

Biometrical Analysis for Genetic Improvement in Wheat [*Triticum aestivum* L.]

THESIS



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by

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CERTIFICATE – I

*This is to certify that the thesis entitled “**Biometrical analysis for genetic improvement in wheat [*Triticum aestivum* L.]**”. Submitted in partial fulfilment of the requirement for the Degree of **MASTER OF SCIENCE in Plant Breeding & Genetics** of Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior is a record of the bonafied research work carried out by Ms. **UPASNA MISHRA** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instruction.*

No part of the thesis has been submitted for any other degree or diploma or has been published. All the assistance and help received during the course of this investigation has been acknowledged by the scholar.

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CERTIFICATE – II

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CHAPTER- I

INTRODUCTION

The common bread wheat (*Triticum aestivum* L.) is the most important cereal crop in India and stands only second largest produce of wheat in the world after china. It is the largest staple food crop of about two billion people (36% of the world population) and an important commodity on the world grain commerce. Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). Wheat is a major contributor to the food security system in India as well, occupying nearly 30.37 million hectares, producing 90.78 million tones and productivity 29.89 quintals/hectare (Anonymous a, 2014-15).

In Madhya Pradesh, it is cultivated in 5.56 million hectares of land with the production of 13.37 million tones and productivity of 24.05 q/ha (Anonymous b, 2014-15). Flour from hard wheat's varieties evolved for the most part from (*T. aestivum*) contains a high percentage of gluten (11-12%) and is used to make bread and fine cakes.

Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. He separated wheat into three groups viz. diploids ($2n=14$), tetraploids ($2n=28$) and hexaploids ($2n=42$) chromosomes. Major cultivated species of wheat include: *Triticum aestivum*, which is a hexaploid species and is widely cultivated in the world; *Triticum durum*, the only tetraploid form of wheat widely used today, and the second most widely cultivated wheat; *Triticum monococcum*, a diploid species with wild and cultivated variants; *Triticum dicoccum*, a tetraploid species. These earliest cultivated forms were diploid (genome AA) (einkorn) and tetraploid (genome AABB) (emmer) wheat's and their genetic relationships indicate that they originated from the south-eastern part of Turkey (Heunet *et al.*, 1997; Nesbitt, 1998; Dubcovsky and Dvorak, 2007).

The objective of this study was to determine the extent of variability of yield and associated traits and the extent of correlation among traits at both phenotypic and genotypic levels and thereby compare the direct and indirect influence of the traits on grain yield. The model of discriminant function suggested by Robinson *et al.*

(1951) helps to identify important combination of yield components useful for selection by formulating suitable selection indices. Path coefficient analysis measures the direct and indirect effect for one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959).

Objectives:

- 1) To estimate the genetic variability for yield and yield contributing traits.
- 2) To estimate the correlation coefficient between yield and yield contributing characters.
- 3) To analyze path coefficients and estimate the direct and indirect effects of various yield components on yield to understand the causes of association.
- 4) To study discriminant function analysis for relative efficiency selection indices of different characters.
- 5) To estimate expected genotypic advances of different trait selection indices.

CHAPTER-II

REVIEW OF LITERATURE

The literature pertaining to various aspects of the present investigation entitled “Biometrical analysis for genetic improvement in wheat [*Triticum aestivum* L.]” has been reviewed under the following heads:

2.1 To estimate the genetic variability and expected genotypic advances.

2.2 To estimate the correlation and path coefficients.

2.3 To study discriminant function.

2.1. Variability and expected genotypic advances:

Ali *et al.* (2008) reported that the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for yield per plant, number of productive tillers per plant and number of grains per spike. The remaining traits recorded moderate to low PCV and GCV estimates. These traits also indicated high genetic advance (except fertility %). Grain yield per plant showed highly significant positive correlation with number of productive tillers per plant, number of spikelets per spike and number of grains per spike and significant positive correlation with spike length. Path coefficient analysis revealed that number of productive tillers per plant and number of grains per spike had the highest direct effect on grain yield per plant and each must be given preference in selection along with optimum plant height to select superior wheat genotypes.

Manal H. Eid (2009) reported that the mean average for plant height, spike length, number of spikes per plant, number of grains per spike, 50% heading date and 1000 grain-weight revealed highly significant differences among genotypes and crosses under both sowing conditions. High heritability accompanied by high genetic advance was observed for spike length and 1000 grain-weight. Low heritability coupled with low genetic advance was for plant height and number of grains per spike. Greater magnitude of heritability coupled with higher genetic advance in some traits under study provided that these parameters were under the control of additive genetic effects.

Ullah *et al.* (2011) reported that the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highly significant ($P < 0.05$) for spike length, days to 50% flowering and plant height. High heritability

estimates were recorded for plant height, days to 50% flowering, days to heading, spikelets per spike and spike length. Plant height, days to physiological maturity and spikelets per spike also indicate high expected genetic advance.

Kolakaret *al.*(2012) reported that the phenotypic and genotypic coefficient of variation was found to be moderate for days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter, spike length, number of spike lets per spike and number of grains per spike, except 1000 grain weight. Results obtained from present investigation has revealed moderate GCV and PCV indicating still there is possibility of improvement of genotypes through these characters. Heritability values for all the characters were found to be high for most of the characters viz., number of days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter length, spike length, number of spikelets per spike, number of grains per spike and grain yield per plot, had shown high heritability and genetic advance as per cent mean.

Shashikalaet *al.* (2012) reported that the variability parameters for eleven (11) traits in the 169 genotypes of wheat by simple lattice design. All the genotypes exhibited significant differences for all the traits. In the present study the phenotypic and genotypic coefficient of variation was found to be moderate for days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter, spike length, number of spike lets per spike and number of grains per spike, except 1000 grain weight. Results obtained from present investigation has revealed moderate GCV and PCV indicating still there is possibility of improvement of genotypes through these characters. Heritability values for all the characters were found to be high for most of the characters viz., number of days to 50 per cent flowering, days to maturity, plant height, peduncle length, number of productive tillers per meter length, spike length, number of spikelets per spike, number of grains per spike and grain yield per plot, had shown high heritability and genetic advance as per cent mean, however, the same character exhibited moderate GCV and PCV hence direct selection of genotypes can be done through these characters for further improvement of genotypes.

Tsegayeet *al.* (2012) reported that the genotypic, phenotypic and environmental coefficient of variation, heritability, genetic advance, correlation coefficients and path coefficients analysis were performed for yield and its contributing parameters in 23 durum wheat genotypes. Analysis of variance for traits

studied showed significant ($P < 0.01$) differences among the genotypes. The estimated values of broad-sense heritability were found between 11% (biological yield) and 90% (days to heading). High heritability coupled with high genetic advance as percent of mean was observed for thousand grain weight, spike length and number of spikelets per spike suggesting selection for these traits would give good response. Phenotypic path analysis described that biological yield (0.679) and harvest index (0.48) have direct contribution towards grain yield.

Degewioneet *et al.* (2013) reported that the High phenotypic coefficient of variation and genotypic coefficient of variation were recorded grain filling period, number of tillers plant-1 and grain yield plot-1. High genetic coefficient of variation along with high heritability and genetic advance were recorded in grain yield plot-1 and days to heading. Positive and Highly significant association were obtained between grain yield plot-1, number of tillers plant-1 and grains spike-1 at both phenotypic and genotypic levels. Path coefficient analysis displayed maximum positive direct effect on grain yield plot-1 mostly by days to heading, grain filling period, number of tillers plant-1 and grains spike-1, was major contributors of towards grain yield plot-1. The two traits which showed significant contribution towards grain yield plot-1 were number of tillers plant-1 and grains spike-1 and these traits should be given emphasis for future bread wheat yield improvement program.

Hokraniet *et al.* (2013) reported character associations for yield and its component traits in 95 advanced generation easily threshable mutant lines of derived dicoccum lines along with five checks (DDK1001, DDK1025, DWR1006, UAS415 and UAS304) of F4M4 progenies of wheat. The character starch content recorded least variability; whereas, seed yield per plant (g) and number of tillers per plant exhibited high variability. Yield per plant had a significant positive phenotypic correlation with starch content, wet gluten and sedimentation value.

Kumar *et al.* (2013) reported that the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for grain yield per plant, harvest index, number of grains per spike, number of tiller per plant and weight per ear. These all traits also indicate high expected genetic advance except harvest index and number of grains per spike.

Kaddemet *et al.* (2014) reported that the High estimates of phenotypic coefficient of variation was recorded for grain yield, but moderate phenotypic coefficient of variation was recorded for harvest index, biological yield, number of tillers per plant,

test weight and spike length. Moderate genotypic coefficient of variation was recorded for test weight, number of tillers per plant, grain yield and spike length. High heritability along with high genetic advance as percent of mean were recorded for spike length and test weight. Positive and highly significant correlation association were obtained for harvest index, plant height, biological yield and test weight with grain yield at both genotypic as well as phenotypic levels.

Kumar *et al.* (2014) reported that the highest estimates of GCV and PCV were observed for grain yield per plant followed by biological yield and harvest index (GCV 22.87 and PCV 23.03). Genetic advance revealed that it was high for plant height, biological yield per plant and moderate estimates were exhibited 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 like plant height, 1000 seed weight and harvest index showed high heritability coupled with high genetic advance.

Maurya *et al.* (2014) reported that the highest genetic variability was observed for yield per plant followed by number of grains per spike, 1000 grain weight and plant height. The highest phenotypic coefficient of variance (PCV) was recorded for yield per plant followed 1000 grain weight and number of grains per spike. The highest genotypic coefficient variance (GCV) was observed for yield per plant while the characters 1000 grains weight, grain per spike and spike length showed moderate value of GCV indicating that there could be used as selection indices for yield improvement. Higher heritability, in broad sense, was recorded for yield per plant, 1000 grain weight, grain per spike and plant height while moderate heritability observed for days to heading days to maturity and spike length.

Yadav *et al.* (2014) reported that genetic variability and diversity for utilization in development of superior varieties. Genotypes were evaluated using a randomized complete block design with three replications. Days to 50 % flowering, days to maturity, plant height, tillers per meter, spike length, grains per spike, test weight, grain yield per plant were recorded. Analysis of variance showed sufficient amount of variability was found in the entire gene pool for all traits studied. Grain yield per plant showed highest genotypic and phenotypic coefficient of variation.

Yahaya *et al.* (2014) reported that the High genetic coefficient of variation was obtained for weight of main spike and awn length. Heritability was found to be high for awn length, spike length, weight of the main spike and plant height. Total tillers per plant, spike length and number of grains per spike had moderate heritability with

high genetic advance. Grain yield per plant was high and positively correlated with effective tiller per plant. A positive significant correlation of yield was observed with length of spike, spikelets per spike, weight of main spike and plant height. Effective number of tiller and weight of the main spike had high heritability with high genetic advance and significant positive correlation with yield.

Choudhary *et al.* (2015) reported that the eighteen wheat genotypes were evaluated for genetic variability, heritability and genetic advance for four yield attributing traits. The PCV and GCV was found to be high for spikelet fertility, number of grains per spike and pollen sterility while, moderate for number of effective tillers per plant and spikelet fertility (field). Higher value of PCV was obtained in all the cases than the GCV for all the characters. The heritability for all the characters was found to be high with high GAM (Genetic advance over mean).

Kabir *et al.* (2015) reported genetic advance and high broad sense heritability for most of the traits. Genetic advance as percent of mean suggested that there is yet scope for further improvement of genotypes for the characters studied. The grain weight of 10 spike, grains/spike and thousand grain weight had high genotypic and phenotypic coefficient of variation. So selection for these three characters will be highly effective and efficient for improvement.

Bhutto *et al.* (2016) reported that the analysis of variance revealed significant differences among the genotypes for plant height, tillers plant⁻¹, spike length, spikelet's spike⁻¹, grains spike⁻¹, seed index and grain yield plant⁻¹. Based on mean performance, variety Sarsabz gave maximum plant height (95.46), produced maximum tillers plant⁻¹ (4.40), gave more grain spike⁻¹ (63.13), TJ-83 gave highest seed index (47.260), and was next ranker in spike length⁻¹ (12.07), spikelet's spike⁻¹ (19.13), grains spike⁻¹ (59.86), and grain yield plant⁻¹ (9.86) among the genotypes. The phenotypic correlations revealed that tillers plant⁻¹ and grains spike⁻¹ were highly positively associated.

Deoraj *et al.* (2016) reported that the significant treatment mean sum of squares for eleven characters studied revealed the presence of considerable amount of variability in F₂'s of 21 crosses, 7 parents and 2 checks. The magnitude of GCV and PCV were high for productive tiller per plant and spikelets per spike; whereas, days to maturity and days to 50 per cent flowering exhibited least GCV and PCV. The high heritability was accompanied with high genetic advance as per cent of mean for length of spike, productive tillers per running meter, 1000 grain weight and

grain yield per plant indicating additive genetic control in the expression of these characters.

2.2 Correlation and path coefficients:

Okuyama *et al.* (2004) reported that the path coefficient analysis, grain yield represented the dependent variable and the number of spikes m⁻², number of grains spike⁻¹, kernel weight, days to anthesis, above-ground biomass m⁻² and plant height were the independent ones. Grain yield showed positive phenotypic correlation with above-ground biomass, number of spikes m⁻² and number of grains per spike. Path analysis revealed positive direct effect and moderate correlation of number of spike m⁻² and number of grains per spike with grain yield.

Mohammad *et al.* (2005) reported that days to heading showed negative and significant correlation with harvest index and grain yield was not found with the biological yield. Days to maturity were negatively correlated at both genotypic and phenotypic levels with biological yield, harvest index and grain yield and the level of negative genotypic correlation was significant with harvest index and grain yield. Plant height showed negative genotypic and phenotypic correlation with harvest index and grain yield. Biological yield had positive significant genotypic and phenotypic correlation with harvest index and grain yield. Harvest index had positive and highly significant genotypic and phenotypic correlation with grain yield. Positive direct effect of days to heading, days to maturity and biological yield with grain yield were observed. Harvest index showed positive and highest direct effect on grain yield. Genotypic and phenotypic correlation coefficients revealed that important characters influencing grain yield (kg/ha) are harvest index and biological yield. Path analysis showed the importance in order of harvest index, biological yield, plant height, days to maturity and days to heading in grain yield.

Aycicek and Yildirim (2006) reported that the correlation coefficients and path analysis were calculated between grain yield and yield components of 20 bread wheat genotypes. Positive and significant correlation was found between yield and plant density, plant height, grain number per spike, grain weight per spike and 1000 kernels weight. Grain yield was negatively and significantly correlated with time to heading. Positive direct effect of plant height and grain weight spike⁻¹ and negative direct effect of time to heading associated with significant correlation with grain yield

Majumder *et al.* (2008) reported that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Spikes per plant, grains per spike, spike length, 100-grain weight and harvest index were the most important characters which possessed positive association with grain yield. Path coefficient analysis revealed that among the different yield contributing characters spike per plant, grains per spike, 100-grain weight and harvest index influenced grain yield per plant directly. The direct effects of these characters on grain yield were positive and considerably high. Moreover, harvest index, days to maturity and spikes per plant had positive and higher indirect effect on grain yield through grains per spike. Thus selection for yield in spring wheat through these characters would be effective.

Anwar *et al.* (2009) reported that the Correlation coefficients were computed for grain yield plant-1, tillers plant-1, spikelets spike-1, 1000 grain weight, spike length, days to heading, days to maturity and plant height from the F1 crosses developed from four lines and three testers including their parents. The results revealed that grain yield plant-1 was positively and significantly correlated with number of tillers plant-1 and days to maturity at genotypic level but non-significantly correlated at phenotypic level. Days to maturity had positive genotypic correlation with grain yield plant-1, number of tillers plant-1 and 1000-grain weight. Days to maturity and tillers plant-1 had positive direct effect on grain yield plant-1 also.

Khan and Dar *et al.* (2009) reported that the Seed yield was significantly and positively associated with number of spikelets plant-1, followed by number of effective tillers and 100-seed weight at both phenotypic and genotypic levels. Seed yield showed a significant negative association with number of seeds spikelet-1 at genotypic level. Among the significant inter-relationships, the association of days to 75% spike emergence with days to maturity and 100-seed weight were significant and positive, but were negative and significantly associated with number of seeds spikelet-1 and number of grains spike-1. Similarly, the associations of spike length with number of seeds spikelet-1, and number of spikelets plant-1 and number of effective tillers were negative and significant. The association of number of spikelets plant-1 with number of effective tillers was also positive and highly significant. Path coefficient analysis revealed that the magnitude of positive direct effect on seed yield was highest through number of spikelets plant-1, followed by number of grains spike-1 and 100-seed weight.

Khokharet *al.* (2009) reported that grain yield per plant was positively and highly significantly correlated with days to maturity but negatively and highly significantly associated with plant height. Days to maturity had highest positive direct effect on yield.

Koksalyagdi (2009) reported that while this trait had a positive direct effect towards increasing the yield, This trait generally had a positive effect on yield indirectly through other traits as well. Seed number per spike and plant height had direct negative effects. Plant density, seed weight per spike and thousand kernel weight increased the yield with the direct effect values of 0.312, 0.295 and 0.286, respectively, based on the average of four years.

Gulmezoglu *et al.* (2010) reported that Path coefficient analysis revealed that grain yield of triticale depended on the effect of four yield components (plant height, grain number per spike and thousand grain weight was positive and protein was negative) whereas grain yield of bread and durum wheat was due mainly to plant height, length of spike, protein, in addition to these, spike weight for durum wheat.

Abinasa *et al.* (2011) reported that the Highly significant differences were revealed among durum wheat genotypes for all traits studied, suggesting the possibility of improving durum wheat for these traits. Plant height and number of kernels per spike showed the highest phenotypic and genotypic coefficients of variations and genetic advance, whereas, days to maturity and test weight had the lowest values. Plant height exhibited highest heritability value of 98.3% while number of spikelets per spike showed minimum value of 36.4%. The genotypic correlations estimated showed positive association of grain yield with days for heading ($r=0.50$), harvest index ($r=0.69$) and kernels number per spike ($r=0.81$). Harvest index (1.13) and biomass (0.81) exhibited the highest positive and significant direct effect on grain yield.

Ashraf *et al.* (2011) reported that the Statistical analysis showed that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. The results revealed positive association in between number of tillers plant⁻¹, number of spikelets spike⁻¹, spike length, number of grains spike⁻¹ and 1000 grain weight with grain yield plant⁻¹ at both genotypic and phenotypic levels. However, days to 50% heading and plant height contributed negatively towards grain yield at both levels. Path analysis showed that maximum positive direct effect on grain yield plant⁻¹ was contributed mostly by

number of grains spike⁻¹, followed by number of tillers plant⁻¹ and 1000-grain weights were the major contributors towards grain yield. Since these three characters had high correlation and also high direct effect thus direct selection for these three characters should be of a major concern for a plant breeder.

Cifci *et al.* (2012) reported that the correlations between traits revealed that important characters, influencing grain yield per spike were spike length, spikelet number per spike and grain number per spike. The results of path analysis also indicated that spike length, spikelet number/ spike and grain number per spike had the maximum direct effects on grain yield per spike.

Iftikhar *et al.* (2012) reported that the obtained results revealed that flag leaf area, spikelets per spike, grains per spike and 1000-grain weight had positive and significant correlation with grain yield at both genotypic and phenotypic levels whereas, spike length was correlated positively and significantly with grain yield at genotypic level but non-significantly at phenotypic level while, tillers per plant showed negative and significant association with grain yield at both levels. Furthermore, path-coefficient analysis revealed that plant height, spike length, grains per spike and 1000-grain weight had positive direct effect on grain yield, whereas, tillers per plant, flag leaf area and spikelets per spike showed negative direct effects on same trait.

Khan and Naqvi (2012) reported that the Path coefficient could be used as an important tool to bring about appropriate cause and effects relationship between yield and yield components. According to obtained results the selection on the basis of number of spikes, number of spikelet's and number of grains in this material would likely to be most useful for increasing grain yield because of their direct positive contribution to grain yield under irrigated condition. However number of spikes, spikelet numbers, spike length and grains number may be used an effective selection criterion for increasing grain yield of wheat under different irrigation levels.

Bhushan *et al.* (2013) reported that the analysis of variance revealed that the treatments were highly significant for all the characters. The higher magnitudes of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for grain yield, biological yield, productive tillers per plant and plant height. The correlation coefficients estimate showed high direct genotypic and phenotypic correlations for the test weight, biological yield, spikelets per spike and grain filling period. While, days to heading, plant height and days to maturity showed

negative correlation with grain yield. Path analysis showed that harvest index had highest direct positive effect on grain yield followed by biological yield, productive tillers per plant, spikelets per spike and test weight thereby indicated that these were main contributors to the grain yield.

Fellahi *et al.* (2013) studied the nature of relation between grain yield and yield components by partitioning the correlation coefficients between grain yield and its components into direct and indirect effects by using simple correlation, stepwise regression and path analysis. The obtained results indicated that grain yield was positively correlated to biological yield, straw yield and number of spike per plant. The results of step by step regression showed that traits including biological yield and harvest index had justified approximately 99.7% of grain yield variations. In the path coefficient analysis, biological yield and harvest index should be considered as the main yield components because these traits showed a positive direct effects towards increasing grain yield with the values of + 1.051 and + 0.364, respectively. Depending on the findings of this study, biological yield and harvest index may be used an effective selection criterion to improve genetic yield potential of bread wheat genotypes.

Gelalcha and Hanchinal (2013) reported that the genotypic as well as phenotypic correlation between grain yield and other yield components such as number of tillers per plant, number of spikes per square meter, number of grains per spike, total biomass per plant, harvest index and 1000 kernel weight were highly significant. Path analysis indicated that biomass, harvest index, days to flowering and plant height imparted significant direct influence on grain yield.

Hannachi *et al.* (2013) reported that the Grain yield per plant was significantly and positively correlated with above ground biomass, straw yield, number of spikes per plant and number of grains per spike. Results of stepwise regression and path analysis revealed that both above ground biomass and harvest index can be a criterion to select high-yielding genotypes in breeding durum wheat programs.

Khan *et al.* (2013) reported that the Significant positive correlation was found for plant height, number of spikes/m² and 1000-grain weight with grain yield. Heading days and maturity days showed negative correlation with grain yield. Maturity days, number of spikes/m² and 1000-grain weight had significant positive direct effects on grain yield. Number of grains/spike had also direct positive effect, but in low magnitude. The indirect effect of heading days and plant height on grain yield was

found mainly through maturity days and 1000-grain weight. It can be concluded that emphasis should be given on heading days and plant height along with 1000-grain weight, number of spikes/m² and number of grains/spike for selection of durum wheat genotypes.

Nukasaniet *al.* (2013) reported that high values of GCV and PCV were recorded for tillers meter-1 and grain yield meter-1, whereas moderate values for rest of the traits. High heritability coupled with high genetic advance were recorded for traits plant height, tillers m-1, grain yield m-1, grain wt spike-1 and spike length indicating that these characters are governed by additive gene effects and directional selection for these traits would be more effective. Correlation and path analysis studies revealed that, three characters, tiller number m-1 > grain weight spike-1 > number of grains spike-1 in that order are the most important characters as these exhibited positive and strong association and maximum positive direct effects on grain yield.

Ashraf *et al.* (2014) reported that the highly significant differences were detected among cultivars for all studied traits. Highly significant and positive correlation estimates were detected between grain yield plant-1 and each of number of tillers plant-1, number of spikelet's spike-1, number of grains spike-1, 1000-grain weight and harvest index. Path analysis showed that maximum positive direct effect on grain yield plant-1 was contributed mostly by number of tillers plant-1, followed by number of grains spike-1, harvest index and 1000-grain weight were the major contributors towards grain yield.

Nasriet *al.* (2014) reported that the results showed that grain yield traits such as the number of fertile spikes, spike weight per unit area, harvest index, biomass. Thousand-grain weight, number of grains per spike, and height plant showed significant positive correlations. Path analysis showed the most significant and positive direct effect ($P = 0.57$) by harvest index and grain yield. Harvest index also showed positive indirect effect ($P = 0.51$) on grain yield. The highest negative direct effect on grain yield was found for the number of fertile spikes ($P = -0.449$) and the highest negative indirect effect for harvest index ($P = -0.35$). Finally, the number of fertile spikes was showed the highest impact on grain yield.

Suleiman *et al.* (2014) reported that the Simple correlation coefficients revealed that the association between the grain yield with leaf area index and days to 95% maturity were positive but non –significant, positive and highly significant (at

1% level of significance) with number of tillers per row- meter, number of grains per spike and 1000- grains weight. Path coefficient analysis revealed that most of the evaluated traits exhibited positive direct effects on grain yield except plant height and days to 50% heading were negative in both seasons, leaf area index and days to 95% maturity were negative in the second season only.

Bagrei and Bybordi *et al.* (2015) reported that results demonstrated that in non-stress condition, grain yield had positive and significant correlation with all traits except for flag leaf area, number of fertile tiller and 1000-grains weight. In drought stress condition, grain yield had positive and significant correlation just with straw yield and harvest index and also had negative and significant correlation with number of fertile tiller and plant height. Path analysis in each experimental condition revealed that under non-stress condition, direct effect of biological yield on grain yield was higher than other traits. Number of fertile tiller with low relative intensity had positive direct effect and plant height had negative direct effect on grain yield.

Singh *et al.* (2015) reported that the positive correlation of the flag leaf with plant height, 100-grain weight, hectoliter weight and protein content whereas, negative correlation was observed with gluten content. Plant height also exhibited positive correlation with hectoliter weight and tiller per plant showed positive correlation with yield per plant. The path coefficient analysis takes into account the cause and effect relationship between the variables which is unique in partitioning the associations into direct and indirect effects through other dependent variables.

Hama *et al.* (2016) reported that the path coefficient analysis, grain yield represented the dependent ones average spike weight (g) no. of spikes/m², Spike yield (kg/h), 1000- Grain weight (g), straw yield (kg/h), biological yield (ton/ ha), harvest index and grain yield (ton/ha). The results confirm that the grain yield correlated negatively and high significantly with 1000- grain weight, whereas grain weight / spike correlated positively and high significantly with 1000-grain. The character No. of grain / spike correlated positively and significantly with spike length, while grain weight / spike showed significant and positive correlation with spike length. The character 1000- grain weight had significant negative correlation with No. of grain / spike. For the first season, the path analysis showed that, 1000-grain weight gave maximum positive direct effect in Grain yield, while maximum negative direct effect recorded by Grain weight / spike. Highest positive indirect effect exhibited by grain weight / spike and No. of grain / spike both of them via 1000- grain

weight, whereas highest negative indirect effect showed by 1000- grain weight via grain weight / spike.

2.3 Discriminant function:

Ferdouset *al.* (2010) reported that the twenty bread wheat genotypes assess the relationship and selection index among yield and important yield attributing characters. Days to maturity, grains per spike, 100-grain weight and harvest index showed significant and positive correlation with grain yield per plant. Path coefficient analysis suggested that grains per spike followed by 100-grain weight and effective tillers per plant contributed maximum to grain yield positively and directly.

Bahariet *al.* (2014) reported that the First group with 6 genotypes including Sabalan, Fengkang, Trakia, Alamout, Bezostaia and Garak 79 genotypes which were the highest considerably all studied characteristic except for eigen-weight of stem at maturity. So this group can be introduced as the best one in measured traits . The second group with 4 genotypes including Azar, Pishtaz, Siosson and Konica2002 were low value genotypes in measured traits. The results from ANOVA and discrimination function analysis show validity of studied genotypes grouping.

Raiyaniet *al.* (2015) reported that the selection indices in 40 genotypes of wheat. Sixty-three selection indices, involving grain yield per plant and five yield components, were constructed using the discriminant function technique. The selection index based on six characters viz., grain yield per plant, days to maturity, number of productive tillers per plant, number of grain per main spike, biological yield per plant and harvest index under limited irrigated condition exhibited maximum gain and relative efficiency.

Shafiuzzamanet *al.* (2015) reported that the differences between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were small for plant height, spike length, spikelets spike-1 and 100 grain weight indicating these characters are less affected by environment and mostly governed by genetic factors Positive correlation found for grain yield plant-1 with spike length, grains spike, 100-grain weight and harvest index. Among them harvest index was significantly correlated with grain yield plant-1 at phenotypic level suggesting that genotypes with high partitioning efficiency gave increase in grain yield plant-1. Spikes plant-1 and harvest index had high positive direct effects on grain yield. The phenotypic correlation of harvest index with grain yield plant-1 also high. The correlation coefficient of spikes plant-1 with grain yield plant-1 was low though their

direct effects were high. Study of selection indices through discriminant function suggests that plant height + grains spike-1+ grain yield plant-1 had the maximum genetic advance and relative efficiency than grain yield alone.

CHAPTER- III

MATERIALS AND METHODS

The experimental materials used and methods adopted during the present investigation entitled “**Biometrical analysis for genetic improvement in wheat [*Triticum aestivum* L.]**” have been described as follows:

Location:

Experiment was conducted at Research Farm, College of Agriculture, Gwalior located in the Gird region (Agro climatic zone No 6, wheat-pearl millet crop zone). The Gwalior is situated at an altitude of 211.52 MSL, 26° 13' N Latitude and 78° 14' E Longitude. The soil is sandy loam, low in available nitrogen, medium in phosphorus and high in potash with pH of 8.5.

Climate:

The summer is hot and dry, May and June are the hottest months and maximum and minimum temperature varies from 47°C to 28.5°C, respectively. December and January constitutes the cooler months of the year and minimum temperature ranges from 7.5°C to 4°C. The average rainfall ranges between 80 to 90 cm most of which is received in the months of July, August and September with few showers in winter months.

During investigation, maximum temperature was ranging from 16.0°C to 34.8°C and minimum temperature from 3.9°C to 17.3°C. Total rainfall received was 708.6 mm (July 14 to April 15) mm during the year 2014-15. The total rainfall received was 200 mm from October to April 2014. Overall season was favorable for crop growth.

Table 3.1: Weekly meteorological data during the crop season (15th Oct. 2014 to 15th April 2015)

STD Week	STD Week period	Temperature		Relative humidity (%)		Rainfall (mm)	Evaporation (mm.)
No.	2014-15	Max	Min	Morn	Even	Weekly	Weekly
42	Oct 15-21	31.9	16.7	89.5	47.2	000.0	3.8
43	Oct 22-28	33.7	16.5	86.5	43.4	000.0	3.6
44	Oct– Nov. 29-4	33.1	15.8	82.8	42.8	000.0	3.8
45	Nov 5-11	32.6	15.4	86.0	46.2	000.0	4.0
46	Nov 12-18	29.1	10.4	91.8	44.5	000.0	2.2
47	Nov 19-25	29.8	8.6	93.5	51.4	000.0	2.8
48	Nov.-Dec. 26-2	30.1	10.2	89.8	46.5	000.0	3.0
49	Dec. 3-9	28.1	8.2	88.8	49.1	000.0	3.6
50	Dec. 10-16	22.3	9.1	96.1	69.5	035.0	1.5
51	Dec. 17-23	19.2	5.1	97.5	73.7	000.0	1.2
52	Dec. 24-31	18.8	4.0	99.2	74.1	000.0	1.0
1	Jan. 1-7	18.7	10.8	94.8	78.1	003.0	1.1
2	Jan.8-14	18.8	5.6	97.5	74.7	000.0	1.3
3	Jan. 15-21	17.0	7.5	97.0	84.0	001.4	0.8
4	Jan. 22-28	16.0	8.7	97.0	92.2	024.0	0.8
5	Jan.-Feb 29-4	21.5	6.6	95.5	70.8	000.0	2.2
6	Feb. 5-11	22.5	8.7	96.0	74.8	004.2	1.8
7	Feb. 12-18	26.9	10.5	94.7	64.7	000.0	3.0
8	Feb. 19-25	30.1	13.9	93.4	67.8	002.4	2.6
9	Feb.-Mar.26-4	26.0	12.3	91.0	73.0	018.4	2.1
10	March 5-11	26.8	10.5	92.7	65.4	002.8	3.2
11	March 12-18	28.2	14.7	93.2	67.2	070.4	3.0
12	March 19-25	31.3	15.0	92.4	55.0	000.0	4.1
13	March-Apr26-1	34.8	18.9	90.1	60.1	026.8	4.6
14	Apr. 2-8	33.5	17.9	85.7	57.4	001.0	4.9
15	Apr. 9-15	33.5	17.7	86.0	61.8	007.4	4.4

Experimental Material: The experimental material consisted of 36 wheat genotypes. The genotypes of wheat sown in Rabi season of 2014-15.

Table: 3.2.Detail of experimental material used for present investigation

S. No.	Hybrid name	Source	S. No.	Hybrid name	Source
1	DBW 170	IIWBR,Kernal	19	RVW 4232	RVSKVV, Gwalior
2	DBW 169	IIWBR,Kernal	20	UAS 369	UAS, Dharwad
3	UAS 372	UAS, Dharwad	21	MP 3440	JNKKVV, Power kheda
4	HI 1610	Delhi	22	NIAW 2595	MPKV, Rahuri
5	UP 2909	GB Pant nagar	23	NIAW 2495	MPKV, Rahuri
6	HI 1608	Delhi	24	GW 473	Vijapur, Gujrat
7	GW 468	Vijapur, Gujrat	25	AKAW 4798	PDKV, Akola
8	JWS 147	Sagar	26	UAS 371	UAS, Dharwad
9	MACS 6671	ARI Pune	27	MACS 6668	ARI Pune
10	DBW 168	IIWBR Kernal	28	GW 471	Vijapur, Gujrat
11	MP 1309	JNKKVV, Power kheda	29	MP 1311	JNKKVV, Power kheda
12	HI 1607	IARI, Indore	30	NIAW 2539	MPKV, Rahuri
13	RAJ 4424	Durgapura	31	PBW 732	PAU, Punjab
14	UAS 370	UAS, Dharwad	32	GW 469	Vijapur, Gujrat
15	WH 1109	Checks	33	GW 470	Vijapur, Gujrat
16	HI1909	Delhi	34	CG 1016	IGKV, Raipur
17	HP 1960	CSKHMPKV, Palampur	35	MACS 6222 C	ARI Pune
18	MP 1310	JNKKVV, Powarkheda	36	HI 1544 C	IARI, Indore

Experimental Details: Experiments were conducted in randomized complete block design with 2 replications. The sowing was done by dibbling seeds in rows with spacing of 20 cm apart and 4-6 cm within row on November 21 (Timely sown environment 2014-15). The recommended packages of practices were adopted for optimum crop growth.



Fig: Experiment carried out in the field of All India coordinated wheat improvement project “Department of Plant Breeding and Genetics”, College of Agriculture, Gwalior (M.P.).

The observations were recorded on the following characters.

- 1. Days to heading (DAS):** Numbers of days were recorded from the date of sowing to the date of 50 per cent grain showing full ear-head emergence.
- 2. Days to maturity (DAS):** Numbers of maturity days were counted from the date of sowing to physiological maturity of the grain.
- 3. Plant height (cm):** Plant height was measured from the base of the plant to top of ear head of main tiller at maturity stage.
- 4. 1000 grain weight (g):** 1000 grains were counted and weight was recorded in gram.
- 5. Grain yield (kg/plot):** The grain yield was recorded kg/plot.

Statistical Methods:

1. Analysis of variance: The mean of each character were analyzed following the procedure given by Panse and Sukhatme (1967) for randomized block design.

(a)The model of randomized compete block design is expressed as follows:

$$y_{ij} = \mu + g_i + b_j + e_{ij}$$

Where,

μ =General mean effect

g_i = Effect of the i^{th} genotype

b_j = Effect of j^{th} replication over the genotype

e_{ij} = Random error associated with each observation

The skeleton of analysis of variance for genotypes explained as follows:

Table 3.3: Analysis of variance in randomized block design for 36 genotypes.

Source of variance	Degree of freedom	Mean sum of square
Replications	(r – 1)	MSS _r
Treatment	(t -1)	MSS _t
Error	(r - 1) (t -1)	MSS _e
Total	(rt - 1)	

Where, r = number of replications, t = number of genotypes, c = number of crosses,

(b)Standard error of mean, critical difference and coefficient of variation:

(i)Standard error of mean: Standard error of mean was calculated using the following formula,

$$S.E(m)_{\pm} = \sqrt{\frac{MSS_e}{r}}$$

Where,

S. E. (m)_± = Standard error of mean

MSS_e = Error mean sum of square

r = Number of replications

(ii)Standard error of difference: Standard error of difference was calculated using the following formula,

$$S.E(m)_{\pm} = \sqrt{\frac{2MSS_e}{r}}$$

Where,

S E (d)_± = Standard error of difference

MSS_e = Error mean sum of squares

r= Number of replications

(iii)Critical difference:It was calculated as formula given below:

C. D. (5%) = S E(d)x 't' value at 5 % level of significance

Where,

C. D. = Critical difference, $S E(d) \pm$ = Standard error difference

't' = t table value at error degree of freedom and at 5% level of significant.

(iv) Coefficient of variation: The coefficient of variation as percentage of mean was estimated as mentioned bellow:

$$cv (\%) = \frac{\sqrt{M_e}}{\bar{X}}$$

Where,

C V (%) = Coefficient of variation in percent, M_e = Error mean sum of square, $\bar{X}$ = Sample mean of observations

(2) Estimation of phenotypic and genotypic coefficients of variation:

The phenotypic and genotypic coefficients of variation in per cent were computed by the following formulae given by Burton (1952).

$$PCV(\%) = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100,$$

$$GCV(\%) = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100,$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

The coefficient of variation were categorized as proposed by Sivasubramanian and MadhavaMenon (1973)

0-10%- Low

10-20% - Moderate

>20%- High

(3) Estimation of heritability and genetic advance:

Heritability in per cent in broad sense was estimated by the following formula given by Singh and Choudhary (1977):

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

$$\text{Genotypic variance} = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance} = \text{genotypic variance} + M_e$$

Where,

M_t = Treatment mean sum of square , M_e = Error mean sum of square and

r = Number of replications

Heritability values are categorized as low, moderate and high (Robinson et al., 1949) and are given below,

0-30%- Low

30-60%- Moderate

>60% - High

Genetic advance G(s): The estimates of expected genetic advance from selection. G(s), was obtained by the formula suggested by Robinson, Comstock, and Harvey (1949).

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

Where,

k = Selection differential in standard deviation units which is 2.06 for 5% selection intensity,

h^2 = Heritability in broad sense, and

σ_p = Phenotypic standard deviation

Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955).

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

Genetic advance as percent of mean was classified as low, moderate and high (Johnson *et al.*, 1955) and values are given below:

0-10% - Low

10-20% - Moderate

>20% - High

(4) Estimation of correlations: Phenotypic and genotypic correlation coefficient between characters were computed utilizing respective components of variance and co-variance, by following formula suggested by Miller *et al.* (1958).

$$r_{XY} = \frac{Cov_{X,Y}}{\sqrt{V_X \cdot V_Y}}$$

Where,

r_{XY} = Correlation coefficient between character X and Y,

Cov_{XY} = Covariance of character X and Y,

V_X = Variance of character X,

V_Y = Variance of character Y

The significance of phenotypic and genotypic correlation coefficients were tested with estimated values compared with the tabulated values of Fisher and Yates (1938) at n-2 d.f. at two levels of probability, viz., 5% and 1%.

(5) Path coefficient analysis: Path coefficient is a standardized partial regression coefficient, which measures the direct influence of one variable upon another and allows partition of correlation coefficient into components of direct and indirect effects. The proportion of direct and indirect contributions of various characteristics to the total correlation coefficients with grain yield per plant, was estimated through path coefficient analysis as suggested by Wright (1921, 1934) and elaborated by Dewey and Lu (1959). To estimates various direct and indirect effect, the following set of simultaneous equations were formed and solved.

$$r_{1y} = P_{1y} + r_{12}P_{2y} + r_{13}P_{3y} + \dots + r_{1i}P_{iy}$$

$$r_{2y} = r_{2y}P_{1y} + P_{2y} + r_{23}P_{3y} + \dots + r_{2i}P_{iy}$$

$$r_{iy} = r_{i1}P_{1y} + r_{i2}P_{2y} + r_{i3}P_{3y} + \dots + P_{iy}$$

Where,

r_{1y} to r_{iy} = Correlation between causal factor 1 to i and dependent character y

r_{12} to $r_{i-1,i}$ = Correlation among causal factors themselves, and

P_{1y} to P_{iy} = Direct effect of characters 1 to i on character y

Residual effect, which measures the contribution of the characters not considered in the causal scheme, was obtained as:

$$\text{Residual effect}(P_{RY}) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{iy} P_{iy}^2 + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy} P_{jy} r_{ij}$$

(6) Discriminant function analysis: Characters of economics value like yield are highly influenced by non-heritable variation and therefore the expected genetic advance for any character has been found to be greater, when the selection pressure is applied with the help of discriminant function technique, than when it is directly on the observed characters

The phenotypic and genotypic variance and co-variance used to compute the correlation provide the basic for constructing the selection index.

The following model suggested by Robinson *et al.* (1951) was used through the set of simultaneous equation of selection indices and development of a require discriminant function.

$$b_1p_{11} + b_2p_{12} + b_3p_{13} + b_4p_{14} + b_5p_{15} = g_{15}$$

$$b_1p_{12} + b_2p_{22} + b_3p_{23} + b_4p_{24} + b_5p_{25} = g_{25}$$

$$b_1p_{13} + b_2p_{23} + b_3p_{33} + b_4p_{34} + b_5p_{35} = g_{35}$$

$$b_1p_{14} + b_2p_{24} + b_3p_{34} + b_4p_{44} + b_5p_{45} = g_{45}$$

$$b_1p_{15} + b_2p_{25} + b_3p_{35} + b_4p_{45} + b_5p_{55} = g_{55}$$

Where,

1. p_{11} , p_{22} , p_{33} , p_{44} and p_{55} represent the estimate of phenotypic variance for the characters numbering x_1 , x_2 , x_3 , x_4 and x_5 respectively.
2. p_{12} , p_{13} , p_{14} , p_{15} represent the phenotypic co-variances of the different combinations of x_1 , x_2 , x_3 , x_4 , and x_5 respectively.
3. g_{15} , g_{25} , g_{35} , g_{45} , g_{55} represent genotypic co-variance of x_1 , x_2 , x_3 , x_4 , x_5 (grain yield) and g_{55} represents genotypic variance of character x_5 (grain yield).

The 'b' values computed from the above formulas indicated the phenotypic weights to be assigned to each of the various characters considered in selection indices. These obtained 'b' values were used for the construction of selection index in the following formulas.

$$Z = b_1x_1 + b_2x_2 + b_3x_3 + b_4x_4 + b_5x_5$$

Where,

$$Z = \text{Selection index}$$

x_1, x_2, x_3, x_4 and x_5 represents phenotypic values of traits x_1, x_2, x_3, x_4 and x_5 , respectively.

b_1, b_2, b_3, b_4 and b_5 represents phenotypic weights assigned to each of the characters i.e. x_1, x_2, x_3, x_4 and x_5 , respectively.

In such a way election indices were constructed for one character, two characters, three characters, four characters, and five characters.

(a) Expected genotypic advance (EGA) of selection index:

The expected genotypic advance from a number of selection indexes was estimated by the following formulas suggested by Robinson, Comstock and Harvey (1951).

$$EGA = \frac{Z}{P} \sqrt{b_1 g_{15} + b_2 g_{25} + b_3 g_{35} + b_4 g_{45} + b_5 g_{55}}$$

Where,

$\frac{Z}{P} = K$ represents selection differential in standard units. Its

Value being 2.06 at 5% intensity of selection.

b_1 to b_5 = represents phenotypic weight of corresponding characters in the selection indices.

g_{18} to g_{55} represents genotypic co-variance of characters x_1 to x_4 with x_5 (grain yield) and g_{55} represent genotypic variance and x_5 (grain yield).

(b) Relative efficiency of selection indices as compared to the straight selection for yield:

Relative efficiency of selection index was computed by comparing its expected genetic advance with expected genetic advance for yield and it is always expressed in percentage. The efficiency of selection for yield is assumed to be 100 percent and used as a basis for comparison of relative efficiency from use of various selection indices (Robinson *et al.*, 1951).

CHAPTER- IV

EXPERIMENTAL RESULTS

The results obtained in the present investigation on different characters studied have been presented under the following aspects:

- 4.1. Analysis of variance
- 4.2. Analysis of mean performance
- 4.3. Variability
- 4.4. Heritability and genetic advance
- 4.5. Analysis of Correlation coefficient
- 4.6. Path coefficient analysis
- 4.7. Discriminant function analysis

4.1. Analysis of variance: Analysis of variance for grain yield per plant and its contributing traits is presented in Table: 4.1 All the 5 characters studied showed significant mean sum of square due to genotypes, viz., Plant height (cm), Days to heading (DAS), 1000 grain weight (g), Days to maturity (DAS), Grain yield (kg/plot). It indicates that there was considerable variability for these characters in the present material.

Table 4.1: Analysis of variance for yield and its attributing characters of wheat genotypes

Source of variation	d.f	Plant height (cm)	Days to heading (DAS)	1000 grain weight (g)	Days to maturity (DAS)	Grain yield (Kg/plot)
Replication	1	70.01	1.13	0.16	46.72**	647142.72*
Genotypes	35	97.24**	25.53**	15.98**	9.33**	186639.77*
Error	35	24.27	0.98	2.64	2.58	88005.29
Total	71	60.89	13.08	9.18	6.53	144503.10

*, ** indicates significance at 5% and 1% respectively

4.2. Mean performance: The mean performance of genotypes has been described for different characters presented in table: 4.2 all Genotypes showed significant variation. The genotypes with significant performance have been described as under.

Plant height: Genotypes significantly varied for plant height ranging from 80.85 (WH 1109) to 109.70 (MP 1309), among these 14, WH 1109, DBW168 and CG 1016 showed significantly dwarf; whereas, MP 1309, UAS 369 and HI 1608 were statistically tall.

Days to heading: Only one genotype significantly varied for earliness, that is, HI 1610 (87.5 DAS) and late that is, RAJ 4424 (103.5 DAS).

1000 grain weight: Genotypes significantly varied for 1000 grain weight and ranged from 24.84 (GW 470) to 36.42 (DBW 170), Among these, out of the significant 9, the genotypes DBW 170 having 36.42g and MACS 6668 36.29g possessed boldest seed size.

Days to maturity: Twenty nine genotypes significantly varied for days to maturity and ranged from 123.50 DAS (HI 1610) to 135.50 DAS (DBW 169); as is clear HI 1610 was earliest maturing; whereas, DBW 169 was very late maturing.

Grain Yield: Fifteen Genotypes were significantly superior as regard to grain yield that ranged from 1510.50 Kg/plot (MP 1311) to 2779 Kg/ plot (HI 1610).

Table 4.2. Mean performance of grain yield (Kg/plot) and its attributing characters in wheat genotypes

S.N	Genotypes	Plant height (cm)	Days to heading (DAS)	1000 grain weight (g)	Days to maturity (DAS)	Grain yield Kg/plot
1	DBW 170	88.00	90.50	36.42	135.00	2559.00
2	DBW 169	100.50	97.00	31.44	135.50	1676.50
3	UAS 372	86.35	93.00	27.41	127.00	1833.00
4	HI 1610	84.85	87.50	35.48	123.50	2779.00
5	UP 2909	97.00	93.50	34.58	134.00	1855.00
6	HI 1608	104.50	95.00	32.98	133.50	1856.00
7	GW 468	86.00	91.50	29.14	133.50	2198.00
8	JWS 147	91.35	97.50	33.10	132.50	2167.50
9	MACS 6671	92.00	97.00	30.43	134.00	2144.50
10	DBW 168	83.70	100.00	31.27	135.00	2071.50
11	MP 1309	109.70	98.50	33.05	132.50	1603.50
12	HI 1607	94.50	89.50	31.43	134.00	2538.50
13	RAJ 4424	96.20	103.50	31.20	134.50	2055.50
14	UAS 370	88.85	93.50	29.79	132.50	2243.00
15	WH 1109	80.85	98.00	31.39	132.50	1855.00
16	HI1909	102.50	96.00	33.87	133.50	2266.50
17	HP 1960	88.70	97.00	30.56	134.00	2029.50
18	MP 1310	95.15	95.50	33.27	132.00	2158.00
19	RVW 4232	94.85	92.00	31.65	133.00	2450.50
20	UAS 369	106.50	92.50	34.18	132.50	2031.00
21	MP 3440	91.00	94.50	29.40	132.00	1968.50
22	NIAW 2595	99.00	93.00	35.69	131.00	1999.00
23	NIAW 2495	102.70	96.00	28.54	133.50	1618.00
24	GW 473	93.20	99.00	31.25	133.00	2521.50
25	AKAW 4798	94.50	93.00	33.08	132.00	2238.50
26	UAS 371	90.35	92.50	26.12	132.50	1874.50
27	MACS 6668	98.20	89.50	36.29	130.00	2588.00
28	GW 471	93.20	89.50	28.93	131.50	2067.00
29	MP 1311	88.50	93.50	29.68	133.00	1510.50
30	NIAW 2539	91.85	98.50	29.99	134.00	1985.50
31	PBW 732	95.35	98.00	29.48	132.50	2242.00
32	GW 469	84.70	90.50	33.05	133.00	2301.50
33	GW 470	93.85	90.00	24.84	132.50	2466.50
34	CG 1016	83.70	91.00	34.66	133.00	2429.50
35	MACS 6222 C	83.85	92.50	26.96	132.50	1886.50
36	HI 1544 C	87.50	93.00	32.32	132.50	2394.00
	Mean	92.88	94.24	31.47	132.58	2123.94
	SE(m)	3.48	0.70	1.15	1.14	209.77
	CD 5%	9.65	1.94	3.18	3.15	581.36
	CV %	5.30	1.05	5.16	1.21	13.97

4.3. Variability(Phenotypic and genotypic coefficient of variation):

The estimation of phenotypic and genotypic coefficient of variation is presented in table: 4.3phenotypic coefficient of variation (PCV) was moderate for Grain yield (17.45%). However, it was low for the traits 1000 grain weight (9.70%), plant height (8.39%), days to heading (3.86%), days to maturity (1.84%).

The moderate genotypic coefficient of variation (GCV) was observed for the grain yield (10.46%); it was low for rest of the traits, that is, 1000 grain weight (8.21%), plant height (6.50%), days to heading (3.72%) and days to maturity (1.39%).

4.4 (a).Heritability (broad sense):

The estimates of broad-sense heritability have been presented in Table 4.3. The Highest heritability was observed for days to heading (92.95%) followed by 1000 grain weight (71.65%) and plant height (60.05%); while it was moderate for days to maturity (56.68%) and grain yield (35.91%).

4.4. (b). Genetic advance (as per cent of mean):

The estimates of expected genetic advance (Table 4.3) was found to be highest (though moderate) for the trait 1000 grain weight (14.31%), followed by that of grain yield (12.91%) and plant height (10.38%). For rest of the traits it was low; such that for days to heading it was 7.37% and for days to maturity it was least 2.15%.

Table-4.3Extent of genetic parameters for yield and its attributing characters in wheat genotypes

S. No	Characters	Mean	Range	PV	GV	PCV (%)	GCV (%)	Broad sense Heritability (%)	Genetic advance	Genetic advance as % of mean
1	Plant height (cm)	92.88	80.9-109.7	60.76	36.48	8.39	6.50	60.05	9.64	10.38
2	Days to heading (DAS)	94.24	89.5-103.5	13.26	12.27	3.86	3.72	92.59	6.94	7.37
3	1000 grain weight (g)	31.47	24.84-36.42	9.31	6.67	9.70	8.21	71.65	4.50	14.31
4	Days to maturity (DAS)	132.58	123.5-135.5	5.95	3.37	1.84	1.39	56.68	2.85	2.15
5	Grain yield (kg/plot)	2123.94	1604-2588	137322.53	49317.24	17.45	10.46	35.91	274.15	12.91

Where, GV = genetic variation PV= phenotypic variation PCV= phenotypic coefficient of variation

GCV= genotypic coefficient of variation

4.5. Correlation analysis:

Genotypic and phenotypic correlation coefficients among grain yield and the traits contributing to it are presented below:

Genotypic correlation coefficient:

Correlation analysis (table: 4.5) revealed that only one character 1000 grain weight showed significant positive correlation with grain yield (0.4881). They were negative for other traits, such as, for days to heading it was (-0.5876) and for plant height it was (-0.4529). All three were statistically significant associations. Days to heading was positively significant correlated with days to maturity (0.5568).

Phenotypic correlation coefficient:

The same (table 4.5) depicts phenotypic correlation coefficients. For days to heading it is a loner, highest, negative and significant with grain yield (-0.3778). It was also positively significant correlated with days to maturity (0.3881).

Table- 4.5. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients of wheat genotypes

Character	Plant height	Days to heading	1000 grain weight	Days to maturity	Grain yield
Plant height	-	0.2359	0.2632	0.1077	-0.4529**
Days to heading	0.1696	-	-0.1152	0.5568**	-0.5876**
1000 grain weight	0.1931	-0.1069	-	-0.1364	0.4881**
Days to maturity	0.2156	0.3881*	-0.0620	-	-0.2298
Grain yield	-0.1798	-0.3778*	0.2759	-0.2812	-

*, ** indicates significance at 5% and 1% respectively.

4.6. Path analysis at genotypic level: Direct effects on grain yield mentioned diagonally and indirect effects (all other values).

Plant height: It exhibited highest but negative direct effect (-0.5095) on grain yield but it had positive indirect effect on grain yield via days to maturity (0.0200) and 1000 grain weight (0.1551); therefore, dwarf plants tend to produce higher grain yield.

Days to heading: It exhibited a negative direct effect (-0.5027) on grain yield but it had positive though small indirect effect on grain yield via days to maturity (0.1032). Therefore, genotypes that set into heading early tend to give higher grain yields.

1000 grain weight: It exhibited highest positive direct effect (0.5896) on grain yield and it had positive indirect effect on grain yield via days to heading (0.0579).

Days to maturity: It exhibited positive direct effect (0.1854) on grain yield.

The residual effects: It was found 0.4782.

Table 4.6 (a): Genotypic Path coefficient matrix of direct and indirect effects of different traits on grain yield in wheat genotypes.

Character	Plant height	Days to heading	1000 grain weight	Days to maturity	Genotypic correlation with Grain yield
Plant height	-0.5095	-0.1186	0.1551	0.0200	-0.4529**
Days to heading	-0.1202	-0.5027	-0.0679	0.1032	-0.5876**
1000 grain weight	-0.1341	0.0579	0.5896	-0.0253	0.4881**
Days to maturity	-0.0549	-0.2799	-0.0804	0.1854	-0.2298

residual effects

0.4782 Dark values denoted direct effect

4.6 (b): Phenotypic path analysis: Direct (diagonal) and indirect effect of various traits on grain yield:

Plant height: It exhibited negative direct effect (-0.1586) on grain yield but it had positive indirect effect on grain yield via 1000 grain weight (0.0520).

Days to heading: It exhibited negative direct effect (-0.2740) on grain yield.

1000 grain weight: It exhibited positive direct effect (0.2695) on grain yield and it had also positive indirect effect on grain yield via days to heading (0.0293) and days to maturity (0.0077).

Days to maturity: It exhibited negative direct effect (-0.1240) on grain yield.

The residual effects: The residual factor value was found 0.8711.

Table 4.6 (b): Phenotypic Path coefficient matrix of direct and indirect effects of different traits on grain yield in wheat genotypes

Character	Plant height	Days to heading	1000 grain weight	Days to maturity	Phenotypic correlation with Grain yield
Plant height	-0.1586	-0.0465	0.0520	-0.0267	-0.1798
Days to heading	-0.0269	-0.2740	-0.0288	-0.0481	-0.3778*
1000 grain weight	-0.0306	0.0293	0.2695	0.0077	0.2759
Days to maturity	-0.0342	-0.1063	-0.0167	-0.1240	-0.2812

residual effects 0.871

Dark values denoted direct effect

4.7. Discriminant function analysis:

Expected genetic advance calculated for different selection indices functions for yield, and traits contributing to yield have been presented in table 4.7. Discriminant functions consisting five indices of single characters, four indices of two characters, six indices of three characters, three indices of four and one index of five characters were calculated and result have been described below.

The genetic advance:

The genetic advance was 274.15 for grain yield which assumed 100 percent efficiency in selection indices. Among the single character indices, days to heading showed highest genetic advance of 258.64, followed by those of 1000 grain weight, plant height and days to maturity 189.01, 160.57 and 79.14, respectively.

Among the two character indices days to heading + grain yield showed highest genetic advance of 321.26, followed by those of 1000 grain weight + grain

yield, plant height + grain yield and days to maturity + grain yield 298.45, 296.58 and 274.16, respectively.

Among the three character indices days to heading + 1000 grain weight + grain yield showed highest genetic advance of 342.06, followed by those of plant height + days to heading + grain yield, plant height + 1000 grain weight + grain yield, days to heading + days to maturity + grain yield, 1000 grain weight + days to maturity + grain yield and plant height + days to maturity + grain yield 335.02, 333.30, 325.73, 298.48 and 297.12 respectively.

Among the four character indices plant height + days to heading + 1000 grain weight + grain yield showed highest genetic advance of 365.86, followed by those of days to heading + 1000 grain weight + days to maturity + grain yield and plant height + 1000 grain weight + days to maturity + grain yield 337.09 and 334.06 respectively. The all five character index showed genetic advance of 372.80.

Among all the results the following index turned out to be resulting into best genetic advance, that is 372.80 and it was a five character index with the following combination: plant height + days to heading + 1000 grain weight + days to maturity + grain yield; followed by four character indices those of plant height + days to heading + 1000 grain weight + grain yield and days to heading + 1000 grain weight + grain yield, 365.86 and 342.06 respectively.

The relative efficiency (%):

The relative efficiency was assumed 100 percent for grain yield in section indices. Among the single character indices revealed that days to heading followed by 1000 grain weight, plant height and day to maturity showed highest relative efficiency of 94.34, 68.94, 58.57 and 28.87 respectively.

Among the two characters indices days to heading + grain yield showed highest relative efficiency of 117.18 followed by those of 1000 grain weight + grain yield, plant height + grain yield and days to maturity + grain yield, 108.86, 108.18 and 100 respectively.

Among the three character indices days to heading + 1000 grain weight + grain yield showed highest relative efficiency of 124.77, followed by those of plant height + days to heading + grain yield, plant height + 1000 grain weight + grain yield, days to heading + days to maturity + grain yield, 1000 grain weight + days to maturity + grain yield and plant height + days to maturity + grain yield 122.20, 121.57, 118.8, 108.87 and 108.38 respectively.

Among the four character indices plant height + days to heading + 1000 grain weight + grain yield showed highest relative efficiency of 133.45, followed by those of days to heading + 1000 grain weight + days to maturity + grain yield and plant height + 1000 grain weight + days to maturity + grain yield 122.96 and 121.85 respectively.

The five character indices revealed plant height + days to heading + 1000 grain weight + days to maturity + grain yield showed relative efficiency of 135.98.

Among all the results the following index turned out to be resulting into best relative efficiency that is 138.98 and it was a five character index with the following combination: plant height + days to heading + 1000 grain weight + days to maturity + grain yield; followed by four character indices those of plant height + days to heading + 1000 grain weight + grain yield and days to heading + 1000 grain weight + grain yield, 133.45 and 124.77 respectively.

Table 4.7: Selection indices for grain yield and their relative efficiency in wheat genotypes

S. No.	Selection index	Discriminant function	Expected genetic Advance	Relative Efficiency (%)
1	2	3	4	5
1	x1 (PH)	-10.00X1	160.57	58.57
2	x2 (DAH)	-9.00X2	258.64	94.34
3	x3 (GW)	-8.00X3	189.01	68.94
4	x4 (DM)	-7.00X4	79.14	28.87
5	x5 (GY)	-6.00X5	274.15	100.00
6	x1.x5	-7.16X1 + 0.33X5	296.58	108.18
7	x2.x5	-24.12X2 + 0.27X5	321.26	117.18
8	x3.x5	19.53X3 + 0.31X5	298.45	108.86
9	x4.x5	-0.44X4 + 0.36X5	274.16	100.00
10	x1.x2.x5	-6.05X1 + -22.58X2 + 0.25X5	335.02	122.20
11	x1.x3.x5	-9.72X1 + 26.05X3 + 0.26X5	333.30	121.57
12	x1.x4.x5	-7.36X2 + 3.78X4 + 0.34X5	297.12	108.38
13	x2.x3.x5	-37.31X2 + 19.40X3 + 0.18X5	342.06	124.77
14	x2.x4.x5	-41.43X2 + 18.48X4 + 0.24X5	325.73	118.8
15	x3.x4.x5	-84.94X3 + -22.89X4 + 0.55X5	298.48	108.87
16	x1.x2.x3.x5	-8.56X + -21.88X2 + 25.20X3 + 0.19X5	365.86	133.45
17	x1.x3.x4.x5	-9.44X1 + 104.49X3 + -113.82X4 + 0.09X5	334.06	121.85
18	x2.x3.x4.x5	26.43X2 + 133.18X3 + -164.39X4 + 0.16X5	337.09	122.96
19	x1.x2.x3.x4.x5	-9.27X1 + -25.18X2 + 25.45X3 + 15.83X4 + 0.20X5	372.80	135.98

PH = Plant height
DM = Days to maturity

DAH = Days to heading
GY = Grain yield

GW = 1000 grain weight

CHAPTER-V

DISCUSSION

The present investigation “Biometrical analysis for genetic improvement in wheat [*Triticum aestivum* L.]” was undertaken to study genetic variability, correlation coefficient, path coefficients, discriminant function technique analysis and expected genotypic advances for yield and yield contributing traits. Present results are discussed in the light of reviews of various research workers.

5.1 Analysis of variance and Mean performance:

Analysis of variance revealed that genotypes were significant for all 5 characters viz., plant height, days to heading, 1000 grain weight, days to maturity and grain yield. Present findings are similar with earlier reports of Zareet *et al.* (2015) and M. Aycicek and T. Yildirim (2006). Mean performance revealed that out of 15 genotypes viz., HI 1610 showed significant highest grain yield (2779 g) along with significantly early in days to heading (87.50), dwarf plant height and bolder seed size as reflected by 1000 grain weight. DBW 170 was recorded significantly bolder seed size as reflected by 1000 grain weight (36.42g) with grain yield. GW 468 was recorded significantly dwarf plant height and late to maturity with grain yield. HI 1607 showed significantly late to maturity with grain yield. UAS 370 showed significantly HI 1909 showed significantly bolder seed size as reflected by 1000 grain weight and late to maturity with grain yield. RVW 4232 showed significantly late to maturity with grain yield. GW 473 showed significantly showed significantly late to maturity with grain yield. AKAW 4798 showed significantly higher grain yield. MACS 6668 showed significantly bolder seed size as reflected by 1000 grain weight with grain yield. PVW 732 late to maturity with grain yield. GW 469 showed significantly dwarf plant height, late to maturity with grain yield. GW 470 showed significantly late to maturity with grain yield. CG 1016 showed significantly dwarf plant height and bolder seed size as reflected by 1000 grain weight, late to maturity with grain yield and HI 1544 C showed significantly dwarf plant height

and late to maturity with grain yield. Present finding are confirmed with Bhutto *et al.* (2016) and Khan *et al.* (2013).

5.2 Phenotypic and genotypic coefficient of variation:

Almost equal magnitude of GCV and PCV showed for days to heading, 1000 grain weight and days to maturity indicating that these characters are less influenced by the environment while grain yield and plant height exhibited high value of PCV over its GCV value, indicating large amount of variation for these characters was due to environment only. Present finding are in confirmation with Degewione *et al.* (2013), Kolakare *et al.* (2012) Maurya *et al.* (2014) and Yadav *et al.* (2014).

5.3 Heritability (Broad sense) and genetic advance:

The Higher heritability was observed for days to heading, 1000 grain weight and plant height while, Moderate heritability were observed for days to maturity and grain yield. Present finding conformed to those of Ali *et al.* (2008), Chaudhary *et al.* (2015), Deoraj *et al.* (2016) and Shashikala *et al.* (2012).

The maximum genetic advance was observed for the character 1000 grain weight (14.31). The moderate genetic advance was observed for the remaining characters. High heritability estimates coupled with high genetic advance were found for 1000 grain weight, plant height, days to heading and grain yield, thereby, suggested effectiveness of selection for the improvement of these traits. These findings are confirmed with Deoraj *et al.* (2016) and Kabir *et al.* (2015).

5.4 Correlation analysis: Phenotypic and genotypic correlation coefficient among grain yield per plant and its contributing characters are presented below:-

5.4.1 Genotypic correlation coefficient:

Correlation analysis revealed that the association between yield and yield contributing characters were found positive and significant only for 1000 grain weight (0.4881). Present finding are confirmed with Ashraf *et al.* (2014), Bagre *et al.* (2015) and Nasir *et al.* (2014).

5.4.2 Phenotypic correlation coefficient:

Correlation analysis revealed that grain yield was significantly but negatively correlated with days to heading. Among the components traits days to heading was significantly positively correlated with days to maturity.

5.5 Genotypic path analysis: Relationship between yield and yield contributing characters were studied in details through path coefficient analysis. Path coefficient analysis performed to disclose the causes and effects of chain relationships of different yield contributing characters with yield.(Majumder *et al.* 2008)

Path coefficient analysis at genotypic level revealed that only two character, 1000 grain weight (0.5896) and days to maturity (0.1854) showed positive direct effect on grain yield and also 1000 grain weight recorded positive indirect effect via days to heading (0.0579) on grain yield. Remaining two characters viz., plant height (-0.5095) and days to heading (-0.5027) exhibited negative direct effect on grain yield but these characters recorded positive indirect effect viz., plant height via 1000 grain weight (0.1551) and days to maturity (0.0200), days to heading via days to maturity (0.1032) on grain yield. The residual factor value was relatively high indicating some other characters which have not been studied. Similar results have been reported by Bhushan *et al.* (2013), Hama *et al.* (2016), Iftikhar *et al.* (2012), Khan *et al.* (2013), Khokhar *et al.* (2009) and Majumdar *et al.* (2008).

5.6 Phenotypic path analysis:

Path analysis at phenotypic level revealed that only one character 1000 grain weight (0.2695) showed positive direct effect on grain yield. Remaining three characters viz., days to heading (-0.2740), plant height (-0.1586) and days to maturity (-0.1240) showed negative direct effect on grain yield but these characters recorded positive indirect effect viz., plant height (-0.1586) via 1000 grain weight (0.0520), 1000 grain weight via days to heading (0.0293) and days to maturity (0.0077). The residual factor value was found high thereby indicating that some more characters may be considered in future study. Present finding are conformed to those of Bagrei and Bybordi (2015).

5.7 Discriminant function analysis:

The technique of discriminant function developed by Fisher (1936) and adopted for plant selection by Smith (1936) it is useful in improvement of yield by combination of characters. For improving yield, index selection is superior on the basis of yield alone. Therefore, discriminant function based on important characters for selection has proved to be very useful in plant and highly helpful to discriminate undesirable genotypes on the basis of their performance. Hazel and Lush (1943) showed that the selection based on such an index is more efficient than selecting individually for the various characters. The basis for the development of the selection indices has been provided by Smith (1936), Hazel (1943) and Robinson *et al.* (1951). Hazel and Lush (1943) stated that the superiority of selection based on index increases with an increase in the number of characters under selection indices. McVetty and Evan (1980) and Esheghiet *al.* (2011) also suggested that the selection indices were reported superior to direct selection in wheat. Strait selection index for grain yield and indirect selection indices consisting components characters along with grain yield were constructed in various combinations and examined to identify their relative efficiency for the selection of superior genotypes. The results of expected genetic gain and relative efficiency were discussed for different selection indices. The maximum genetic advance (GA) and relative efficiency (RI) in single character direct selection index of grain yield was 274.15 and assumed as 100 per cent, respectively. However, in two character combinations indices (days to heading + grain yield) increased genetic advance up to 321.26 and relative efficiency 117.18 per cent. In three character combinations indices (days to heading + 1000 grain weight + grain yield) increased genetic advance up to 342.06 and relative efficiency 124.77 per cent. In four character combinations (plant height + days to heading + 1000 grain weight + grain yield), the highest genetic advance and relative efficiency were 365.86 and 133.45 per cent, respectively. Genetic advance and relative efficiency increased considerably when selection index was based on two or more characters with an increase in the character combinations. Finally all five character combination index (plant height + days to heading + 1000 grain weight + days to maturity + grain yield) recorded highest genetic advance of 372.80 and relative efficiency 135.98 per cent. Ferdous *et al.* (2011) and Kemelew (2011) were also reported similar opinion that an increase in characters result in an increase in genetic gain and that the selection indices improve

the efficiency than the straight selection for grain yield alone. Present finding are confirm with Raiyani *et al.* (2015) and Shafiuzzaman *et al.* (2015).

CHAPTER - VI

SUMMARY, CONCLUSION AND SUGGETIONS FOR FURTHER WORK

SUMMARY

The present investigation entitled “Biometrical analysis for genetic improvement in wheat [*Triticum aestivum* L.]” was undertaken to study the inheritance of grain yield and its components in 36 test genotypes. An experiment was conducted in a randomized complete block design with two replications at experimental area of Research Farm, College of Agriculture, Gwalior, (M.P.) during 2014-2015. Observations were recorded on randomly selected 5 plants for grain yield and different yield contributing traits viz., Plant height, Days to heading, 1000 grain weight, Grain yield, Days to maturity in each plot. The findings of present investigation are summarized as under:

1. Analysis of variance revealed that genotypes were significantly differed for all characters and suggested considerable variability for all yield and its attributing characters in the present material.
2. Among genotypes tested, HI 1610 seems to be the best, because, it is highest yielder, early flowering, early maturing, bold grain size and dwarf.
3. Almost equal magnitude of GCV and PCV showed for days to heading, 1000 grain weight and days to maturity indicating that these characters are less influenced by the environment while grain yield and plant height exhibited high value of PCV over its GCV value, indicating relatively large amount of variation for these characters was due to environment alone.
4. The Higher heritability was observed for days to heading, 1000 grain weight and plant height. High heritability estimates coupled with high genetic advances were found for 1000 grain weight, plant height, days to heading and grain yield suggested better effectiveness of selection for the improvement of these traits.
5. Genotypic correlation analysis revealed that the association between yield and yield contributing characters were found positive and significant only for 1000 grain weight. Selection for these characters can directly be followed for immediate yield improvement of wheat crop.

6. Genotypic path coefficient analysis revealed that 1000 grain weight(0.5896) and days to maturity (0.1854) showed positive direct effect on grain yield; whereas, at phenotypic level, it was only 1000 grain weight (0.2695).
7. All the indirect effects at both at genotypic and phenotypic levels have been found to contribute only to a small and inexplicable extent, therefore, requires no further discussion, though, they do make a contribution by a small margin.
8. The maximum efficiency in selection for grain yield was exhibited by a discriminant function involving plant height, days to heading, 1000 grain weight, days to maturity and grain yield which had high genetic advance and relative efficiency of 372.80 and 135.98 per cent, respectively.

CONCLUSION:

It is concluded that:

1. High heritability coupled with high genetic advance recorded for traits 1000 grain weight, plant height, days to heading and grain yield and that these characters are governed by additive gene effects; a directional selection for these traits would be more effective for desired genetic improvement.
2. Correlation between yield and 1000 grain weight was found positive and significant and therefore selection for this character can lead to yield improvement wheat.
3. The path analysis confer that traits 1000 grain weight and days to maturity showed genotypic positive direct effect on grain yield thus selection should be considered for both component traits in future wheat breeding programme.
4. The present study also revealed that the discriminant function method of making selection in plant appears to be the more useful over classical breeding methods; and hence due weightage may be given to the promising selection indices for grain yield advancement in wheat breeding programme.

SUGGESTIONS FOR FURTHER WORK:

1. The best genotype HI 1610 outperformed over all other genotypes; therefore, it may consider as parent in future breeding improvement programme.
2. The five characters discriminant function index plant height + days to heading + 1000 grain weight + days to maturity + grain yield may be used with advantage to maximize genetic advance and relative efficiency of selection than grain yield alone.

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