

Salient study on genetic architecture through variability and genetic advance in linseed (*Linum usitatissimum*L.)

Kailash Ram

Department of Ag. Botany, Government Degree College, Jakhini, Varanasi (UP) India

Abstract

Linseed (*Linum usitatissimum* L.) is a significant oilseed crop, and its improvement can be achieved through genetic selection. This study examines the genetic structure of linseed by assessing genetic variability, heritability, and genetic advancement across various linseed genotypes. The research discovered substantial diversity across all variables which provides strong evidence for selection possibilities. A higher phenotypic coefficient of variation (PCV) compared to the genotypic coefficient of variation (GCV) indicates that environmental factors shape how traits develop while some traits showed no response to environmental changes. The essential yield components which include the number of capsules per plant and 1000-seed weight show high heritability together with significant genetic progress because of dominant additive gene effects. The presence of non-additive gene effects explains why traits show limited genetic progress despite having high heritability. The results show that using these selection criteria will lead to significant yield increases which enable the development of better linseed varieties.

Keywords: Oilseed Crop, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), *Linum Usitatissimum*, Limited Genetic Progress etc.

I. Introduction

Context and Significance of Linseed

Linseed (*Linum usitatissimum* L.), commonly referred to as flax, is among the most ancient cultivated crops, esteemed for its oil-laden seeds and superior fabric. The presence of alpha-linolenic acid (omega-3 fatty acid) and lignans and dietary fiber makes this plant economically and nutritionally important [1]. In India, linseed cultivation occurs across all agro-climatic zones with farmers cultivating it on less productive areas. The crop has not reached yield results that match other oilseeds because its genetic progress and breeding methods face significant limitations. The process of increasing linseed yield requires scientists to establish complete genetic knowledge of the plant which exists between different genotypes in the population.

Concept of Genetic Variability in Agricultural Enhancement

All crop development programs depend on genetic variation because it provides essential genetic materials needed for their breeding selection work [2]. The selection of superior linseed lines depends on the genetic diversity which exists for agronomic and yield-related traits within the species. Multiple genes control quantitative traits which include seed yield and plant height and capsule count per plant while environmental factors also influence these traits [2]. Therefore, researchers must assess both phenotypic and genotypic differences to identify which traits are passed down through heredity and which traits result from environmental factors. Researchers use the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) as standard tools to assess variability and demonstrate how traits are passed down through generations.

The Significance of Heritability and Genetic Progress

The term variability describes the genetic differences which exist between different genotypes while heritability together with genetic progress shows how traits will be passed down through generations and their expected improvements through artificial selection. Breeders use heritability measurement to calculate selection success because it shows how much genetic factors contribute to total variance [3]. Genetic advancement needs to be assessed together with heredity because it helps researchers identify the specific patterns through which genes operate. The combined presence of high heritability and important genetic progress shows that additive gene effects control the trait which improves selection success. Breeding strategies need to change for traits which demonstrate high heritability together with low genetic gain because these traits show evidence of non-additive gene effects.

Importance of Investigating Genetic Architecture in Linseed

The genetic structure of linseed can be understood through its heritable traits which display different degrees of variability. The studies will help identify key characteristics which significantly boost crop yield and can be improved through controlled selection. The research enables researchers to choose appropriate breeding methods which include pure line selection and hybridization and population enhancement [4]. The need to increase linseed crop production has become crucial because of changing weather patterns and rising demand for oilseed crops. The research requires complete assessments of genetic diversity and genetic elements to achieve permanent genetic improvements in linseed.

II. Literature Review

Current investigations conducted at this site have produced critical findings about genetic diversity and inheritance patterns and genetic progress in linseed (*Linum usitatissimum* L.) which scientists utilize for agricultural improvements. *Kumar et al. (2019)* [5] in the Journal of Pharmacognosy and Phytochemistry documented significant heterogeneity across linseed genotypes regarding parameters including plant height, branch count, capsules per plant, and seed output. The study results showed heritability estimates for 1000-seed weight and capsule count per plant that reached statistical significance while the researchers found high genetic progress rates for seed production and biological yield which demonstrated that additive gene effects dominate and direct selection methods work effectively.

Banjare et al. (2019) [6] in the Journal of Pharmacognosy and Phytochemistry studied yellow-seeded linseed genotypes and found that both genotypic and phenotypic coefficients of variation showed high values for the number of capsules per plant and seed yield. They also indicated significant heritability for days to blooming and plant height, underscoring considerable genetic diversity and its use in selection strategies.

Singh et al. (2019) [7] in the Journal of Pharmacognosy and Phytochemistry (Special Issue) showed that plant height, seed yield, and 1000-seed weight showed both significant heritability and considerable genetic improvement which made them suitable for breeding through simple selection methods. The same publication presented data from *Paul et al. (2020)* [8] which showed that seed yield and branch count exhibited high PCV and GCV values because the genotypes showed extensive genetic diversity which breeders could use for genetic improvement.

Kasana et al. (2019) [9] performed their research through the International Journal of Agricultural Invention which demonstrated that their analysis of mean performance with variability assessment showed better genotypes, which proved that superior breeding lines should be chosen for research projects. The International Journal of Chemical Studies published *Abate et al. (2020)* [10] research which showed that yield components and oil quality traits have high heritability and genetic advancement rates because these traits arise from additive gene action that makes them possible to enhance through selection. Researchers conducted studies from 2019 to 2020 which proved that linseed maintains high genetic diversity. The integrated evaluation of heritability and genetic advancement is essential for pinpointing features suitable for selection and enhancing yield potential.

III. Materials and Methods

The researchers conducted their research about genetic diversity and heritable traits and genetic improvement in linseed (*Linum usitatissimum* L.) by using multiple genotypes which they collected from different agricultural climate zones [11]. The research used improved varieties together with breeding lines and local landrace varieties for assessment during the rabi season in field conditions. The researchers used a randomized block design (RBD) with three replications to conduct the experiment which helped them minimize environmental differences while obtaining statistical results. The research team established identical farming plots for each genotype which they cultivated according to specific planting distances while following agricultural practices throughout the crop development stage.

The research team collected data from randomly chosen plants of each genotype which included essential quantitative traits that measured days until 50% flowering and days until maturity and plant height (cm) and primary branch count per plant and capsule count per plant and seed count per capsule and 1000-seed weight (g) and seed yield per plant (g). The breeding strategies selected these characteristics because they directly affect yield and their breeding value. The research team used standard protocols for documenting observations which helped them achieve precise results while maintaining observation consistency. The researchers used statistical methods to analyze the collected data which resulted in determining the study's variability parameters. The researchers used analysis of variance (ANOVA) to determine whether the differences between genotypes reached a significant level [12]. The researchers calculated genotypic and phenotypic variances by using mean square values which they obtained from ANOVA. The researchers calculated phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) based on these estimations to measure how much all populations differed from each other.

Heritability in the broad sense was quantified as the ratio of genotypic variance to phenotypic variance which scientists expressed as a percentage [13]. The genetic progress was computed using selection intensity and phenotypic standard deviation and heritability estimations which scientists expressed as a percentage of the mean to enable comparison between different traits. The metrics showed how gene action operated and how selection methods achieved their desired outcomes.

The researchers used correlation analysis to study the relationships between different traits. Using path coefficient analysis, the researchers then broke down the correlation coefficients into direct and indirect effects. This helped them identify the main traits that affected seed production.

S. No.	Trait	Symbol	Measurement Method	Unit
1	Days to 50% flowering	DFF	Number of days from sowing to when 50% plants flowered	Days
2	Days to maturity	DM	Number of days from sowing to physiological maturity	Days
3	Plant height	PH	Measured from base to tip of main stem at maturity	cm
4	Number of primary branches per plant	PB	Count of primary branches on selected plants	Number
5	Number of capsules per plant	CP	Total capsules counted per plant at harvest	Number
6	Number of seeds per capsule	SC	Average seeds counted from randomly selected capsules	Number
7	1000-seed weight	TSW	Weight of 1000 randomly selected seeds	g
8	Seed yield per plant	SY	Weight of seeds obtained from individual plant	g

Table 1: List of Traits Recorded and Their Measurement Methods in Linseed, Source: Author Findings

S. No.	Parameter	Formula	Description
1	Genotypic variance	$\sigma^2g = (MSg - MSe) / r$	Variation due to genetic factors
2	Phenotypic variance	$\sigma^2p = \sigma^2g + \sigma^2e$	Total observed variation
3	Genotypic coefficient of variation (GCV)	$(\sqrt{\sigma^2g} / \text{Mean}) \times 100$	Genetic variability
4	Phenotypic coefficient of variation (PCV)	$(\sqrt{\sigma^2p} / \text{Mean}) \times 100$	Total variability
5	Heritability (broad sense)	$h^2 = (\sigma^2g / \sigma^2p) \times 100$	Proportion of genetic variation
6	Genetic advance (GA)	$GA = k \times \sigma p \times h^2$	Expected improvement under selection
7	Genetic advance as % of mean	$(GA / \text{Mean}) \times 100$	Relative gain from selection

Table 2: Statistical Parameters Used for Genetic Analysis, Source: Author Findings

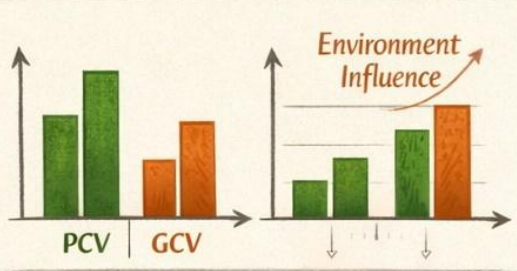
IV. Findings and Analysis

Degree of Genetic Variation

The analysis of variance showed that there were significant differences between linseed genotypes for all factors that were looked at. The research showed that the experimental material contained multiple genetic variations. The researchers used the different traits of crop varieties to identify the best breeding candidates. The phenotypic coefficient of variation (PCV) estimates was higher than the genotypic coefficient of variation (GCV) estimates for all traits. The environmental elements caused the traits to develop in specific ways. For the traits of 1000-seed weight and plant height, the PCV and GCV values showed only slight differences. The findings show that genetic factors determine these traits while environmental elements have no effect. The PCV and GCV results showed high values for both the number of capsules per plant and the number of seeds produced per plant. The selection process became easier because the traits exhibited high levels of diversity. The results demonstrate that the germplasm contains sufficient genetic variation which breeders can use to enhance growth and related traits.

Degree of Genetic Variation in Linseed

Significant differences among linseed genotypes were observed for all traits studied, indicating substantial genetic variability.



Phenotypic Coefficient (PCV) > Genotypic Coefficient (GCV)

Environmental vs. Genetic Variation



1000-Seed Weight
& Plant Height

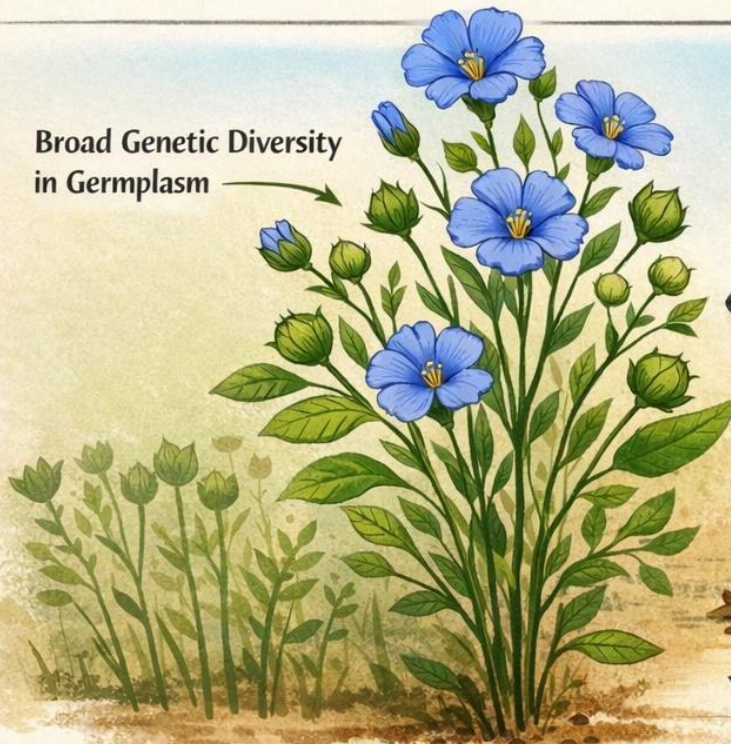
Low Disparity,
Mainly Genetic Control



Capsules Per Plant
& Seeds Per Plant

High Variation,
High Selection Potential

Broad Genetic Diversity
in Germplasm



Breeding & Selection



Yield Improvement

Significant Potential for Enhancing Yield & Traits

Estimates of Heritability and Their Importance

The heritability estimates for different traits showed different levels of genetic control through their broad heritability measurement. The heritability of plant height and 1000-seed weight and number of capsules per plant showed that these traits have a genetic basis which accounts for most of their observed variations. The observed characteristics exhibited superior selection reliability, as evidenced by their consistent presence across diverse testing conditions. Both the number of branches per plant and the number of seeds per capsule displayed moderate heritability, a reflection of the influence of both genetic and environmental determinants on their expression. Research showed that seed yield per plant has low heritability because this trait depends on multiple genetic factors and environmental conditions. The results demonstrate that heritability serves as an important selection criterion but needs to be evaluated together with other genetic traits to enable proper selection.

Genetic Progress and Characteristics of Gene Function

The genetic progress evaluation provides a better practical method to assess selection-based improvements than other methods. The study identified a substantial genetic advancement which represented a percentage of the average for three traits which included the number of capsules per plant and seed yield per plant and the number of major branches. The combination of high heritability with significant genetic advance shows that additive gene effects control the traits which can be improved through basic selection methods. The heritability of flowering and maturation time was moderate to high, yet genetic progress was limited, suggesting that non-additive gene interactions, including dominance and epistasis, govern these traits. Consequently, direct selection is ineffective for certain characteristics, necessitating alternative breeding strategies, such as hybridization and recurrent selection.

Correlation of Characteristics and Yield Factors

The correlation research found significant positive links between seed yield per plant and its various component traits which included the total number of capsules per plant and the total number of seeds in each capsule and the 1000 seed weight. The research results indicate that increasing these features will result in higher seed production. The path coefficient analysis showed that the number of capsules per plant had the strongest direct positive effect on seed yield while the number of seeds per capsule and seed weight followed in strength. The research results prove that these traits function as fundamental selection factors which linseed breeders must consider during their breeding programs. The study found that plant height and branch quantity together with additional traits created indirect effects which led to yield changes through their impact on main yield components. The selection of these interrelated traits together with their concurrent selection will produce better results for overall production efficiency.

Impact of Environment on Trait Stability

The environmental effect on trait development shows through the different levels of PCV and GCV measurement between various traits. Traits which display minimal differences between their PCV and GCV values show 1000-seed weight as a stable trait which does not change with environmental conditions. The seed yield per plant characteristic exhibited more environmental effects through their measurement difference between PCV and GCV. The testing across multiple environments serves as a necessary process to discover genotypes which remain constant in performance during different environmental conditions. The assessment of linseed genotype adaptability requires the study of genotype-environment interaction effects. Breeders need to include environmental factors during their process of identifying suitable genotypes which will maintain performance through different agricultural climate conditions.

Consequences for Linseed Enhancement

The study results proved that three specific plant features which include number of capsules per plant and seeds contained in each capsule together with 1000-seed weight, function as critical determinants of seed yield, while displaying genetic characteristics that researchers can use for selection purposes. The existing characteristics show both substantial variation and heritability, which enables genetic advancement, thus demonstrating the potential for successful selection from first generation subjects. For traits that show non-additive gene behavior, breeding methods should include both hybridization and population improvement techniques. The implementation of these findings in breeding programs will lead to the development of linseed varieties that produce high yields with consistent performance. The breeding process gains substantial benefits from using modern molecular techniques which work together with traditional selection methods to enhance both breeding efficiency and accuracy.

Consequences for Breeding

The assessment of genetic variation together with heritable traits and genetic progress in linseed establishes a solid foundation for developing successful breeding programs. Additive gene action mostly

determines the traits which include capsule count per plant and seeds counted per capsule together with 1000-seed weight because these traits show high heritability while presenting substantial genetic advancements. The selection of these traits during the early generations will help yield improvement programs because they serve as essential selection points for plant development.

The traits which show moderate to high heritability together with minor genetic advancement demonstrate that non-additive genetic factors control the days required to reach flowering and maturity. The genetic potential of specific traits needs to be developed through hybridization and heterosis breeding or recurrent selection because conventional selection methods fail to work with these particular traits.

The observation of substantial genetic variation among different genotypes provides researchers with the opportunity to pick the best parents for breeding programs. The introduction of different genotypes will create a broader genetic base which will result in the development of transgressive segregants that perform better than both parent strains.

The combination of traditional breeding methods together with molecular techniques such as marker-assisted selection will lead to quicker identification of advantageous genotypes. The selection process together with hybridization methods should follow a planned process which uses genetic information to create high-yield linseed cultivars with stable performance.

V. Conclusion

The research demonstrates how genetic diversity and heritability together with genetic progress contribute to understanding the genetic makeup of linseed (*Linum usitatissimum* L.) The research shows that different genotypes lead to substantial genetic progress through selection breeding methods. The number of capsules per plant and 1000-seed weight exhibit strong heritability and high genetic advancement because their traits depend mostly on additive gene effects which breeders can develop through basic selection methods. Breeding programs need to implement hybridization and population enhancement methods to develop traits which depend on non-additive gene effects. The testing process must take place across multiple locations because environmental factors affect specific traits which need to assess the stability and adaptability of selected genotypes. Traditional breeding methods combined with modern genetic technologies will enhance the success of linseed breeding programs which aim to create high-yielding climate-resilient cultivars that suit different agro-ecological zones.

Reference

- [1]. Shim, Y. Y., Gui, B., Arnison, P. G., Wang, Y., & Reaney, M. J. (2014). Flaxseed (*Linum usitatissimum* L.) bioactive compounds and peptide nomenclature: A review. *Trends in food science & technology*, 38(1), 5-20.
- [2]. Kaur, V., Kumar, S., Yadav, R., Wankhede, D. P., Aravind, J., Radhamani, J., ... & Kumar, A. (2018). Analysis of genetic diversity in Indian and exotic linseed germplasm and identification of trait specific superior accessions. *Journal of Environmental Biology*, 39(5), 702-709.
- [3]. Feldman, M. W., & Lewontin, R. C. (1975). The Heritability Hang-Up: The role of variance analysis in human genetics is discussed. *Science*, 190(4220), 1163-1168.
- [4]. Paul, S., Bhateria, S., & Kumari, A. (2015). Genetic variability and interrelationships of seed yield and yield components in linseed (*Linum usitatissimum* L.). *SABRAO Journal of Breeding & Genetics*, 47(4).
- [5]. Ahmed, E. (2017). Genetic studies of yield and yield component of Linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*, 1, 872-875.
- [6]. Kumar, S., Sharma, A., Choudhary, A., Purushottam, M., & Chauhan, M. P. (2018). Applying correlation and path coefficient to study genetic variability in linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(2), 2593-2595.
- [7]. Ranjith, P., Ghorade, R. B., Kalpande, V. V., & Dange, A. M. (2017). Genetic variability, heritability and genetic advance for grain yield and yield components in sorghum. *International Journal of Farm Sciences*, 7(1), 90-93.
- [8]. Ahmed, E. (2017). Genetic studies of yield and yield component of Linseed (*Linum usitatissimum* L.). *Journal of Pharmacognosy and Phytochemistry*, 1, 872-875.
- [9]. Pandey, A., Mishra, S. P., & Yadav, S. K. (2015). ESTIMATES OF VARIABILITY PARAMETERS FOR YIELD AND ITS COMPONENTS IN LINSEED (*LINUM USITATISSIMUM* L.). *Journal of Plant Development Sciences* Vol, 7(2), 177-179.
- [10]. Tyagi, A. K., Sharma, M. K., Surya, M. S., Kerkhi, S. A., & Chand, P. (2014). Estimates of genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) germplasm. *Progressive Agriculture*, 14(1), 37-48.
- [11]. Tyagi, A. K., Sharma, M. K., Surya, M. S., Kerkhi, S. A., & Chand, P. (2014). Estimates of genetic variability, heritability and genetic advance in linseed (*Linum usitatissimum* L.) germplasm. *Progressive Agriculture*, 14(1), 37-48.
- [12]. van Eeuwijk, F. A., Malosetti, M., Yin, X., Struik, P. C., & Stam, P. (2005). Statistical models for genotype by environment data: from conventional ANOVA models to eco-physiological QTL models. *Australian Journal of Agricultural Research*, 56(9), 883-894.
- [13]. Al-Tabbal, J. A., & Al-Fraihat, A. H. (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. *Journal of Agricultural Science*, 4(3), 193.