GENETIC VARIABILITY IN BOLD SEEDED LINSEED
(*Linum usitatissimum* L.)

M. Sc. (Ag.) Thesis

by

Jhanendra Kumar Patel

DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
INDIRA GANDHI KRISHI VISHWAVIDYALAYA
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Submitted to the
Indira Gandhi Krishi Vishwavidyalaya, Raipur

by

Jhanendra Kumar Patel

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CERTIFICATE – I

This is to certify that the thesis entitled **"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"** submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Jhanendra Kumar Patel** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma or has been published/ published part has fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by his.

Chairman

Date: 13-08-2020

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

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Member	(Dr. K. P. Verma)	
Member	(Dr. R. R. Saxena)	
Member	(Dr. Rajeev Shrivastav)	13/8/2020

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This is to certify that the thesis Viva-voce in respect of **Mr. Jhanendra Kumar Patel** student of **M.Sc. (Ag.)** has been conducted under the chairmanship of Head of the Department/Dean (in case of out campii) along with Advisory Committee on **07-09-2020**. The necessary corrections have also been made as per comments/suggestions made by the Advisory Committee and Head of the Department/Dean.

Date: 7.9.2020

Signature of Major Advisor

Name: Dr. S. S. Rao

CERTIFICATE II

This is to certify that the thesis entitled **"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"** submitted by **Jhanendra Kumar Patel** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur, in partial fulfilment of the requirements for the degree of **Master of Agriculture** in the **Department of Genetics and Plant Breeding** has been approved by the external evaluator and Student's Advisory Committee after oral examination, under the chairmanship of head of the Department.

Signature of Head of the Department

(Name: Dr. A K Sarawgi)

Date: 7.09.2020

Major Advisor ____________________ 7/9/2020

Faculty Dean ____________________

Approved/Not approved

Director of Instructions ____________________

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%	Percent
°C	Degree Celsius
Cm	Centimeter
d.f.	Degree of freedom
et al.	and others
G	Gram
Ha	Hectares
i.e.	that is
viz.	For example
M	Meter
Mm	Millimeter
*	Significance at 5%
**	Significance at 1%

LIST OF ABBREVIATIONS

ABBREVIATION	DESCRIPTION
Approx.	Approximately
S.N.	Serial number
CV	Coefficient of variation
C.D.	Critical difference
GA	Genetic Advance
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
No.	Number
SD	Standard deviation
$h^2_{(bs)}$	Heritability in broad sense
DUS	Distinctiveness, uniformity and stability

THESIS ABSTRACT

(a) Title of the thesis	:	"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"
(b)Full name of student	:	Jhanendra Kumar Patel
(c)Major subject	:	Genetics and Plant Breeding
(d)Name and Address of the major advisor	:	Dr. S. S. Rao, Principal Scientist (Genetics and Plant Breeding) and Dean, College of Agriculture, Raipur
e)Degree to be awarded	:	Master of science in Agriculture

13/8/2020

Signature of Major Advisor

jhanendra patel

Signature of the student

14.8.2020

Date 13.08.2020

Signature of the head of
the department

ABSTRACT

Linseed (*Linum usitatissimum* L.) is an annual self-pollinated crop with originating either in the Middle East or the Indian regions. The bold seeded linseed alone has never been exploited for yield improvement of crop and its oil yield potential. Hence, for the present investigation the different source for variability of bold seed character in germplasm is taken. Generally in linseed the comparing bold seeded with medium and small seeded, the advantage lies with better germination and seedling vigour giving robust plant growth which ultimately produces more branches and capsule and finally will produce more seed yield and seed oil content, respectively.

Keep in view the above mention points, the recent experiment was conducted entitled **"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"** was managed at "Research cum instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh" during 2019-20 *rabi* season. The material were used in the research work comprises of 45 bold seeded genotypes along with checks (RLC-92 and R-552). The experiment was laid out in RCBD with 3 replications. The observations taken for different agro-morphological traits based on linseed descriptor, Kanpur (2010) "National guidelines for the conduct of tests for Distinctness, Uniformity and Stability in linseed, India" published as per "Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), Kanpur, (2010)" are "plant height (cm), days to 50 percent flowering, days to maturity, number of primary branches per plant, number of secondary branches per pant, total number of branches per plant, number of capsules per plant, 1000-seed weight (g), oil content (%), seed yield per plant (g) and harvest index (%)."

Analysis of variance disclosed that "significant differences exist for all the traits taken under study from bold seeded linseed genotypes. It indicates that there is presence of sufficient amount of variation among the bold seeded genotype of linseed for seed yield and its contributing traits." The highest seed weight (8.75 g) and seed yield per plant (2.26 g) observed for R-4275 genotypes. The "highest genotypic coefficient of variation observed for number of capsules per plant followed by number of secondary branches per plant, number of primary branches per plant and harvest index (%). However, highest value phenotypic coefficient of variation observed for number of capsules per plant subsequently, number of secondary branches per plant, harvest index (%) and number of primary branches per plant."

"Highest heritability showed by 1000-seed weight (g) followed by plant height (cm), number of primary branches per plant, number of secondary branches per plant and number of capsules per plant whereas, the highest genetic advance recorded for number of capsules per plant subsequently, number of secondary branches per plant, number of primary branches per plant and harvest index (%)."

This shows that certain traits are influenced by additive gene action and selection will be rewarded for the improving such traits.

Association analysis showed that “positive and significant correlation of 1000-seed weight with number of capsules per plant and total number of branches per plant. In contrast, seed yield per plant observed positive and significant correlation with 1000-seed weight (g), harvest index (%) and days to 50% flowering.”

Diversity analysis through D^2-analysis was carried out among 45 bold seeded genotypes of linseed. Cluster analysis distributes the 45 genotypes into 8 clusters. Cluster I has maximum number of genotypes *i.e.* 27 genotypes. Based on “intra-cluster distance, the most diverse clusters among all clusters were cluster III whereas, the highest inter cluster D^2 values were observed between cluster VI and IV (711.93) followed by cluster VI and V (696.75), cluster VI and II (551.16), cluster III and II (487.20) and cluster VIII and IV (461.72). Highly diverse genotypes can be used in hybridization programme.”

Present investigation revealed that about the best bold seeded genotype of linseed with respect to various traits including “1000-seed weight (g) are R-4275 followed by R-4285, R-3579, R-3990 and R-3772 whereas, for seed yield per plant (g) R-4275 followed by RLC-92 (check), RLC-175, R-4285 and R-552 (check), they were represented high yielding genotypes of linseed.” In this, high yield and bold seed offers ample opportunity to enhance linseed cultivation.

शोध ग्रन्थ सारांश

(अ) शोध ग्रन्थ का शीर्षक	:	"बड़े बीज वाले अलसी (लाइनम यूसीटाटीसीमम) में आनुवांशिक परिवर्तनशीलता"
(ब) छात्र का पूरा नाम	:	झानेन्द्र कुमार पटेल
(स) मुख्य विषय	:	आनुवंशिकी एवं पादप प्रजनन विभाग
(द) मुख्य सलाहकार का नाम और पता	:	डॉ. एस. एस. राव, प्रमुख वैज्ञानिक (आनुवंशिकी एवं पादप प्रजनन विभाग) एवं अधिष्ठाता, कृषि महाविद्यालय, रायपुर
(इ) उपाधि से सम्मानित किया जाता है	:	कृषि विज्ञान में स्नातकोत्तर

jhanendra patel
छात्र का हस्ताक्षर

मुख्य सलाहकार का हस्ताक्षर

14.8.2020
विभागाध्यक्ष के हस्ताक्षर

दिनाँक 13.08.2020

सारांश

अलसी (लाइनम यूसीटाटीसीमम) एक वार्षिक स्व-परागण वाली फसल है जिसकी उत्पत्ति या तो मध्य पूर्व या भारतीय क्षेत्रों में होती है। बड़े बीज वाले अलसी का उपयोग फसल की उपज में सुधार और इसकी तेल उपज क्षमता के लिए कभी भी शोध नहीं किया गया है। वर्तमान में जर्मप्लाज्म में बड़े बीज चरित्र की परिवर्तनशीलता के लिए अलग स्रोत उपस्थित है।आम तौर पर बड़े बीज वाले अलसी की तुलना, मध्यम और छोटे बीज से की जाती है। इसका लाभ बेहतर अंकुरण और अंकुर शक्ति के लिए होता है, जो कि मजबूत

पौधे की वृद्धि देता है जो अधिक शाखाएँ और कैप्सूल का उत्पादन करता है और अंत में अधिक बीज उपज और बीज तेल सामग्री का उत्पादन करेगा।

उपर्युक्त बिंदुओं को ध्यान में रखते हुए, वर्तमान शोध "**बड़े बीज वाले अलसी (लाइनम यूसीटाटीसीमम) में आनुवांशिक परिवर्तनशीलता**" शीर्षक से 2019-20 के दौरान रबी मौसम "अनुसंधान सह अनुदेशात्मक प्रक्षेत्र, आनुवंशिकी एवं पादप प्रजनन विभाग, कृषि महाविद्यालय, इंदिरा गांधी कृषि विश्व विद्यालय, रायपुर, छत्तीसगढ़" में किया गया था। अनुसंधान कार्य में उपयोग की जाने वाली जैविक सामग्री मे चेक (आरएलसी-92 एवं आर-552) सहित 45 बड़े बीज वाले आनुवंशिक रूप शामिल थे। शोध 3 प्रतिकृति के साथ आर सी बी डी में किया गया था। अलसी वर्णनकर्ता, कानपुर, (2010) के आधार पर विभिन्न कृषि-रूपात्मक लक्षणों) "पौधे की ऊंचाई (सेमी), पुष्पन के ५० प्रतिशत दिन, परिपक्वता के दिन, प्रति पौधा प्राथमिक शाखाओं की संख्या, प्रति पौधा माध्यमिक शाखाओं की संख्या, प्रति पौधा कुल शाखाओं की संख्या, प्रति पौधा कैप्सूल की संख्या 1000-बीज वजन (ग्राम), तेल मात्रा (%), प्रति पौधा बीज उपज (ग्राम) और फसल सूचकांक (%)" अलसी, भारत में विशिष्टता, एकरूपता और स्थिरता के लिए परीक्षणों के संचालन के लिए राष्ट्रीय दिशा-निर्देश" कैटलॉग में प्रकाशित अलसी परियोजना समन्वित इकाई, कानपुर, (२०१०), के अनुसार लिया गया है।

विचरण के विश्लेषण से ज्ञात होता हैं कि "बड़े बीज वाले अलसी आनुवंशिक रूप के अध्ययन के तहत लिए गए सभी लक्षणों के लिए महत्वपूर्ण अंतर मौजूद हैं। यह इंगित करता है कि बीज की उपज और इसके योगदान के लिए बड़े बीज वाले अलसी के आनुवंशिक रूप के बीच पर्याप्त मात्रा में विविधता मौजूद है। उच्चतम बीज वजन (8.75 ग्राम) और बीज उपज प्रति पौधा (2.26 ग्राम) आर-4275 जीनोटाइप के लिए देखा गया। "विभिन्न जीनोटाइपिक भिन्नता का गुणांक, प्रति पौधा कैप्सूल की संख्या के बाद प्रति पौधा द्वितीयक शाखाओं की संख्या, प्रति पौधा प्राथमिक शाखाओं की संख्या और फसल सूचकांक (%) के लिए देखा गया जबकि, विभिन्न फेनोटाइपिक भिन्नता का गुणांक, प्रति पौधा कैप्सूल की संख्या के बाद प्रति पौधा द्वितीयक शाखाओं की संख्या, फसल सूचकांक (%) और प्रति पौधा प्राथमिक शाखाओं की संख्या के लिए देखा गया।

" उच्चतम आनुवंशिकता, 1000-बीज वजन (ग्राम) के बाद पौधों की ऊँचाई (सेमी), प्रति पौधा प्राथमिक शाखाओं की संख्या, प्रति पौधा द्वितीयक शाखाओं की संख्या और प्रति पौधा कैप्सूल की संख्या के लिए दर्ज किया गया है, जबकि, सबसे अधिक आनुवंशिक अग्रिम, प्रति पौधा कैप्सूल की संख्या के बाद प्रति पौधा द्वितीयक शाखाओं की संख्या, प्रति पौधा प्राथमिक शाखाओं की संख्या और फसल सूचकांक (%) लिए दर्ज किया गया है।" इससे पता चलता है कि लक्षण एडिटिव जीन एक्शन से प्रभावित हैं और इस तरह के लक्षणों में सुधार के लिए चयन को अवसर प्रदान करेगा।

सह संबंध विश्लेषण से यह पता चलता है कि "प्रति पौधा कैप्सूल की संख्या और प्रति पौधा कुल शाखाओं की संख्या के साथ 1000-बीज वजन का सकारात्मक और महत्वपूर्ण सहसंबंध है । इसके विपरीत, प्रति पौधा के बीज की उपज का 1000-बीज वजन (ग्राम), फसल सूचकांक (%) और पुष्पन के ५० प्रतिशत दिन के साथ सकारात्मक और महत्वपूर्ण सहसंबंध देखा गया।"

डी ^{2}-विश्लेषण के माध्यम से विविधता का विश्लेषण बड़े बीज वाले अलसी के 45 जीनोटाइप के बीच किया गया। क्लस्टर विश्लेषण, 45 जीनोटाइप को 8 क्लस्टर में विभाजित करता है। क्लस्टर I में अधिकतम जीनोटाइप यानी 27 जीनोटाइप हैं। " अंतरा-क्लस्टर दूरी के आधार पर, सभी क्लस्टर के बीच सबसे विविध क्लस्टर, क्लस्टर III है , जबकि क्लस्टर VI और IV (711.93) के बाद क्लस्टर VI और V (696.75), क्लस्टर VI और II (551.16), क्लस्टर III और II (487.20) और क्लस्टर VIII और IV (461.72)के बीच उच्चतम अंतर क्लस्टर D^2 मान देखे गए। संकरण कार्यक्रम में अत्यधिक विविध जीनोटाइप का उपयोग किया जा सकता है।"

वर्तमान जांच में पता चलता है कि 1000-बीज वजन (ग्राम) सहित विभिन्न लक्षणों के संबंध में बड़े बीज वाले अलसी के सर्वश्रेष्ठ जीनोटाइप आर-4275 के बाद आर-4285, आर-3579, आर -3990 और आर-3772 है, जबकि प्रति पौधा के बीज की उपज (ग्राम) के लिए आर-4275 के बाद आरएलसी-92 (चेक), आरएलसी-175, आर-4285 और आर-552 (चेक) है। वे अलसी के उच्च उपज वाले जीनोटाइप का प्रतिनिधित्व करते थे। यह उच्च उपज और बड़े बीज वाले अलसी की खेती को बढ़ाने का पर्याप्त अवसर प्रदान करेगा

CHAPTER I
INTRODUCTION

Linseed (*Linum usitatissimum* L.) is an annual self-pollinated crop with originating either in the Middle East or the Indian regions (Vavilov, 1951). The generic name *Linum* derives from Celtic word ‘lin’ means ‘thread’ and the species name *usitatissimum* (Latin word) means “very useful”. *Linum usitatissimum*, only cultivated species of the genus *Linum* of family Linaceae is cultivated for oil from the beginning of agriculture eight thousand years ago and somewhat later for fibre (Zohary and Hopf, 1999).

Allaby *et al*. (2005) suggested that the cultivated species arise from a single domestication event from *L. bienne*, and the first domestication characters included selection for annual habit, non-shattering of capsules and more effective self-fertilization (Fu, 2011).

Later it was introduced into New World (The Americas) after extensive dissemination throughout Asia and Europe (Soto-Cerda *et al.* 2013). The high biological diversity of the genus Linum is considered to occur in near the Mediterranean Sea of the Indian subcontinent (Genesar and Morris, 2003; Fu, 2005; Kaur *et al.*, 2017). Differential selection for fibre and oil purpose has resulted in two distinct morphotypes of linseed-flax type and linseed type, respectively. The taller, less branched fiber flax type is grown in the cool-temperate regions of Russia, Western Europe, China and shorter, more branched, larger seeded linseed type is grown in continental climate regions of India, USA, Argentina and Canada.

Linseed has two origin centers *i.e.*, South West Asia, mainly in India (Vavilov, 1935; Richharia, 1962) and the Mediterranean region of Europe (Darlington, 1963).

Given increasing demand of linseed because of several benefits for health, there is steady need to increase genetic potential for oilseed yield. As per the Food and Agriculture Organization statistical data (FAOSTAT, 2018), currently overall world production of linseed is around 3.18 million tonnes, with Canada (34%), Russia (15%), and China (13%) being the major producers. In the world, India is the 6th largest producer adding 13% and 5.5% to global linseed area and production respectively. In world, India is the foremost growing country of linseed ranking 4th in area 3.20 lakh ha (11%) and production of 1.74 lakh tonnes followed by Kazakhstan, Russia and Canada, with annual area whereas, in terms of productivity India (543.8 Kg/ha) is far behind to Switzerland (2525 Kg/ha), Kyrgyzstan (2257.1 Kg/ha), Tunisia (2142.6 Kg/ha) and France (1909.1 Kg/ha) (FAOSTAT, 2018). In India, linseed is mostly occupied under rainfed (63%), utera (25%) and irrigated (17%) conditions and in famished conditions in the major linseed producing states of India are Madhya Pradesh, Chhattisgarh, Maharashtra, Jharkhand, Uttar Pradesh and Odisha. Currently, linseed is grown in Chhattisgarh in 29900 ha with 1030 tonnes production and average productivity 344 Kg/ha (INDIASTAT, 2017). Production and area wise, Chhattisgarh is one of the significant linseed producing states of India. In Chhattisgarh, Durg, Rajnandgaon, Bilaspur, Raigarh, Raipur, Dhamtari, Sarguja, Raipur and Kabirdham are the prime growing districts of linseed. In Chhattisgarh, linseed is grown as a rabi crop under rainfed (63 %) and in utera (25 %) under sub-marginal lands.

The nutriment quality of linseed, the top-level thing is mentioned to be the presence of omega fatty acids in high amount. There are 2 classes of omega fatty acids is present *i.e.* omega-3 fatty acids and omega-6 fatty acid. Omega-3 fatty acids are three types *i.e.* Linolenic acid, docosahexanoic acid (DHA) and eicosapentaenoic acid (EPA) which are nutrimentally important. All the 3 fatty acids have been shown to lower the chance of risk of cardiovascular problems in human (Hurteau, 2004). Linseed comprises of mixtures of fatty acids. Flax type of linseed is mainly enriched in poly-unsaturated fatty acids *i.e.* α-linolenic acids (ALA) being an essential omega-3 fatty acid and linoleic acid (LA) being omega-6 fatty acid. Linoleic acid and ALA comprises 16% and 57% of the total fatty acids in linseed and making flaxseed as the richest source of ALA (Ganorkar and Jain, 2013).

The swift drying properties and rancidity are the major drawback of linseed oil, with a focus on value addition for edible purposes. Because of this property it is widely used in varnish and paint industries of the country. Presence of high amounts of omega-3 fatty acid cause the drying effect of linseed oil. Being highly unsaturated, it reacts with oxygen as it comes into contact with air and then dries up. Linseed is being used in food-markets, where seeds are being used as a nutritional beneficial ingredient for health to strengthen food products (Flax Council of Canada, 2017).

The fibre is widely used in linen for textile industry, thread/rope and packaging materials; paper for cigarette, currency notes and artwork (Mackiewicz-Talarczyk *et al*., 2008). To use as a rope/thread, the strength, repeated flexibility, non-elasticity and its recyclable nature with a low density was quite desirable, value in using. The oil extracted from the seeds has unique drying properties having utility in production of varnish, inks, paints and linoleum flooring (Newkirk, 2008; Czemplik *et al*., 2011).

Linseed is rich in oil (fatty acids), dietary fibre and protein. An examine of brown seeded linseed reported 41 % fat, 20 % protein, 28 % total dietary fiber, 7.7 % moisture and 3.4 % ash, which is the mineral-rich residue left after the burning of samples. The oil content of seeds differs significantly from 33-45 % (Gill, 1987).

The medicinal value of linseed is also very rich. Most often, it is used in condition such as high cholesterol and laxative. It has a beneficial effect on platelets, which induce coagulation of the blood vessel. It is considered beneficial for treatment of cancer too. In painkillers, the linseed is very common use.

For genetic improvement of any crop, wide genetic diversity is basic requirement. The progress in developing a superior variety largely depends on the genetic basis of diverse parent selection and the breeding approach followed. However, in developing countries, linseed is the most neglected oilseed crop grown on marginal land with poor management. Lack of availability of improved varieties to suit the diverse agro-climatic condition is the reason for low yield of linseed crop. Therefore, to overcome the low yield levels of this crop, the development of high yielding variety is topmost priority.

The knowledge of genetic variability enables a breeder to devise proper selection strategies as selection depends on the existence of available genetic variability. Broad range of genetic variability in the segregating population largely determined by the genetic variation exists among the genotypes, which provide ample opportunity for better selection. Furthermore, selection utilizes the heritable proportion of existing variability hence, knowledge of heritability is also very much essential for crop improvement processes. Evaluation of variability for yield and yield attributing characters gets to be completely essential prior to planning for a suitable breeding methodology for genetic advancement. Genetic parameters like phenotypic and genotypic coefficient of variation are important for identifying the amount of variability show within the germplasm. Heritability along with high genetic advance would be more helpful tool in foreseeing the resultant effect in best genotypes selection for yield and its attributing characters. It helps in assessing the environmental effect on the expression of the genotypic and reliability of traits.

Present investigation focused with this hypothesis that in linseed the bold seededness alone has never been exploited for yield improvement of crop and its oil yield potential. Hence, for the present investigation the different source for variability of bold seed character in germplasm is taken. Segregating material and varieties have been collected and studied for various genetic parameters *viz;* heritability, genetic advance and correlation *etc.* for bold seededness with other yield attributes development of bold seeded varieties. Generally in linseed the comparing bold seeded with medium and small seeded, the advantage lies with better germination and seedling vigour giving robust plant growth which ultimately produces more branches and capsule and finally will produce more seed yield and seed oil yield respectively.

Recognizing the advantage and desire for such comprehensive study in bold seeded linseed, the recent investigate entitled **“Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)”** was managed at Research-Cum-Instructional-Farm, Department of Genetics and Plant Breeding, College of

Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh during 2019-20 *rabi* season with objective follows:-

1. Identification of bold seeded genotypes of linseed.
2. To estimate the amount of genetic variability and association analysis for yield & yield contributing traits in bold seeded genotypes of linseed.
3. To work out genetic divergence analysis in bold seeded genotypes of linseed.
4. To estimate oil content in bold seeded genotypes of linseed.

CHAPTER II

REVIEW OF LITERATURE

“The prime aim of the present study is to work for the better understanding of bold seeded linseed. It is also to be well understood about the diversity among different genotypes of bold seeded linseed itself**.”**

The relevant literature reviewed on various aspects of the present investigation entitled **“Genetic variability in bold seeded linseed** (*Linum usitatissimum* L.)” has been presented under the following heads:

2.1 Studies on morphological characters of bold seeded linseed

2.2 Studies on genetic variability and association analysis

2.3 Studies on genetic divergence analysis

2.1 Studies on morphological characters of bold seed linseed

In the study of Arora (2003) reported that weight of thousand seeds ranged from 5.01 to 6.05 g and seed length ranged between 4.50 to 5.45 mm per seed in three varieties of linseed. The seeds were reported to be flat and pointed and the width ranged between 0.90 to 1.45 mm. Seed density was reported to range from 0.69 to 0.72 g/ml.

Diederichsen *et al.* (2006) at Canada observed that accession of linseed (*Linum usitatissimum)* and noticed colour of seed, weight of seed and oil content held by Plant Gene Resources of Canada. These studies help us to understand variation and correlation between weight of seed, seed colour and oil content in cultivated linseed (*Linum usitatissimum* L.). Gene bank accession had 2934 seed presently grown at SK, Saskatoon, Canada, which is originating from seventy two countries utilized to observed variation of seed character. Based on single observations for all accessions, the overall mean and standard deviation was 5.95 ± 1.22 mg/seed for weight of seed and 38.3 ± 1.74% for oil content. Among 3 intra-specific groups of linseed, seed weight, concentration of oil, amount of oil per seed increased in the following order: fiber flax (convar. *elongatum*), intermediate flax (convar. *usitatissimum*), and large seeded linseed (convar. *mediterraneum*). In 52 North American cultivars, there was a weak positive association of high oil content with high seed weight.

Worku *et al.* (2015) at Ethiopia studied that evaluation of variation in 198 accession of linseed which is based on oil content and morphology character in Ethiopia. We focused to form and use a set of morphological descriptors to examine level and patterns of variance in germplasm of Ethiopia from tropical highland in one ninety eight Ethiopian traditional varieties. The Ethiopian traditional varieties with both fiber and oilseed stem branching morphology, though most of the seed were small. Oil quality of traditional variety was evaluated and content of oil was low as 30 percent than 47 percent observed elsewhere. Flowering days and maturity days differs more and high heritable.

2.2 Studies on genetic variability and association analysis

2.2.1. Analysis of variance

Mirza *et al.* (1996) at Bangladesh estimated 30 linseed genotypes for yield and yield contributing traits. Analysis of variance indicated significantly variation between genotypes of linseed for all character except number of primary branches per plant and weight of seed and noticed that higher heritability along with higher genetic advance as mean percentage for plant height, number of capsules per plant and seed yield.

Dubey *et al*. (2006) at Kanpur noticed high variation between 10 characters for number of branches per plant, 1000-seed weight and yield of seed per plant while low variable for height of plant and oil content.

Sood *et al.* (2012) at Palampur studied 38 linseed genotypes. They evaluated the variation level in oil content and fatty acid composition of linseed cultivars, elite lines and hybrids. 2 saturated (steric and palmitic acid) and 3 unsaturated fatty acids (linoleic, linolenic and Oleic acid) identified by gas chromatography represented 8.81 percent and 90.89 percent of the total oil, respectively. Wide range of variation was recorded for linolenic acid followed by oleic acid, while linoleic acid has recorded highest GCV.

Belete and Yohannes (2013) at Ethiopia study was carried out in twenty five genotypes of linseed derived from various crosses including checks. The analysis of variance revealed significant amount of differences among the genotypes for number of capsules per plant, seed yield per plant and 1000 seed weight.

Paul *et al*. (2016) at Palampur analyzed 32 genotypes for 9 morphological traits. There were highly significant differences among the genotypes for number of primary branches per plant. plant height, total number of branches per plant, number of capsules per plant, 1000 seed weight, harvest index and seed yield per plant and non-significant differences for number of seeds per capsule, indicating the existence of variability among the genotypes.

Chauhan *et al*. (2018) at Faizabad analyzed sixty six genotypes of linseed for the morphological traits to investigate the genetic diversity between and within the genotypes. There were highly significant differences among the genotypes for seed yield per plant, number of primary branches per plant, total number of branches per plant, number of capsules per plant, number of seeds per capsule and 1000 seed weight indicating the presence of variability among the genotypes.

2.2.2. Genotypic and phenotypic coefficient of variation

Singh (2001) at Allahabad observed various qualitative traits of 20 genotypes of linseed and examine that variation of phenotypic coefficient was high for number of primary branches per plant while variation of genotypic coefficient high for 50% flowering days followed by seed yield per plant and number of secondary branches per plant.

Naik and Satapathy (2002) at Odisha evaluated that high GCV and PCV for number of capsules per plant, number of primary branches per plant and 1000 seed weight.

Adugna and Labuschagne (2003) at Ethiopia examined that 60 accession of linseed from Ethiopia for 11 traits to evaluate the diversity of accession. The variation of phenotypic coefficient varied from 1.90 percent for number of seeds per capsule to 142.72 percent for plant height whereas, variation of genotypic coefficient ranged from 1.52 percent to 118.88 percent for same traits. They evaluated that yield of seed per plant had low heritability and higher for flowering days. The genetic gain was 3.16 percent for maturity days and 24.26 percent for height of plant.

Saeidi *et al.* (2003) at Iran studied genetic variability in linseed genotypes. They noticed that there was considerable variation of phenotypic and genotypic coefficient among the genotypes for number of capsules per plant and yield of seed per plant.

Awasthi and Rao (2005) at Raipur studied variability for the following ten characters *viz*., "days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, number of seeds per plant, 100-Seed weight, seed yield per plant." Higher genetic variation was found for number of seeds per capsule followed by number of capsules per plant, seed yield per plant, number of primary branches per plant and number of secondary branches per plant.

Dandigadasar *et al*. (2012) studied genetic variability in genotypes of linseed. They noticed wide ranging for variation of genotypic and phenotypic coefficient for number of capsules per plant followed by yield of seed per plant and number of seeds per capsule.

Belete and Yohannes (2013) at Ethiopia studied in 25 linseed genotypes. They found a high genotypic and phenotypic coefficient of variation was recorded for number of seeds per plant and number of capsules per plant.

Bibi *et al*. (2013) at Islamabad estimated in 19 linseed genotypes. They observed that coefficient variation was found higher for seed yield per plant followed by number of capsules per plant and harvest index (%).

Reddy *et al*. (2013) at Nagpur studied in 23 genotypes of linseed. They observed that phenotypic and genotypic coefficient of variation was found higher for trait number of branches per plant followed by seed yield per plant, number of capsules per plant and omega-6-fatty acid.

Pali and Mehta (2014) at Raipur studied in 48 linseed varieties. They noticed that high genotypic variation was found for number of seeds per plant followed by number of capsules per plant, 1000-seed weight and harvest index.

Kanwar *et al.* (2014) at Raipur studied on 36 linseed genotypes were evaluated for genetic variability. They observed high genotypic and phenotypic coefficient of variation values for seed yield per plant followed by number of capsules per plant, biological yield per plant, number of primary branches per plant and number of secondary branches per plant.

Kumar *et al*. (2015) at Allahabad estimated that harvest index and yield of seed had higher variation of genotypic and phenotypic coefficient showed best deal variability in those traits which signifies the effectiveness of selection of beneficial type for enhancement.

Patel *et al.* (2015) at Palampur disclosed that high variation of genotypic and phenotypic coefficient was found for number of capsules per plant followed by yield of seed per plant and weight of thousand seeds.

Chandrawati *et al.* (2016) at Kanpur experimented in 58 linseed genotypes. They noted that the high estimates of genotypic coefficient of variation and phenotypic coefficient of variation were observed for number of capsules per plant, number of branches per plant and seed yield per plant while low for number of seeds per capsules and oil content.

Paul and Kumari (2018) at Palampur conducted experiment among 18 genotypes of Linseed. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the observed traits *i.e.* days to 50% flowering, number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, 1000 seed weight and seed yield per plant.

Tewari and Singh (2018) at Kanpur experimented on 73 genotypes including checks Shekhar and T-397 to study the genetic variability in linseed. They observed high phenotypic and genotypic coefficients of variation estimates for seed yield per plant and number of secondary branches per plant.

Dhirhi and Mehta (2019) at Raipur assessed 20 hybrids of linseed for genetic variability. The variation of phenotypic and genotypic coefficient was observed for days to flowering and days to maturity showed less difference. Differences between variation of genotypic and phenotypic coefficient were recorded for plant height followed by number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, number of seeds per capsule, seed yield per plant, 1000-seed weight and total number of branches per plant, indicating these traits are highly influenced by environment.

Singh *et al.* (2019) at Meerut studied in 40 accessions of linseed to estimate the high value of phenotypic and genotypic coefficient of variation was recorded for number of primary branches per plant, number of secondary branches per plant, seed yield per plant and biological yield per plant.

Upadhyay *et al.* (2019 a) at Raipur experimented in 25 linseed genotype. They noted that the phenotypic coefficient of variation higher than genotypic coefficient of variation for all the traits. The highest genotypic coefficient of variation was recorded for number of seeds per plant followed by seed yield per plant, number of seeds per capsule, 1000-seed weight, number of capsules per plant, plant height, days to 50% flowering and days to maturity. The highest phenotypic coefficient of variation was recorded for number of seeds per plant followed by seed yield per plant, number of seeds per capsule, 1000-seed weight, number of capsules per plant, plant height, days to 50% flowering and days to maturity.

Upadhyay *et al.* (2019 b) at Raipur experimented in 63 linseed genotype. They revealed that the highest variation of genotypic coefficient was recorded for number of capsules per plant followed by number of seeds per plant and seed yield per plant. The highest phenotypic coefficient of variation was recorded for number of seeds per plant followed by number of capsules per plant, seed yield per plant and seed length.

2.2.3. Heritability and genetic advance

Rede and Rao (1999) at Raipur estimated that higher heritability in broad sense along with higher genetic advance for number of effective capsules per plant followed by number of primary branches per plant, number of secondary branches per plant, and weight of dry matter shows the contribution of additive genetic variance in these traits.

Payasi *et al*. (2000) at Sagar (M.P.) were evaluated eighty linseed genotypes under four farming conditions for genetic variability analysis with regard to twelve quantitative traits. They found higher heritability along with higher genetic advance as mean percentage for yield of seed per plant and flower initiation days and concluded that these characters applied for enhancement in yield.

Akbar *et al.* (2003) at Pakistan noticed that higher heritability for plant height, number of capsules per plant, seed yield per plant, weight of thousand seed. Except height of plant, all the character was correlated significant and positive with seed yield.

Saeidi *et al.* (2003) at Iran revealed that higher heritability for number of seedling per meter square, days to 50 percent flowering, days to maturity and height of plant of both brown and yellow-seeded linseed genotypes whereas, low heritability for number of capsules per plant, number of seeds per capsule, 1000-seed weight and seed yield per plant of linseed genotypes.

Kant *et al.* (2005) at Kanpur evaluated higher heritability coupled with moderate genetic advance as mean percent was noticed for yield of seed per plant, number of primary branches per plant and number of capsules per plant provides scope for the enhancement through selection. Higher heritability accompanying lower genetic advance as mean percent was reported for remaining traits shows selection of genotype is not more effective for these character.

Kumar *et al.* (2012) at Meerut evaluated high heritability for plant height, number of capsules per plant, yield of seed per plant, maturity days, content of linolenic acid, content of oleic acid and biological yield per plant. It shows that presence of more effect of additive genetic component in the inheritant of these traits. Expect high genetic advance for height of plant, 50% flowering, maturity days, number of primary branches per plant, number of secondary branches per plant, diameter of stem, weight of thousand seed, number of capsules per plant, stearic acid, biological yield per plant, seed yield per plant, harvest index, oleic acid and linoleic acid.

Vardhan and Rao (2012) at Raipur observed 30 diverse genotypes of linseed for variable evaluation yield and yield component under 3 environmental conditions viz., sowing late, irrigated and rainfed, independently. Under all 3 condition yield of seed per plant indicated high variation of genotypic coefficient. Under irrigated condition maturity days had high heritability, whereas higher genetic advance as mean percentage for yield of seed per plant under both irrigated and rainfed condition. Under irrigated condition weight of hundred seed had high heritability coupled with high genetic advance.

Belete and Yohannes (2013) at Ethiopia studied in 25 linseed genotypes. High heritability coupled with high genetic advance as mean percentage was recorded for number of seeds per plant which indicating this trait would be effective for selection.

Bibi *et al*. (2013) at Islamabad studied in 19 linseed genotypes. They evaluated high heritability for days to commencement of flowering followed by days to complete flowering, days to maturity, weight of thousand seed, number of capsules per plant and harvest index. High heritability along with high genetic advance was found for yield of seed per plot, number of capsules per plant, plant height and seed yield per hactare.

Reddy *et al*. (2013) at Nagpur studied in 23 genotypes of linseed. They observed that higher heritability along with higher genetic advance showed quite simple selection would be advantageous for the enhancement of the trait like plant height, number of branches per plant, weight of thousand seed, number of capsules per plant, seed yield per plant and omega-6-fatty acid.

Kanwar *et al.* (2014) at Raipur studied in 36 genotypes of linseed. They observed high heritability along with high genetic advance as mean percentage was found for number of capsules per plant followed by seed yield per plant, biological yield per plant, plant height and number of primary branches per plant, indicating effect of additive gene action for these characters.

Pali and Mehta (2014) at Raipur worked in 48 linseed varieties. They observed that higher heritability along with higher genetic advance as mean percentage was found for number of seed per plant followed by number of seeds per capsule, number of capsules per plant, number of secondary branches per plant, yield of seed per plant and hundred seed weight whereas, number of primary branches per plant had moderate heritability.

Rajanna *et al*. (2014) at Raichur used 10 genotypes of linseed *viz.*, PCL-45, LCK-1101, RLC-133, BAU13-09, RL-10193, SLS-87, PKDL-133, NDL-2010-1-27, NL-97-26 and LMS-2010-1-27 and 4 checks *viz.*, Padmini (Zonal check), T-397 (National check) and 2 local checks (S-36 and NL-115). 1000 seed weight and seed yield per plant showed that the higher values of heritability coupled with higher genetic advance as mean percentage.

Kumar *et al*. (2015) at Palampur estimated 12 hybrids together with 7 parents and studied that high heritability along with high genetic advance as mean percentage for yield of straw per plant, yield of seed per plant, weight of thousand seed shows chief additive gene action for all traits.

Chandarwati *et al.* (2016) at Kanpur worked on 58 genotypes of linseed. They revealed that broad sense heritability was found high for the trait days to 50% flowering followed by oil content, number of capsules per plant and plant height in the first year. In the second year also these traits showed high heritability. The trait number of branches per plant, number of seeds per capsules showed lowest heritability in the first year and husk weight per plant in the second year. Genetic advance as mean percentage was found highest for husk weight per plant followed by number of capsules per plant and number of branches per plant in the first year and was highest for number of capsules per plant followed by days to 50% flowering and test weight in the second year. The oil content had lowest genetic advance in both the year.

Dash *et al*. (2016) at Odisha disclosed that moderate heritability and moderate genetic advance for weight of thousand grains suggested the chief role of non additive gene action.

Kasana *et al.* (2016) at Kanpur conducted experiment in 151 genotypes of linseed. They disclosed that the high heritability estimated for number of capsules per plant followed by plant height, days to flowering, size of corolla, number of seeds per capsule, 1000 seed weight, seed yield per plant, days to maturity, oil content and capsule size whereas, low for number of primary branches per plant. The maximum value of genetic advance as mean percentage has been observed for number of capsules per plant followed by plant height, days to flowering, days to maturity, size of corolla, oil content, seed yield per plant, 1000-seed weight, capsule size and number of primary branches per plant. The minimum value of genetic advance as mean percentage has been noted for number of seeds per capsule.

Siddiqui *et al.* (2016) at Lucknow (Uttar Pradesh) experimented on 151 accessions of linseed. They noted that high heritability along with high genetic advance as mean percentage for plant weight followed by number of secondary branches per plant, number of capsules per plant, and seed yield per plant, which implies that heritability is due to additive gene effects and that selection would be effective.

Kumar *et al.* (2017) at Meerut worked in 35 genotypes of linseed. They evaluated that higher heritability along with genetic advance as mean percentage was noticed for the traits like biological yield per plant and capsules per plant. While, high heritability along with moderate genetic advance as mean percent was recorded for 50% flowering days and plant height.

Paul and Kumari (2018) at Palampur conducted experiment among 18 genotypes of Linseed. They observed high heritability and high genetic advance for yield of seed per plot and straw yield per plot. The result suggested that the significance of additive gene effect for their inheritance and phenotypic selection would be effective.

Tewari and Singh (2018) at Kanpur experimented on 73 genotypes including checks Shekhar and T-397. High heritability was recorded for all the traits except oil content and 1000-seed weight. High heritability along with high genetic advance as mean percent was recorded for seed yield per plant followed by number of secondary branches per plant, number of primary branches per plant and number of capsules per plant.

Singh *et al.* (2019) at Meerut experimented on 40 diverse linseed accessions. They observed high heritability along with high genetic advance as mean percentage for the traits *viz.,* number of secondary branches per plant followed by number of primary branches per plant, biological yield per plant and seed yield per plant, indicating predominance of additive gene action in the expression of these traits. High estimates of genetic advance as mean percentage were recorded for number of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and biological yield per plant.

Upadhyay *et al.* (2019) at Raipur experimented in 25 genotype of linseed. They revealed that the 'highest heritability estimate was recorded for days to 50% flowering followed by plant height, days to maturity and seed yield per plant' indicating predominance of additive gene action in the expression of these traits. The highest genetic advance as mean percentage was noted for number of capsules per plant followed by seed yield per plant and 1000 seed weight. The minimum genetic advance was seen for days to 50% flowering.

2.2.4. Association analysis in linseed

Payasi *et al*. (2000) at Sagar (M.P.) were evaluated eighty linseed genotypes. They noticed that yield of seed per plant was associate negative with 50%

flowering days while positive associate with number of secondary branches per plant, number of seeds per capsule and number of capsules per plant.

Akbar *et al.* (2003) at Pakistan estimated that seventeen genotypes of linseed consider having high significant differences. Seed yield per plant positively and significantly correlated with trait like number of capsules per plant, number of branches per plant and number of seeds per capsule. The direct contribution of number of seeds per capsule have more significant correlate followed by weight of thousand seed and number of capsules per plant.

Yadav (2001) observed that phenotypic correlation is lesser than genotypic correlation coefficient. The outcome shows that yield of seed per plant was positively associated with number of capsules per plant followed by maturity days, number of seeds per capsule at genotypic level, 1000 seed weight and height of plant at both genotypic and phenotypic level.

Tadesse *et al.* (2002) at Sinana and Robe of Ethiopia experimented on 81 diverse linseed accessions of Ethiopia were analyzed "yield of seed per plot was significantly associated with seed weight, seed yield per plant, biomass and harvest index at both locations. However, at Sinana, height of plant and content of oil were also significantly associated with yield of seed per plot." Analysis over locations also supported that biomass and harvest index are the important for seed yield per plot. Seed weight was found to be an important trait in indirect selection for content of oil.

Adunga and Labuschagne (2003) at Ethiopia studied in 60 accessions of linseed. They observed that yield of seed per plot was significant and positive for yield of seed per plant, 1000 weight of seed and number of capsules per plant. These 3 yield traits were also strongly and positively associated with plant height, number of branches per plant, flowering days and days to maturity.

Akbar *et al*. (2003) at Pakistan estimated that seed yield per plant correlate significantly and positively with number of capsules per plant and number of branches per plant, significantly with weight of thousand seed and associate negative and non-significantly with number of capsules per plant, number of branches per plant, significantly with weight of thousand seed.

Saeidi *et al*. (2003) at Iran recorded seed yield per plant and evaluate higher and positively association with basal branching per plant and number of capsules per plant, although higher and negative association with number of seedling per m^2.

Dubey *et al*. (2006) at Kanpur observed that significantly positive association for branches per plant, weight of thousand seed and number of capsules per plant with yield of seed per plant.

Kumari and Rao (2007) evaluated association analysis in linseed genotypes. They noticed that number of primary branches per plant, number of capsules per plant, number of secondary branches per plant and weight of thousand seeds had positively correlation with seed yield per plant.

Nagaraja *et al.* (2009) evaluated that yield of seed had significant and positive correlated with number of branches per plant, number of capsules per plant, weight of thousand seed and harvest index. For many trait coefficient of genotypic association was high compared to phenotypic association.

Patel and Rao (2009) evaluated association analysis in genotypes of linseed. They noticed that seed yield per plant had significant and positive correlated with number of capsules per plant, number of seeds per capsule, weight of hundred seed and flowering days.

Gauraha *et al.* (2011) at Raipur disclosed that number of secondary branches per plant, number of capsules per plant, number of primary branches per plant, number of seeds per plant, 1000 seed weight and days to maturity had the strong positive association with seed yield per plant. Genotypic correlations were higher than the corresponding phenotypic correlations.

Savita *et al.* (2011) at Karnataka disclosed association between yield and its component shows that seed yield per plant correlate positively and significantly with oil yield per plant, number of capsules per plant, number of primary branches per plant, number of secondary branches per plant, number of seeds per capsule, total number of branches per plant, harvest index and weight of thousand seed at both genotypic and phenotypic levels.

Dandigadasar *et al.* (2012) noted yield of seed per plant had positive significant association with number of branches per plant, number of capsules per plant and harvest index at both phenotypic and genotypic level. Genotypic coefficients association was higher than corresponding phenotypic coefficient for most trait combinations.

Sood *et al.* (2012) at Palampur evaluated the variation level in oil content and fatty acid composition of linseed cultivars, elite lines and hybrids. Oil content showed weak positive association with weight of seed. Linoleic acid had negative association with linoleic, oleic and stearic acid however, palmitic acid also showed positive association with oleic acid.

Belete and Yohannes (2013) at Ethiopia study was carried out in 25 linseed genotypes. They observed that seed yield per plant highly significant and positive correlated with number of primary branches per plant, number of secondary branches per plant, number of capsules per plant and number of seeds per plant whereas, 1000 seed weight showed highly significant and negative correlation.

Bibi *et al*. (2013) at Islamabad studied in 19 genotypes of linseed. They noticed yield of seed correlate positive to all character except flower initiation days and harvest index. Yield of seed per plot significantly positive correlate with height of plant and number of capsules per plant.

Reddy *et al.* (2013) at Nagpur observed that yield and morphology character of twenty three genotypes to find out the phenotypic and genotypic association and contribute to this character to yield direct and indirect in linseed. The association of phenotypic and genotypic coefficients gets similar in direction among different character but in magnitude coefficient of genotypic association more when compared to phenotypic association.

Bayark *et al.* (2014) at Turkey studied in eighty one genotypes of linseed. They noticed positive association between oil content and palmitic acid. “Linolenic acid had negative and non-significant association with oil content. Additionally, significant and positive association was recorded between oleic, palimitic acid and linoleic, stearic acid. Linolenic acid noted significant and negative association with oleic, stearic and linoleic acid. These results explained that high oil content will result in low palmitic acid and increase in linolenic acid will result in decrease in oleic, linoleic and stearic acids.”

Ibrar *et al.* (2014) at Pakistan evaluated correlation of phenotypic and genotypic coefficient to form a way for the enhancement of yield in linseed. Estimation of genotypic association indicated that seed yield of linseed was positive affected by number of primary branches per plant, number of capsules per plant, number of seeds per capsule, weight of thousand seeds and oil content, whereas, negatively associated with days to complete flowering, flower initiation days and physiological maturity days. Phenotypic correlation evaluation outcome indicated same findings except weight of thousand seeds had positive and significant effect on seed yield.

Pali and Mehta (2014) at Raipur worked in 48 linseed varieties. They noticed number of primary branches per plant, number of secondary branches per plant, that number of capsules per plant and weight of thousand seed was positively associated with seed yield per plant which indicates higher positive direct effect on seed yield.

Rajanna *et al.* (2014) at Karnataka used ten linseed genotypes for association analysis. They disclosed variation of genotypic and phenotypic association and examined that yield of seed was significantly and positively correlation with number of capsules per plant, technical plant height and height of plant.

Tariq *et al.* (2014) at Pakistan observed positively correlation with number of primary branches per plant, height of plant, number of seeds per capsule, number of capsules per plant and thousand seed weight.

Chaudhary *et al.* (2016) at Faizabad investigated with 160 linseed genotypes with 3 checks in augmented block design. Association studies disclosed that seed yield per plant showed highly significant and positive correlation with harvest index followed by number of capsules per plant, number of seeds per capsule, biological yield per plant and plant height.

Chandarwati *et al.* (2016) at Kanpur worked on 58 genotypes of linseed. They noted that the capsule weight per plant showed significantly positive correlation with number of capsules per plant, seed weight per plant, number husk weight per plant, test weight and significantly negative association with plant height. Seed weight per plant had significantly positive association with number of capsules per plant, test weight. It had significant and positive association only with test weight though with comparatively low magnitude. The association among other morphological traits revealed that days to 50% flowering had positive and significant correlation with plant height and number of branches per plant. Number of branches was positively and significantly associated with number of capsules per plant, and plant height in both the years.

Kasana *et al.* (2016) at Kanpur conducted experiment in 151 genotypes of linseed. They noted that seed yield per plant showed significantly and positively correlation with 1000-seed weight, capsule size and number of capsules per plant and negative correlation with number of seeds per capsule, days to maturity and size of corolla at both phenotypic and genotypic level.

Naik *et al.* (2016) at Odisha observed that under normal sowing, soil stress and late sowing condition, correlation coefficient analysis of yield of seed and yield contributing trait in linseed. Yield of seed is the dependent attribute and independent attributes was yield contributing character like 50% flowering days, height of plant, weight of thousand or hundred seed, number of primary branches per plant, maturity days, height of technical plant, number of secondary branches per plant, number of capsules per plant and number of seeds per capsule under normal sowing environment and environment confers that it is the most principle selection criterion for enhancement of yield of seed.

Paul *et al*. (2016) at Palampur observed 16 genotypes of linseed to estimate the correlation. Coefficient of correlation disclosed that in order to increased yield of seed, direct selection of plant is done on the basis of 3 character would be effective such that height of plant, number of seeds per capsule and number of capsules per plant which have maximal genotypic and phenotypic association.

Sharma *et al*. (2016) at Palampur worked in 30 genotypes of linseed to evaluate the coefficient of genotypic and phenotypic correlation. The result showed that seed yield had positively and significantly correlation with number of secondary branches per plant followed by number of seeds per capsule, number of capsules per plant, harvest index, 1000-seed weight and oil content.

Kumar *et al.* (2017) at Uttar Pradesh worked in 35 genotypes of linseed. They noticed that seed yield per plant had positive and significant association with days to 50% flowering, capsules per plant, biological yield per plant, harvest index, seed per capsule and height of plant.

Ankit *et al.* (2018) at Meerut worked on 40 diverse genotypes of linseed. They estimate correlation coefficient the higher genotypic correlation values than the corresponding phenotypic correlation values indicated the existence of strong inherent association among the various traits. Seed yield per plant showed highly positive and significant correlation with biological yield per plant and 1000 seed weight.

Dhirhi and Mehta (2019) at Raipur observed 20 hybrids of linseed to estimate the correlation. Plant height had highly positive and significant association with number of secondary branches per plant and number of capsules per plant at both genotypic and phenotypic level. It also showed positive and significant association with number of capsules per plant at only genotypic level.

2.3 Studies on genetic divergence analysis

Mahto (2004) worked on 26 genotypes of linseed found BAUL 9, BAUL 116, BAUL 144-2, BAUL 149-2, BAUL 160, BAUL 189-2 and BAUL 285-1 showed wide genetic divergence over environment present in Chhota Nagpur Division of Bihar.

Begum *et al.* (2007) at Gazipur-1701 studied genetic divergence in linseed. They reported that the highest inter-cluster distance was recorded among clusters V, IV and II, while the lowest between cluster III and I. The highest intra-cluster distance was recorded in cluster III indicates that maximum variability within the clusters.

Khan *et al.* (2013) at Pakistan experimented on 55 accessions of linseed including a check variety (Chandni) under rainfed conditions. Dendrogram based on Euclidean distance coefficient using ten quantitative characters, grouped all the accessions of linseed into 13 clusters. Cluster II was the highest and had 33 accessions followed by Cluster I having 11 accessions. Best performing accessions of Clusters I and II could be used in hybridization programme for the development of high yielding varieties by crossing with accessions of Clusters VII, VIII, IX and X followed by selection in segregating populations.

Paul *et al*. (2016) at Palampur district of Himachal Pradesh analyzed 32 genotypes for 9 morphological traits in 2 consecutive years (E-I, E-II) to analyze the pattern of genetic diversity. “The cluster analysis based on Tocher’s method classified the genotypes into 8 (E-I) and 6 (E-II) major groups of different sizes during both the years. The maximum distance was found between clusters V and VII (E-I) and between clusters IV and V (E-II).” The genotypes from these clusters can be utilized for the improvement of seed yield in linseed breeding programmes. In both years, weight of thousand seeds contribute maximum in E-I and E-II total genetic divergence among genotypes.

Chauhan *et al*. (2018) at Faizabad analyzed sixty six genotypes of linseed for the morphological traits to investigate the genetic divergence between and within the genotypes. The cluster analysis classified linseed genotypes in to nine major groups. The maximum inter-cluster diversity was observed between cluster V and VIII. Based on mean performance of the genotypes and inter-cluster distance the crosses between ICAR Sel-1 and L-9, NDC 2005-34, H660, LCK 87042, NDL2005-22, GS335 is recommended to get use full transgressive segregants in linseed.

Kaur et al. (2018) at Delhi analysed the genetic diversity of linseed. Cluster analysis classified the accessions under 4 divergent clusters which indicated fair association of genetic diversity and geographical diversity. Few trait specific promising accessions such as “IC0096488, IC0096487 (large capsule size), IC0096490 (high oil content and bold seeds), IC0096496, IC0096539 (early flowering and maturity), IC0054954, IC0054949 (bold seeds), EC0718827 (tall, large corolla), and EC0718835 (high seed yield per plant)” were identified with high estimates of heritability for the mentioned traits.

Kumari *et al.* (2018) at Bihar studied in 31 linseed genotypes using D^2 analysis, On the basis of D^2 analysis, genotypes were grouped into six divergent clusters in which cluster I was largest with twelve genotypes followed by cluster II and cluster V. The results showed the highest contribution of linolenic acid towards genetic diversity. However, inter cluster D 2 value was found highest between cluster II and VI followed by V and VI. On the basis of cluster mean, the genotypes of cluster IV were characterized by the highest cluster mean for seed yield per plant and cluster II for oil content and linolenic acid.

Paul and Kumari (2018) at Palampur conducted experiment among 18 genotypes of Linseed for divergence analysis. The cluster analysis classified the genotypes into 2, 3 and 3 clusters in Env. I, Env. II and pooled over the environments, respectively indicating that pattern of cluster was different in Env. I. Therefore, in Env. I, parents should be selected from cluster combination from clusters I and II, in Env. II and in pooled over the environments from clusters I and III. The character weight of thousand seeds contributed maximum towards total genetic divergence in Env. I, Env. II and in pooled over the environment among 18 genotypes under study.

Patial *et al.* (2019) at Palampur estimate genetic divergence through cluster analysis. Cluster analysis showed 34 genotypes of linseed differentiated into three clusters. Mean value for each cluster revealed that genotypes in cluster I had highest values for plant height followed by capsules per plant and oil content, cluster II showed highest values for plant height followed by capsules per plant and technical height and cluster III showed highest value for capsule per plant, plant height, oil content and technical height.

CHAPTER III

MATERIALS AND METHODS

The recent investigation entitled **“Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)”** was conducted at the Research-cum-Instructional Farm, at Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India during *rabi* 2019-20 to evaluate the genetic variability and genetic diversity among genotypes of bold seeded linseed.

3.1 Geographical situation

Raipur is located in the southern part of Chhattisgarh , 21°16’ N latitude and 81°31 E longitude including an altitude of 289.56 meter over the mean sea level.

3.2 Climate

The climatic conditions of Raipur are subtropical. The region received 1200-1400mm annual rainfall during *kharif* season, out of which about 8 percent is received in rabi season. Rainfall patterns had wide variations from year to year during rainy season. The data related to weekly rainfall, rainy days, relative humidity, minimal and maximal temperatures of entire period of growing crop have been represented are shown in Figure 3.1.

3.3 Experimental material

The experimental materials consists of forty-five (45) lines of bold seeded linseed genotypes including check variety taken from linseed germplasm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur Chhattisgarh, India. The genotype was obtained by selection of seed from linseed germplasm in *rabi* 2019-2020. The selection was made according to linseed 1000-seed weight (more than 6.5 grams). During *rabi* 2019-20 experiment was in randomized complete block design (RCBD) with 3 replication. The forty-five lines were sown including check variety (RLC-92 and R-552) on 7th December, 2019 in a single row of 2.5m length with spacing of 30 cm between rows and 6 cm between plants. The recommended packages of practices were done for controlling pest and diseases (Table 3.1).

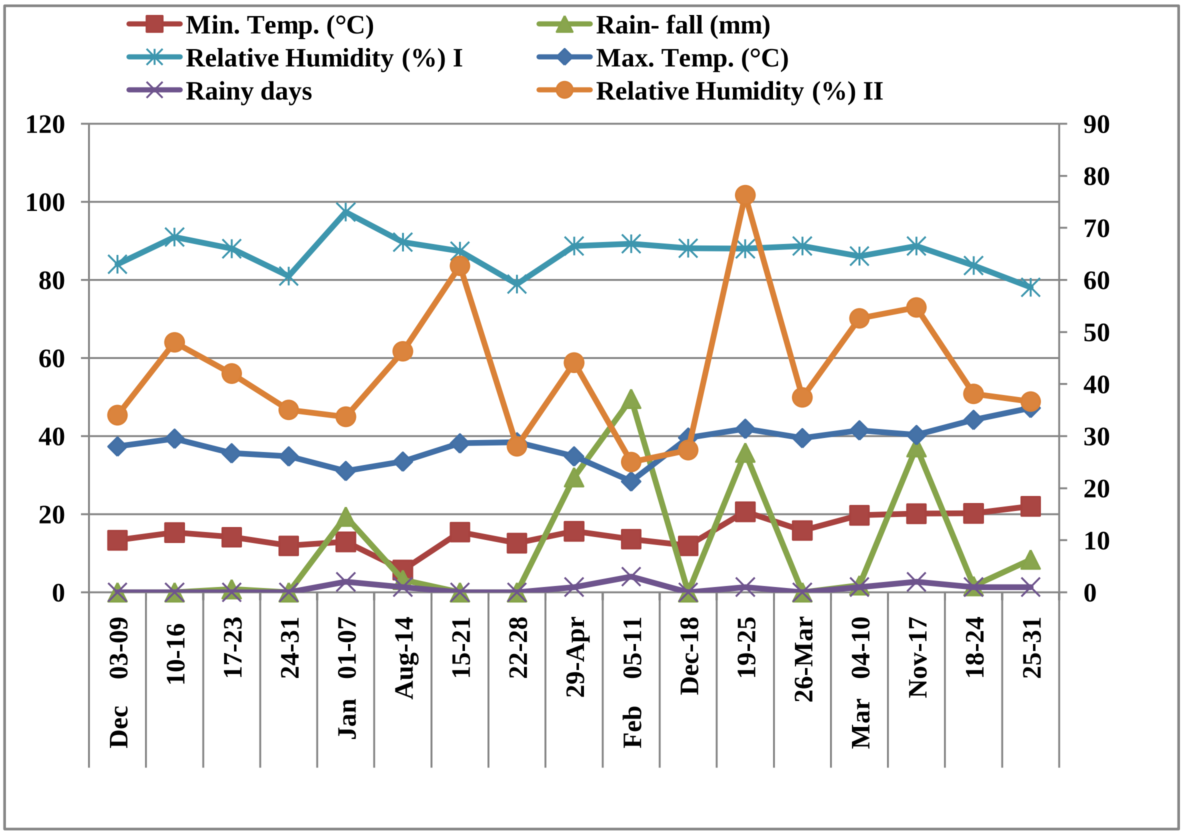

Fig. 3.1: Graphical representation of weekly meteorological data during *rabi* crop periods (2019-20)

Table 3.1: Experimental material used in the present study

S.N.	Genotypes	S.N.	Genotypes	S.N.	Genotypes	S.N.	Genotypes
1	R-3312	13	R-4167	25	R-4222	37	R-4285
2	R-3313	14	R-4176	26	R-4225	38	R-4287
3	R-3570	15	R-4186	27	R-4231	39	R-4288
4	R-3579	16	R-4188	28	R-4245	40	R-4290
5	R-3643	17	R-4189	29	R-4255	41	RLC-173
6	R-3667	18	R-4190	30	R-4257	42	RLC-175
7	R-3772	19	R-4192	31	R-4268	43	RLC-177
8	R-3788	20	R-4199	32	R-4270	44	RLC-92©
9	R-3892	21	R-4203	33	R-4272	45	R-552©
10	R-3990	22	R-4205	34	R-4275		
11	R-4140	23	R-4211	35	R-4280		
12	R-4153	24	R-4215	36	R-4283		

Sources of germplasm and checks: I.G.K.V., Raipur.

© = Checks

3.4 METHODLOGY

3.4.1. Observations recorded:

In this study, observations on seed yield and its components along with morphological traits based on linseed descriptor, Kanpur (2010) “National guidelines for the conduct of tests for Distinctness, Uniformity and Stability in linseed, India” published as per Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), Kanpur, (2010) have to recorded with following details

1- Plant growth habit
2- Plant height (cm)
3- Days to commencement of flowering
4- Days to 50 percent flowering
5- Size of corolla (mm)
6- Flower shape
7- Flower size (mm)
8- Colour of corolla
9- Petal aestivation
10- Petal venation colour
11- Stamen: filament colour
12- Anther colour
13- Capsule size (mm)
14- Number of capsules per plant
15- Days to maturity
16- Number of primary branches/plant
17- Number of secondary branches/plant
18- Total number of branches/plant
19- 1000 seed weight (g)
20- Oil content (%)
21- Seed yield/ plant (g)
22- Harvest index (%)

Techniques adopted for taking observations were as follows:

3.4.1.1. Days to commencement of flowering: counted as number of days from sowing to the day on which flowering has commenced at least one of the plant in the row of the particular genotype.

3.4.1.2. Days to 50% flowering: counted as number of days from sowing to the day on which 50% plant in a plot flowered.

3.4.1.3. Days to maturity: counted as number of days from sowing to the days on which plant present in a plot turn into golden colour.

3.4.1.4. Plant height at maturity (cm): measured in centimeters from the base of the plant to the top of main shoot.

3.4.1.5. Number of primary branches per plant: measured as counting of number of primary branches in each base of the plant.

3.4.1.6. Number of secondary branches per plant: measured as counting of number of secondary branches present in primary branches.

3.4.1.7. Total number of branches per plant: measured as counting the total number of both primary and secondary branches in each plant.

3.4.1.8. Number of capsules per plant: measure as counting the total number of seed bearing capsules of the each selected plant.

3.4.1.9. 1000 seed weight (g): weight of 1000 well developed seed of genotype collected from bulk of five plants which was recorded and expressed in gram.

3.4.1.10. Seed yield/plant (g): measured as by weighing the clean seed from each selected plant and expressed in gram as seed yield per plant.

3.4.1.11. Harvest index (%): measured in per cent by applying following formula,

$$\text{Harvest index (\%)} = \frac{\text{Economical} \quad \text{yield}}{\text{Biological} \quad \text{yield}} \times 100$$

3.4.1.12. Oil content (%): Oil content was evaluated by instrument named Dopi Minispic Pulsed NMR (Nuclear Magnetic Resonance). Earlier linseed seed sample is oven dried before oil estimation and gives direct value of percent in seeds.

Table 3.2: DUS (Distinctness, Uniformity and Stability) descriptors for linseed genotypes under study. As per Catalogue on linseed germplasm, Project Coordinating Unit (Linseed), Kanpur, (2010).

S.N.	Characters	Range
1.	Plant growth habit	Erect Semi-erect Bushy
2.	Days to commencement of flowering	Early Medium Late
3.	Colour of corolla	Blue White Light blue Violet
4.	Petal aestivation	Twisted Semi twisted Valvate
5.	Petal venation colour	Blue White Violet
6.	Flower shape	Disc Funnel Tubular
7.	Flower size	Small (<15mm) Medium (15-20mm) Large (>20mm)
8.	Stamen filament colour	Colourless Coloured below anther
9.	Anther colour	Blue Grey Yellow
10.	Capsule size	Small (<7mm) Medium(7-8mm) Bold (>8mm)

3.4.2. STATISTICAL ANALYSIS:-

“All the statistical analysis has to be done with aid of windostat version 9.2 from indostat service, Hyderabad.” The data were processed with the aid of different standard statistical procedure as mention below.

3.4.2.1. Analysis of variance

The statistics for diverse traits were bought into light to analyse the variability usually relevant to the Randomized Complete Block Design along with the formula suggested by “Panse and Sukhatme (1967)”. The linear model for Randomized Complete Block Design is as follows:

$$\boxed{Y_{ij} = \mu + g_i + r_j + e_{ij}}$$

Whereas,

Y_{ij} = Yield of j^{th} genotype in i^{th} replication.

μ = General mean

g_i = Effect of i^{th} genotype

r_j = Effect if j^{th} replication

e_{ij}= Error component

Table 3.3: Analysis of variances

Source of Variation	**Degree of freedom**	**Mean sum of square**	**Expected mean sum of squares**	**(F) Calculated**
Replication	(r-1)	MSR	$t\ \sigma^2 r$	MSR/MSE
Genotype	(g-1)	MSG	$r\ \sigma^2 t$	MSG/MSE
Error	(r-1) (g-1)	MSE	$\sigma^2 e$	
Total	(rg-1)			

Whereas,

r = replication number,

g = genotypes number.

The replicated data were subjected to variances analysis and test of significance as per the method of Fisher (1935).

3.4.2.2. Assessment of variability parameters

All the observed traits were analysed for each of the test genotypes taken under study were evaluated with the help of various variability parameters as mentioned below:

3.4.2.2.1. Mean

The average of recorded observation was evaluated as follow,

$$X = \frac{\Sigma Xi}{n}$$

Where,

X = Mean,

ΣX_i = Sum of all observations,

N = total number of all observations.

3.4.2.2.2. Range

A lowest and highest value of traits gives range which is expressed as follows,

Range = Highest value – Lowest value

3.4.2.2.3. Standard deviation

It is defined as the square root of the mean of the squared deviation of the individual values from the mean. It indicates a sort of group standard spread of values around their mean. It is the most widely used measures of dispersion.

$$SD = \sqrt{\frac{\Sigma d2}{N}}$$

Where,

SD= Standard deviation

N= Total number of observations

3.4.2.2.4. Coefficient of Variation (%)

The coefficient of variation is unit-free measures. It expressed as percentage. It is defined as the ratio of standard deviation to the mean. A phenotypic and genotypic coefficient of variation was estimated as per the formula proposed by “Burton (1952)”.

$$\text{CV (\%)} = \frac{SD}{\text{x}} \times 100$$

Where,
SD =Standard deviation
X = Mean

3.4.2.3. Genetic Parameters

3.4.2.3.1. Genotypic and phenotypic coefficient of variation (%)

Estimation of variation of phenotypic and genotypic coefficient was calculated as suggested by Burton (1952).

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

Category	**Range**
Low	less than 10 percent
Moderate	between 10-20 percent
High	more than 20 percent

3.4.2.3.2. Heritability (%)

It is the ratio of genotypic variances to the phenotypic variances (total variance).

Heritability in terms of broad sense (bs) was evaluated by using formula given by Allard (1960). It expressed as %.

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

Where,

$\sigma^2 g$= genotypic variances,

$\sigma^2 p$ = phenotypic variances.

The evaluations of heritability were categories as low, medium and high according to Robbinson(1966).

Category	**Range**
Lower	less than 50 percent
Medium	between 50-70 percent
Higher	more than 70 percent

3.4.2.3.3. Genetic advance

It is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic value of the parental population. The expected genetic advance signifies the change in a population in the direction of exclusive region under some selection pressure next to single generation of selection. The expected genetic advance or gain under selection is estimated by following method suggested by "Johnson *et al*. (1955)."

$$\text{Genetic advance (GA)} = h^2_{(bs)} \times K \times \sigma_p$$

Where,

$h^2_{(bs)}$ = Heritability in term of broad sense

σ_p = Phenotypic standard deviation of the original population

K = Selection intensity at 5% = 2.06 suggested by "Allard (1960)"

3.4.2.3.4. Genetic advance as percentage of mean:

$$\textbf{Genetic advance as percentage of } \bar{\mathbf{x}} = \frac{GA}{\bar{x}} \times 100$$

Whereas,

GA = Genetic advance

$\bar{x}$ = Population mean

The genetic advance as mean % was categories as low, moderate, high as given by Johnson *et al.,* Falconer and Mackey (1996).

Categories of genetic advances:-

Category	**Range**
Lower	Less than 10 percent
Moderate	Between 10-20 percent
Higher	More than 20 percent

3.4.2.4. ASSOCIATION ANALYSIS

For evaluating coefficient of phenotypic and genotypic association, make all possible combination pair. Correlation coefficient analysis have been carried out with the aid of following formula given by Miller *et al.* (1958), Hanson *et al.*, (1956) and Johnson *et al.,* (1955).

The component of genotypic co-variance among two characters and the component of phenotypic co-variance were obtained in the same way like for the component of variance. This co-variance was utilized to evaluate phenotypic and genotypic association among the pair of traits are as follows:-

3.4.2.4.1. Genotypic correlation coefficient between character x and y

$$r_{xy(g)} = \frac{\mathrm{Cov\ (g)X.Y}}{\sqrt{\sigma^2\mathrm{(g)X} \times \sigma^2\mathrm{(g)Y}}}$$

Where,

$R_{xy(g)}$ = Genotypic correlation coefficient between x and y

Cov $_{(g)}$ xy = Genotypic covariance between x and y

$\sigma^2{}_{x\ (g)}$ = Genotypic variance of character x

$\sigma^2{}_{y\ (g)}$ = Genotypic variance of character y

3.4.2.4.2. Phenotypic correlation coefficient between character x and y

$$r_{xy\ (p)} = \frac{\mathrm{Cov\ (p)X.Y}}{\sqrt{\sigma^2\mathrm{(p)X} \times \sigma^2\mathrm{(p)Y}}}$$

Where,

$r_{xy\,(p)}$ = Phenotypic correlation coefficient between x and y

Cov $_{(p)}xy$ = Phenotypic covariance between x and y

$\sigma^2 x_{(p)}$ = Phenotypic variance of character x

$\sigma^2 y_{\,(p)}$ = Phenotypic variance of character y

3.4.2.5. Testing for significance of correlation coefficients-

‘t’ test was applied to test the significance of correlation coefficients. ‘t’ values were estimated by using the following formula:

$$T = \frac{r}{\sqrt{1-r^2}}\, x \sqrt{n-2}$$

Comparing the‘t’ values at (n-2) degree of freedom, we test the significance of correlation coefficient (r). If calculated value of t is higher than the tabular value of‘t’ at (n-2) degree of freedom at given probability level, the coefficient of correlation is considered significant.

3.4.2.6. Methodology for Mahalanobis D^2 statistics diversity analysis

The D^2 statistics was developed by P.C. Mahalanobis in 1936 and Rao in 1952 suggested the application of this technique for genetic diversity assessment between the populations. Between any two populations, the generalized distance is given by formula,

$$\Delta = \Sigma\Sigma\lambda_{ij}\sigma_i\sigma_j$$

Where,

$D^{2\,=}$ Generalized distance square,

λ_{ij} = Reciprocal of the common dispersal matrix

$\sigma_{i\,=\,(}\mu_{i1}-\mu_{i2})$

$\sigma_{j\,=\,(}\mu_{j1}-\mu_{j2})$

μ = General mean

Since the formula for computation requires reversal of higher order determinant, the transformations of the original correlated unstandardized character means (Xs) to standardized uncorrelated variable (Ys) was performed to simply the computational procedures. The D^{2-}values of any two uncorrelated genotypes are obtained as the corresponding uncorrelated (Ys) values (Rao, 1952).

3.4.2.6.1. Clustering of D^2 values

Using Tocher's method, all the n (n-1)/2 D^2 values were clustered as described by Rao (1952).

3.4.2.6.1.1. Intra cluster distance

The formula given by Singh and Chaudhary (1977), the intra cluster distances were calculated.

$$\text{Square of intra cluster distance} = \frac{\Sigma Di^2}{n}$$

$\frac{\Sigma Di^2}{n}$ = Sum of distance between all possible combinations of the genotypes included in a cluster.

N = All possible cluster number

3.4.2.6.1.2. Inter cluster distance

The formula given by Singh and Chaudhary (1977), the inter cluster distances were calculated.

$$\text{Square of intra cluster distance} = \frac{\Sigma Di^2}{n_i n\mathrm{j}}$$

$\frac{\Sigma Di^2}{n_i n\mathrm{j}}$= Sum of distance between all possible combinations ($n_i n$j) of the genotypes included in a cluster study.

n_i= Number of entries in a cluster i,

n_j = Number of entries in a cluster j.

CHAPTER-IV
RESULTS AND DISCUSSION

The recent study entitled **"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"** was conducted with the main objective to study the variation and divergence present among the bold seeded genotypes and to analyse the association in different traits among the bold seeded genotypes of linseed. For that, an experiment was performed in Randomized Complete Block Design with 3 replications in 45 bold seeded (more than 6.5 g 1000-seed weight) genotypes of linseed along with the checks (RLC-92 and R-552). Five competitive plants have been selected randomly from each plot for recording observations." The data were recorded for seed yield and its contributing traits and the results obtained presented under the following topics:

4.1 Mean performance of bold seeded genotypes of linseed.

4.2 Analysis of variance and genetic parameters of bold seeded genotypes of linseed.

4.3 Association analysis of bold seeded genotypes of linseed.

4.4 Divergence analysis of bold seeded genotypes of linseed through cluster analysis.

4.1 Mean performance of genotypes of bold seeded genotypes of linseed

The mean performance of genotypes when compared with checks (RLC-92 and R-552) for seed yield and its contributing traits in bold seeded genotypes of linseed is given in Table 4.1 and discussed below:-

4.1.1. Plant height (cm)

Plant height ranged from 48.5 cm (R-3643) to 70.7 cm (R-4140) with a mean value 62.9 cm. R-4140 (70.7 cm) has high plant height when compared to best performing checks RLC-92 with a mean 62.4 cm.

4.1.2. Days to 50 % flowering

Days to 50% flowering ranged from 55.3 days (R-3892 and R-4225) to 69.0 days (R-4287) with a mean 59.0 days. Earliest days to 50% flowering was recorded in R-3892 (55.3 days) and R-4225 (55.3 days). Whereas, best performing checks R-552 was recorded 60.7 days for days to 50% flowering.

4.1.3. Days to maturity

Days to maturity ranged from 111.3 days (R-552) to 133.3 days (RLC-175) with a mean 119.9 days. R-4211 (111.7 days) has high when compared to the mean value of best performing checks R-552 (111.3 days) for days to maturity. R-4211 (111.7 days) was followed by R-3788 (113.0 days) and R-3892 (114.0 days) for days to maturity.

4.1.4. Number of primary branches per plant

Number of primary branches per plant ranged from 1.4 (RLC-177) to 4.8 (R-4290) with a mean value 5.9. R-4290 having the maximum number of primary branches per plant when compared to the best performing checks R-552 with a mean 2.7. R-4290 mean was followed by R-4288 (4.6) and R-4275 (4.2).

4.1.5. Number of secondary branches per plant

Number of primary branches per plant ranged from 11.0 (RLC-92) to 27.33 (RLC-175) with a mean value 15.8. RLC-175 having high mean value of number of secondary branches per plant. RLC-175 mean was followed by R-3312 (23.5) and R-4290 (20.7).

4.1.6. Total number of branches per plant

Total number of branches per plant ranged from 18.2 (R-4189) to 40.6 (R-3579) with a mean value 28.4. R-3579 having maximum total number of branches per plant when compared to the best performing checks R-552 (28.4). R-3579 mean was followed by 4167 (37.10) and R-3312 (35.9).

4.1.7. Number of capsule per plant

Number of capsules per plant ranged from 36.3 (R-4231) to 87.5 (R-4211) with a mean value 58.0. R-4211 having more number of capsules per plant when compared to the best performing checks R-552 (38.5). R-4211 mean was followed by R-4275 (86.7) and R-4199 (86.1).

4.1.8. 1000-Seed weight (g)

1000-seed weight ranged from 6.68 g (R-4187) to 8.74 g (R-4275) with a mean value 7.3g. R-4275 having highest 1000-seed weight when compared to the best performing checks R-552 (7.61 g). R-4275 mean was followed by R-4285 (8.47 g) and R-3579 (8.24 g).

4.1.9. Oil content (%)

Oil content ranged from 30.3% (R-4285) to 42.7% (R-552) with a mean value 35.2%. R-4140 (39.4%) having highest oil content when compared to the best performing checks R-552 (42.7%). R-552 mean was followed by 39.4% (R-4140) and 39.1% (R-3579).

4.1.10. Seed yield per plant (g)

Highest seed yield per plant was recorded for R-4275 (2.26 g) which is followed by R-3579 (2.1 g) and R-4199 (2.0 g). The minimum value was found in R-4215 (1.42 g) and R-4222 (1.49 g). Whereas, best checks RLC-92 was recorded (2.24 g) seed yield per plant.

4.1.11. Harvest Index (%)

Harvest index ranged from 17.1 % (R-3570) to 35.0 % (R-552) with a mean value of 23.3 %. R-552 having maximum harvest index which is followed by RLC-175 (31.6 %) and R-4285 (31.2 %).

Table 4.1: Mean performance for seed yield and yield contributing traits during 2019-20 at Raipur (C.G.)

S.N	Genotypes	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches/plant	No. of secondary branches/ plant	Total no. of branches/ plant	No. of capsules/ plant	1000-Seed weight	Oil content (%)	Seed yield (g)	Harvest Index (%)
1	R-3312	54.7	58.33	122.7	3.6	23.5	35.9	49.9	6.78	35.2	1.68	27.9
2	R-3313	61.1	56.00	114.3	3.9	16.7	30.0	45.2	6.76	33.3	2.00	25.0
3	R-3570	67.2	58.33	122.0	4.0	19.0	29.5	55.9	6.85	34.9	1.64	17.1
4	R-3579	65.9	61.33	125.7	3.9	20.1	40.6	81.8	8.24	39.1	2.10	26.1
5	R-3643	48.5	58.00	115.7	3.1	15.0	31.1	47.7	7.38	34.3	1.76	29.3
6	R-3667	52.3	56.67	115.0	3.8	19.3	31.7	71.2	7.29	34.6	1.69	28.1
7	R-3772	52.2	55.67	115.3	3.3	14.4	33.3	84.8	7.99	34.3	1.74	29.0
8	R-3788	70.4	55.67	113.0	2.9	15.2	35.1	67.9	7.49	33.6	1.82	18.2
9	R-3892	64.6	55.33	114.0	2.7	14.7	32.3	63.6	6.99	34.1	1.54	19.2
10	R-3990	69.0	58.67	125.0	3.7	13.2	31.3	70.7	7.99	35.5	1.61	17.9
11	R-4140	70.7	61.67	125.3	2.9	11.9	30.5	46.1	7.61	39.4	1.84	18.4
12	R-4153	58.3	58.00	116.0	2.9	11.5	34.8	47.8	6.69	38.7	1.45	20.7
13	R-4167	64.8	58.33	119.0	3.0	15.6	37.1	70.3	7.34	33.8	1.90	23.7
14	R-4176	55.0	57.00	115.3	3.1	13.0	26.9	63.4	6.78	34.0	1.60	26.7
15	R-4186	52.8	57.00	116.3	3.4	12.5	22.7	56.3	7.30	34.5	1.76	29.4
16	R-4188	56.0	56.00	114.7	2.5	14.5	21.3	38.8	7.48	35.0	1.83	25.7
17	R-4189	67.0	61.00	125.3	2.6	11.7	18.2	60.3	7.06	34.3	1.98	21.9
18	R-4190	65.1	58.33	118.3	2.9	11.7	18.3	72.7	7.07	33.7	1.95	24.4
19	R-4192	63.9	57.33	117.0	2.7	11.7	23.1	80.1	6.72	34.7	1.70	21.2
20	R-4199	55.4	56.67	117.0	4.0	15.8	25.7	86.1	7.47	33.3	2.03	29.0
21	R-4203	62.8	60.00	123.3	3.3	16.2	26.2	45.1	6.75	36.0	1.52	19.0
22	R-4205	61.6	62.00	124.7	2.9	16.4	27.8	57.9	7.61	32.0	1.79	22.3
23	R-4211	63.5	57.33	111.7	3.3	18.3	28.6	87.5	7.70	30.7	1.76	21.9
24	R-4215	64.5	59.00	123.0	2.8	16.0	27.9	69.6	6.79	36.3	1.42	17.7
25	R-4222	64.0	58.00	116.7	3.5	16.5	27.2	41.6	6.87	37.7	1.50	18.7
26	R-4225	58.5	55.33	118.0	3.1	15.0	25.9	40.8	7.31	34.0	1.81	25.9
27	R-4231	65.9	58.00	119.7	3.2	13.7	25.2	36.3	7.08	35.3	1.77	22.1
28	R-4245	70.2	57.00	117.7	3.2	14.8	26.4	49.8	6.89	37.0	1.86	18.6
29	R-4255	62.5	57.67	120.3	3.1	17.3	26.5	76.4	6.87	36.0	1.60	20.0
30	R-4257	66.1	57.67	118.7	3.0	13.9	25.1	62.8	6.82	37.7	1.55	17.2

S.N.	Genotypes	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches/plant	No. of secondary branches/ plant	Total no. of branches/ plant	No. of capsules/ plant	1000-Seed weight	Oil content (%)	Seed yield (g)	Harvest Index (%)
31	R-4268	68.7	57.7	118.7	3.3	16.6	27.6	41.9	7.3	31.3	1.73	19.3
32	R-4270	62.8	57.3	117.7	3.3	16.0	25.9	43.7	7.0	36.7	1.65	20.7
33	R-4272	64.2	59.3	124.0	2.9	15.0	27.1	65.7	7.2	34.7	1.68	20.9
34	R-4275	64.0	56.3	118.0	4.2	17.9	28.9	86.7	8.7	31.7	2.26	28.3
35	R-4280	68.4	59.7	122.7	3.4	14.5	25.9	63.7	7.2	34.0	1.71	19.0
36	R-4283	65.1	61.3	124.0	2.7	13.2	24.1	47.1	7.5	34.7	1.82	26.0
37	R-4285	65.3	59.3	116.3	2.9	11.7	23.3	51.5	8.5	30.3	2.20	31.2
38	R-4287	64.6	69.0	130.7	3.7	17.3	28.5	42.7	6.7	37.3	1.63	23.3
39	R-4288	66.8	64.3	125.7	4.6	18.3	30.1	78.7	7.3	38.0	2.00	21.8
40	R-4290	67.5	59.3	124.3	4.8	20.7	31.2	61.4	7.2	36.7	1.81	20.1
41	RLC-173	66.5	61.7	126.3	3.3	19.3	31.0	40.5	7.6	33.4	1.50	18.7
42	RLC-175	58.6	66.0	133.3	3.9	27.3	33.1	41.4	7.7	35.5	2.21	31.6
43	RLC-177	68.1	63.0	125.3	1.4	15.0	28.3	40.1	7.8	36.3	1.90	20.8
44	RLC92©	62.4	63.0	118.3	1.7	11.0	27.9	38.4	7.5	38.1	2.24	28.0
45	R-552©	53.8	60.7	111.3	2.7	16.7	28.4	38.6	7.6	42.7	2.10	35.0
	Mean	62.7	59.0	119.9	3.2	15.8	28.4	58.0	7.3	35.2	1.80	23.3
	CV %	2.03	2.2	2.8	5.7	6.5	12.1	8.8	0.7	4.0	9.30	9.2
	CD at 5%	2.07	2.1	5.5	0.3	1.7	5.6	8.3	0.1	2.3	0.27	3.5
	SEm±	0.73	0.7	1.9	0.1	0.6	2.0	2.9	0.03	0.8	0.10	1.2

4.2 Analysis of variance and variation parameters of bold seeded genotypes of linseed

4.2.1. Analysis of variance

On the basis of sound genetics information genetic enhancement of linseed crop either through direct enhancement of traits in which plant breeder is interested or indirect enhancement through component traits can be effectively achieved. In order to touch the eventual goal of getting high quality seed yield, study of presence of genetic variability for seed yield and its improvement, and the nature of correlation among themselves is a crucial prerequisite.

The analysis of variance for seed yield per plant and its contributing traits in the present investigation of bold seeded genotypes of linseed disclosed that significantly differences among the genotypes. These suggested that there were inherent genetic differences for all the genotypes. High significant differences among mean square exhibited genetic variances which were required to work out an enhancement of crop in effective programme.

The table showed that genotypic mean sum of squares was observed to be significantly for all the traits. This showed that presence of variation for seed yield per plant and its relative traits of bold seeded genotypes of linseed. (Table 4.2)

Table 4.2: Analysis of variance for seed yield and its contributing traits in bold seeded linseed during 2019-20 at Raipur (C.G.)

S. N	Source of variance	DF	PH	DTF	DM	PB	SB	TB	C	SW	OC	SY	HI
1.	Replication	2	1.5	5.2	9.4	0.1	3.0	4.2	79.6	0.07	5.4	0.01	1.7
2.	Genotype	44	92.6**	25.1**	74.7**	1.2**	32.0**	62.0**	743.6**	0.7**	17.3**	0.1**	62.9**
3.	Error	88	1.6	1.7	11.4	0.03	1.05	11.8	26.1	0.003	2.0	0.03	4.6

* Significant at 5% level, ** Significant at 1% level

PH- Plant height (cm)	**C- Number of capsules per plant**
DTF- Days to 50% flowering	**SW- 1000 Seed weight (g)**
DM- Days to maturity	**OC- Oil content (%)**
PB- Primary branches per plant	**SY- Seed yield per plant (g)**
SB- Secondary branches per plant	**HI- Harvest index (%)**
TB- Total branches per plant	**DF- Degree of freedom**

4.2.2. GENETIC VARIABILITY

Results of genetic variability revealed that under study for all the traits phenotypic coefficient of variation was higher than genotypic coefficient of variation which indicates that environment having masking effect on the expression of genetic variability (Table 4.3). This range of variation was found for all the traits indicated enough scope to study considerable range of variation was reported for all the traits. The evaluation of PCV and GCV were categorized as high (>20%), moderate (10-20%) and low (<10%) according to Sivasubramanian and Madhavamenon (1973).

The highest magnitude of genotypic coefficient of variation was noticed for number of capsules per plant (26.6%) which is followed by number of secondary branches per plant (20.4%).

The moderate magnitude for number of primary branches per plant (19.3%) which is followed by harvest index (18.9%), total number of branches per plant (14.4%) and seed yield per plant (10.7%).

The low magnitude of genotypic coefficient of variation was noticed in plant height (8.9%) followed by 1000 seed weight (6.5%), oil content (6.4%), days to 50% flowering (4.7%) and days to maturity (3.8%).

The highest magnitude of phenotypic coefficient of variation was noticed for number of capsule per plant (28.1%) followed by number of secondary branches per plant (21.4%), harvest index (21.1%) and number of primary branches per plant (20.1%).

The moderate magnitude of phenotypic coefficient of variation for total number of branches per plant (18.8%) and seed yield per plant (14.1%).

The low magnitude of phenotypic coefficient of variation was found in plant height (9.0%) followed by oil content (7.6%), 1000 seed weight (6.6%), days to 50% flowering (5.2%) and days to maturity (4.7%).

“The characters viz., number of capsule per plant, plan number of secondary branches, number of primary branches per plant, seed yield per plant and harvest index exhibiting high genotypic and phenotypic coefficient of variation showed the presence of considerable amount of variability for these characters for all genotypes.” Hence, there is enough scope for enhancement of these traits.

These results fall in line with those of Belete and Yohannes (2013), Reddy *et al.*, (2013), Patel *et al.* (2015), Chandrawati *et al.* (2016), Paul and Kumari (2018), Singh *et al.* (2019) and Upadhyay *et al.* (2019 b) noticed “highest magnitude of genotypic variation was observed seed yield per plant (g).”

Result similar to those of Reddy *et al*. (2013), Bibi *et al*., (2013), Pali and Mehta (2014), Kanwar *et al.* (2014), Patel *et al.*, (2015), Chandrawati *et al.* (2016), Tewari and Singh (2018) and Upadhyay *et al.* (2019 a) reported “high variation of genotypic and phenotypic coefficient for number of capsules per plant, number of secondary branches per plant and harvest index.”

Table 4.3: Genetic Parameter of variation for seed yield and its contributing traits in bold seeded linseed during 2019-20 at Raipur (C.G.)

S. N.	Characters	Mean	Range		Critical Differences (5%)	Coefficient of Variation (%)		h^2 (bs) %	GA	GA % mean
			Max.	Min.		PCV (%)	GCV (%)			
1	**Plant height (cm)**	62.7	70.7	48.5	2.1	9.0	8.8	94.9	11.0	17.6
2	**Days to 50% flowering**	59.0	69.0	55.3	2.1	5.2	4.7	82.3	5.2	8.8
3	**Days to maturity**	119.9	133.3	111.3	5.5	4.7	3.8	64.8	7.6	6.3
4	**No. of primary branches/plant**	3.2	4.8	1.4	0.3	20.2	19.3	92.0	1.2	38.2
5	**No. of secondary branches/plant**	15.8	27.3	11.0	1.7	21.4	20.4	90.7	6.3	39.9
6	**Total no. of branches/plant**	28.4	40.6	18.2	5.6	18.8	14.4	58.7	6.5	22.7
7	**No. of capsule/plant**	58.0	87.5	36.3	8.3	28.1	26.6	90.1	30.2	52.1
8	**1000-Seed weight (g)**	7.3	8.7	6.7	0.1	6.6	6.5	98.7	0.1	13.5
9	**Oil content (%)**	35.2	42.7	30.3	2.3	7.6	6.4	71.4	3.9	11.2
10	**Seed yield (g)**	1.8	2.3	1.4	0.3	14.2	10.7	57.1	0.3	16.7
11	**Harvest Index (%)**	23.3	35.0	17.1	3.5	21.1	18.9	80.8	8.2	35.1

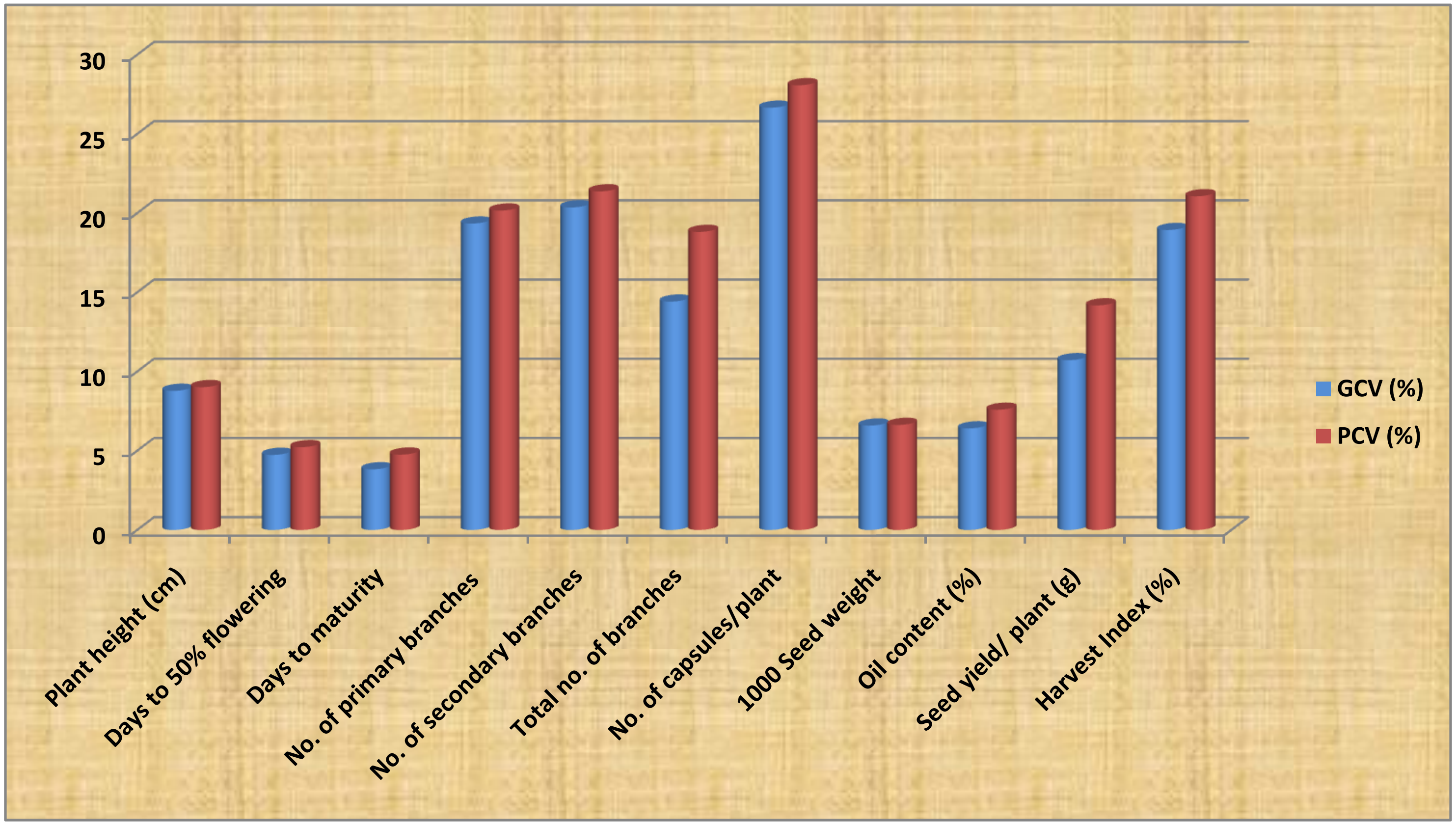

Fig. 4.1: Graphical representation of comparison of PCV (Phenotypic coefficient of variation) and GCV (Genotypic coefficient of variation) of seed yield and its contributing trait in bold seeded linseed during 2019-20 at Raipur (C.G.)

4.2.3. Heritability and Genetic advance

Heritability compute the degree of similarity between breeding value and phenotypic. Heritability is strictly well found for the population from which they are derived. For different population estimation of same characters may vary. Difference present in estimation of heritability is mainly due to environmental variance. The environment variance is depending on the situation of cultivar and management where more uniform condition increases heritability and more variable condition decreases the heritability. Heritability evaluates efficiency by which we can utilize the genotypic variability in breeding programme. The concept of heritability in broad sense is more helpful to know the relative effect of environment and genotype to determine the phenotypic difference. According to Robbinson (1966) estimation of heritability have been broadly categories into low (<50%), medium (50-70%), high (>70%) classes.

On a basis of scientific, genetic advance gives an estimation of reliable gain at a specified intensity of selection which is a chief implement in plant breeding. Therefore, heritability coupled with genetic advance is helpful in laying emphasis in selection for seed yield and its component. However, the proportion of enhancement in trait would be more reliable on the amount of variability in the population where selection has to be done. According to Johnson *et al.*, (1996) estimate genetic advance as mean percent was broadly categories into low (<10%), medium (10-20%) and high (>20%) classes.

Heritability in broad sense was recorded for each of the yield contributing trait under study (Table: 4.3). The highest heritability was recorded for 1000 seed weight (98.7%), plant height (94.9%), number of primary branches per plant (92.0%) and number of secondary branches per plant (90.7%), days to 50% flowering (82.3%), harvest index (80.8%) and oil content (71.4%). (Table 4.3)

The moderate heritability was noticed for days to maturity (64.8%), total number of branches per plant (58.7%) and seed yield per plant (57.1%). (Table 4.3)

The high amount of genetic advance as mean percent was observed for number of capsules per plant (52.1%) followed by number of secondary branches per plant (39.9%), number of primary branches per plant (38.2%), harvest index (35.0%) and total number of branches per plant (22.7%).

The moderate amount of genetic advance was recorded for plant height (17.6%) followed by 1000 seed weight (13.5%), seed yield per plant (16.7%) and oil content (11.1%).

The low genetic advance was recorded for the trait days to 50% flowering (8.8%) followed by days to maturity (6.3%).

These results fall in line with those of Pali and Mehta (2014), Chandarwati *et al.* (2016), Singh *et al.* (2019) and Upadhyay *et al.* (2019) reported "high heritability for 1000 seed weight, plant height, number of primary branches per plant and number of secondary branches per plant."

Kumar *et al.* (2012), Kasana *et al.* (2016), Siddiqui *et al.* (2016), Kumar *et al.* (2017), Singh *et al.* (2019) and Upadhyay *et al.* (2019) reported "high genetic advance for number of capsules per plant, number of secondary branches per plant, number of primary branches per plant and harvest index."

Kanwar *et al.* (2014), Pali and Mehta (2014), Rajanna *et al*. (2014), Kumar *et al*. (2015), Kasana *et al.* (2016), Tewari and Singh (2018) and Singh *et al.* (2019) reported "high heritability and high genetic advance for number of capsules per plant, number of primary branches per plant, number of secondary branches per plant and seed yield per plant."

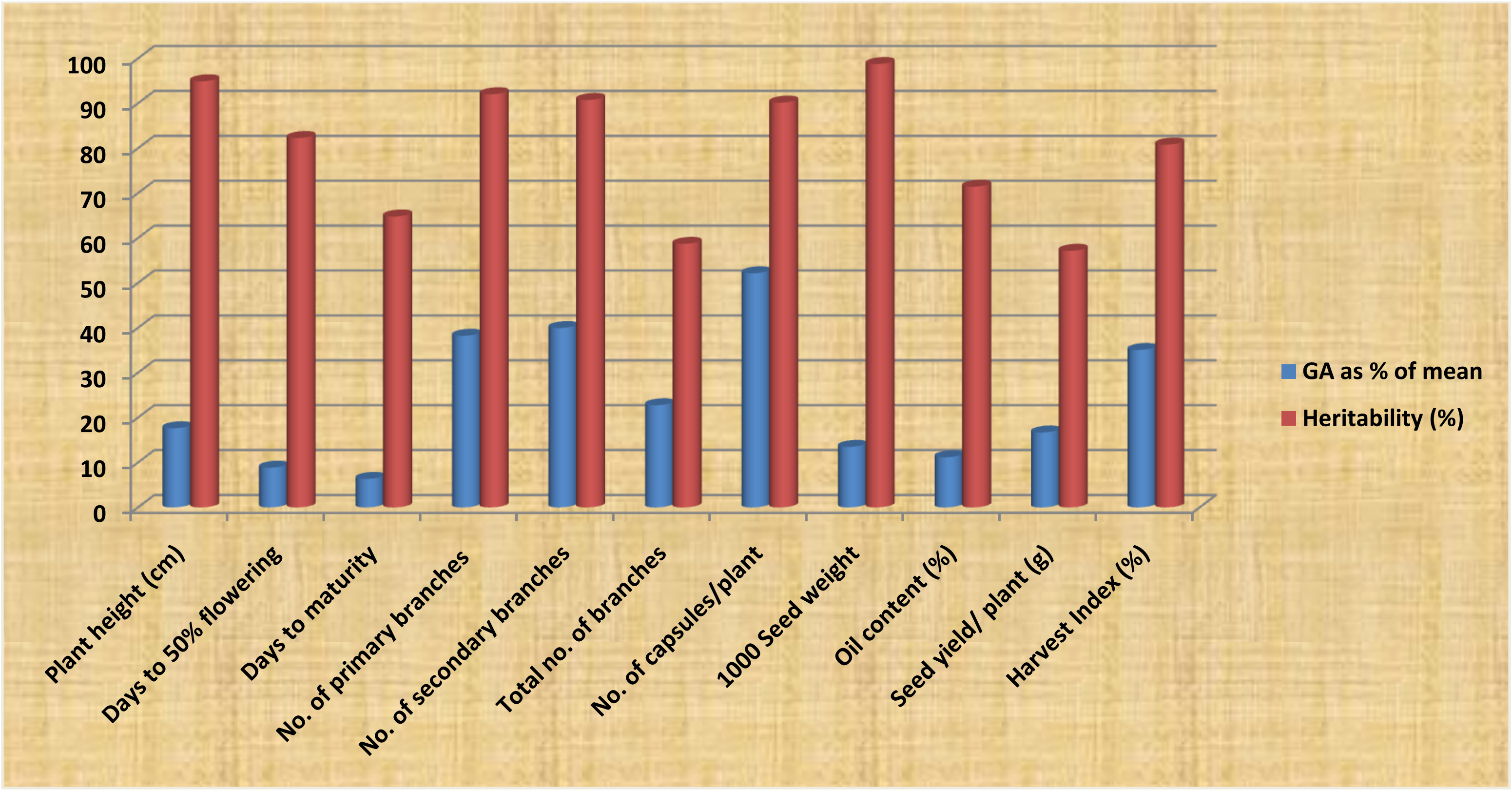

Fig.4.2: Heritability and genetic advance as mean percent for seed yield and its contributing characters in bold seeded linseed 2019-20 at Raipur (C.G.)

4.3 Association analysis among seed yield and its contributing traits in bold seeded genotypes of linseed

Seed yield or economical yield is the most important character of any crop which is the resultant of both genetic as well as environmental factors. Hence, in direct selection of yield through its associated character is very much useful for devising efficient breeding strategies for evolving high yielding varieties. The statistical technique such as correlation coefficient helps in establishing relationship or association among the entire yield and its component traits, which can be utilized in the proper selection processes for improving the desirable trait as well as yielding ability of the crop.

The high significant and positive correlation of seed yield per plant with 1000 seed weight suggested that heavy weight seed might have higher seed yield. Therefore, selection based on 1000 seed weight could be depending on rich seed yield for the development of varieties. Similar finding have also been reported by Patel and Rao (2009), Gauraha *et al.* (2011), Savita *et al.* (2011), Chandarwati *et al.* (2016), Kasana *et al.* (2016) and Sharma *et al*. (2016).

The genotypic and phenotypic correlation coefficients of seed yield and its component traits are shown in Table 4.4 and Table 4.5 respectively. Correlation analysis in bold seeded linseed revealed that seed yield per plant positively and significantly correlated with “days to 50% flowering (r_g=0.220, r_p=0.211) and 1000 seed weight (r_g=0.688, r_p=0.519) whereas, positive correlation with days to maturity(r_g=0.019, r_p=0.007), number of primary branches per plant(r_g=0.052, r_p=0.029), number of secondary branches per plant(r_g=0.094, r_p=0.076) and number of capsules per plant(r_g=0.050, r_p=0.059)” at both genotypic and phenotypic level.

Similar findings have also been noticed by Gauraha *et al.* (2011), Ibrar *et al.* (2014), Pali and Mehta (2014), Rajanna *et al.* (2014), Tariq *et al.* (2014), Kasana *et al.* (2016), Kumar *et al.* (2017) and Dhirhi and Mehta (2019) reported that “days to maturity, number of primary branches per plant, number of secondary branches per plant and number of capsules per plant had positive association with seed yield per plant.”

Savita *et al.* (2011), Rajanna *et al.* (2014), Chaudhary *et al.* (2016), Chandarwati *et al.* (2016), Kasana *et al.* (2016), Sharma *et al*. (2016), Kumar *et al.* (2017) and Ankit *et al.* (2018) noticed that seed yield per plant shows positive and significantly correlated with days to 50% flowering and 1000 seed weight.

Table 4.4: Genotypic correlation coefficient for seed yield and contributing traits in bold seeded linseed during 2019-20 at Raipur (C.G.)

	PH	DF	DM	PB	SB	TB	C	SW	OC	SY	HI
PH	**1.000**										
DF	0.251**	**1.000**									
DM	0.424**	0.907**	**1.000**								
PB	-0.043	0.000	0.203*	**1.000**							
SB	-0.117	0.262**	0.414**	0.608**	**1.000**						
TB	-0.060	0.085	0.146	0.329**	0.543**	**1.000**					
C	0.015	-0.299**	-0.159	0.337**	0.025	0.172*	**1.000**				
SW	0.024	0.078	0.035	-0.003	0.077	0.219*	0.231**	**1.000**			
OC	0.002	0.408**	0.220**	-0.056	0.021	0.219*	-0.278**	-0.260**	**1.000**		
SY	-0.020	0.220**	0.019	0.052	0.094	-0.044	0.050	0.688**	-0.042	**1.000**	
HI	-0.755**	0.038	-0.245**	0.043	0.141	0.023	-0.034	0.436**	-0.037	0.596**	**1.000**

* Significant at 5% level, ** Significant at 1% level

PH- Plant height (cm)
DF- Days to 50% flowering
DM- Days to maturity
PB- Primary branches per plant
SB- Secondary branches per plant
TB- Total branches per plant
C- Number of capsules per plant
SW- 1000 Seed weight (g)
OC- Oil content (%)
SY- Seed yield per plant (g)
HI- Harvest index (%)

Table 4.5: Phenotypic correlation coefficient of seed yield and contributing traits in bold seeded linseed during 2019-20 at Raipur (C.G.)

	PH	DF	DM	PB	SB	TB	C	SW	OC	SY	HI
PH	**1.000**										
DF	0.226**	**1.000**									
DM	0.334**	0.603**	**1.000**								
PB	-0.038	-0.006	0.176*	**1.000**							
SB	-0.110	0.233**	0.313**	0.572**	**1.000**						
TB	-0.044	0.056	0.056	0.253**	0.467**	**1.000**					
C	0.016	-0.257**	-0.117	0.307**	0.024	0.096	**1.000**				
SW	0.023	0.073	0.019	-0.004	0.066	0.167	0.218*	**1.000**			
OC	0.024	0.290**	0.130	-0.056	0.009	0.187*	-0.269**	-0.207*	**1.000**		
SY	-0.029	0.211*	0.007	0.029	0.076	-0.017	0.059	0.519**	-0.081	**1.000**	
HI	-0.671**	0.071	-0.185*	0.029	0.127	0.010	-0.014	0.391**	-0.064	0.688**	**1.000**

* Significant at 5% level, ** Significant at 1% level.

PH- Plant height (cm)
DF- Days to 50% flowering
DM- Days to maturity
PB- Primary branches per plant
SB- Secondary branches per plant
TB- Total branches per plant

C- Number of capsules per plant
SW- 1000 Seed weight (g)
OC- Oil content (%)
SY- Seed yield per plant (g)
HI- Harvest index (%)

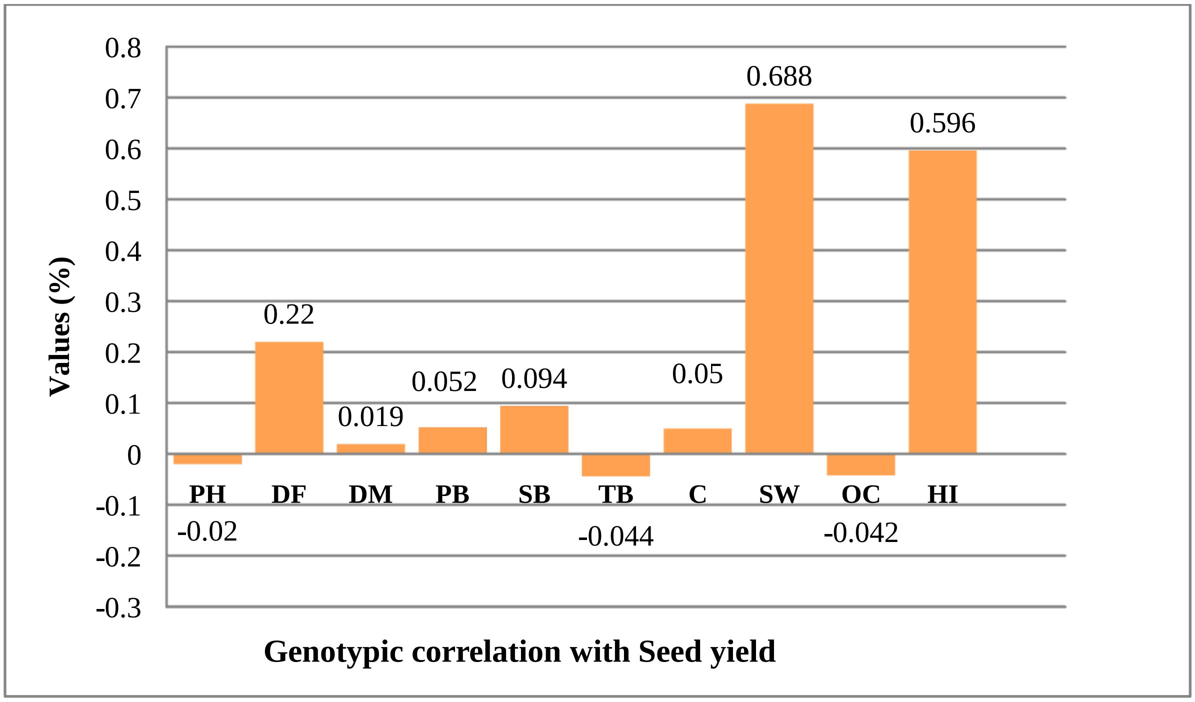

Fig.4.3: Graphical representation of genotypic correlation among seed yield/plant (g) and yield contributing characters in bold seeded linseed genotypes.

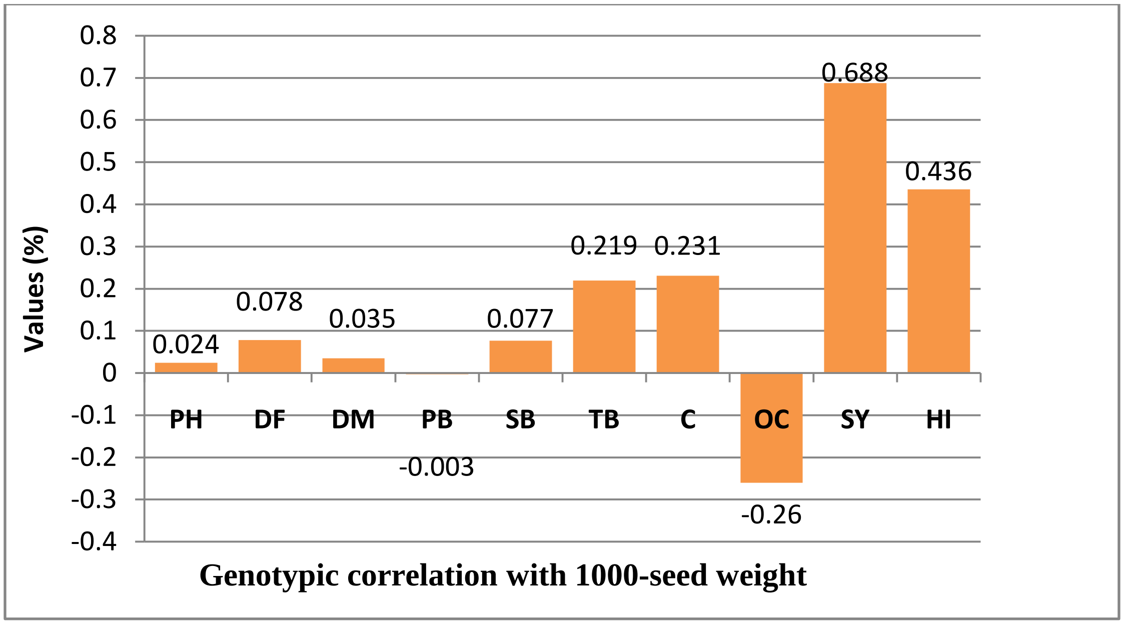

Fig.4.4: Graphical representation of genotypic correlation among 1000-seed weight (g) and yield contributing characters in bold seeded linseed genotypes.

4.4 Genetic divergence analysis through Mahalanobis D^2 clusters analysis

The existence of genetic divergence among the 45 genotypes of bold seeded linseed was examined by employing Mahalanobis D^2-statistics. The clustering pattern of 45 genotypes on the basis of the D^2-statistics analysis has been presented in Table 4.6. The genotypes were a grouped into eight distinct clusters. The highest number of genotypes appeared in cluster I which possessed 27 genotypes namely, R-3313, R-3570, R-3892, R-4167, R-4188, R-4189, R-4190, R-4192, R-4203, R-4205, R-4211, R-4215, R-4222, R-4225, R-4231, R-4245, R-4255, R-4257, R-4268, R-4270, R-4272, R-4280, R-4283, R-4288, R-4290, RLC-92 and RLC-173. The second highest number of genotypes was found in cluster II which was comprised of 8 genotypes namely, R-3312, R-3643, R-3667, R-3772, R-4176, R-4186, R-4199 and R-552. Cluster III comprised of 5 genotypes *viz.;* R-3579, R-3788, R-3990, R-4140 and RLC-177. The lowest genotypes were found in cluster IV (R-4153), V (R-4287), VI (R-4275), VII (RLC-175) and VIII (R-4285). They all possessed only one genotype.

4.4.1. Intra and inter clusters distance

The estimate of intra and inter cluster distance represent by D^2 values have been given in Table 4.7. The maximum intra-cluster distance was obtained for cluster III (90.91) followed by cluster II (75.97) and cluster I (72.47).

The minimum intra-cluster D^2 values were shown by cluster IV (0.00), V (0.00), VI (0.00), VI (0.00), VII (0.00) and VIII (0.00), they all have only one genotype.

The highest inter cluster D^2 values were observed between cluster VI and IV (711.93) followed by cluster VI and V (696.75), cluster VI and II (551.16), cluster III and II (487.20) and cluster VIII and IV (461.72).

The lowest inter-cluster D^2 value was found between cluster V and IV (63.19) followed by cluster VIII and VI (114.87).

4.4.2. Inter cluster mean

Cluster III (68.82) showed the highest cluster mean for plant height followed by cluster VIII (65.27) and cluster V (64.63). The lowest cluster mean was showed by cluster II (53.10).

Cluster V (69.00) showed the highest cluster mean for days to 50% flowering followed by cluster VII (66.00) and cluster III (60.07). The lowest cluster mean was showed by cluster VI (56.33).

Cluster VII (133.33) showed the highest cluster mean for days to maturity followed by cluster V (130.67) and cluster III (122.87). The lowest cluster mean was showed by cluster IV (116.00).

Cluster VI (4.20) showed the highest cluster mean for number of primary branches per plant followed by cluster VII (3.87) and cluster V (3.73). The lowest cluster mean was showed by cluster VIII (2.87).

Cluster VII (27.33) showed the highest cluster mean for number of secondary branches per plant followed by cluster VI (17.93) and cluster V (17.33). The lowest cluster mean was showed by cluster IV (11.53).

Cluster IV (34.80) showed the highest cluster mean for total number of branches per plant followed by cluster III (33.19) and cluster VII (33.07). The lowest cluster mean was showed by cluster VIII (23.33).

Cluster VI (86.73) showed the highest cluster mean for number of capsules per plant followed by cluster II (62.26) and cluster III (61.31). The lowest cluster mean was showed by cluster VII (41.40).

Cluster VI (8.75) showed the highest cluster mean for 1000 seed weight followed by cluster VIII (8.47) and cluster III (7.83). The lowest cluster mean was showed by cluster V (6.69).

Cluster IV (38.67) showed the highest cluster mean for oil content followed by cluster V (37.33) and cluster III (36.81). The lowest cluster mean was showed by cluster VIII (30.33).

Cluster VI (2.26) showed the highest cluster mean for seed yield per plant followed by cluster VII (2.21) and cluster VIII (2.18). The lowest cluster mean was showed by cluster IV (1.45).

Cluster VII (31.62) showed the highest cluster mean for harvest index followed by cluster VIII (31.18) and cluster II (29.30). The lowest cluster mean was showed by cluster III (20.28).

Table 4.6: Genotypes included in different clusters based on D^2 analysis in bold seeded linseed

Clusters No.	No. of genotypes	Name of the genotypes
I	27	R-3313, R-3570, R-3892, R-4167, R-4188, R-4189, R-4190, R-4192, R-4203, R-4205, R-4211, R-4215, R-4222, R-4225, R-4231, R-4245. R-4255. R-4257, R-4268, R-4270, R-4272, R-4280, R-4283, R-4288, R-4290, RLC-92, RLC-173
II	8	R-3312, R-3643, R-3667, R-3772, R-4176, R-4186, R-4199, R-552
III	5	R-3579, R-3788, R-3990, R-4140, RLC-177
IV	1	R-4153
V	1	R-4287
VI	1	R-4275
VII	1	RLC-175
VIII	1	R-4285

Table 4.7: Average intra and inter cluster distance

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**72.47**							
II	283.02	**75.97**						
III	156.73	487.20	**90.91**					
IV	144.83	151.86	392.79	**0.00**				
V	157.15	187.89	385.98	63.19	**0.00**			
VI	394.10	551.16	204.92	711.93	696.75	**0.00**		
VII	215.77	192.22	265.41	301.18	204.09	279.31	**0.00**	
VIII	309.16	305.41	234.12	464.72	461.99	114.87	181.30	**0.00**

Table 4.8: Cluster means for yield and its components in 45 bold seeded linseed genotypes

Cluster No.	No. of genotypes	PH	DF	DM	PB	SB	TB	C	SW	OC	SY	HI
I	27	64.51	58.75	120.00	3.17	15.50	26.95	56.88	7.14	34.96	1.75	21.35
II	8	53.10	57.50	116.08	3.37	16.27	29.48	62.26	7.33	35.36	1.79	29.30
III	5	68.82	60.07	122.87	2.88	15.08	33.19	61.31	7.83	36.81	1.85	20.28
IV	1	58.30	58.00	116.00	2.93	11.53	34.80	47.80	6.70	38.67	1.45	20.76
V	1	64.63	69.00	130.67	3.73	17.33	28.47	42.73	6.69	37.33	1.63	23.33
VI	1	64.00	56.33	118.00	4.20	17.93	28.87	86.73	8.75	31.67	2.26	28.29
VII	1	58.60	66.00	133.33	3.87	27.33	33.07	41.40	7.69	35.47	2.21	31.62
VIII	1	65.27	59.33	116.33	2.87	11.73	23.33	51.47	8.47	30.33	2.18	31.18

PH- Plant height (cm)
DF- Days to 50% flowering
DM- Days to maturity
PB- Primary branches per plant
SB- Secondary branches per plant
TB- Total branches per plant

C- Capsule per plant
SW- 1000 Seed weight (g)
OC- Oil content (%)
SY- Seed yield per plant (g)
HI- Harvest index (%)

Table 4.9: Morphological characters of bold seeded linseed during *rabi* 2019-20 at Raipur (C.G.)

S.N	Genotypes	Plant growth habit	Days to commencement of flowering	Colour of corolla	Petal venation colour	Petal aestivation	Flower shape	Flower size (mm)	Corolla length (mm)	Corolla width (mm)	Anther colour	Stamen: filament colour	Capsule size (mm)
1	R-3312	SE	S	B	B	ST	F	M	M	M	B	CL	Bo
2	R-3313	SE	S	B	B	ST	F	M	M	M	G	CL	Bo
3	R-3570	SE	S	B	B	ST	F	M	M	M	G	CL	M
4	R-3579	SE	S	B	B	ST	F	M	M	M	B	CL	Bo
5	R-3643	SE	S	B	B	ST	F	M	M	M	G	CL	M
6	R-3667	SE	S	V	V	ST	Tu	M	M	M	B	CL	M
7	R-3772	SE	S	B	B	ST	F	M	M	M	B	CL	M
8	R-3788	SE	S	B	B	ST	F	M	M	M	B	CL	M
9	R-3892	SE	S	B	B	ST	F	M	M	M	B	CL	M
10	R-3990	SE	S	W	W	ST	D	M	M	Wi	Y	CL	M
11	R-4140	SE	S	B	B	ST	F	M	M	M	G	CL	M
12	R-4153	SE	S	DB	B	ST	F	M	M	M	B	CL	Bo
13	R-4167	SE	S	B	B	ST	F	M	M	M	B	CL	M
14	R-4176	SE	S	W	W	ST	D	M	M	M	Y	CL	M
15	R-4186	SE	S	W	W	ST	D	M	M	Wi	Y	CL	M
16	R-4188	SE	S	B	B	ST	F	M	M	M	B	CL	M
17	R-4189	SE	S	LB	B	ST	F	M	M	M	G	CL	M
18	R-4190	SE	S	LB	B	ST	F	M	M	M	G	CL	M
19	R-4192	SE	S	LB	B	ST	F	M	M	M	B	CL	M
20	R-4199	SE	S	B	B	ST	F	M	M	M	B	CL	M
21	R-4203	SE	S	LB	B	ST	F	M	M	M	G	CL	M
22	R-4205	SE	S	B	B	ST	F	M	M	M	B	CL	M
23	R-4211	SE	S	LB	B	ST	F	M	M	M	B	CL	M
24	R-4215	SE	S	V	V	ST	Tu	M	M	M	B	CL	M

S.N	Genotypes	Plant growth habit	Days to commencement of flowering	Colour of corolla	Petal venation colour	Petal aestivation	Flower shape	Flower size (mm)	Corolla length (mm)	Corolla width (mm)	Anther colour	Stamen: filament colour	Capsule size (mm)
25	R-4222	SE	S	B	B	ST	F	M	M	M	G	CL	M
26	R-4225	SE	S	B	B	ST	F	M	M	Wi	B	CL	M
27	R-4231	SE	S	B	B	ST	F	M	M	M	B	CL	M
28	R-4245	SE	S	B	B	ST	F	M	M	Wi	G	CL	M
29	R-4255	SE	S	B	B	ST	F	M	M	Wi	B	CL	M
30	R-4257	SE	S	W	W	ST	D	M	M	M	Y	CL	M
31	R-4268	SE	S	B	B	ST	F	M	M	M	B	CL	M
32	R-4270	SE	S	B	B	ST	F	M	M	M	G	CL	M
33	R-4272	SE	M	B	B	ST	F	M	M	M	B	CL	M
34	R-4275	SE	M	B	B	ST	F	M	M	M	B	CL	Bo
35	R-4280	SE	S	B	B	ST	F	M	M	Wi	B	CL	M
36	R-4283	SE	M	B	B	ST	F	L	M	M	G	CL	M
37	R-4285	SE	S	LB	B	ST	F	M	M	M	G	CL	Bo
38	R-4287	SE	M	B	B	ST	F	L	M	M	B	CL	M
39	R-4288	SE	M	B	B	ST	F	L	M	M	B	CL	M
40	R-4290	SE	M	B	B	ST	F	L	M	Wi	B	CL	M
41	RLC-173	SE	S	B	B	ST	D	L	M	M	B	CL	Bo
42	RLC-175	SE	S	B	B	Tw	D	L	M	M	B	CL	Bo
43	RLC-177	SE	S	B	B	ST	D	L	M	M	G	CBA	Bo
44	RLC-92	E	S	B	B	ST	D	L	M	M	B	CL	M
45	R-552	SE	S	V	V	ST	F	M	M	M	B	CL	Bo

SE- Semi-erect
W- White
L- Large
E- Erect
V- Violet
Wi- Wide
S- Short day
ST- Semi twisted
G- Grey
M- Medium
Tw- Twisted
Y- Yellow
B- Blue
F- Funnel
Cl- Colorless
LB- Light blue
D- Disc
CBA- Coloured below anther
DB- Dark blue
Tu- Tubular
Bo- Bold

Fig. 4.5: Graphical representation of morphological characters in bold seeded linseed genotypes through pie charts

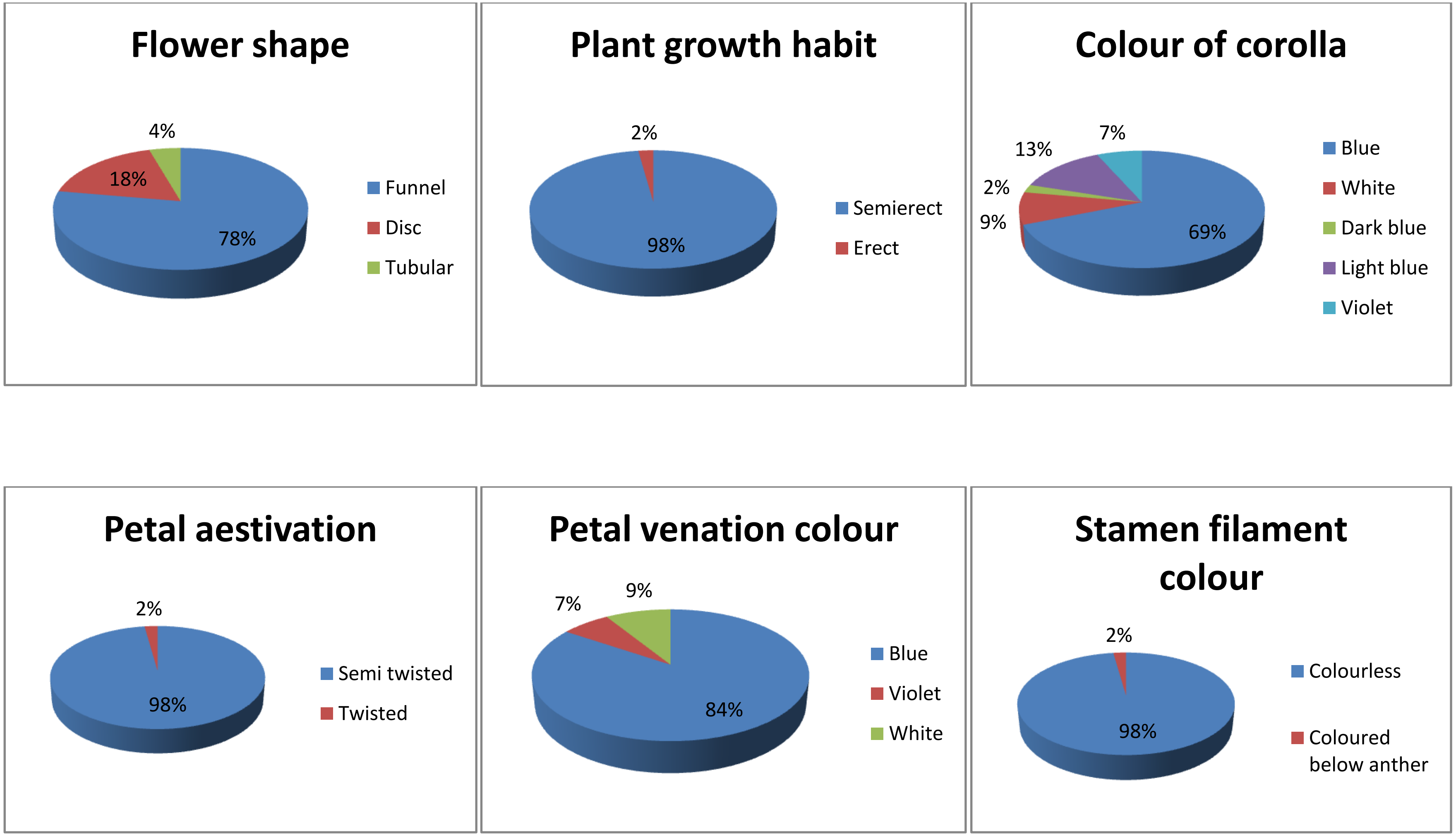

Fig. 4.6: Graphical representation of morphological characters in bold seeded linseed genotypes through pie charts

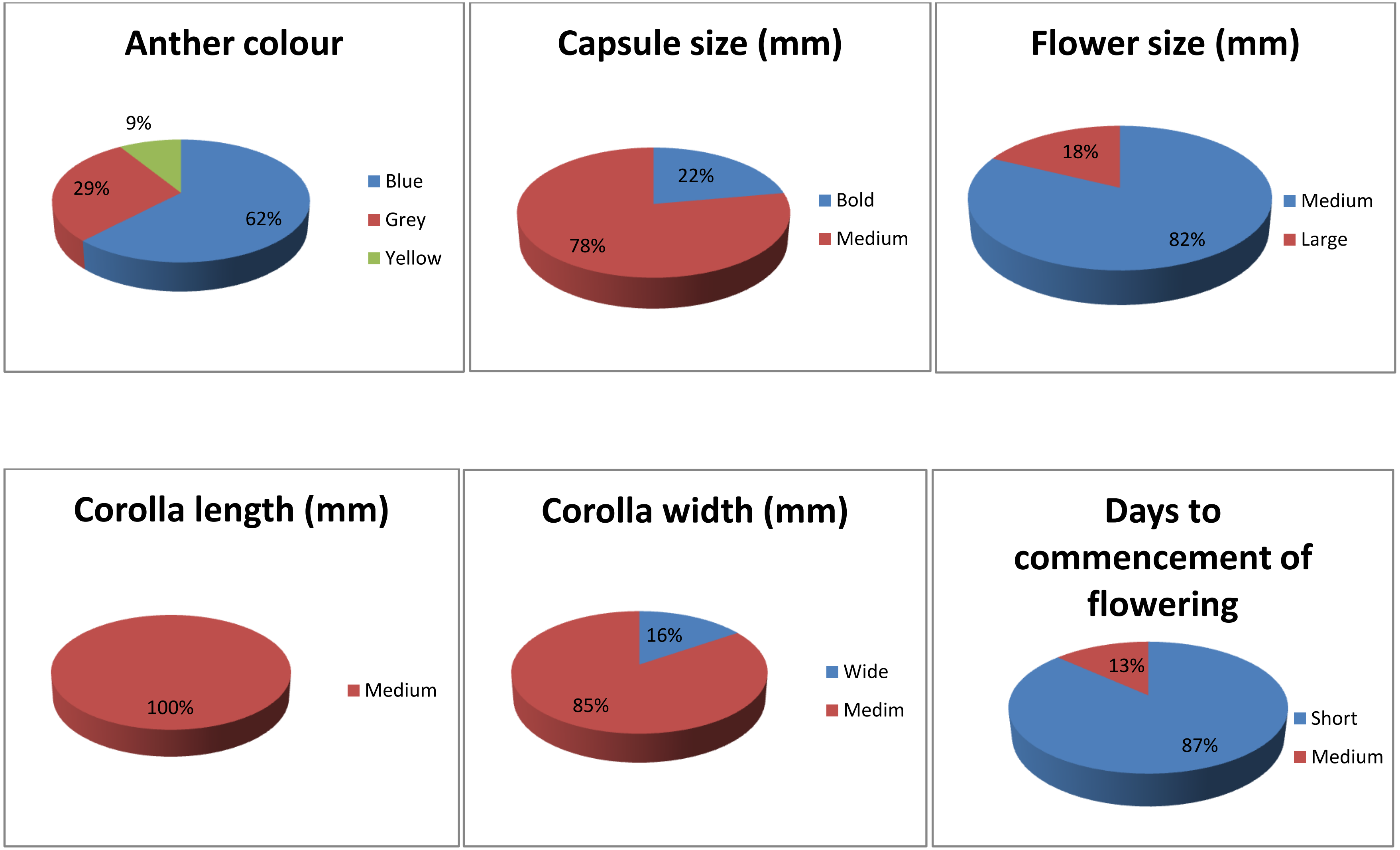

Fig. 4.7 Pictorial presentation of morphological characteristics of bold seeded linseed

Fig. 4.7 (A) Flower colour

White **Blue** **Light blue** **Violet**

Fig. 4.7 (B) Flower shape

Funnel **Disc** **Tubular**

Fig. 4.7 (C) Petal aestivation

Twisted **Semi-twisted** **Valvate**

Fig. 4.7 (D) Petal venation colour

Blue **White** **Violet**

Fig. 4.7 (E) Anther colour

Blue **Grey** **Yellow**

Fig. 4.7 (F) Plant growth habit

Erect **Semi-erec**

CHAPTER V
SUMMARY AND CONCLUSION

The bold seeded linseed alone has never been exploited for yield improvement of crop and its oil yield potential. Hence, for the present investigation the different source for variability of bold seed character in germplasm. Advance segregating material and varieties have been collected and studied for various genetic parameters *viz;* heritability, genetic advance and correlation *etc.* for bold seededness with other yield attributes develop meant of bold seeded varieties. Generally in linseed the comparing bold seeded with medium and small seeded, the advantage lies with better germination and seedling vigour giving robust plant growth which ultimately produces more branches and capsule and finally will produce more seed yield and seed oil yield respectively. The present experiment entitled **"Genetic variability in bold seeded linseed (*Linum usitatissimum* L.)"** was conducted with the main objective to study the variation and divergence present among the bold seeded genotypes and to analyse the association in different traits among forty-five bold seeded linseed genotypes, which is being summarized below-

- Analysis of variance for all the traits showed the sufficient amount of variability present among bold seeded linseed genotypes.
- The highest genotypic coefficient of variation was noted for "number of capsules per plant which was followed by number of secondary branches per plant, number of primary branches per plant and harvest index" whereas, phenotypic coefficient of variation was found to be the highest in "number of capsules per plant followed by number of secondary branches per plant, harvest index and number of primary branches per plant" indicating the presence of considerable amount of variability for those traits among the genotypes.
- In genetic variability analysis "the phenotypic coefficient of variation and genotypic coefficient of variation for days to flowering and days to maturity showed less difference" signifying influence of genetic causes in the expression of these traits.

- 1000-seed weight (g) exhibited the highest heritability which was followed by “plant height (cm), number of primary branches per plant, number of secondary branches per plant and number of capsules per plant” whereas, moderate heritability showed by “seed yield per plant (g) and total number of branches per plant”.
- The highest amount of genetic advance was recorded for “number of capsules per plant which was followed by number of secondary branches per plant, number of primary branches per plant, harvest index (%) and total number of branches per plant”. The least value of genetic advance was seen for “days to maturity”.
- The “number of capsules per plant, number of primary branches per plant, number of secondary branches per plant and harvest index.” recorded high broad sense heritability along with high genetic advance as mean percentage while, moderate heritability along with moderate genetic advance observed for seed yield per plant (g)”.
- Highest positive and significant correlation was observed for “1000- seed weight and days to 50% flowering” and positive correlation with “days to maturity followed by number of primary branches per plant, number of secondary branches per plant and number of capsules per plant”.
- 1000-seed weight (g) lies between 6.68 g and 8.74 g with a mean value 7.31 g. R-4275 (8.75 g) exhibit highest value for 1000-seed weight (g) which was followed by R-4285 (8.47 g) and R-3579 (8.24 g) whereas, in all checks R-552 recorded highest 7.61 g for 1000-seed weight (g).
- Seed yield per plant (g) lies between 1.41 g to 2.26 g with a mean value 1.79 g. R-4275 (2.26 g) exhibit highest value for seed yield per plant whereas, in the all checks RLC-92 recorded highest 2.24 g for seed yield per plant (g).
- Oil content (%) recorded highest for check R-552 (42.67 %) which was followed by R-4140 (39.4 %) and R-3579 (39.1 %).
- Diversity analysis through D^2 analysis carried out among 45 bold seeded linseed genotypes. Genotypes were classified into VIII clusters. Maximum number of genotypes appeared in cluster I which possessed 27 genotypes

followed by clusters II and cluster III which was comprised of 8 genotypes and 5 genotypes, respectively. “The highest intra-cluster value was recorded for cluster III (90.91) followed by cluster II (75.97) and cluster I (72.47) while lowest intra-cluster distance obtained for cluster IV to VIII (0.00). Based on intra-cluster distance, the most diverse cluster among all clusters was cluster I. The maximum inter-cluster D^2 values were showed between cluster VI and cluster IV (711.93) which was followed by cluster VI and cluster V (696.75) whereas, minimum between cluster VIII and cluster VI (114.87)”. Based on inter-cluster values, it can be concluded that genotypes of the cluster I and II could be selected for hybridization programmes as they are expected to produce high seed yield.

Conclusions

- Analysis of variance shows that variation among treatment is highly significant for all the characters whereas, variation among replication is non-significant for all the characters. It means significant amount of variability present among the genotypes.
- The existence of variability among the breeding materials is highly essential for devising proper selection strategies and also useful in the selection of diverse parents for utilising in the future hybridization programmes.
- Association analysis in bold seeded linseed revealed that “1000-seed weight (g) was significantly and positively associated with number of capsules per plant, total number of branches per plant and harvest index (%)” which indicates that increase in one variable will cause increase in other and *vice versa.*
- “Seed yield per plant were positively and significantly correlated with 1000-seed weight and days to 50% flowering”. A significant positive correlation between the traits is desirable as it leads to improvement of both the characters simultaneously.

- Bold seeded linseed genotypes were identified with good agro morphological characters. This will help to initiate the research work with bold seeded linseed genotypes in our state.

Suggestions for future research work

- Bold seeded linseed genotypes may be used as parent in breeding programmes. More diverse parents should be involved in hybridization programmes in order to incorporate desirable genes in a single genotype.
- In most of crops, “seed yield is an important trait and the cumulative result of a number of component traits controlled by polygenes and highly influenced by the environmental factors. Hence, yield alone would not be effective for selection of superior genotypes”. In order to make the selection effective one has to give emphasis on the yield attributing traits.
- The existing variability in the gene pool offers an opportunity for selecting superior genotypes, which can be obtained through evaluation.
- Knowledge of correlation among the traits in the expression of desirable traits such as 1000-seed weight and seed yield per plant in case of bold seeded linseed will provide an additional assistance in deciding the selection criteria for selecting dual purpose linseed genotypes.
- In order to improve the desirable traits among the germplasms and to carry out any successful breeding programs, the assessment of the available genetic variation and insight of association among the traits are highly desirable.
- Chhattisgarh state has a huge amount of linseed germplasms containing diverse alleles of important genes which could be utilized in the near future for improving nutritional status of the crop.

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APPENDIX

Table: Meteorological data recorded during crop growth season

(December 2019 to March 2020)

S. N.	**Date**	**Max. Temp. (°C)**	**Min. Temp. (°C)**	**Rain-fall**	**Rainy days**	**Relative Humidity (%) I**	**Relative Humidity (%) II**
1	**Dec 03-09**	28	13.3	0	0	84	34
2	**10-16**	29.5	15.3	0	0	91	48
3	**17-23**	26.7	14.1	0.8	0	88	42
4	**24-31**	26.1	11.9	0	0	81	35
5	**Jan 01-07**	23.3	12.9	19.4	2	97.4	33.7
6	**08 to 14**	25.1	5.7	3.2	1	89.7	46.3
7	**15-21**	28.6	15.4	0	0	87.4	62.7
8	**22-28**	28.8	12.6	0	0	78.9	28
9	**29-Apr**	26.1	15.6	29.5	1	88.7	44.1
10	**Feb 05-11**	21.3	13.6	49.6	3	89.3	25
11	**12 to 18**	29.7	11.9	0	0	88.1	27.3
12	**19-25**	31.4	20.6	35.8	1	88	76.3
13	**26-Mar**	29.6	15.8	0	0	88.7	37.4
14	**Mar04-10**	31.1	19.7	1.8	1	86.1	52.6
15	**11 to 17**	30.2	20.1	37.2	2	88.7	54.7
16	**18-24**	33.1	20.2	1.6	1	83.7	38.1
17	**25-31**	35.4	22	8.4	1	78.1	36.6

RESUME

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