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**Dissertation report
(AGR- 690)**

**“STUDY OF GENETIC COMPONENTS OF VARIABILITY FOR YIELD &
YIELD RELATED TRAITS IN WHEAT (*Triticum aestivum* L.)”**

Thesis submitted to
Lovely Professional University, Punjab
In partial fulfillment of the requirements for the
Degree of

Master of Science (Agriculture)

In

Genetics and Plant Breeding

Submitted By

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CERTIFICATE

This is to certify that the Dissertation entitled “**Study of genetic components of variability for yield & yield related traits in wheat (*Triticum aestivum* L.)**” is a bonafide record of independent research work done by **K. Rajaneesh** (Reg. No.: 11616666) under our supervision and submitted to Lovely Professional University in partial fulfillment for the award of the Degree of Master of Agriculture. (Genetics & Plant Breeding)

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I hereby declare that the project work entitle “**Study of genetic components of variability for yield & yield related traits in wheat (*Triticum aestivum* L.)**”Is an authentic record of my work carried out at lovely professional university as requirements of project work for the award of degree of Master of Science in Genetics and Plant Breeding, under the guidance of Dr. Anant Madakemohekar Assistant professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab.

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INTRODUCTION

Cultivation of wheat began to spread beyond the Fertile Crescent after about 8000 BCE. Jared Diamond traces the spread of cultivated emmer wheat starting in the Fertile Crescent sometime before 8800 BCE. Archaeological analysis of wild *emmer* indicates that it was first cultivated in the southern Levant with finds dating back as far as 9600 BCE. Genetic analysis of wild *einkorn* wheat suggests that it was first grown in the Karacadag Mountains in southeastern Turkey.

Wheat (*Triticum aestivum*) is the first important and strategic cereal crop for the majority of world's populations. It is the most important staple food of about two billion people (36% of the world population). Worldwide, wheat provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). It exceeds in acreage and production every other grain crop (including rice, maize, etc.). Triticeae is one of the tribes containing more than 15 genera and 300 species including wheat and barley. Wheat belongs to the tribe Triticeae (= Hordeae) in the grass family Poaceae (Gramineae) (Briggle and Reitz, 1963) in which the one to several flowered spikelets are sessile and alternate on opposite sides of the rachis forming a true spike. Wheats (*Triticum*) and ryes (*Secale*) together with *Aegilops*, *Agropyron*, *Eremopyron* and *Haynalidia* form the subtribe Triticineae (Simmonds, 1976). Linnaeus in 1753 first classified wheat. In 1918, Sakamura reported the chromosome number sets (genomes) for each commonly recognized type. This was a turning point in *Triticum* classification. It separated wheat into three groups. Diploids had 14 ($n=7$), tetraploids had 28 ($n=14$) and the hexaploids had 42 ($n=21$) chromosomes.

Wheat is an edible grain, one of the oldest and most important of the cereal crops. Though grown under a wide range of climates and soils, wheat is best adapted to temperate regions with rainfall between 30 and 90 cm. Winter and spring wheats are the two major types of the crop, with the severity of the winter determining whether a winter or spring type is cultivated. Winter wheat is always sown in the fall; spring wheat is generally sown in the spring but can be sown in the fall where winters are mild. Therefore, today wheat is grown all over the world, with different varieties sown according to the various climates. The greatest portion of the wheat flour produced is used for bread making.

Wheat grown in dry climates is generally hard type, having protein content of 11-15 percent and strong gluten (elastic protein). The sticky gluten of bread wheat entraps the carbon dioxide (CO₂) formed during yeast fermentation and enables leavened dough to rise. The hard type of wheat produces flour best suited for bread making. The wheat of humid areas is softer, with protein content of about 8-10 percent and weak gluten. The softer type produces flour suitable for cakes, crackers, cookies, pastries and household flours. Durum wheat (*Triticum turgidum* L.). Although most wheat is grown for human food and about 10 percent is retained for seed and industry (for production of starch, paste, malt, dextrose, gluten).

Wheat (*Triticum species*) is a crop of global significance. It is grown in diversified environments. It is a staple food of millions of people. Approximately one-sixth of the total arable land in the world is cultivated with wheat. Whereas paddy is mainly cultivated in Asia, wheat is grown in all the continents of the world. It supplies about 20 per cent of the food calories for the world's growing population. Global wheat production touched 622.2 million tonnes in 2009 -12 India is the second largest producer of wheat after China. Wheat has a distinct place among the food grain crops.

World trade in wheat is greater than for all other crops combined. Globally, wheat is the leading source of vegetable protein in human food. It has a higher protein content than other major cereals such as maize (corn) or rice. In terms of total production, it is second to rice as the main human food crop and ahead of maize (maize is used more for animal feeds).

Wheat was a key factor enabling the emergence of city-based societies at the start of civilization. It was one of the first crops that could be easily cultivated on a large scale, and its seeds could be stored for long periods in a dry climate.

Wheat, best known and most widely cultivated of the wheats, is cultivated for the grain, used whole or ground. Fine ground, it is the source of flour for the world's bread making. Main use is for flour and bread-stuffs known by various names throughout the world. Grain also is the source of alcoholic beverages, beer, industrial alcohol made into synthetic rubber and explosives. Bran from flour milling also an important livestock feed; germ is valuable addition to feed concentrate. Grain fed to livestock whole or coarsely ground. Starch is used for pastes and sizing textiles. Straw made into mats, carpets, baskets, and used for packing material, cattle bedding, and paper manufacturing. Some wheat is cut for hay.

With these points in view, the present investigation entitled “**Study of genetic components of variability for yield & yield related traits in wheat (*Triticum aestivum* L.)**” will be undertaken with the following

Objectives.

1. To identify superior lines based on yield and its component traits.
2. To estimate genetic parameter of variability for yield and yield related traits
3. To study genotypic and phenotypic association among traits.
4. To estimate path coefficient analysis of traits under study on seed yield.

2. Review of literature

M.J. Baloch *et al* ,(2013) research was carried out to examine the correlations of yield components with grain yield and to determine the extent of transmission of traits from parents to their offspring by heritability estimates. The experimental material consisted of eight wheat genotypes viz. Moomal, Kiran-95, Sarsabz, TD-1, Imdad, Sahar, Sasuee and Sundar. The heritability estimates in broad sense were higher for plant height, tillers plant, spike length, spikeletes spike, grains spike, grain yield plant, seed index and harvest index which suggested that these traits had more genetic variance and less influenced by the environmental factors, hence could be improved through selection from segregating populations.

Shoaib Ur Rehman *et al*, (2015) studied the behaviour of 100 wheat genotypes under drought stress an experiment was conducted following randomized complete block design (RCBD) with three replications. Heritability assessed the relative significance of gene action in genetic variation and plays vital role in selection process for yield improvement in collaboration with genetic advance. PCA and heritability along with genetic advance suggested that these traits and diverse genotype should be given importance in selection programs to get better grain yield in wheat under rainfed conditions.

MA Rahman *et al*, (2016) studied 12 wheat genotypes to study their variability and select genotypes for improvement of wheat. There was significant variation for all the 13 characters studied indicating the presence of considerable variations for selection. Heading days (HD), plant/ m² (PPM), spikelet per spike (SPS) and 1000 grains weight (TGW) exhibited high heritability coupled with a moderate genetic advance. Grain yield had positive and highly significant association with heading days, maturity days and 1000 grains weight at both genotypic and phenotypic levels. These results suggested that use of these traits in selecting high yielding genotypes would bring out good results and supplement empirical breeding approach.

Athar Hussain Bhutto *et al* , (2016) studied correlation and regression analysis for yield traits in wheat genotypes. The experiment was laid out in a RCBD with three replications to examine correlation and regression. Seven traits, viz.; plant height, tillers plant , spike length, spikelet's spike, grains spike, seed index and grain yield plant were studied. Thus estimation of correlation and regression analysis among yield and yield components may provide effective selection criteria to improve wheat grain yield. The results from correlation and regression of plant height indicated significantly positive association with spikelet's spike.

Birhanu Mech *et al* (2016) studied sixty four wheat genotypes were tested in 8x8 simple lattice design at Ginchi, The objective was to study the extent of genetic variability, heritability and genetic advance. The phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) values for all the traits studied. Medium phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were recorded for

plant height, number of kernels per spike, thousand kernels weight, grain yield per plot, biomass yield per plot and harvest index.

Berhanu Meles *et al*, (2017) studied Forty-nine wheat genotypes were tested at Axum, with the objective of assessing the extent of genetic variation, correlation and path analysis of wheat genotypes in yield and grain quality traits using 7 x 7 triple lattice design. Data were collected for 17 agronomic and grain quality characters. For each of the test entries, samples of 500 g grains were taken from each plot for quality analysis. This suggests selection based on phenotype of genotypes could be effective to improve characters. Thus selection for higher mean values of biomass yield and harvest index could be considered simultaneously for selection of higher grain yield.

Anzer U Islam *et al*, (2017) studied 100 wheat genotypes for various morpho-physiological traits under timely sown and late sown conditions. Yield and yield contributing traits were found significant under both conditions. Correlation coefficients revealed that number of productive tillers, 1000 grain weight, number of grains per spike, biological yield, flag leaf area, grain filling duration and grain filling rate gave the positive associations with grain yield in both environments. Consequently, selection can be based on these traits in both environments for breeding of bread wheat under heat stress condition.

Sheraz Ahmad Khan *et al*, (2017) studied a set of 27 genotypes were tested for estimation of heritability, genetic advance and association of yield and yield related traits in wheat. For all the studied traits, mean squares showed the presence of significant variation ($p \leq 0.01$) among the genotypes. Heritability estimates were observed high ($h^2 > 0.60$) for all the traits. These results suggest that all the traits showing significant correlation with grain yield needs better attention in future wheat breeding programs for increasing yield.

Arshad Iqba (2017) studied that Heritability plays a vital role in selection. An experiment with . The randomized complete block design with three replications was used in the experiment. Data were recorded on yield and some other important plant traits like days to heading (days), days to maturity (days), flag leaf area (cm²), spike length (cm), . Mean performance of genotypes showed that all the spring wheat genotypes performed well for all the traits. Spring wheat cultivar Tatara showed best performance for maturity, similarly, genotype SM12 performed well for grains spike-1 and grain weight spike-1, whereas, genotype SM4 performed well for grain yield.

Muhammad Yaqoob (2016) studied Twenty four wheat lines developed by different research institutes of Pakistan were tested at Arid Zone Research Institute, under rainfed conditions. The experiment was laid out in RCBD with three replications. All candidate lines along with well adapted local variety "Hashim-08" Row to row distance was kept as 25 cm. The results revealed significant differences for all traits except number of grains per spike. The presence of

considerable amount of genetic variability revealed that genotypes under study were genetically diversified as these were developed through various sources under different ecological zones.

Vichitra Kumar Arya (2017) studied forty nine genotypes of wheat were studied for generating scientific information on nature and magnitude of genetic variability and diversity for designing breeding programme. The experiment was conducted in randomized complete block design in three replications. The data were recorded on days to 50% flowering, plant height, peduncle length, spike length, number of spikelets per spike, number of grains per spike, 1000grain weight, harvest index and gluten content. Analysis of variance revealed significant differences among the genotypes for all the characters under study. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for grain yield per plant.

Jaydev Kumar (2017) studied 10 diverse parents and their 45 F1's of bread wheat for yielding and physiological characters during season of Rabi . Analyses of variance in 55 (45 F1's with their 10 parents) bread wheat genotypes for eighteen characters were showed highly significant differences indicate the presence of extensive amount of genetic variability. According to results, effective genotypes based on either mean performance and high heritability coupled with high genetic advance for interesting traits can be used further improvement of yield and its related traits through ideal breeding

Arshad Jamil (2017) studied genetic diversity, heritability and genetic advances for few characters which relate to yield in bread wheat. Sixty wheat genotypes obtained from NARC, The experiment was laid out in (RCBD) having 3 replications. The aspects for recording data included number of tillers plant-1, plant height, number of spikelet's spike, number of grain spike-1, 1000-grain weight and grain yield plant. ANOVA showed significant differences for all the characters studied. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were high for grain yield per plant and 1000-grain yield. The overall results showed that selection should lead to a fast genetic improvement of the material.

Materials and Methods

The materials used and methods applied during the present course of investigation on “Study of heterosis and combining ability for yield and its component traits in barley (*Hordeum vulgare* L.)” are being presented, followed by statistical procedures used. Twenty five elite and diverse pure lines of barley were received from the B.H.U., Varanasi. The experiments will be conducted at Agricultural Research Farm of School of Agriculture, Lovely Professional University as per following detailed plan of work.

3.1.1 Experimental site

The experiments will be conducted during the *rabi* (winter) season of 2017-18 at Agricultural Research Farm of School of Agriculture, Lovely Professional University. The experimental area is quite uniform in respect of topography and fertility. The soil of experimental site is sandy loam.

3.2 Experimental material

25 varieties of barley will be collected and these genotypes will be sown in five rows of 2 m length having a spacing of 25 cm x 10 cm following single seed per hill to keep the plant population at optimum level in three replications by using RCBD design.

3.3 Observations recorded

Ten competitive plants from each of the parents and F_1 s', 20 plants from backcrosses (B_1 and B_2) and 50 plants from each F_2 population from each replication were randomly selected and tagged for recording of data on following quantitative traits.

3.3.1 Days to 50 % flowering

The number of days taken from sowing to heading in main spike of 50 % plants of a plot will be recorded.

3.3.2 Days to maturity

The number of days will be recorded from sowing to physiological maturity of main spike in hundred per cent plants.

3.3.3 Plant height (cm)

At the physiological maturity, the height of individual tagged/sampled plant will be measured in centimeters from the ground level to the tip of terminal spikelet (excluding the awn) of the main shoot.

3.3.4 Number of effective tillers

At the physiological maturity, the total number of spike bearing tillers in each plant will be recorded.

3.3.5 Spike length (cm)

Length of main spike (cm) will be measured from the base to the tip of the terminal spikelet, excluding the awn.

3.3.6 Awn length (cm)

Length of the awn will be measured in centimeter.

3.3.7 Number of grains per spike

The number of grains per spike will be counted from main spike after the harvesting of plant.

3.3.8 1000 grain weight (g)

One thousand threshed grains will be taken randomly after sun drying at 12% moisture level and weighted in gram with the help of electric balance.

3.3.9 Harvest index

Harvest index will be calculated as,

$$\text{Harvest Index} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

3.3.10 Grain yield per plant (g)

The weight of filled grains of each plant in gram will be recorded.

3.4 Statistical analysis

3.3 The data recorded on fifteen Assessment of seed yield and Quality Traits in Recombinant Inbred Lines of Rice were subjected to the following analysis.

3.4.1 Mean

Mean is calculated by the following formula:

$$\bar{X} = \sum X_i / n$$

where,

$\sum X_i$ = Summation of all the observation

n = Total number of observation

3.4.2 Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes.

3.4.3 Analysis of variance

The trial was analysed as randomized complete block design. The model for the design is as follows:-

$$y_{ij} = \mu + T_i + B_j + e_{ij}$$

Where,

Y_{ij} = Observed value of i th treatment in the j th replication

M = General mean

T_i = Effect of treatment

B_j = Effect of i th block

e_{ij} = Error in i th treatment in j th block

The mean data of 5 plants were subjected to variance analysis and test of significance as per the method of Fisher (1935).

Table: 3.1 ANOVA for randomized complete block design

Source of Variation	Degree of freedom	Mean sum of squares	Expected mean sum of squares
Replications	r-1	Mr	
Treatments	t-1	Mt	$\sigma^2 e + r \sigma^2 g$
Error	(r-1) (t-1)	Me	$\sigma^2 e$

r = Number of replication; t = Number of treatment

Table: 3.7 The structure of analysis of variance is as follows:-

Source of variation	Degree of freedom	M_s
Blocks	(r-1) = 2	M_r
Treatments	(t-1) = 18	M_t
Methods	(m-1) = 11	M_m
Pedigree's	(pd-1) = 3	M_{pd}
Bulks	(b-1) = 3	M_b
SSD,s	(s-1) = 3	M_s
Bulks Vs. SSD,s	= 1	$M_{b \text{ vs. } s}$
Ped's Vs.(Bulk's + SSD,s)	= 1	$M_{p \text{ vs. } (b+s)}$
Parents	(p-1) = 6	M_p
Methods Vs. parents	= 1	$M_{m \text{ vs. } p}$
Error	(r-1)(t-1) = 36	M_e

r = NO. of replications

t = NO. of treatments

m = NO. of methods

pd	=	NO. of pedigrees
b	=	NO. of bulks
s	=	NO. of SSD,s
p	=	NO. of parents
M_r	=	Mean sum of square due to replication
M_t	=	Mean sum of square due to treatments
M_m	=	Mean sum of square due to methods
M_{pd}	=	Mean sum of square due to pedigree methods
M_b	=	Mean sum of square due to bulk methods
M_s	=	Mean sum of square due to bulk methods
$M_{b \text{ vs. } s}$	=	Mean sum of square due to bulk Vs. SSD methods
$M_{p \text{ vs. } (b+s)}$	=	Mean sum of square due to pedigree Vs. (Bulk+SSD)
M_p	=	Mean sum of square due to parents
$M_m \text{ vs. } p.$	=	Mean sum of square due to (methods Vs. Parents)
M_e	=	Mean sum of square due to error.

3.4.4 Variability

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952).

Phenotypic coefficient of variation (PCV)

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

$$P C V = (\sigma p / \bar{X}) \times 100$$

$$\text{where, } \sigma p = \sqrt{\sigma^2 p}$$

Genotypic Coefficient of Variation (GCV)

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

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

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

The estimates of PCV and GCV were classified as low, moderate and high according to Sivasubramanian and Madhavamenon (1973).

< 10 per cent = low

10-20 per cent = moderate

> 20 per cent = high

3.4.5 Heritability (broad sense)

It is the ratio of genotypic variance to the phenotypic variance. Heritability for the present study was calculated in broad sense by adopting the formula suggested by Hanson *et al.*(1950).

$$h^2(\text{bs}) \% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,

$h^2(\text{bs})$ = heritability in broad sense,

σ^2_g = Genotypic variance,

σ^2_p = Phenotypic variance

3.4.6 Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. Expected genetic advance (GA) was calculated by the method suggested by Johnson *et al.* (1955)

$$GA = K \cdot \sigma_p \cdot h^2$$

where,

GA = Genetic advance

K = Constant (Standardized selection differential) having the value of 2.06 at 5 per cent selection intensity

h^2 = Heritability of the character

σ_p = Phenotypic standard deviation

3.4.7 Genetic advance as percentage of mean

It was calculated by the following formula

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

GA was categorized as

> 20 per cent = high

10-20 per cent = moderate

< 10 per cent = low

3.4.8 Correlation coefficient analysis

Correlation coefficients were calculated for all the character combinations at genotypic and phenotypic levels as per the formula given by Miller *et al.* (1958).

where,
$$r(X_i X_j) = \frac{\text{Cov.}(X_i X_j)}{\sqrt{\text{Var}(X_i)\text{Var}(X_j)}}$$

$X_i X_j$ = Coefficient of correlation between characters X_i and X_j

$\text{Cov}(X_i X_j)$ = Covariance between characters X_i and X_j

$\text{Var}(X_i)$ = Variance of character X_i

$\text{Var}(X_j)$ = Variance of character X_j

3.4.9 Path coefficient analysis

The cause and effect relationship is well defined in path coefficient analysis. It is possible to represent the whole system of variables in the form of a diagram known as path diagram. Path coefficient analysis can be defined as the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, in other words it is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects, i.e. it measures the direct and indirect contribution of various independent characters on a dependent character.

Designing new plant type, the knowledge of direct and indirect influence of yield contributing characters, path coefficient analysis was under taken in parents and crosses. Wright (1921) proposed the original technique; analysis was carried out by modified method devised by Dewey and Lu. (1959). Following set of simultaneously equations were formed and solved for estimating direct and indirect effects.

Genotypic path coefficients were calculated separately for yield and yield components. The dependent variable was yield plant⁻¹. The unexplained variation in the dependent variable was obtained as residual factor from the following equation.

$$r_1 Y = P_1 Y + r_{12} P_2 Y + r_{13} P_3 Y + \dots + r_{1i} P_i Y.$$

$$r_2 Y = r_{21} P_1 Y + P_2 Y + r_{23} P_3 Y + \dots + r_{2i} P_i Y.$$

.

$$r_{kY} = r_{k1} P_1Y + r_{k2} P_2Y + r_{k3} P_3Y + \dots + r_{k} P_kY.$$

Where,

r_1Y to r_kY = Coefficient of correlation between causal factors 1 to i and dependent character Y

P_1Y to P_kY = Direct effect of characters 1 to i on character Y.

r_{12} to r_{k-1} , = Coefficient of correlation among causal factors.

The above equations were written in a matrix form as under-

$$\begin{matrix}
 \text{A} & & \text{C} & & \\
 \left[\begin{matrix} r_1Y \\ r_2Y \\ \cdot \\ \cdot \\ r_kY \end{matrix} \right] & & \left[\begin{matrix} 1 & r_{12} & r_{13} \dots r_{1i} \\ r_{21} & 1 & r_{23} \dots r_{2i} \\ \cdot & & \\ \cdot & & \\ r_{k1} & r_{k2} & r_{k3} \dots 1 \end{matrix} \right] & & \left[\begin{matrix} P_1Y \\ P_2Y \\ \cdot \\ \cdot \\ P_kY \end{matrix} \right]
 \end{matrix}$$

Then,

$$B = [C]^{-1} A$$

Where,

$$[C]^{-1} = \left[\begin{matrix} C_{11} & C_{12} & C_{13} \dots C_{1i} \\ C_{21} & C_{22} & C_{23} & C_{2i} \\ \cdot & & & \\ \cdot & & & \\ C_{i1} & C_{i2} & C_{i3} & C_{ii} \end{matrix} \right]$$

Then the direct effects were calculated as follows -

$$P_1Y = \sum_{i=1}^k C_{1i} r_{iy}$$

$$P_2Y = \sum_{i=1}^k C_{2i} r_{iy}$$

$$P_k Y = \sum_{i=1}^k C_{ki} r_{ky}$$

Residual effect was obtained as per for formula given below –

$$R = \sqrt{1 - \sum d_i r_{ij}}$$

Where,

d_i = Direct effect of the i^{th} character

r_{ij} = Correlation coefficient of the i^{th} character with j^{th} character.

Path coefficient were to be rated based on the scales given below. (Lenka and Mishra 1973).

> 1.0	Very high
0.30 – 0.99	High
0.2 – 0.29	Moderate
0.1 – 0.19	Low
0.00 – 0.09	Negligible

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