant showed the highest direct positive effect on grain yield/plant which was followed by harvest index.

Sabit *et al.* (2017) studied path coefficient analyses in nineteen wheat genotypes and reported that plant height, days to 50% flowering, spike length, peduncle length, biological yield, harvest index and main spike weight displayed positive direct effects on grain yield per plant at both genotypic and phenotypic levels.

2.4 Genetic divergence

Dwivedi and Pawar (2005) studied the genetic divergence among 72 lines of bread wheat, for 12 yield and other quality-attributing traits (number of days to heading, number of days to maturity, plant height, number of tillers/plant, number of grains/spike, grain weight/spike, 1000-grain weight, total biomass, grain yield/plant, protein content, sedimentation value and hectoliter weight) and they were evaluated using Mahalanobis' D^2 analysis. Based on D^2 values, the genotypes were grouped into 8 clusters, with cluster I having the highest number of genotypes and cluster VIII with the lowest number of genotypes. The genotypes of clusters I, III and IV were identified as diverse and had higher mean values for most of the important yield component traits.

Ali *et al.* (2008) revealed that the cluster analysis grouped 70 wheat genotypes into 4 different clusters. Five genotypes of China were grouped in cluster I that showed the maximum diversity. Genetic diversity was partially related to the geographic origin. From the cluster mean values, Chinese genotypes deserved consideration for their direct release as a variety(s) or as parents in hybridization programmes to develop high-yielding wheat varieties. The genotypes in cluster II may be used for the improvement of plant height and 1000 grain weight in wheat.

Kumar *et al.* (2009) identified superior genotypes on the basis of the data on genetic divergence and mean performance of yield and other traits, diverse and superior genotypes namely, HUW 533, K 68, K 9465, K 65, K 816, HD 2891, HD 2643, HD 2687, HD 2824, PBW 343, HD 2733, Kalyan sona and Sonalika. Further, on the basis of cluster means, cluster VI has been identified for selecting parents for incorporating grain yield/plant, tillers /plant and plant height, cluster V for spike length, grains /spike and early maturity and cluster III for 1000 grain weight.

Hailegiorgis *et al.* (2011) grouped the 49 bread wheat genotypes into 22 different clusters. This indicated the presence of wide diversity among the tested genotypes. From cluster mean values, genotypes in cluster 9 and 13 deserve consideration for their direct use as parents in hybridization programs to develop high yielding wheat varieties. The genotypes in cluster 3 and 16 could be used for improvement of protein and gluten contents, early maturity and other desirable characters other than grain yield.

Mollasadeghi *et al.* (2012) emphasized that diversity was essential to any change, after the requisite genetic variation. Genetic diversity to investigate genetic variation of 12 bread wheat genotypes based on phenological and morphological traits. It was shown by estimating the phenotypic and genotypic coefficients of variation for various traits that the studied genotypes were of more genetic variation in terms of traits such as plant height, spike length, grain number/spike and grain weight/spike, 1000-grain weight and days to heading

than of other traits. Studied genotypes fell into two categories using cluster analysis. Mean of square between the categories was significant for all traits except grain yield, spike length and date of heading.

Degewione and Alamerew (2013) studied twenty six bread wheat (*Triticum aestivum* L.) genotypes and observed genetic divergence grouped into six clusters. The crosses between genotypes selected from cluster-III with cluster-VI and cluster V with cluster VI were expected to produce better genetic recombination and segregation in their progenies. Therefore, these bread wheat genotypes could to be crossed and selected to develop high yielding pure line variety.

Singh *et al.* (2014) evaluated genotypes for divergence including Tocher's and Euclidian methods which indicated the presence of appreciable amount of genetic diversity in the experimental materials. The thirteen wheat genotypes were grouped into four clusters by both Tocher's and Euclidian methods of divergence. But the clusters of both methods were different on the basis of the genotypes and their numbers present in the cluster.

Meena *et al.* (2014) grouped all the 324 spring wheat lines into 19 clusters using Ward's method. Extreme divergence was observed among clusters. By using D^2 statistics, the highest inter cluster distance (584.72) was found between Clusters VIII and XIX. Cluster VIII recorded highest mean values for chlorophyll content, peduncle length, biomass, grains/spike, 1000grain weight and grain yield. The major contributing trait towards genetic divergence was found to be AUDPC (60.36%).

Khare *et al.* (2015) studied thirty Mexican wheat (*Triticum aestivum* L.) genotypes and studied ten different traits. These genotypes were grouped into six different clusters by using Mahalanobis D^2 analysis. Cluster V had maximum number of (12) genotypes while, cluster I had only one genotypes. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the traits studied. Maximum generalized distances were observed between clusters I and

VI. Yield per plant, gluten content (%) and plant height showed maximum contribution to the total genetic divergence. The genotypes present in cluster I and VI could be used as parents in hybridization programmes to develop high yielding wheat varieties.

Mishra *et al.* (2015) evaluated twenty three wheat genotypes for 9 agromorphological and physiological traits *viz.*, early vigor, leaf firing, days to heading, plant height, number of tillers/m, chlorophyll content Index (CCI) at 3 stages and grain yield. The cluster analysis showed that there was significant genetic diversity among tested wheat genotypes that indicated the presence of excellent opportunity to bring about improvement through hybridizing the selected genotypes present in distant clusters.

Uddin *et al.* (2015) reported that the cluster analysis based on squared Euclidean distance and UPGMA method, categorized the RILs into six groups. Analysis revealed high inter-cluster difference between cluster III and cluster VI followed by cluster IV and VI and among cluster V and cluster VI. Cluster I contained genotypes having maximum mean value for days to heading, flag leaf area and grains /spike, whereas cluster IV contained genotypes having maximum mean value for plant height, number of spikes, 1000-grain weight and grain yield.

Arya *et al.* (2017) found that high heritability coupled with high genetic advance was observed for grain yield/plant. Based on D^2 -Statistics, 49 genotypes were grouped into eight clusters. The highest inter-cluster distance among clusters indicated wide genetic diversity among genotypes belonging to different clusters.

2.5 Principal component analysis

Meena *et al.* (2014) reported first 5 principal components (PC1, PC2, PC3, PC4 and PC5) accounted for proportionate values of 20.66, 17.96, 15.07, 8.28, and 7.38%, respectively, contributing 69.35% of the total variability. The second PCs had high positive PC value for plant height, biomass, and 1000-grain weight.

Bhanupriya *et al.* (2014) studied forty nine germplasm of bread wheat along with 4 checks. Principal component analysis (PCA) indicated that five

components (PC1 to PC5) accounted for about 75 % of the total variation. Out of total principal components retained PC1, PC2 and PC3 with values of 25.9%, 17.1% and 13.3% respectively contributed more to the total variation. The first principal component had high positive loading for 9 characters out of 16 viz. weight of grains/spike, number of grains/spike, number of spikelets/spike, spike length, plant height, days to heading, days to heading, grain protein content and yield/plant which contributed more to the diversity.

Ali *et al.* (2015) observed 52 advanced lines of bread wheat including 6 improved varieties. Principal component (PC) analysis resulted in six principal components (PCs) having Eigen value >1 which contributed 70.90% of the total variability amongst the wheat genotypes assessed for various morpho-physiological traits. The PC I contributed maximum towards the variability (24.10%) and this variability was mainly conditioned by yield attributes like spikelets/spike, grains/spike, days to 50% heading, spike length and grain yield.

MATERIALS AND METHODS

The present investigation entitled “Genetic Analysis for Yield, its Components and Quality Characters in Wheat” was carried out during the *Rabi* season of 2017-18. The techniques followed and materials used during the course of investigation are presented under following subheads.

3.1 Experimental site

The experiment was carried out at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture Jabalpur (M.P). The experimental area occupied was quite uniform in respect to topography and fertility.

3.2 Climate and weather

Jabalpur region has semi humid and subtropical climate. It is situated at 23.90° North latitude and 79.58° East longitude at an altitude of 411.87 m above the mean sea level. The main features of the region are hot and dry summer and cool winter with occasional showers. The average rainfall is about 1400 mm, which is mostly received during July to September. The minimum and maximum temperatures vary between 8 °C in January to 45 °C in May. The crop was grown under normal crop season. The meteorological data of crop season (*rabi* 2017-18) is presented in Appendix II. The soil of experimental field was heavy black, clayey, uniform in its topography and free from waterlogged condition. It is deep, well drained alluvial in origin and has fairly good moisture holding capacity.

3.3 Experimental material

The experimental material comprised 60 genotypes of wheat (*Triticum aestivum* L.), procured from All India Coordinated Research Project on Wheat, Jabalpur (M.P). These genotypes were grown in a Randomized Complete Block Design (RCBD) with two replications. Each plot consisted of four rows of 2.75 m length and 20 cm apart. The details of wheat genotypes presented in Table 3.1 and experimental details were as follows.

Experimental design	RCBD
Year	Rabi 2017-18
Replications	2
Genotypes	60
Row length	2.75
Row to row distance	20
Date of sowing	18/11/2017
Date of harvesting	27/03/2018
Fertilizer dose	100:60:40

3.4 Observations recorded

The observations were recorded on five random selected competitive plants for each genotype and from each replication for the following characters.

3.4.1 Quantitative traits

- 1. Days to 50% heading (days):** The number of days required from sowing to 50% ear emergence was recorded in days.
- 2. Days to maturity (days):** The number of days required from sowing to achieve physiological maturity was recorded in days.
- 3. Plant height (cm):** The height of the main shoot of each plant was recorded from the base of the plant to the tip of the main spike.
- 4. Number of effective tillers/plant:** It was recorded by counting the number of productive tillers present in one plant excluding non-productive tillers at the time of maturity.

Table 3.1: Genotypes of wheat used as experimental material

S.No.	Entry Name	S.No.	Entry Name	S.No.	Entry Name
1	STNT-2	21	MP-3471	41	MP-3506
2	STNT-3	22	MP-3472	42	MP-3507
3	PBW-343/CDWR-9563	23	MP-3474	43	MP-3323/MP-3298
4	STNT-5	24	MP-3476	44	MP-3324/NIAW-1395
5	STNT-6	25	MP-3478	45	MP-3324/MP-3222
6	STNT-7	26	MP-3479	46	MP-3342/PBWK-998-4
7	STNT-8	27	MP-3480	47	MP-3342/PBWK-343/K-918
8	STNT-10	28	MP-3481	48	MP-3335/GW-322-J-485
9	STNT-11	29	MP-3489	49	MP-3382
10	STNT-12	30	MP-3491	50	MP-3372/NIAW-1395
11	STNT-13	31	MP-3492	51	MP-1201
12	STNT-14	32	MP-3493	52	PBW-343/CBW-9563
13	STNT-15	33	MP-3494	53	JW-3288
14	STNT-16	34	MP-3495	54	PBW-14
15	STNT-17	35	MP-3496	55	IPPSN-102
16	STNT-21	36	MP-3497	56	IPPSN-201
17	STNT-22	37	MP-3499	57	IPPSN-137
18	STNT-25	38	MP-3500	58	HI-1544
19	STNT-34	39	MP-3501	59	MP-3336
20	MP-3468	40	MP-3504	60	HD-2864

5. Number of spikelets/spike: Total number of spikelets were counted in each spike of the sampled plants and averaged to find average number of spikelets per spike.

6. Ear length (cm): The length of the ear was recorded in cm from base to tip of ear excluding awns.

7. Ear weight (g): It is calculated by using following formula:

$$\text{Ear weight (g)} = \frac{\text{Weight of ears (g)}}{\text{Number of ear}}$$

8. Peduncle length (cm): The length of the main shoot was recorded in cm from the base to the tip of the first flag leaf up to the base of ear.

9. Number of ears per plant: Number of ears were counted in each plant of the sampled plants and averaged to find average number of ears per plant.

10. Number of grains/ear: Total number of grains per main spike was counted after threshing the individual spike.

11. Thousand grain weight (g): Thousand seeds of each line were counted in duplicate, weighted and mean of two samples were recorded in grams.

12. Biological yield/plant (g): Each of the selected plants was harvested at maturity and weight recorded in grams after complete sun dry excluding roots.

13. Harvest index (%): The harvest index was calculated by using the following formula and expressed in percentage.

$$\text{Harvest index (\%)} = \frac{\text{Grain yield/plant (g)}}{\text{Biological yield/plant (g)}} \times 100$$

14. Grain yield/plant (g): Individual plant was hand threshed, cleaned and weighed in grams.

3.4.2 Physiological traits

1. Chlorophyll content: Chlorophyll content was estimated in 4th leaf from the top (fully expanded leaflet) with the help of chlorophyll meter (SPAD-502 plus). Readings measured in 3 plants per plot at grain filling stages. Chlorophyll content is expressed in terms of SPAD units.

2. Canopy temperature (°C): Canopy temperature was recorded by the CTD instrument at grain filling stage by Infra Red Thermometer (Model LT 300 Sixth Sense).

3. Relative Water Content (%): RWC was measured from flag leaves at anthesis. Immediately after cutting at the base of lamina, leaves were sealed within plastic bags and transferred to the laboratory. Fresh weight (FW) was measured after excision and the full turgid weight (TW) after the dehydration of the leaves by placing them in a test tube containing 100 ml distilled water for 24 hours at room temperature (about 21°C). After soaking, leaves were carefully blotted dried with tissue paper. Dry weight (DW) was measured after oven drying at 70°C for 72 hrs. The RWC was calculated from the equation as:

$$\text{RWC (\%)} = \frac{(\text{FW}-\text{DW})}{(\text{TW}-\text{DW})} \times 100$$

where,

FW = Fresh weight of the flag leaf

TW = Turgid weight of the flag leaf

DW = Dry weight of the flag leaf

RWC = Relative Water Content of flag leaf

3.4.3 Quality traits

1. Protein (%): Protein content of each genotype was estimated using micro-Kjeldal method (Markham, 1942) as described below:

Preparation of digestion mixture:

Mixed thoroughly 2.5 g of powdered selenium dioxide (SeO_2), 100 g potassium sulphate (K_2SO_4) and 20g of copper sulphate ($\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$). Mixed CuSO_4 and K_2SO_4 in 1:10 ratio. Copper sulphate acted as catalyst and potassium sulphate increased boiling point of sulphuric acid.

Preparation of mixed indicator:

Mixed thoroughly 10 ml of Bromocresol green (0.1% in 95% alcohol) and 2 ml of Methyl red (0.1% in 95% alcohol).

Digestion:

1. Weighed exactly 0.25g of dry homogenized sample into clean and dry digestion flask taking care that no sample/particles adhere to the sides of the flask.

2. Added a pinch (approximately 0.5g) of digestion mixture and 10.0 ml of concentrated sulphuric acid. 3. Heated the flask on an electric heater in a fume hood. Gradually increased the heat to keep the contents boiling. Continued heating until the solution was colorless/very light green. 4. Cooled and added distilled water, shook carefully and after attaining room temperature, carefully transferred the contents into 100 ml volumetric flask. Washed the digestion flask several times with small portion of distilled water and transferred the washings into the same volumetric flask and shook to make up the volume and shook again for uniform concentration.

Distillation and titration:

About 10 ml of 2% boric acid was taken in a 100 ml conical flask. Added 2-3 drops of mixed indicator (color was pink) and placed the flask under the condenser taking care to see the end of the condenser was dipping in boric acid solution. Exact 10 ml of digested material was measured and placed into the distilling portion (Vacuum jacket) of the set followed by 10 ml of distilled water and 10 ml 40% NaOH. Immediately stopper was placed on the mouth of apparatus. Steam distilled the mixture by opening the steam inlet and keeping

the other outlets closed except the receiving end of the condenser. The liberated ammonia was collected in the boric acid which resulted in the colour change of the solution from pink to blue. Distilled for 5-6 min or until the volume in the conical flask increased by 2 to 2.5 folds (30-40 ml). Closed the steam inlet, washed down the tip with a few ml of distilled water, removed the conical flask containing the distillate and titrated against standard 0.1N HCl until the colour changed to light pink. Note down the titrated value. A blank preparation (identically prepared except that it did not contain the sample) was also run.

Calculate crude protein content by multiplying the nitrogen content with 5.68. The nitrogen content of the sample was calculated based on the following formula:

$$\text{N\%} = \frac{(\text{ml H}_2\text{SO}_4 \text{ used} - \text{ml blank}) \times \text{normality} \times 14.007}{\text{Amount of sample taken}} \times 100$$

2. Sedimentation value (SDS value in ml): It measures the quality of proteins and is based on the fact that gluten protein absorbs water and swells considerably when treated with lactic acid in the presence of Sodium Dodecyl Sulphate (SDS). The volume of sediment depends on the extent of swelling of gluten protein and correlates significantly (+0.7) with loaf volume.

Apparatus: Stop clock, water bath, 100 ml stopper measuring cylinder (these should have identical internal Diameter and the distance between the 0 and 100 ml graduations should be 160 mm approximately) and 50 ml measuring cylinders.

Reagents:

1. Lactic acid solution: 3 ml of 88% lactic acid is diluted (1: 8 v/v) to 27 ml with distilled water.

2. SDS solution (2%): Dissolve 20g SDS (Sodium dodecyl sulphate “Specially pure”) in distilled water to make 1 litre.

3. Lactic acid-SDS stock solution: Add 20 ml of Reagent (1) to (2).

The desired SDS/lactic acid reagent may be prepared by dissolving 20 g SDS in one liter of distilled water, to this 20 ml of stock dilute lactic acid prepared by diluting one part by volume of lactic acid 88% with 8 parts by volume of distilled water. The reagent is shaken or otherwise agitated until homogeneous.

Method:

The following method permits four determinations to be carried out at the same time, an additional four tests may be started during the period in which first four sediments are setting. 50 ml of distilled water should be poured in each of the required number of 100 ml cylinders prior to starting the test, similarly the required number of 50 ml measuring cylinders should each be pre-filled with 50 ml SDS/lactic acid reagent.

Add 6 g whole meal to 50 ml water (cylinder 1) and start the stop clock. Shake rapidly for 15 seconds, keep the clock running continuously throughout the rest of the experiment. The time for commencement of the other preparations are given, in minute, in Table 3.1.

Table 3.2 Shake and rest interval for SDS value determination

Cylinder No.	15 sec. shake in water	15 sec. shake in water	15 sec shake in water, add 50 ml SDS, invert 4 times	Invert 4 times	Invert 4 times	Invert 4 times	Read sedimentation value
1	0.0	2.0	4.0	6.0	8.0	10.0	30.0
2	0.5	2.5	4.5	6.5	8.5	10.5	30.5
3	1.0	3.0	5.0	7.0	9.0	11.0	31.0
4	1.5	3.5	5.5	7.5	9.5	11.5	31.5

3.5 Statistical analysis

Statistical analysis was performed for following parameters:

3.5.1 Analysis of variance

3.5.2 Genetic variability

3.5.2.1 Mean and range

3.5.2.2 Coefficient of variation

3.5.2.3 Heritability

3.5.2.4 Genetic advance

3.5.3 Correlation coefficient analysis

3.5.4 Path coefficient analysis

3.5.5 Genetic divergence using Mahalanobis D^2 analysis

3.5.6 Principal component analysis

3.5.1 Analysis of variance

The data on yield, yield components and quality traits were statistically analyzed on the basis of model described by Cochran and Cox (1950) for Randomized Complete Block Design. In order to test the significance of treatments, critical difference was computed (Fisher and Yates, 1963).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

where,

Y_{ij}	=	Performance of i^{th} genotype in j^{th} block
μ	=	General mean
b_i	=	True effect of i^{th} block
t_j	=	True effect of j^{th} treatment
e_{ij}	=	Random errors which are supposed to be identically and independently distributed with normal distribution having zero mean and variance σ^2_e .

Skeleton of Anova for Randomized Complete Block Design

Source of Variation	d.f.	Sum of Squares	Mean Squares	F ratio	Expected mean squares
Replication	(r-1)	R _{ss}	M ₁	F _{e(R)} = M ₁ /M ₃	
Genotypes	(g-1)	G _{ss}	M ₂	F _{e(g)} = M ₂ /M ₃	$\sigma^2_e + r \sigma^2_g$
Error	(r-1)(g-1)	E _{ss}	M ₃		σ^2_e
Total	(rg-1)				

$$1. \text{Genotypic variance } (\sigma^2_g) = \frac{M_2 - M_3}{r}$$

$$2. \text{Phenotypic variance } (\sigma^2_p) = \frac{M_2 - M_3}{r} + M_3$$

$$3. \text{Environmental variance } M_3 = \sigma^2_e$$

where,

r = Number of replications

g = Number of genotypes

M₁ = Mean square due to replication

M₂ = Mean square due to genotype

M₃ = Mean square due to error

A significant value of F-test 5% and 1% level indicates that the genotypes differ significantly among themselves, which requires computing the critical difference (CD).

$$\text{Standard error of difference of mean SE (d)} = \sqrt{\frac{2 \text{EMS}}{r}}$$

Critical difference (CD) = SE_(d) x t_α at error degree of freedom

where,

t_α = t-value at 5% and 1% probability level

EMS = Error mean square from ANOVA

The significance of the computed mean squares was tested making ratio of respective mean square against error mean square. The calculated value of F (Fc) compared with table value of F (Ft) at n₁ and n₂ (error d.f.) degrees of freedom. If calculated value of F is >F tabulated at given probability level is said to be significant.

3.5.2 Genetic variability

3.5.2.1.1 Mean

The mean of recorded observation was calculated as follows:-

$$\text{Mean}(\bar{x}) = \frac{\sum x_i}{n}$$

where,

\bar{x} = mean value of character

$\sum x_i$ = Summation of all values of observation

n = Number of observed values

3.5.2.1.2 Range

Range is observed as minimum and the maximum among series of observation and thus provides the information about the variability present in the genotypes.

3.5.2.2 Coefficient of variation

3.5.2.2.1 Phenotypic coefficient of variation (PCV)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

$$\sqrt{\sigma^2 p} = \sigma p$$

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

where,

3.5.2.2.2 Genotypic coefficient of variation (GCV)

$$\sqrt{\sigma^2 g} = \sigma g$$

$$\text{GCV (\%)} = (\sigma g / \bar{X}) \times 100$$

where,

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

$\sigma^2 g$ = Genotypic variance

σg = Genotypic standard deviation

$\sigma^2 e$ = Environment variance

\bar{X} = General Mean

3.5.2.3 Heritability

Heritability in broad sense was estimated by the following formula given by Hanson *et al.* (1956):

$$h^2 \text{ (bs)\%} = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The range of heritability was categorized as low (below 50 per cent), moderate (50-70 per cent) and high (above 70 per cent) as followed by Johnson *et al.* (1955).

3.5.2.4 Genetic advance

The estimates of expected genetic advance from selection, $G(s)$, was obtained by the formula suggested by Johnson *et al.* (1955).

$$G(s) = K \times h^2 \times \sigma_p$$

where,

K = Selection intensity (value of K at 5% 2.06),

h^2 = Heritability in broad sense, in fraction

σ_p = Phenotypic standard deviation

3.5.2.5 Genetic advance as percentage of mean

It was calculated by the following formula:

$$\text{GA as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

The range of genetic advance as percent of mean is classified as suggested by Johnson *et al.* (1955).

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

3.5.3 Correlation coefficients analysis

Correlation coefficients were calculated for paired combination of all characters under study at genotypic and phenotypic levels with the help of formula suggested by Miller *et al.* (1958).

$$r_{ij} = \frac{Cov(ij)}{\sqrt{(\sigma^2 i)(\sigma^2 j)}}$$

where,

r_{ij} = Correlation coefficient between i^{th} and j^{th} traits

$Cov(ij)$ = Covariance between i^{th} and j^{th} traits

$\sigma^2 i$ = Variance of i^{th} trait

σ^2_j = Variance of j^{th} trait

To test the significance of phenotypic correlation coefficients, the estimated values were compared with the tabulated values of Fisher and Yates (1963) at $n-2$ d.f. at two levels of probability, viz., 5% and 1%.

$$T_{\text{cal.}} = \frac{r}{\sqrt{(1 - r^2)}} \times \sqrt{n - 2} \quad \text{at } (n - 2) \text{ d. f.}$$

3.5.4 Path coefficient analysis

It is standardized partial coefficient method to detect the direct and indirect effects of the independent variable on dependent variable. It permits separation of correlation into components of direct and indirect effects.

The method of path coefficient was developed by Wright (1921) and modified by Dewey and Lu (1959). The following set of simultaneous equations were formed and used for estimation of direct and indirect effects on seed longevity.

Path coefficients were obtained by simultaneous equations which express basic relationship between correlation and path coefficient.

$$r_{1y} = P_{1y} + P_{2y}r_{12} + P_{3y}r_{13} + \dots + P_{(n-1)y}r_{1(n-1)}$$

$$r_{2y} = P_{2y} + P_{1y}r_{21} + P_{3y}r_{23} + \dots + P_{(n-1)y}r_{2(n-1)}$$

$$r_{3y} = P_{3y} + P_{2y}r_{32} + P_{1y}r_{31} + \dots + P_{(n-1)y}r_{3(n-1)}$$

$$y = P_{(n-1)y} + P_{(n-2)y}r_{(n-1)(n-2)} + \dots + P_{(n-(n-1))y}r_{(n-1)(n-1)}$$

where,

y = is the dependent variable i.e. yield per plant

r = Genotypic or phenotypic correlation coefficients between a pair of character

n = Total number of characters under study

Apart from these variations, unexplained residual variation is also there which is an account of residual factor which is calculated by following formula.

Residual effect:

$$1 = R^2 + P_1y^2 + P_2y^2 + \dots + [p(n-1)y]^2 + 2\{p_1yP_2y r_{12} + P_1y P_3y r_{13} + P_1y P_4y r_{14} + \dots + p(n-2)y p(n-1)y r(n-2)\}$$

$$1 = R^2 + X$$

where,

X is equal to sum of all terms of right hand side of equation except R^2 .

$$\text{Or } R^2 = (1-X)$$

Therefore,

$$= \sqrt{(1 - X)}$$

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

- >1.00 = Very high
- 0.3-0.99 = High
- 0.2-0.29 = Moderate
- 0.1-0.19 = Low
- 0.0-0.09 = Negligible

3.5.5 Genetic divergence using Mahalanobis D^2 analysis

3.5.5.1 Genetic divergence

D^2 analysis: Mahalanobis (1928) defines D^2 analysis as follows.

$$D^2P = b_1d_1 + b_2d_2 + \dots + b_p d_p$$

A resource for group distance based on multiple characters with $X_1, X_2, X_3, \dots, X_p$ as the multiple measurements available on each individual and $d_1,$

$d_2 \dots d_p$ as x_1, x_2, \dots, x_p respectively is the difference in the means of two populations. The 'P' values are to be estimated that the ratio of variance between the populations to the variance within the populations is maximized. Taking variance and covariance under consideration, the D^2 value may be estimated by this formula.

$$D^2 = \sum w_{ij} \sum (x_1 - x_2) (x_1 - x_2)$$

where,

w_{ij} is the inverse of estimated variance and covariance matrix

3.5.5.2 Step to estimate D^2 value

3.5.5.2.1 Collection of data:

Data were collected considering "V" population and "P" characters which have been measured on each individual.

3.5.5.2.2 Test of significance

According to Wilk's criteria, a simultaneous test of difference between mean values of number of correlated variance is done (Rao, 1948).

Using pivotal condensation method, the determinant of error and error variety matrix will be calculated.

$$A = \begin{vmatrix} W \\ S \end{vmatrix} = \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

$$V(\text{State}) = -m \log e = - \frac{(p+g+1)}{2} [n] \log e$$

Where

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

P = Number of variance or character

Q = Degree of freedom for population

N = Degree of freedom for error + variety

E = Constant (2.7183)

V (state) is distributed as X^2 with Pq degree of freedom.

The tabulated value of X^2 for Pq degree of freedom at 5% level is compared with the X^2 value for testing the significance.

3.5.5.2.3 Transformation of correlated values

Transformation is done by using pivotal consideration method. The correlated variables are first transformed into uncorrelated once and D^2 values are calculated.

3.5.5.2.4 Computation of D^2 values

The D^2 value obtained for a pair of population is taken as the calculated value of X^2 and is tested against the tabulated value of X^2 at "P" degree of freedom, where "P" is the number of characters considered.

3.5.6.2.5 Contribution of individual characters towards divergence

In all combination, each character is ranked on the basis of $d_i = Y_{ij} - Y_{ik}$ values. Rank 1 is given to the highest mean difference where "P" is the total number of characters.

3.5.5.2.6 Grouping of varieties into various clusters by Tocher's method

Populations are grouped in order to their relative genetic distance from each other in the first step grouping of different varieties into distinct clusters. The two population having the least distance from each other are considered first to which a third population having the smallest D^2 value from the first two population is added, then comes the fourth population and so on. There is disrupt increase in the average D^2 at certain stage by adding a particular population, then this population is not added in the cluster.

Similarly, second cluster is formed. The process is continued till all the populations are included into one or other cluster.

3.5.5.2.7 Average intra cluster distance

The formula is used for measuring the intra cluster distance is as follows

$$\sum Di^2/n$$

where,

$\sum Di^2/n$ is the sum of distance between all possible contributions (n) of the population included in the cluster.

3.5.5.2.8 Average inter-cluster distance

First of all, the distance clusters are measured. The clusters are taken one by one and their distances from other cluster are calculated.

3.5.6: Principal component analysis (PCA)

PCA is a well-known method of dimension reduction (Massy, 1965; Jolliffe, 1986), which seeks linear combinations of the columns of \mathbf{X} with maximal variance, or equivalently, high information. It is routinely applied in chemometrics with the goal of providing the most compact representation of the data. The original p variables $\mathbf{X} = [\mathbf{x}_1 \dots \mathbf{x}_p]$ are transformed in a new predictor set $\mathbf{T} = [\mathbf{t}_1 \dots \mathbf{t}_k]$, with $k \leq \min(n - 1, p)$. The new variables \mathbf{t}_j , called *scores*, are a weighted average of the original \mathbf{X} variables. The *principal components* are the eigen vectors, \mathbf{u}_j from the eigen decomposition of $\mathbf{X}\mathbf{X}$ (and of the sample covariance matrix \mathbf{S} , up to a constant). PCA sequentially maximises the variance of a linear combination of the original predictor variables

$$\mathbf{U}_j = \arg \max \text{Var}(\mathbf{X}\mathbf{u}),$$

$$\mathbf{u}=1$$

Subject to the constraint that $\mathbf{u}'_i \mathbf{S}\mathbf{u}_j = 0$ for all $1 \leq i < j$. This ensures that $\mathbf{t}_j = \mathbf{X}\mathbf{u}_j$ is uncorrelated with all the previous linear combinations $\mathbf{t}_i = \mathbf{X}\mathbf{u}_i$. The principal components are ordered in terms of the amount of variation of the original data they account for. The first principal component direction has the property that $\mathbf{t}_1 = \mathbf{X}\mathbf{u}_1$ has the largest sample variance among all normalized linear combinations of the columns of \mathbf{X} . Each subsequent component gives combinations with the largest possible variance which is uncorrelated with those that have been taken earlier.

There are various standard approaches to find the principal components, e.g. taking the singular value decomposition of \mathbf{X} . In chemometrics, it is common to estimate the principal components using the nonlinear iterative partial least-squares (NIPALS) algorithm (Wold, 1966). This is because the number of required components is usually much less than the total possible number ($k - p$). In fact, the NIPALS algorithm does not calculate all the principal components at once, but it first calculates \mathbf{t}_1 and \mathbf{u}_1 from the \mathbf{X} matrix. Then the outer product $\mathbf{t}_1\mathbf{u}_1'$ is subtracted from \mathbf{X} and the residual \mathbf{X}_2 is calculated. In turn, this residual can be used to calculate \mathbf{t}_2 and \mathbf{u}_2 .

RESULTS

The results obtained from the present investigation “Genetic Analysis for Yield, its Components and Quality Characters in Wheat” are presented under the following heads.

4.1 Characterization

4.2 Analysis of variance

4.3 Genetic variability

4.3.1 Range and mean performance

4.3.2 Coefficient of variation

4.4 Heritability

4.5 Genetic advance

4.6 Correlation coefficient analysis

4.7 Path coefficient analysis

4.8 Genetic divergence

4.9 Principal component analysis

4.1 Characterization

In the present experiment, 60 wheat genotypes were characterized on the basis of thirteen morphological traits *viz.*, plant growth habit, foliage colour, ear time of emergence, ear waxiness, flag leaf length, ear shape in profile, ear density, awns length, awn colour, ear colour, peduncle length, grain shape and grain colour. Their categorization is mentioned in Table 4.1.

4.1.1 Plant growth habit

Based on plant growth habit, genotypes were categorized in three groups *viz.*, erect, semi erect, intermediate/spreading. Sixteen genotypes were having erect, thirty seven having semi erect and seven were having spreading type.

4.1.2 Foliage colour

On the basis of foliage colour, genotypes were categorized into three groups *viz.*, pale green, green and dark green. Seven genotypes having pale

green, twenty eight germplasm lines were having green and twenty one were having dark green.

4.1.3 Ear time of emergence

Based on ear time of emergence, genotypes were categorized in three groups *viz.*, very early, early and medium. All the genotypes under study had early emergence.

4.1.4 Ear waxiness

Based on ear waxiness, genotypes were categorized in five groups *viz.*, absent, weak, medium, strong and very strong. Thirty eight genotypes had weak, seven medium, thirteen strong and absent in two germplasm

4.1.5 Flag leaf length

Based on flag leaf length, genotypes were categorized in three groups *viz.*, short, medium and long. Two genotypes had short length, thirty eight had medium length and twenty had long flag leaf length.

4.1.6 Ear Shape in profile

On the basis of ear shape in profile, genotypes were categorized in four groups *viz.*, tapering, parallel, club shaped and fusiform. Fifty genotypes had tapering and ten had parallel shape.

4.1.7 Ear Density

Based on ear density, genotypes were categorized in five groups *viz.*, very lax, lax, medium, dense and very dense. Twenty six genotypes lines had lax, thirty three medium and one was dense.

4.1.8 Awns Presence

Based on awns presence, genotypes were categorized in two groups *viz.*, present or scurs and awned. All sixty genotypes showed awn presence.

4.1.9 Awns length

On the basis of awns length, genotypes were categorized in five groups *viz.*, very short, short, medium, long and very long. Four genotypes showed very short, ten short, thirty three had medium, twelve had long and one had very long length of awns.

Table 4.1 Morphological description of genotypes of wheat

S. N O.	NAME OF ENTRY	PLANT GRO WTH HABIT	FOLIAGE COLOUR	EAR TIME OF EMERGENCE	EAR WAXINESS	FLAG LEAF LENGTH	EAR SHAPE IN PROFILE	EAR DENSITY	AWNS PRESENCE	AWNS LENGTH	AWN COLOUR	EAR COLOUR	GRAIN COLOUR	GRAIN SHAPE
1	STNT-2	SEMI ERECT	GREEN	EARLY	MEDIUM	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
2	STNT-3	SEMI ERECT	GREEN	EARLY	STRONG	LONG	TAP	MEDIUM	PRESENT	LONG	LIGHT BLACK	WHITE	AMBER	OBLONG
3	STNT-4	ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	ELLIPTICAL
4	STNT-5	SPREADING	PALE GREEN	EARLY	ABSENT	LONG	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	WHITE	WHITE	ELLIPTICAL
5	STNT-6	SEMI ERECT	GREEN	EARLY	STRONG	LONG	TAP	MEDIUM	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	RED	OBLONG
6	STNT-7	SPREADING	DARK GREEN	EARLY	WEAK	LONG	TAP	LAX	PRESENT	MEDIUM	DULL WHITE	WHITE	AMBER	OBLONG
7	STNT-8	SPREADING	DARK GREEN	EARLY	STRONG	LONG	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
8	STNT-10	ERECT	PALE GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	WHITE	OBLONG
9	STNT-11	SPREADING	GREEN	EARLY	WEAK	LONG	TAP	LAX	PRESENT	MEDIUM	DULL WHITE	WHITE	WHITE	OBLONG
10	STNT-12	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	RED	OBLONG
11	STNT-13	SEMI ERECT	GREEN	EARLY	STRONG	MEDIUM	TAP	LAX	PRESENT	LONG	LIGHT BLACK	WHITE	AMBER	OBLONG
12	STNT-14	ERECT	PALE GREEN	EARLY	MEDIUM	LONG	TAP	MEDIUM	PRESENT	MEDIUM	DULL BLACK	LIGHT BLACK	AMBER	OBLONG
13	STNT-15	SEMI ERECT	PALE GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
14	STNT-16	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	OVATE
15	STNT-17	SEMI ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG

16	STNT-21	SEMI ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	OBLONG
17	STNT-22	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	LONG	LIGHT BLACK	WHITE	AMBER	ELLIPTICAL
18	STNT-25	SEMI ERECT	PALE GREEN	EARLY	STRONG	LONG	TAP	LAX	PRESENT	SHORT	DULL BLACK	LIGHT BLACK	AMBER	OBLONG
19	STNT-34	SEMI ERECT	PALE GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
20	MP-3468	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	ELLIPTICAL
21	MP-3471	ERECT	DARK GREEN	EARLY	WEAK	LONG	PARALLEL	DENSE	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	WHITE	OBLONG
22	MP-3472	SEMI ERECT	GREEN	EARLY	STRONG	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	DULL BLACK	WHITE	AMBER	ELLIPTICAL
23	MP-3474	SEMI ERECT	GREEN	EARLY	STRONG	LONG	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	ELLIPTICAL
24	MP-3476	SEMI ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	DULL BLACK	DULL BLACK	AMBER	ELLIPTICAL
25	MP-3478	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	DULL WHITE	WHITE	AMBER	OVATE
26	MP-3479	SPREADING	DARK GREEN	EARLY	MEDIUM	LONG	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
27	MP-3480	ERECT	GREEN	EARLY	WEAK	MEDIUM	PARALLEL	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OVATE
28	MP-3481	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	LIGHT BLACK	WHITE	RED	OBLONG
29	MP-3489	SEMI ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	SHORT	LIGHT BLACK	WHITE	AMBER	OVATE
30	MP-3491	SEMI ERECT	GREEN	EARLY	STRONG	LONG	PARALLEL	MEDIUM	PRESENT	MEDIUM	DULL WHITE	LIGHT BLACK	AMBER	OBLONG
31	MP-3492	SEMI ERECT	GREEN	EARLY	WEAK	LONG	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG

32	MP-3493	SEMI ERECT	PALE GREEN	EARLY	MEDIUM	MEDIUM	TAP	LAX	PRESENT	VERY SHORT	LIGHT BLACK	WHITE	AMBER	OBLONG
33	MP-3494	SEMI ERECT	PALE GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	AMBER	ELLIPTICAL
34	MP-3495	SEMI ERECT	GREEN	EARLY	STRONG	MEDIUM	TAP	LAX	PRESENT	VERY LONG	LIGHT BLACK	LIGHT BLACK	AMBER	ELLIPTICAL
35	MP-3496	SEMI ERECT	DARK GREEN	EARLY	WEAK	LONG	TAP	LAX	PRESENT	LONG	LIGHT BLACK	WHITE	AMBER	OBLONG
36	MP-3497	SPREADING	DARK GREEN	EARLY	WEAK	LONG	PARALLEL	MEDIUM	PRESENT	VERY SHORT	LIGHT BLACK	WHITE	AMBER	OBLONG
37	MP-3499	SEMI ERECT	PALE GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OVATE
38	MP-3500	ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	VERY SHORT	LIGHT BLACK	LIGHT BLACK	AMBER	OVATE
39	MP-3501	SEMI ERECT	DARK GREEN	EARLY	STRONG	MEDIUM	TAP	MEDIUM	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
40	MP-3504	ERECT	GREEN	EARLY	STRONG	MEDIUM	PARALLEL	MEDIUM	PRESENT	LONG	DULL BLACK	LIGHT BLACK	AMBER	OBLONG
41	MP-3506	ERECT	DARK GREEN	EARLY	MEDIUM	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	DULL BLACK	RED	OBLONG
42	MP-3507	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	OVATE
43	MP-3323/MP-3298	SEMI ERECT	DARK GREEN	EARLY	ABSENT	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	LIGHT BLACK	WHITE	AMBER	OBLONG
44	MP-3324/NIAW-1395	ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	LAX	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
45	MP-3324/MP-3222	ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
46	MP-3342/PBWK-998-4	ERECT	PALE GREEN	EARLY	WEAK	SHORT	PARALLEL	MEDIUM	PRESENT	SHORT	LIGHT BLACK	DULL BLACK	WHITE	OBLONG

47	MP-3342/PBWK-343/K-918	ERECT	PALE GREEN	EARLY	WEAK	SHORT	PARALLEL	LAX	PRESENT	VERY SHORT	LIGHT BLACK	DULL BLACK	AMBER	OBLONG
48	MP-3335/GW-322-J-485	ERECT	GREEN	EARLY	WEAK	MEDIUM	PARALLEL	LAX	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	AMBER	OBLONG
49	MP-3382	SEMI ERECT	DARK GREEN	EARLY	MEDIUM	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	WHITE	WHITE	AMBER	OBLONG
50	MP-3372/NIAW-1395	ERECT	GREEN	EARLY	WEAK	MEDIUM	PARALLEL	MEDIUM	PRESENT	LONG	LIGHT BLACK	LIGHT BLACK	WHITE	OBLONG
51	MP-1201	INTERMEDIATE	GREEN	EARLY	WEAK	LONG	TAP	MEDIUM	PRESENT	MEDIUM	WHITE	WHITE	AMBER	OBLONG
52	PBW-343/CBW-9563	ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	AMBER	OVATE
53	JW-3288	SEMI ERECT	DARK GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	DULL WHITE	WHITE	AMBER	OBLONG
54	PBW-14	ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	LIGHT BLACK	WHITE	OBLONG
55	IPPSN-102	SEMI ERECT	GREEN	EARLY	WEAK	MEDIUM	TAP	MEDIUM	PRESENT	MEDIUM	DULL WHITE	WHITE	AMBER	OBLONG
56	IPPSN-201	SEMI ERECT	GREEN	EARLY	WEAK	LONG	PARALLEL	MEDIUM	PRESENT	MEDIUM	LIGHT BLACK	WHITE	AMBER	OBLONG
57	IPPSN-137	SEMI ERECT	GREEN	EARLY	MEDIUM	LONG	TAP	LAX	PRESENT	MEDIUM	DULL WHITE	WHITE	AMBER	OBLONG
58	HI-1544	ERECT	GREEN	EARLY	STRONG	MEDIUM	TAP	MEDIUM	PRESENT	SHORT	BLACK	WHITE	AMBER	OVATE
59	MP-3336	ERECT	GRREN	EARLY	MEDIUM	LONG	TAP	LAX	PRESENT	MEDIUM	WHITE	WHITE	AMBER	OBLONG
60	HD-2864	SEMI ERECT	DARK GREEN	EARLY	STRONG	LONG	TAP	MEDIUM	PRESENT	MEDIUM	DULL BLACK	DULL BLACK	AMBER	OBLONG

Table 4.2 Frequency distribution of morphological traits

Traits	Classes	Number of entry	Percentage of entry (%)
Plant growth habit	Erect	16	26.66
	Semi-erect	37	61.66
	Intermediate/spreading	7	11.66
Foliag Colour	Pale green	11	18.33
	Green	28	46.66
	Dark green	21	35
Ear Time of emergence	Very early	00	00
	Early	60	100
	Medium	00	00
Ear Waxiness	Absent	2	3.33
	Weak	38	63.33
	Medium	7	11.66
	Strong	13	21.66
	Very strong	00	00
Flag leaf Length	Short(<20.0cm)	2	3.33
	Medium(20.1-30.0cm)	38	63.33
	Long(>30cm)	20	33.33
Ear Shape in profile	Tapering	50	83.33
	Parallel	10	16.66
	Clubbed	00	00
	Fusiform	00	00
Ear Density	Very lax	00	00
	Lax	26	43.33
	Medium	33	55
	Dense	1	1.66
	Very dense	00	00
Awns Presence	Present/Scurs	60	100
	Owned	00	00

Awn Length	Very short (<6.0cm)	4	6.66
	short (6.0-7.5cm)	10	16.66
	medium (7.51-9.0cm)	33	55
	Long (9.0-10.5)	12	20
	very long (>10.5cm)	1	1.66
Awn Colour	White	3	5
	Dull white	7	11.66
	Dull black	6	10
	Light Black	44	73.33
Ear Colour	White	26	43.33
	Light black	29	48.33
	Dull black	5	8.33
Grain Colour	White	7	11.66
	Amber	49	81.66
	Red	4	6.66
Grain Shape	Round	00	00
	Ovate	9	15
	Oblong	42	70
	Elliptical	9	15

4.1.10 Awn colour

Based on awn colour, genotypes were categorized in three groups *viz.*, white, dull white, dull black and light black. Three genotypes lines had white, seven had dull white, six had dull black and forty four had light black colour.

4.1.11 Ear colour

On the basis of ear colour, genotypes were categorized in three groups *viz.*, white, light brown and dark brown. Twenty six had white, twenty nine had light brown and five had dark brown in ear colour.

4.1.12 Grain shape

Based on grain shape, genotypes were categorized in four groups *viz.*, round, ovate, oblong and elliptical. Nine genotypes lines had ovate, forty two had oblong and nine had elliptical in shape.

4.1.13 Grain colour

On the basis of grain colour, genotypes were categorized in three groups *viz.*, white, amber and red. Seven genotypes lines had white, forty nine had amber and four in red colour.

4.2 Analysis of variance

The analysis of variances for all the traits studied has been presented in table 4.3 Mean squares due to genotypes were highly significant for all the traits, indicating the presence of sufficient genetic variability in the existing material. Six traits *viz.*, biological yield/plant, plant height, sedimentation value, relative water content, number of grains/spike, 1000 grain weight, grain yield/plant, days to 50% heading, harvest index and chlorophyll content exhibited the value of higher magnitude.

Table:- 4.3 (a) Analysis of variance for yield, its components and quality traits in wheat

S.No.	Source of variations	d.f.	Mean sum of squares for traits									
			DFH	DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E
1	Replications	1	5.6333	120.0000	9.6730	0.0496	0.7728	0.0418	0.1733	2.9079	0.1976	9.9015
2	Genotypes	59	21.7028**	9.6435**	138.6133**	1.9083**	3.4819**	3.1215**	0.6183**	15.9613**	1.7819**	31.8098**
3	Error	59	4.8706	2.9322	15.2521	0.7410	0.5824	0.4629	0.1023	2.2933	0.7983	4.6797

Table:- 4.3 (b) Analysis of variance for yield, its components and quality traits in wheat

S.No.	Source of variations	d.f.	Mean sum of squares for traits								
			TGW	BY/P	HI	CC	CT	RWC	PC	SDS	GY/P
1	Replications	1	0.0267	0.5936	0.0843	2.3269	1.3104	1.1880	0.0496	2.3019	0.0725
2	Genotypes	59	28.1833**	156.9897**	21.6497**	20.5837*	8.3854**	57.0418**	1.8474**	98.5722**	22.5718**
3	Error	59	1.0337	12.5915	3.8852	11.1690	1.3462	7.3037	0.0346	0.1467	3.4772

* indicates significance at 5 % level of significance

** indicates significance at 1% level of significance

DFH- Days to 50% heading, DM- Days to maturity, PH- Plant height(cm), NET/P- Number of effective tillers/plant, NS/S- Number of spikelets/spike, EL- Ear length(cm), EW- Ear weight(g), PL- Peduncle length(cm), NE/P- Number of ears/ plant, NG/E- Number of grains/ear, TGW- 1000- grain weight(g), BY/P- Biological yield/plant(g), HI- Harvest index(%), CC- Chlorophyll content(SPAD 502), CT- Canopy temperature(°c), RWC- Relative water content(%), PC- Protein Content(%), SDS- Sedimentation value(%), GY/P- Grain yield/plant(g).

4.3 Genetic variability

4.3.1 Range and mean performance of the genotypes

Range (maximum and minimum) and mean performance of the sixty genotypes of wheat for nineteen traits are presented in Table 4.4

4.3.1.1 Days to 50% heading

The average days for 50 percent heading were 67.43 days and it ranged from 60.50 to 73.50 days. Genotype STNT-10 and MP-3504 was recorded early heading (60 days), while the genotype MP-3507 was having the maximum (73.50 days) for 50 percent heading.

4.3.1.2 Days to maturity

Days to maturity ranged from 112.50 to 122.50 days with mean value of 118.52 days. Genotype MP-3506 was earliest in maturity, while MP-3479, MP-3481, MP-3492, MP-3501 were late.

4.3.1.3 Plant height (cm)

Plant height varied from 68.16 to 109 cm with an overall mean performance of 97.24 cm. Genotype STNT-13 recorded maximum plant height (108.99 cm) whereas genotype MP-3342/PBWK-343/K-918 exhibited the minimum (68.16) cm plant height.

4.3.1.4 Number of effective tillers/plant

Number of effective tillers/plant ranged from 6.83 to 10.68 with an average performance of 9.19. The maximum number of effective tillers/plant (10.68) were recorded in genotype MP-3497, while it was minimum (6.83) in MP-3342/PBWK998-4.

4.3.1.5 Number of spikelets/spike

Maximum number of spikelets/spike was observed in MP-3336(C) (19.66) spikelets/spike, while it was minimum (14.33) in genotypes MP-3342/PBWK-343/K-918. The average number of spikelets/spike was 17.36 and it ranged from 14.33 to 19.66 spikelets / spike.

4.3.1.6 Ear length (cm)

Ear length ranged from 8.10 to 13.75 cm with overall mean performance of 10.81 cm. The maximum ear length was noted in genotype MP-3495, while minimum (8.10) was exhibited in genotype MP-3342/PBWK998-4.

4.3.1.7 Ear weight (g)

Maximum ear weight was observed in MP-3495 (4.02 g), while it was least (1.25 g) in genotype MP-1201. The average ear weight was 2.83 g and it ranged from 1.25 to 4.02 g.

4.3.1.8 Peduncle length (cm)

Maximum peduncle length was observed in MP-3336(check) (24.66 cm), while it was minimum (10.55 cm) for genotype MP-3481. The average peduncle length was 19.77 cm and it ranged from 10.55 to 24.67 cm.

4.3.1.9 Number of ear/plant

Number of ear/plant ranged from 6.75 to 10.53 with an overall mean performance of 9.11. The maximum value (10.52) ear/plant was noted in genotype MP-3497, while minimum (6.75) ear/plant was exhibited by genotype MP-3342/PBWK998-4.

4.3.1.10 Number of grains/spike

Maximum number of grains/spike was observed in MP-3336 (56.66), while it was least (41.00) in genotype MP-3382(check). The average number of grains/spike was 49.72 and it ranged from 41.00 to 56.67 grains/spike.

4.3.1.11 Thousand seed weight (g)

Comparatively bold seeds were observed in genotype MP-3495 with maximum 1000 seed weight (51.14 g) and it was minimum in MP-3497(35.15). The weight of 1000 seeds varied between 35.15 g to 51.14 g, while the average mean value was 43.27 g.

4.3.1.12 Biological yield/plant (g)

Maximum Biological yield/plant was recorded in STNT-3 (65.61 g) and minimum in genotype MP-3342/PBWK998-4 (31.99 g). The average Biological yield/plant was 47.56 g and it ranged from 31.99 g to 65.61 g.

4.3.1.13 Harvest index (%)

The harvest index varied from 31.63 percent to 44.83 percent with a mean value of 37.10%. Genotype MP-3495 depicted highest harvest index (44.83%) whereas, genotype MP-3480 was recorded minimum harvest index (31.63%).

4.3.1.14 Chlorophyll content (SPAD Units)

Chlorophyll content was maximum recorded in Genotype MP-3500(55.14), and minimum in Genotype STNT-6(41.39). Chlorophyll content had mean value of 49.24 it ranged from 41.39 to 55.14.

4.3.1.15 Canopy temperature (°C)

The average value of canopy temperature was recorded as 23.25 °C which varied from 20.20 °C (STNT-5) to 26.65 °C(MP-3495).

4.3.1.16 Relative water content (%)

Minimum relative water content i.e. 70.17 (JW-3288) while maximum of 88.98 (STNT-22) with mean value of 77.64.

4.3.1.17 Protein

The average value of protein percentage was recorded as 12.71% which varies from 11.27% (IPPSN-102) to 14.42% (STNT-6).

4.3.1.18 Sedimentation value (ml)

The mean value of sedimentation was recorded 47.71 ml. Higher sedimentation value was recorded 59.11ml (MP-3491) and lowest 34.29 ml (HD-2864).

4.3.1.19 Grain yield/plant (g)

Maximum grain yield/plant was recorded in PBW-343/CDWR-95-63-3(24.43 g). Whereas genotype MP-3372/NIAW-1395(11.12 g) was poor

yielder. The average grain yield/plant was 17.61 g and it ranged from 11.12 g to 24.43 g.

4.3.2 Coefficient of variations

Estimation of components of genetic parameters of variation for yield and its attributes exhibited a wide range of variation for the traits studied (Table 4.4). Result indicate that the value of phenotypic coefficient of variation was of higher magnitude than that of genotypic coefficient of variation for all the traits showing that the environment had an important role in influencing the expression of the traits.

4.3.2.1 Phenotypic coefficient of variation

The phenotypic coefficient of variation (Table 4.4) ranged from 2.12% for days to maturity to 21.23 % for ear weight. The phenotypic coefficient of variations was highest for traits viz., ear weight (21.23%) followed by grain yield/plant (20.49%), biological yield/plant (19.36%), peduncle length (15.28) sedimentation value (14.73) number of effective tillers/plant (12.53%), number of ear/plant (12.47), ear length (12.39). However, it was exhibited low for traits like days to maturity (2.12%), days to 50% heading (5.41%). The rest of the traits such as harvest index (9.63) canopy temperature (9.49) plant height (9.02) 1000 grain weight (8.83%) number of grains/spike (8.59%) number of spikelets/spike (8.21%), chlorophyll content (8.09), protein content (7.64) and relative water content (7.31) exhibited moderate phenotypic coefficient of variation.

4.3.2.2 Genotypic coefficient of variation

It is revealed from the Table 4.4 that genotypic coefficient of variation varied from 1.55% for days to maturity to 17.96% for ear weight. High genotypic coefficient of variation was noted for ear weight (17.96) followed by biological yield (17.87), grain yield/plant (17.54), sedimentation value (14.70) and peduncle length (13.23%). Days to maturity (1.55%), days to 50% heading (4.30%) and chlorophyll content (4.41) showed genotypic coefficient of variation. While it was moderate for rest of the traits such as ear length (10.67), 1000 grain weight (8.51), number of effective tillers/plant (8.31), plant height (8.08%), canopy temperature (8.07), harvest index (8.03%), number of

ear/plant (7.70), protein content (7.49), number of grains/ear (7.41), number of spikelets/spike (6.94), relative water content (6.42).

4.4 Heritability

The heritability (BS) was computed for each of the traits by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors. The estimates of heritability (BS) for all the traits have been discussed as follows (Table 4.4). It was partitioned as very high (above 90%), high (70 to 90%), medium (50-70%) and low (less than 50%).

Very high heritability estimates were observed for sedimentation value (99.70%), protein content (96.30), 1000 grain weight (92.90%) however, high heritability for Biological yield/plant (85.10%), plant height (80.20%), relative water content (77.30), peduncle length (74.90%), number of grains/ear (74.40%), ear length (74.20%), grain yield/plant (73.30%), canopy temperature (72.30%), ear weight (71.60%) and number of spikelets/spike (71.30%). Moderate for harvest index (69.90%), days to 50% heading (63.30), days to maturity (53.40%) and low for number of effective tillers/plant (44.10%), number of ear/plant (38.10%) and chlorophyll content (29.60%).

4.5 Genetic advance

Based on the estimate of heritability (BS) expected genetic advance was computed on the hypothetical selection at 5 percent best individual ($K=2.06$). Due to masking influence of environment upon traits concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the traits in relation to environment genetic advance as percentage of mean was calculated to predict the genetic gain (Table 4.4).

Genetic advance as percentage of mean ranged from 2.33% for days to maturity to 33.96% for biological yield/plant. The highest estimate of genetic advance as percentage of mean was recorded for biological yield/plant (33.96%) followed by ear weight (31.31%), grain yield/plant (30.94%), sedimentation value (30.24%) peduncle length (23.57%).

Ear length (18.92%), 1000 grain weight(16.91%), protein content (15.15%),plant height(14.90%), canopy temperature (14.14%),harvest index (13.80%), number of grains/ear (13.16%), number of spikelets/spike(12.07%), relative water content (11.63%), number of effective tillers/plant (11.37%) showed moderate value of genetic

Table 4.4 : Parameters of genetic variability for yield, its components and quality characters in wheat

S.NO.	Traits	General Mean	Range		GCV (%)	PCV (%)	h ² (bs)	Genetic Advance	Genetic Advance as % of Mean
			Min.	Max.					
1	DFH	67.4330	60.5000	73.5000	4.3020	5.4050	63.30%	4.7560	7.0530
2	DM	118.5170	112.5000	122.5000	1.5460	2.1160	53.40%	2.7570	2.3260
3	PH	97.2380	68.1600	108.9950	8.0770	9.0200	80.20%	14.4860	14.8980
4	NET/P	9.1880	6.8300	10.6800	8.3140	12.5260	44.10%	1.0450	11.3690
5	NS/S	17.3610	14.3300	19.6600	6.9350	8.2110	71.30%	2.0950	12.0670
6	EL	10.8100	8.0950	13.7500	10.6660	12.3850	74.20%	2.0450	18.9230
7	EW	2.8280	1.2500	4.0200	17.9640	21.2290	71.60%	0.8850	31.3140
8	PL	19.7670	10.5500	24.6650	13.2250	15.2840	74.90%	4.6600	23.5740
9	NE/P	9.1070	6.7500	10.5250	7.7010	12.4720	38.10%	0.8920	9.7940
10	NG/E	49.7190	41.0000	56.6650	7.4080	8.5910	74.40%	6.5420	13.1580
11	TGW	43.2720	35.1500	51.1450	8.5140	8.8330	92.90%	7.3160	16.9080
12	BY/P	47.5600	31.9950	65.6150	17.8660	19.3610	85.10%	16.1520	33.9610
13	HI	37.1010	31.6300	44.8250	8.0330	9.6310	69.60%	5.1210	13.8020
14	CC	49.2440	41.3950	55.1450	4.4060	8.0910	29.60%	2.4340	4.9420
15	CT	23.2450	20.2000	26.6500	8.0710	9.4900	72.30%	3.2870	14.1400
16	RWC	77.6360	70.1650	88.9800	6.4230	7.3060	77.30%	9.0320	11.6340
17	PC	12.7060	11.2700	14.4200	7.4930	7.6350	96.30%	1.9250	15.1490
18	SDS	47.7130	34.2900	59.1100	14.7030	14.7250	99.70%	14.4300	30.2430
19	GY/P	17.6140	11.1250	24.4350	17.5430	20.4900	73.30%	5.4500	30.9400

DFF- Days to 50% heading, DM- Days to maturity, PH- Plant height(cm), NET/P- Number of effective tillers/plant, NS/S- Number of spikelets/spike, EL- Ear length(cm), EW- Ear weight(g), PL- Peduncle length(cm), NE/P- Number of ears/plant, NG/E- Number of grains/ear, TGW- 1000- grain weight(g), BY/P- Biological yield/plant(g), HI- Harvest index(%), CC- Chlorophyll content(SPAD 502), CT- Canopy temperature(°c), RWC- Relative water content(%), PC- Protein content(%), SDS- Sedimentation value(%), GY/P- Grain yield/plant(g).

4.6 Correlation coefficient analysis

Correlation coefficient was worked out at phenotypic and genotypic levels for all possible combinations of nineteen yield and its attributing traits (table 4.5 and 4.6). Results indicated that genotypic correlation coefficient, in general, were of higher magnitude than the corresponding phenotypic correlation coefficient for all the traits.

The results of phenotypic correlation coefficients have been discussed only as the genotypic and environmental correlation were mostly influenced by the environmental conditions, hence phenotypic correlation will give the correct idea about the association between two variables.

4.4.1 Days to 50% heading

Days to 50 percent heading recorded highly significant and positive association with canopy temperature (0.4141) followed by days to maturity (0.2347). Highly significant and negative association of this trait was observed with number of spikelets/spike (-0.3418), relative water content (-0.3353), number of grains/ear (-0.3346) and grain yield/plant (-0.2176).

4.4.2 Days to maturity

Days to maturity revealed highly significant and positive associated with plant height (0.2946) followed by ear length (0.2359), relative water content (0.2355), protein content (0.2168), biological yield/plant (0.2063). It was found highly significant and negative association with harvest index (-0.2190).

4.4.3 Plant height (cm)

Plant height showed highly significant and positive correlation with ear length (0.5439) followed by relative water content (0.4779), biological yield/plant (0.4607, number of spikelets/spike (0.4292), number of grains/ear (0.4007), grain yield/plant (0.3147), peduncle length (0.3122). Highly significant and negative association of this trait was observed with canopy temperature (-0.5261) followed by harvest index (-0.2713).

4.4.4 Number of effective tillers/plant

Number of effective tillers/plant expressed significant positive correlation with number of ear/plant (0.9585), grain yield/plant (0.5886), biological

yield/plant (0.4669), harvest index (0.3508) and ear length (0.1825). Significant and negative association was exhibited with canopy temperature (-0.1472).

4.4.5 Number of spikelets/spike

Number of spikelets/spikes showed highly significant positive association with number of grains/ear (0.9396) followed by ear length (0.5239), biological yield/plant (0.5054), grain yield/plant (0.4367). Highly significant and negative association was exhibited with canopy temperature (-0.2512).

4.4.6 Ear length (cm)

Ear length recorded highly significant and positive associated with biological yield/plant (0.6166) followed by grain yield/plant (0.5832), ear weight (0.5399), number of grains/ear (0.5043), relative water content (0.3677) and 1000 grain weight (0.3513). It was found highly significant and negative association with canopy temperature (-0.3238).

4.4.7 Ear weight (g)

Ear weight recorded highly significant and positive association with grain yield/plant (0.4490), biological yield/plant (0.3864), 1000 grain weight (0.3510) number of grains/ear (0.2418).

4.4.8 Peduncle length (cm)

Correlation coefficient of peduncle length showed significant and positive with number of ear/plant (0.1371) while significant and negative association was exhibited with chlorophyll content (-0.1998).

4.4.9 Number of ear/plant

Number of ear/plant recorded high significant and positive correlation with grain yield/plant (0.5598) followed by biological yield/plant (0.4359) and harvest index (0.3537).

4.4.10 Number of grains/ear

Number of grains/ear expressed a highly significant and positive correlation with biological yield/plant (0.4680), relative water content (0.4091), grain yield/plant (0.4048), while highly significant and negative association was exhibited with canopy temperature (-0.3078).

4.4.11 1000 grain weight (g)

Thousand grain weight was recorded highly significant and positive association with grain yield/plant (0.4280), biological yield/plant (0.3157) and harvest index (0.2644).

4.4.12 Biological yield/plant (g)

Correlation coefficient of biological yield/plant was recorded highly significant and positive with grain yield/plant (0.8805) and relative water content (0.4198). Highly significant and negative association was exhibited with canopy temperature (-0.3936)

4.4.13 Harvest index (%)

Harvest index exhibited highly significant and positive correlation with grain yield/plant (0.3789) followed by canopy temperature (0.2666).

4.4.14 Chlorophyll content (SPAD Units)

Chlorophyll content was showing significant positive association with canopy temperature (0.1960).

4.4.15 Canopy Temperature (°C)

Canopy temperature had highly significant and negative association with protein content (-0.5660) followed by relative water content (-0.5469).

4.4.16 Relative Water Content

Relative water content had significant positive association with grain yield/plant (0.2176).

4.4.17 Protein Content

Protein percentage had highly significant positive association with sedimentation value (0.6597).

4.4.18 Sedimentation Value

Sedimentation value was not showing significant association with any character.

4.4.19 Grain yield/plant (g)

Correlation coefficient of grain yield/plant was recorded highly significant and positive with biological yield/plant (0.8805) followed by) number of effective tillers/plant (0.5886), ear length (0.5832), number of ear/plant (0.5598), ear weight (0.0.4490), 1000 grain weight (0.4280), harvest index (0.3789), plant height (0.3147).

Table 4.5: Phenotypic correlation among yield, Its components and quality traits in wheat

	DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E	TGW	BY/P	HI	CC	CT	RWC	PC	SDS	GY/P
DFH	0.2347**	-0.2847**	-0.1167	-0.3418**	-0.2906**	-0.1387	0.1097	-0.1175	-0.3346**	-0.1742	-0.2331*	-0.0036	-0.2131*	0.4141**	-0.3353**	0.0190	0.0938	-0.2176*
DM		0.2946**	-0.0136	0.1543	0.2359**	0.1460	0.1012	-0.0184	0.1212	-0.0994	0.2063*	-0.2190*	-0.0289	-0.0780	0.2355**	0.2168*	0.1914*	0.0911
PH			0.1694	0.4292**	0.5439**	0.1516	0.3122**	0.1548	0.4007**	0.0829	0.4607**	-0.2713**	-0.0334	-0.5261**	0.4779**	0.1302	0.0001	0.3147**
NET/P				0.1980*	0.1825	-0.0560	0.1351	0.9585**	0.1598	0.0974	0.4669**	0.3508**	-0.0677	-0.1472	0.1052	0.0646	-0.1038	0.5886**
NS/S					0.5239**	0.2907	-0.0801	0.1650	0.9396**	0.1576	0.5054**	-0.1035	0.1759	-0.2512**	0.4014**	0.0202	-0.0360	0.4367**
EL						0.5399**	0.0130	0.2054*	0.5043**	0.3513**	0.6166**	-0.0258	0.0429	-0.3238**	0.3677**	0.0302	-0.0542	0.5832**
EW							-0.1066	-0.0556	0.2418**	0.3510**	0.3864**	0.1398	-0.0134	-0.1400	0.1158	0.0028	0.0785	0.4490**
PL								0.1371	-0.0804	0.0266	0.1302	-0.0235	-0.1998*	-0.0953	-0.0392	0.0514	-0.0360	0.1105
NE/P									0.1247	0.0986	0.4359**	0.3537**	-0.0342	-0.1099	0.0483	0.1020	-0.0707	0.5598**
NG/E										0.1326	0.4680**	-0.0973	0.1400	-0.3078**	0.4091**	-0.0165	-0.0639	0.4048**
TGW											0.3157**	0.2644**	-0.0606	-0.0922	-0.0147	-0.0324	-0.0749	0.4280**
BY/P												-0.0973	0.0075	-0.3936**	0.4198**	0.0399	0.0548	0.8805**
HI													-0.0957	0.2666**	-0.3690**	-0.0424	-0.2803**	0.3789**
CC														0.1960	0.0655	0.0318	0.1268	-0.0493
CT															-0.5469**	-0.5660**	-0.0275	-0.2510**
RWC																-0.0048	0.0289	0.2176*
PC																	0.6597**	0.0203
SDS																		-0.0769
GY/P																		

*significant level at 5%

**significant at level at 1%

DFH- Days to 50% heading, DM- Days to maturity, PH- Plant height(cm), NETP- Number of effective tillers/plant, NSS- Number of spikelets/spike, EL- Ear length(cm), EW- Ear weight(g), PL- Peduncle length(cm), NEP- Number of ears/plant, NGE- Number of grains/ear, TGW- 1000- grain weight(g), BYP- Biological yield/plant(g), HI- Harvest index(%), CC- Chlorophyll content(SPAD 502), CT- Canopy temperature(°c), RWC- Relative water content(%), PC- Protein content(%), SDS- Sedimentation value(%), GYP- Grain yield/plant(g).

Table 4.6: Genotypic correlation among yield, its components and quality traits in wheat

		DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E	TGW	BY/P	HI	CC	CT	RWC	PC	SDS	GY/P
DFH		0.3813	-0.4197	-0.1360	-0.4433	-0.3131	-0.1199	0.0828	-0.1461	-0.4484	-0.1987	-0.2578	0.1130	-0.4735	0.5430	-0.5140	0.0210	0.1179	-0.2164
DM			0.4786	0.2000	0.1966	0.4127	0.1152	0.1377	0.1064	0.1221	-0.1586	0.3369	-0.2814	0.0059	-0.2105	0.4395	0.2939	0.2574	0.2264
PH				0.3727	0.5519	0.7139	0.1997	0.3638	0.4210	0.4937	0.0980	0.5472	-0.3739	-0.0171	-0.7179	0.6694	0.1611	0.0008	0.3934
NET/P					0.2129	0.2319	-0.0374	0.2594	1.0018	0.1569	0.1373	0.4843	0.2395	-0.3662	-0.2098	0.0492	0.1026	-0.1469	0.5792
NS/S						0.6408	0.3677	-0.0637	0.1498	0.9970	0.1705	0.5692	-0.1767	0.2546	-0.4436	0.4869	0.0135	-0.0456	0.5125
EL							0.6268	0.0609	0.2422	0.6228	0.3990	0.6843	-0.0375	0.0570	-0.3995	0.4229	0.0516	-0.0585	0.6927
EW								-0.0761	-0.0534	0.3544	0.3807	0.4475	0.2650	0.1250	-0.1677	0.0753	0.0366	0.0986	0.5995
PL									0.3270	-0.0859	0.0207	0.1675	-0.0394	-0.3852	-0.1391	0.0005	0.0665	-0.0433	0.1421
NE/P										0.0887	0.1507	0.4272	0.2406	-0.4150	-0.1528	-0.0261	0.1624	-0.1047	0.5225
NG/E											0.1658	0.5372	-0.1985	0.1758	-0.4842	0.5080	-0.0299	-0.0772	0.4752
TGW												0.3224	0.3039	-0.0803	-0.1150	-0.0245	-0.0150	-0.0767	0.4723
BY/P													-0.2368	-0.0022	-0.4858	0.4882	0.0535	0.0626	0.8876
HI														-0.2442	0.4145	-0.5241	-0.0408	-0.3308	0.2317
CC															0.2557	0.2093	0.0397	0.2307	-0.1298
CT																-0.7276	-0.0725	-0.0382	-0.3077
RWC																	0.0188	0.0356	0.2480
PC																		0.6703	0.3810
SDS																			-0.0850
GY/P																			

4.7 Path coefficient analysis

Path coefficient analysis measures direct and indirect contribution of various independent characters on the dependent character. It reveals whether the association of these independent characters with yield is due to their direct effect on yield or is consequence of their indirect effect via other component characters.

In this study, path coefficient analysis was carried out using genotypic and phenotypic correlation, taking grain yield/plant as a dependent variable. Path coefficients are rated as per the scales given by Lenka and Mishra (1973). The estimates of path coefficient are furnished in Table 4.7 and 4.8.

4.7.1 Direct Effects

At genotypic level, highest positive direct effect was recorded for biological yield/plant (0.8887) followed by number of spikelets/spike (0.6858), harvest index (0.3759), ear length (0.1248) and number of ear/plant (0.1045). However peduncle length (0.0412), ear weight (0.0260) whereas, 1000 grain weight (0.0045) exhibited very low negligible positive direct effect on yield/plant. Whereas, number of grains/ear (-0.6291) exerted highest negative direct effect on grain yield/plant followed by plant height (-0.1710). However, negligible negative direct effect was showed by number of effective tillers/plant (-0.0781) followed by days to 50% heading (-0.0420).

4.7.2 Indirect Effects

The indirect effects on grain yield/plant at genotypic level through different traits are presented below in table 15.

4.7.2.1 Days to 50% heading

The indirect effects of days to 50% heading on grain yield/plant via, number of grains/ear (0.0187), number of spikelets/spike (0.0185), plant height (0.0175) were although positive but of least importance due its very low values.

4.7.2.2 Days to maturity

All the indirect effect of days to maturity via all other traits were negligible of either sign

4.7.2.3 Plant Height (cm)

The positive but low indirect effects of plant height on grain yield/plant via days to 50% heading (0.0716) and harvest index (0.0638), however majority of negative indirect effect of plant height on grain yield/plant were negative via ear length (-0.1218), number of spikelets/spike. Most of the indirect effect of plant height via other traits were negative and negligible.

4.7.2.4 Number of effective tillers/plant

The majority of indirect effect of effective number of tillers/plant via all other traits were extremely low in magnitude of either sign.

4.7.2.5 Number of spikelets/spike

High positive indirect effects of number of spikelets/spike via, number of grain/ear (0.6837) followed by ear length (0.4395), biological yield/plant (0.3904), plant height (0.3785), ear weight (0.2521), days to maturity (0.1348), however negative indirect effect of number of spikelets/spike via days to 50% heading (-0.304), harvest index (-0.1212), indirect effect via other traits were very low in magnitude of either sign hence they are not of any significance.

4.7.2.6 Ear length (cm)

Majority of indirect effect of ear length via other traits were positive but very low in magnitude. However low negative indirect effect ear length via maturity (-0.039) was observed.

4.7.2.7. Ear weight (g)

The positive indirect effect of ear weight via ear length (0.0163), biological yield/plant (0.0116) and all other traits were extremely low of either sign, hence negligible and of little importance.

4.7.2.8. Peduncle length (cm)

The positive indirect effects of peduncle length on grain/yield via number of ear/plant (0.0135), number of effective tillers/plant (0.0107) whereas, all other traits were very low in magnitude of either sign hence they are not of any significance.

4.7.2.9 Number of ear/plant

Number of ear/plant exhibited positive indirect effect via number of effective tillers/plant (0.1046), biological yield/plant (0.0446), plant height (0.0440), peduncle length (0.0342), ear length (0.0253), harvest index (0.0251), 1000 grain weight (0.0157), days to maturity (0.0111) and number of spikelets/spike whereas other traits are negligible.

4.7.2.10 Number of grains/ear

The positive indirect effect of number of grains/ear on grain yield/plant via, days to 50% heading (0.2821), harvest index (0.1249), peduncle length (0.0541) whereas, negative indirect effect on grain yield/plant via, number of spikelets/spike (-0.6272), ear length (-0.3918), biological yield/plant (-0.3380), plant height (-0.3106), ear weight (-0.2230) and 1000 grain weight (-0.1043).

4.7.2.11 Thousand grain weight (g)

Majority of indirect effects of 1000-grain weight via, all other traits were very low in magnitude of either sign hence they are not of any significance.

4.7.2.12 Biological yield/plant (g)

Biological yield/plant had maximum positive indirect effect on via ear length (0.6082), followed by number of spikelets/spike (0.5059), plant height (0.4863), number of grains/ear (0.4775), number of effective tillers/plant (0.4304), ear weight (0.3977), number of ear/plant (0.3797), days to maturity (0.2994), 1000 grain weight (0.2865), peduncle length (0.1488) whereas negative indirect effect via, days to 50% heading (-0.2290) followed by harvest index (-0.2104).

4.7.2.13 Harvest index

The positive indirect effect of harvest index via 1000 grain weight (0.1142), ear weight (0.0996), number of ear/plant (0.0905), number of effective tillers/plant (0.0900), days to 50% heading (0.0425) whereas negative indirect effect via, plant height (-0.1410), days to maturity (-0.1060), biological yield/plant (-0.0890) and number of grains/ear (-0.0746).

Table 4.7 Phenotypic path coefficient table showing direct and indirect effects of various independent traits on grain yield/plant in wheat

	DH	DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E	TGW	BY/P	HI	rPyi
DH	0.0127	0.003	-0.0036	-0.0015	-0.0044	-0.0037	-0.0018	0.0014	-0.0015	-0.0043	-0.0022	-0.003	0	-0.2176
DM	-0.0019	-0.0082	-0.0024	0.0001	-0.0013	-0.0019	-0.0012	-0.0008	0.0002	-0.001	0.0008	-0.0017	0.0018	0.0911
PH	-0.0032	0.0033	0.0113	0.0019	0.0048	0.0061	0.0017	0.0035	0.0017	0.0045	0.0009	0.0052	-0.0031	0.3147
NET/P	-0.0035	-0.0004	0.0051	0.0299	0.0059	0.0055	-0.0017	0.004	0.0287	0.0048	0.0029	0.014	0.0105	0.5886
NS/S	-0.0018	0.0008	0.0022	0.001	0.0052	0.0027	0.0015	-0.0004	0.0009	0.0049	0.0008	0.0026	-0.0005	0.4367
EL	-0.0069	0.0056	0.0129	0.0043	0.0124	0.0237	0.0128	0.0003	0.0049	0.012	0.0083	0.0146	-0.0006	0.5832
EW	-0.0032	0.0034	0.0035	-0.0013	0.0068	0.0126	0.0234	-0.0025	-0.0013	0.0057	0.0082	0.009	0.0033	0.449
PL	0.0005	0.0004	0.0014	0.0006	-0.0004	0.0001	-0.0005	0.0044	0.0006	-0.0004	0.0001	0.0006	-0.0001	0.1105
NE/P	0.0033	0.0005	-0.0043	-0.0269	-0.0046	-0.0058	0.0016	-0.0038	-0.028	-0.0035	-0.0028	-0.0122	-0.0099	0.5598
NG/E	-0.0033	0.0012	0.004	0.0016	0.0094	0.005	0.0024	-0.0008	0.0012	0.01	0.0013	0.0047	-0.001	0.4048
TGW	-0.0011	-0.0006	0.0005	0.0006	0.001	0.0021	0.0021	0.0002	0.0006	0.0008	0.0061	0.0019	0.0016	0.428
BY/P	-0.2074	0.1836	0.4099	0.4155	0.4497	0.5487	0.3438	0.1159	0.3878	0.4164	0.2809	0.8898	-0.0866	0.8805
HI	-0.0017	-0.1015	-0.1258	0.1626	-0.048	-0.012	0.0648	-0.0109	0.164	-0.0451	0.1226	-0.0451	0.4636	0.3789
Residual														0.0716

Note: Diagonal bold figure are the direct effect and the off diagonals are indirect effects

rPyi - phenotypic correlation between yield (y) and ith independent character

Table 4.8: Genotypic path coefficient table showing direct and indirect effects of various independent traits on grain yield/plant in wheat

	DH	DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E	TGW	BY/P	HI	rGyi
DH	-0.0417	-0.0159	0.0175	0.0057	0.0185	0.0131	0.005	-0.0035	0.0061	0.0187	0.0083	0.0108	-0.0047	-0.2164
DM	0.0067	0.0175	0.0084	0.0035	0.0034	0.0072	0.002	0.0024	0.0019	0.0021	-0.0028	0.0059	-0.0049	0.2264
PH	0.0716	-0.0816	-0.1706	-0.0636	-0.0941	-0.1218	-0.0341	-0.0621	-0.0718	-0.0842	-0.0167	-0.0933	0.0638	0.3934
NET/P	0.0106	-0.0156	-0.0291	-0.0781	-0.0166	-0.0181	0.0029	-0.0202	-0.0782	-0.0122	-0.0107	-0.0378	-0.0187	0.5792
NS/S	-0.304	0.1348	0.3785	0.146	0.6858	0.4395	0.2521	-0.0437	0.1027	0.6837	0.1169	0.3904	-0.1212	0.5125
EL	-0.0391	0.0515	0.0891	0.0289	0.0799	0.1248	0.0782	0.0076	0.0302	0.0777	0.0498	0.0854	-0.0047	0.6927
EW	-0.0031	0.003	0.0052	-0.001	0.0095	0.0163	0.026	-0.002	0.0014	0.0092	0.0099	0.0116	0.0069	0.5995
PL	0.0034	0.0057	0.015	0.0107	-0.0026	0.0025	-0.0031	0.0412	0.0135	-0.0035	0.0009	0.0069	-0.0016	0.1421
NE/P	-0.0153	0.0111	0.044	0.1046	0.0157	0.0253	-0.0056	0.0342	0.1045	0.0093	0.0157	0.0446	0.0251	0.5225
NG/E	0.2821	-0.0768	-0.3106	-0.0987	-0.6272	-0.3918	-0.223	0.0541	-0.0558	-0.6291	-0.1043	-0.338	0.1249	0.4752
TGW	-0.0009	-0.0007	0.0004	0.0006	0.0008	0.0018	0.0017	0.0001	0.0007	0.0008	0.0045	0.0015	0.0014	0.4723
BY/P	-0.2291	0.2994	0.4863	0.4304	0.5059	0.6082	0.3977	0.1488	0.3797	0.4775	0.2865	0.8887	-0.2104	0.8876
HI	0.0425	-0.1058	-0.1406	0.09	-0.0664	-0.0141	0.0996	-0.0148	0.0905	-0.0746	0.1142	-0.089	0.3759	0.2317

Residual Effect = 0.0800

Note: Diagonal bold figure are the direct effect and the off diagonals are indirect effects

rGyi - genotypic correlation between yield (y) and ith independent character

DFF- Days to 50% heading, DM- Days to maturity, PH- Plant height(cm), NET/P- Number of effective tillers/plant, NS/S- Number of spikelets/spike, EL- Ear length(cm), EW- Ear weight(g), PL- Peduncle length(cm), NE/P- Number of ears/plant, NG/E- Number of grains/ear, TGW- 1000- grain weight(g), BY/P- Biological yield/plant(g), HI- Harvest index(%), CC- Chlorophyll content(SPAD 502), CT- Canopy temperature(°c), RWC- Relative water content(%), PC- Protein content(%), SDS- Sedimentation value(%)

4.8 Genetic divergence (D^2)

D^2 statistics measures the degree of divergence and determines the Relative proportion of each component trait to the total divergence. It measures the forces of differentiation at two levels, i.e. intra-cluster and inter-cluster levels. Analyses of covariance for all possible combination of traits were done for genetic divergence. The uncorrelated variables i.e. transformed variables when obtained by pivotal condensation method, the original mean values (x_1 to x_n) are transformed into standard divergence uncorrelated (y_1 to y_n) variables.

4.8.1 Contribution of individual traits toward divergence

The percentage contributions of different traits towards total genetic divergence of the sixty wheat genotypes are depicted in the table 4.9

Table 4.9: Percent contribution of 14 characters towards total genetic divergence

S.NO.	SOURCE	TIMES RANKED 1 ST	CONTRIBUTION %
1	Days to 50% heading	36	2.03%
2	Days to maturity	18	1.02%
3	Plant height	165	9.32%
4	Number of effective tillers/plant	17	0.96%
5	Number of spikelets/spike	57	3.22%
6	Ear length	68	3.84%
7	Ear weight	51	2.88%
8	Peduncle length	127	7.18%
9	Number of ear/plant	18	1.02%
10	Number of grain/ear	9	0.51%
11	Thousand grain weight	650	36.72%
12	Biological yield/plant	269	15.20%
13	Harvest index	168	9.49%
14	Grain yield/plant	117	6.61%

Thousand grain weight contributed maximum towards genetic divergence (36.72) followed by biological yield/plant (15.20%), harvest index (9.49%), plant height (9.32%), peduncle length (7.18%), grain yield/plant (6.61%), ear length (3.84%), number of spikelets/spike (3.22%), ear weight (2.88%), days to 50% heading (2.03%), days to maturity and number of ear/plant (1.02%), number of effective tillers/plant (0.96%) and number of grain/ear (0.51%).

4.8.2 Grouping of genotypes in to various clusters

The traits comprising of sixty wheat genotypes were grouped into eleven clusters based on divergence analysis. Distribution of genotypes into different clusters is presented in the Table 4.10

Table 4.10: Clustering pattern of 60 wheat genotypes based on D² analysis

S.No	Cluster No.	No. of Germplasm	Germplasm included in the cluster
1	I	16	STNT-5 , STNT-21 , STNT-11 , STNT-12 , STNT-14 , MP-3474 , PBW-343/CDWR-95-63-3(STNT-4) , MP-3323/MP-3298 , STNT-34 , MP-3493 , MP-3324/MP-3222 , STNT-8 , HI-1544 , MP-3500 , STNT-6 , STNT-10
2	II	1	PBW-14
3	III	16	MP-3324/NIAW-1395 , IPPSN-102 , PBW-343/CBW-9563 , MP-3471 , MP-3335/GW322-J-485 , MP-3372/NIAW-1395 , MP-3501 , MP-3491 , STNT-22 , MP-3499 , MP-3476 , IPPSN-201 , MP-3478 , MP-1201 , STNT-16 , MP-3497
4	IV	10	STNT-13 , STNT-15 , MP-3472 , STNT-17 , IPPSN-137 , MP-3494 , MP-3382 , MP-3504 , MP-3342/PBWK998-4 , MP-3496
5	V	7	STNT-7 , MP-3480 , STNT-2 , MP-3489 , STNT-3 , MP-3468 , MP-3492
6	VI	1	HD-2864
7	VII	1	MP-3479
8	VIII	1	MP-3336
9	IX	1	MP-3495
10	X	5	MP-3481 , MP-3507 , MP-3506 , MP-3342/PBWK343/K918 , JW-3288
11	XI	1	STNT-25

Out of eleven clusters, cluster I and III had largest population consisting of 16 genotypes in even cluster followed by cluster IV (10 genotypes), cluster V (7 genotypes), cluster X (5 genotypes). While remaining clusters viz. cluster II, cluster VI, cluster VII, cluster VIII, cluster IX and cluster XI had one genotype in each cluster.

4.8.3 Inter and intra cluster distance

Considering the inter and intra cluster distances (Table 4.11), the highest inter cluster distance was observed between cluster V and cluster IX (156.94) followed by cluster III and XI (136.61), cluster V and XI(130.73), cluster VII and IX (121.13), cluster V and VI (120.43), cluster VII and XI (118.05), cluster III and IX (116.67), cluster VIII and XI (115.92), cluster X and XI (114.93), cluster V and X (105.65).

The minimum inter cluster distance was observed between clusters VI and IX (18.44), cluster II and IV (27.89), cluster I and II (32.22), cluster VI and VIII (32.7) and cluster II and VI (33.98).

Maximum intra cluster distance was revealed in cluster X (62) followed by cluster IV (36.54), cluster V (31.50), cluster III (31.39) and cluster I (25.45). The remaining clusters viz. cluster II, cluster VI, cluster VII, cluster VIII, cluster IX and cluster XI were mono genotypic hence having zero intra cluster distance.

4.8.4 Cluster mean

Cluster mean for all the traits are summarized in Table 4.12. The higher average inter cluster mean was exhibited in days to maturity followed by plant height, days to 50% heading, Biological yield/plant, and number of grains/ear.

Highest mean value for a maximum number of traits was exhibited by cluster IX for ear length (13.75), ear weight (4.02), number of ear/plant (9.92), 1000 thousand grain weight (51.15), harvest index (44.83) followed by cluster VIII for number of spikelets/spike (19.66), peduncle length (24.67), number of grain/ear (51.15), grain yield/plant (23.39), in cluster II for number of effective tillers/plant (10.00), in cluster V for biological/yield (59.94), in cluster VI for days to 50% heading (71.50), in VII cluster for days to maturity (122.00) and cluster XI for plant height (105.67).

However, lowest mean value for maximum number of traits was exhibited by cluster X for plant height (84.13), number of effective tillers/plant (7.66), number of ear/plant (7.56), biological/yield (38.93) followed by cluster VII number of spikelets/spike (16.33), peduncle length (12.97), number of grain/ear (46.50) followed by cluster XI for days to 50% heading (62.00), days to maturity (117.00), ear weight (1.85), in cluster III for 1000 grain weight (39.05) and grain yield/plant (15.47) in cluster II for ear length (9.35) and cluster V harvest index (32.73).

Table 4.11: Average intra and inter-cluster distances between eleven clusters in wheat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI
CLUSTER I	25.45	32.22	54.35	40.39	59.84	41.91	49.25	40.41	62.29	62.02	69.64
CLUSTER II		0	36.8	27.89	75.92	33.98	37.61	45.83	64.65	35.44	73.02
CLUSTER III			31.39	60.49	77.62	82.4	51.21	71.04	116.67	69.23	136.61
CLUSTER IV				36.54	81.12	52.67	65.78	65.34	68.32	66.94	55.64
CLUSTER V					31.5	120.43	63.67	85.73	156.94	105.65	130.73
CLUSTER VI						0	68.4	32.7	18.44	62.64	70.89
CLUSTER VII							0	85.73	121.13	57.75	118.05
CLUSTER VIII								0	56.63	72.09	115.92
CLUSTER IX									0	96.99	66.67
CLUSTER X										62	114.93
CLUSTER XI											0

Table 4.12: Cluster mean for 14 characters in Wheat

Characters	DFH	DM	PH	NET/P	NS/S	EL	EW	PL	NE/P	NG/E	TGW	BY/P	HI	GY/P
CLUSTER I	65.63	118.34	101.36	9.53	17.94	11.47	3.2	19.52	9.37	51.55	45.4	53.68	38.04	20.43
CLUSTER II	68.5	117.5	85.83	9.96	16.67	9.35	2.5	18.84	9.88	47.83	43.93	41.83	39.99	16.75
CLUSTER III	68.28	119.03	95.73	9.02	16.8	10.24	2.71	20.07	8.92	47.92	39.05	41.37	37.27	15.47
CLUSTER IV	67.3	118.15	97.6	8.93	16.7	10.22	2.57	20.97	9.05	47.41	45.48	42.36	36.76	15.58
CLUSTER V	67.71	118.93	102.45	9.69	18.07	11.09	2.56	21.8	9.57	51.59	41.57	59.94	32.73	19.64
CLUSTER VI	71.5	119.5	94.33	9.83	17.67	12.1	3.07	18.98	9.75	51	49	51.33	44.76	22.91
CLUSTER VII	70	122	88	9.67	16.33	10.69	2.51	12.97	9.58	46.5	41.4	50.4	34.34	17.29
CLUSTER VIII	70.5	119	90.33	9.83	19.66	12.8	3.73	24.67	9.73	56.67	46.58	57.83	40.41	23.39
CLUSTER IX	68.5	118.5	103	10.00	18	13.75	4.02	18.78	9.92	51.5	51.15	49	44.83	21.94
CLUSTER X	69.1	117.1	84.13	7.66	17.13	10.22	2.78	15.36	7.56	49.97	43.29	38.93	36.52	14.04
CLUSTER XI	62	117	105.67	9.85	18.33	11.52	1.85	19.2	9.76	53	50.8	44.56	37.4	16.67

DFF- Days to 50% heading, DM- Days to maturity, PH- Plant height(cm), NET/P- Number of effective tillers/plant, NS/S- Number of spikelets/spike, EL- Ear length(cm), EW- Ear weight(g), PL- Peduncle length(cm), NE/P- Number of ears/plant, NG/E- Number of grains/ear, TGW- 1000- grain weight(g), BY/P- Biological yield/plant(g), HI- Harvest index(%), CC- Chlorophyll content(SPAD 502), CT- Canopy temperature(°c), RWC- Relative water content(%), PC- Protein content(%), SDS- Sedimentation value(%), GY/P- Grain yield/plant(g).

4.9 Principal components analysis (PCA)

PCA is a well-known method of dimension reduction that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set (Massay, 1965; Jolliffe, 1986). It is a mathematical procedure that transforms a number of (possibly) correlated variables into a (smaller) number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

In the present investigation, PCA performed for quantitative traits of wheat are presented in Table 4.13, 4.14, 4.15, 4.16, 4.17, 4.18 and 4.19. Out of nineteen, only 10 principal components (PCs) exhibited more than 0.5 Eigen value and showed about 91.33% variability among the traits studied. Out of which, only 6 principal components were given due importance for further explanation. The PC1 had the highest variability (27.693 %) followed by PC2 (15.020%), PC3 (10.501%), PC4 (8.953%) and PC5 (8.143%), PC6 (5.99) for traits under study (Table 4.13).

Scree plot explained the percentage of variance associated between eigen values and principal components with each PC obtained by drawing a graph. First principal component recorded the highest variation 27.693% (PC1) followed by 15.020% (PC2), 10.501% (PC3), 8.953% (PC4), 8.143 (PC5) and 5.99% (PC6). Total variation of six PCs was recorded to be 76.300%. Semi curve line obtained after eighth PC with little variation observed in each PC indicated that maximum variation was found in PC1; therefore selection of lines for characters under PC1 may be desirable (Figure 5.)

Rotated component matrix revealed that first six PCs are representing maximum variability (76.300%) hence, the traits falling in these six PCs may be given due importance in wheat breeding. It revealed that the first principal component (PC1) which accounted for the highest variation (27.693%) was mostly related with yield traits such as plant height, number of spikelets/spike, ear length, number of grains/ear, biological yield/plant, grain yield/plant, relative water content. The second principal component (PC2) was

dominated by yield related traits viz., number of effective tillers/plant, number of ear/plant, harvest index and 1000 grain weight, while PC3 consisted with traits viz., days to maturity, peduncle length and protein content. Fourth principal component(PC4) was related with ear weight, sedimentation value, fifth principal component(PC5) with chlorophyll content and sixth principal component(PC6) with days to 50% heading, canopy temperature (Table 4.14 and 4.15). On the basis of PCA, most of the important yield attributing traits were present in PC1, PC2 and PC3.

PC scores of genotypes

The PC scores of the each component (PC1, PC2, PC3, PC4 PC5 and PC6) had positive and negative values (Table 4.16, Table 4.17, Table 4.18 and Table 4.19). These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of principal component. High PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. In PC1, the positive scores ranged from 4.054 (STNT-5) to 0.573 (MP-3472), while negative value ranged from -4.615 (JW-3288) to -0.630 (MP-3491). In PC2, the positive value of the component ranged from 3.467 (HD-2864) to 0.619 (MP-3382) and negative value ranged from -3.903 (MP-3491) to -0.823 (MP-3476). In PC3, the positive value of the components ranged from 3.042 (STNT-16) to 0.655 (STNT-11) and negative from -3.486 (MP-3506) to -0.692 (JW-3288). In PC4, the positive value of the components ranged from 2.744 (MP-3323/MP-3298) to 0.557 (MP-3492), while negative value ranged from -2.230 (STNT-7) to -0.568 (MP-3372/NIAW-1395). In PC5, the positive value of the components ranged from 3.409 (MP-3497) to 0.531 (MP-3491), while negative value ranged from -2.597 (MP-3474) to -0.520 (PBW-343/CBW-9563). IN PC6, the positive value of the components ranged from 2.923 (MP-3507) to 0.517 (MP-3478), while negative value ranged from -2.438 (MP-3504) to -0.500 (MP-3472).

In PC1, the genotype STNT-5(4.054) had the highest PC score followed by STNT- (3.941), STNT-3 (3.414), STNT-12 (3.363), STNT-14 (3.218), STNT-6 (3.090), STNT-11 (2.873), STNT-21 (2.860), STNT-10 (2.660), STNT-15 (2.505), STNT-13 (2.00), STNT-2 (1.927), MP-3336 (1.917),

STNT-7 (1.882), MP-3495 (1.880), MP-3474 (1.804), STNT-25 (1.761), MP-3489 (1.725), MP-3468 (1.634), STNT-17 (1.305), MP-3323/MP-3298 (1.177), STNT-8 (1.173), STNT-34 (1.090), MP-3492(1.089), MP-3481 (1.072), STNT-22 (1.054), HD-2864 (1.048) and MP-3472 (0.573). Maximum negative Values were recorded by JW-3288 (-4.615) followed by MP-3342/PBWK-343/K-918 (-4.332), MP-3372/NIAW-1395 (-4.117), MP-1201 (-3.769), MP-3324/NIAW-1395 (-3.086), IPPSN-201 (-2.920), MP-3382 (-2.830), PBW-14 (-2.689), MP-3494 (-2.539), IPPSN-102 (-2.502), IPPSN-137 (-2.441), MP-3335/GW-322-J-485 (-2.291), HI-1544 (-2.257), MP-3504 (-1.801), MP-3471 (-1.675), PBW-343/CBW-9563 (-1.530), MP-3476 (-1.324), MP-3506 (-1.304), MP-3493(-1.191), MP-3499 (-1.171), MP-3507 (-1.041), MP-3496 (-0.894) And MP-3491 (-0.630), for traits viz., plant height, number of spikelets/spike, ear length, number of grains/ear, biological yield/plant, grain yield/plant, relative water content.

In PC2, germplasm HD-2864 (3.467) scored maximum followed by PBW-14 (2.956), MP-3500 (2.897), MP-3495 (2.792), IPPSN-137 (2.722), MP-3336 (2.705), PBW-343/CBW-9563 (2.540), MP-3323/MP-3298 (2.155), MP-3335/GW-322-J-485 (2.072), MP-3324/MP-3222 (1.925), MP-3497 (1.742), MP-3504 (1.661), MP-3468 (1.436), STNT-25 (1.243), STNT-11 (1.052), STNT-21 (1.009), STNT-15 (0.932), STNT-10 (0.879), STNT-5 (0.866), MP-3499 (0.811), HI-1544 (0.781), IPPSN-201 (0.667), MP-3474 (0.625), MP-3382 (0.619) for the traits number of effective tillers/plant, number of ear/plant, harvest index and 1000 grain weight. Maximum negative values were recorded by MP-3491 (-3.903) followed by MP-3481 (-3.157), MP-3501 (-2.400), MP-3496 (-2.382), MP-3372/NIAW-1395 (-2.165), MP-3489 (-2.086), STNT-22 (-2.056), STNT-16 (-1.998), MP-3506 (-1.973), STNT-17 (-1.942), STNT-13 (-1.734), STNT-3 (-1.706), MP-3507 (-1.565), STNT-2 (-1.359), MP-3494 (-1.351), STNT-8 (-1.276) MP-3493 (-1.240), MP-3342/PBWK-998-4 (-1.201), STNT-7 (1.156), MP-3471 (-1.152), MP-3478 (-1.062), MP-3476 (-0.823).

In PC3, highest PC scores were obtained by STNT-16 (3.042) followed by MP-3472 (3.014), IPPSN-201 (2.779), MP-3479 (2.297), MP-1201 (2.059), MP-3474 (1.934), IPPSN-137 (1.782), MP-3468 (1.662), MP-3489 (1.639),

STNT-13 (1.639), MP-3480 (1.532), MP-3335/GW-322-J-485 (1.499), STNT-15 (1.132), MP-3492 (1.094), MP-3324/MP-3222 (0.996), MP-3382 (0.942), MP-3491 (0.911), MP-3501 (0.886), MP-3496 (0.869), STNT-6 (0.763) and STNT-11 (0.655). Maximum negative values were recorded in MP-3506 (-3.486), followed by STNT-8 (-2.205), MP-3499 (-2.198), STNT-10 (-1.994), MP-3342/PBWK-998-4 (-1.987), PBW-343/CBW-9563 (-1.765), STNT-22 (-1.703), STNT-14 (-1.634), IPPSN-102 (-1.602), STNT-21 (-1.501), STNT-25 (-1.397), MP-3507 (-1.136), MP-3504 (-1.105), MP-3324/NIAW1395 (-1.015), STNT-34 (-0.944), STNT-12 (-0.940), MP-3481 (-0.897), STNT-4 (-0.873), MP-3342/PBWK-343/K-918 (-0.820), MP-3495 (-0.802), PBW-14 (-0.799), STNT-2 (-0.781), HD-2864 (-0.743) and JW-3288 (-0.692) for characters viz., days to maturity, peduncle length and protein content.

In PC4, the highest value for characters viz., ear weight, sedimentation value was noted for genotypes MP-3323/MP-3298 (2.744) followed by STNT-11 (2.719), MP-3481 (2.231), MP-3382 (2.220), MP-3335/GW-322-J-485 (2.009), MP-3324/MP-3222 (1.871), MP-3507 (1.815), STNT-12 (1.701), MP-3495 (1.621), MP-3494 (1.548), MP-3496 (1.511), MP-3491 (1.475), MP-3336 (1.456), MP-3342/PBWK-343/K-918 (0.927), MP-3474 (0.752), MP-3504 (0.735), MP-3493 (0.688), MP-3324/NIAW-1395 (0.666), MP-3506 (0.637), STNT-6 (0.609) and MP-3492 (0.557). Maximum negative values were recorded in STNT-7 (-2.230) followed by MP-3468 (-2.165), STNT-25 (-2.149), MP-3480 (-1.924), STNT-15 (-1.897), IPPSN-137 (-1.877), STNT-22 (-1.784), STNT-1 (-1.670), HI-1544 (-1.605), MP-3476 (-1.325), STNT-8 (-1.270), IPPSN-201 (-1.227), MP-3342/PBWK-998-4 (-1.064), STNT-10 (-1.044), PBW-14 (-1.036), STNT-2 (-0.965), MP-1201 (-0.916), STNT-13 (-0.915), MP-3471 (-0.879), MP-3499 (-0.810), IPPSN-102 (-0.661) and MP-3372/NIAW-1395 (-0.568).

In PC5, the highest value for chlorophyll content was noted for genotype MP-3497 (3.409) followed by MP-3499 (2.849), MP-3480 (2.039), MP-3504 (1.896), MP-3472 (1.733), MP-3500 (1.714), MP-3506 (1.648), STNT-13 (1.564), STNT-2 (1.492), MP-3489 (1.302), STNT-25 (1.125), MP-3335/GW-322-J-485 (0.999), MP-3493 (0.955), MP-3324/MP-3222 (0.950), STNT-10 (0.802), STNT-16 (0.704), STNT-34 (0.679), STNT-3 (0.662), PBW-

14 (0.620), MP-3507 (0.585) and MP-3491 (0.531). Maximum negative values were recorded in MP-3474 (-2.597) followed by MP-3471 (-2.393), HD-2864 (-2.312), MP-3336 (-1.629), STNT-22 (-1.556), IPPSN-137 (-1.411), MP-3492 (-1.387), STNT-6 (-1.377), STNT-5 (-1.306), MP-3342/PBWK-343/K-918 (-1.144), STNT-21 (-1.077), STNT-4 (-0.979), HI-1544 (-0.925), STNT-7 (-0.886), MP-3496 (-0.860), MP-3478 (-0.851), MP-3494 (-0.812), MP-3342/PBWK-998-4 (-0.787), MP-3468(-0.562), IPPSN-201 (-0.532) and PBW-343/CBW-9563 (-0.520).

In PC6, the highest value for days to 50% heading canopy temperature were noted for genotype MP-3507 (2.923), MP-3497 (2.217), MP-3336 (1.597), MP-3491 (1.567), MP-3481 (1.535), MP-3468 (1.476), MP-3492 (1.468), PBW-343/CBW-9563 (1.416), MP-3489 (1.384), MP-3372/NIAW-1395 (1.211), MP-3499 (1.200), HD-2864 (1.152), IPPSN-102 (1.035), MP-3493 (0.868), MP-3495 (0.676), PBW-14 (0.557) and MP-3478 (0.517). Maximum negative values were recorded in MP-3504 (-2.438) followed by STNT-17 (-2.315), STNT-12 (-1.539), MP-3476 (-1.529), JW-3288 (-1.456), STNT-34 (-1.437), MP-3382 (-1.265), MP-3474 (-1.161), MP-3324/NIAW-1395 (-1.141), STNT-5 (-1.071), MP-3342/PBWK-343/K-918 (-0.935), STNT-11 (-0.935), STNT-25 (-0.865), MP-3323/MP-3298 (-0.796), MP-3496 (-0.760), STNT-8 (0.575), STNT-13 (-0.531) and MP-3472 (-0.500).

Germplasm having common PC scores with positive value

On the basis of PC scores maximum positive values was recorded in STNT-5 (4.054) followed by HD-2864 (3.467), STNT-3 (3.414), MP-3497 (3.409), STNT-12 (3.363), STNT-6 (3.090), STNT-16 (3.042), MP-3472 (3.014), PBW-14 (2.956), MP-3507 (2.923), MP-3500 (2.897), STNT-11 (2.873), MP-3499 (2.849), MP-3495 (2.792), MP-3323/MP-3298 (2.744), MP-3336 (2.705) STNT-15 (2.506), MP-3382 (2.220), MP-3335/GW-322-J-485 (2.072), MP-3474 (1.934), MP-3324/MP-3222 (1.925), STNT-25 (1.761), MP-3489 (1.725), MP-3468 (1.662), MP-3491 (1.568) and MP-3492 (1.468) which fell more than one PCs.

Germplasm having common PC scores with negative value

Maximum negative values were recorded in JW-3288 (-4.615) followed by MP-3342/PBWK-343/K-918 (-4.342), MP-3342/PBWK-998-4 (-4.332), MP-3372/NIAW-1395 (-4.117), MP-3506 (-3.486), MP-3481 (-3.157) MP-3324/NIAW-1395 (-3.086), IPPSN-201 (-2.920), PBW-14 (-2.689), MP-3494 (-2.539), IPPSN-102 (-2.502), IPPSN-137 (-2.441), MP-3504 (-2.438), MP-3471 (-2.393), MP-3496 (-2.382), HI-1544 (-2.257), STNT-7 (-2.230), STNT-8 (-2.205), MP-3499 (-2.198), STNT-25 (-2.149), STNT-22 (-2.056), PBW-343/CBW-9563 (-1.765), STNT-13 (-1.734), MP-3507 (-1.565), MP-3476 (-1.529) and STNT-2 (-1.359) which are common in more than one PCs.

On the basis of yield and yield attributing traits, out of top six principal component the value of PC1 was highest than PC2, PC3, PC4, PC5 and PC6. Germplasm lines showing maximum positive PC scores and common in PC1, PC2 PC3 and PC5 for the traits viz., plant height, number of spikelets/spike, ear length, number of grains/ear, biological yield/plant, grain yield/plant, relative water content, number of effective tillers/plant, number of ear/plant, harvest index and 1000 grain weight, days to maturity, peduncle length and protein content and chlorophyll content are STNT-6, STNT-10, STNT-11, STNT-13, STNT-15, STNT-25, MP-3468, MP-3472, MP-3474, MP-3489, MP-3492, MP-3495, MP-3323/MP-3298 and MP-3324/MP-3222 for yield and yield attributing traits. Thus, selection of these lines can help in further development of new high yielding quality varieties. Maximum negative values were recorded in MP-3342/PBWK-998-4, MP-3506, MP-3507, 3342/PBWK-343/K-918, MP-3324/NIAW-1395, PBW-14, IPPSN-102, MP-3494, MP-3496, STNT-8, STNT-22, PBW-343/CBW-9563 and MP-3471 germplasm lines for traits days to days to maturity, harvest index relative water content and protein content (%).

Table 4.13: Eigen values, percentage of total variation and cumulative eigen values for corresponding 19 traits in wheat genotypes

Characters	Principal Component(PC)	Eigenvalue	Variability (%)	Cumulative %
DH	PC1	5.262	27.693	27.693
DM	PC2	2.854	15.020	42.714
PH	PC3	1.995	10.501	53.215
NET/P	PC4	1.701	8.953	62.168
NS/S	PC5	1.547	8.143	70.310
EL	PC6	1.138	5.990	76.300
EW	PC7	0.839	4.416	80.716
PL	PC8	0.779	4.099	84.815
NE/P	PC9	0.695	3.660	88.476
NG/E	PC10	0.544	2.863	91.339
TGW	PC11	0.408	2.147	93.487
BY/P	PC12	0.348	1.831	95.318
HI	PC13	0.248	1.305	96.623
GY/P	PC14	0.213	1.123	97.746
CC	PC15	0.186	0.977	98.723
CT	PC16	0.179	0.941	99.665
RWC	PC17	0.030	0.159	99.824
PC	PC18	0.023	0.123	99.947
SDS	PC19	0.010	0.053	100.000

Table 4.14: Principle components for 19 traits of wheat genotypes

Traits	Principal Components					
	PC1	PC2	PC3	PC4	PC5	PC6
DH	-0.533	0.149	0.372	0.105	-0.376	0.485
DM	0.256	-0.250	0.566	0.150	-0.147	0.494
PH	0.736	-0.228	0.207	-0.291	-0.128	-0.137
NET/P	0.273	0.728	0.416	-0.228	0.328	0.068
NS/S	0.772	-0.143	-0.239	0.058	0.246	0.289
EL	0.797	0.012	-0.072	0.126	-0.256	0.118
EW	0.430	0.103	-0.244	0.561	-0.455	0.019
PL	0.099	-0.124	0.482	-0.318	-0.315	-0.046
NE/P	0.257	0.732	0.388	-0.207	0.384	-0.008
NG/E	0.760	-0.154	-0.241	0.004	0.237	0.267
TGW	0.371	0.432	-0.143	0.304	-0.281	-0.317
BY/P	0.820	0.220	0.067	0.096	-0.078	0.089
HI	-0.163	0.747	-0.148	0.199	-0.038	-0.142
GY/P	0.713	0.544	0.003	0.171	-0.062	0.058
CC	0.088	-0.269	-0.235	0.331	0.634	0.077
CT	-0.625	0.243	-0.078	0.339	0.210	0.420
RWC	0.681	-0.419	0.023	-0.277	0.068	-0.033
PC	0.139	-0.193	0.615	0.474	0.258	-0.317
SDS	0.024	-0.384	0.522	0.596	0.129	-0.220

Table 4.15: Interpretation of rotated matrix for the traits having maximum values in each PCs

	PC1	PC2	PC3	PC4	PC5	PC6
Traits	Plant height	No. of effective tillers/plant	Days to maturity	Ear weight	Chlorophyll content	Days to heading
	No. of spikelets/spike	No. of ear/plant	Peduncle length	Sedimentation value	–	Canopy temperature
	Ear length	Thousand grain weight	Protein content	–	–	–
	No. of grain/ear	Harvest index	–	–	–	–
	Biological yield/plant	–	–	–	–	–
	Grain yield/plant	–	–	–	–	–
	Relative water content	–	–	–	–	–

Table 4.16: PC scores of wheat germplasm having positive values > 0.5 in each PCs

S.NO.	Genotypes	PC1	PC2	PC3	PC4	PC5	PC6
1	STNT-2	1.928	-1.359	-0.781	-0.965	1.491	-0.345
2	STNT-3	3.414	-1.706	0.191	-0.420	0.662	0.346
3	STNT-4	3.941	-0.389	-0.873	0.319	-0.979	-0.034
4	STNT-5	4.054	0.866	-0.292	-0.263	-1.306	-1.071
5	STNT-6	3.090	-0.402	0.763	0.609	-1.377	-0.181
6	STNT-7	1.882	-1.156	-0.419	-2.230	-0.886	0.013
7	STNT-8	1.173	-1.276	-2.205	-1.270	-0.298	-0.575
8	STNT-10	2.660	0.879	-1.994	-1.044	0.802	-0.353
9	STNT-11	2.874	1.052	0.655	2.719	0.321	-0.909
10	STNT-12	3.363	-0.426	-0.940	1.701	-0.438	-1.539
11	STNT-13	2.000	-1.734	1.639	-0.915	1.564	-0.531
12	STNT-14	3.218	-0.170	-1.634	-0.349	-0.163	0.168
13	STNT-15	2.506	0.932	1.132	-1.897	-0.102	-0.176
14	STNT-16	0.301	-1.998	3.042	-1.670	0.704	-0.412
15	STNT-17	1.306	-1.942	0.204	0.417	0.237	-2.315
16	STNT-21	2.860	1.009	-1.501	0.028	-1.077	0.074
17	STNT-22	1.054	-2.056	-1.703	-1.784	-1.556	0.113
18	STNT-25	1.761	1.243	-1.397	-2.149	1.125	-0.865
19	STNT-34	1.090	0.019	-0.944	-0.169	0.679	-1.437
20	MP-3468	1.635	1.436	1.662	-2.165	-0.562	1.477
21	MP-3471	-1.675	-1.152	0.006	-0.879	-2.393	0.479
22	MP-3472	0.573	0.282	3.014	-0.295	1.733	-0.500
23	MP-3474	1.804	0.625	1.934	0.752	-2.597	-1.161
24	MP-3476	-1.324	-0.823	-0.172	-1.325	0.161	-1.529
25	MP-3478	-0.191	-1.062	0.363	-0.057	-0.851	0.517
26	MP-3479	-0.204	-0.428	2.297	0.441	0.278	0.302
27	MP-3480	0.415	-0.164	1.532	-1.924	2.039	-0.396
28	MP-3481	1.072	-3.157	-0.897	2.231	-0.400	1.535
29	MP-3489	1.725	-2.087	1.639	0.064	1.302	1.384
30	MP-3491	-0.630	-3.903	0.911	1.475	0.531	1.568

31	MP-3492	1.089	0.349	1.094	0.557	-1.387	1.468
32	MP-3493	-1.191	-1.240	-0.086	0.688	0.955	0.868
33	MP-3494	-2.539	-1.351	-0.097	1.548	-0.812	-0.359
34	MP-3495	1.880	2.792	-0.802	1.622	0.149	0.676
35	MP-3496	-0.894	-2.382	0.869	1.511	-0.860	-0.760
36	MP-3497	-0.025	1.742	0.096	-0.233	3.409	2.217
37	MP-3499	-1.171	0.811	-2.198	-0.810	2.849	1.200
38	MP-3500	-0.236	2.898	-0.304	-0.089	1.715	0.300
39	MP-3501	-0.423	-2.400	0.886	0.230	0.399	0.357
40	MP-3504	-1.801	1.661	-1.106	0.735	1.896	-2.438
41	MP-3506	-1.304	-1.973	-3.486	0.637	1.648	-0.434
42	MP-3507	-1.041	-1.565	-1.136	1.816	0.585	2.930
43	MP-3323/MP-3298	1.177	2.155	0.389	2.744	0.299	-0.796
44	MP-3324/NIAW-1395	-3.086	-0.410	-1.015	0.666	-0.210	-1.141
45	MP-3324/MP-3222	-0.442	1.925	0.996	1.871	0.950	-0.091
46	MP-3342/PBWK-998-4	-4.332	-1.201	-1.987	-1.064	-0.787	-0.437
47	MP-3342/PBWK-343/K-918	-4.342	0.019	-0.820	0.927	-1.144	-0.935
48	MP-3335/GW-322-J-485	-2.291	2.072	1.499	2.009	0.999	-0.076
49	MP-3382	-2.830	0.619	0.942	2.220	-0.102	-1.265
50	MP-3372/NIAW-1395	-4.117	-2.165	-0.009	-0.568	-1.230	1.211
51	MP-1201	-3.769	0.270	2.059	-0.916	0.053	-0.004
52	PBW-343/CBW-9563	-1.530	2.540	-1.765	0.194	-0.520	1.416
53	JW-3288	-4.615	0.410	-0.692	0.103	-0.080	-1.456
54	PBW-14	-2.689	2.957	-0.799	-1.036	0.620	0.557
55	IPPSN-102	-2.502	0.172	-1.602	-0.661	-1.226	1.035
56	IPPSN-201	-2.920	0.667	2.780	-1.227	-0.532	-0.012
57	IPPSN-137	-2.441	2.723	1.782	-1.877	-1.411	-0.227
58	HI-1544	-2.257	0.781	-0.356	-1.605	-0.925	-0.199
59	MP-3336	1.918	2.705	0.376	1.456	-1.629	1.597
60	HD-2864	1.048	3.467	-0.743	-0.436	-2.312	1.152

Table 4.17: List of selected genotypes in each principal component having positive values

PC1	PC2	PC3	PC4	PC5	PC6
STNT-5 (4.054)	HD-2864 (3.467)	STNT-16 (3.042)	MP-3323/MP-3298(2.744)	MP-3497 (3.409)	MP-3507 (2.923)
STNT-4 (3.941)	PBW-14 (2.956)	MP-3472 (3.014)	STNT-11 (2.719)	MP-3499 (2.849)	MP-3497 (2.217)
STNT-3 (3.414)	MP-3500 (2.897)	IPPSN-201 (2.779)	MP-3481 (2.231)	MP-3480 (2.039)	MP-3336 (1.597)
STNT-12 (3.363)	MP-3495 (2.792)	MP-3479 (2.297)	MP-3382 (2.220)	MP-3504 (1.896)	MP-3491 (1.567)
STNT-14 (3.218)	IPPSN-137 (2.722)	MP-1201 (2.059)	MP-3335/GW322-J-485(2.009)	MP-3472 (1.733)	MP-3481 (1.535)
STNT-6 (3.090)5	MP-3336 (2.705)	MP-3474 (1.934)	MP-3324/MP-3222 (1.871)	MP-3500 (1.714)	MP-3468 (1.476)
STNT-11 (2.873)	PBW-343/CBW-9563 (2.540)	IPPSN-137 (1.782)	MP-3507 (1.815)	MP-3506 (1.648)	MP-3492 (1.468)
STNT-21 (2.860)	MP-3323/MP-3298 (2.155)	MP-3468 (1.662)	STNT-12 (1.701)	STNT-13 (1.564)	PBW-343/CBW-9563(1.416)
STNT-10 (2.660)	MP-3335/GW322-J-485(2.072)	MP-3489 (1.639)	MP-3495 (1.621)	STNT-2 (1.492)	MP-3489 (1.384)
STNT-15 (2.505)	MP-3324/MP-3222 (1.925)	STNT-13 (1.639)	MP-3494 (1.548)	MP-3489 (1.302)	MP-3372/NIAW-1395(1.211)
STNT-13 (2.00)	MP-3497 (1.742)	MP-3480 (1.532)	MP-3496 (1.511)	STNT-25 (1.125)	MP-3499 (1.200)
STNT-2 (1.927)	MP-3504 (1.661)	MP-3335/GW322-J-485(1.499)	MP-3491 (1.475)	MP-3335/GW322-J-485(0.999)	HD-2864 (1.152)
MP-3336 (1.917)	MP-3468 (1.436)	STNT-15 (1.132)	MP-3336 (1.456)	MP-3493 (0.955)	IPPSN-102 (1.035)
STNT-7 (1.882)	STNT-25 (1.243)	MP-3492 (1.094)	MP-3342/PBWK-343/K-918(0.927)	MP-3324/MP-3222 (0.950)	MP-3493 (0.868)
MP-3495 (1.880)	STNT-11 (1.052)	MP-3324/MP-3222 (0.996)	MP-3474 (0.752)	STNT-10 (0.802)	MP-3495 (0.676)
MP-3474 (1.804)	STNT-21 (1.009)	MP-3382 (0.942)	MP-3504 (0.735)	STNT-16 (0.704)	PBW-14 (0.557)

STNT-25 (1.761)	STNT-15 (0.932)	MP-3491 (0.911)	MP-3493 (0.688)	STNT-34 (0.679)	MP-3478 (0.517)
MP-3489 (1.725)	STNT-10 (0.879)	MP-3501 (0.886)	MP-3324/NIAW-1395 (0.666)	STNT-3 (0.662)	
MP-3468 (1.634)	STNT-5 (0.866)	MP-3496(0.869)	MP-3506 (0.637)	PBW-14 (0.620)	
STNT-17 (1.305)	MP-3499 (0.811)	STNT-6 (0.763)	STNT-6 (0.609)	MP-3507 (0.585)	
MP-3323/MP-3298 (1.177)	HI-1544 (0.781)	STNT-11 (0.655)	MP-3492 (0.557)	MP-3491 (0.531)	
STNT-8 (1.173)	IPPSN-201 (0.667)				
STNT-34 (1.090)	MP-3474 (0.625)				
MP-3492 (1.089)	MP-3382 (0.619)				
MP-3481 (1.072)					
STNT-22 (1.054)					
HD-2864 (1.048)					
MP-3472(0.573)					

Table 4.18: PC scores of wheat germplasm having negative values > 0.5 in each PCs

S.NO.	Genotypes	PC1	PC2	PC3	PC4	PC5	PC6
1	STNT-2	1.928	-1.359	-0.781	-0.965	1.491	-0.345
2	STNT-3	3.414	-1.706	0.191	-0.420	0.662	0.346
3	STNT-4	3.941	-0.389	-0.873	0.319	-0.979	-0.034
4	STNT-5	4.054	0.866	-0.292	-0.263	-1.306	-1.071
5	STNT-6	3.090	-0.402	0.763	0.609	-1.377	-0.181
6	STNT-7	1.882	-1.156	-0.419	-2.230	-0.886	0.013
7	STNT-8	1.173	-1.276	-2.205	-1.270	-0.298	-0.575
8	STNT-10	2.660	0.879	-1.994	-1.044	0.802	-0.353
9	STNT-11	2.874	1.052	0.655	2.719	0.321	-0.909
10	STNT-12	3.363	-0.426	-0.940	1.701	-0.438	-1.539
11	STNT-13	2.000	-1.734	1.639	-0.915	1.564	-0.531
12	STNT-14	3.218	-0.170	-1.634	-0.349	-0.163	0.168
13	STNT-15	2.506	0.932	1.132	-1.897	-0.102	-0.176
14	STNT-16	0.301	-1.998	3.042	-1.670	0.704	-0.412
15	STNT-17	1.306	-1.942	0.204	0.417	0.237	-2.315
16	STNT-21	2.860	1.009	-1.501	0.028	-1.077	0.074
17	STNT-22	1.054	-2.056	-1.703	-1.784	-1.556	0.113
18	STNT-25	1.761	1.243	-1.397	-2.149	1.125	-0.865
19	STNT-34	1.090	0.019	-0.944	-0.169	0.679	-1.437
20	MP-3468	1.635	1.436	1.662	-2.165	-0.562	1.477
21	MP-3471	-1.675	-1.152	0.006	-0.879	-2.393	0.479
22	MP-3472	0.573	0.282	3.014	-0.295	1.733	-0.500
23	MP-3474	1.804	0.625	1.934	0.752	-2.597	-1.161
24	MP-3476	-1.324	-0.823	-0.172	-1.325	0.161	-1.529
25	MP-3478	-0.191	-1.062	0.363	-0.057	-0.851	0.517
26	MP-3479	-0.204	-0.428	2.297	0.441	0.278	0.302
27	MP-3480	0.415	-0.164	1.532	-1.924	2.039	-0.396

28	MP-3481	1.072	-3.157	-0.897	2.231	-0.400	1.535
29	MP-3489	1.725	-2.087	1.639	0.064	1.302	1.384
30	MP-3491	-0.630	-3.903	0.911	1.475	0.531	1.568
31	MP-3492	1.089	0.349	1.094	0.557	-1.387	1.468
32	MP-3493	-1.191	-1.240	-0.086	0.688	0.955	0.868
33	MP-3494	-2.539	-1.351	-0.097	1.548	-0.812	-0.359
34	MP-3495	1.880	2.792	-0.802	1.622	0.149	0.676
35	MP-3496	-0.894	-2.382	0.869	1.511	-0.860	-0.760
36	MP-3497	-0.025	1.742	0.096	-0.233	3.409	2.217
37	MP-3499	-1.171	0.811	-2.198	-0.810	2.849	1.200
38	MP-3500	-0.236	2.898	-0.304	-0.089	1.715	0.300
39	MP-3501	-0.423	-2.400	0.886	0.230	0.399	0.357
40	MP-3504	-1.801	1.661	-1.106	0.735	1.896	-2.438
41	MP-3506	-1.304	-1.973	-3.486	0.637	1.648	-0.434
42	MP-3507	-1.041	-1.565	-1.136	1.816	0.585	2.930
43	MP-3323/MP-3298	1.177	2.155	0.389	2.744	0.299	-0.796
44	MP-3324/NIAW-1395	-3.086	-0.410	-1.015	0.666	-0.210	-1.141
45	MP-3324/MP-3222	-0.442	1.925	0.996	1.871	0.950	-0.091
46	MP-3342/PBWK-998-4	-4.332	-1.201	-1.987	-1.064	-0.787	-0.437
47	MP-3342/PBWK-343/K-918	-4.342	0.019	-0.820	0.927	-1.144	-0.935
48	MP-3335/GW-322-J-485	-2.291	2.072	1.499	2.009	0.999	-0.076
49	MP-3382	-2.830	0.619	0.942	2.220	-0.102	-1.265
50	MP-3372/NIAW-1395	-4.117	-2.165	-0.009	-0.568	-1.230	1.211
51	MP-1201	-3.769	0.270	2.059	-0.916	0.053	-0.004
52	PBW-343/CBW-9563	-1.530	2.540	-1.765	0.194	-0.520	1.416
53	JW-3288	-4.615	0.410	-0.692	0.103	-0.080	-1.456
54	PBW-14	-2.689	2.957	-0.799	-1.036	0.620	0.557
55	IPPSN-102	-2.502	0.172	-1.602	-0.661	-1.226	1.035
56	IPPSN-201	-2.920	0.667	2.780	-1.227	-0.532	-0.012
57	IPPSN-137	-2.441	2.723	1.782	-1.877	-1.411	-0.227
58	HI-1544	-2.257	0.781	-0.356	-1.605	-0.925	-0.199
59	MP-3336	1.918	2.705	0.376	1.456	-1.629	1.597
60	HD-2864	1.048	3.467	-0.743	-0.436	-2.312	1.152

Table 4.19: List of selected genotypes in each principal component having negative values

PC1	PC2	PC3	PC4	PC5	PC6
JW-3288 (-4.615)	MP-3491 (-3.903)	MP-3506 (-3.486)	STNT-7 (-2.230)	MP-3474 (-2.597)	MP-3504 (-2.438)
MP-3342/PBWK-343/K-918 (-4.342)	MP-3481 (-3.157)	STNT-8 (-2.205)	MP-3468 (-2.165)	MP-3471 (-2.393)	STNT-17 (-2.315)
MP-3342/PBWK-998-4 (-4.332)	MP-3501 (-2.400)	MP-3499 (-2.198)	STNT-25 (-2.149)	HD-2864 (-2.312)	STNT-12 (-1.539)
MP-3372/NIAW-1395 (-4.117)	MP-3496 (-2.382)	STNT-10 (-1.994)	MP-3480 (-1.924)	MP-3336 (-1.629)	MP-3476 (-1.529)
MP-1201 (-3.769)	MP-3372/NIAW-1395 (-2.165)	MP-3342/PBWK-998-4 (-1.987)	STNT-15 (-1.897)	STNT-22 (-1.556)	JW-3288 (-1.456)
MP-3324/NIAW-1395 (-3.086)	MP-3489 (-2.0867)	PBW-343/CBW-9563 (-1.765)	IPPSN-137 (-1.877)	IPPSN-137 (-1.411)	STNT-34 (-1.437)
IPPSN-201 (-2.920)	STNT-22 (-2.056)	STNT-22 (-1.703)	STNT-22 (-1.784)	MP-3492 (-1.387)	MP-3382 (-1.265)
MP-3382 (-2.830)	STNT-16 (-1.998)	STNT-14 (-1.634)	STNT-16 (-1.670)	STNT-6 (-1.377)	MP-3474 (-1.161)
PBW-14 (-2.689)	MP-3506 (-1.973)	IPPSN-102 (-1.602)	HI-1544 (-1.605)	STNT-5 (-1.306)	MP-3324/NIAW-1395 (-1.141)
MP-3494 (-2.539)	STNT-17 (-1.942)	STNT-21 (-1.501)	MP-3476 (-1.325)	MP-3372/NIAW-1395 (-1.230)	STNT-5 (-1.071)
IPPSN-102 (-2.502)	STNT-13 (-1.734)	STNT-25 (-1.397)	STNT-8 (-1.270)	IPPSN-102 (-1.226)	MP-3342/PBWK-343/K-918 (-0.935)
IPPSN-137 (-2.441)	STNT-3 (-1.706)	MP-3507 (-1.136)	IPPSN-201 (-1.227)	MP-3342/PBWK-343/K-918 (-1.144)	STNT-11 (-0.909)

MP-3335/GW-322-J-485 (-2.291)	MP-3507 (-1.565)	MP-3504(- 1.105)	MP-3342/PBWK-998-4 (-1.064)	STNT-21 (-1.077)	STNT-25 (-0.865)
HI-1544 (-2.257)	STNT-2 (-1.359)	MP-3324/NIAW-1395 (-1.015)	STNT-10 (-1.044)	STNT-4 (-0.979)	MP-3323/MP-3298 (-0.796)
MP-3504 (-1.801)	MP-3494 (-1.351)	STNT-34 (-0.944)	PBW-14 (-1.036)	HI-1544 (-0.925)	MP-3496 (-0.760)
MP-3471 (-1.675)	STNT-8 (-1.276)	STNT-12 (-0.940)	STNT-2 (-0.965)	STNT-7 (-0.886)	STNT-8 (-0.575)
PBW-343/CBW-9563 (-1.530)	MP-3493 (-1.240)	MP-3481 (-0.897)	MP-1201 (-0.916)	MP-3496 (-0.860)	STNT-13 (-0.531)
MP-3476 (-1.324)	MP-3342/PBWK-998-4 (-1.201)	STNT-4(-0.873)	STNT-13 (-0.915)	MP-3478 (-0.851)	MP-3472 (-0.500)
MP-3506 (-1.304)	STNT-7 (-1.156)	MP-3342/PBWK-343/K-918 (-.820)	MP-3471 (-0.879)	MP-3494 (-0.812)	
MP-3493 (-1.191)	MP-3471 (-1.152)	MP-3495 (-0.802)	MP-3499 (-0.810)	MP-3342/PBWK-998-4 (-0.787)	
MP-3499 (-1.171)	MP-3478 (-1.062)	PBW-14 (-0.799)	IPPSN-102 (-0.661)	MP-3468 (-0.562)	
MP-3507 (-1.041)	MP-3476 (-0.823)	STNT-2 (-0.781)	MP-3372/NIAW-1395 (-0.568)	IPPSN-201 (-0.532)	
MP-3496 (-0.8949)		HD-2864 (-0.743)		PBW-343/CBW-9563 (-0.520)	
MP-3491 (-0.630)		JW-3288 (-0.692)			

DISCUSSION

India is the second largest producer of wheat with record food production in the recent past from a gradual transition, chronic shortage to self-sufficiency in the important cereal crops especially in wheat. This has been achieved due to hard and painstaking work of wheat scientist by manipulating the yield components and consequent availability of right type of plant ideotype and sound production technology.

Improving yield, quality and stress resistance are the main objectives of the entire breeding programmes. Along with the superior yield performance and quality traits, stabilizing wheat production was also one of the aim of any breeding experiment now a days. Yield reflects the contribution of all the components traits and is considered as the final result of many traits. Every plant contains an inherent production capacity that operates on water, energy, nutrients and other natural resources required for normal plant growth. The ultimate aim of the plant breeder is to improve the yield or economic produce by improving the efficiency of plant genotypes through the study of different characters.

Global climate change and global warming in particular has started to show its impact on crop production. Wheat is one of the most sensitive crop to heat and it had been estimated that rise in temperature by 1°C may lead to yield losses between 3–17% (average 11%) in north-western India.

The experimental finding of the present investigation have been discussed under the following heads.

5.1 Characterization

5.2 Analysis of variance

5.3 Parameters of genetic variability

5.4 Heritability

5.5 Genetic advance

5.6 Correlation coefficient

5.7 Path coefficient

5.8 Genetic divergence analysis (D^2 analysis)

5.9 Principal component analysis

5.1 Characterization

Characterization with distinct morphological markers is essential for identification of germplasm and intellectual property protection. India has enacted legislation for the Protection of Plant Varieties and Farmer's Right in 2001 in order to provide incentives for development and fulfill obligations under Trade Related Intellectual Property Right (TRIPs). Novelty, Distinctiveness, Uniformity and Stability are the essential requirements for grant of protection to varieties/ germplasm / variation either. Germplasm were characterized on the basis of morphological traits *viz.*, plant growth habit, foliage colour, ear time of emergence, ear waxiness, flag leaf length, ear shape in profile, ear density, awns length, awn colour, ear colour, peduncle length, grain shape and grain colour. From the study, we can easily identify different wheat germplasm and can use these characters as an identification key.

5.2 Analysis of variance

The main objective of the present investigation was to study the genetic variability present in the experimental material. The analysis of variance revealed highly significant variation for all the traits, indicating the presence of sufficient genetic variability in the existing material. Traits *viz.*, biological yield/plant, plant height, sedimentation value, relative water content, number of grains/spike, 1000 grain weight, grain yield/plant, days to 50% heading, harvest index and chlorophyll content exhibited the value of higher magnitude. The findings of (Mohibullah et al., 2011), (Tsegaye et al., 2012), (Bhushan et al., 2013), (Rajpoot et al., 2013), (Singh and Upadhyay 2013), (Rajdeep et al., 2014), (Kaddem et al., 2014) and (Ghuttai et al., 2015), (Mecha et al., 2016), (Rahmam et al., 2016), (Kumar et al., 2017), (Kabir et al., 2017), (Sabit et al., 2017) (Ahmed et al., 2018) for all yield related traits are similar to that of the present findings.

5.3 Genetic variability

5.3.1 Mean and range performance of the genotype

The mean performance of the genotypes revealed a wide range of variability for all the traits. The variation was highest for plant height followed by biological yield/plant, sedimentation value, relative water content, 1000 grain weight, number of grains/ear, peduncle length, chlorophyll content, days to 50% heading, grain yield/plant, harvest index, days to maturity, canopy temperature, number of spikelets/spike, ear length, number of ear/plant, number of effective tillers/plant, protein content and ear weight.

The findings were quite similar to as reported by (Tsegaye et al., 2012), (Kabir et al., 2017), (Kumar et al., 2017), (Ahmed et al., 2018). (Ghuttai et al., 2015) for biological yield/plant and moderate variation for harvest index, (Rajpoot et al., 2013) and (Ghuttai et al., 2015) for plant height, number of grains/spike, peduncle length, (Rajpoot et al., 2013) for days to maturity, days to 50% heading, grain yield/plant.

5.3.2 Coefficient of variation

In the present findings phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the traits studied, however the differences was narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The finding of (Rajpoot et al., 2013), (Singh and Upadhyay 2013), (Rajdeep et al., 2014), (Kumar et al., 2014) and (Desheva and Kyosev 2015).

The phenotypic coefficient of variation ranged from 2.11 for days to maturity to 21.22% for ear weight and genotypic coefficient of variation varied from 1.54% for days to maturity to 17.96% for ear weight. The phenotypic and genotypic coefficient of variation high for characters viz., ear weight, grain yield/plant, biological yield/plant, peduncle length, sedimentation value, number of effective tillers/plant, number of ear/plant, ear length. Similarly result have been obtained by (Kumar et al., 2014) for grain yield/plant, biological yield/plant, (Singh et al., 2015) for grain yield/plant and sedimentation value, (Tiwari et

al.,2016) for grain yield/plant, biological yield/plant, ear weight, (Mohammad Yakoob 2016) for grain yield/plant, effective tillers/plant, (Rahman et al.,2016) for number of spikelets/spike, (Ali and Abdulla 2016) for grain yield/plant and biological yield/plant, (Chimdesa et al., 2017) for grain yield/plant, biological yield/plant, number of effective tillers/plant, number of spikelets/spike, ear length, (Kumar et al.,2017) for grain yield/plant and biological yield/plant, number of effective tillers/plant, (Chethana et al., 2017) for number of grain yield/plant, effective tillers/plant and peduncle length, (Sabit et al., 2017) for biological yield/plant, grain yield/plant, number of effective tillers/plant and peduncle length, (Sharaan et al., 2017) for grain yield/plant and number of effective tillers/plant, (Kumar et al., 2017) for grain yield/plant and canopy, (Arya et al., 2017) for grain yield/plant, (Ahmed et al., 2018) for grain yield/plant, biological yield/plant and number of ear/plant.

Harvest index, canopy temperature, plant height, 1000 grain weight, number of grains/ear, number of spikelets/spike, chlorophyll content, protein content and relative water content showed moderate (GCV) and (PCV). Similarly finding of (Mecha et al., 2016) for harvest index, plant height, number of grains/ear and 1000 grain weight, (Chimdesa et al., 2017) for harvest index, number of grains/ear and 1000 grain weight, (Kumar et al., 2017) for plant height.

Days to maturity, days to 50% heading showed lowest genotypic coefficient of variation. The finding of (Kabir et al., 2017), (Bisht and Gahalain 2009) for days to 50% heading, was similar to the present finding which indicated that there is limited scope for improvement. The finding of (Bisht and Gahalain 2009) for number of spikelets /spike, (Bisht and Gahalain 2009), (Mecha et al., 2016), (Chimdesa et al., 2017) for days to maturity.

Contradictory results obtained by (Rahman et al., 2016) for days to 50% heading, (Kabir et al., 2017) for harvest index, number of grains/ear and plant height.

5.4 Heritability

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular trait or a set of trait is very

important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate trait for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative traits. The estimated values of heritability in broad sense were classified as very high (more than 90%), high (more than 70- 90%), medium (50-70%) and low (less than 50%).

Result indicated that the heritability estimates were observed very high for sedimentation value, protein content, 1000 grain weight, high for biological yield/plant, plant height, relative water content, peduncle length, number of grains/ear, ear length, grain yield/plant, canopy temperature, ear weight, number of spikelets/spike and medium for harvest index, days to 50% heading and days to maturity and very low in number of effective tillers/plant, number of ear/plant and chlorophyll content.

High values of broad sense heritability for the above traits depicted that they were least influenced by environmental modification. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable. Similarly result obtained by (Mecha et al., 2016), (Sharaan et al., 2017), (Tsegaye et al., 2012) for ear length, (Mishra and Shukla 2013) for sedimentation value, (Bhushan et al., 2013) for biological yield/plant, (Bhushan et al., 2013) for ear weight and biological yield/plant, (Singh and Upadhyay 2013), (Rajdeep et al., 2014) and (Ghuttai et al., 2015) for number of grains/ear, (Rahman et al., 2016) for 1000 grain weight and number of spkelets/spike, (Chethana et al., 2017) for plant height and peduncle length, (Chimdesa et al., 2017) for peduncle length and plant height, (Kumar et al., 2017) for plant height, ear length, 1000 grain weight and grain yield/plant, (Kumar et al., 2017) for 1000 grain weight and plant height, (Shah et al., 2017) for plant height, 1000 grain weight, grain yield/plant and biological yield/plant and ear length, (Sabit et al., 2017) for plant height, number of grains/ear, 1000 grain weight, grain yield/plant, biological yield/plant, ear length and peduncle length.

Contradictory results finding by (Shah et al., 2017) for days to 50% heading, days to maturity and harvest index, (Kumar et al., 2017) for number of effective tillers/plant, (Arya et al. 2017) for grain yield/plant.

5.5 Genetic advance

Heritability however indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection (Johnson et al., 1955). Estimates of genetic advance were helps to predict the extent of improvement that can be achieved for improving the different traits. The estimated values of genetic advance as percent of mean are classified as high (more than 35%), moderate (20 - 35%) and low (less than 20%).

Genetic advance as percentage of mean ranged from 2.33% for days to maturity to 33.96% for biological yield/plant. The highest estimate of genetic advance as percentage of mean was recorded for biological yield/plant followed by ear weight, grain yield/plant, sedimentation value, peduncle length. Ear length, 1000 grain weight, protein content, plant height, canopy temperature, harvest index, number of grains/ear, number of spikelets/spike, relative water content, number of effective tillers/plant showed moderate value of genetic advance as percentage of mean. Whereas, low estimates were observed for days to maturity, chlorophyll content, days to 50% heading and number of ear/plant.

The results were in consonance with (Suleiman et al., 2014), (Mecha et al., 2016), (Bhushan et al., 2013) for grain yield/plant, (Tsegaye et al., 2012), (Kaddem et al., 2014) and (Desheva and Kyosev 2015) for peduncle length, (Bhushan et al., 2013) and (Kumar et al., 2014) for biological yield/plant. (Rahman et al., 2016) moderate for 1000 grain weight and number of spikelets/spike and least for days to 50% heading, (Chimdesa et al., 2017) for grain yield/plant , biological yield/plant, peduncle length, 1000 grain weight, days to maturity, days to 50% heading, ear weight, relative water content, protein content and low for days to maturity, (Kabir et al., 2017) moderate for harvest index, (Kumar et al., 2017) for grain yield/plant, biological yield/plant

and moderate for plant height, (Kumar et al., 2017) for grain yield/plant and moderate for plant height, number of effective tillers/plant, ear length and 1000 grain weight, (Sharaan et al., 2017) for grain yield/plant, (Shah et al., 2017) for grain yield/plant, biological yield/plant and moderate for plant height, 1000 grain weight and low for days to 50% heading.

5.6 Correlation coefficient analysis

Wide range of variation in quantitative traits provides the basis for selection in plant breeding programme. The knowledge of association among the traits is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant traits and determines the component trait on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. Correlation coefficient provides a clear picture of the extent of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component traits help in improving the efficiency of selection for yield by making proper choice and balancing one component with another.

In present investigation, an attempt has been made to estimate the phenotypic correlation in all trait combinations with the objective to get information about the nature, extent and direction of selection pressure to achieve practical and usable results. In general, genotypic correlation coefficients were higher in magnitude than the phenotypic correlation coefficients. This indicates that although there is strong inherent association between the various pairs of traits studied the low phenotypic correlation would result from the masking and modifying effects of environment on the association of all the traits at gene level. The findings were in agreement to (Majumder et al., 2008).

Correlation coefficient of grain yield/plant was recorded highly significant and positive with biological yield/plant followed by number of effective tillers/plant, ear weight, ear length, number of ear/plant, 1000 grain

weight, harvest index, plant height indicating that these traits are the primary yield determinant in wheat. These findings agreed with the earlier findings of (Gelalcha and Hanchinal 2013), (Fellahi et al., 2013) and (Kaddem et al., 2014), (Phougat et al., 2017), (Chimdesa et al., 2017) for biological yield/plant, harvest index, (Rajpoot et al., 2013), (Gelalcha and Hanchinal 2013) and (Rajdeep et al., 2014) for number of effective tillers/plant, 1000 grain weight, (Khan et al., 2013) and (Kaddem et al., 2014) for plant height, (Suleiman et al., 2014) for number of ear/plant and 1000 grain weight, (Poor et al., 2015), (Rahman et al., 2016) for 1000 grain weight, (Rajpoot et al., 2015) for 1000-grain weight, (Kabir et al., 2017) for 1000 grain weight and harvest index, (Sabit et al., 2017) for biological yield/plant and ear weight, (Shah et al., 2017) for biological yield/plant, harvest index, ear length, 1000 grain weight and plant height.

Among the other pairs of traits, high and positive correlation was found for Days to 50 per cent heading with days to maturity and canopy temperature, days to maturity with high and positive correlation with plant height, ear length, relative water content, protein content, biological yield/plant, Plant height with ear length, relative water content, biological yield/plant, number of spikelets/spike, number of grains/ear, grain yield/plant and peduncle length, Number of effective tillers/plant with number of ear/plant, grain yield/plant, biological yield/plant, harvest index and ear length, Number of spikelets/spike with number of grains/ear, ear length, biological yield/plant, grain yield, Ear length with biological yield/plant, grain yield/plant, ear weight, number of grains/ear, relative water content, 1000 grain weight, Ear weight with grain yield/plant, biological yield/plant, 1000 grain weight, number of grains/ear, Peduncle length with number of grains/ear, Number of ear/plant with grain yield/plant, biological yield/plant and harvest index, Number of grains/ear with biological yield/plant, relative water content and grain yield/plant, 1000 grain weight with grain yield/plant, biological yield/plant and harvest index, Biological yield/plant with grain yield/plant and relative water content, Harvest index with grain yield/plant and canopy temperature, Chlorophyll content with canopy temperature, Canopy temperature with protein content and relative water content, Relative water content with grain yield, Protein content with sedimentation value.

The association analysis revealed that biological yield/plant, harvest index, number of grains/ear, number of effective tillers/plant, number of spikelets /spike, ear length, ear weight, plant height and 1000 grain weight are the important traits and may be selected to increase the grain yield. Present findings also revealed that by making selection for a particular trait, simultaneous improvement in the associated trait may also be achieved.

5.7 Path coefficient analysis

The correlation coefficient between characters exhibits the relationship existing between pair of characters. But a dependent character is an interaction of product of many mutually associated component characters and change in anyone component will disturb whole network of cause and effect system.

The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relationship between the variables, the path coefficient partition the association into direct and indirect effects via other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved. This is simply standardized partial regression coefficient. Path diagram facilitates the understanding of the nature of cause and effect system. The path analysis suggested by Dewey and Lu (1959) helps to resolve these correlations further and throws more light on the way in which component traits contribute towards specifically identifying important component characters.

In the present investigation path coefficient analysis has been performed at genotypic and phenotypic level taking grain yield as dependent variable. In general genotypic direct and indirect effects were slightly higher in magnitude as compared to phenotypic effects.

In the present study biological yield/plant, number of spikelets/spike, harvest index, ear length, number of ear/plant, peduncle length and ear weight had positive direct effect and on grain yield/plant direct selection for these traits may rewarded in other words these traits should given importance while practicing selection, aimed at improvement of grain yield in wheat. The results are in propinquity with (Singh and Dwivedi 2002), (Phougat

et al., 2017) for harvest index and biological yield/plant, (Majumder et al., 2008), (Suleiman et al., 2014) for number of ear/plant, (Tsegaye et al., 2012), (Fellahi et al., 2013), (Gelalcha and Hanchinal 2013) and (Bhushan et al., 2013) for biological yield/plant, harvest index and, (Rajpoot et al., 2013) for ear length, (Tiwari et al. 2016) for biological yield, harvest index and ear weight, (Chimdesa et al., 2017) for biological yield/plant, harvest index and ear length, (Sabit et al., 2017) for biological yield/plant, harvest index, ear length, peduncle length and ear weight. (Singh et al., 2003) for biological yield/plant. (Majumder et al., 2008) for harvest index.

Whereas, number of grains/ear had the highest negative direct effect on grain yield/plant followed by plant height, number of effective tillers/plant and days to 50% heading. Similarly result were obtained by (Suleiman et al., 2014) for plant height and days to 50% heading, (Chimdesa et al., 2017) for days to 50% heading.

Other traits plant height expressed higher positive indirect effect on grain yield on it through days to 50% heading and harvest index. Similar traits viz., Number of spikelets/spike for (ear length, biological yield/plant, plant height), Ear length for (plant height, biological yield, number of spikelets/spike, ear weight and number of grains/ear), Number of ear/plant for (number of effective tillers/plant, biological yield/plant, plant height, peduncle length), Number of grains/ear for (days to 50% heading, harvest index , peduncle length), Biological yield/plant for (ear length, number of spikelets/spike, plant height, number of grains/ear, number of effective tillers/plant, ear weight, number of ear/plant), Harvest index for (1000 grain weight, ear weight, number of ear/plant, number of effective tillers/plant), hence simultaneous selection for these traits can be made for the improvement of yield. The findings are in accordance to the findings of (Majumder et al., 2008) and (Khan et al., 2013).

The traits viz. biological yield/plant, harvest index, ear length, number of ear/plant and ear weight had positive correlation coefficient values and positive direct effect on grain yield/plant. This indicates true relationships with grain yield/plant and direct selection for these traits would result in higher breeding efficiency for improving yield. Thus, these traits might be reckoned as the most important component trait for grain yield/plant. Majority of indirect

effects of various independent traits via other traits were extremely low of either signs.

5.8 Genetic divergence

Genetic divergence means estimation of genetic distance between two or more genotypes in order to achieve best combination for hybridization. D^2 statistic helps in the selection of genetically divergent parents for their exploitation in hybridization programmes. The technique measures the degree of diversification and determines the relative proportion of each components trait to the total divergence. It measures the forces of differentiation at two levels i.e. intra cluster and inter cluster levels. It provides reliable estimates of genetic divergence and a large number of germplasm lines can be evaluated at a time for genetic diversity by this technique. In the present investigation, 60 genotypes were grouped into eleven clusters using Tocher's method. The intra and inter cluster distance was calculated by using D^2 values.

5.8.1 Contribution of individual characters towards genetic divergence

The variance of cluster mean of different traits indicated that there is a significant variation for all the traits. Hence, traits like 1000 grain weight contributed maximum towards genetic divergence followed by biological yield/plant, harvest index, plant height, peduncle length, grain yield/plant, ear length, number of spikelets/spike, ear weight, days to 50% heading and other characters viz, days to maturity and number of ear/plant, number of effective tillers/plant, number of grains/ear did reported very negligible percentage contribution towards divergence. These findings corroborated with the earlier findings of (Mishra et al., 2015), (Mollasadeghi et al., 2012) for 1000 grain weight and plant height, (Khare et al., 2015) found that maximum contribution to total genetic divergence genotypes present in cluster I and IV.

5.8.2 Grouping of genotypes into different clusters

The maximum number of genotypes (16) were found in the cluster I and III followed by cluster IV (10), cluster V (7), cluster X (5). While remaining cluster II, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X and cluster XI were mono-genotypic. From the composition of genotypes of most of the clusters, it was found that the genotypes included in clusters are heterogeneous

in terms of their origins. These results revealed that geographic diversity might not be an important factor in determining genetic divergence. These findings are in agreement with the results obtained by (Dwivedi and Pawar 2005) obtained highest number of genotypes in cluster I and lowest in VIII, (Ali et al., 2008) obtained maximum diversity in cluster I, (Kumar et al., 2009), (Singh et al., 2014), and (Uddin et al., 2015), (Khare et al., 2015) resulted maximum genotypes in cluster V and XII and cluster I only 1 genotype was present.

5.8.3 Intra and inter cluster divergence D² values

The inter cluster distances were found higher than the intra cluster distance revealing a considerable amount of genetic diversity among the genotypes studied. The highest inter cluster distance was observed between cluster V and cluster IX (STNT-7, MP-3480, STNT-2, MP-3489, STNT-3, MP-3468, MP-3492, MP-3495) followed by cluster III and XI, cluster V and XI, cluster VII and IX, cluster V and VI, cluster VII and IX and cluster VII and XI. The genotypes grouped in these clusters can be used in breeding programme in order to get a wide spectrum of variability and transgressive segregants. These findings are in agreement with the results obtained by (Ali et al., 2008), (Hailegiorgis et al., 2011), (Degewione et al., 2013), (Desheva and Kyosev 2015) and (Uddin et al., 2015), (Khare et al., 2015) obtained maximum distance between cluster II and IV, (Ahmed et al., 2018) obtained highest D² value in cluster I and II, (Meena et al., 2014) resulted highest inter cluster distance in cluster VIII and XIX.

The minimum inter cluster distance was found between clusters II and IV, cluster I and II and cluster VI and VIII indicated that they were genetically closure clusters. Selection of parents from such clusters may be avoided because it may result in narrow genetic base. (Ahmed et al., 2018) resulted lowest D² value in cluster X and XI.

Maximum intra cluster distance was recorded in cluster X (MP-3481, MP-3507, MP-3506, MP-3342/PBWK343/K918, and JW-3288) followed by cluster IV, cluster V, cluster III. The minimum intra cluster distance was expressed by cluster I. The cluster II, cluster VI, cluster VII, cluster VIII, cluster IX, and cluster XI were mono-genotypic hence the intra cluster distance was

zero. (Ahmed et al., 2018) obtained result in 12 groups maximum intra cluster distance in cluster II and minimum in cluster X indicated close relation among genotypes.

Highest mean value for a large number of traits was exhibited in cluster IX for ear length, ear weight, harvest index, number of effective tillers/plant, number of ear/plant and 1000 grain weight followed by cluster VIII for number of spikelets/spike, peduncle length, number of grains/ear and grain yield/plant, cluster V for biological yield/plant, cluster VI for days to 50% heading, cluster VII for days to maturity, cluster XI for plant height. These findings are in close harmony with the earlier findings of (Dwivedi and Pawar 2005) found that cluster I, II and IV identified diverse and high mean value for yield attributed traits, (Ali et al., 2008), (Kumar et al., 2009), (Hailegiorgis et al., 2011) and (Uddin et al., 2015). (Meena et al., 2014) resulted highest mean value for chlorophyll content, peduncle length and number grains/ear.

5.8.4 Genotypes identified as most diverse parents in hybridization programme

Crossing among the genotypes in cluster V (STNT-7, MP-3480, STNT-2, MP-3489, STNT-3, MP-3468, MP-3492) and cluster IX (MP-3495) were identified as genetically most diverse parents, which can be utilized for future crop improvement programme may lead to maximum diversity in the segregating population and develop high yielding varieties in wheat.

5.9 Principal component analysis

Principal component analysis (PCA) is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (i.e. accounts for as much of the variability in the data as possible) and each succeeding component in turn has the highest variance possible under the constraint that it is orthogonal to the preceding components. The resulting

vectors are an uncorrelated orthogonal basis set. The principal components are orthogonal because they are the eigen vectors of the covariance matrix, which is symmetric.

In the present investigation PCA was performed for quantitative and qualitative traits of wheat. Out of nineteen, only ten principal components (PCs) exhibited more than 0.5 Eigen value and showed about 91.33% variability. Therefore, only six principal components were given due importance for the further explanation. The PC1 had the highest variability (27.693 %) followed by PC2 (15.020%), PC3 (10.501%), PC4 (8.953%), PC5 (8.143%) and PC6 (5.99%) for traits under study.

The PC1 showed positive effect for the specific traits under study that is plant height, number of spikelets/spike, ear length, number of grains/ear, biological yield/plant, grain yield/plant and relative water content. PC2 was more related to yield traits viz., number of effective tillers/plant, number of ear/plant, harvest index and 1000 grain weight while PC3 was consisting of traits viz., days to maturity, peduncle length and protein content. PC4 was related to traits ear weight and sedimentation value. PC5 was consisting only chlorophyll content. Days to 50% heading and canopy temperature was in PC6. On the basis of PCA most of the important yield and yield attributing traits were present in PC1 PC2 and PC3.

On the basis of principle component scores high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. STNT-5 had the highest PC score followed by STNT-4, STNT-3, STNT-12, STNT-14, STNT-6, STNT-11, STNT-21, STNT-10, STNT-15, STNT-13, STNT-2, MP-3336, STNT-7, MP-3495, MP-3474, STNT-25, MP-3489, MP-3468, STNT-17, MP-3323/MP-3298, STNT-8, STNT-34, MP-3492, MP-3481, STNT-22, HD-2864 and MP-3472 in PC1 indicated that these genotypes possesses high values of traits viz., plant height, number of spikelets/spike, ear length, number of grains/ear, biological yield/plant, grain yield/plant and relative water content which are mainly yield attributing traits. The highest PC score of HD-2864, PBW-14, MP-3500, MP-3495, IPPSN-137, MP-3336, PBW-343/CBW-9563, MP-3323/MP-3298, MP-3335/GW322-J-485, MP-3324/MP-3222, MP-3497, MP-3504, MP-3468, STNT-25, STNT-11, STNT-

21, STNT-15, STNT-10, STNT-5, MP-3499, HI-1544, IPPSN-201, MP-3474 and MP-3382 in PC2 was mainly related with number of effective tillers/plant, number of ear/plant, harvest index and 1000 grain weight which are mainly yield attributing traits. The highest PC scores was obtained by STNT-16 followed by MP-3472, IPPSN-201, MP-3479, MP-1201, MP-3474, IPPSN-137, MP-3468, MP-3489, STNT-13, MP-3480, MP-3335/GW322-J-485, STNT-15, MP-3492, MP-3324/MP-3222, MP-3382, MP-3491, MP-3501, MP-3496, STNT-6 and STNT-11 in PC3 for characters namely, days to maturity, peduncle length and protein content. PC scores in PC4 were recorded the highest value for characters viz. ear weight and sedimentation value by the genotypes MP-3323/MP-3298 followed by STNT-11, MP-3481, MP-3382, MP-3335/GW322-J-485, MP-3324/MP3222, MP-3507, STNT-12, MP-3495, MP-3494, MP-3496, MP-3491, MP-3336, MP-3342/PBWK-343/K-918, MP-3474, MP-3504, MP-3493, MP-3324/NIAW-1395, MP-3506, STNT-6 and MP-3492. PC5 scores highest for the genotypes viz., MP-3497, MP-3499, MP-3480, MP-3504, MP-3472, MP-3500, MP-3506, STNT-13, STNT-2, MP-3489, STNT-25, MP-3335/GW322-J-485, MP-3493, MP-3324/MP-3222, STNT-10, STNT-16, STNT-34, STNT-3, PBW-14, MP-3507 and MP-3491 for only chlorophyll content. In PC6 the highest score for days to 50% heading and canopy temperature was recorded for genotypes MP-3507 followed by MP-3497, MP-3336, MP-3491, MP-3481, MP-3468, MP-3492, PBW-343/CBW-9563, MP-3489, MP-3372/NIAW-1395, MP-3499, HD-2864, IPPSN-102, MP-3493, MP-3495, PBW-14 and MP-3478.

Similar findings for plant height, in PC1 was reported by (Bhanupriya et al., 2014), but in contradiction (Meena et al., 2014) obtained higher value for plant height and 1000-grain weight in PC2. It can be concluded from the above results that yield contributing traits were having the highest variation in PC1 followed by PC2 and PC3.

Table 4.20: Promising genotypes identified for yield and quality

S.No.	Genotypes	Traits
1	MP-3468	biological yield/plant, grain yield/plant, plant height , protein content, number of ear/plant, harvest index, number of grains/ear , days to heading, days to maturity
2	MP-3474	biological yield/plant, grain yield/plant, plant height , protein content, relative water content, days to maturity, number of grains/ear, number of spikelets/spike, sedimentation value, ear weight
3	MP-3489	biological yield/plant, grain yield/plant, plant height , protein content, relative water content, days to maturity, days to 50% heading, number of grains/ear, number of spikelets/spike
4	MP-3492	biological yield/plant, grain yield/plant, plant height , protein content, sedimentation value, , number of ear/plant, harvest index, 1000 grain weight
5	MP-3324/MP-3222	number of effective tillers/plant, number of ear/plant, harvest index, 1000 grain weight, protein content, days to heading sedimentation value, ear weight, peduncle length, chlorophyll content
6	MP-3335/GW-322-J-485	number of effective tillers/plant, number of ear/plant, harvest index, 1000 grain weight, protein content, sedimentation value, ear weight, peduncle length, chlorophyll content
7	STNT-13	biological yield/plant, grain yield/plant, plant height , protein content, relative water content, days to maturity, number of grains/ear, number of spikelets/spike

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FUTURE RESEARCH WORK

6.1 Summary

The present investigation “Genetic Analysis for Yield, its Components and Quality Characters in Wheat” was carried out during *Rabi* season of 2017-18 at the Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jabalpur (M.P).

The experimental material comprised of 60 genotypes of wheat collected from AICRP on wheat, College of Agriculture Jabalpur (M.P). These genotypes were planted in Randomized Complete Block Design (RCBD) with two replications. This investigation was carried out to estimate the genetic variability, heritability, genetic advance, correlation coefficient, path coefficient, genetic divergence analysis and principal component analysis to identify the importance of individual character and formulating selection criteria for improvement in yield and quality of wheat. On the basis of results, the present investigation is summarized as follows:

The analysis of variance revealed that mean sum of squares due to genotypes was highly significantly for all the traits, indicating the presence of sufficient genetic variability in the existing material. Traits viz., biological yield/plant, plant height, sedimentation value, relative water content, number of grains/spike, 1000 grain weight, grain yield/plant, days to 50% heading, harvest index and chlorophyll content exhibited the value of higher magnitude for variability.

The values of phenotypic coefficient of variation for all the traits under study were found more than genotypic coefficient of variation. High genotypic and phenotypic coefficient of variation were found for ear weight, grain yield/plant, biological yield/plant, peduncle length, sedimentation value, number of effective tillers/plant, number of ear/plant, ear length whereas, harvest index, canopy temperature, plant height, 1000 grain weight, number of grains/ear, number of spikelets/spike, chlorophyll content, protein content and relative water content showed moderate (GCV) and (PCV).

The heritability estimates were observed very high for sedimentation value, protein content, 1000 grain weight, biological yield/plant, plant height, relative water content, peduncle length, number of grains/ear, ear length, grain yield/plant, canopy temperature, ear weight, number of spikelets/spike and medium for harvest index, days to 50% heading and days to maturity.

The highest estimate of genetic advance as percentage of mean was recorded for biological yield/plant followed by ear weight, grain yield/plant, sedimentation value, peduncle length. Ear length, 1000 grain weight, protein content, plant height, canopy temperature, harvest index, number of grains/ear, number of spikelets/spike, relative water content, number of effective tillers/plant showed moderate value of genetic advance as percentage of mean.

Grain yield/plant was recorded highly significant and positive correlation with biological yield/plant followed by number of effective tillers/plant, ear weight, ear length, number of ear/plant, 1000 grain weight, harvest index, plant height indicating that these traits are the primary yield determinant in wheat.

Biological yield/plant showed highest positive effect on grain yield/plant followed by number of spikelets/spike, harvest index, ear length, number of ear/plant, peduncle length and ear weight. Direct selection for these traits may rewarded in other words these traits should give importance while practicing selection, aimed at improvement of grain yield in wheat.

From the results of correlation and path analysis, it was clear that the yield components which were showing significant correlation with the grain yield/plant was mainly due to its direct effect and partially due to indirect effect via other characters.

Sixty genotypes of wheat were grouped in eleven clusters based on D^2 values. Wide range of diversity has been recorded in terms of genetic distance D^2 values. Thus, it was evident that considerable amount of genetic divergence was present in the material under study. Inter crossing of genotypes from different clusters showing superior mean performance may help in obtaining superior recombinants for achieving higher yield and superior quality.

These genotypes from different clusters may be utilized as parents in crossing programme to isolate desirable segregants for yield and quality traits.

Out of nineteen traits, only ten principal components (PCs) exhibited more than 0.5 Eigen value and showed about 91.33 % variability.

On the basis of principal component analysis twenty eight genotypes are ranked into PC1 followed by twenty four in PC2 and twenty one genotypes on PC3, which possess higher number of values for the yield and quality attributing traits. MP-3468, MP-3474, MP-3492, MP-3489, MP-3324/MP-3222, MP-3335/GW-322-J-485, STNT-13, STNT-25, MP-3481 and MP-3495 were identified as promising genotypes because they fell into more than one PCs. Whereas, STNT-5, STNT-4, STNT-3, STNT-12, STNT-14, STNT-6, STNT-11 and STNT-21 was found the best as it possessed higher value for more number of important traits.

6.2 Conclusion

Based on the results the following conclusions are drawn from the present investigation.

1. Higher magnitude of PCV and GCV were observed for traits viz., ear weight, grain yield/plant, biological yield/plant, peduncle length, sedimentation value and number of effective tillers/plant. Thus the above characters were given due to importance for further work.

2. High heritability was observed for sedimentation value, protein content, 1000 grain weight, biological yield/plant and plant height, while high genetic advance as % of mean observed for biological yield/plant, ear weight, grain yield/plant, sedimentation value, peduncle length and ear length. This indicates that these traits may be controlled by additive gene action and attention should be required at time of selection.

3. Correlation and path analysis indicated that biological yield/plant, harvest index, ear length, ear weight and number of ears/plant are more important traits for wheat improvement.

4. Genetic divergence showed that 1000 grain weight exhibited highest percent contribution towards total genetic divergence (36.72%)

followed by biological yield/plant (15.20). Maximum cluster distance between cluster V & IX (156.94) followed by cluster III&XI (136.61). Suggests that crossing between genotypes of these clusters may yield better recombinant and superior segregants.

5. On the basis of PCA the promising genotypes identified for yield and quality viz., MP-3468, MP-3474, MP-3492, MP-3489, MP-3324/MP-3222, MP-3335/GW-322-J-485 and STNT-13.

6.3 Suggestions for further work

1. Diverse genotypes for yield components and quality traits should be used as donor parents for recovery of better recombinants.
2. The desirable and stable genotypes identified for yield and quality traits should involve in further breeding programmes.
3. The study should be conducted over years and locations for testing their stability.
4. The diversity of the genotypes will be further confirmed using molecular markers

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Appendix –I: Mean Performance of various genotype for yield, its components and quality characters in wheat

Genotypes	DFH	DM	PH	NETPP	NSPS	EL	EW	PL	NEPP	NGPE	TGW	BY	HI	CC	CT	RWC	PC	SDS	GY
STNT-2	63.00	116.50	102.83	9.50	18.33	10.95	2.68	19.22	9.44	53.17	36.86	58.58	33.08	50.90	21.00	83.45	12.70	49.95	19.39
STNT-3	67.00	119.00	106.83	9.50	18.83	11.00	3.07	24.05	9.38	54.33	41.42	65.62	32.33	55.05	20.70	83.78	13.29	45.97	21.24
STNT-4	61.50	121.50	103.00	9.35	18.50	11.62	3.65	21.90	8.41	53.17	46.43	64.23	38.05	52.10	20.50	88.42	12.26	42.00	24.44
STNT-5	64.50	118.00	108.66	9.65	18.67	13.33	3.17	20.17	9.58	53.67	47.37	64.33	37.05	44.82	20.20	78.41	13.18	43.88	23.91
STNT-6	67.50	119.50	108.33	9.18	19.33	11.42	3.28	22.42	9.05	55.83	43.33	53.83	41.08	41.40	21.75	79.30	14.42	50.33	22.19
STNT-7	67.50	117.50	106.16	9.32	18.16	11.23	2.65	23.08	9.26	52.17	40.66	57.00	34.04	47.85	20.55	83.00	11.73	41.73	19.45
STNT-8	66.50	117.00	104.83	8.50	18.17	11.39	2.92	20.82	8.36	52.33	42.40	43.66	37.52	52.93	20.43	81.20	11.63	38.39	16.45
STNT-10	60.50	116.50	99.67	9.82	19.33	11.65	3.04	19.48	9.76	55.67	46.35	47.18	36.69	48.73	21.35	78.70	11.87	40.41	17.33
STNT-11	66.50	119.50	102.83	9.82	18.00	12.98	3.67	16.82	9.71	51.67	46.39	63.82	37.58	50.67	20.90	73.40	14.24	57.38	23.98
STNT-12	62.00	117.50	103.83	9.33	18.33	12.03	3.92	16.85	9.26	52.33	47.46	60.67	36.40	50.95	21.85	86.70	13.70	54.18	22.09
STNT-13	67.00	119.50	109.00	9.82	18.67	11.05	2.58	20.47	9.77	53.83	43.13	42.33	34.16	49.32	20.65	85.56	14.00	53.44	14.50
STNT-14	63.00	118.50	99.83	9.66	19.00	11.48	3.32	19.27	9.54	54.83	45.75	57.50	36.54	48.70	20.65	86.50	11.29	49.09	21.00
STNT-15	67.50	119.50	107.50	10.15	18.67	11.12	2.63	22.80	10.10	53.67	46.51	45.67	36.77	47.02	20.31	77.65	12.02	47.53	16.83
STNT-16	69.00	121.00	108.67	10.00	16.67	10.64	2.51	21.00	9.74	48.00	37.50	41.33	33.32	49.27	20.23	87.08	13.94	52.71	13.83
STNT-17	62.00	117.50	99.00	8.83	18.33	10.14	2.76	21.19	8.76	52.67	47.40	48.00	33.59	48.62	20.40	79.00	14.24	54.98	16.17
STNT-21	63.50	119.00	107.00	9.66	18.00	13.35	3.68	19.15	9.55	51.67	46.48	59.29	37.05	48.95	22.40	78.75	11.49	43.23	22.00
STNT-22	63.50	119.50	108.17	7.50	18.00	12.08	3.06	19.65	7.42	51.83	40.65	41.00	37.38	46.84	20.85	88.98	11.58	38.04	15.34
STNT-25	62.00	117.00	105.67	9.85	18.33	11.52	1.85	19.20	9.76	53.00	50.80	44.56	37.40	48.92	22.15	81.62	11.95	37.07	16.67
STNT-34	63.00	117.50	102.17	9.66	17.67	10.48	3.03	17.21	9.55	50.67	45.55	45.99	36.71	50.00	20.75	81.14	12.72	47.36	16.88
MP-3468	70.50	119.50	101.67	10.18	17.33	11.64	2.25	23.23	9.92	49.83	45.04	64.46	34.11	47.50	24.45	87.78	11.63	41.38	22.00
MP-3471	70.00	120.00	100.50	7.50	16.33	9.57	3.08	21.88	7.42	47.00	41.13	42.23	37.02	46.40	22.75	75.85	12.02	40.67	15.67
MP-3472	68.00	121.00	104.66	10.15	18.00	9.49	1.88	20.20	10.07	51.83	44.50	45.13	36.92	48.71	21.95	76.29	14.15	57.96	16.67

MP-3474	68.00	120.50	105.67	9.66	16.00	11.92	3.40	21.87	9.54	46.33	46.48	59.38	37.22	45.50	20.50	75.79	12.73	58.17	22.11
MP-3476	62.00	117.00	98.33	9.50	15.00	11.34	2.57	21.24	9.38	42.83	39.42	43.66	35.50	50.00	22.10	75.47	12.33	45.90	15.50
MP-3478	68.00	121.00	96.00	9.17	16.67	11.22	2.89	17.00	9.07	47.83	35.57	45.82	36.73	46.07	21.85	82.29	12.79	49.76	16.83
MP-3479	70.00	122.00	88.00	9.67	16.33	10.69	2.51	12.97	9.58	46.50	41.40	50.40	34.34	46.20	21.95	87.61	13.94	55.03	17.29
MP-3480	67.00	117.00	99.00	10.18	17.67	10.34	2.17	20.32	10.05	50.83	38.17	51.78	31.63	48.23	23.15	83.60	13.09	52.13	16.39
MP-3481	69.50	122.50	97.66	7.00	18.50	12.25	3.64	10.55	6.92	53.00	43.80	45.50	32.12	53.66	22.60	81.87	13.13	52.26	14.61
MP-3489	68.50	121.00	99.50	9.50	18.50	11.07	2.16	22.77	9.39	53.50	41.08	59.85	32.01	54.10	22.85	83.05	12.84	58.67	19.14
MP-3491	69.00	121.00	100.33	7.33	18.83	10.59	2.84	21.48	7.24	54.00	39.60	37.02	32.50	49.85	26.00	77.40	14.04	59.11	12.07
MP-3492	70.50	122.00	101.17	9.66	17.67	11.42	2.99	19.97	9.55	47.33	47.80	62.33	31.93	48.38	24.85	76.54	12.07	49.43	19.90
MP-3493	67.50	121.00	97.66	8.65	17.00	10.55	2.34	18.12	8.58	48.66	43.08	44.94	35.97	52.22	25.95	75.73	13.62	43.48	16.22
MP-3494	70.50	118.50	97.00	7.50	15.67	10.87	2.70	20.77	7.40	44.33	48.58	41.33	34.93	53.38	25.80	73.46	12.73	53.41	14.34
MP-3495	68.50	118.50	103.00	10.00	18.00	13.75	4.02	18.78	9.92	51.50	51.15	49.00	44.83	53.28	26.65	80.14	12.13	44.23	21.94
MP-3496	67.00	119.50	103.16	7.22	16.00	12.35	3.25	24.05	8.60	45.33	43.54	40.82	34.56	52.80	25.35	74.18	13.90	54.62	14.13
MP-3497	67.50	120.00	98.33	10.68	18.67	11.03	2.21	17.68	10.53	53.50	35.15	42.78	42.03	54.22	26.00	73.29	12.82	41.28	17.98
MP-3499	64.50	117.50	91.33	9.66	18.00	10.14	2.20	14.37	9.57	51.83	37.48	43.50	38.91	55.07	26.05	76.10	11.63	37.33	16.92
MP-3500	67.50	118.00	89.00	10.17	17.66	9.88	2.75	21.15	10.06	50.50	45.15	49.16	42.70	55.15	25.30	75.21	12.06	39.87	20.99
MP-3501	66.50	122.00	96.33	8.50	17.67	11.19	2.53	23.84	8.39	50.33	40.55	43.16	36.60	52.25	23.90	77.88	13.21	52.67	15.80
MP-3504	60.50	113.00	89.17	9.33	16.00	9.38	2.36	16.99	9.76	45.50	45.58	43.33	42.00	52.07	24.20	72.54	12.95	50.24	18.23
MP-3506	62.50	112.50	80.83	7.50	18.67	10.42	2.77	14.87	7.33	53.33	43.74	37.00	34.68	54.18	23.75	74.44	12.03	47.23	12.87
MP-3507	73.50	119.50	88.33	7.83	18.83	10.62	2.79	13.75	7.72	53.83	40.65	46.50	34.00	51.90	25.80	71.97	11.96	53.60	15.86
MP-3323/MP-3298	70.00	115.00	96.50	9.83	18.00	11.86	3.43	18.98	9.74	51.83	46.50	54.18	41.10	49.48	24.35	74.13	14.32	57.54	22.26
MP-3324/NIAW-1395	68.00	114.50	88.83	8.83	16.00	8.97	3.05	19.95	8.74	46.00	41.48	40.22	37.84	49.20	24.40	73.65	11.58	58.12	15.24
MP-3324/MP-3222	68.00	119.50	92.83	10.00	17.00	9.88	3.26	18.03	9.86	48.50	44.43	46.50	40.38	49.47	24.75	73.09	13.76	53.14	18.76
MP-3342/PBWK-998-4	70.00	115.50	86.33	6.83	15.33	8.10	2.21	17.93	6.75	43.50	43.78	32.00	36.09	47.50	24.75	76.73	11.50	41.38	11.56

MP-3342/PBWK-343/K-918	72.00	116.50	68.16	7.67	14.33	8.59	2.76	17.73	7.60	46.03	44.80	33.33	39.40	46.88	24.10	72.16	12.65	51.01	13.12
MP-3335/GW-322-J-485	70.00	119.00	87.17	10.00	16.67	9.14	3.47	19.62	9.89	43.47	40.93	41.33	42.89	50.53	25.75	72.56	13.84	54.78	17.73
MP-3382	69.00	118.50	85.50	9.33	15.33	9.55	2.79	21.10	9.26	41.00	46.41	43.17	40.60	51.82	25.20	72.61	13.90	56.07	17.49
MP-3372/NIAW-1395	72.00	119.50	91.33	7.33	15.67	8.65	2.66	20.70	7.25	44.83	36.77	32.66	34.07	48.50	24.75	73.22	11.48	50.32	11.13
MP-1201	72.00	118.50	88.83	9.67	15.33	8.65	1.25	21.75	9.55	43.83	39.70	40.33	37.35	46.21	25.00	74.34	12.85	52.70	15.12
PBW-343/CBW-9563	68.50	118.00	86.50	9.67	17.33	10.43	3.46	18.73	9.56	50.00	42.03	44.33	41.32	47.30	26.10	73.01	11.42	37.50	18.34
JW-3288	68.00	114.50	85.67	8.33	15.33	9.22	1.96	19.92	8.27	43.67	43.47	32.32	42.41	46.72	25.85	70.17	13.65	43.25	13.73
PBW-14	68.50	117.50	85.83	10.00	16.67	9.35	2.50	18.84	9.88	47.83	43.93	41.83	39.99	47.08	25.80	70.64	11.51	37.76	16.75
IPPSN-102	71.00	116.50	90.67	9.17	16.67	10.09	3.15	19.53	9.21	48.00	40.65	44.22	35.13	47.52	24.55	71.68	11.27	39.27	15.65
IPPSN-201	71.00	119.50	100.33	9.83	15.33	10.20	2.44	22.77	9.75	43.50	36.25	38.33	37.82	45.41	23.95	70.58	13.58	49.20	14.48
IPPSN-137	71.50	119.00	94.67	10.16	15.00	10.21	2.54	24.19	10.03	42.50	45.39	41.83	37.98	44.17	23.10	71.36	12.52	35.68	15.88
HI-1544	70.50	115.00	99.97	9.50	16.50	9.75	2.32	20.17	9.36	47.16	43.32	44.33	36.68	45.53	24.05	71.13	12.03	38.24	16.28
MP-3336	70.50	119.00	90.33	9.83	19.66	12.80	3.73	24.67	9.73	56.67	46.58	57.83	40.41	43.70	25.10	71.31	13.06	46.44	23.39
HD-2864	71.50	119.50	94.33	9.83	17.67	12.10	3.07	18.98	9.75	51.00	49.00	51.33	44.76	43.63	21.80	74.78	11.37	34.29	22.91
MEAN	67.43	118.51	97.23	9.18	17.36	10.80	2.82	19.76	9.10	49.71	43.3	47.6	37.1	49.2	23.2	77.6	12.7	47.7	17.6
S.E.	1.56	1.21	2.76	0.60	0.53	0.48	0.22	1.07	0.63	1.52	0.71	2.50	1.39	2.36	0.82	1.91	0.13	0.27	1.31
Range Lowest	60.5	112.5	68.16	6.83	14.33	8.095	1.25	10.55	6.75	41	35.15	31.995	31.63	41.395	20.2	70.165	11.27	34.29	11.125
Range Highest	73.5	122.5	108.995	10.68	19.66	13.75	4.02	24.665	10.525	56.665	51.145	65.615	44.825	55.145	26.65	88.98	14.42	59.11	24.435

Appendix – II: Weekly meteorological parameters during *Rabi* season (November to April 2017-18)

Month	Meteo. Weeks	Temperature (°C)		SunShine hrs.	Rainfall (mm)	R. H. (%)		Wind Speed	Vapour Pressure (MM)		Evapo. (mm)	Rainy days
		MaX.	Min.			Morning	Evening		Morning	Evening		
Nov.	47	27.6	10.1	5.9	0	86	31	3.1	11	8.5	2.4	0
	48	28.1	5.1	8.6	0	82	21	2.3	7.1	5.6	2.4	0
Dec.	49	26.7	8.1	6.7	0	80	30	3	7.9	8.2	2.1	0
	50	27.5	9	6.6	0	88	35	2.4	9.3	9.5	2.1	0
	51	24.8	5.5	4.2	0	88	32	2.5	7.2	7.4	1.2	0
	52	25.2	3.9	7.3	0	86	28	2.4	6.4	6.4	2.1	0
Jan.	1	28.8	9.7	7.8	0.0	87	30	2.8	6.1	6.4	2.0	0
	2	24.7	12.6	9.1	0.0	88	29	2.3	6.6	6.6	2.0	0
	3	28.4	10.5	9.3	0.0	88	30	2.4	6.9	7.4	2.3	0
	4	31.0	12.7	9.2	0.0	86	25	3.3	7.1	5.9	2.8	0
	5	26.7	6.8	9.8	0.0	85	28	2.4	6.9	7.4	3.0	0
Feb.	6	26.6	12.4	5.4	0.0	81	52	3.4	9.5	10.9	2.6	0
	7	25.2	11.5	6.4	18.0	91	45	3.6	10.3	9.8	2.6	3
	8	31.2	12.5	9.8	0.0	80	28	2.8	10.0	9.7	3.1	0
	9	32.4	14.0	8.9	15.0	79	26	2.8	11.1	9.3	3.6	1
Mar.	10	30.9	14.1	6.9	1.0	75	33	2.9	10.5	10.4	3.2	0
	11	33.3	15.4	7.4	0.8	74	30	3.7	11.4	9.8	4.0	0
	12	34.4	14.7	8.4	17.0	64	20	3.5	10.2	8.0	4.8	1
	13	37.0	13.5	9.1	8.7	54	18	3.9	9.0	0.0	6.1	0
April	14	38.0	18.1	11.4	10.8	56	22	4.3	7.5	0.0	6.0	0
	15	37.0	20.6	15.3	17.9	67	40	4.8	7.4	0.0	5.2	0

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