ESTIMATION OF CORRELATION AND PATH ASSOCIATION IN RAPESEED (BRASSICA NAPUS L.) WITH THE FEASIBILTY OF DEVELOPING F1 HYBRID IN LINE X TESTER MATING DESIGN

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ABSTRACT

The presented study was carried out at Mata Gujri College, Fatehgarh Sahib's experimental farm, Department of Agriculture during 2020-2021, 2021-2022. The National Bureau of Plant Genetic Resources, New Delhi provided the eight parents (IC 571662, IC 311734, IC 571697, IC 589680, IC 589670), three testers (EC 338978, EC 338975, EC 338976), and one check that made up the experimental material. Fifteen f1s using the line x tester mating design were grown in a randomised block design. The number of primary branches, number of secondary branches, plant height, number of siliquae per plant, siliquae length, test weight, biological yield, and harvest index are all shown at the phenotypic level of path coefficient of analysis of various traits contributing to the seed yield per plant. All of these traits show a positive value, but the days to first flowering, days to 50% flowering, and days to harvest index remain significant negative values. Additionally, the two F1 hybrids (IC 311734 x EC 338976 and IC 311734 x EC 338975) for the best parents' seed output per plant are available. Furthermore, no cross has a substantial negative value.

INTRODUCTION

Brassica napus is also used to make honey. This crop has numerous selected cultivars that ensure higher product quality and better processing methods.

Brassica napus is used for the production of vegetable oil and animal feed. The oil is extracted from the seeds of *Brassica napus* is used as a food stuff and as well as in many products such as candles, lipsticks, industrial lubricants, etc. The remaining *Brassica napus* meal is then used for production of superior livestock feed. The oilseeds Third-largest source of oils in the world, brassica have steadily increased in production as a result of traditional and contemporary plant breeding techniques. (Sabaghnia *et al.,* 2010). Today, agriculture has taken the shape of a commercial profession and oilseed crops are being cultivated by farmers owing to good remunerative prices. The demand for oilseeds and their products is ever increasing and has become an essential part of our daily diet in view of changing life style and burgeoning population.

In India, mustard is one of the most important oilseeds crops. It makes up over 13% of the edible oil produced worldwide. In northern India, seeds are mostly used for human consumption for frying and cooking purposes, and they contain 38–40% oil. Furthermore, its oil is a crucial raw resource for industrial goods like paints, lubricants, soap, and other items. Although oil cakes have a high glucosinolate concentration, they are not appropriate for use as animal feed despite their high protein level.

Since there are now more species and varieties of Brassica produced in Canterbury for seed, it is important to recognise the threat to cultivar purity posed by the variety of species present. Many of these species are hybrids, necessitating a much higher criterion for cultivar purity. These seed crops are also utilised for oilseed crop types that are grown in Europe and North America. Due to several reports on gene flow from genetically modified (GM) crops to allied crops and weeds, cross-pollination in mustard has grown in previous years.

The main focus of mustard breeding has been to create homozygous plants by taking use of the genetic variety that is present. Increasing output and stability with an efficient plant type that carries the genes for larger seed and oil content is highly desirable. The release of such lines depends on the knowledge of combining ability and genetic architecture of the population (Parkash *et al.,* 2012).

The coefficient of variance does not provide any information regarding heritability; instead, it shows the extent of variability for different features. Because of this, understanding heredity is censorious, allowing for greater selection effectiveness by isolating the influence of the environment from overall variability. If the variance is first evaluated in terms of heritability and is attributed to additive genes, breeders can attain the best selection response.

Dewey and Lu's (1959) To determine the amount and direction of the direct and indirect effects of different yields and its distributing properties, the route coefficient approach was employed. When combined, the correlation and route coefficients offer more useful data that can be applied more successfully to crop improvement initiatives. If the yield and its characteristics are directly correlated, indicating a genuine relationship between them, then selecting for the feature directly will be more advantageous for crop improvement.

MATERIALS AND METHOD

1. Experimental Site and Condition
The studies were conducted at Mata Gujri College's Experimental Farm in Fatehgarh Sahib. With coordinates between 30°27' and 30°46' north latitude and 76°04' and 76°38' east longitude, this place is 246 meters above sea level. The farm is located 35 km from Patiala and 42 km from Chandigarh. The area has scorching, dry summer breezes and foggy winters. There are three different seasons in Fatehgarh Sahib's subtropical semi-arid climate: hot, dry summers, a monsoon period, and freezing winters. December and January can have temperatures as low as 4°C, while May and June can see temperatures as high as 42°C.

2. Experimental materials
There were fifteen F1 hybrids and eight genotypes of mustard in the experimental material. In the 2020–21 Rabi season, the parents were crossed in the Line tester mating design.

Table 2.1: Parents used in crossing programme with line × tester mating design.

Sr.no.	Genotypes	Sources
Lines (Females)		
1.	IC 571662	NBPGR
2.	IC 311734	Do
3.	IC 571697	Do
4.	IC 589680	Do
5.	IC 589670	Do
Tester (Males)		
6.	EC338978	Do
7.	EC338975	Do
8.	EC338976	Do

3. Plan of work
The experiment was conducted at the Experimental Farm, Department of Agriculture, Mata Gujri College, Fatehgarh Sahib, Punjab, during two consecutive winter seasons: 2020–21 and 2021–22. The detailed procedures and methodologies employed during these seasons are described below:

First Year (Winter 2020–21)
Experimental Setup
- Objective: To generate and evaluate F1 hybrids using a line × tester mating design.
- Material: Five elite lines of mustard were selected for the experiment.
- Design: The experimental layout was set up using a Randomized Block Design (RBD) with three replications to ensure robust data and reliable results.

Procedures
1. Crossing: A total of 15 crosses were made using the selected lines. Each of the five lines was crossed with each of the three testers, resulting in a comprehensive set of hybrids. This design aimed to assess the combining ability and performance of the different lines and testers.
2. Selfing of parents: To maintain genetic purity, individual plants of the parent lines were selfed. This step ensured that the seeds used for crossing were true to type, providing accurate results for the hybrid evaluation.
3. Collection of F1 Seeds: After the completion of the crosses, F1 seeds from each hybrid combination were harvested separately. These seeds were prepared for further evaluation in the subsequent year.

Second Year (Winter 2021–22)
Experimental setup
- Objective: To evaluate the performance of F1 hybrids and analyze their yield characteristics.
- Material: The 15 F1 hybrids from the previous year, which included eight genotypes and one check variety, were used for this phase.
- Design: The experiment was conducted using a Randomized Block Design (RBD) with three replications, similar to the previous year, to maintain

consistency in the experimental conditions and results.

Procedures
1. Planting and Spacing: Each of the 15 F1 hybrids and the check variety were grown with a population size of 20 plants per treatment. Standard spacing was maintained to ensure uniform growth and to minimize competition between plants.
2. Data Collection: Various yield characteristics were recorded throughout the growing season. This included measurements such as plant height, number of branches, siliquae per plant, and seed yield, among others. The data collected were used to evaluate the performance and potential of the hybrids.
3. Collection of F2 Seeds: After the evaluation of F1 hybrids, F2 seeds were collected separately for each hybrid. These seeds were preserved for future experimentation and analysis, such as assessing segregation patterns and further selection for desirable traits.

Summary: The experiment conducted over the two years aimed to identify promising mustard hybrids through careful design and execution of crosses, followed by rigorous evaluation of their performance. By employing a systematic approach in crossing, evaluating F1 hybrids, and collecting F2 seeds, the study provided valuable insights into the genetic potential and breeding value of the mustard lines involved.

METHODS
1. Field layout
The experimental material comprising of eight genotype *i.e.* 5 parents and three tester were grown in Randomized Block Design with three replications.

2. Observation
From each replication, five competing plants will be chosen at random to record the observations for every character. For various statistical studies, the average of the data from each replication with regard to distinct characters will be employed.

We kept track of observations for the following quantitative parameters
1. Field layout
Eight genotypes (three testers and five parents) made up the experimental material that was cultivated in a Randomised Block Design (RBD) with three replications. By guaranteeing that every genotype is assigned at random to the experimental units in every block, this strategy reduces the variability among treatments and offers a more precise assessment of the treatment effects.

2. Observations
Five rival plants were randomly selected from each replication to document observations for every character.

The mean of the data for each replication in terms of unique characters was used for a variety of statistical analyses. The following quantitative parameters' observations were monitored:
1. Days to first flowering
The number of days from the date of sowing the mustard crop to the date when the plants first began to bloom was recorded.

2. Days to 50% flowering
The number of days from the date of sowing until 50% of the plants in the field had flowered was noted.

3. Number of primary branches per plant
At maturity, the number of branches growing from the main stem was recorded for each chosen plant in each replication.

4. Number of secondary branches/plant
At maturity, the secondary branches that grew from the primary branches of each plot's chosen plants were counted in each replication.

5. Plant height (cm)
All of the tagged plants' mature plant heights, including the inflorescence, were measured using a metre scale and centimetres to measure from the base of the axis to the top.

6. Number of Siliquae/Plant
All of the siliquae, which were abundant in seeds and found on both the primary and secondary branches, were counted from each plot's selected trousers in each replication at maturity.

7. Siliquae length (cm)
Only ten siliquae of each chosen plant in each plot, measured from the upper base to the top, were randomly selected.

8. Number of seeds/siliquae
The number of seeds from each genotype's ten randomly chosen siliquae of each selected plant was counted. and employed to calculate the siliquae length.

9. Days to maturity
The days of maturity was recorded from the sowing date to the date of maturity, the date when all the plants in line appearance turned in yellow colour.

10. Biological Yield/Plant (g)
The eight plants in every row that was harvested at the point and they are attached to the ground level after that they were collected, than sun dried until the weight was constant.

11. Seed Yield/Plant (g)
At the maturity level, the all selected plants of each genotype in every replication was threshed separately with mechanical method and properly cleaned in the

laboratory. The grains are weighed on the electric balance and the yield was recorded in the grams.

12. Harvested index (%)
The harvested index was taken as a ration of grain yield to the total biomass expressed as percent:
Harvest index = Grain yield (g) × 100/Biological yield (g)

13. Test weight (g)
The 1000-seeds weight was randomly taken from the every selected plant and after that the weighed of the seeds in grams on electric in the laboratory.

Hybridization programme
Using the line tester mating design, each of the eight lines was crossed, resulting in the production of fifteen hybrids. The following day, the healthy flower bids from the fresh flush were open to being chosen for emasculation and pollination. The chosen buds were manually emasculated between 4:00 and 5:00 p.m. with forceps and needles. In order to prevent contamination from other or foreign pollen, the emasculated blooms are then covered with butter paper sheets and stapled to both sides. The pollination of the emasculated bloom was completed between 7.30 and 10.30 am the next day. The male father selected the well-opened flowers with dehisced anther, carefully removed the butter paper beg, and contacted the stigma with the male flower's anther. Because they were simple to identify and prevented pollen contamination, the female flower was likewise quickly covered in another shade of butter paper beg. Every pollinated flower had a label attached to its petal that included the date of crossing, the names of the male and female parents, and other identification information.

3.7. Statistical analysis
The mean values of nine plants in each parent and F1 plot over all three replications were used for statistical analysis. Hyderabad-based Indo Stat conducted data analysis.

3.7.1. Analysis of variance
For every genotype, it was conducted using the Randomised Block design (RBD) analysis method (Panse and Sukhatme, 1989). Three sources of variance were identified: replication, treatment, and error. These accounted for half of the overall variance.
The model of ANOVA is given as: $Y_{ij} = \mu + t_i + r_j + e_{ij}$,
Here,
i = 1, 2, 3...........55;
j = 1, 2, 3;
Null hypothesis,
H_o = $t_1 = t_2$ .... t_{55}

The numbers r and g represent the number of replications and treatments, respectively, and the degrees of freedom (D.F.) for replication, treatment, and error, respectively, are (r-1)(g-1). Calculations are made for the sum of squares for error (ESS), treatment (GSS), and replication (RSS). The mean square is ESS/(r-1)(g-1) for error (Me), GSS/(g-1) for treatment (Mg), and RSS/(r-1)(r-1) for replication (Mr). Mr/Me is the replication F-value, while Mg/Me is the treatment F-value. There are (rg-1) degrees of freedom for the total sum of squares (TSS). If the calculated F-value is greater than the tabulated F-value, indicating significance at the 5% or 1% level of significance, the standard error (SE) and critical difference (CD) are computed as SE. The crucial difference (CD) is derived by multiplying SE.d by the t-value at the 5% or 1% significance level at the error degrees of freedom. The standard error of the difference (SE.d±) is computed as $\sqrt{(2.MSE)/r}$.

Table 3.7.1: Analysis of variance (Anova).

Source	D.F.	Sum of Square	Mean square	F- Value
Replication	(r-1)	RSS	RSS/(r-1)= Mr	Mr/Me
Treatment	(g-1)	GSS	GSS/(g-1)= Mg	Mg/Me
Error	(r-1) (g-1)	ESS	ESS/(r-1)(g-1)= Me	
Total	(rg-1)	TSS		

The standard error and critical difference were computed as standard error if F calculated value > F tabulated value, which indicated that the corresponding source of variation is significant at the 5% or 1% level of significance, or vice versa. (SE. d±)=$\frac{\sqrt{2.MSE}}{r}$ SEd x t value at 5% or 1% level significance at error degree of freedom is the crucial difference (CD).

Test of significance
A difference between treatments was deemed statistically significant "if the calculated value was higher than the tabulated value of F for n1 and n2 degrees of freedom at the 5% or 1% level of significance. However, it was deemed statistically insignificant if it was less than the tabulated value, indicating that there isn't a true difference between the genotypes."

3.7.2. Line x tester analysis
Using the approach described by Kempthorne (1957) "and further developed by Arunachalam (1974), the "line x tester" analysis was performed to estimate the variances of general and particular combining abilities and their consequences. On a small scale, line tester analysis was utilised to ascertain the GCA and SCA of

various lines." This is how analysis of variance is formatted":

Table 3.7.2 Line x tester analysis.

Source of variation	DF	SS	MSS	Expected MSS
Replications	(r-1)	-	-	-
Lines (Females)	(l-1)	SS (l)	M (l)	$\sigma^2 e + r(Cov.FS - 2.Cov.HS) + rt.Cov.H.S.$
Testers (Males)	(t-1)	SS (t)	M (t)	$\sigma^2 e + r(Cov.FS - 2.Cov.HS) + l.Cov.H.S.$
Lines x Tester	(l-1)(t-1)	SS (lt)	M (lt)	$\sigma^2 e + r(Cov.FS - 2.Cov.HS)$
Error	(r-1)(T-1)	SS (e)	M (e)	$\sigma^2 e$

3.7.3. Genetic components

$$Cov. HS (line) = \frac{M_l - M_{lt}}{rt}$$

$$Cov.HS (tester) = \frac{M_t - M_{lt}}{rl}$$

$$CovHS (average) = \frac{1}{r.(2lt - l - t)} . \left[\frac{(l-1).M_l + (t-1).M_t}{1 + t - 2} - M_{lt} \right]$$

$$CovFS = \left[\left\{ \frac{(M_l - M_e) + (M_t - M_e) + (M_{lt} - M_e)}{3r} - M_{lt} \right\} + \left\{ \frac{6r.Cov.HS - r.(1 + t).Cov.HS}{3r} \right\} \right]$$

3.7.4. Degree of dominance
It was calculated using the formula suggested by Kempthorne and Curnow (1961).

$$Degree\ of\ dominance = \sqrt{\frac{\sigma^2_{sca}}{2.\sigma^2_{sca}}} \ \ or \ \ \sqrt{\frac{\sigma^2_D}{\sigma^2_A}}$$

3.7.5. Proportional contribution of lines, Testers and Their interactions

$$Contribution\ of\ lines\ (\%) = \left[\frac{SS(l)}{SS(Crosses)} \right] x\ 100$$

$$Contribution\ of\ testers\ (\%) = \left[\frac{SS(t)}{SS(Crosses)} \right] x\ 100$$

$$Contribution\ of\ lines \times testers\ (\%) = \left[\frac{SS(lt)}{SS(Crosses)} \right] x\ 100$$

3.7.6. Gene action
Gene action was worked out following Kempthorne (1957)

$$Cov.HS = \left[\frac{1 + F}{4} \right] . \sigma^2_A$$

Additive genetic variance $\sigma^2 A = 4\ Cov.HS.$ (Average) with F=1

$$\sigma^2_{sca} = \left[\frac{1 + F}{4} \right] . \sigma^2_D$$

Dominance variance $(\sigma^2 D) = \sigma^2 sca$ with F=1

3.8. Coefficient of variation
Phenotypic and genotypic coefficient of variation for different characters was be estimated as suggested by Burton and De Vane (1953).

CV (%) = [SD/Mean] × 100

Phenotypic coefficient of variation (PCV)	=	$\dfrac{\text{Phenotypic Standard Deviation}}{\text{General Mean}}$
	=	$\dfrac{\sigma_P}{\overline{X}}$ x 100
Genotypic coefficient of variation (GCV)	=	$\dfrac{\text{Genotypic Standard Deviation}}{\text{General Mean}}$
	=	$\dfrac{\sigma_g}{\overline{X}}$ x 100

3.8.1. Estimation of heritability
Heritability was estimated as

$[h^2 = \sigma^2_g/\sigma^2_p]$

Where, $[\sigma^2_g = (V_L - V_E) / R]$ V_L = Variance due to lines, V_E = Variance Due to environment (error variances), R = replication, $\sigma^2_p = \sigma^2_g + V_E$.

3.8.2. Estimation of genetic advance:-
The expected Genetic advance was be estimated using the formula as suggested by Johnson *et al.* (1955).

GS = (k) (σ_p) (H)

3.8.3. Estimation of correlation analysis
Correlation coefficients analysis measures the mutual relationship between various characters at genotypic (g), phenotypic (p) and environmental levels with the help of following formula:-

Genotypic correlation coefficient between characters x and y This coefficient measures the correlation between two characters x and y based on their genotypic values. It is calculated using the formula:

rxy (g) = Covxy (g) √ (Var x (g) x Vary (g))

2. Phenotypic correlation coefficient between characters x and y

rxy (p) = Covxy (p) √ (Varx (p) x Vary (p))

These coefficients provide insight into the strength and direction of the relationships between different characters, helping in understanding how traits are associated with each other at different levels of genetic and environmental influence.

3.8.4. Path coefficient analysis
The path coefficient analysis was computed using the following formula by Dewey and Lu (1959). The following equations, which represented the fundamental connection between genotypic correction (r) and path coefficient (P), were simultaneously selected to yield the path coefficient.

$r_{14}= P_{14}+ r_{12} P_{24}+ r_{13} P_{34}$
$r_{24}= r_{21} P_{14} + P_{24} + r_{23} P_{34}$
$r_{34}= r_{31} P_{14} + P_{32} + r_{24} P_{34}$

where, "r_{14}, r_{24} and r_{34} are genotypic correlation of components characters with yield (dependent variable) and r_{13}, r_{23} and r_{24} are genotypic correlations among the component characters (independent variable) and $r_{12} P_{24}$, $r_{13} P_{34}$, $r_{21} P_{14}$, $r_{23} P_{34}$, $r_{31} P_{14}$ and $r_{24} P_{34}$ are indirect effects." The direct effects are calculated by the following set of equations:

$P_{14}= C_{11} r_{14}+ C_{12} r_{24}+ C_{13} r_{34}$
$P_{24}= C_{21} r_{14} + C_{22} r_{24} + C_{23} r_{34}$
$P_{34}= C_{31} r_{14} + C_{32} r_{32} + C_{24} r_{34}$

Where, "C_{11}, C_{12}, C_{23} and C_{33} are constants derived by using abbreviated Doul tittle's technique and P_{14}, P_{24} and P_{34} are the estimates of direct effects."

Residual effect
It assesses the influence of other potential independent variables that were left out of the dependent variable analysis. The direct effect and simple correction coefficient are used to estimate the residual effect, as shown below:

$I = P^2x_4 + P^2_{14} + P^2_{24} + P^2_{34} + 2P_{14}r_{12}P_{24} + 2P_{14}r_{13}P_{34} + 2P_{24}r_{22}P_{34}$

DISCUSSION
Prior to initiating an efficient and successful breeding program, it is crucial to identify superior parents that will reliably transmit desirable traits to their offspring. This step is fundamental for ensuring that the various qualities of interest are inherited in a predictable manner (Dhillon and Singh, 1979). Superior F1 hybrids or segregants are not always produced by parents that exhibit high mean performance for yield and other qualities. Therefore, selecting parents based solely on their individual performance might not always result in optimal hybrid outcomes.

Challenges in handling multiple crosses
Given the vast number of potential crosses that can arise from a diverse set of parents, it becomes impractical to analyze and manage all possible combinations. To address this, it is essential to strategically select a small number of parents that possess high genetic potential aligned with specific breeding objectives. This targeted approach helps in managing resources efficiently and focusing on crosses that are most likely to yield beneficial results.

In plant breeding, the concept of combining ability has become a vital tool for selecting appropriate parents and specific crosses for further exploitation. Combining ability refers to the ability of a parent to contribute favorable alleles to its progeny, thereby enhancing desired traits. There are two main types of gene effects that are crucial in this context:

- Measures the additive effects of genes and indicates how well a parent can contribute to the performance of its progeny. Parents with high GCA are typically good general contributors to the traits of interest.
- **Specific Combining Ability (SCA):** Measures non-additive gene effects, such as dominance and epistasis, which influence the performance of specific crosses. SCA helps in identifying particular crosses that exhibit superior performance due to interactions between specific alleles.

Understanding these gene effects allows breeders to tailor their strategies more effectively. By leveraging information on the type of gene action present in a population, breeders can design breeding plans that maximize the potential benefits of both additive and non-additive genetic effects.

One of the widely used methods for assessing combining ability is the Line × Tester analysis (Kempthorne, 1957). This approach involves crossing a set of inbred lines (lines) with a set of testers to evaluate their combining abilities. The Line × Tester design is particularly useful for:

- **Germplasm screening:** Identifying promising germplasm and valuable donor parents that can be used in breeding programs.

- **Evaluating crosses:** Determining which crosses have high potential for desirable traits, such as seed yield or disease resistance.

Application in current study
The current study utilizes the Line × Tester design to assess the combining ability of various parents and crosses with respect to seed yield per plant and its constituent parts. This design helps in:

- **Identifying effective parents:** Determining which parental lines have high general combining ability for desirable traits.
- **Selecting promising crosses:** Finding specific crosses that exhibit high specific combining ability, indicating potential for superior performance.

The following sections of the study provide a comprehensive analysis of the findings, focusing on the genetic potential of different parents and the performance of various crosses. This detailed discussion helps in understanding the effectiveness of the selected breeding strategies and the potential for achieving the breeding objectives.

Heritability and Genetic Advance
Correlation Coefficients and Path analysis
Heritability and Genetic advance
Heritability and genetic advance are crucial metrics in plant breeding that help determine the potential for improving traits through selection.

The estimation of heritability for specific traits is important for identifying which traits are more likely to respond to selection. High heritability indicates that a significant proportion of the variation in a trait is due to genetic differences rather than environmental factors, making the trait a good candidate for selection. Ravali et al. (1952) proposed that heritability estimates, in conjunction with the Genotypic Coefficient of Variation (GCV), are valuable for predicting genetic gains and making effective selections.

In this context, traits such as days to 50% blooming, test weight, days to maturity, number of secondary branches, plant height, number of siliquae per plant, yield per plant, siliquae length, biological yield, number of primary branches, harvest index, and days to first flowering have shown high heritability. This suggests that these traits are strongly influenced by genetic factors, as supported by studies from Singh et al. (2011) and Tiwari et al. (2017).

Genetic advance refers to the expected improvement in a trait under selection. The highest genetic advance has been observed for traits such as test weight, number of primary branches, number of secondary branches, days to 50% flowering, days to maturity, days to first flowering, siliquae length, biological yield, yield per plant, plant height, harvest index, and siliquae length. This finding aligns with the results of Acharya and Pati (2008), indicating that these traits are likely to show substantial improvement through selective breeding.

Overall, focusing on traits with high heritability and genetic advance can enhance the effectiveness of breeding programs and lead to significant improvements in crop performance.

Correlation
In plant breeding, understanding correlations between traits is essential for improving specific characteristics, especially when direct selection for certain traits is challenging. Correlation analysis helps breeders make informed decisions by revealing relationships between traits and guiding indirect selection methods. This approach provides valuable insights into how traits are related and helps in designing more efficient breeding programs.

Correlations can be categorized into two main types: genetic and phenotypic.
1. **Genetic correlation:** Genetic correlation measures the degree to which two traits share a common genetic basis. It reflects the relationship between

traits that arise from their shared genetic factors, such as linkage or pleiotropy. A high genetic correlation indicates that selecting for one trait may simultaneously improve another due to their underlying genetic linkage. For example, if plant height and yield are genetically correlated, selecting plants with greater height might also enhance yield. Genetic correlation is crucial for understanding the genetic relationships between traits and making decisions about which traits to select together.

2. **Phenotypic correlation:** Phenotypic correlation reflects the relationship between traits as observed in the actual phenotypes of plants. It includes both genetic and environmental influences. This type of correlation can be influenced by factors such as environmental conditions, measurement errors, and interactions between traits. Phenotypic correlation provides practical information about how traits are related in real-world conditions and can guide breeders in selecting traits that are easier to measure and assess.

By analyzing both genetic and phenotypic correlations, breeders can design selection strategies that maximize improvements across multiple traits. For example, if a breeder wants to enhance yield, they may look for traits that are positively correlated with yield and select for those traits, even if direct selection for yield itself is difficult. Understanding these correlations helps in developing breeding programs that efficiently target desired outcomes while managing the complexities of trait interactions.

Path analysis
Simple correlation measures the bilateral relationships between two variables, providing insights into how they are related. However, these correlations often do not fully capture the complexity of relationships among multiple variables. To enhance understanding and manage these relationships more effectively, path analysis techniques are employed.

Path analysis allows for a more detailed examination of the direct and indirect effects of one variable on another, revealing the underlying structure of relationships among variables. For instance, at the phenotypic level, the harvest index exhibited the largest path coefficient, indicating a strong direct positive effect on seed yield per plant. This suggests that improvements in the harvest index can lead to higher seed yields. Conversely, the test weight had the lowest path coefficient, reflecting a weaker direct effect on seed yield per plant. This finding aligns with similar results reported by Ray et al. (2014), who observed a similar pattern in their study.

At the genotypic level, path analysis revealed that days to first flowering had the lowest path coefficient, while the harvest index showed the greatest direct positive impact on seed yield per plant. This indicates that genetic variations affecting the harvest index have a significant influence on seed yield. These results are consistent with findings by Awasthi et al. (2020), who also identified the harvest index as having a major direct effect on seed yield.

CONCLUSION
Several findings emerge from the path coefficient analysis of the different variables that influence the amount of seed produced by each plant. Positive values can be shown in traits including test weight, biological yield, harvest index, plant height, number of siliquae per plant, length of siliquae, number of primary branches, and secondary branches. This suggests that a larger seed output per plant is linked to increases in these features. Days to 50% blooming, days to maturity, and days to first flowering, on the other hand, show negative significant values, indicating that longer times for these phases are associated with decreased seed output.

These tendencies at the phenotypic level agree with the findings at the genotypic level. Days to flowering and maturity continue to have a negative impact, but the positive contributions of primary branches, secondary branches, plant height, number of siliquae per plant, siliquae length, test weight, biological yield, and harvest index do not.

In terms of inheritance, compared to other features, plant height has the least heritable component, as indicated by its lowest significant value. On the other hand, the largest genetic advance value is seen in the number of siliquae per plant, indicating the greatest possibility for development through breeding. However, test weight has the lowest genetic progress value, meaning selective breeding is less likely to improve it. These results are essential for creating successful breeding plans to maximise seed.

Abbreviations used

r	=	number of replications
T	=	total number of treatments
l	=	number of lines
t	=	number of testers
$\sigma^2 e$	=	variance due to error
Cov.HS	=	Covariance between half-sibs
Cov.FS	=	Covariance between Full-sibs
Yij	=	Phenotypicobservationin the ith treatment of jth replication;
μ	=	Overall mean;
ti	=	Effect of the ith treatment;
rj	=	Effect of jth replication;
ei	=	Random error associated with ith genotype and jthreplication;
M_l	=	Mean squares due to lines
M_t	=	Mean squares due to testers
M_{lt}	=	Mean squares due to lines x testers interaction
M_e	=	Mean squares due to error

$\sigma^2 g(testers) = Cov. H.S. (testers)$

σ^2g(lines) = Cov. H.S. (lines)

gca variance (σ^2g) = Cov. H.S. (average)

sca variance (σ^2s) = $\dfrac{M_{lt} - M_e}{r}$

σ^2_{sca} = Estimated variance due to sca

σ^2_{gca} = Estimated variance due to gca

l = Lines

t = Testers

lt = Line * tester interaction

F = Inbreeding co-efficient

k = Selection differential

σ_p = Phenotypic standard deviation

H = Heritability

rxy (g) = Genotypic correlation coefficient between x and y

rxy (p) = Phenotypic correlation coefficient between x and y

Covxy (g) = Genotypic covariance between x and y

Covxy (p) = Phenotypic covariance between x and y

Var x (g) = Genotypic variance of x

Var x (p) = Phenotypic variance of x

Var y (g) = Genotypic variance of y

Var y (p) = Phenotypic variance of y

REFRENCES

1. Acharya N N and Pati P. Gentic variability, correlation and path analysis in mustard (*Brassica napus* L.) *Environment and Ecology*, 2008; 26: 2165-2168.
2. Arunachalam V. Genetic distance in plant breeding. *Indian Journal Genetics, 1981;* 41: 226 236.
3. Awasthi D, Tiwari V K and Kandalkar V S. Studies of correlation and path analysis in germplasm of Indian mustard (*Brassica juncea*). *International Journal of Plant Sciences, 2020;* 15(2): 101-106.
4. Burton G W and Devane E W. Estabilishing heritability in tall fescue *(Festuca arundinaceae)* from replicated clonal material. *Journal of Agronomy*, 1953; 45: 478-481.
5. Dewey D R and Lu K H. A correlation and path *c*oefficient analysis of components of crested wheat grass seed production. *Argonomy Journal, 1959;* 51: 515-518.
6. Dhillon B S and Singh J. Evolution of factorial partial diallel crosses. *Crop Sciences,* 1979; 19(2): 192-195.
7. Kempthorne O. An introduction to genetic statistics. John Wiley and sons. Incharge New York, 1957; 458-471.
8. Kempthorne O. An introduction to genetic statistics. John Wiley and sons. Incharge New York, 1957; 458-471.
9. Panse V G and Sukhatme P V. Statistical methods for Agricultural workers. ICAR, New Delhi, 1967; 2, 9: 361.
10. Patra T, Maiti S and Mitra B. Variability, correlation and path analysis of the yield attributing characters of mustard (*Brassica spp.*). *Research On Crops, 2006;* 7(1): 191-193.
11. Prakash S, Kiriti P B, Bhat S R, Quiros C F and Chopra V L. Brassica and its close alies: Cytogenetics and Evolution. *Plant Breeding Reviews, 2012;* 31: 21-187.
12. Ravali B, Reddy K R, Saidaiah P and Shivraj N. Variability, Heritability and Genetic Advance in Brinjal (*Solanum melongena* L.). *International Journal Current Microbiology Applied Science, 2017;* 6(6): 42-47.
13. Ray K, Pal A K, Banerjee H and Phonglosa A. Correlation and Path Analysis studies for growth and yield contributing traits in Indian mustard (*Brassica juncea*). *International Journal of Bio-resource and Stress Management*, 2014; 5(2): 200-206.
14. Sabaghnia N, Dehghani H, Alizadeh B and Mohghaddam M. Interrelationship between seed yield and 20 related traits of 49 canola (*Brassica napus* L.) genotypes in non-stressed and water-stressed environments. *Spanish Journal Agriculture Research,* 8: 356-370.
15. Singh M, Tomar A, Mishra C N and Srivastava S B L. Studies on genetic components for seed yield and its contributing traits in Indian mustard [*Brassica juncea* (L.) Czern & Coss]. *Journal of Oilseed Brassica, 2011;* 2(2): 83-86.
16. Tiwari V K, Tomar S S and Awasthi D and Gupta J C. Morphology parameters in breeding for higher yield in Indian mustard (*Brassica juncea* L.Czeren & Coss). 2ⁿᵈ National Brassica Conference on Brassicas for addressing edible oil and nutritional security, held at *Punjab Agricultural University Ludhiana,* 2014; *40:* 14-16.
17. Tomar J, Tomar S S, Singh R and Vivek. Effect of imazethapyr on blackgram and residual effect on wheat and mustard crops. *In:Extended Summary of Biennial Conference of Indian Society of Weed Science, 2015;* 15-17.
18. Verma R R, Combining Ability Anaysis for yield and its Components through Diallel Crosses in Indica Coiza [*Brassica juncea (L.)Czern and Coss.*]. *Indian Journal Agricultural Research, 2000;* 34(2): 91–96.