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GENETIC DIVERSITY STUDY OF LINSEED GENOTYPES
ON ACIDIC SOIL AT BEDI TRIAL SITE, CENTRAL
HIGHLAND OF ETHIOPIA

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List of Abbreviations

AFLP	Amplified Fragment Length Polymorphism
BC	Before the Birth of Christ
CV	Coefficient of Variation
CSA	Central Statistical Authority
CSO	Central Statistical Organization
DAP	Diammonium Phosphate
DMRT	Duncan's Multiple Range Test
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agriculture Organization of United Nations
HARC	Hollela Agricultural Research Centre
IAR	Institute of Agricultural Research
IBC	Institute of Biodiversity Conservation
ITS	Internal Transcribed Spacer
LCD	Least Common Difference
RAPD	Random Amplification of Polymorphic DNA
SAS	Statistical Analysis System

Abstract

Linseed (Linum usitatissimum L. 2n = 30) is the second most important oilseed crop in production after noug in the higher altitudes of Ethiopia. It is suited to a wide range of soil types but it is sensitive to and performs poorly on the acidic soils. Sixty-four linseed genotypes, consisting of six exotic, one standard check and 47 single plant selection from different crosses were evaluated by simple lattice design with two replications for their tolerance to acidic soil at Bedi Trial Site in Central Ethiopia during 2009/2010 cropping season. Data were collected for 14 characters and statistically analyzed. Analysis of variance showed significant differences among the genotypes for root length, days to flowering, days to maturity, plant height, seed yield per plot, seed yield per plant, tillers per plant, number of primary branches per plant, 1000 seed weight, oil yield and oil content. However, the numbers of capsules per plant and secondary branches per plant were non-significant. High phenotypic and genotypic coefficients of variations were recorded for seed yield per plant, seed yield per plot, oil yield per plot, number of primary branches and tillers per plant. Conversely, oil content, 1000 seed weight, days to flowering and days to maturity showed low phenotypic and genotypic coefficient of variations. Heritability in the broad sense is adequately high for all characters and comparatively higher heritability was observed for oil content, 1000 seed weight and days to maturity. Relatively, higher heritability was coupled with high genetic advance for days to flowering, days to maturity, plant height, capsules per plant and vigourity. High heritability, associated with low predicted genetic advance, was estimated for oil content, seed yield per plant, 1000 seed weight, root length, tillers per plant, primary and secondary branches per plant. Simple correlation coefficient analysis revealed that seed and oil yields (kg/ha) had positive and significant correlation with seed yield per plant, tillers per plant, primary and secondary branches, capsules per plant, and vigourity. Significant and positive correlation was observed for oil content only with 1000 seed weight but negative correlation with vigourity and tillers per plant. Positive and significant correlation of days to maturity with root length and plant height was observed. Root length had positive and significant correlation with days to maturity, plant height, seed yield per plant, tillers per plant, vigourity of plants, seed yield per plot, primary and secondary branches per plant, capsules per plant and oil yield. The study showed that linseed genotypes with longer root lengths such as Omega X CI-1525/B/3, Chilalo X R-12-N27G/P2/S2, CDC-1747XCI-1652/S2, PGRC/E10306 X Chilalo/B/4, etc., were among higher seed yielders. In general, seed yield of the genotypes increased with increase in root length and these genotypes are thought to be more tolerant to acidic soil. Cluster analysis of genotypes from six different sources grouped them into seven different classes. Analysis of Mahalanobis's D^2 showed significant genetic distances between all clusters except between the first and the second clusters. Generally, no clear cut relationship was observed among different sources of genotypes since genotypes from the different sources of origin fell into the same cluster and genotypes of the same source were distributed into different clusters, indicating that genotypes from the same origin may have different genetic background and vice-versa. Principal component analysis revealed that seed yield per hectare, oil yield per hectare, vigourity of plants and oil content were the most determining characters in grouping genotypes into the clusters.

Key words: *Clustering genotypes, genetic diversity, linseed (Linum usitatissimum L.), soil acidity*

1. Introduction

Linseed belongs to the genus *Linum*. The genus *Linum* has several wild species and a cultivated species of which *Linum usitatissimum* L. is grown for its oil and fiber. The wild species are of little economic value. Almost all the species are annual herbs; some are shrubs. The genus is reported to have been originated in Southwestern Asia and the Mediterranean area of Europe (Kaul and Das, 1986). There are strong indications that *Linum* originated in India, from where it spread northward and westward, probably also to Ethiopia (Adugna Wakjira *et al.*, 2004). Most of the linseed cultivars have been developed by crossing within linseed gene pool of *Linum usitatissimum* (Orhan and Evans, 1996).

Linseed stands fourth after mustard, sesame and groundnut in edible oil production of the world (Aruchalam, 1981). Linseed has been a traditional crop in Ethiopia and it is the second most important oil crop in production after noug (*Guizotia abyssinica* CASS) in the higher altitudes (Adugna Wakjira and Adefris Tekilewolde, 1995). Ethiopia is considered to be the secondary center of diversity, and now the 5th major producer of linseed in the world after Canada, China, United States and India (Adugna Wakjira, 2007).

The way in which plants grow and carry out their different activities is a result of several environmental factors. These factors include light, temperature, water, atmospheric gases, wind as well as soil (edaphic) and physiographic (nature of land surface) factors. Acidity or alkalinity of soil (the pH of the soil) influences the biological activity in soil and the availability of certain minerals. Thus, the pH of soil has a greater influence on the growth and development of plants (<http://www.botany.uwc.ac.za/sci-ed/ecology/abiotic/abiot>).

There are some traits considered important in most linseed breeding programs: earliness, high oil content and seed yields, resistance to biotic and abiotic stresses. Among them, yield receives the greatest attention in cultivar development, as it does in other crop species. Genetic improvement of yield and yield components are, nevertheless, the most difficult to achieve due to the complex nature of their inheritance and the numerous environmental factors that influence yield and its components (Orhan and Evans, 1996).

Several studies have been carried out on linseed genotypes regarding improvement of yield, genotype-environment interaction and phenotypic stability. Even though the hitherto research efforts made resulted in a release of improved linseed varieties, little is known about genetic

diversity of linseed genotypes on acid soil in the Ethiopian context. Many studies on mechanism of acid soil tolerance were carried out on cereal crops, particularly on maize and wheat (Delhaize *et al.*, 1993a); Riede and Anderson, 1996; Ninamango *et al.*, 2003; Pineros *et al.*, 2005). This may possibly be due to an attempt to increase yield of food crops to feed the ever growing population of the world.

In addition to the above mentioned gaps, most of the small-scale farmers are not aware of the status of their soils in Ethiopia (EIAR, 2007). In view of this situation, practical and cheap options for soil acidity amelioration have paramount importance. Evaluation of genetic diversity among the linseed genotypes is important so as to select and promote linseed genotypes that perform well on the stress environment, including soil acidity.

Adding lime is one way of correcting soil acidity problem. But lime is expensive, environmentally unfriendly and in some situations subsoil acidity restricts the benefit of lime because it takes decades to correct acidity at depth, and thus plants with better tolerance to acidity have immediate application (Doss *et al.*, 1979; Smith *et al.*, 1994). There is considerable variation in tolerance amongst crop species and between cultivars and within species to acidic soils (Coventry, 1986). Thus, developing cultivars with improved tolerance to acidic soil stress is a solution to address this problem. Consequently, the present study was carried out to evaluate the genetic diversity of different linseed genotypes in terms of their performance on acidic soil so that the end users, particularly small-scale farmers, could use the varieties that adapt and give better yield on the acidic soil.

2. Literature Review

2.1. Botany and taxonomy of linseed

The genus *Linum* belongs to family Linaceae and subfamily Linoideae. *Linum* is the largest of the eight genera of the family Linaceae and comprises of over 180 species of which *Linum usitatissimum* is economically the most important species and is the source of linen and linseed oil. It is an erect, herbaceous annual, which branches corymbosely above the main stem (Fernald, 1950). Two types of *Linum usitatissimum* are cultivated: the linseed type, grown for seed oil, is a relatively short plant which produces many secondary branches compared to the flax type, grown for the fiber extracted from the stem, which is taller and is less branched (Gill, 1987).

The leaves of linseed are simple, sessile, linear-lanceolate with entire margins, and are borne on main stems and branches. The inflorescence is a loose terminal raceme. Flowers are borne on long erect pedicels, are hermaphrodite, hypogynous and are composed of five sepals, five petals (blue), five stamens, and a compound pistil of five carpels each separated by a false septum. The fruit is a capsule, composed of five carpels and may contain up to 10 seeds. The seed is oval, lenticular, 4-6 mm long with a smooth, shiny surface, brown to light-brown and yellow in color. Seeds contain 35-45% oil and 20-25% protein (Fernald, 1950; Gill, 1987).

Cultivated linseed reproduces by means of seed. Because of its flower structure and the sticky nature of the pollen, pollen grains are rarely transferred by insects (Beard and Comstock, 1980), and thus linseed is a highly self-pollinated species. The pollen is viable for only a few hours, from the time of anther dehiscence until about the time the petals dehisce - between 4 and 7 hours (Dillman, 1938; Lay and Dybing, 1989). As the flower opens, the anthers come together and form a cap over the stigma. In over 8,000 observations in a linseed variety, Dillman (1938) found no natural crossing.

2.1.1. The species identity of *Linum usitatissimum* L.

Linseed ($2n = 30$) is an important oilseed crop which belongs to the family Linaceae. It is the only widely grown and economically important species. It is believed that this crop species may have originated from *Linum angustifolium* Huds ($2n = 30$), native to the Mediterranean region. *Linum usitatissimum* L. is the only species with non-dehiscent or semi-dehiscent

capsules suitable for modern cultivation of the family Linaceae (Getinet Alemaw and Nigussie Alemayehu, 1997).

Linum usitatissimum is an erect annual, forming a short taproot with fibrous branches which may extend 90-120 cm in light soils. Linseed species grown for oil production has a relatively high variability in flower color, plant height, flowering and maturity duration, and capsule size and wilts resistance (IBC, 2008). The stem is thin and wiry, the degree of branching depends upon plant type and density; the leaves are unstalked, small, narrow and pointed and dark or grayish-green in color. The flowers are produced near the top of the stems while the flowering period may last for some weeks, individual flowers are short-lived. Linseed flowers are commonly bright blue, but may be pale blue or white (Robbelen *et al.*, 1989).

2.1.2. Phylogenetics

Joshua *et al.* (2009) made phylogenetic analyses by using 44 species representing all the eight genera of subfamily Linoideae including 37 species of *Linum*, with data from the chloroplast and the nuclear internal transcribed spacer (ITS), with *Hugonia* (Linaceae subfamily Hugonioideae) as out group. They reported that Linoideae are monophyletic, but *Linum* is not. *Anisadenia*, *Reinwardtia*, and *Tirpitzia* are found to be the basal members of Linoideae. The rest of the subfamily forms two major lineages: a blue-flowered clade (*Linum* sections *Linum* and *Dasylinum*) and a yellow-flowered clade (*Linum* sects. *Linopsis*, *Syllinum*, and *Cathartolinum*, and the genera *Cliococca*, *Hesperolinon*, *Radiola*, and *Sclerolinon*).

The wild progenitor of the cultivated linseed has long been hypothesized to be *Linum angustifolium* Huds (Hjelmquist, 1950; Helbaek, 1959). This hypothesis is supported by morphological (Diederichsen and Fu, 2006) and cytological studies (Gill and Yermanos, 1967a; Gill and Yermanos, 1967b). Many authors reported that cultivated linseed was derived from two or more ancestral forms (De Candolle, 1904; Vavilov, 1926; Richharia, 1962).

The available studies based on molecular markers are limited. A phylogenetic study of *Linum usitatissimum* based on amplified fragment length polymorphism (AFLP) carried out by Diederichsen and Richards (2003) on 17 species of *Linum* has revealed no compatibility with the traditional sections of the species. McDill and Simpson (2005) carried out a more comprehensive phylogenetic study of *Linum* based on DNA sequence variation from multiple chloroplast markers and the nuclear encoded internal transcribed spacer region. Their analysis of approximately 70 species indicated that blue-flowered *Linum* species were sister to a

predominantly yellow-flowered lineage although some consider *Linum angustifolium* and *Linum bienne* to be the same species (Zohary and Hopf, 2000). However, genome comparisons with molecular markers of these three species (*Linum angustifolium*, *Linum bienne* and *Linum usitatissimum*) confirmed that they are very closely related genetically and *Linum bienne* can be considered as a subspecies of *Linum usitatissimum*, rather than a separate species (Muravenko *et al.*, 2003).

Fu *et al.* (2002) also carried out Random Amplification of Polymorphic DNA (RAPD) variations study genetic relationship of 12 linseed accessions representing seven linseed species in the genus *Linum* and they found large variations among the linseed species. They reported that *Linum usitatissimum* and *Linum angustifolium* had a higher RAPD similarity than the other pairs of linseed species and these two species were consistently clustered in the same group with all of the similarity coefficients used. This further consolidated the hypothesis of *Linum angustifolium* as the wild progenitor of the cultivated linseed.

2.2. Center of origin and its geographic distribution

The center of origin of linseed has not yet been identified with certainty (Lay and Dybing, 1989), but it is believed to have been disseminated from Egypt (Cooke, 1903) where it was in use during the time of the Pharaohs. Flax fabrics from Egyptian mummy-clothes were dated at more than 4500 years (De Candolle, 1904; Matthews, 1908). Similarly, Adugna Wakjira (2007) reported that Egyptian mummies provided evidence of the use of the oil by 1400 B.C. It is believed that Phoenicians were responsible for transporting linseed into Europe from the Near East (Rosberg, 1996; Stephens, 1997) during the period from 2500 to 1200 B.C. Linseed cultivation by Aryans extended north to Russia and Finland (De Candolle, 1904). During the Colonial Era, European colonists transported linseed to North America, New Zealand, and Australia (Rosberg, 1996).

Many speculative centers of origins for linseed are reported with many existing theories. Among the eight independent centers of origin of the world most important cultivated plants (Vavilov, 1926), *Linum* species were reported to have originated in four centers: the Central Asiatic, the Near Eastern, the Mediterranean, and the Abyssinian centers. Gill (1987) and Richharia (1962) also considered these four possible centers as areas of linseed origin.

Finally, an area east of the Mediterranean toward India has been suggested as another center of origin because a diverse form of linseed is found in the area (De Candolle, 1904; Zeven,

1982; Zeven and Zhukovsky, 1989). Whereas, Adugna Wakjira (2007) pointed out that India could not be considered as the centre of origin though it is an important centre of genetic diversity of linseed because of the absence of its progenitor, *Linum angustifolium*.

Adugna Wakjira (2007) indicated that specialization of *Linum usitatissimum* L. into its two basic types, namely fiber flax and linseed, was occurred early: Mediterranean and European types developed into fiber flax; short-season types adapted to the warmer climates of western Asia, the Indian subcontinent and Ethiopia developed into linseed types. *Linum usitatissimum* is now grown widely in many parts of the world, including the tropics. Fiber flax is cultivated in cool and humid temperate climates, whereas linseed is grown in warmer climates.

2.3. Economic importance of linseed

Linseed is oilseed crop and one of the oldest cultivated plants (Bhatty and Rowland, 1990). Linseed comes in two basic varieties: brown and yellow or golden. Most types of linseed have similar nutritional characteristics and equal amounts of short-chain omega-3 fatty acids. The exception is a type of yellow linseed called linola or solin, which has a completely different fatty acid and is very low in omega-3. Although brown linseed can be consumed as readily as yellow, and has been grown for thousands of years, its oil is better known as an ingredient in paints and is used as, fiber and cattle feed (<http://www.flaxcouncil.ca/english/index.jsp?p=g3&mp=nutrition>).

Linseed oil is used as a raw material for agro-industries (IBC, 2008). In view of its diverse industrial uses, especially for the manufacture of high quality paper, instant drying inks, paints, etc, linseed oil is very important industrially (Khan *et al.*, 2000). In Ethiopia, linseed is mainly used for domestic consumption as cooking oil. It is of increasing importance for the food industry in highly developed consumer markets due to the specific non-saturated fatty acids (Wijnands *et al.*, 2007).

2.3.1. Nutritional importance

Linseed contains a mixture of fatty acids. It is rich in polyunsaturated fatty acids, particularly α -linolenic acids (ALA), the essential ω -3 fatty acids, and linoleic acids (LA), the essential ω -6 fatty acids. These two polyunsaturated fatty acids are essential for humans. Human must obtain these fatty acids from the fats and oils in foods because human bodies cannot make

them. Likewise, the amino acid pattern of linseed protein is similar to that of soybean protein, which is viewed as one of the most nutritious plant proteins (Morris, 2005).

Linseed oil had been used in Ethiopia mostly for industrial purposes because of its high content of linolenic (polyunsaturated) acid, which is known for its fast drying quality due to its three auto-oxidative double bonds, e.g. in the manufacture of paints, varnishes, soaps, printing inks, oilcloth and linoleum tiles (Adugna Wakjira *et al.*, 2004). It is now grown primarily for food and to generate revenue, either in local markets or by export. For food, the seeds are usually roasted, ground, mixed with spices and water, and served with various local breads. It is also consumed in soups, with porridges and cooked potatoes, etc. Limited amounts are also pressed locally for its edible oil, which is often blended with other high quality vegetable oils such as that from noug, which contains about 750 g/kg linoleic acid. Blending is undertaken to minimize rancidity and to maintain acceptable taste and flavor of cooking oils (Adefris Tekilewolde *et al.*, 1992).

Linseed oil is suitable for human consumption, and is used as a nutritional supplement. It has also numerous medicinal uses. It is rich in omega-3 fatty acids, especially alpha-linolenic acid that appears to be beneficial for heart disease, inflammatory bowel disease, arthritis and a variety of other health conditions. It also contains a group of chemicals called lignans that may play a role in the prevention of cancer ([http://wiki.medpedia.com/ Flaxseed Oil](http://wiki.medpedia.com/Flaxseed%20Oil)). For the last 15 years, there has been a steadily growing interest in the medicinal value of linseed, including experimental evidence for its use in the prevention of cancer and cardiovascular and kidney diseases (Alister *et al.*, 2003).

2.4. Cultivation of linseed in Ethiopia

Ethiopia is also considered to be the center of diversity for linseed (Vavilov, 1926). However, other authors (Richharia, 1962; Gill, 1987) have also discussed Abyssinian center among four possible centers of linseed origin. Adugna Wakjira *et al.* (2004) described that linseed has been cultivated in Ethiopia since antiquity. In tropical Africa linseed production is concentrated in the Ethiopian highlands, where linseed has been grown since time immemorial.

Wijnands *et al.* (2007) stated that the diverse climatic conditions enabled the country to grow a wide range of oilseeds, in which it has a long tradition. As in many parts of Africa, in

Ethiopia linseed is grown for oil. It is widely grown on the highland of northern and central Ethiopia usually rather on poor soil or after the fields have been planted for two or three years with grain crops. Sowing is usually done in June and the crop matures in November (Adugna Wakjira and Labuschagne, 2003).

The principal linseed growing regions in Ethiopia are located at altitudes between 1800 and 2800 meter above the sea level , although it occasionally grows at altitudes as low as 1680 m or as high as 3430 m (CSO, 1984). Arsi, Bale, Chercher Mountains, Eastern Welega, Eastern Gojam, Tigray, and Southeast Welo, and Shewa are the major areas of production where frost is a problem for other oilseed crops such as noug and Ethiopian mustard (*Brassica carinata* A.Braun). Linseed is a major oilseed and rotation crop for barley in higher elevations of Arsi, Bale, Gojam, Gonder, Wello, Shewa and Welega. High yields of wheat, barley and teff can be obtained following linseed (Getinet Alemaw and Nigussie Alemayehu, 1997). In Ethiopia, in terms of area and production, linseed occupies the second position among the oilseed crops next to noug. The area under this crop is about 177, 000 ha with an average yield of 970 kg/ha (CSA, 2008).

The crop is traditionally grown on marginal and sub-marginal lands with minimum frequency of plowing and no weeding (Adefris Tekilewolde *et al.*, 1992). In spite of low productivity, Ethiopian Landraces of linseed possess economically important traits such as large number of capsules per plant, high seed weight, resistance to most of the diseases and high number of tillers per plant (Tadele Tadesse *et al.*, 2009). The crop is mainly grown by small-scale farmers for local consumption. According to the Central Statistical Authority (CSA, 2008) estimate of the area ploughed, production and yield of linseed has generally shown an increase from 2000 to 2008 for private holdings (Table 1).

Table 1. Estimates of area, production and yield of linseed in Ethiopia for private holdings from 2000-2008.

Year	2000	2001	2002	2003	2004	2005*	2006	2007	2008*
Area ('000 ha)	130.52	98.60	131.88	142.90	250.70	261.37	174.11	152.13	176.75
Production ('000q)	640.5	510.5	427.9	773.6	1518.4	1672.0	1082.2	1403.0	1714.9
Yield (q/ha)	4.91	5.18	3.24	5.41	6.06	6.40	6.22	9.22	9.70

Source: CSA (2000-2008), *Forecasted, q/ha = quintal per hectare

2.4.1 Agro-ecology of linseed

Ethiopia has several climatic zones suitable for various types of agricultural undertakings. More than half of the country has a highland climate, 1500 meter above sea level (m.a.s.l.) suitable for various field and horticultural crops (Tesfaye Zegeye, 2003). Linseed is well suited to a cool, humid climate but is susceptible to severe frost as well as drought (Adane Choferie, 2008).

Linseed is suited to a wide range of soil types but establishment can be difficult on heavy clay soils, as well as soils of a gravelly or dry sandy nature, which has to be avoided. A fine tilth and adequate moisture are required to ensure good establishment. Cultivations should minimize soil compaction so that the taproot is able to penetrate down to available water. Daniel (2006) reported that linseed will tolerate weakly saline (pH 9.0-11.0) to weakly acidic soil (pH 6.1-6.5). According to Melvyn (2004) optimum pH of soil for linseed growth ranges from 6.0-7.0. Adugna Wakjira (2007) reported that linseed will not perform well on soils with pH less than 5.0 or above 7.0 and sensitive to soil acidity and alkalinity. Omafra (2009) also recommended that soil pH below 6.1 needs lime for the growth of linseed.

Linseed requires cool temperature during its growing period for better yield. The yield potential of modern cultivars of linseed is estimated at about 3.0 t/ha (tons per hectare). The average seed yield in Ethiopia is nearly 0.9 t/ha, while improved cultivars with good management yielded up to 2.5 t/ha in favourable areas (Adugna Wakjira, 2007). It grows well within temperature ranges of 10 °C to 30 °C; but it performs best between 21 °C and 22 °C. It prefers dry and sunny weather with well-distributed moderate rain over the growing season (Getinet Alemaw and Nigussie Alemayehu, 1997). The same authors detailed that good seed yield can be achieved with a midday relative humidity of 60–70%, and rainfall of 150–200 mm distributed over the three months (July to September) growing period. Temperatures of –6 °C may kill the crop in the seedling stage and frost may also cause injuries during the flowering and green capsule stages. Adugna Wakjira (2007) pointed out that rainfall towards maturity of the crop may cause secondary flowering and hence uneven maturity. Heavy rain and strong winds may cause lodging, thereby, reducing yield.

2.5. Soil acidity and its causes

Soil acidity is among the important environmental factors, which can affect plant growth, and can seriously limit crop production (Douglas and Dwight, 1995). Soils are not homogenous and its pH can vary considerably from one spot in the field to another. It also varies with depth of the soil. Soils in different geographic regions may have different pH because of different factors (Charles, 2000). The major causes of soil acidity, such as rainfall and leaching, acidic parent material, organic matter decay, harvest of high yielding crops and fertilizers are described here under.

2.5.1. Rainfall and leaching

In time of excessive rainfall, water passing through soil leaches the soil profile's basic elements (calcium, magnesium, sodium, and potassium) that prevent soil acidity (Jeff, 1999). These basic cations are replaced by acidic cations such as aluminum (Al^{3+}) and hydrogen (H^+). For this reason, soils formed under high rainfall conditions are more acidic than those formed under arid conditions (Charles, 2000; Uchinda and Hue, 2000). Soil acidity resulting from mineral leaching due to high rainfall is a problem of increasing concern in crop production in the highlands of Ethiopia (EIAR, 2007).

2.5.2. Acidic parent material

Mark *et al.* (2000) stated that the minerals from which a soil is formed partly determine whether it is acid or alkaline. Soils that develop from weathered granite are likely to be more acidic than those developed from shale or limestone (Jeff, 1999). Soils formed from acidic rocks have a lower pH than those formed from basic rocks or alkaline parent material. Soil parent material and the climate under which a soil was formed are important determinants of soil acidity.

2.5.3. Organic matter decay

The accumulation of organic matter has been suggested to be one of the causes of soil acidification. Organic matter decay produces hydrogen ions (H^+), which are responsible for acidity. Like that from rainfall, acidic soil development from decaying organic matter is insignificant in the short term. Robert (2007) detailed that many forms of organic matters can also acidify, depending on the plant from which the organic matter is derived. The same

author added that some plants contain significant quantities of organic acids. As their residues are decomposed, the organic acids naturally affect the soil acidity. Other plants are acidifying simply because of the low concentrations of bases they contain (Douglas and Dwight, 1995). If the plant does not contain enough bases to satisfy microbial needs, the decomposition of the plant debris will not only give off carbon dioxide, but will also remove base nutrients such as calcium and magnesium from the soil (Robert, 2007).

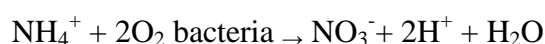
2.5.4. Harvest of high-yielding crops

Harvest of high-yielding crops plays significant role in increasing soil acidity. During growth, crops absorb basic elements such as calcium, magnesium, and potassium to satisfy their nutritional requirements. As crop yields increase, more of these lime-like nutrients are removed from the field. When these basic cations are removed from the soil, they are replaced with H^+ in order to maintain electrical neutrality (Charles, 2000).

2.5.5. Fertilizers

Where available, application of inorganic fertilizer without soil test, on the long run, can increase soil acidity. It is also due to side effects of inorganic fertilizer on intensely cultivated soils (Mercy and Ezekiel, 2007). Nitrogen fertilizer has been blamed for the increase in soil acidity problems. This is revealed when ammonia fertilizer materials are applied to the soil acidity is produced, but the form of nitrogen removed by the crop is similar to that found in fertilizer. In reality, nitrogen fertilizer increases soil acidity by increasing crop yields, thereby increasing the amount of basic elements being removed (Jeff, 1999).

Both chemical and organic fertilizers may eventually make the soil more acidic. Hydrogen is added in the form of ammonia-based fertilizers (NH_4^+), urea based fertilizers [$CO(NH_2)_2$], and as proteins (amino acids) in organic fertilizers. Transformations of these sources of nitrogen into nitrate (NO_3^-) release H^+ to create soil acidity. Therefore, fertilization with fertilizers containing ammonium or even adding large quantities of organic matter to a soil will ultimately increase the soil acidity and lower the pH (Charles, 2000).



2.6. Effect of soil acidity on crops

Soil acidity influences many chemical and biological reactions that control plant nutrient availability and element toxicity (Sumner *et al.*, 1991). Acidic soil often causes the stunting and yellowing of leaves, resulting in the decrease in growth and yield of crops as the pH levels falls. Additionally, plants grown in adverse pH conditions may be more prone to disease and fungal attack (SGS, 2009). Soil pH affects the soil microbial activity and populations, many soil chemical reactions, and nutrient availability, thereby, reducing crop productivity (Robert *et al.*, 2007).

2.6.1. Aluminum toxicity

Plants don't need aluminum to grow and it is not an essential plant nutrient. Since many plant species are sensitive to micro-molar concentrations of aluminum, the potential for soils to be aluminum toxic is considerable (Charles, 2000). Its toxicity is the primary limitation to crop production on approximately 50% of the world's potentially arable lands, including many developing countries, where food security is most tenuous (Emmanuel and Peter, 1995). The most striking effect of aluminum in acid soils is stunting of the root system. Toxic aluminum cations (Al^{3+}) solubilized by the acidity rapidly inhibits root growth and subsequent uptake of water and nutrients (Bona *et al.*, 1991; Baligar and Fageria, 2001). Restricted root systems can lead to nutrient deficiencies or drought symptoms of the crop even if moisture is available further down the soil profile (Charles, 2000).

Fortunately, most of the Al is bound by ligands or occurs in other non-phototoxic forms such as aluminosilicates and precipitates. However, solubilization of toxic aluminum cations is enhanced by low pH of acidic soil. When the soil pH is lower than 5.5, Al^{3+} is released to the soil and enters into root tip where it causes inhibition of cell elongation and cell division, leading to root stunting accompanied by reduced water and nutrient uptake (Pandal *et al.*, 2009).

2.7. Crop species tolerance to soil acidity

Because acidity of soils is such a potential constraint to agriculture, understanding the mechanisms and genes conferring tolerance to acidic soil stress has been a focus of intense research over the past decade (Kochian *et al.*, 2004). Plant species and genotypes within species greatly differ in their tolerance to acidic stress (Zhang *et al.*, 2004). However, there is

little information about the mechanisms of aluminum toxicity and the genetic difference in aluminum tolerance of plants in general and in linseed in particular. Wissemeier *et al.* (1992) suggested that the use of plant genotypes tolerant to high aluminum and manganese supplies in the soil might make a substantial contribution to improve crop production since soil amelioration to overcome Al and Mn toxicities often has ecological and economical limits. Differences in Al and Mn tolerance as well as their genetic control have been demonstrated, not only between but also within plant species (Mark, 1993).

Genotypes differ from each other in genetic make up for growth and yield (Muhammad *et al.*, 2005). Linseed breeding endeavor is a continuous process to evolve potential varieties that are genetically better yielding than the prevalent ones (Khan *et al.*, 2000). Thus, it is desirable for breeders to have as much information as possible on the genetic control of important agronomic and morpho-physiological characteristics of the crop; the knowledge of such system is incomplete (Orhan and Evans, 1996). Furthermore, the critical information on genetic mechanisms governing plant responses to stresses like soil acidity is quite limited (Redhu *et al.*, 1990).

There is considerable variation in tolerance amongst crop species and between cultivars within species to acid soils (Gerardo *et al.*, 2005). The knowledge of this tolerance often dictates which crop and what variety is grown in regions having acidic soils. Difference in the genotypes is essential to meet different purposes of the crop such as increased yield (Joshi and Dhawan, 1986), wider adaptations to environmental stresses such as drought, soil acidity and alkalinity, desirable quality, pest and disease resistance (Nove *et al.*, 1982).

A different reaction of crop species to acid soils has long been established but only recently has the possibility of breeding for tolerance to aluminum and manganese, within a species been recognized (Brendan, 1986). Several studies have identified key genes that regulate Al³⁺ tolerance in different species of crops. For example, a gene encoding Al-activated malate transporter, *TaALMT1*, was identified using a near isogenic line of wheat, while a gene encoding citrate transporter (*Alt_{SB}*) was identified in the major Al-tolerant quantitative trait loci in sorghum (Sasaki *et al.*, 2004; Magalhaes *et al.*, 2007).

Barley cultivars and lines that tolerate toxic levels of Al or low soil pH have been reported. Stolen and Andersen (1978) found a single gene (*Pht*), explaining most of the differences for low soil pH tolerance in a group of spring barleys. Reid (1971) reported a single gene (*Alp*) controlling aluminum tolerance in winter cultivars of barleys Dayton and Smooth Awn 86.

Ph1 and *Alp* were located on chromosome four by simple trait association (Stolen and Andersen, 1978). Genetic and molecular mapping research has also shown that Al tolerance in barley is controlled by a single locus which is located on chromosome 4H (Jun-ping *et al.*, 2006). Tolerance was dominant in all published studies. Minor gene effects also have been postulated (Reid, 1971). Minella and Sorrells (1992) attributed the range of variation among barley cultivars to a single locus, with different alleles conferring different degrees of tolerance to aluminum.

Genetic variation in response to Al toxicity has been found even among cultivars within the same species (Foy and Fleming, 1978; Aniol and Gustafson, 1984). Therefore, it is possible to develop new crop varieties with higher Al tolerance using a cytogenetic manipulation approach. For this purpose, it is important to know which chromosomes in plants contain genes for Al tolerance. In hexaploid wheat, major genes influencing tolerance to Al are located on the short arm of chromosome 5A and the long arms of chromosome 2D and 4D (Takagi *et al.*, 1983; Aniol and Gustafson, 1984; Aniol, 1990). Using wheat-rye addition lines, major genes influencing Al tolerance in rye were located on chromosomes 3R, 4R, and the short arm of 6R (Aniol and Gustafson, 1984). However, the physiological processes controlled by these genes are still unknown.

All plants are affected by the extremes of pH but there is wide variation in their tolerance of acidity and alkalinity (Belinda, 2000). Most plants grow best within a pH range of 6.5 to 7.2. Plants that are resistant to Al toxicity, or by extension acid-soil, are those, “. . . that exhibit superior root growth which ultimately results in enhanced plant vigor on acidic, Al-toxic soils or solutions” (Kochian, 1995). There are two major mechanisms by which plants respond to aluminum toxicities: aluminum tolerance and aluminum avoidance. Aluminum tolerance and aluminum exclusion imply the existence of specific and different mechanisms responsible for that resistance.

2.7.1. Aluminum tolerance mechanism

Regarding aluminum tolerance mechanism, it was suggested that there are/is gene/s in aluminum toxicity tolerant crops that confer the ability to tolerate aluminum in the plant symplasm (inner side of the plasma membrane in which water and low-molecular solutes can freely diffuse between plant cells). The genetics of aluminum tolerance has been looked at primarily in several important crop plants with particular emphasis on wheat. Riede and

Anderson (1996) reported variation in aluminum tolerance between wheat varieties. In their experiment, they found out that aluminum tolerance is under the control of a single gene difference. Aniol (1990) detailed that Al tolerance is a dominant, quantitative trait that can be controlled by one or more major genes and several minor genes depending on the type of crops

2.7.2. Aluminum avoidance mechanism

The avoidance mechanism includes exclusion of Al from sensitive sites such as Al exclusion from root and organic compounds exudation for forming Al complex. The exudation of organic acids such as malate, citrate, succinate, and oxalate from roots has been suggested to play a role in aluminum exclusion (Nursyamsi *et al*, 2002). Several recent studies have shown that Al resistance in wheat involves exclusion of Al from the root apex. Delhaize *et al.*, 1993b) reported malate as the predominant organic acids released in Al-tolerant genotypes, from the root tips of the wheat where it binds to Al, thereby, preventing its entry. Kochian *et al.* (2004) also observed the continuous organic acid exudation as the root of wheat grows through the soil, thus maintaining the Al-chelating barrier around the root apex as it encounters new regions of acid soil.

2.8. Heritability

Heritability, in the broad sense, is defined as the proportion of phenotypic variance that is attributable to an effect for the whole genotype, comprising the sum of additive, dominance, and epistatic effects (Allard, 1960; Nyquist, 1991). Similarly, heritability in the narrow sense is defined as the proportion of phenotypic variance among individuals in a population that is due to heritable genetic effects, expressed as the ratio of the additive genetic variance to the total phenotypic variance (Falconer and Mackay, 1996).

A broad-sense heritability estimate provides information on the relative magnitude of genetic and environmental variation in the population (Rafi and Nath, 2004). Since broad sense heritability does not give a clear picture of transmissibility of variation from generation to generation (because the genetic variation includes the fixable additive and non-fixable dominance and epistatic variation), its utilization is limited in plant improvement program. In contrast, estimate of heritability in a narrow sense can give clearer picture than that of broad sense (Falconer and Mackay, 1996). Narrow sense heritability is most important in plant

selection programs, because response to artificial (and natural) selection depends on additive genetic variance. Moreover, resemblance between relatives is mostly driven by additive genetic variance (Hill *et al.*, 2008). But in the absence of separate estimate of narrow sense heritability, the broad sense heritability can offer some useful information such as forecasting genetic gain.

Since heritability is a proportion, it can vary in value from 0 (meaning none of the phenotypic variation in the population is genetic) to 1 (meaning all of the phenotypic variation in the population is genetic). For many traits in many populations, values of heritability are somewhere between 0 and 1, meaning that some of the differences among individuals are genetic and contribute to heritability but other differences depend directly on the environment and do not contribute to heritability. Heritability values can be used as a measuring scale to determine genetic relationship between parents and progeny as well as other degrees of relatives (Memon *et al.*, 2007). Better heritability values recorded points to the possibility of improvement in the parameters. Therefore, attention may be focused on important traits while producing genotypes (Ahmed *et al.*, 2007).

Heritability plays a predictive role in breeding, expressing the reliability of phenotypes as a guide to its breeding value (Tazeen *et al.*, 2009). It is understood that only the phenotypic value can be measured directly while breeding values of individuals are derived from the phenotypic value by appropriate analyses. It is breeding value, which determines how much of the phenotype would be passed on to the next generation (Rehman and Alam, 1994). Heritability indicates the degree of connection between phenotypic value and breeding value (Falconer, 1989). The efficiency of the process of selection depends upon the kind and magnitude of variation. There is a direct relationship between heritability and response to selection, which is referred to as genetic progress (Tazeen *et al.*, 2009)

Studies conducted by various researchers have shown that high heritability alone is not enough for selection; it must be accompanied with substantial amount of genetic advance (Memon *et al.*, 2007; Mangi *et al.*, 2008). High value of heritability and predicted genetic advance indicates that selection among genotype would be effective (Ghandorah and El-Shawaf, 1993). High heritability (broad sense) associated with high genetic advance reveals strong contribution of additive genetic variance for expression of the traits (Iqbal and Khan, 2003). However, if a character or trait is controlled by non additive gene action, even if it has high heritability value, it would result in low genetic advance (Ahmed *et al.*, 2007).

Heritability and genetic advance (breeding value) enables the breeders to use best genetic stock for improving the crop (Mangi *et al.*, 2008). The success of any breeding program depends upon amount of genetic diversity existing in germplasm and it is prerequisite to have a good knowledge of heritability and genetic advance present in different yield associated parameters (Waqar-ul Haq *et al.*, 2008).

2.9. Correlation coefficient

Correlation is a measure of a linear association between traits. Correlations between characters are frequent features of plant breeding. It is indicated by the correlation coefficient (r) and measures the degree of association, genetic or non-genetic, between two or more traits (Hallauer and Miranda, 1998). It measures the mutual association between two variables but does not permit to know the cause and effect relationship of traits contributing directly or indirectly towards economic yield (Shivanna *et al.*, 2007). The value of correlation coefficient, which is a ratio of the covariance between the two variables and the geometric mean of their variances, ranges from -1 to +1, the extreme values indicating perfect negative and positive association, respectively (Gomez and Gomez, 1984).

The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain for the primary trait under consideration. Sadek *et al.* (2006) pointed out that estimation of simple correlation between various agronomic characters may provide good information necessary for crop breeders, when selection is based on two or more traits simultaneously. Information obtained from correlation coefficients for characters could also be useful as indicators of the more important ones under consideration.

Becker (1993) stated that correlation studies are of interest to plant breeders because traits that are correlated with main breeding objectives may be useful for indirect selection. Tadesse *et al.* (2009) noted that information on the extent and nature of interrelationship among characters help in formulating efficient scheme of multiple trait selection. Traits under consideration may have strong correlation or not at all. Grafius (1959) indicated that a positive genetic correlation between two desirable traits makes the job of the plant breeder easy for improving both traits simultaneously. On the other hand, a negative correlation between two desirable traits impedes or makes it impossible to achieve a significant improvement in both traits.

In crop breeding sciences, one usually faces a group of variables which are associated due to complex interactions. Associations between characters signify the importance of such genetic causes as pleiotropic action of gene and linkages (Harlan, 1939; Ginzburg and Nikoro, 1973). Govindaraj *et al.* (2009) also indicated that existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all.

Environment plays an important role in correlation. In some cases, environment affects two traits simultaneously in the same direction or sometimes in different directions. Genetic and environmental causes of correlation combine together and give phenotypic correlation. The dual nature of phenotypic correlation makes it clear that the magnitude of genetic correlation cannot be determined from phenotypic correlation (Usman *et al.*, 2006).

Prior to launching of any breeding program, thorough knowledge of the nature and extent of association between yield components is essential (Ahmed and Saleem, 2003; Shivanna *et al.*, 2007). Yield is a quantitative character and is influenced by both genetics and environmental conditions. Therefore, in plant improvement, the effects of yield parameters as well as heritability and environmental factors should be taken into consideration. Investigation of the interrelationships between yield and its components will improve the efficiency of a breeding program with appropriate selection criteria. Mehmet and Telat (2006) recommended that study of direct and indirect effects of yield components to increase the yield provides the basis for its successful breeding program and hence the problem of yield decrease can be more effectively tackled on the basis of performance of yield components and selection for closely related characters.

Mevlut *et al.* (2008) stated that correlation analyses are being widely used in many crop species by plant breeders to understand the nature of complex interrelationships among traits and to identify the sources of variation in yield. Seed yield is a complexly inherited trait as its manifestation is an outcome of intricate interaction of several traits and environment. Therefore, proper understanding of association of different traits provides more reliable criterion for selection to achieve the goal of high yield (Muhammad *et al.*, 2001). Yield components, not only directly affect the yield, but also indirectly by affecting other yield components in negative or positive ways (Roopa and Ravikumar, 2008). High yield through yield attributes, as primary interest in crop improvement, requires understanding the magnitude of correlations among various yield traits (Tadele Tadesse *et al.*, 2009).

Yield and yield related components correlation studies of linseed were undertaken by different researchers. Ram *et al.* (2004) reported that oil yield had strong coherent association with seed yield, followed by number of capsules, oil content and number of primary and secondary branches. Tadele Tadesse *et al.* (2009) also reported that seed yield per plot show positive and highly significant association with plant height, thousand seed weight, seed yield per plant and oil content at phenotypic level.

Muhammad *et al.* (2003) studied five traits in eight linseed genotypes and found that seed yield per plant had highly significant positive correlation with number of branches per plant, number of capsules per plant, significant with 1000 seed weight and non significant negative correlation with plant height. Adugna Wakjira and Labuschagne (2003) reported positive significant correlation for seed yield per hectare with seed yield per plant, 1000 seed weight, and capsules per plant. The same authors found positive strong correlation for seed yield per plant, 1000 seed weight and capsules per plant with plant height, branches per plant, days to flowering and maturity.

3. Objectives

3.1. General objective

To study the genetic diversity of 64 genotypes of linseed in terms of their performance on Bedi Acidic Soil in Central Highland of Ethiopia

3.2. Specific objectives

1. To examine the genetic diversity of linseed genotypes on Bedi acidic soil and determine phenotypic and genotypic coefficient of variation, heritability and genetic advance of main traits;
2. To identify high yielding and adaptable genotypes of linseed on acidic soil;
3. To determine the magnitude of relationships among yield and yield related characters;
4. To estimate the genetic distance of the genotypes and classify them in different groups based on their genetic distances;
5. To generate useful information for future breeding program for acidic soils

4. Materials and Methods

4.1. Description of the study area

The experiment was carried out in the field at Bedi Trial Site, which is located at about 20 kilometers (km) West of Addis Ababa. This place is situated in West Shewa Zone and its geographical coordinates are 9° 7' 0" North, 38° 39' 0" East. The trial site is among the highland areas of the region where soil acidity has been limiting crop production. Holleta Agricultural Research Centre (HARC) is currently carrying out different studies on cereals, pulses, and oilseeds to screen out tolerant crop varieties to acidic soil at Bedi. The soil type of Bedi is clay loam. The altitude is 2730 m.a.s.l. The soil pH of the trial site is 5.11 (Table 2), which is strongly acidic.

Table 2. Exchangeable cations and pH of soil of Bedi trial site

Exchangeable cations	Amount	Unit
Aluminum (Al^{+3})	1.73	Centimole/g of soil
Calcium (Ca^{+2})	7.0324	Milliequimolar/100g of soil
Magnesium (Mg^{+2})	2.755	Milliequimolar/100g of soil
pH	5.11	Hydrogen ion concentration in moles/liter at 25 ⁰ C
Altitude	2730	Meter above the sea level

Source: Holetta Agricultural Research Center, Soil Analysis and Plant Physiology Team, 2009/2010

4.2. Experimental materials

The details of experimental materials used for this study are given in Appendix III. Sixty-four linseed genotypes, which were obtained from HARC, were used for this study. They consisted of one released and 63 elite lines. The released line, known as Tolle, was used as a standard check. Tolle was a variety that had shown good performance on acidic soil in the previous tests and thus used as a standard check for this experiment. All genotypes are driven from a single plant selection of crosses (beyond F₈) except six exotic genotypes. Appendix III provides names of genotypes, pedigrees (origins) and major merits of the genotypes.

4.3. Experimental design and procedure

A field-based screening method was used to test performance of linseed genotypes on acidic soil. Sixty-four linseed genotypes were laid in simple lattice design with two replications at random. Each replication had eight blocks and each block was represented by eight plots. A plot of two rows each of 3 m length and 20 cm spacing between rows was used. The path between blocks was 1.7 m. The crop was planted on June 23rd, 2009. Each genotype was sown at seed rate of 25 kg/ha by hand drilling the seeds in rows. A fertilizer rate of 23/23 kg/ha N/P₂O₅ (30 kg/ha urea + 50 kg/ha DAP) was applied at planting by incorporating them with the soil prior to sowing the seeds. All other cultural practices were undertaken uniformly for plots as per the recommendations.

4.4. Data collection

Data were collected under two categories (on plot and single plant bases) as shown below:

4.4.1. On plot bases

Days to 50% flowering (DF): days from sowing to the stages when 50% of plants have started flowering were computed.

Days to 90% maturity (DM): The number of days from date of sowing to a stage at which 90% of the plants have reached physiological maturity was calculated. It is the time when 90% of the capsules change their color into brown. The growing time of linseed was calculated as the period from sowing until seed maturity, the day when upper part of plants with their seed capsules had turned brown and seeds rattled in their capsules.

Thousand seed weight (TSW): The weight (g) of 1000 seeds from randomly sampled seeds per plot measured by using sensitive balance.

Vigourisity (VIG): Vigourisity measures density of plant population in the plot. Vigourisity of plot is ranked from 5 to 1 based on their relative vigourisity and converted to 100% scale.

Oil content (OC): The proportion of oil in the seed to total oven dried seed weight as measured by nuclear magnetic resonance spectrometer (Appendix I).

Seed yield per plot (SYP): Seed yield per plot was measured in grams after moisture of the seed is adjusted to 7%. It was converted to seed yield per hectare (SYH) by extrapolating the area of 1.2 m² to the hectare basis.

Oil yield (OYH): The amount of oil in kg/ha obtained by multiplying seed yield by corresponding oil percentage obtained from oil analysis.

$$OY = OC \times SYH$$

4.4.2. On single plant basis

Data on single plant basis was collected from five plants randomly taken from the plots. The mean of these five plants was used for statistical analysis.

Tillers per plant (TPP): The average number of tillers per plant was counted from the five randomly taken plants.

Primary branches per plant (PB): The average number of branches on the main stem per plant was counted from the five randomly taken plants.

Secondary branches per plant (SB): The average number of branches arising from primary branches per plant was counted from the five randomly obtained plants

Number of capsules per plant (NCP): The average number of capsules was counted from the five randomly taken plants.

Root length (RL): The average length (cm) of fresh taproot was measured from the five randomly obtained plants.

Plant height (PH): The average height (cm) of five randomly taken plants was measured from the ground to the highest part of plant at the harvesting time.

Seeds yield per plant (SYP): The weight of seeds of five randomly taken plants was measured in grams after moisture of the seed is adjusted to 7% and then divided by five. Adjusted yield is a yield that is determined after the moisture is driven off.

4.5. Statistical procedures

Data was collected for 14 agro-morphological characters on each of the 64 genotypes studied and were subjected to various statistical analyses.

4.5.1. Analysis of variance

Analysis of variance for each character was computed as per Montgomery (1991) using AGROBASE 2000 Software (Agronomix Software, Inc., 2000).

Table 3. Analysis of variance (ANOVA) for 14 characters of 64 linseed genotypes

Source of variation	Df	SS	MS	F-value	Pr>F
Replication (r)	r-1	SSr	MSr	MSr/Mse	
Genotypes (g)	g ² -1	SSg	MSg	MSg/Mse	
Block within replication (b)	r (b-1)	SSb	MSb	MSb/Mse	
Intra-block error (e)	(b-1) (rb-b-1)	SSE	Mse		
Total	rb ² -1	SST			

where: r = number of replication, g = number of genotypes, df = degree of freedom, b = block, SS = Sum of squares, MS = mean squares, SSr and MSr are sums of squares and mean of replication, respectively; SSg and MSg are sums of squares and mean of genotypes, respectively; SSb and MSb are sums of squares and mean of blocks within replication respectively, SSE and MSe are sums of squares and mean of intra-block error, respectively and SST is sum of squares of the total

4.5.2. Analysis of genetic parameters

Estimation of genetic parameters were done to identify and ascertain the genetic variability among the genotypes and to determine the extents of environmental effects on various characters. Components due to genotypic variance (σ^2g), environmental variance (σ^2E), and broad-sense heritability (h^2) were calculated by adopting the following formulas suggested by different biometricians:

I. Phenotypic and genotypic variation

The phenotypic and genotypic variances and coefficient of variation were calculated according to the methods suggested by Burton and de Vane (1953).

Genotypic variance

$$\text{Genotypic variance, } \sigma^2G = \frac{(\sigma^2e + r\sigma^2g) - \sigma^2e}{r}$$

r

Where, σ^2_g = mean square of genotypes (treatment),

σ^2_e = environmental variance (error mean square)

r = number of replication

Phenotypic variance

Phenotypic variance, $\sigma^2_P = \sigma^2_g + \sigma^2_e$

$$PCV = \frac{\sigma_P}{\bar{X}} \times 100$$

X

Where, PCV = phenotypic coefficient of variation

X = grand mean

σ_P = the phenotypic standard deviation

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

X

Where, GCV = genotypic coefficient of variation

σ_g = the genotypic standard deviation

II. Heritability in the broad sense, $h^2 = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e}$

III. Genetic Advance (GA): Genetic advance as the percent of mean was calculated by dividing the genetic advance with the mean and multiply it by 100.

$$GA = h^2 \sigma_p K$$

Where, h^2 = heritability in the broad sense

K = selection differential at 5% intensity of selection, that is 2.06.

σ_p = the phenotypic standard deviation

IV. GA% (as % of mean) = GA/grand mean x 100

4.5.3. Analysis of correlation coefficient (r)

The associations among oil content, seed yield and yield related traits themselves were estimated using simple Pearson's product moment correlation coefficients by using MSTAT (MSTAT, 1988) software of version 1.0. Using the r table at appropriate degrees of freedom and probability level, significance of the correlation coefficients were tested. The phenotypic correlation coefficients were calculated by using the formula suggested by Gomez and Gomez (1984) as:

$$r_{p_{xy}} = \frac{Covp_{xy}}{\sqrt{\sigma^2 p_x \sigma^2 p_y}}$$

Where: $r_{p_{xy}}$ = phenotypic correlation coefficient between traits x and y.

$Covp_{xy}$ = Phenotypic covariance between traits x and y

$\sigma^2 p_x$ = Phenotypic variance of trait x

$\sigma^2 p_y$ = Phenotypic variance of trait y

4.5.4. Cluster analysis

Clustering of genotypes was performed by canonical roots method using procedures of SAS (SAS Institute, 2002) version 9.00 software to group sets of genotypes into possible homogenous classes.

4.5.4.1. Genetic distance between clusters

Genetic distances between clusters were estimated by Mahalanobis's (1936) D^2 statistics using the same software as in clustering as:

$$D^2_{ij} = (\bar{x}_i - \bar{x}_j)' cov^{-1} (\bar{x}_i - \bar{x}_j)$$

Where, D^2_{ij} = the distance between cases i and j;

\bar{x}_i and \bar{x}_j = vectors of the values of the variables for cases i and j and

cov^{-1} = the pooled within groups variance matrix.

The D^2 values obtained for pairs of clusters were considered as the calculated value of chi-square (X^2) and were tested for its significance both at 1% and 5% probability levels against the tabulated value of X^2 for 'p' degree of freedom, where p is the number of significant characters (p = 9 in present case), as suggested by Singh and Chaudhary (1985). If calculated $X^2 >$ tabulated X^2 , it indicates significance of the D^2 values.

5. Results

5.1. Mean values of the 14 traits of linseed genotypes studied

Mean values of the characters of the 64 linseed genotypes tested are presented in Table 4 below. Duncan's Multiple Range Test (DMRT) was carried out for only highly significant characters among the genotypes.

Table 4. Mean values of the 14 characters of 64 linseed genotypes studied for their performance on acidic soil at Bedi trial site, 2009/2010

Trt. no	Name of genotypes	SYH	OYH	OC	SYP	TSW	RL	TPP	PB	SB	NCP	VIG	DF	DM	PH
1	Omega X CI-1525/B/1	1938.5 ^c	726.7 ^h	37.6 ^a	2.1	5.5 ^a	13.8 ^h	2.5	9.6	11.5	34.0	70.9 ^e	101.4 ^f	179.1 ^k	68.3 ^d
2	Omega X CI-1525/B/2	2566.7 ^j	993.0 ^m	38.4 ^b	2.3	6.1 ¹	11.7 ^e	2.4	9.8	11.2	33.7	89.9 ^g	101.5 ^g	161.9 ^d	66.3 ^c
3	Omega X CI-1525/B/3	2339.9 ^a	889.1 ¹	37.5 ^a	2.0	5.4 ^a	14.7 ^j	2.3	10.5	11.4	43.8	95.3 ⁱ	99.0 ^e	159.4 ^c	74.4 ^g
4	CI-1652 X Omega /B/4	2378.4 ^a	946.8 ^m	40.0 ^f	2.8	6.4 ^s	12.4 ^g	2.0	7.7	11.0	35.9	80.6 ^e	96.8 ^e	175.0 ^j	74.7 ^g
5	CI-1652 X Omega /B/8	2215.0 ^g	869.3 ⁱ	39.2 ^d	2.6	6.0 ^l	13.4 ^h	3.2	7.9	13.1	39.2	95.1 ⁱ	91.9 ^d	175.0 ^j	79.7 ^h
6	CI-1652 X Omega /B/10	2224.1 ^h	875.6 ^j	39.5 ^d	1.9	6.6 ^u	13.5 ^h	3.1	8.2	10.2	38.7	91.1 ^g	90.3 ^a	178.8 ^j	79.4 ^h
7	PGRC/E10306XCI-1525/B/1	1942.6 ^e	744.2 ^g	38.6 ^c	2.1	6.2 ^r	14.4 ^j	2.1	6.8	7.9	32.0	89.7 ^g	90.5 ^a	169.9 ^g	76.5 ^g
8	CI-1652X/PGRC/E10306/B/7	1560.5 ^k	616.9 ^e	40.0 ^f	1.0	6.4 ^s	12.9 ^f	2.7	7.7	12.5	35.3	87.4 ^e	99.8 ^e	178.8 ^j	76.9 ^g
9	PGRC/E10306XCI-1652/Y/1	1876.7 ^e	746.8 ^g	39.9 ^f	2.4	6.9 ^v	15.1 ^j	2.4	10.0	13.7	45.6	82.9 ^e	100.9 ^f	183.1 ^m	95.8 ^a
10	Omega X Chilao/Y/7	2244.7 ^h	900.4 ¹	39.8 ^e	2.2	5.9 ^j	12.2 ^e	2.2	8.2	9.9	34.5	97.9 ^j	98.5 ^e	165.0 ^f	87.9 ^m
11	CDC-1747XCI-1652/S2	2292.4 ^a	875.2 ^j	38.1 ^a	2.1	5.8 ⁱ	13.0 ^f	2.5	7.8	11.8	37.7	92.3 ^g	99.0 ^e	169.9 ^g	82.4 ^j
12	CI-1525XR12-N27G/S4	1933.2 ^e	755.8 ^g	39.3 ^d	2.2	6.0 ^l	12.5 ^f	1.8	7.4	10.6	29.4	80.6 ^e	99.3 ^e	165.1 ^f	78.2 ^g
13	R12-N27G X CI-1525/S3	1958.6 ^e	735.4 ^g	37.5 ^a	1.7	5.6 ^b	11.8 ^e	2.3	7.8	11.2	41.9	93.1 ^h	100.9 ^f	147.0 ^a	74.7 ^g
14	CI-1525XR12-D33C/S1	2283.3 ^g	897.7 ¹	39.1 ^d	1.8	5.9 ^j	12.3 ^e	2.8	9.0	11.2	36.8	96.1 ^j	101.8 ^g	171.8 ^h	75.9 ^g
15	CI-1525XR12-D33C/S4	1870.3 ^c	731.9 ^g	39.5 ^d	2.0	5.5 ^a	12.8 ^f	1.9	7.0	10.8	30.0	85.7 ^e	102.5 ^h	161.0 ^d	81.5 ^j
16	CI-1525XR12-D33C/S9	1984.7 ^f	759.5 ^g	38.8 ^c	2.6	6.6 ^u	13.8 ^h	2.6	7.6	10.3	37.2	81.4 ^e	89.8 ^a	182.8 ^l	74.9 ^g
17	CI-1525XCDC1747V&E/S8	2170.4 ^g	855.8 ⁱ	39.4 ^d	2.5	5.7 ^c	12.8 ^f	3.2	9.3	14.0	41.7	86.6 ^e	97.8 ^e	179.3 ^k	70.9 ^e
18	CI-1525XR12-N27G/S13	1907.4 ^e	762.1 ^h	39.9 ^e	2.6	6.1 ^q	11.2 ^d	2.3	8.1	13.0	46.0	88.7 ^e	103.9 ^j	166.0 ^f	79.2 ^h
19	CI-1652XCDC1747/S6	1868.0 ^e	734.5 ^g	39.4 ^d	1.9	5.8 ^g	13.1 ^f	2.3	7.3	12.1	32.4	83.0 ^e	96.8 ^e	170.1 ^h	79.3 ^h
20	Omega X chilalo/Y	2235.8 ^h	876.6 ^j	39.5 ^d	1.9	5.5 ^a	12.2 ^e	1.8	7.6	10.3	38.4	84.3 ^e	99.2 ^e	165.2 ^f	78.6 ^h
21	CI-1652XPGRC/E10306/Y/2	2058.3 ^f	809.1 ^h	39.3 ^d	1.7	6.0 ^l	12.0 ^e	2.1	6.2	11.1	33.7	91.8 ^g	99.7 ^e	165.2 ^f	84.1 ^k
22	R-12-D33CX CI-1525/P1/S2	2278.2 ^h	888.4 ^k	38.9 ^c	1.6	5.8 ⁱ	11.4 ^e	1.9	7.3	11.7	34.8	88.8 ^e	101.7 ^g	162.2 ^e	83.3 ^j
23	R-12-D33CX CI-1525/P3/S1	1911.4 ^e	755.1 ^g	39.5 ^d	1.8	5.8 ⁱ	12.4 ^e	2.4	9.2	12.5	28.3	85.4 ^e	99.4 ^e	174.1 ⁱ	80.4 ^j
24	Chilalo X R-12-N27G/P2/S2	2420.9 ^b	935.3 ¹	38.7 ^c	2.9	5.8 ⁱ	14.5 ^j	2.8	8.4	12.1	38.4	92.1 ^g	103.1 ⁱ	174.0 ⁱ	78.3 ^h
25	CI-1525XR-12-N27G/P4/S2	1741.1 ^e	674.7 ^f	38.9 ^c	1.8	6.0 ^l	11.5 ^e	2.2	7.9	11.3	44.6	78.1 ^e	101.4 ^f	159.8 ^c	80.7 ^j
26	CI-1525X R-12-N27G/P2/S2	1783.3 ^c	697.2 ^g	38.7 ^c	2.3	6.0 ^l	11.3 ^d	2.2	7.2	10.7	35.0	81.6 ^e	101.5 ^g	164.7 ^f	77.7 ^g
27	CI-1525X R-12-N27G/P2/S3	2200.9 ^h	869.4 ⁱ	39.6 ^e	1.9	5.9 ^j	12.1 ^e	1.8	9.2	12.3	39.0	89.5 ^g	98.4 ^e	164.7 ^f	77.8 ^g
28	CI-1525X R-12-N27G/P1/S3	2073.7 ^f	825.6 ⁱ	39.8 ^e	2.2	5.8 ⁱ	12.4 ^e	2.3	8.5	11.8	36.7	91.7 ^g	100.2 ^f	164.8 ^f	76.6 ^g
29	R-12-N27G X CI-1525/P4/S1	2208.1 ^g	855.0 ⁱ	38.6 ^c	1.5	5.8 ⁱ	12.0 ^e	1.8	6.3	10.9	29.6	90.2 ^g	98.3 ^e	164.7 ^f	80.6 ^j
30	CI-1525X CDC1747/P4/S1	2316.9 ^a	909.8 ¹	39.5 ^d	1.9	6.0 ^l	11.4 ^e	2.5	7.4	10.0	38.2	81.3 ^e	99.8 ^e	173.5 ⁱ	82.8 ^j
31	CI-1525X CDC1747/P2/S3	2033.2 ^f	815.3 ^h	40.2 ^f	1.4	6.0 ^l	12.8 ^f	2.2	8.1	11.0	37.5	83.9 ^e	97.9 ^e	180.7 ^l	83.4 ^j

	Table 4. continued	SYH	OYH	OC	SYP	TSW	RL	TPP	PB	SB	NCP	VIG	DF	DM	PH
32	CI-1525X CDC1747/P1/S2	2156.0 ^f	885.1 ^k	41.0 ^g	1.7	6.0 ^l	13.1 ^g	2.0	7.3	11.1	40.0	89.5 ^g	91.2 ^b	185.6 ^m	74.3 ^g
33	R12-D33C X CI-1525/P2/S3	1816.1 ^e	719.9 ^g	39.5 ^d	2.5	6.1 ^l	12.4 ^e	2.5	8.1	10.8	38.6	80.5 ^e	100.2 ^g	179.2 ^k	78.8 ^h
34	CI-1525XR12-N27G/P1/S1	2004.0 ^e	782.9 ^h	38.6 ^c	2.2	6.1 ^l	12.0 ^e	2.3	7.7	10.4	32.7	92.5 ^g	102.2 ^h	165.0 ^f	76.3 ^g
35	CI1525XCDC1747/VandE/S4	2504.2 ⁱ	975.8 ^m	38.8 ^c	2.2	6.1 ^l	12.3 ^e	1.8	7.5	12.9	36.5	89.9 ^g	101.2 ^f	165.0 ^f	78.9 ^h
36	PGRC/E10306 X Chilalo/B/4	2100.6 ^f	810.7 ^h	38.4 ^c	2.7	6.0 ^l	14.3 ^j	2.1	8.0	12.8	39.5	84.1 ^e	101.5 ^g	183.1 ^m	83.2 ^j
37	Chilalo X Omega/10	2166.9 ^f	844.8 ⁱ	38.7 ^c	2.0	5.8 ⁱ	13.2 ^g	2.1	7.0	10.9	34.1	84.6 ^e	99.6 ^e	165.0 ^f	80.2 ⁱ
38	CDCI-1747XCI-1652/S1	1977.1 ^e	767.9 ^h	38.5 ^c	2.1	5.7 ^c	11.7 ^e	2.4	7.8	12.0	36.1	79.7 ^e	100.0 ^f	178.8 ^j	79.9 ⁱ
39	R12-N27G X CI-1525/S6	2137.6 ^f	829.0 ⁱ	39.4 ^d	2.3	5.4 ^b	13.6 ^h	1.9	5.6	10.3	27.4	79.3 ^e	95.2 ^e	185.5 ^m	85.5 ^k
40	CI-1525/S6 X R12-N27G/S12	1948.6 ^e	824.3 ^h	42.1 ^g	2.0	6.0 ^l	12.1 ^e	2.3	7.3	11.6	40.5	75.9 ^e	95.5 ^e	178.9 ^j	83.4 ^j
41	PGRC/E10306 X Chilalo/Y	1464.9 ^p	574.6 ^d	38.8 ^c	1.3	5.8 ⁱ	13.9 ⁱ	2.2	7.9	10.0	35.9	78.1 ^e	103.2 ^j	183.3 ^m	90.4 ^m
42	PGRC/E10306 X Chilalo/Y/2	1382.4 ^m	541.6 ^d	38.4 ^b	1.8	6.0 ^l	14.0 ⁱ	1.9	6.7	10.2	33.8	80.1 ^e	99.3 ^e	185.1 ^m	85.9 ^k
43	PGRC/E10306XChilalo/B/4/A	1440.4 ^p	564.9 ^d	39.0 ^d	1.3	5.9 ^j	14.2 ^j	1.7	5.3	9.5	27.2	76.5 ^e	102.2 ^h	183.1 ^m	86.0 ^l
44	PI-523353 SPS1	1318.2 ^m	585.9 ^d	44.2 ^h	1.2	6.4 ^s	11.4 ^e	1.5	6.2	9.4	28.7	66.7 ^c	98.6 ^e	156.7 ^b	64.3 ^c
45	CI-1525XR-12D33C/S2	1840.0 ^e	705.0 ^g	37.9 ^a	1.8	6.4 ^s	13.2 ^g	2.3	5.8	11.4	31.3	81.2 ^e	94.1 ^e	175.7 ^j	83.8 ^j
46	CI-1525XR-12N27G/S13/A/	2008.7 ^e	774.2 ^h	38.5 ^c	1.4	6.1 ^q	12.7 ^f	2.0	5.8	8.8	32.5	85.3 ^e	100.1 ^f	174.0 ⁱ	87.0 ^l
47	CI-1525XR-12N27G/S13/B/	1500.4 ^p	593.0 ^d	39.1 ^d	2.1	6.0 ^l	12.6 ^f	1.8	6.8	9.8	29.7	85.9 ^e	100.8 ^g	174.1 ⁱ	84.1 ^k
48	PI-523353 SPS2	1239.5 ^m	534.5 ^d	43.1 ^h	1.3	6.6 ^u	11.4 ^e	1.9	7.1	9.8	37.6	71.5 ^e	102.0 ^g	157.0 ^b	63.5 ^c
49	PGRC/E10306 X Chilalo/B/2	1562.4 ^p	588.6 ^d	38.2 ^a	1.9	5.4 ^b	13.2 ^g	2.2	6.3	10.3	32.5	73.6 ^e	94.2 ^e	179.2 ^k	78.3 ^h
50	PI-523353 SPS3	1840.3 ^e	751.0 ^g	44.1 ^h	1.3	6.3 ^r	10.8 ^b	1.6	7.6	9.8	37.9	68.7 ^d	102.8 ^h	156.5 ^b	67.9 ^d
51	R-12N27G/S13 XCI-1525/S4	2104.8 ^f	804.3 ^h	38.7 ^c	1.7	5.9 ^j	13.9 ⁱ	2.2	7.1	10.1	32.1	60.1 ^a	100.8 ^g	183.0 ^m	73.5 ^g
52	Omega X CI-1525/B/3	1305.1 ^m	531.1 ^c	40.9 ^g	1.1	5.7 ^c	13.2 ^g	2.1	7.6	12.4	28.5	64.3 ^b	101.6 ^g	183.1 ^m	78.3 ^g
53	PGRC/E10306X Chilalo/B/4/	1739.2 ^e	653.8 ^e	37.9 ^a	2.3	6.0 ^l	13.8 ^g	2.2	6.5	10.5	30.5	70.8 ^e	100.7 ^f	173.6 ⁱ	88.2 ^m
54	CI- 1652 X CDC 1747/S3	2102.5 ^f	786.9 ^h	37.9 ^a	1.2	5.7 ^c	11.0 ^b	2.5	7.0	10.8	31.6	84.9 ^e	101.6 ^g	169.9 ^g	79.9 ^h
55	CDC 1747 X CI- 1652/S15	1851.2 ^e	680.9 ^g	37.8 ^a	2.0	5.7 ^c	12.1 ^e	3.2	9.5	12.0	42.7	83.4 ^e	92.3 ^c	175.0 ^j	82.1 ⁱ
56	PI-523353 SPS4	1171.0 ^q	491.7 ^b	42.5 ^g	0.8	6.6 ^u	9.8 ^a	1.5	6.8	10.5	34.4	63.1 ^a	101.1 ^f	155.4 ^a	67.0 ^d
57	PGRC/E10306 X Chilalo/Y/3	1704.4 ^e	669.3 ^f	39.4 ^d	2.3	5.9 ^j	13.3 ^g	1.6	6.9	10.7	31.6	81.6 ^e	98.7 ^e	167.3 ^g	97.6 ⁿ
58	Omega X CI-1525/Y/43	1432.2 ^p	564.2 ^d	39.0 ^d	1.4	6.1 ^q	11.2 ^d	2.1	6.3	9.1	30.1	73.6 ^e	91.3 ^b	170.2 ^h	82.7 ^j
59	Omega X CI-1525/Y/44	1245.7 ^m	491.9 ^b	39.2 ^d	1.9	5.4 ^b	13.2 ^g	1.7	6.9	10.1	34.2	57.0 ^a	100.3 ^f	183.2 ^m	79.8 ^h
60	Omega X CI-1525/B/44	1036.8 ^q	412.9 ^a	39.5 ^d	1.4	5.7 ^c	13.5 ^h	2.4	6.6	10.7	33.1	60.3 ^a	91.6 ^c	183.3 ^m	72.6 ^g
61	PI-523353 SPS5	1196.3 ^m	515.7 ^d	42.6 ^g	1.6	7.0 ^v	10.7 ^b	2.4	6.7	10.5	33	51.8 ^a	98.7 ^e	162.2 ^e	62.6 ^c
62	Omega X CI-1525/14/A	1983.2 ^e	771.1 ^h	38.9 ^c	1.1	6.5 ^s	11.9 ^e	2.0	6.8	10.5	36.3	76.8 ^e	99.1 ^e	183.0 ^m	80.8 ⁱ
63	PI-523353 SPS	1045.0 ^q	484.5 ^b	44.0 ^h	2.2	6.9 ^u	11.1 ^c	2.3	5.7	9.2	35.3	55.4 ^a	99.3 ^e	152.7 ^a	57.9 ^a
64	Tolle	2093.3 ^f	797.1 ^h	38.5 ^b	1.8	6.0 ^l	11.5 ^e	2.4	6.4	10.8	33.3	74.1 ^e	98.5 ^e	174.1 ⁱ	67.3 ^d
	Mean	1894.32	744.3	39.5	1.9	6.0	12.6	2.21	7.5	11.0	35.3	81.0	99	172	78.5
	C.V. (%)	17.97	16.9	2.2	28.2	3.03	7.5	19.2	18.4	14.8	18.2	7.9	3.9	3.7	6.6

Where: SYH= Seed yield per hectare, OYH= Oil yield per hectare, OC= Oil content per plot (%), SYP= Seed yield per plant (g), TSW= Thousand seed weight, RL = Root length per plot (cm), TPP= Tillers per plant, PB = Primary branches per plant, SB= Secondary branches per plant, NCP= Number of capsules per plant, VIG= Vigourity or stand of the plot (%), DF=Days to 50% flowering, DM = Days to 90% maturity and PH= Plant height per plot. Means within the same column followed by similar letters are not significantly different according to DMRT at 5% level of probability

5.2. Analysis of variance for 14 characters of linseed genotypes

The result of analysis of variance is presented below (Table 5). From the 14 traits measured, six characters (RL, OC, TSW, PH, VIG and DM) have shown very highly significant variations ($P < 0.001$) among the genotypes, while three characters (SYH, OYH and DF) displayed highly significant differences ($P < 0.01$). Three characters (SYP, TPP and PB) revealed significant differences at 0.1 probability level. However, the remaining two characters (NCP and SB) were not statistically different for the evaluated genotypes though they had wide ranges (Table 6).

Table 5. Mean sum of square of different sources of variations for 14 quantitative characters of 64 linseed genotypes.

Characters	Sources of variation in mean square			
	Genotypes (63)	Block (14)	Replication (1)	Intra-block error (49)
RL	131.18***	56.7	2.8	43.5
SYP	22.2*	11.4	4.1	14.0
SYH	12814110.1**	7593747.1	1099119.3	5680628.1
OC	265.0***	65.4	95.2	36.8
OYH	1721456.0**	1182392.1	43305.4	773178.9
TSW	16.1***	0.6	0.02	1.6
PH	6120.3***	2423.5	795.0	1314.0
NCP	2261.8	1265.1	206.1	2028.2
TPP	17.2*	4.6	1.5	8.8
PB	152.1*	28.6	31.4	92.8
SB	152.0	68.1	128.0	130.6
VIG	9854.1***	6595.0	1122.2	2003.3
DF	1543.5**	254.4	144.5	731.125
DM	11040.2***	617.0	197.5	1984.0

***, **, * indicate significance at 0.001, 0.01 and 0.1 probability levels, respectively; numbers in parentheses refer to degrees of freedom. SYH = seed yield per hectare, OYH = oil yield per hectare, OC = oil content (%), SYP = seed yield per plant (g), TSW = 1000- seed weight (g), RL= root length (cm), TPP = tillers per plant, PB = primary branches per plant, SB = secondary branches per plant, NCP= number of capsules per plant, VIG = vigourity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height

Seed yield per hectare showed significant differences among genotypes at 0.01 probability levels. The top five high seed yielding genotypes identified and short-listed for further breeding program are given in Table 6 below.

Table 6. The top five high seed yielders of linseed genotypes on Bedi acidic soil with their respective sources of origin and clusters

Treatment number	Name of genotypes	SYH	Source	Cluster no
2	Omega X CI-1525/B/2	2566.7	SPS from a cross between yellow-seeded USA (Omega) and standard variety (CI-1525/B/2)	VI
35	CI1525 X CDC1747/VandE/S4	2504.2	SPS from a cross between standard (CI-1525) and Canadian (CDC1747) varieties	VI
24	Chilalo X R-12-N27G/P2/S2	2420.9	SPS from a cross between standard variety (Chilalo) and regenerant from tissue culture	VI
4	CI-1652 X Omega /B/4	2378.4	SPS from a cross between standard variety (CI-1652) and yellow-seeded USA	VI
3	Omega X CI-1525/B/3	2339.9	SPS from a cross between yellow-seeded USA and standard variety (CI-1525)	III

Oil content (%) revealed highly significant ($P < 0.001$) variations for the 64 linseed genotypes tested. Six exotic genotypes from the USA had high oil content, ranging from 42.5-44.2% (Table 7).

Table 7. The top six linseed genotypes that yielded high oil content (%) on Bedi acidic soil, 2009/10

Treatment number	Name of genotypes	Oil content (%)	Source	Cluster no
44	PI-523353 SPS1	44.2	Exotic (USA)	V
50	PI-523353 SPS3	44.1	Exotic (USA)	II
63	PI-523353 SPS	44.0	Exotic (USA)	VII
48	PI-523353 SPS2	43.1	Exotic (USA)	V
61	PI-523353 SPS5	42.6	Exotic (USA)	V
56	PI-523353 SPS4	42.5	Exotic (USA)	V

Highly significant differences were also observed among the genotype for days to maturity at 0.001 probability level. Seven early maturing genotypes comprised of all exotic genotypes and one genotype of single plant selection from crosses between regenerant from the tissue culture are given in Table 8 below.

Table 8. Number of days of early matured linseed genotypes on Bedi acidic soil

Treatment number	Name of genotypes	Number of days	Source	Cluster no
13	R12-N27G X CI-1525/S3	147.0	SPS from acrosses between regenerant from the tissue culture and standard variety (CI-1525/S3)	I
63	PI-523353 SPS	152.7	Exotic (USA)	VII
56	PI-523353 SPS4	155.4	Exotic (USA)	V
50	PI-523353 SPS3	156.5	Exotic (USA)	II
48	PI-523353 SPS2	157.0	Exotic (USA)	V
44	PI-523353 SPS1	156.7	Exotic (USA)	V
61	PI-523353 SPS5	162.2	Exotic (USA)	V

5.3. Analysis of genetic parameters

5.3.1. Genotypic and phenotypic coefficient of variation

Analysis of genetic parameters viz. genotypic variance, phenotypic variance, phenotypic and genotypic coefficient variations, heritability in the broad sense and an expected genetic advance were given in Table 9. Estimated genetic variance ranged from 0.26 for 1000 seed weight to 203398.68 for seed yield (kg/ha). Likewise, the phenotypic variance ranged from 0.29 for the 1000 seed weight to 339585.95 for seed yield. Phenotypic coefficient of variation ranged between 5.72 for oil content and 43.63 for seed yield per plant, and genotypic coefficient of variation ranged between 5.01 days to maturity and 31.30 for seed yield per plant. The comparison of genetic coefficient of variation with the phenotypic coefficient of variation for 14 characters is given in Figure 1 below.

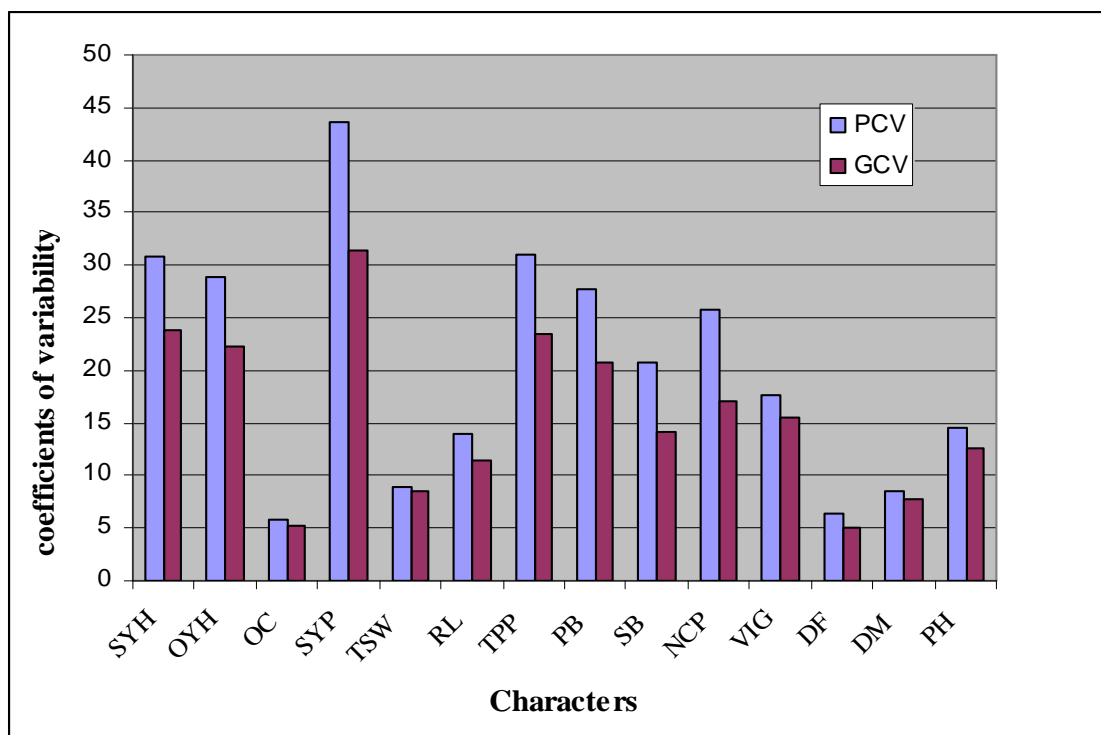


Figure 1. Phenotypic and genotypic coefficients of variability for 14 quantitative characters in linseed

Where, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, SYH = seed yield per hectare, OYH = oil yield per hectare, OC = oil content (%), SYP = seed yield per plant (g), TSW = 1000 seed weight (g), RL= root length (cm), TPP = tillers per plant, PB = primary branches per plant, SB = secondary branches per plant, NCP= number of capsules per plant, VIG = vigourisity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height (cm)

5.3.2. Heritability in the broad sense

In this study, heritability values were found to be sufficiently high for most of the characters (Table 9) and relative comparison was made among the characters. Heritability in the broad sense for different characters measured ranged from 43.63 to 89.66%. 1000 seed weight showed the highest (89.66%) heritability, while the lowest (43.63 %) heritability was observed for capsules per plant.

5.3.3. Genetic advance

Regarding the genetic advance at 5% selection intensity, the highest genetic gain was predicted for seed yield (kg/ha) followed by oil yield (kg/ha), while the lowest genetic advance was predicted for tillers per plant (Table 9). The highest genetic gain as percent of mean was observed for seed yield per plant (46.46%) followed by seed yield per hectare, which was predicted to be 38.02 (%). On the other hand, the lowest genetic gain as percent of mean was observed for oil content (9.74%) followed by days to flowering. Comparison of

heritability with genetic advance as mean % (Figure 2) was made as effectiveness of selection depends upon genetic advance of the character selected along with heritability.

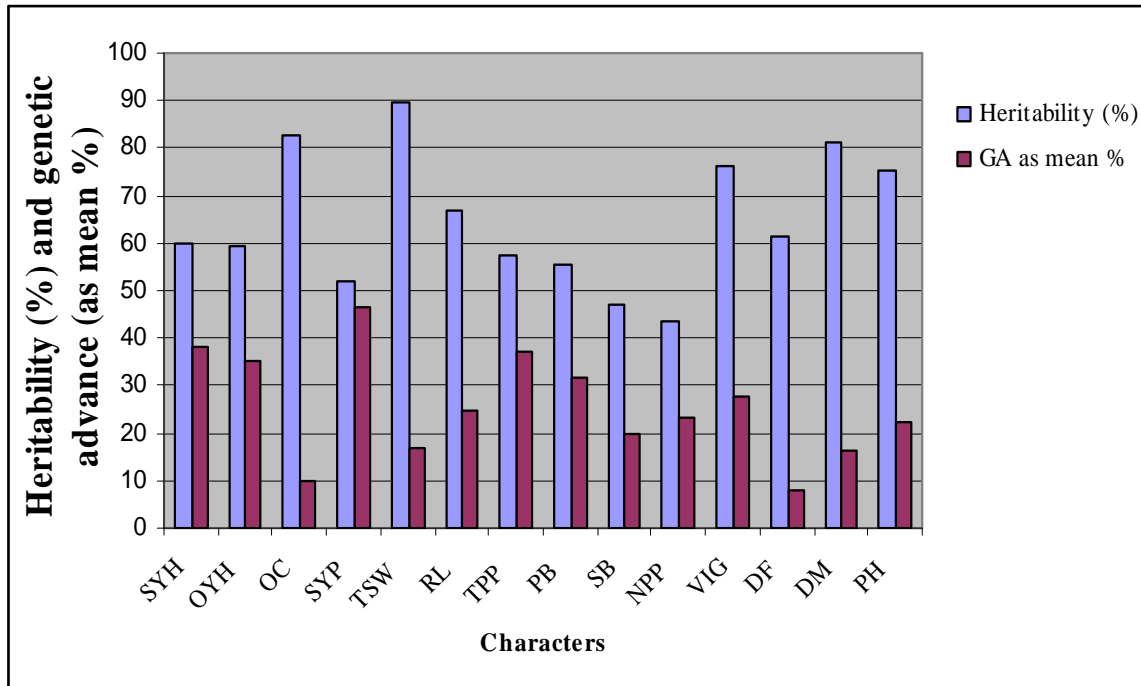


Figure 2. Broad sense heritability (%) and expected genetic advance (as mean %) for 14 quantitative characters of 64 linseed genotypes

Where, SYH = seed yield per hectare, OYH = oil yield per hectare, OC = oil content (%), SYP = seed yield per plant (g), TSW = 1000- seed weight (g), RL = root length (cm), TPP = tillers per plant, PB = primary branches per plant, SB = secondary branches per plant, NCP= number of capsules per plant, VIG = vigourisity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height (cm)

Table 9. Estimates of heritability (in the broad sense) and expected genetic advance for 14 characters of linseed genotypes tested at Bedi, 2009/10

Characters	Mean		Grand mean (X)	C.V. (%)	Genotypic variance	Phenotypic variance	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (%)	Genetic advance (k = 5%)	Genetic advance as mean %
	Mini	Maxi									
SYH	1036.80	2566.70	1894.32	17.97	203398.68	339585.95	30.76	23.81	60.00	720.27	38.02
OYH	412.90	993.00	744.33	16.90	27324.70	45955.22	28.80	22.21	59.46	262.67	35.29
OC	37.50	44.20	39.45	2.20	4.21	5.10	5.72	5.20	82.55	3.84	9.74
SYP	0.80	2.90	1.89	28.20	0.35	0.68	43.63	31.30	51.90	0.89	46.46
TSW	5.40	7.00	6.00	3.03	0.26	0.29	8.98	8.50	89.66	0.99	16.66
RL	9.80	15.10	12.58	7.50	2.08	3.12	14.04	11.46	66.70	3.15	25.00
TPP	1.50	3.20	2.21	19.20	0.27	0.47	31.02	23.51	57.45	0.82	37.03
PB	5.30	10.50	7.49	18.40	2.41	4.33	27.78	20.73	55.66	2.39	31.90
SB	7.90	14.00	10.98	14.80	2.41	5.14	20.65	14.14	46.89	2.19	19.97
NCP	27.20	46.00	35.29	18.20	35.90	82.28	25.70	17.00	43.63	8.15	23.10
VIG	51.80	97.90	81.06	7.90	156.41	205.59	17.69	15.43	76.08	22.48	27.73
DF	89.80	103.90	98.78	3.90	24.50	40.01	6.40	5.01	61.23	7.98	8.08
DM	147.00	185.60	171.57	3.70	175.24	216.46	8.58	7.72	80.96	27.78	16.19
PH	57.90	97.60	78.48	6.60	97.15	129.00	14.47	12.56	75.31	17.63	22.46

Where: SYH = seed yield (kg/ha), OYH = oil yield (kg/ha), OC = oil content (%), SYP = seed yield per plant (g), TSW = 1000- seed weight (g), RL = root length (cm), TPP = tillers per plant, PB = primary branches per plant, SB = secondary branches per plant, NCP= number of capsules per plant, VIG = vigourisity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height (cm)

5.4. Correlation coefficient analysis

Pearson's correlation coefficients (r) that were computed for 14 characters of the linseed genotypes to assess the possible interrelationship between any two traits have shown both positive and negative associations (Table 10). The correlation coefficient among most of the quantitative characters was highly significant. From 91 correlations made for the 14 quantitative characters at the phenotypic level, 49 correlation coefficients were statistically significant irrespective of directions of association. Among the significant correlations, 37 correlation coefficients were significant at 0.1% probability level, while six at 1% percent probability level. The remaining six showed significance at 5% probability level. Vigourisity of the genotypes per plot had significant correlation with most of the characters considered. On the other hand, days to flowering had less number of correlation characters. The highest phenotypic correlation was observed between seed yield per hectare with oil yield per hectare as shown in Figure 3 below.

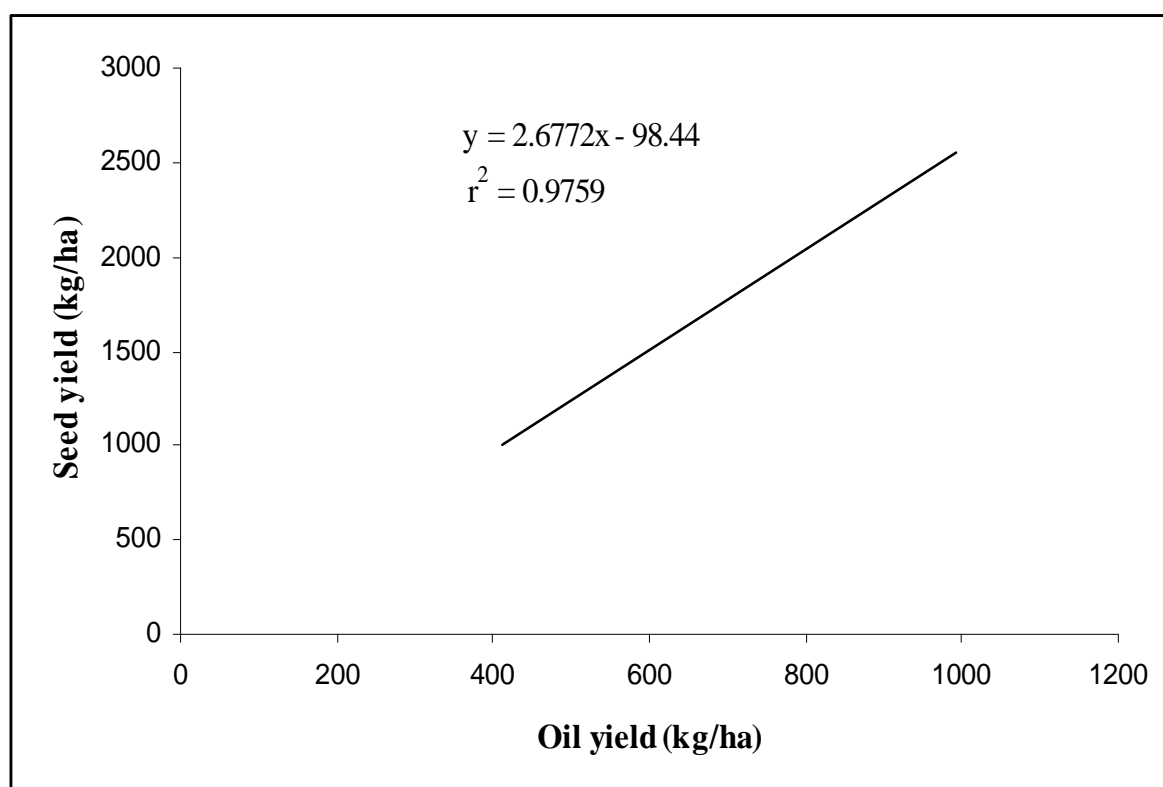


Figure 3. Biplot of seed yield (kg/ha) against the oil yield (kg/ha) of the test genotypes

Oil content had highly positive correlation only with the 1000 seed weight (figure 4). Characters such as oil yield per hectare, number of capsules per plant and days to flowering showed positive and non-significant correlation with the oil content. On the other hand, seed yield per plant, number of primary and secondary branches had negative non-significant correlation with the oil content.

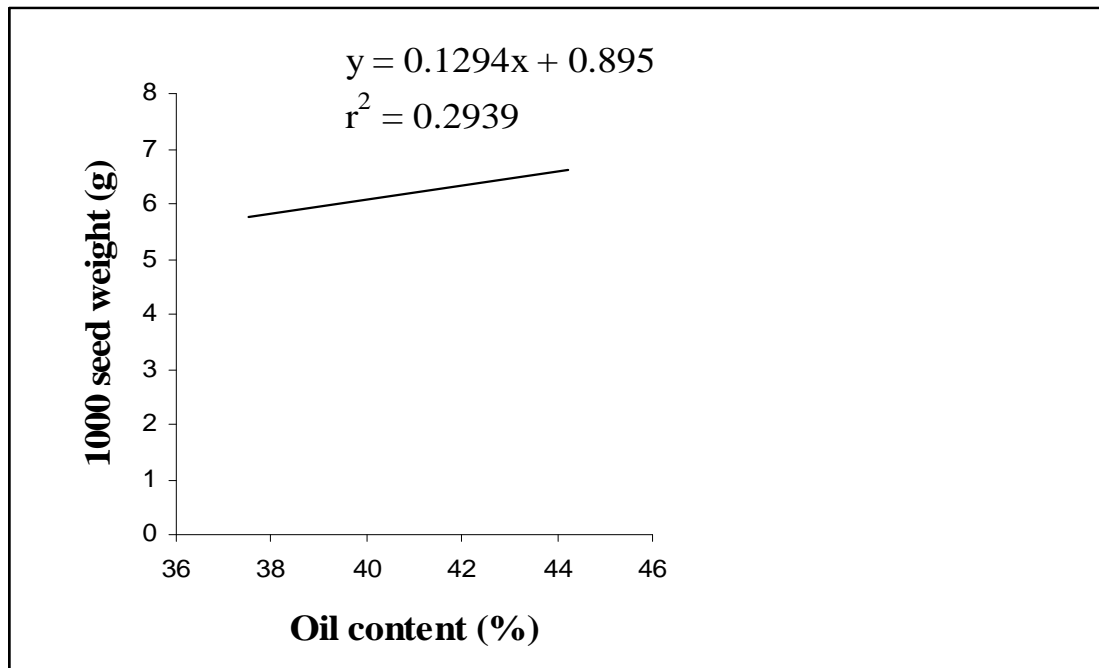


Figure 4. Biplot of 1000 seed weight (g) of the test genotypes against the oil content (%)

Days to maturity showed highly significant positive association with plant height and root length. On contrary, days to maturity and plant height had highly significant negative correlation with oil content (Figure 5).

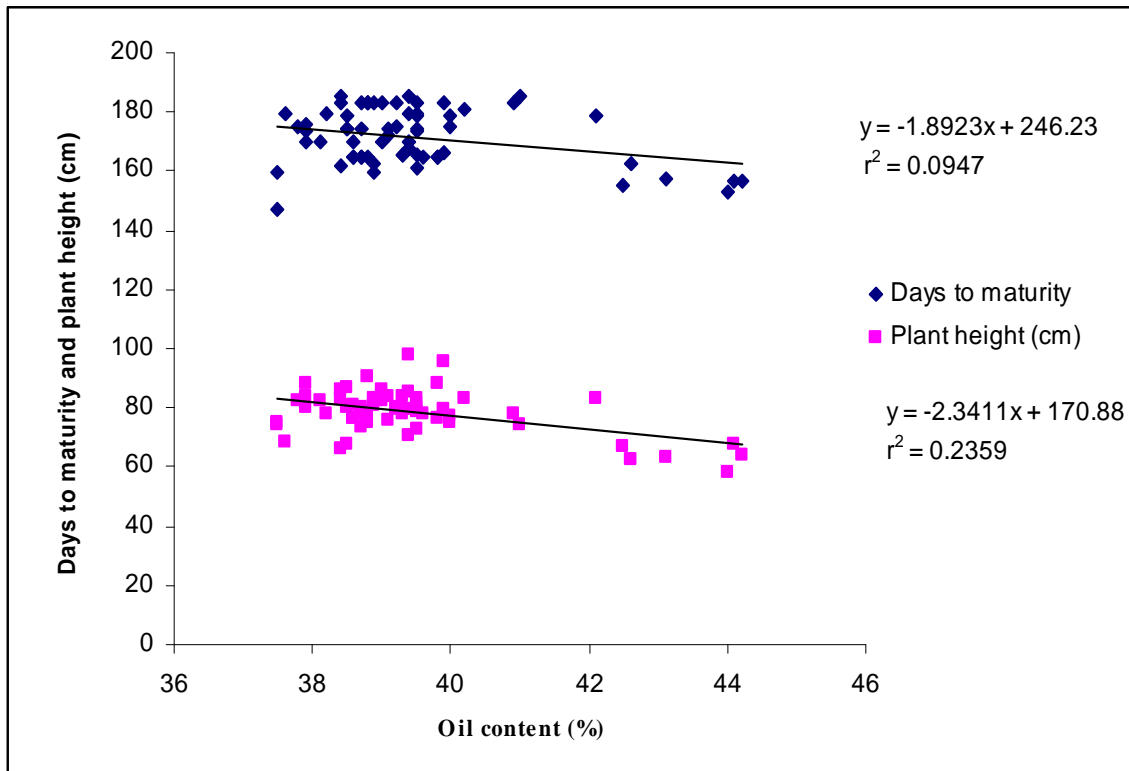


Figure 5. Biplot of plant height (cm) and days to maturity against the oil content (%) of genotypes

Understanding the relationship between root system and yield related traits is an important objective in crop breeding programs, particularly on acidic soil. Accordingly, the biplot of seed yield per hectare against root length was shown (Figure 6).

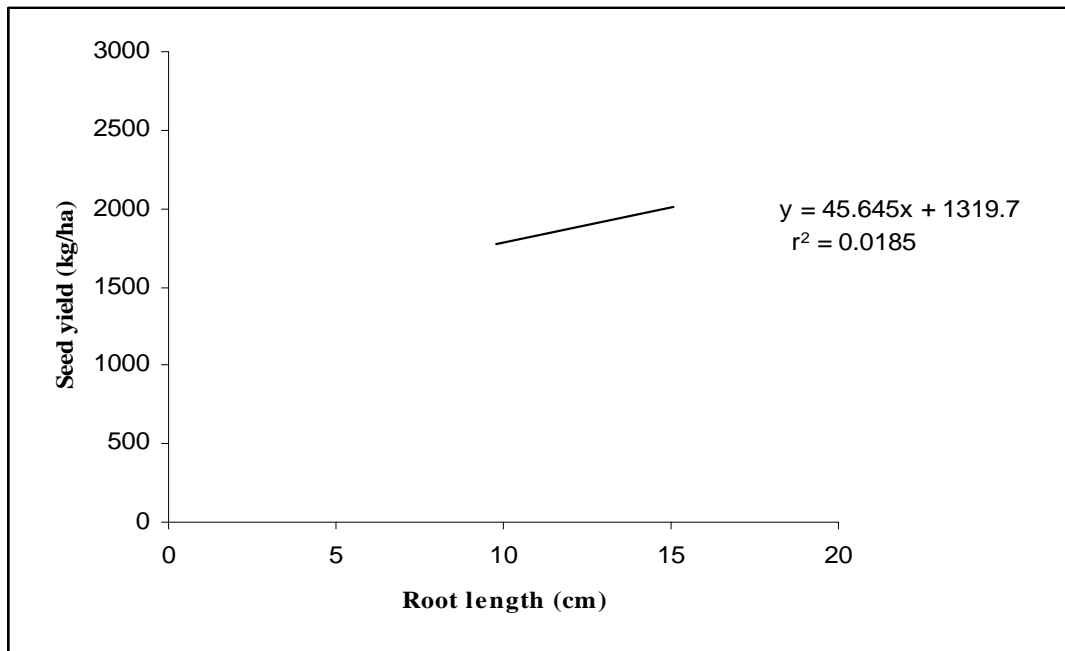


Figure 6. Biplot of seed yields (kg/ha) of genotypes against their root lengths (cm)

Furthermore, seed yield per hectare had highly significant correlation (Figure 7) with vigouricity of the population of linseed plants per plot.

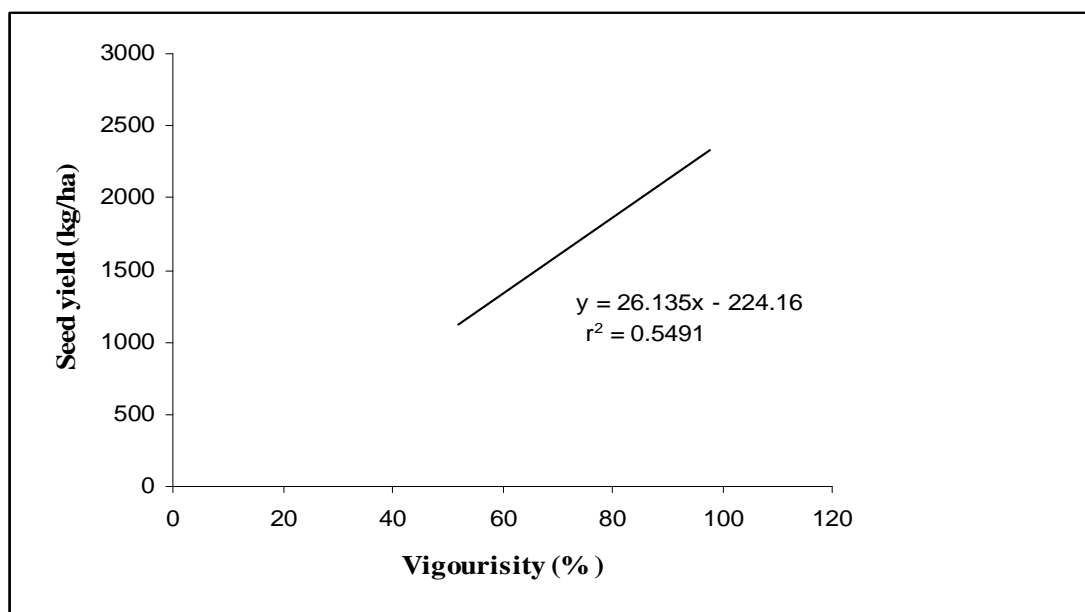


Figure 7. Biplot of seed yield per hectare of genotypes against their vigouricity

Table 10. Pearson's correlation coefficients (r) among possible pairs of 14 characters of 64 linseed genotypes tested at Bedi acidic soil in 2009/10

Charac.	SYH	OYH	OC	SYP	TSW	RL	TPP	PB	SB	NCP	VIG	DF	DM	PH
SYH	1.000	0.983***	-0.146	0.561***	-0.160	0.197*	0.341***	0.447***	0.308***	0.341***	0.748***	-0.161	-0.016	0.215*
OYH		1.000	0.027	0.566***	-0.079	0.152	0.310**	0.452***	0.327***	0.369***	0.710***	-0.061	-0.065	0.156
OC			1.000	-0.075	0.502***	-0.359***	-0.224*	-0.040	-0.009	0.110	-0.296**	0.031	-0.371***	-0.405***
SYP				1.000	-0.041	0.305***	0.391***	0.371***	0.408***	0.451***	0.353***	-0.158	0.146	0.132
TSW					1.000	-0.231	-0.023	-0.152	-0.185*	0.067	-0.252**	-0.119	-0.153	-0.225*
RL						1.000	0.232*	0.133	0.170	0.092	0.229*	-0.287**	0.646***	0.458***
TPP							1.000	0.521***	0.431***	0.470***	0.362***	-0.279**	0.259**	0.037
PB								1.000	0.644***	0.696***	0.414***	0.141	-0.004	0.024
SB									1.000	0.515***	0.337***	0.141	0.165	0.159
NCP										1.000	0.315***	-0.063	-0.064	0.020
VIG											1.000	-0.187	-0.073	0.433***
DF												1.000	-0.295***	-0.114
DM													1.000	0.427***
PH														1.000

Where: ***, **, *= Significant at P <0.001, 0.01 and 0.05 levels, respectively.

SYH = seed yield per hectare, OYH = oil yield per hectare, OC = oil content (%), SYP = seed yield per plant (g), TSW = 1000- seed weight (g), RL= root length (cm), TPP = tillers per plant, PB = primary branches per plant, SB = secondary branches per plant, NCP= number of capsules per plant, VIG = vigourisity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height (cm)

5.5. Cluster analysis of genotypes

The result of cluster analysis made on 64 linseed genotypes is presented in Table 11. The 64 genotypes of linseed from six sources (Appendix IV) were clustered into seven diversity classes based on D^2 value computed for nine highly significant characters. Among the 21 paired generalized squared distance measured, all of them are found to be significant except one. Fifteen and five squared distances were significant at 1% and 5% probability levels, respectively.

Cluster I, the largest of all, included 19 (29.7%) genotypes (Table 11) that comprised four genotypes of single plant selection (SPS) from crosses between Canadian and standard varieties, one standard variety that used as a standard check, two genotypes of SPS from a cross between yellow seeded USA (Omega) and standard varieties, three genotypes of SPS from crosses between yellow seeded PGRC/E and standard varieties and eleven genotypes of SPS from crosses between regenerants from the tissue culture and standard varieties. The second cluster comprised of 11 (17.2%) genotypes, one an exotic genotype from the USA, two genotypes of SPS from crosses between Canadian and standard varieties, two genotypes of SPS from crosses between yellow seeded PGRC/E and standard varieties and six genotypes from the SPS of crosses between regenerants from tissue culture and standard varieties.

Cluster III was the second largest group and consisted of 15 (23.4%) linseed genotypes. Of these, four genotypes were SPS from a cross between Canadian and standard varieties, six from a cross between yellow seeded USA and standard varieties, four from a cross between standard varieties and regenerant from the tissue culture and one genotype of the SPS from the crosses between yellow seeded PGRC/E and standard variety.

Cluster IV was the third smallest in the dendrogram (Appendix V), and contained six (9.4%) genotypes from two sources. Four genotypes are of SPS from crosses between yellow seeded PGRC/E and standard varieties. The rest two genotypes contained in this cluster are from the SPS of crosses between yellow seeded USA and standard variety and SPS from crosses between regenerant from tissue culture and standard variety.

Cluster V comprised of seven (10.9%) genotypes, four of them are the exotic ones from the USA, one from the SPS of crosses between yellow seeded PGRC/E and two from SPS of crosses between yellow seeded USA and standard varieties. Cluster VI, the second smallest

cluster, contained four (6.3%) genotypes, of which two genotypes are of SPS from crosses between yellow seeded USA and standard varieties, one from SPS of crosses between regenerant from the tissue culture and standard variety and the remaining one is from crosses between Canadian and standard variety.

Cluster VII, the smallest cluster of all, contained two (3.1%) genotypes from two different sources, one exotic genotype from the USA and the second one from SPS of crosses between yellow seeded USA and standard variety.

Table 11. Classification of 64 linseed genotypes into clusters based on nine highly significant characters of 64 linseed genotypes

Cluster	Treatment number	Number of genotype	Name of genotypes			
I	1, 7, 12, 13, 16, 18, 21, 23, 28, 31, 34, 36, 38, 40, 46, 51, 54, 62 and 64	19	Omega X CI-1525/B/1 CI-1525XR12-D33C/S9 CI-1525XR-12-N27G/P1/S3 CI-1747XCI-1652/S CI- 1652XCDC1747/S3	PGRC/E10306XCI-1525/B/1 CI-1525XR12-N27G/S13 CI-1525X CDC1747/P2/S, CI-1525/S6XR12-N27G/S12 Omega X CI-1525/14/A	CI-1525XR12-N27G/S4 CI-1652XPGRC/E10306/Y/ CI-1525XR12-N27G/P1/S1 CI-1525XR-12N27G/S13/A/ Tolle	R12-N27G X CI-1525/S3 R-12-D33CXCI-1525/P3/S1 PGRC/E10306 X Chilalo/B/4 R-12N27G/S13 XCI-1525/S4
	9, 15, 19, 25, 26, 33, 45, 50, 53, 55 and 57	11	PGRC/E10306XCI1652/Y/1 CI-1525XR-12N27G/P2/S2 PGRC/E10306XChilalo/B/4/	CI-1525XR12-D33C/S4 R12-D33CXCI-1525/P2/S3 CDC 1747 X CI- 1652/S15	CI-1652XCDC1747/S6 CI-1525XR-12D33C/S2 PGRC/E10306 X Chilalo/Y/3	CI-1525XR-12-N27G/P4/S2 PI-523353 SPS3
III	3, 5, 6, 10, 11, 14, 17, 20, 22, 27, 29, 30, 32, 37 and 39	15	Omega X CI-1525/B/3 CDC-1747XCI-1652/S2 R-12-D33CXCI-1525/P1/S2 CI-1525X CDC1747/P1/S2	CI-1652 X Omega /B/8 CI-1525XR12-D33C/S1 CI-1525X R-12N27G/P2/S3 Chilalo X Omega/10	CI-1652 X Omega /B/10 CI-1525XCDC1747V&E/S8 R-12-N27G X CI-1525/P4/S1 R12-N27G X CI-1525/S6	Omega X Chilao/Y/7 Omega X chilalo/Y CI-1525XCDC1747/P4/S1
IV	8, 41, 43, 47, 49 and 58	6	CI-1652X\PGRC/E10306/B/7 PGRC/E10306X Chilalo/B/2	PGRC/E10306 X Chilalo/Y Omega X CI-1525/Y/43	PGRC/E10306XChilalo/B/4/A CI-1525XR-12N27G/S13/B/	
V	42, 44, 48, 52, 56, 59 and 61	7	PGRC/E10306XChilalo/Y/2 PI-523353 SPS4	P-I523353 SPS1 Omega X CI-1525/Y/44	PI-523353 SPS2 PI-523353 SPS5	Omega X CI-1525/B/3
VI	2, 4, 24 and 35	4	Omega X CI-1525/B/2	CI-1652 X Omega /B/4	Chilalo X R-12-N27G/P2/S	CI-15DJF25XCDC1747/VandE/S4
VII	60 and 63	2	Omega X CI-1525/B/44,	PI-523353 SPS		

5.5.1. Genetic distances between clusters

Genetic distances between the clusters are presented in Table 12. All clusters were highly and significantly divergent with each other except between cluster I and Cluster II. The maximum distance was found between cluster VI and cluster VII ($D^2 = 509.51$). The second most divergent clusters were cluster V and cluster VI. The genetic divergence between clusters I and IV ($D^2 = 69.77$), I and V ($D^2 = 137.43$), I and VI ($D^2 = 57.96$) and I and VII ($D^2 = 233.86$) were highly and significantly ($P < 0.01$) divergent. Cluster II was highly and significantly divergent with all the clusters except cluster I. Similarly, cluster III was highly and significantly divergent with all clusters, but only at 5% probability level with cluster VI. Highly significant divergence was also observed for cluster IV with all clusters except with cluster V, which was significantly diverged with it. Cluster V was highly and significantly divergent with all clusters except VII and IV. Highly and significant divergence were also observed for cluster VII with all clusters except cluster V and VI, which are only significant at 5% probability level.

Table 12. Pairedwise generalized squared distances (D^2) among 64 linseed genotypes in seven clusters

Clusters	I	II	III	IV	V	VI	VII
I	0	11.34	16.98*	69.77**	137.43**	57.96**	233.86**
II		0	49.93**	30.74**	79.43**	115.41**	158.89**
III			0	148.42**	241.45**	17.05*	362.31**
IV				0	17.71*	253.80**	61.30**
V					0	366.43**	15.83*
VI						0	509.51*
VII							0

* $P < 0.01$ ($X^2 = 21.67$), * $P < 0.05$ ($X^2 = 16.92$)

5.5.2. Cluster means

Cluster means indicated the differences among the clusters for most of the traits (Table 13). Cluster I and II constituted intermediate genotypes for most of the traits. Cluster III was characterized by the highest oil yield, and vigourisity but lowest 1000 seed weight. Cluster IV comprised genotypes with fewer days to maturity. On the other hand, Cluster V has been found to contain genotypes with the shorter root length and less vigourisity. Cluster VI was characterized by the highest seed yield,

root length, days to flowering and days to maturity. In contrast, cluster VII comprised of genotypes with the lowest seed yield, oil yield and shorter days to flowering, but it contained genotypes with high oil content and 1000 seed weight.

Table 13. Mean values of nine quantitative characters for the seven clusters formed

Cluster Trait	I	II	III	IV	V	VI	VII	Grand mean
SYH	2003.4	1811.9	2231.3	1493.5	1265.5	2465.6	1040.9	1758.9
OYH	779.4	705.9	874.7	583.7	527.5	962.7	448.7	697.5
OC	39.0	39.4	39.2	39.0	41.6	39.0	41.8	39.9
TSW	6.0	6.1	5.8	5.9	6.3	6.1	6.3	6.1
RL	12.6	12.7	12.7	13.0	12.0	13.2	12.3	12.6
VIG	82.7	79.8	89.5	79.2	64.5	88.1	57.9	77.4
DF	99.0	99.3	97.4	98.6	100.2	100.7	95.5	98.7
DM	172	170.0	171.0	166.0	169.0	179.0	167.0	170.6
PH	78.3	83.0	80	83.1	71.6	74.5	65.3	76.5

5.5.3. Principal component analysis

Four principal components (PCs) extracted about 82% (Table 14) of the entire variation of the genotypes. About 38% of the total variance explained by the first PC was due chiefly to variation in seed yield per hectare, oil yield per hectare, vigourity per plot, plant height and oil content. About 22% of the whole variance explained by the second PC originated mainly from variation in the days to maturity and root length. The third PC accounting for about 13% of the entire variance resulted largely from variation in days to flowering and 1000 seed weight. The fourth PC constituted 8.46% of the variation and demonstrated mainly by 1000 seed weight, plant height and days to flowering.

Table 148. Percent and cumulative variances and Eigenvectors on the first four principal components in 64 genotypes of linseed

Parameters	PCA1	PCA2	PCA3	PCA4
Eigen value	4.58	2.02	1.18	0.76
Variance (%)	38.39	22.48	13.11	8.46
Cumulative (%)	38.39	60.87	73.98	82.44

Characters	Eigen vectors			
SYH	0.44	0.33	0.19	-0.0001
OYH	0.41	0.38	0.24	0.05
OC	-0.42	0.17	0.22	0.01
TSW	-0.29	0.12	0.45	0.69
RL	0.27	-0.46	0.13	0.28
VIG	0.43	0.25	0.09	-0.37
DF	0.02	0.19	-0.75	0.42
DM	0.16	-0.54	0.21	0.11
PH	0.32	-0.30	-0.17	-0.52

Where: SYH = seed yield per hectare, OYH = oil yield per hectare, OC = oil content (%), TSW = 1000- seed weight (g), RL= root length (cm), VIG = vigourisity of plot (%), DF = days to flowering, DM = days to maturity and PH = plant height (cm)

6. Discussion

6.1. Analysis of variance for agronomic characteristics

Analysis of variance showed highly significant differences for most of the characters among the linseed genotypes studied (Table 5). Furthermore, maximum source of variation for all characters were also observed for the genotypes, illustrating presence of adequate variations among them. These differential responses of the genotypes to soil acidity imply the possibility of developing tolerant linseed varieties and improving different characters including seed yield through selection and cross-breeding. Adane Choferie (2008) evaluated 12 genotypes of linseed at eight different locations for several characters and reported similar results to the present study.

The genotypes greatly varied for seed yield (kg/ha). The mean seed yield ranged from 1036.8 to 2566.7 kg/ha for Omega X CI-1525/B/44, which was the lowest yielder of all the genotypes, and Omega X CI-1525/B/2, respectively. Tolle, a standard check for the experiment, scored 2093.3 kg/ha. Twenty-two genotypes (34.4%) provided higher yield than the standard check, whereas the rest genotypes (64.1%) gave lower yield than the standard check. The genotypes evaluated varied substantially in seed yields and these variations in yield could be exploited in future breeding programs on acidic soils. The top five high seed yielding genotypes identified were given in Table 6. Therefore, these top seed yielding genotypes found to be superior and could be more tolerant to acidic soils. On the contrary, PI-523353 SPS2, PI-523353 SPS5, PI-523353 SPS4, PI-523353 SPS and Omega X CI-1525/B/44 were the poor seed yielders providing 1239.5 kg/ha, 1196.3 kg/ha, 1171 kg/ha, 1045 kg/ha and 1036.8 kg/ha, respectively. All the above poor yielders, except Omega X CI-1525/B/44, are exotic, brown seeded genotypes introduced from the USA. But they possessed higher oil contents (42-44%).

Significant differences among the genotypes considered were also observed for oil content (%). It ranged from 44.2% for deep brown exotic variety from the USA, P-I523353 SPS1, to 37.5 % for two brown-seeded varieties: Omega X CI-1525/B/3 and R12-N27G X CI-1525/S3 (Table 4). Six exotic linseed varieties from the USA used for this experiment gave higher oil contents (Table 7). These genotypes were relatively shorter and gave lesser seed yields and, they also had shorter root lengths. However, they should be appreciated and utilized for their higher oil contents and early maturity for the specific breeding program. In general, 49 genotypes (76.5%) gave higher oil content than the standard check variety. On the other hand, twelve genotypes (18.8%) were measured to have lower oil content than the standard check. The rest two genotypes (3.13%), CI-1747 X CI-1652/S1 and CI-1525 X R-12N27G/S13/A/, gave an equal amount of oil content to that of standard variety. Adane Choferie (2008) reported 37.1%, 37.9% and 37.8% means oil content from eight different locations that are not prone to soil acidity for Tolle, PGRC/E10306 X Chilalo/B/4 and Omega X chilalo/Y genotypes, respectively. In this study Tolle, PGRC/E10306 X Chilalo/B/4 and Omega X chilalo/Y gave 38.5, 38.4 and 39.5% oil contents, respectively which are about the same with previous findings for these genotypes. This indicates the opportunity of improving the oil contents of genotypes of linseed on acidic soil.

As far as oil yield is concerned, higher mean oil yield of 993.0 kg/ha, 975.8 kg/ha and 946.8 kg/ha were obtained from the brown-seeded linseed genotypes, Omega X CI-1525/B/2, CI-1525XCDC1747/VandE/S4 and CI-1652 X Omega /B/4, respectively. Tolle gave 797.1 kg/ha oil yield. Among the 64 linseed genotypes computed for the oil yield per hectare, 26 genotypes (40.6%) provided higher than standard check, while 38 genotypes (59.4%) were lower in their oil yield than the standard check (Table 4). Therefore, the higher oil yielders can be further exploited in the future breeding programs.

Genotypes showed highly significant differences ($P < 0.01$) for their root lengths. It ranged from 15.1 to 9.8 cm for the genotypes PGRC/E10306 X CI-1652/Y/1 and PI-523353 SPS4, respectively. Of the 64 genotypes, 12 genotypes (nearly 19%) had root lengths shorter than the standard check, while 51 genotypes (80%) had the root grown taller than the standard check. The remaining one genotype had equal root length with the standard check. The differential response of root growth among the genotypes indicates their variation in this regard that may lead to tolerance to soil acidity as root is the target site for the aluminum toxicity in acidic soil. Moreover, the linseed genotypes

studied had generally shown increase of yield with the increase of root lengths though few outliers are observed in both extremes.

Ali *et al.* (2004) examined root of different crops for their rooting ability with depth in natural soil profiles including linseed under rain-fed condition between seasons and observed that yield of crops were related to rooting ability below 30 cm soil depth. The same authors witnessed that increase in yield was observed for linseed as rooting ability at depth was increased. From above correlation magnitudes it can be inferred that the longer the root lengths, the higher the plant heights, providing the increased seed yield per plot and per plant. This could be due to the fact that genotypes that tolerate the soil acidity send their roots deep to the soil utilizing minerals and getting access to more moisture. Similar results were reported in the past in different crops such as wheat and barley that exhibited soil acidity tolerance (Pavan and Bingham, 1982; Kinraide and Parker, 1989; Tang *et al.*, 2001). As plants obtain minerals and moisture from the deeper part of the soil, they keep on growing and mature lately. Foster *et al.* (1998) examined drought resistance among linseed cultivars and concluded that tall and late maturing cultivars needed more water to be grown successfully for better yield. This possibly resulted in the increased seed yield of the genotypes. Therefore, these traits can indirectly be used for future breeding when the increased seed yield is desired on acidic soil.

Significant differences were also observed among linseed genotypes for days to maturity (DM). All exotic genotypes from the USA (Table 8) used for this experiment showed early maturity than nearly all the rest genotypes. On the other hand, CI-1525XCDC1747/P1/S2 and R12-N27G X CI1525/S6 were late maturing genotypes (186 days).

Days to maturity is an important agronomic trait of crops depending on agro-ecology and harvesting season. December and January months experience frost in Ethiopia, particularly in highland areas (Walter and Dechassa Lemessa, 2000). Linseed is frost sensitive during two stages: at a young seedling during the first few days of emergence and during flowering and pod development (Mills, 1987). As early frost can be damaging to linseed, especially if the development has been delayed, it is therefore vital to screen for and grow early maturing linseed varieties in frost susceptible environment so that they can escape the frost. Adugna Wakjira *et al.* (2005) studied genetic variability among sixty accessions of linseed collections in Ethiopia and reported wide ranges in days to maturity. They suggested that wide ranges in days to maturity can offer great

flexibilities for the development of suitable varieties for the various agro-ecological zones of Ethiopia. Therefore, different cultivars can be developed for specific agro-ecological regions to make use of the available potentials of both the genotypes and the environment.

6.2. Estimates of genetic parameters

6.2.1. Phenotypic and genotypic coefficient of variation

Higher phenotypic and genotypic variance values for seed and oil yield and relatively intermediate phenotypic and genotypic variance values for days to flowering, vigourisity per plot, days to maturity, capsules per plant and plant height were obtained in this experiment (Table 9). However, the phenotypic and genotypic variation values cannot be used for comparing the degree of variability for different characters as the means of the characters to be measured could also be different (Okelola *et al.*, 2007). Therefore, for the comparison purpose coefficients of variations were used.

Phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficient of variation (GCV) for 1000 seed weight, oil contents and days to maturity (Figure 1). This suggests that these characters were least influenced by the environment and selection for these characters will be more effective as compared to the rest characters. An intermediate difference in phenotypic coefficient of variation and genotypic coefficient of variation was observed for the root length, plant height, vigourisity per plot and days to flowering. Number of capsules per plant, tillers per plant, primary, and secondary branches per plant, seed yield per plant and oil and seed yield (kg/ha) showed considerable differences between phenotypic coefficient of variation and genotypic coefficient of variation, which reflected considerable environmental effect on these characters. In general, the phenotypic coefficients of variations were comparatively higher than the genotypic coefficients of variations for all characters, indicating environmental effect constitutes a greater portion of the total phenotypic variation.

6.2.2. Broad sense heritability

The heritability estimate showed broad ranges of variation (Table 9) among the 14 characters measured. Thousand seed weight was found to be the most heritable trait in the genotypes, with heritability of 89.66%, followed by oil content (82.55%) and days to maturity (80.96%). This

indicates that selection for these traits in the genotypes would be most effective for the expression of these traits in the succeeding generations. Therefore, a good improvement can be made if some of these traits are considered as selection criteria in future breeding program. Similar findings had been reported for 1000 seed weight (Dewan *et al.*, 1992; Yadav and Gupta, 1999; Muhammad *et al.*, 2003), maturity period (Dewan *et al.*, 1992) and oil content (Yadav and Gupta, 1999). According to Singh (1990), if a heritability of a character is high, selection for such a character is fairly easy as the selected character will be transmitted to its progeny. This is because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to the phenotype.

High heritability was observed for seed yield per plot (60.00%), oil yield (59.46%), root length (66.70%), vigourity per plots (76.08), days to flowering (61.23%) and plant height (75.31%), suggesting possibility of obtaining better yield providing progeny in the future breeding on acidic soil if some of these characters are considered as selection criteria. Earlier workers also reported similar findings for plant height and days to flowering (Yadav and Gupta; 1999; Muhammad *et al.*, 2003) and seed yield per plot in linseed (Muhammad *et al.*, 2003).

On the other hand, comparatively lower heritability was observed for primary branches per plant (55.66%), secondary branches per plant (46.89%), tillers per plant (57.45%), number of capsules per plant (46.63%) and seed yield per plant (51.90%). But, Muhammad *et al.* (2003) reported high heritability for the number of capsules per plant. The lower heritability for these characters is due to larger phenotypic variances, indicating greater environmental influences. Gemechu Keneni (1996) suggested that selection for a character with low heritability may be considerably difficult or virtually impractical due to the masking effect of the environment on the genotypic effects.

Heritability value by itself cannot provide the amount of genetic progress that would result from selection of the best individuals (Johnson *et al.*, 1955b). The studies carried out by various researchers have shown that high heritability alone is not enough for selection; it must be accompanied with substantial amount of genetic advance (Memon *et al.*, 2007; Mangi *et al.*, 2008). To be used as a selection criterion for the breeding improvement, it has to be coupled with higher

predicted genetic gain. According to Allard (1960), the higher the heritability and genetic gain values, the better will be the chance to select genotypes with good performance.

6.2.3. Expected genetic advance

Progresses that could be expected from selecting the top 5 % of the genotypes varied between 0.82 and 720.27, or as a percent of mean between 8.08% and 46.46% (Table 9). The highest expected genetic gain was observed for seed yield (kg/ha) followed by oil yield. The highest predicted genetic gain obtained for the seed and oil yield were not due to the higher heritability, but it is attributed to higher variance components estimated for them. Relatively higher predicted genetic advance (gain) was observed for days to maturity, plant height, number of capsules per plant, vigourisity and days to flowering.

In this study, relatively higher heritability associated with higher predicted genetic advance was observed for days to flowering, days to maturity, plant height, capsules per plant and vigourisity of genotypes. These traits therefore, deserve greater attention in future breeding programs for evolving better linseed varieties. Earlier researchers have reported additive gene effects in linseed for plant height (Kumar and Chauhan, 1980; Marchenkow, 1988), days to flowering (Badwal *et al.*, 1972) and seed yield (Vijayakumar *et al.*, 1975). Agronomic characters in crop show high heritability coupled with high genetic advance when they are governed by additive gene effect (Iqbal and Khan, 2003). In the present study, such conclusion cannot be made since a genetic component of additive gene effect is not partitioned.

Conversely, high genetic advance coupled with low heritability was observed for seed yield and oil yield (Table 9), which was attributed by the high phenotypic variances of the characters. Comparatively, high heritability with low predicted genetic advance was estimated for oil content, seed yield per plant, 1000 seed weight, root length, tillers per plant, primary and secondary branches per plant. The association of high heritability with low predicted genetic advance was reported to be attributed by predominant effects of non additive gene (Ahmed *et al.*, 2007). Dominance effects in linseed have been reported by several investigators in the past for seed yield per plant, number of branches, number of capsules per plant (Badwal *et al.*, 1972; Kumar and Chauhan, 1980; Patil and Chopde, 1983; Singh *et al.*, 1987) and 1000 seed weight (Kumar and

Chauhan, 1980). It is not possible to make such generalizations as the effects of genetic components were not partitioned from the non genetic components.

Furthermore, relatively higher heritability and genetic advance as mean % was observed for seed and oil yields (kg/ha) and seed yield per plant (Figure 2), while high heritability coupled with low genetic advance as mean % was observed for the 1000 seed weight and oil content. The rest of characters had shown intermediate heritability and genetic advance as mean percent.

6.3. Correlation between traits

In this study, seed yield per plant had highly significant positive correlation with seed yield per plot, oil yield, root length, number of tillers per plant, primary and secondary branches per plant, capsules per plant and vigourisity of the plot (Table 10). Similarly, it had positive non-significant correlation with plant height and days to maturity. However, negative non-significant correlation with seed yield per plant was observed for days to flowering and 1000 seed weight. This indicates that increase in positively associated characters contribute to increase in yield per plant. Therefore, for selection purposes to improve seed yield per plant, it is suggested that emphasis should be given to the positively correlated traits.

Similar positive significant correlation with seed yield per plant has been reported for capsules per plant (Noor-ul-Islam *et al.*, 2000; Akbar *et al.*, 2003; Muhammad *et al.*, 2003; Dubey *et al.*, 2006; Osman *et al.*, 2006; Adane Choferie, 2008), branches per plant (Akbar *et al.*, 2003; Muhammad *et al.*, 2003; Dubey *et al.*, 2006; Osman *et al.*, 2006; Adane Choferie *et al.*, 2008), 1000 seed weight and plant height (Noor-ul-Islam *et al.*, 2000; Akbar *et al.*, 2003). However, other researchers (Muhammad *et al.*, 2003; Dubey *et al.*, 2006; Osman *et al.*, 2006; Adane Choferie, 2008) reported positive significant correlation of seed yield per plant with 1000 seed weight. Disparity in association of 1000 seed weight with seed yield per plant may be attributed to variation in the environmental and genotypes under investigation.

The highest and linear correlation ($r = 0.983$, $P < 0.001$) was observed for seed yield per hectare with the oil yield per hectare (Figure 3). Seed yield per hectare also showed highly significant positive association with vigourisity of plots ($r = 0.748$, $P < 0.001$), seed yield per plant ($r = 0.561$, $P < 0.001$), number of primary branches per plant ($r = 0.477$, $P < 0.001$), number of secondary

branches per plant ($r = 0.308$, $P < 0.001$), number of capsules per plant ($r = 0.341$, $P < 0.001$) and tillers per plant ($r = 0.341$, $P < 0.001$). Similar results were reported by Tadele Tadesse *et al.* (2009) that seed yield per hectare had highly significant positive correlation with seed yield per plant. Similarly, it also showed medium correlation with root length and height of plant ($P < 0.01$). The positive significant association of these characters with seed yield per plot indicates these characters could be useful for improvement of seed yield (kg/ha) through indirect selection.

On the other hand, negative non-significant associations were observed for seed yield (kg/ha) with days to flowering, days to maturity, thousand seed weight and oil content per plot. Negative non-significant associations for days to flowering and maturity with seed yield were also reported by earlier studies (Badwal *et al.* 1970; Patil *et al.* 1980). Therefore, improvement of seed yield in linseed is possible by using appropriate breeding strategy through selection for tillers per plant, primary branches per plant, secondary branches per plant, number of capsules per plant, plant height, vigourisity and plant root on acid stressed soil as shown in this study. Similarly, oil yield had positive correlation with primary branches ($r = 0.452$, $P < 0.001$), secondary branches ($r = 0.327$, $P < 0.001$), number of capsules per plant ($r = 0.710$, $P < 0.001$) and vigourisity of plots ($r = 0.710$, $P < 0.01$). Intermediate and positive correlation was observed for tillers per plant with oil yield.

Positive and non-significant correlations were also observed for root length and plant height with the oil yield. But it had negative and non-significant correlation with 1000 seed weight, days to flowering and days to maturity. Both seed yield and oil yield had positive and very significant correlation with seed yield per plant, primary branches, secondary branches, number of capsules per plant, and vigourisity. Oil yield and seed yield show the highest, positive and highly significant correlation among the 14 traits correlated (Figure 3). This information, therefore, can be used in the future breeding as these two traits could possibly be improved simultaneously.

Highly significant positive correlation of oil content with 1000 seed weight ($r = 0.502$, $P < = 0.001$) was observed (Figure 4). Tadele Tadesse *et al.* (2009) also reported significant positive correlation of oil content with 1000 seed weight. This indicates that genotypes with heavy seed weight are associated with high amount of oil content. The result suggested that indirect selection for increased seed oil content in linseed is possible by selecting for higher seed weight.

On the other hand, the association of oil content with root length, days to maturity and plant height was negative and highly significant. It had also medium and low negative correlation with vigourisity per plot and tillers per plant, respectively. Negative significant correlation of oil content with plant height was also reported by Osman *et al.* (2006). Tadele Tadesse *et al.* (2009) also reported negative but low association of oil content with days to flowering and days to maturity. Genotypes with high oil contents, as shown in this study, were short, early maturing and less vigorous. Genotypes providing higher oil content with short plant height are important to select and breed in the environment where lodging is the problem. Furthermore, early maturing genotypes with higher oil content are important to breed in the areas where frost is severe as early maturing genotypes could escape the potential damages.

Highly significant positive correlation of days to maturity with root length ($r = 0.646$, $P < 0.001$), and plant height ($r = 0.427$, $P < 0.001$) were observed, but it had highly significant negative correlations with days to flowering and oil content. Adane Choferie (2008) also reported significant positive correlation of days to maturity with plant height. According to the present study, early maturing genotypes are generally genotypes with shorter plant height and low seed yielders (Figure 5). On the other hand, late maturing genotypes with higher root length were high seed yielders but low in oil content.

Root length of the linseed genotypes considered had highly significant positive correlation with seed yield per plant. It had also positive significant correlation with number of tillers per plant, vigourisity and seed yield per hectare (Figure 6). Positive and medium correlation with primary branches, secondary branches, capsules per plant and oil yield were also observed. From this, it can be inferred that linseed genotypes that are tolerant to soil acidity are probably those which exhibited better root penetration to the soil as they matured late and provided higher seed yield. For selection purposes, it is suggested that emphasis should be given to characters like, plant height, root lengths, vigourisity, branches per plant, capsules per plant and days to maturity for yield improvement among the genotypes in general and on acidic soil in particular. However, root lengths of the linseed genotypes are not the sole factor to consider as selection criterion for high yield.

Many researchers (Sidlauskas and Bernotas, 2003; Mehmet and Telat, 2006; Mevlut *et al.*, 2008) reported that yield is the end product of several characters, which are polygenic in inheritance and

thus are highly influenced by environment. Therefore, it is important to consider many parameters along with root length that attribute to the increase of yield in linseed breeding program on acidic soil.

Root length has also shown positive and significant correlation with vigourisity per plot. The vigourisity plot had very significant correlation with seed yield (Figure 7) and oil yield (kg/ha) and seed yield per plant. As it is shown in this study, the superiority in vigourisity of genotypes has resulted in the increased yield and this further indicated that the genotypes with better tolerance to soil acidity had better growth expressed by differential vigourisity among the genotypes.

6.4. Clustering genotypes

Divergence analysis is usually performed by using D^2 techniques of Mahalanobis to classify the diverse genotypes for hybridization purpose (Mahalanobis, 1936). Genetic improvement through hybridization and selection depends upon the extent of genetic diversity between parents. Hybridization of genetically divergent parents could lead to the development of desirable recombinants and transgressive segregants, that in turn, may lead to the development of better performing varieties than the released varieties. Crossing genotypes belonging to distant clusters for wide Mahalanobis distance (D^2) could maximize transgressive segregation.

The cluster analysis revealed that linseed genotypes originated from six different sources (Appendix IV) were randomly distributed to the different clusters with no definite pattern showing their distinct diversity. The six exotic genotypes from the USA used in the present experiment were randomly distributed in cluster II, V and VII with no definite pattern though they tend to be clustered more in cluster V (Table 11).

Generally, no clear cut relationship between the original sources of the tested genotypes and their genetic diversity was observed since genotypes from the different sources fell into the same cluster and genotypes of the same source were distributed into different clusters, indicating that genotypes from the same origin may have different genetic background and genotypes from different origins might have the same clusters. Chandra (2004) studied 57 varieties of linseed collected from different geographic source and reported that genotypes having genetic similarity were grouped into the same clusters and that most of the clusters at individual level included were the varieties of different geographic regions. Adugna Wakjira *et al.* (2005) studied the genetic variability of 60 accessions of linseed collected from different regions in Ethiopia and from exotic origins and reported that accessions from different geographical regions were not necessarily clustered according to their geographic origins or specific collection sites, indicating that clustering phenomenon were not necessarily based on the geographic origins of the collections. Gemechu Keneni (1996) also suggested that selection of parents for hybridization need not necessarily be based on geographic diversity but genetic diversity must form the sound base for parental selection.

6.4.1. Genetic distances between clusters

Analysis of Mahalanobis's D^2 showed significant differences between all clusters except between cluster I and cluster II (Table 12), indicating high genetic diversity among the genotypes which should be exploited in future breeding efforts. Crosses between genotypes selected from cluster VII with cluster VI, cluster VII with cluster I, cluster I with cluster VII, cluster IV with cluster VI, cluster V with cluster VI and cluster III with cluster V are expected to provide relatively better genetic recombination and segregation in their progenies since they had maximum distances. On the other hand, inter-cluster distances have been found to be non-significant between cluster I and II ($D^2 = 11.34$), suggesting close relationship between clusters and hybridization between these two clusters will not result in more promising varieties.

6.5. Principal components

In order to assess the pattern of variations, principal component analysis (PCA) was done by considering the nine significant characters simultaneously. It is a method that reduces data dimensionality without much loss of information and identifies most important gradients by performing a covariance analysis between factors (Cooley and Lohnes, 1971). It involves a

mathematical procedure that transforms a number of possibly correlated variables into a smaller number of uncorrelated variables called principal components. The first principal component accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible (Jolliffe, 2002). According to Noor - ul-Islam *et al.* (2000) principal component analysis removes the effect of multi-collinearity on character association enabling breeders to apply selection per changing population structure in favorable direction.

PCA showed that the first four principal components accounted for 82.44% of the total variation, of which nearly 61% was contributed by the first two principal components (PCA1 and PCA2) (Table 14). Normally it is assumed that characters with larger absolute values closer to unity within the first principal component influences the clustering more than those with lower absolute values closer to zero (Chahal and Gosal, 2002). Accordingly, characters with relatively greater weight in PCA1 (seed yield per hectare, oil yield per hectare, vigourisity and oil content in this case) had higher relative contribution to the total diversity and they were the ones that most differentiated the genotypes.

However, most of the characters individually contributed small effects ($\pm 0.42- 0.44$) to the total variation and, therefore, the grouping of genotypes into different clusters was rather dictated by the number of characters. Therefore, such characters as seed yield per hectare, oil yield per hectare, vigourisity, oil content, root length, days to maturity, days to flowering, 1000 seed weight and plant height were the most determinant in total 82% variations of genotypes.

7. Conclusion and Recommendation

7.1. Conclusion

Soil acidity is one of the crop production problems of increasing concern in the highlands of Ethiopia decreasing yield adversely. Under such situation, it is important to have practical and simple amelioration options. One of the options is selecting and breeding crop genotypes that tolerate soil acidity and hence screening linseed varieties for such purposes became necessary as an immediate solution. Consequently, 64 linseed genotypes were evaluated to study their genetic diversity on acidic soil. Analysis of variance revealed the presence of significant differences for most characters studied, indicating adequate variability among the genotypes.

High seed yielders relatively depicted longer root length, suggesting their tolerance to soil acidity. Therefore, emphasis should be given to them in the future yield improvement breeding program on acidic soil. Exotic genotypes from the USA showed early maturity, short plant height and low seed yield. They had high oil content. Therefore, they can be exploited for their high oil contents and early maturity in a particular breeding program.

Slightly higher PCV than GCV were observed for 1000 seed weight, days to maturity and oil contents, indicating less effect of environment so that they could be easily improved in future breeding on acidic soil. Generally, PCV were comparatively higher than GCV for all characters, illustrating the existence of environmental influences. Oil content, 1000 seed weight and days to maturity had higher broad sense heritability and are useful for selection in future breeding as inheritance of these traits in the progeny would be higher. Furthermore, high heritability associated with high genetic advance for days to flowering, days to maturity, plant height, capsules per plant and vigourisity were observed. However, high estimates of heritability with low genetic advance were observed for oil content, seed yield per plant, 1000 seed weight, root length, tillers per plant, primary and secondary branches per plant.

Seed yield (kg/ha) was positively and significantly correlated with oil yield per hectare, seed yield per plant, root length, tillers per plant, primary and secondary branches per plant, plant height and vigourisity, suggesting any positive increase in such traits will accelerate the boost in seed yield per

plot as indirect selection through yield components is effective. Oil yield (kg/ha) was positively and significantly correlated with seed yield per plant, tillers per plant, primary and secondary branches per plant, capsules per plant and vigouricity. Generally, improving the yield related traits by indirect selection will increase the yield.

Genotypes were grouped into seven different clusters, narrowing down duplication of genotypes with similar genetic background. Therefore, it is important to assess genetic diversity of linseed genotypes during the parental selection for possible linseed improvement program. Significant paired wise generalized squared distances were observed for all possible pairs of clusters except for cluster I and Cluster II. Maximum distances were found between cluster VI and cluster VII, VI and IV, III and VII and V and VI. Parental selection of individual genotypes from these clusters would be useful for the future hybridization to generate agronomical desirable progenies.

Principal component analysis revealed that the most variations among the genotypes were attributed by the seed yield per hectare, oil yield per hectare, oil content and vigouricity.

7.2. Recommendation

Information generated by the current study can be used by research centers for further breeding and improvement of linseed genotypes for their tolerance to acidic soils. However, detailed and exhaustive study is needed to determine the genetic and morpho-physiological basis of tolerance to soil acidity and such study should be on varying level of soil acidity in controlled environment to determine the extent to which the genotypes tolerate soil acidity.

The present study has shown significant variation among genotypes for most of characters considered. Improvement in yield could be achieved by selecting for high yielding genotypes or for yield related components positively associated to yield.

Although evaluation for soil acidity in linseed using the quantitative traits could provide vital information, morphological comparisons have some limitations including the influence of environment, subjectivity in the character evaluation and management practices. Therefore, a molecular genetic analysis such as mapping of molecular marker and quantitative trait loci associated with soil acidity tolerance need to be done in order to arrive at more comprehensive conclusions.

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9. Appendices

Appendix I. Determination of oil content using nuclear magnetic resonance (NMR)

NMR operates on the principle that when oil, or seeds containing liquid, are placed in a strong permanent magnetic field, the nuclei of hydrogen atoms of the oil molecules behave like tiny rod magnets and align themselves parallel to the field. By applying a second magnetic field in the form of electromagnetic radiation with a specified frequency (resonance conditions) the orientation of the nuclei is changed with the absorption of a fine amount to energy per hydrogen nucleus. The corresponding loss of energy of the radio frequency sender is used to measure the amount of hydrogen atoms and thus the amount of oil present in the sample holder. In order to improve the precision of the measurements resonance can be suspended and restored after some microseconds. By this means a thousand or more single NMR-signals may be summed and averaged (Robbelen *et al.*, 1989). In this experiment, 22 gm of seeds was dried in an oven for two and half hours at 78 °c; cooled for 30 minutes. Then oil contents of seeds were measured based on the above procedures.

Appendix II. Monthly meteorological data of the HARC 20 km away from Bedi site during 2009/2010

Months	May	June	July	Aug	Sep	Oct	Nov	Dec	Jan
Rainfall (mm)	10.6	64.8	208.8	242.	75.9	15.6	6.4	39.4	6.0
T ⁰ c max.	23.4	21.2	19.1	18.7	20.1	22.3	22.7	24.2	23.7
T ⁰ c min	5.0	8.6	9.8	10.4	8.8	6.6	2.9	7.2	5.3
T ⁰ c mean	14.2	14.9	14.5	14.6	14.5	14.5	12.8	15.7	14.5

Source: Holleta Agricultural Research Center Metrology Section, 2009/2010

Appendix III. List of 64 linseed genotypes used for the experiment, their pedigree/ origin and major merits, 2009/2010 cropping season

Trt.No	Name of genotypes	Pedigree/ origin	Major merits
1	Omega X CI-1525/B/1	*SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525/B/1)	High yielder and bold-seeded
2	Omega X CI-1525/B/2	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525/B/2)	High yielder, brown and bold-seeded
3	Omega X CI-1525/B/3	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525/B/3)	High yielder, brown and bold-seeded
4	CI-1652 X Omega /B/4	SPS from a cross between standard variety (CI-1652) and yellow-seeded USA (omega)	High yielder, brown and bold-seeded
5	CI-1652 X Omega /B/8	SPS from a cross between standard variety (CI-1652) and yellow-seeded USA (omega)	High yielder, brown and bold-seeded
6	CI-1652 X Omega /B/10	SPS from a cross between standard variety (CI-1652) and yellow-seeded USA (omega)	High yielder, brown and bold-seeded
7	PGRC/E10306XCI-1525/B/1	SPS from a cross between yellow-seeded PGRC/E (10306) and standard variety (CI-1525)	High yielder, brown and bold-seeded
8	CI-1652X\PGRC/E10306/B/7	SPS from a cross between standard variety (CI-1652) and yellow-seeded PGRC/E (P10306)	High yielder, brown and bold-seeded
9	PGRC/E10306XCI-1652/Y/1	SPS from a cross between yellow-seeded PGRC/E (P10306) and standard variety (CI-1652)	High yielder and yellow-seeded
10	Omega X Chilao/Y/7	SPS from a cross between yellow-seeded USA (omega) and standard variety (Chilalo)	High yielder and yellow-seeded
11	CDC-1747XCI-1652/S2	SPS from a cross between Canadian (CDC-1747) and standard variety (CI-1652)	High yielder and brown-seeded
12	CI-1525XR12-N27G/S4	SPS from a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
13	R12-N27G X CI-1525/S3	SPS from a cross between regenerant from the tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
14	CI-1525XR12-D33C/S1	SPS from a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
15	CI-1525XR12-D33C/S4	SPS from a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
16	CI-1525XR12-D33C/S9	SPS from a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
17	CI-1525XCDC1747V&E/S8	SPS from a cross between standard variety (CI-1525) and Canadian (CDC1747)	High yielder and brown-seeded
18	CI-1525XR12-N27G/S13	SPS a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
19	CI-1652XCDC1747/S6	SPS from a cross between standard variety (CI-1652) and Canadian (CDC1747)	High yielder and brown-seeded
20	Omega X chilalo/Y	SPS a cross between yellow-seeded USA (Omega) and standard variety (Chilalo)	High yielder and yellow-seeded
21	CI-1652XPGRC/E10306/Y/2	SPS from a cross between standard variety (CI-1652) and yellow- seeded PGRC/E (P10306)	High yielder and yellow-seeded
22	R-12-D33CX CI-1525/P1/S2	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
23	R-12-D33CX CI-1525/P3/S1	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
24	Chilalo X R-12-N27G/P2/S2	SPS from a cross between standard variety (Chilalo) and regenerant from tissue culture	High yielder and brown-seeded
25	CI-1525XR-12-N27G/P4/S2	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
26	CI-1525X R-12-N27G/P2/S2	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
27	CI-1525X R-12-N27G/P2/S3	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
28	CI-1525X R-12-N27G/P1/S3	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded

Appendix III continued

29	R-12-N27G X CI-1525/P4/S1	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
30	CI-1525X CDC1747/P4/S1	SPS from a cross between standard variety (CI-1525 and Canadian (CDC1747)	High yielder and brown-seeded
31	CI-1525X CDC1747/P2/S3	SPS from a cross between standard variety (CI-1525 and Canadian (CDC1747)	High yielder and brown-seeded
32	CI-1525X CDC1747/P1/S2	SPS from a cross between standard variety (CI-1525 and Canadian (CDC1747)	High yielder and brown-seeded
33	R12-D33C X CI-1525/P2/S3	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
34	CI-1525XR12-N27G/P1/S1	SPS a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
35	CI-1525XCDC1747/VandE/S4	SPS from a cross between standard variety (CI-1525) and Canadian (CDC1747)	High yielder and brown-seeded
36	PGRC/E10306 X Chilalo/B/4	SPS from a cross between yellow-seeded PGRC/E (P10306) and standard variety (Chilalo)	High yielder and brown-seeded
37	Chilalo X Omega/10	SPS from a cross between standard variety (Chilalo) and yellow-seeded USA (omega)	High yielder and brown-seeded
38	CDCI-1747XCI-1652/S1	SPS from a cross between Canadian and standard varieties (CI-1652/S1)	High yielder and brown-seeded
39	R12-N27G X CI-1525/S6	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
40	CI-1525/S6 X R12-N27G/S12	SPS a cross between standard variety (CI-1525) and regenerant from the tissue culture	High yielder and brown-seeded
41	PGRC/E10306 X Chilalo/Y	SPS a cross between yellow-seeded (P10306) and standard variety (Chilalo)	High yielder and yellow-seeded
42	PGRC/E10306 X Chilalo/Y/2	SPS a cross between yellow-seeded (P10306) and standard variety (Chilalo)	High yielder and yellow-seeded
43	PGRC/E10306XChilalo/B/4/A	SPS a cross between yellow-seeded (P10306) and standard variety (Chilalo)	High yielder and brown-seeded
44	PI-523353 SPS1	Exotic (USA)	High oil content (>40%)
45	CI-1525XR-12D33C/S2	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
46	CI-1525XR-12N27G/S13/A	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
47	CI-1525XR-12N27G/S13/B	SPS from a cross between standard variety (CI-1525) and regenerant from tissue culture	High yielder and brown-seeded
48	PI-523353 SPS2	Exotic (USA)	High oil content (>40%)
49	PGRC/E10306 X Chilalo/B/2	SPS from a cross between yellow-seeded PGRC/E (P10306) and standard variety (Chilalo)	High yielder and brown-seeded
50	PI-523353 SPS3	Exotic (USA)	High oil content (>40%)
51	R-12N27G/S13 XCI-1525/S4	SPS from a cross between regenerant from tissue culture and standard variety (CI-1525)	High yielder and brown-seeded
52	Omega X CI-1525/B/3	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525)	High yielder and brown-seeded
53	PGRC/E10306XChilalo/B/4/B	SPS from a cross between yellow-seeded PGRC/E (P10306) and standard variety (Chilalo)	High yielder and brown-seeded
54	CI-1652 X CDC 1747/S3	SPS from a cross between standard variety (CI-1652) and Canadian (CDC1747)	High yielder and brown-seeded
55	CDC 1747 X CI-1652/S15	SPS from a cross between Canadian (CDC1747) and standard variety (CI-1652)	Lower ALA (omega-3)
56	PI-523353 SPS4	Exotic (USA)	High oil content (>40%)
57	PGRC/E10306 X Chilalo/Y/3	SPS from a cross between yellow-seeded PGRC/E and standard variety (Chilalo)	High yielder and brown-seeded
58	Omega X CI-1525/Y/43	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525)	High yielder and yellow-seeded
59	Omega X CI-1525/Y/44	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525)	High yielder and yellow-seeded

Appendix III continued

60	Omega X CI-1525/B/44	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525)	High yielder and brown-seeded
61	PI-523353 SPS5	Exotic (USA)	High oil content (>40%)
62	Omega X CI-1525/14/A	SPS from a cross between yellow-seeded USA (omega) and standard variety (CI-1525)	High yielder and brown-seeded
63	PI-523353 SPS	Exotic (USA)	High oil content (>40%)
64	Tolle	SPS from a cross between standard varieties (CI-2698 and P.136611)	Widely adapted and released

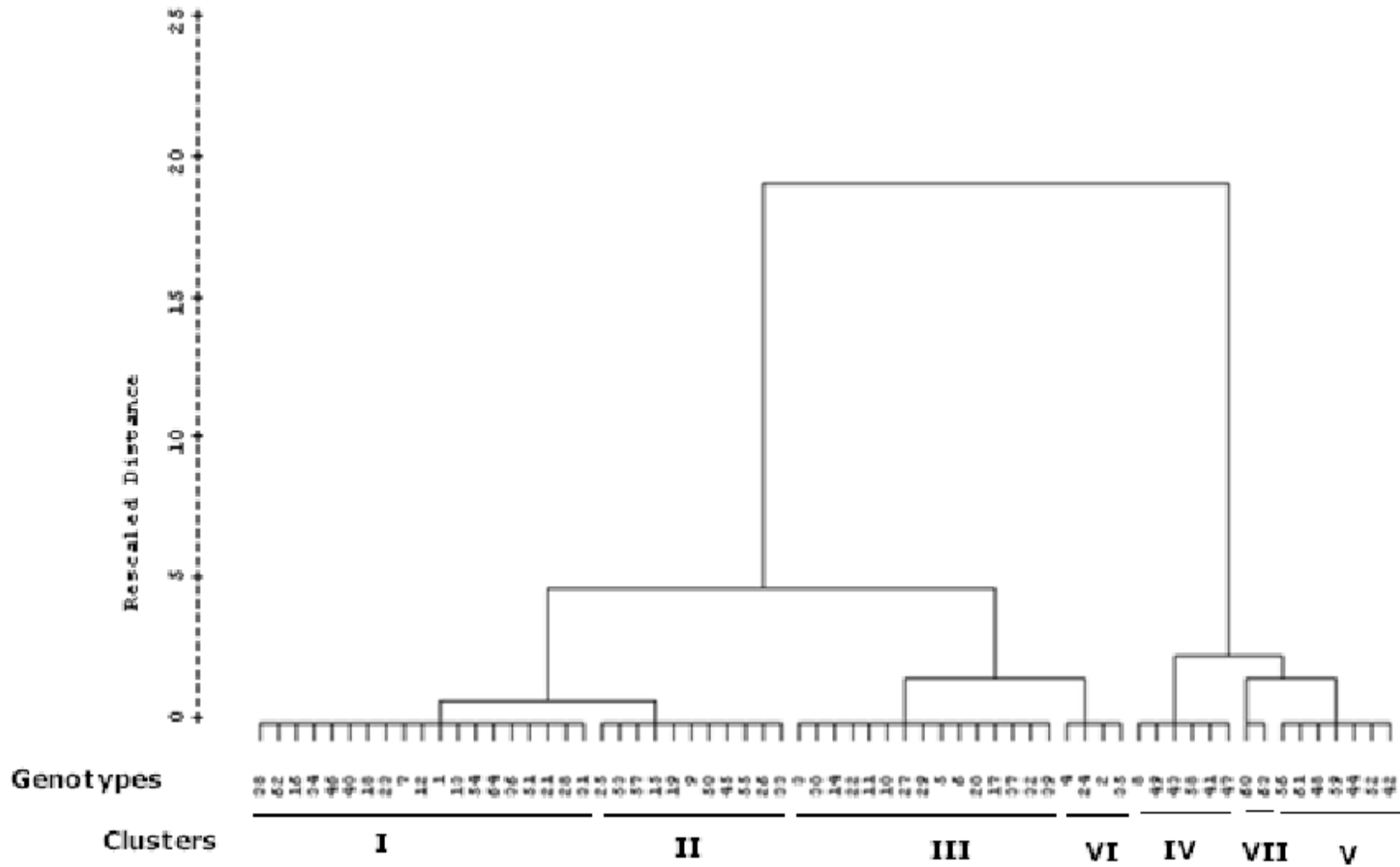
* SPS: Single Plant Selection

Source: Holleta Agricultural Research Center (HARC), 2009/2010

Appendix IV. Category of 64 linseed genotypes based on their original sources

Source	Number of genotypes	Treatment numbers
Exotic (from the USA)	6	44, 48, 50, 56, 61, and 63
The standard variety (standard check)	1	64
SPS from crosses between yellow seeded PGRC/E and standard varieties	11	7, 8, 9, 21, 36, 41, 42, 43, 49, 53 and 57
SPS from crosses between yellow seeded USA (Omega) and standard varieties	14	1, 2, 3, 4, 5, 6, 10, 20, 37, 52, 58, 59, 60 and 62
SPS from crosses between Canadian and standard varieties	10	11, 17, 19, 30, 31, 32, 35, 38, 54 and 55
SPS from crosses between regenerant from tissue culture and standard variety	22	12, 13, 14, 15, 18, 16, 22, 23, 24, 25, 26, 27, 28, 29, 33, 34, 39, 40, 45, 46, 47 and 51

Appendix V. Dendrogram showing the distribution of 64 linseed genotypes into seven clusters



Declaration

I, here, declare that this thesis is entirely my own work and it has never been submitted for a degree in any other university and all sources of materials used for it have been duly acknowledged.

Name: Legesse Burako

Signature: _____

Place: Faculty of Science, Addis Ababa University

Date: _____

Advisor

Name: Kifle Dagne (PhD)

Signature: _____

Date: _____