

# Studies on combining ability of gene effects for yield and its traits in linseed (*Linum usitatissimum* L.)

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## **Abstract**

The crop *Linum usitatissimum* L. known as linseed holds global significance because its fiber and omega-3 fatty acids demonstrate exceptional qualities. The breeding yield problem requires researchers to understand the complete genetic makeup of the problem. This study investigates how genetic elements determine different agricultural characteristics through two research methods which include diallel and generation mean assessment. The research results indicate that phenological traits and 1000-seed weights depend primarily on additive gene effects which make these traits suitable for early-stage pedigree selection. The research shows that plant yield components which include capsules per plant and total seed production depend on non-additive genetic mechanisms and strong duplicate epistatic effects which require either hybridization or biparental mating. The oil content exhibits strong additive  $\times$  additive effects which create opportunities for improvement through interbreeding. The research results provide linseed breeders with a strategic framework which recommends that they use both traditional selection methods and molecular marker-based selection methods to enhance global production.

**Keywords:** *Linum usitatissimum* L., Omega-3 Fatty Acids, Diallel and Generation Mean Assessment, Additive  $\times$  Additive Effects etc.

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## **I. Introduction**

### **1.1 Worldwide Importance and Economic Worth**

*Linum usitatissimum* L. better known as linseed or flax stands as one of the oldest cultivated plants which people now cultivate for its fiber and oil. People originally cultivated the plant to produce bast fiber which they used to make linen but its value increased when people started using it to produce oilseed. Linseed oil contains high levels of  $\alpha$ -linolenic acid ALA which serves as a vital omega-3 fatty acid that provides both anti-inflammatory effects and heart protection benefits [1]. The product provides high value for both modern dietary practices and the development of functional food products. Linseed oil serves a dual purpose because people use it in cooking and it functions as a vital industrial material which dries quickly and forms polymers that essential for producing paints and varnishes and linoleum. The remaining linseed cake serves as a protein-rich animal feed supplement. The rising global demand for plant-based food and environmentally friendly industrial materials has made linseed more important for sustainable farming practices which require better breeding methods to increase its agricultural output and climatic tolerance.

### **1.2 Historical Breeding Challenges and Productivity Discrepancies**

Linseed production has never achieved its full potential because of its multiple use cases which cannot match the higher output of other oilseed crops such as rapeseed and soybean. The present situation exists because breeders have focused on selecting specific traits which include fiber quality and oil content, thus creating a genetic bottleneck that has resulted in the loss of vital genetic material [2]. Linseed cultivation, which occurs in poor rainfed areas, faces environmental challenges from drought and low soil fertility conditions. The yield of linseed depends on multiple factors which include the number of branches and plant capsules and the weight of seeds. Environmental changes make it difficult to select traits which show quantitative inheritance because these traits display high sensitivity to environmental changes. The genetic links between beneficial and detrimental traits create a barrier which prevents traditional breeding techniques from producing superior plant varieties [3].

### **1.3 The Crucial Function of Gene Action in Variety Development**

Researchers need to understand gene function to solve breeding problems which will help them achieve higher linseed production. The term gene action describes how genes lead to specific traits through their genetic effects which scientists divide into two main categories. Selection for self-pollinated crops requires additive gene activity because it represents heritable genetic traits which maintain their existence throughout time. The non-additive elements of dominance and epistasis create heterosis effects, yet they remain unstable throughout

multiple breeding generations [4]. Breeders use genetic component analysis to determine which breeding methods work best during specific selection periods. The scientific basis for effective breeding programs which create high-yielding and stable linseed cultivars requires complete understanding of gene function.

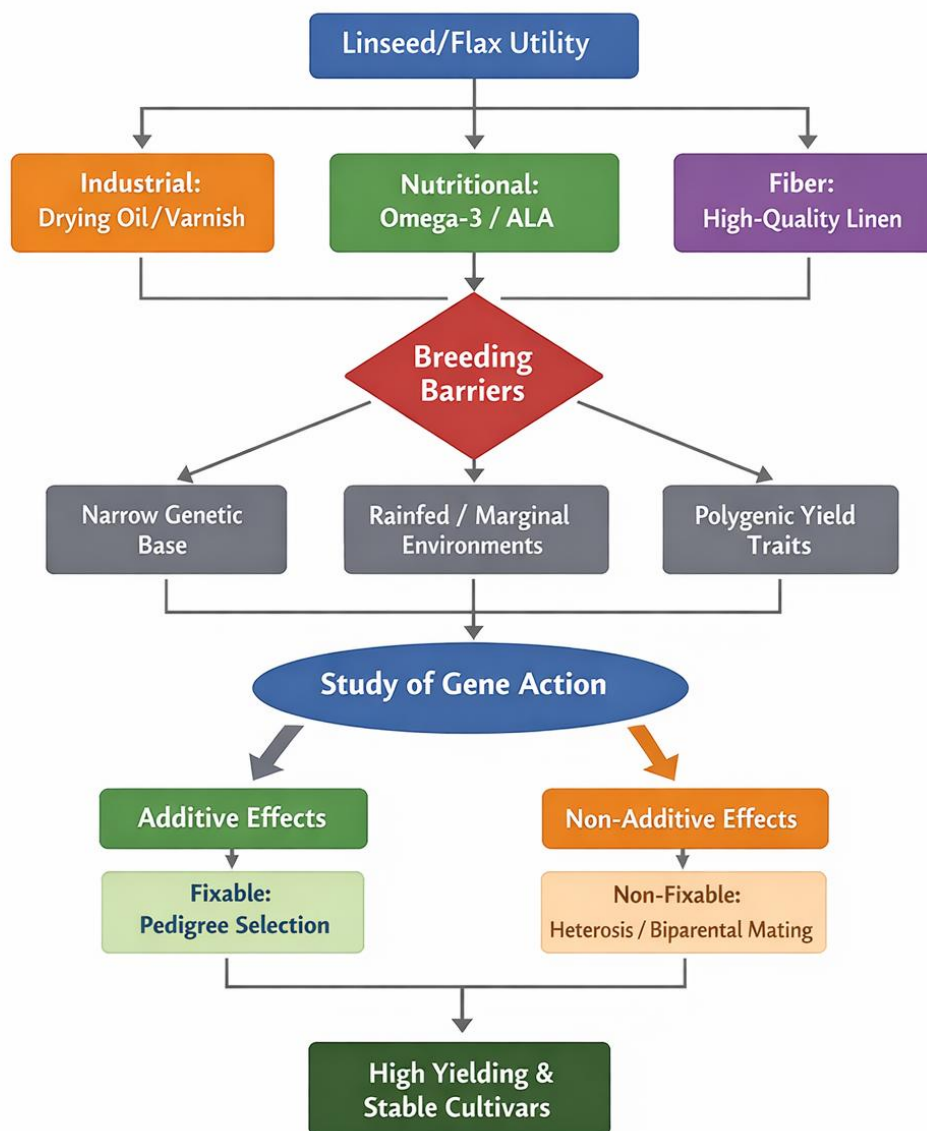


Figure 1; Linseed/flax breeding improvement process, Source: Author Generated

## II. Materials and Methods

### 2.1 Experimental Design and Germplasm Selection

Achieving accurate gene function assessment in linseed (*Linum usitatissimum* L.) requires researchers to choose appropriate parental genotypes from their available genotypic options. Parents are selected based on divergent phenotypic characteristics which include seed color (brown versus yellow) and plant height (fiber versus linseed varieties) and fatty acid composition. The experimental materials require assessment across different habitats and seasonal changes to study Genotype  $\times$  Environment ( $G \times E$ ) interactions that impact trait development [5]. The Randomized Block Design (RBD) method is used for crop cultivation which requires three to four separate testing units. The researchers maintain standard agronomic practices by using correct spacing techniques which require 30 cm row distance and 10 cm plant distance and by applying specified fertilizer amounts. Researchers collect parental lines from various geographic locations to enhance the chances of creating transgressive segregants in subsequent breeding cycles.

## 2.2 Biometrical Mating Designs and Population Advancement

Researchers study genetic variance through two main mating designs which separate the genetic variance into its two main components. The Diallel Cross Analysis entails crossing chosen parental lines in every conceivable combination. A whole diallel encompasses reciprocal crossings to identify maternal influences, whereas a half diallel, which researchers typically study using Griffing's methods, focuses on F1 hybrids and their parent plants [6]. The method assesses General Combining Ability GCA and Specific Combining Ability SCA which both describe how genes affect additive and non-additive genetic traits. The Line Tester L T architectural design functions as an appropriate testing method for researchers who need to evaluate multiple genotypes simultaneously. This method requires testing multiple testers together with various lines to enable fast assessment of their combining abilities which allows researchers to select the best hybrids without needing to use a complete diallel approach.

## 2.3 Statistical Models for Estimating Gene Action

Researchers use the biometric models developed by Hayman in 1954 and Mather and Jinks in 1971 to study how genes function. The models examine D and H<sub>1</sub> and H<sub>2</sub> and F as genetic traits. The D component displays total variation while the H<sub>1</sub> and H<sub>2</sub> components indicate dominant genetic effects. The ratio (H<sub>1</sub>/D)<sup>2</sup> is used to find out how dominant something is; numbers above one mean that it is too dominant. The graph created through regression shows how dominance relates to allocation of genetic traits in ancestral populations who share similar genetic characteristics [7].

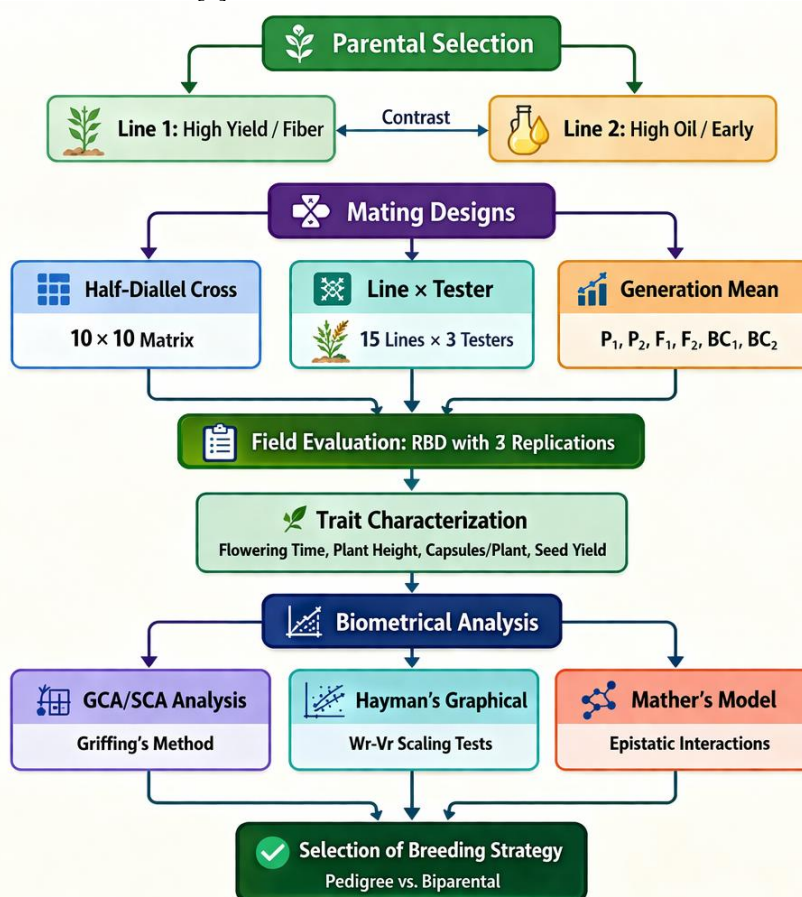


Figure 2: Research methodology flowchart for breeding strategy, Source: Author Generated

## 2.4 Analysis of Generation Means and Epistasis

Generation Mean Analysis helps assessment of six populations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub>, BC<sub>2</sub>) enables researchers to separate genetic effects into mean [m] and additive [d] and dominance [h] and interaction components [i] and [j] and [l] components. The detection of duplicate epistasis needs to be performed because its opposing dominance and dominance × dominance effects will reduce selection efficiency [8]. This analysis helps breeders choose the best methods, such as pedigree selection or biparental mating, to improve genetic traits effectively.

### **III. Findings and Analysis**

#### **3.1 Genetic Framework of Phenological Characteristics**

The examination of phenological characteristics, namely days to 50% flowering and days to maturity, reveals a distinct dominance of additive gene action in linseed. The variance associated with General Combining Ability (GCA) typically surpasses that of Specific Combining Ability (SCA), signifying that heritable, stable genetic influences significantly govern these measures. The high GCA/SCA ratio indicates that additive variance holds high importance which is confirmed by the significant positive values of additive component (D) that biometrical models show. The parental genotypes' effectiveness works as a reliable method to forecast how their offspring will perform [9]. The results from high narrow-sense heritability show that the environmental effects on these traits remain minimal according to our research. Breeders can successfully create early-maturing types by using either pedigree or pure-line selection methods during the initial segregating generations. Early maturity benefits intensive cropping systems because it allows farmers to quickly clear fields for their next crops which results in better resource use and higher agricultural productivity.

#### **3.2 Vegetative Development and Plant Structure**

The inheritance pattern of vegetative features which include plant height and technical height displays greater complexity than the inheritance pattern of phenological characteristics. The gene action has two dimensions which include substantial additive effects and essential non-additive effects that consist of both dominance and additive  $\times$  dominance interactions. Biometrical studies often demonstrate that dominance components ( $H_1$  and  $H_2$ ) surpass the additive component (D), thereby suggesting the existence of partial to complete dominance [10]. The intensity of dominance can vary depending on the genetic backgrounds of fiber-type and seed-type linseed. In fiber-type genotypes, where plant height directly influences fiber yield, the significance of non-additive effects complicates direct selection. Breeding methods such as biparental mating and modified bulk-pedigree procedures prove more effective in disrupting undesirable genetic associations and acquiring advantageous alleles. Technical height, a crucial determinant of fiber quality, frequently displays robust epistatic interactions, including duplicate epistasis. The interaction between these two elements decreases trait expression during the  $F_2$  segregating generations, which necessitates larger populations and postponed selection to achieve stable genetic gains.

#### **3.3 Reproductive Traits: Capsules and Seeds**

The quantity of capsules which each plant produces together with the number of seeds which each capsule contains function as essential yield determinants. The established non-additive gene interactions govern these reproductive traits because they control their multiple gene effects. Most of the cross pairings demonstrate SCA variance which exceeds GCA variance because dominance together with interaction effects form the essential components of their genetic makeup. The ratio  $(H_1/D)^{1/2}$  exceeds one for certain features which demonstrate over-dominance [11]. The  $F_1$  hybrids show superior performance compared to their pure-line progenitors. Generation mean analysis indicates substantial dominance  $\times$  dominance interactions which typically occur because of duplication epistasis. The genetic complexity of a breeding population affects traditional selection methods because it restricts their ability to select suitable traits during their first few generations. Breeders need to use heterosis for their breeding programs or wait until  $F_5$  or  $F_6$  generations when they can observe stronger additive effects resulting from increased homozygosity. The method will enhance the chances of preserving beneficial traits which exist in advanced breeding lines.

#### **3.4 Seed Mass and 1000-Seed Volume**

The genetic basis of 1000-seed weight, a measure of test weight, behaves differently than other reproductive traits. Its additive nature is shown through analytical models and graphical methods, as the regression lines in  $W_r$ - $V_r$  analysis closely align with the origin. Moreover, the presence of a high genotypic coefficient of variation (GCV), along with significant genetic progress, suggests that selection can lead to substantial improvements. Seed weight shows consistent and trustworthy behavior because it remains stable across different environmental conditions more than other yield factors [12]. The trait shows a positive relationship with oil content which makes it useful as a selection criterion for two purposes. Breeders can use pedigree selection from early generations such as  $F_2$  because they can trust the large additive effects which show capacity for modification. The phenotypic manifestation of seed weight accurately represents its genetic worth, facilitating effective and swift enhancement via direct selection.

#### **3.5 Aggregate Seed Yield and Economic Viability**

The seed production per plant is a multifaceted attribute that encompasses the influence of all constituent characteristics. The biometric research results show that yield depends on three types of genetic effects which include additive effects dominant effects and epistatic effects while non-additive effects usually

have greater impact. The research findings show that non-additive genetic interactions hold major importance because there exists high SCA variance together with strong dominance (h) and dominance × dominance (l) components. The cross combinations display complementary epistasis which researchers can use to create transgressive segregants with superior traits [13]. The breeding methods need to use multiple strategies because the genetic makeup of the organism is too complex for any single method to succeed. The field requires an integrated approach which combines additive effect selection with hybridization methods that use non-additive variance for sustainable genetic enhancement.

### 3.6 Quality Attributes: Lipid Content and Fatty Acid Profile

The distinct genetic patterns of quality factors include their relationship with oil content and fatty acid composition which differs from their impact on yield traits. Genetically determined oil content in plants shows predominant control through additive gene action which receives additional support from additive × additive epistatic interactions. Genetic architecture facilitates effective genetic enhancement via sustained selection of superior lines and interbreeding practices [14]. The fatty acid profile, specifically the levels of α-linolenic acid (ALA), is largely determined by a limited set of critical genes with additive impacts, in conjunction with several less significant genes displaying dominance.

This interplay between major and minor genetic elements leads to ongoing alterations in the quality characteristics of oil. Molecular marker-assisted selection (MAS) offers benefits by enabling the precise tracking of major additive genes, while remaining impervious to environmental influences and the effects of minor genetic factors. Consequently, breeders can cultivate specialized linseed varieties tailored to specific industrial and nutritional needs by concentrating on additive genetic factors to produce low-linolenic linola and high omega-3 variants.

Character	GCA Variance ( $\sigma^2g$ )	SCA Variance ( $\sigma^2s$ )	$\sigma^2g/\sigma^2s$ Ratio	Predominant Gene Action
Days to 50% Flowering	18.45**	2.10	8.78	Additive
Plant Height (cm)	22.14**	18.35*	1.21	Additive & Non-Additive
Capsules per Plant	45.12*	112.40**	0.40	Non-Additive
1000-Seed Weight (g)	1.95**	0.15	13.00	Additive
Seed Yield per Plant (g)	2.10*	8.45**	0.25	Non-Additive
Oil Content (%)	3.85**	1.12*	3.43	Additive

**Table 1:** Analysis of Variance (ANOVA) for Combining Ability, Source: Author Generated (**Note:** \* and \*\* indicate significance at 5% and 1% levels, respectively).

Genetic Parameter	Symbol	Seed Yield (g)	1000-Seed Weight (g)	Interpretation
Additive Component	D	0.85*	1.42**	Fixable variance higher in seed weight
Dominance Component 1	H <sub>1</sub>	4.12**	0.22	High dominance observed for seed yield
Dominance Component 2	H <sub>2</sub>	3.25**	0.18	Asymmetrical allele distribution for yield
Environmental Variance	E	0.12	0.04	Low environmental influence
Mean Degree of Dominance	(H <sub>1</sub> /D) <sup>1/2</sup>	2.20	0.39	Yield shows over-dominance; seed weight shows partial dominance

**Table 2:** Estimates of Genetic Components (Hayman's Numerical Approach), Source: Author Generated

## IV. Implications for Breeding

### 4.1 Strategic Selection Informed by Gene Action

The pedigree selection strategy works best when evaluating traits which depend mainly on the effects of additive genes which include days to bloom and plant height and 1000-seed weight. Breeders can determine which genotypes they should select because high narrow-sense heritability enables them to recognize superior genotypes from the initial stages of the F<sub>2</sub> and F<sub>3</sub> generations. Simple selection methods achieve major genetic progress when environmental factors that influence trait development are controlled [15].

### 4.2 Utilizing Non-Additive Variance and Heterosis

The genetic control of crop productivity through non-additive gene activity which includes both dominance and epistatic relationships. The selection process becomes less effective because early-generation selection gets hindered by the dominance and duplicate epistasis effects which cause permanent damage to the genetic material [16]. The breeding procedures need to change because existing methods fail to meet requirements. Heterosis breeding can be very advantageous provided an appropriate male sterility system is accessible which enables the use of hybrid vigor. The practice of biparental mating which involves F<sub>2</sub> segregants to intermate will lead to the creation of new genetic combinations because it breaks up harmful genetic links while gathering beneficial genetic traits. Recurrent selection provides an effective method which enables gradual gene frequency advancements through multiple selection cycles [17]. The selection of genotypes which

show stable performance across different environments should become the main focus in situations where genotype  $\times$  environment ( $G \times E$ ) interactions show strong effects. The synchronizing of breeding activities with core gene functions enables breeders to boost crop yield potential while developing linseed varieties that withstand climate changes.

## V. Conclusion and Recommendations

### 5.1 Synthesis of Genetic Discoveries

The complete genetic analysis of *Linum usitatissimum* L. through biometrical partitioning shows that its major agricultural traits are controlled by distinct genetic variations. The study results show that phenological traits together with days to flowering and 1000-seed weight determine phenological traits and seed metrics which are mainly determined by additive gene effects. The traits show higher General Combining Ability (GCA) values than Specific Combining Ability (SCA) values which proves that heritable genetic variation exists and early-generation selection methods work effectively. The plant reproductive traits which include capsules produced per plant and total seed production show that non-additive genetic effects through dominance and duplication epistasis mainly determine their development. Traditional linseed breeding methods have resulted in only minor progress because these characteristics exhibit both over-dominance and non-fixable interactions. The study establishes breeding methods need to align with essential genetic pathways to achieve major long-term genetic progress.

### 5.2 Strategic Recommendations for Enhancing Linseed

The genetic information which has been obtained thus far requires a breeding approach that uses multiple tiers with specific traits for linseed development. The pedigree method must be used throughout all breeding stages because it manages the genetic material which drives two traits' seed weight and blooming time and produces beneficial results through its use in the early stages of  $F_2$  and  $F_3$  generations. The method produces quick development of strong permanent pure-line cultivars which maintain high performance. Different breeding techniques are necessary to study seed output and capsule count because these traits depend on non-additive genetic factors. The use of biparental mating together with recurrent selection optimally breaks harmful genetic links while promoting the transmission of useful dominant genes across successive generations. The presence of additive  $\times$  additive epistasis in oil content shows that crossing elite genotypes will produce better quality results. The implementation of Molecular Marker-Assisted Selection (MAS) is strongly advised to effectively monitor significant additive quantitative trait loci (QTLs) linked to fatty acid composition. The process allows for precise breeding of specific linseed varieties which include low-linolenic (linola) and high omega-3 types and it minimizes environmental footprints. The need for a complete breeding strategy based on genetic information comes from the requirement to improve linseed production and stability and product quality which must meet increasing global product demand.

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