Dissertation report
(AGR 690)

"STUDY OF GENETIC VARIABILITY FOR YIELD, ITS COMPONENT AND DROUGHT RELATED TRAITS IN BARLEY (*Hordeumvulgare* L.)"

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

Master of Science (Agriculture)

In

Genetics & Plant Breeding

By

MYLARU SRAVANI
11615189

Department of Genetics & Plant Breeding
School of Agriculture
LPU, Jalandhar (Punjab) 144411

November 2017

CERTIFICATE

This is to certify that the Dissertation entitled **"Study of genetic variability for yield, its component and drought related traits in barley (*Hordeum vulgare* L.)"** is a bonafide record of independent research work done by **MYLARU SRAVANI,** (Reg. No.: 11615189) 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)

Signature of Student	Signature of Guide
Mylaru sravani	Dr. Madakemohekar Anant H
Reg. No. 11615189	UID: 19767
School of Agriculture	Designation: Assistant Prof.
LPU, Jalandhar, Punjab School of Agriculture	

DECLARATION

I here by declare that the project work entitle **"Study of genetic variability for yield, its component and drought related traits in barley (*Hordeumvulgare* 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. Madakemohekar Anant Hanumant, Assistant professor, School of Agriculture, Lovely Professional University, Phagwara, Punjab.

Mylaru sravani
Reg. No. 11615189

INDEX

1. INTRODUCTION

Barley (*Hordeumvulgare* L.) is one of the world's most ancient food crops. It has been an important cereal crop since the early stages of agricultural innovations 8,000-10,000 years ago (Giles and Bothmer, 1985). It is an economically important cereal crop, ranking fourth after wheat, rice and maize in the world, both in terms of quantity produced and in area of cultivation (FAO, 2014). Barley originates from the Eastern Mediterranean region where plants experience many abiotic stresses in the field. It is grown in many areas where climatic conditions are unfavorable. Though its commercial value is less than that of wheat but it replaces the later in the dry regions in areas of too low and erratic rainfall. Because of low input requirement and better adaptation, it survives easily under rainfed condition and known as poor men's crop (Verma*et al*., 2010). World production of barley is 292.9 million tonnes with highest production from Europe region (59.6%) followed by Asian region (14.9%). Russian federation is the highest producing country which produces near about 20.02 million tonnes, while India has thirteenth rank (USDA, 2015).

Cultivated barley is a member of the genus *Hordeum,* and it has descended from wild barley (*Hordeumspontaneum* Koch), which still grows in the Middle East of the world. Both cultivated and wild barley are diploid species, with fourteen chromosomes (2n= 14). Based on the morphology, *Hordeumvulgare* L. is the only cultivated species which has two – distant phenotypic forms *viz.*, six rowed (*Hordeumvulgare*, *H. hexasstichum*) and two rowed (*H. distichum*). In spite of differences in spike morphology they have same chromosome number (2n=14), and intercross freely to produce fertile hybrids (Poehlman, 1987). Barley has much genetic variation which provides the basis for classifying the species. There are many ways to classify barley among each other. One way to classify barley is to identify whether there are two, four or six rows of spikelet's on the spike. Wild barley has two rows, and most cultivated barley is of six-rowed type. Another way to classify barley is to describe the beards (awns) link with the kernels. Barley can also be described by adherence of chaff on grains (hulled) or hull-less (naked), height (dwarf, semi-dwarf and tall), seed color (colorless, white, yellow and blue) and feed or malt type. Some hull-less cultivars are more digestible due to higher-protein, lysine and in some instance glutamine content.

This has been very well explained that semi dwarf wheat and rice varieties as well as hybrids of maize and millets gave substantial increase in yield (15-20%) on high-input management but subsequently their adverse effect on soil fertility, ground water table and pollution of drinking water caused human health hazard and environmental pollution which have been quite alarming. There is no scope to raise the yield by raising fertilizers and irrigation level. It means technology revolution has reached to the freezing point in wheat and rice; maize and millets because of genetic ceiling in yield. Therefore, barley especially huskless barley is an option to produce more from less input in India where 70 percent of cultivated area is under rainfed condition.

Its production has become more intense and complex in recent years. Due to this reason, it is necessary to carry out experiments to estimate the response of barley plants to a variety of adverse conditions, such as low and high solar energy availability, shortage or excess of water in soil, high temperature and salinity, which affects photosynthesis and yield formation (Kalaji, 2012). There is a need for the development of new barley cultivars that tolerate abiotic and biotic stresses for the improvement of crop productivity (Ellis *et al*., 2000). This will require good understanding of the available genetic variation in both wild and cultivated barley. The rate of progress, however, will depend on the occurrence of desirable genetic variation and the availability of precise methods of identification, selection and transfer of superior genes (Ellis *et al*., 2000).

Proper choice of parents on the basis of their combining ability status for putative drought tolerant attributes as well as productive traits and selection in typical target environment will help in combining complex traits, such as, productivity and drought tolerance (Hanamaratti*et al*., 2004). The concept of combining ability helps the breeder to determine the nature of gene action involved in the expression of quantitative traits of economic importance. The choice of suitable breeding method for the improvement of drought tolerance traits primarily depends on the relative importance of GCA and SCA variances. A hybrid is commercially valuable only when it exhibits significantly high standard heterosis over the best locally adapted variety or hybrid. Apart from high vigor and yield, the hybrids can be a potential genetic source for better root system with higher efficiency to absorb moisture effectively for tolerating drought condition. Existence of heterosis for desired traits will be a boon to drought tolerance breeding since most

of the hybrids developed so far lack tolerance to abiotic stresses. The generation mean analysis is one of most appropriate methods of genetic analysis for quantitative traits (Eshghi and Akhundova, 2009).In this method, epistatic effects as well as additive and dominance effects can be estimated. Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is being transferred generation after generation. Because efficiency of selection mainly depends on additive genetic action, influence of the environment and interaction between genotype and environment as well.

The magnitude of additive gene effect is particularly useful in the development of pureline varieties. Drought is predominantly controlled by additive genes as has been reported by Solmon*et al*. (2003). Likewise, the information concerning dominance and epistatic gene effects (non-additive components) is also valuable for development of hybrid varieties (Sharma and Tandom, 1997: and Munir*et al*., 2007). Several barley workers have tried to estimate the various gene effects; genetic variance and combining ability through exploiting different mating design, such as, diallel, half-diallel, line x tester, partial-diallel, triallel and generation mean analysis etc.

With these points in view, the present investigation entitled **"Study of genetic variability for yield, its component and drought related traits in barley (*Hordeumvulgare* L.)"** will be undertaken with the following

objectives.

1. To identity superior lines based on yield and quality, drought tolerant 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

Various biometrical procedures are used by plant breeders for estimation of genetic value of parents and evaluation of varieties and hybrids in terms of their genetic makeup in different adverse conditions need to reviewed before the start of any research programme. A vast literatures in respect of combining ability and gene action, heterosis and inbreeding depression for various yield e traits have been reviewed and brief account of which are presented in this chapter as follows,

V. L. Aidun *et al*., (1989) observed Two populations, developed from three two-rowed malting barley (Hordeum vulgare L.) lines. Estimates of genetic advance indicated that moderate gains could be achieved with stringent selection pressure (5%) against hull peeling. A great deal of variability was found within the F. and F. generations indicating potential for improvement through selection. Based on results obtained. selection for hull adherence would best be incorporated into the later generations of an already established breeding program.

Nanak Chand *et al*., (2008) Thirty diverse elite barely lines and six checks were grown in the three environments with two replications during *Rab*i to study coefficient of variability, heritability and expected genetic advance for ten characters *i.e.*, days to ear emergence, days to maturity, total tillers per plant, number of effective tillers per plant, plant height (cm), number of grains per spike, 1000-grain weight (g), biological yield per plant (g) The characters which showed higher estimates of genetic advance coupled with higher estimates of heritability reflecting additive gene action, were grain yield per plant and number of grains per spike followed by biological yield per plant .Thus, selection of these characters should emphasized in barley improvement programme

Roham eshghi *et al*., (2011) In order to study selection indices for improving hulless barley grain yield and its components, 75 F2 plants resulting from the two crosses ICNBF93-369×ICNBF-582 and SB91925×ICB-102607 were evaluated regarding plant height, number of tillers per plant, spike length, multiplication of broad-sense heritability values and values of direct effects of path analysis. The results also indicated that taking advantage of led to almost similar genetic

advance in the traits under study. Hence, using the Brim-Williams index is recommended due to simplicity of calculations and interpretation of results, so as to improve the grain yield and its components.

Emine Budkali carpici and Necmettin celik (2012) studied sought to determine the correlations between grain yield and yield components and to measure the direct and indirect effects of yield components on grain yield in barley. This research was conducted with ten varieties of two-rowed barley. Agronomic traits such as grain yield, plant height, spike length, kernel number per spike, harvest index and 1000-kernel weight were determined..Correlation analyses indicated that the grain yield was positively and significantly associated with all the yield components except 1000-kernel weight. Because of the significant effects of the harvest index, spike number per m2 and kernel number per spike on grain yield

Rao Wali Muhammad *et al.*, (2013) Fifteen lines with four testers were crossed in a line x tester (L× T) mating design to estimate the variability, heritability and genetic advance for yield and its component traits in barley (*Hordeum vulgare* L.). The mean squares due to replications were positive and significant for days to 50 per cent flowering, days to maturity, biological yield plant-1 and amylose content while, mean square due to treatments were positive and highly significant for all the characters. High PCV and GCV were recorded for grain main spike-1 and number of grains ear-1. High heritability coupled with high genetic advance was noted for biological yield plant-1 These characters were mainly under the influence of additive gene action and thus, there is ample scope for the improvement of traits through simple selection

J. Singh et al., (2014) studied fourteen genotypes of Barley (Hordeum vulgare L.). The mean data estimated were subjected to analysis of variance, correlation coefficient and path analysis to identify promising genotypes for ten quantitative traits, The character association study revealed significant positive association of grain yield per plant with 1000 grain weight (r y p = 0.83), peduncle length (r p = 0.51), number of effective tillers per plant (r p =0.46) and plant height (r p =0.18). Hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes. Path coefficient analysis revealed high positive direct effect of 1000 grain weight followed (0.72) by number of effective tillers per plant (0.62), number of grains per ear

Yadav *et al*., (2015) observed a total of 45 F1s along with their parents and F2 populations were evaluated in a randomized block design with 3 replications during *Rabi* . The various traits measured were days to 50% flowering, days to maturity, plant height, flag leaf area, grain yield , harvest index, grain size, husk content and protein content. The degree of genotypic and phenotypic coefficient of variation was high for tiller, spike grain yield, flag leaf area, harvest index, 1000 grain weight, Data on eight morphological traits, i.e. plant height (PH), flag leaf area (FLA), number of tillers per plant (NTP), spike length (SL), heritability for kernel yield per plant (KYP) and number of kernels per spike (NKSP) were 99.11% and 98.96%, respectively, with higher value of genetic advance provided the evidence that these plant attributes might be under the control of additive genetic effects and selection breeding can be beneficial for improvement of barley genotypes

Rao *et al.*, (2015) The current study was made to work out the heritability and genetic diversity among seven barley genotypes. Data on eight morphological traits, i.e. plant height (PH), flag leaf area (FLA), number of tillers per plant (NTP), spike length (SL), number of spikelets per spike (NSPK), number of kernels per spike (NKSP), hundred kernel weight (HKWT) and kernel yield per plant (KYP) were collected and analysed. Phenotypic coefficient of variability (PCV) was higher than genotypic coefficient of variability (GCV) for all the traits. Estimates of broad sense heritability for kernel yield per plant (KYP) and number of kernels per spike (NKSP) were 99.11% and 98.96%, respectively, coupled with high value of genetic advance. High amount of broad sense heritability with higher value of genetic advance provided the evidence that these plant attributes might be under the control of additive genetic effects and selection breeding can be beneficial for improvement of barley genotypes.

.

Addisu and Shumet (2015) Accordingly, thirty six barley landraces were Evaluated The plot design used for the experiment was a randomized complete block design with three replications. The analysis of variance for the 36 barley landraces revealed significant difference among the landraces for the 13 quantitative characters studied. The greater difference between GCV and PCV was observed spike and peduncle length indicating that these characters were influenced by environmental factors to greater extent. Heritability coupled with high genetic advance was

observed for characters biomass per plant, grain yield and number of tiller per plant indicating that selection for these characters could be more effective due to additive gene action. Thus, this study revealed the presence of sufficient variability among the barley landraces in the country that can be exploited for germplasm enhancement.

Madakemohekar *et al*., (2015) A study was undertaken to analyze the genetic variability, correlation and path coefficient analysis of yield and its contributing traits in 14 parents and their 40 F_1 crosses for twelve component characters, grown at BHU Agricultural Research Farm, during Rabi season of 2013-14. High GCV and PCV were observed for number of effective tiller per plant, stomatal conductance, spike length and awn length. High heritability coupled with high genetic advance was obtained with number of grains per plant, effective tillers per plant, stomatal conductance, spike length and awn length. Path coefficient analysis revealed that among the different yield contributing characters, number of effective tiller per plant, harvesting index, 1000 grain weight and number of grains per panicle influenced grain yield per plant directly. The direct effects of these characters on grain yield were positive and considerably high.

Lodhi *et al*., (2015) Selected 105 genotypes of barley (*Hordeum vulgare* L.) were evaluated in randomized block design with High GCV and PCV were observed for peduncle length (27.23, 34.43), grain yield per plant (21.23, 32.23) . Heritability in broad sense ranged from 29.00 (Spike length without awn) to 76.00 (Days to Maturity). High heritability coupled with high genetic advance as percent of mean was observed for plant height and grains per ear. There was positive significant correlation of seed yield per plant with grains per ear (rp= 0.47), effective tillers per plant (rp= 0.36), 1000 grain weight (rp= 0.25) and Plant Height (rp= 0.19) hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes

Hailu *et al.,* (2016) studied Sixty four barley genotypes were tested in 8 × 8 simple lattice design at Atsbi, Ofla and Quiha environments in Tigray region. The objective was to estimate the extent of association between pairs of characters in genotypic and phenotypic levels and thereby compare the direct and indirect effects of the characters. Analysis of variance (ANOVA) revealed that there was a significant difference ($p<0.001$) Grain yield had positive and highly significant phenotypic and genotypic correlation with 1000-kernel weight and biological yield in all environments except harvest index at Ofla. On the other hand, grain yield had negative and

highly significant correlation at genotypic level with days to heading and days to maturity only at Ofla.

Ahmadi *et al*., (2016) studied Forty barley pure lines the number of grains per spike followed by peduncle length, early vigor and grain yield. The broad heritability estimates ranged from 24% for grain yield to 96% for the number of grains per spike. The pure lines No. 29, 13, 9 and 33 were identified as the superior lines for semi-arid environmental conditions. Our results indicate that check cultivars could be improved by selecting for pure lines with taller peduncle and the number of grains per spike, but with heavier grains. Therefore, these lines can be used as genetic material

Shrimali *et al.,* (2017) observed path analysis for 30 genotypes of Barley in a Randomize Block Design (RBD) with three replications in two environments. The seed yield per plant was found to be positively and significantly associated with plant height, biological yield per plant, test weight, number of spikelets per spike and spike length in both the environments. Path coefficient analysis indicated that biological yield per plant and harvest index. were the important characters for selection of high yielding genotype as this exerted high positive direct effect as well as showed high and positive correlation with seed yield.

Sunil *et al.*, (2017) studied One hundred and seventy barley germplasm lines (101 two rowed and 69 six rowed) and three standard checks (BH393 six rowed, BH946 six rowed and BH885 two rowed) were evaluated for ten quantitative traits using augmented block design consisting of 10 complete blocks. Path coefficient analysis revealed that all the characters had direct and positive association with grain yield/plant except peduncle extrusion length which had negative direct effect in case of two

3. MATERIAL 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 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 collect and these genotypes will be sowin 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 replication by using RCBD design.

3.3 Observations recorded

Ten competitive plants from each of the parents and F_1s', 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 bemeasured 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 gramwill berecorded.

a. **Statistical analysis**

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

3.4.1 Mean

Mean is calculated by the following formula:

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

where,

$\sum Xi$ = 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:-

$Y_{ij} = m + T_i + B_j + e_{ij}$

Where,

Y_{ij} = Observed value of ith treatment in the jth replication

M = General mean

T_i = Effect of treatment

B_j = Effect of ith block

e_{ij} = Error in ith treatment in jth block

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

Table: 3.1ANOVA 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 $v_{s.S}$
Ped's Vs.(Bulk's + SSD,s)	= 1	$M_{pvs.\ (b+s)}$
Parents	(p-1) = 6	M_p
Methods Vs. parents	= 1	$M_{m\ Vs.}$ 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 $v_{s.S}$ = Mean sum of square due to bulk Vs. SSD methods

$M_{pvs.\ (b+s)}$ = Mean sum of square due to pedigree Vs. (Bulk+SSD)

M_p = Mean sum of square due to parents

M_m v_s. 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)

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

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

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

Genotypic Coefficient of Variation (GCV)

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

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).

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

where,

$h^2 (bs)$ = heritability in broad sense,

$\sigma^2 g$ = Genotypic variance,

$\sigma^2 p$ = 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)

$$G\ A = K.\sigma_p\ h^2(bs)$$

where,

GA = Genetic advance

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

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

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, $$r(XiXj) = \frac{Cov.(XiXj)}{\sqrt{Var(Xi)Var(Xj)}}$$

XiXj = Coefficient of correlation between characters Xi and Xj

Cov (XiXj) = Covariance between characters Xi and Xj

Var (Xi) = Variance of character Xi

Var (Xj) = Variance of character Xj

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.

$r_1Y = P_1Y + r_{12} P_2Y + r_{13} P_3 Y +\ldots\ldots\ldots\ldots\ldots+ r_1i P_1Y.$

$r_2Y = r_{21} P_1Y + P_2 Y + r_{23} P_3Y +\ldots\ldots\ldots\ldots\ldots+ r_{21} p_1Y.$

.

.

.

$r_k y = r_{k1} P_1Y + r_{k2} P_2Y + r_{k3}P_3Y + \ldots\ldots\ldots\ldots + r_k P_kY.$

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-

$$A = \begin{bmatrix} r_1Y \\ r_2Y \\ . \\ . \\ r_kY \end{bmatrix} \qquad C = \begin{bmatrix} 1 & r_{12} & r_{13}\ldots\ldots\ldots\ldots r_{1i} \\ r_{21} & 1 & r_{23}\ldots\ldots\ldots\ldots r_{2i} \\ . & & \\ . & & \\ r_{k1} & r_{k2} & r_{k3}\ldots\ldots\ldots\ldots 1 \end{bmatrix} \qquad \begin{bmatrix} P_1Y \\ P_2Y \\ . \\ . \\ P_kY \end{bmatrix}$$

Then,

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

Where,

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13}\ldots\ldots\ldots\ldots C_{1i} \\ C_{21} & C_{22} & C_{23} & C_{2i} \\ . & & & \\ . & & & \\ C_{i1} & C_{i2} & C_{i3} & C_{ii} \end{bmatrix}$$

Then the direct effects were calculated as follows -

$$P_1Y = \sum_{i=1}^{k} C_{1i}\, r_iy$$

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

$$P_k Y = \sum_{i=1}^{k} C_{ki} r_k y$$

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

Reference

Aidun, V. L., Harvey, B. L. and Rossnagelt, B. G. (1989). Heritability and genetic advance of hull peeling in two-row barley. *Journal of Plant Sciences*, 70: 481-485.

Arun, K., Jaydev, K, U,. (2017) Genotypic correlation and path coefficient analysis for yield and yield contributing traits in released varieties of barley (Hordeum. vulgare) *Journal of Applied and Natural Science*, 9 (1): 192 – 195.

Emine, B. C. and Celik, N. (2012). Correlation and path coefficient analyses of grain yield and yield components in two-rowed of barley (*Hordeum vulgare* convar. *distichon*) varieties. *Not. Sci. Biol.* 4(2): 128-131

Fekadu, A. and Gegnaw, S. T. (2015). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) Landraces in Ethiopia. International Journal of Plant Breeding and Genetics. 9 (2) : 68-76.

Jaya, A., Shekhawa, S., and Sunita, K., (2017) . Correlation and Path Analysis Studies in Barley (*Hordeum vulgare* L.) Genotypes under Normal and Limited Moisture Conditions. *International Journal of Current Microbiology and Applied Sciences*, 6(8) : 1850-1856.

Lodhi, R., Prasad, L. C., Madakemohekar, A. H., Bornare, S. S. and Prasad, R. (2015). Study of genetic parameters for yield and yield contributing trait of elite genotypes of barley (H*ordeum vulgare L*.). *Indian Res. J. Genet. & Biotech.*, 7(1): 17 – 21.

Muhammad, R. W., Qayyum, A., Shoib, L., Hamza, A. and, Malik, M. Y. (2012). Variability, heritability and genetic advance for some yield and yield related traits in barley (*Hordeum vulgare* L.) genotypes in arid conditions. *Journal of Food, Agriculture & Environment*, 10(3&4) : 626 - 629.

Manoj, K., Vishwakarma, S. R., Bharat, B. and Kumar, A. (2013). Estimation of genetic parameters and character association in barley (*Hordeum vulgare* L.). *Journal Wheat Research*,. 5(2): 76-78

Madakemohekar, A. H., Prasad, L. C., Lal, J. P., Lodhi, R. D. and Prasad, R. (2015). Studies on genetic variability, correlation and path analysis for yield and its contributing traits in barley *(Hordeum vulgar* L.*)* under rainfed environment. *Indian Res. J. Genet & Biotech*., 7(3): 305 –310.

Nanak, C., Vishwakarma, S. R,. Verma, O. P. and Kumar, M. (2008). Worth of genetic parameters to sort out new elite barley lines over heterogeneous environments. *Barley Genetics Newsletter*, 38 : 10-13.

Roham, E., Ojaghi, J. and Samira, S. (2011). Genetic gain through selection indices in hulless barley. *International journal of agriculture & biology*, 13(2): 191-197

Singh, J., Prasad, L. C., Madakemohekar, A. H. and Bornare, S. S. (2014). Genetic variability and character association in diverse genotypes of barley (hordeum vulgare l.). *The international quarterly of journal of life sciences*, 9(2): 759-761.

Yadav, S. K., Singh, A. K., Praveen, P. and Smita, S. (2015). Genetic variability and direct selection criterion for seed yield in segregating generations of barley (*Hordeum vulgare* L.). *American Journal of Plant Sciences*, (6):1543-1549.