ASSESSMENT OF TISSUE CULTURE DERIVED REGENERANTS OF LINSEED (*Linum usitatissimum* L.) IN ETHIOPIA

BY

ADUGNA WAKJIRA GEMELAL

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CHAPTER 1

INTRODUCTION

Linseed (*Linum usitatissimum* L.) is the second most important oil crop of Ethiopia and it has been in production since antiquity (Getinet and Nigussie, 1992). The country is considered as a centre of diversity for linseed (Adefris *et al.*, 1992). It was grown on about 148 000 hectares with a production of about 68 000 tonnes and with a productivity of about 0.46 t ha^{-1} in 1996 (CSA, 1997). The main linseed producing areas of Ethiopia are the southeastern regions of Arisi with the adjoining areas of Bale and Chercher mountains, eastern Wellega, eastern Gojam and Semen mountains, Tigray, western Wello and the central highlands of Shewa. The principal regions of linseed production have an altitude range of 1200 to 3500 meters above sea level and the crop performs best within 2200-2800 m. Linseed requires cool temperatures during its growing period to produce good yields. The mean temperature can range from 10°C to 30°C although it does best from 21-22°C (Appendix 2). The crop grows well within a 12 to 18-hour photoperiod.

In Ethiopia, linseed is used both as food crop and cash crop mainly for industrial purposes. Linseed oil is famous for making varnishes, paints and the like due to its high (45-65%) linolenic fatty acid, which is known for its fast drying quality (auto-oxidative) because of its triple bonds, C18:3 (Rowland *et al.*, 1995). On the other hand, it is one of the essential fatty acids responsible for numerous health benefits (Carter, 1993). However, it reduces the keeping quality of its oil, causing rancidity in edible oils within few days after extraction. On the other hand, the oil from linseed has many industrial uses as a drying agent in paints and varnishes and in the manufacture of soaps, printer inks oilcloth and linoleum tiles. Hence, the seed of linseed is mostly used for oil production. Moreover, roasted and crushed seeds are also used to prepare stew or the local food known as *fit-fit* (linseed stew mixed with local bread). Similarly, the same crushed seeds are often mixed with water to prepare soft drinks, which are sometimes used as medicine to treat diseases like amoebic dysentery (Carter, 1993). The cake remaining after oil extraction is a good feed to animals.

Linseed is often grown in rotation with cereals to prevent the build-up of diseases, as it is immune to cereal diseases. Linseed is frost tolerant as compared to other oilseeds and it has the advantage of being grown in the high altitude areas, where frost frequently occurs. The major production constraints of linseed in Ethiopia include: low seed yield (less than 0.5 t ha^{-1}); low oil content (less than 40%); poor edible oil quality (>40% linolenic fatty acid); diseases (Fusarium wilt, pasmo, and powdery mildew) and parasitic and other weeds.

The linseed research programme in Ethiopia was started in 1962 by then Debrezeit Agriculture Experiment Station (now Research Centre). However, from the late 1960's, it was transferred to the Holetta Research Centre. Establishing a wide genetic base of germplasm is the foundation practice for all breeding programmes. Thus, germplasm collection and evaluation was one of the initial activities. The past varietal tests of local and exotic germplasm have led to the release of five varieties (Appendix 3). The current linseed improvement research is geared towards developing high yielding and disease tolerant varieties adapted to the major growing areas of the country.

Acquisition of germplasm from exotic sources has been the main strategy of variety development programme at Holetta. Consequently, four of the released varieties were selections out of the exotic sources. That is to say, good emphasis has been given to the introduction of exotic materials from abroad, which is similar to the history of wheat in the United States of America. Cox and Murphy (1990) reported that, until the 1930s, all wheat produced in the United States of America was harvested from some 28-foundation introductions or by direct selection from them. Including exotic germplasm is thus believed to reduce genetic vulnerability, broadening the genetic variability available for breeding and selections. Introgressing useful exotic materials into elite lines with BC_2 to BC_4 progenies (88-97% adapted and 3-12% exotic) was found an acceptable and useful practice (Cox and Murphy, 1990).

Linseed is regarded as a self-pollinating crop and has a considerable heritage in terms of classical breeding techniques. The pedigree method has been used most widely in developing improved linseed cultivars, although other methods such as single-seed descent and bulk breeding methods could be used, too (Kenaschuk, 1975; Salas and Friedt, 1995). That means, cultivars of linseed represent pure or true breeding lines.

Further cultivar improvement is also feasible, particularly by application of biotechnology i.e. tissue and cell culture techniques (Rowland *et al.*, 1988a). It is possible to obtain haploid and doubled haploid plants reproducible through anther- or microspore- culture, which allows the rapid fixation of rarely segregating genotypes and a substantial reduction of the breeding cycle (Nichterlein *et al.*, 1991; Nichterlein and Friedt, 1993). In other words, breeding of linseed using haploid techniques has the potential advantages of the rapid development of completely homozygous lines within one generation and the development of efficient means of genotypic selection (Chen *et al.*, 1998). According to Friedt *et al.* (1995), anther culture is currently the most successful method for producing doubled-haploid lines in linseed. The plant regeneration frequency from linseed anther culture has been improved by optimising plant growth conditions (Nichterlein *et al.*, 1991), culture temperatures and cytokinin concentration in the regeneration medium (Chen *et al.*, 1998). Consequently, anther culture is being applied effectively in the breeding programmes of linseed. In fact, the application of such tissue or cell culture has been practiced since mid 1970's (Murray *et al.*, 1977). But it became more feasible with the development of *in vitro* selection system where various artificial stresses like herbicides, salts, disease toxins, etc. are used to select potentially resistant cells that are regenerated into the whole plant (Rowland *et al.*, 1988a).

The Ethiopian linseed research programme has good linkages with research institutions in Northern America, like the University of Saskatchewan in Canada. Subsequently, tissue culture derived regenerants or somaclones (at R_6 and R_7 stages) were introduced to Ethiopia in 1990 (Adugna and Adefris, 1995). Somaclones or regenerants refers to the spontaneous genetic aberrations occurring in cells growing *in vitro* (Larkin and Scowcroft, 1981). Since both terms are often interchangeably used, the same will be done in this study.

The regenerants were initially obtained from hypocotyl and callus of three linseed cultivars (McGregor, Norlin and Dufferin) on modified MS culture medium (Murashige and Skoog, 1962) in the early 1980's, at the University of Saskatchewan (Rowland *et al.*, 1988a; Adugna and Adefris, 1995). After inspections for quarantine purposes in 1991, they were tested for wilt (*Fusarium* spp.) resistance in sick-plots in 1992 at Holetta Research Centre. Then those materials that showed relatively better performance than the standard checks were evaluated in a series of experiments across several environments in

Ethiopia since 1995. The main purpose of introducing the regenerants into Ethiopia was to assess and identify useful variants for either direct release or to use them as germplasm sources in the breeding programme.

Nationally, the cultivar improvement programme of linseed is conducted under the Ethiopian Agricultural Research Organisation (EARO) in collaboration with the Regional Research Centres such as Adet, Sinana and Areka. The research results are dispatched to the farmers through the Ministry of Agriculture (MoA), the Extension Division of EARO and by some non-governmental organisations. The use of improved varieties and practices has shown encouraging yield increase over farmers' methods. Adugna (1992) reported a mean seed yield advantage of 0.27 t ha^{-1} and a marginal rate of return of 76.8% from improved varieties and their practices over that of the farmers. Seed yields up to 2.5 t ha^{-1} were also obtained from experimental plots at Holetta, Adet, Kulumsa, Bekoji and Sinana and about half of this amount can be obtained from farmers fields by using the improved production technologies (Adefris *et al.*, 1992; Adugna and Adefris, 1995). These evidences indicate the potentials of increasing the productivity of linseed in the country. Likewise, varieties with low linolenic fatty acid are required to expand the market opportunities of linseed as edible oils. In order to achieve these projected targets, adaptive and innovative research efforts are needed. In fact, the current cultivar improvement programme is directed towards developing high yielding varieties together with improved nutritional and industrial values.

According to Crossa (1990), data from multilocation trials possess three main agricultural objectives: (i) to accurately estimate and predict yield based on experimental data; (ii) to determine yield stability and pattern of response of genotypes or agronomic treatments across environments; and (iii) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years and at new sites. With respect to these, genotypes by environment (G x E) interactions are important issues confronting plant breeders and agronomists worldwide and especially in countries like Ethiopia, where its agro-ecology is very diversified (Appendix 4).

Crop breeders have been striving to develop improved genotypes that are superior in seed yield, quality and other desirable agronomic characteristics over a wide range of environmental conditions. However, due to the wide occurrence of G x E interactions,

stable and high yielding genotypes are not easily available as required. The interactions of genotypes with environments were partly described (Becker and Leon, 1988) as a result of differential reactions to environmental stresses, such as drought, extreme temperatures, diseases and other factors. In fact, the function of experimental design and statistical analysis of multilocation trials is to minimise and eliminate this unexplainable and unpredictable extraneous variability, which was termed as noise (Gauch 1988; Crossa, 1990). Consequently, many plant breeders use estimates of various stability parameters to assist them in identifying superior genotypes in the presence of G x E interactions.

Accordingly, this study was planned to analyse and understand the comparative performance of linseed regenerants along with other crosses and the standard checks across several environments of Ethiopia with the help of different statistical tools. The specific objectives of this study were:

1. To assess the seed yield, oil content and other agronomic characteristics of the linseed regenerants and study their potential use in the linseed breeding programme of Ethiopia;

2. To evaluate the adaptation potential, investigate the G x E interactions and stability performance of the tested entries across the 18 environments of Ethiopia;

3. To compare the relative importance of the regenerants with other breeding materials, and investigate their patterns and relationships;

4. To determine the relative contributions of different linseed characteristics to yield and oil content; and,

5. To understand and describe the existing variety testing environments and generate some recommendations that could contribute to the future improvements of linseed research in Ethiopia.

CHAPTER 2

LITERATURE REVIEW

2.1 Introduction

In this literature survey, attempts were made to collect and present the concepts and results of recent studies on two main aspects of linseed breeding. The first one is in relation to tissue culture derived regenerants, which are the initial steps of the recent biotechnological innovations that have opened new opportunities for the production of novel crop varieties (Larkin and Scowcroft, 1981). In this regard, the overall applications and contributions of biotechnology in general and that of tissue culture in particular are discussed in view of linseed breeding. In fact, techniques of modern biotechnology range from the complex methods of recombinant DNA technology, through intermediate methodologies such as cell and tissue culture, to relatively simple and routine procedures such as chemical mutagenesis and screening (Murphy, 1994). With respect to the oil crops, biotechnology deals with two major goals, to maximise the oil yield and to manipulate the oil quality in order to meet the various needs of food and industrial applications. Hence, it is felt appropriate to assess and highlight this important area of research.

The second aspect of this chapter deals with the genotype by environment (G x E) interactions and stability analysis. As stated by Crossa (1990), data collected from multi-location trials are intrinsically complex and have three fundamental dimensions: structural pattern, non-structural noise and relationships among genotypes, environments and their interactions. Pattern implies that a number of genotypes respond to certain environments in significant and interpretable manner, while noise suggests that the responses are unpredictable and uninterpretable. This literature study, thus, tries to describe some of the conventional and new approaches of stability analysis that are applied for multi-environment trials. Subsequently, the improved productivity of linseed is expected from growing superior genotypes developed by assembling many favourable genes that could work well together in the environments that may allow them to express their superiority, for which this study is eventually targeted. That is why this chapter has capitalised on the basic themes of tissue culture-derived materials and G x E interactions. Indeed, that is one

of the feasible strategies for increasing linseed productivity in view of sustainability and environmental sensitivity.

2.2 Overview of biotechnological applications in improvement of oilseeds

2.2.1 Rationale and potentials

From the earliest days of agriculture and crop cultivation, plant breeding has been the main technology for improving food, feed and other consumable products (Frey, 1992). Although these practices are still of paramount importance, they stand to benefit considerably from applications of biotechnology based on research in emerging fields such as molecular biology, cell culture and genetic engineering (Rattray, 1990). Adoption of such technologies will be required if oils and fats industry is to keep pace with ever-increasing consumer demand for a higher standard of living. To this effect, applications of biotechnology in its several forms will have a major role to play. Combinations of the new techniques of genetic engineering and breeding procedures with older agricultural practices associated with crop growth are expected to give the required increased productivity and provision of products of uniform and desirable properties. For instance, development of novel crops for either edible or non-edible oils and fats is being driven by different demands of industries as shown in Table 2.1.

Murphy (1994) reported that vegetable oils were produced globally at the rate of about 62 million tons (MT) per year (i.e. 4.3% annual increase in production) in the 1990s and the demand by the year 2000 was estimated to rise to about 90 MT. Of the 62 MT productions, about 13 MT are used for industrial purposes (i.e. major uses for non-edible industry). There is a considerable need for the expansion of industrial crop production. The prospects for oil crop production are thus good in both the short and long terms. In the short term, the continued rise in demand for edible oils and increasing demand for industrial oils will be matched by the available land set-aside and other surplus land from cereal and animal production. An accelerating demand is expected for renewable oleochemicals and other products derived from vegetable oils. The application of modern biotechnology to oil crops

will hence allow these opportunities to be grasped through an appropriate collaboration between the public and private sectors.

Table 2.1. Objectives of biotechnology in the modification of fatty acid composition of oilseeds (Rattray, 1990)

Oilseeds	Fatty acid	Objective	Expected result
Linseed	Linolenic (18:3)	reduction	oil stability
Soybean	Stearic (18:0)	increase	margarine industry
	Linolenic (18:3)	reduction	oil flavour & stability
Rapeseed	Caprylic (8:0)	increase	oleochemical industry
	Capric (10:0)	increase	oleochemical industry
	Palmitic (16:0)	increase	margarine industry
	Linolenic (18:3)	reduction	oil stability
	Erucic (22:1)	increase	oleochemical industry
	Erucic (22:1)	decrease	edible oil food industry
Sunflower	Oleic (18:1)	increase	olive oil substitute
Safflower	Oleic (18:1)	increase	olive oil substitute

For the major value component of oil crops (i.e. oils), there are two goals for improvement in biotechnology. These are to maximise the oil yield and to manipulate the oil quality suitable for various industrial applications. Besides enhancing the yield and value of the oil, biotechnology can also be employed to improve the quality of products, such as seed proteins. It can also assist in reducing or eliminating undesirable components such as high linolenic fatty acid level in edible oil of linseed (Rowland et al., 1995) or high glucosinolate content in rapeseed (Murphy, 1994). Finally, biotechnology can improve the disease resistance and it can accelerate the development of new varieties via hybridisation of distant materials.

Generally speaking, biotechnology may create favourable conditions for the rational design of oil crops architecture to optimise seed yield, growing time, flowering time, desiccation rates, harvesting potential and other useful agronomic characters. An additional important goal for oil crop biotechnology is to translate its achievement to the agriculture systems of developing countries, like Ethiopia which are currently depending on imported vegetable oils but which have the potential to be come self-sufficient or even to export such oils in the days to come. In other words, the latest crop improvement techniques, which follow the molecular approaches, need to be incorporated into the conventional breeding methods to generate useful outcomes within the shortest possible time. This should not be done only in the narrow social frame of the developed nations and less diverse agricultural systems, but also for the broader social benefits in developing countries for increasing food security and biodiversity.

Currently, it is possible to select resistant cells or tissues *in vitro* against various types of biotic and abiotic stresses, and superior varieties can be developed within five or six years by anther culture and similar techniques. Fertile plants can be recovered from callus (McHughen and Swartz, 1984); suspension and protoplast culture in major crops (somaclones), thus a new cultivar can be developed with fewer efforts (Rowland *et al.*, 1988a). For example, a high yielding, bold-seeded and shattering resistant somaclone (Pusa Jai kisan) of oilseed brassica (*Brassica juncea* L.) was released for commercial cultivation in India (Katiyar and Chopra, 1995).

Breeding programmes have permitted the development of commercial oilseed cultivars (Rowland *et al.*, 1995; Katiyar and Chopra, 1995), which provide a relatively constant range of values for the contents of both oil and protein in seed (Table 2.2). Attempts to select high oil producing varieties from cell suspension or undifferentiated callus culture has not proved possible since oil and fat accumulation occurs during oilseed maturation (Rattray, 1990). Perhaps, increased oil productivity *per se* may have limited economic importance, particularly with present commercial cultivars, since the pleiotropic effects of developed varieties may have deleterious consequences resulting in lower plant vigour and yield. This was true with the development of sunflower seed with remarkable oil content of 63%. It has been found to be associated with a marked tendency to seed shattering with consequent oil loss during harvesting (Fick, 1983).

Table 2.2. The oil, protein and fatty acid contents of linseed and other major oil seeds, value as % of dry mass (Rattray, 1990; Luhs and Friedt, 1994)

Crop	Oil	Protein	Palmitic	Stearic	Oleic	Linoleic	Linolenic	Eruicic	Iodine value
Linseed	42-45	16-31	4-7	2-8	12-38	5-27	40-65	-	169-196
Soybean	15-22	30-50	7-14	3-6	18-26	50-57	5-10	-	125-138
Sunflower	25-48	15-20	3-10	1-10	14-35	55-75	-	-	122-139
Rapeseed *	37-50	20-33	3-6	1-3	50-66	18-28	6-14	0-5	110-115
Peanut	40-45	25-30	6-16	1-7	35-72	13-45	-	-	84-102

* Low erucic acid types; - = nil

Greater possibilities for advances through biotechnology would appear to modify the oil and fat composition to furnish a more desirable product in fatty acid composition. Specific modifications in seed oil and fat composition are being sought via biotechnology to furnish "designer oil and fats" (Murphy, 1994). The primary attentions are given to a particular tailoring of certain plant oils and fat industry as indicated in Tables 2.1 and 2.2. Successful modifications of fatty acid composition will require more definite knowledge of fatty acid biosynthesis and storage of tricylglycerol deposition. Currently, however, little is known about the molecular composition of the genetic factors involved (Rattray, 1990). In summary, biotechnology is assisting the improvement of oil crops in two ways. Firstly, the potential and efficiency of classical breeding programmes are being enhanced by increasing the genetic diversity within breeding lines and by using marker-assisted selection programmes to transfer useful genes into elite agronomic background within shorter period of time. Secondly, genetic engineering is being used to isolate genes from unrelated species and to transfer these into advanced breeding lines, and these two approaches are seen as complimentary to each other.

2.2.2. Brief accounts of tissue-culture derived regenerants/ somaclones

Recent advances in plant breeding and biotechnology have opened up new opportunities for the production of novel varieties of crops (Larkin and Scowcroft, 1981; Murphy, 1994). According to Pauls (1995), plant biotechnology can be defined as the application of tissue

culture and molecular genetics to develop or produce a commodity from plants. Tissue culture refers to the maintenance and propagation of plant parts in biologically pure and controlled environments. Molecular genetics includes techniques for isolating, characterising, recombining, multiplying and transferring discrete fragments of DNA that contain genes coding for specific traits (Pauls, 1995). To be more effective and efficient, plant biotechnology has to be well integrated into the established plant breeding and crop production practices.

The potential gene pools available to plant breeders have been extended enormously following the development of wide crossing techniques, for example protoplast fusion, embryo rescue and the marker based selection methods for rapid identification of valuable traits in variety screening programmes. It is well known that two important prerequisites, the presence of sufficient genetic variation and the availability of efficient selection procedures are required in plant breeding. In order to meet the former and broaden the genetic variation of crops, wild species, mutation and hybridisation techniques have been utilised (Frey, 1992). Nevertheless, during the past decades, another source of variation has become apparent. It was the variation induced by cell and tissue culture, which was designated as somaclonal variation (Larkin and Scowcroft, 1981; Scowcroft, 1984).

The events of somaclonal variation have been reported in many crops (Ahloowalia, 1986; Van den Bulk, 1991; Cheng *et al.*, 1992; Rowland *et al.*, 1995). And the regenerants most frequently observed are those which are easy to detect, for example, plants with chlorophyll deficiency and those with chromosomal aberrations such as polyploidy and aneuploidy (Ahloowalia, 1986). The various plant characteristics that can be altered as a result of plant regeneration from cells and tissue culture comprises of agronomically useful traits, such as disease resistance (Van den Bulk, 1991). Somaclonal variants have also been described in rapeseed for black leg disease susceptibility (Katiyar and Chopra, 1995) and in tomato for growth habit, fruit colour and male sterility (Evans and Bravo, 1986; Evans, 1987).

Studies on improving winter wheat by inducing somaclonal variation have shown highly variable R_1 plants in plant height, maturity, awnedness and spike number (Cheng *et al.*, 1992). The same authors estimated the somaclonal variation frequencies to 14.2% on R_1 plant basis and 5.3% on the R_2 spike basis. Moreover, studies on the use of somaclonal variation and *in vitro* selection for chilling tolerance improvement in rice, indicated

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significantly higher survival rates in the R_3 with *in vitro* than the control plants (Bertin and Bouharmont, 1997). They also indicated that the percentage of regenerating calli greatly varied depending on variety, length of culture and callus temperature treatment. Hence, all of these evidences demonstrate the potential of somaclonal variation for production of new breeding lines in crops.

The other successful application of somaclonal variation in plant breeding was the selection of sugar cane against disease resistance. Clones with resistance to eyespot disease (*Helminthossporium saccari*), downy mildew (*Sclerospora saachari*) and fijii disease were produced by regenerating plants from callus of susceptible parents (Scowcroft, 1984). The selection of disease resistant regenerants might be more efficient if cells or tissues are exposed to a selective pressure, as shown by Carlson (1973) for wildfire disease of tobacco caused by *Pseudomonas syringae* pv. Tabaci. Several studies have been conducted since then to obtain regenerants with increased levels of disease resistance (Evans and Bravo, 1986). Therefore, the successful application of somaclonal variation could be determined by the frequency of occurrence of specific traits, stable variants and the efficiency of the procedures for selecting these regenerants.

The causes of somaclonal variants or regenerants could be alterations in chromosome number and structure, point mutations, mitotic recombinations, and the amplification, deletion, transposition or methelation of DNA sequences in nuclear, mitochondorical or chloroplast genomes (Van den Bulk, 1991). The chromosomal or molecular changes may result in stable changes, which are transmitted sexually to the progeny while epigenetic alterations that frequently occur are not transmitted to the progenies. Evans and Bravo (1986) indicated that the use of somaclonal variation was evident to develop new cultivars of horticultural crops and ornamental plants based on the experimental results of tomato and tobacco. Successful applications of tissue culture were also reported for clonal propagation of elite selections, which enabled the growers to produce uniform and high quality products (Ahloowalia, 1986; Van den Bulk, 1991). Moreover, tissue culture technologies were also used for preservation of valuable germplasm in addition to overcoming breeding barriers (incompatibilities) via embryo rescues, somatic and gametic embryogenesis (Evans and Bravo, 1986; Evans, 1987). According to Janick (1990), the potential agricultural uses of somatic and gametic embryogenesis are as follows: rapid clonal propagation; freeing plants of viruses; germplasm preservation; metabolite production; and crop variety improvement.

The last point, which deals with crop development, is usually applied through embryo rescue, exploitation of somaclonal and gametoclonal variation, protoplast fusion, transformed cells, and production of homozygous lines via androgenesis. Hence, *in vitro* selection has been proposed as an effective methodology to screen for variants such as herbicide resistant genotypes. However, only few plant traits are expressed at cellular level. Traits of paramount importance to the breeder (e.g. yield, maturity, height and lodging resistance) are not expressed at cellular of tissue level (Frey, 1992). Furthermore, a number of variants selected for tolerance to abiotic stresses such as salinity, acidity, heavy metals, etc. have been reported ephemeral (Rattray, 1990) and thus, *in vitro* selection may not be widely used to select quantitatively inherited traits (Frey, 1992).

2.2.3. Cytogenetic basis of the regenerants/ somaclones

The existence of chromosomal changes in plant tissue culture has been reported in the forms of polyploidy, aneuploidy and abnormal cell divisions since the early 1960's (Orton 1984; Evans and Bravo, 1986). According to Evans and Bravo (1986), most of the variations in early reports were attributed to the readily detected chromosome instability of cultured plant cells. In many of these studies, the extent of chromosome instability was reported to be proportional to the length of time the cells remained in culture. Recognition of the spontaneous variation inherent in long-term cultures led to the use of cell culture for mutagenesis and selection of genetic variants and for direct recovery of novel genotypes from cell cultures via somaclonal variation.

Alterations from cultured cells have been referred to as phenotypic or genotypic changes. The genotype refers to the sum total of the genetic information, while phenotype is recognised to be a combination of genetic and environmental factors. The phenotypic changes that are not the result of genetic alternations are referred to as epigenetic changes. It is, therefore, appropriate to characterise variation in the plant or cell culture phenotype as a genetic or epigenetic change. The distinction between these two types of changes is only conclusively demonstrated by detailed genetic evaluation, often requiring several sexual generations. The term somaclone or regenerant (R), given to self-fertilised progenies as R_1,

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R_2, R_3, etc. refers to the plants regenerated from cell cultures originating from somatic tissue (Larkin and Scowcroft, 1981).

Phenotypic variation has been reported in a number of plant species regenerated via organogenesis or embryogenesis (Evans and Bravo, 1986). These authors indicated that genetic variation was first detected as altered chromosome number in cultured plant cells like carrot. The most frequently reported variation has been polyploidy (Skirvin, 1978), attributed to selective growth; normally non-dividing polyploid cells, existing in the original ex-plant. It has also been reported that the frequency of polyploids cells is dependent on the concentration and type of cytokinin used in the culture medium. Polyploid plants have been recovered in many commercially important species including tobacco, tomato and alfalfa (Evans and Bravo, 1986). Aneuploid changes involving the gain or loss of a few chromosomes have also been frequently reported in plant cell cultures. These changes have been attributed to ageing of cultures. Chromosome rearrangements have been detected in clones of potatoes regenerated from mesophyl protoplasts (Shepard, 1982).

Inheritance of somaclonal variation was also demonstrated for wheat in both segregated and uniform variant families and spike lines (Cheng et al., 1992). They reported about 70% of the 134 variant selections were inherited, indicating both recessive and dominant gene mutations at one, two or three loci. Similarly, the progeny of tomato plants regenerated from leaf-derived callus were examined and 13 distinct single gene mutations were recovered among 230 regenerated plants (Evans and Bravo, 1986). According to them, this frequency of visual somaclonal variation is substantially greater than the cell mutagenesis rate from several cell selection experiments.

A mitochondrially encoded male sterility of cytoplasmic genetic variation has been detected from regeneration of corn cell culture (Evans and Bravo, 1986). Thus, somaclonal variation has resulted in numerical and structural chromosomal changes, in nuclear genetic modifications and cytoplasmic genetic variation. This wide spectrum of variation suggests that by using appropriate selection methods, all classes of genetic variation could be recovered and used for crop improvement. Evidence from several laboratories suggests that variability is dependent on hormone concentration of culture medium, donor ex-plants and pre-exists in the tissue used to establish cell culture. According to Cocking and Riley (1981), and Ahloowalia (1994), the causes of somaclonal variations are point mutations, changes in

chromosome number and structure, activation of transposons, methylation of DNA, changes in plastid and in chloroplast DNAs, segregation of existing chimeral tissues and non-specified environmental interactions that are often called epigenetic variations. While most regenerants were used as a germplasm sources, only few somaclones have been of direct value without further breeding (Ahloowalia, 1986; 1994).

Recent indications of somaclonal variation in several crop plants have stimulated interest in application of this method for crop improvement. For example, studies with sugar cane suggested that clones with disease resistance could be regenerated from callus induced from sensitive plants. Most of these variants have been attributed to changes in chromosome number. Potato variants have been isolated with resistance to early blight and with altered growth habit, tuber shape, colour and maturity date. These variants were attributed to changes in chromosome number and structure (Shepard, 1982). While these variants can be stably propagated asexually, the genetic inheritance of this variation in sugar cane and potato has not been well explained.

Based on the tomato experimental evidence, Evans and Bravo (1986) have concluded the following points regarding the genetic base of somaclonal variation:

- Chromosome number variation can be recovered in regenerated plants;
- Several single gene mutations have been recovered in different tomato varieties;
- Somaclones include dominant, semi-dominant and recessive nuclear mutations;
- The frequency of single gene mutation was one in every 20-25 regenerated plants;
- New single gene mutations not previously reported have been recovered;
- The mutants were of clonal origin;
- Mitotic recombination might also account for somaclonal variation;
- Mutations in chloroplast DNA can also be recovered; and,
- Agriculturally useful variants leading to development of new breeding lines have been recovered via somaclonal variation.

2.3. Applications of tissue-culture and other bio-techniques in linseed breeding

2.3.1. Tissue- and cell-culture

In linseed, tissue culture has been carried out since mid 1970's (Murray *et al.*, 1977; McHughen and Swartz, 1984; Ling and Binding, 1987; Rowland *et al.*, 1988a). Regeneration of plants was obtained from shoot tips, hypocotyls, cotyledons and roots of linseed, the regeneration frequencies of the latter being rather low (Murray *et al.*, 1977). McHughen and Swartz (1984) reported the regeneration of salt-tolerant linseed lines *in vitro*. Moreover, Ti-plasmid mediated transformation of linseed *in vitro* (McHughen *et al.*, 1986), and the selection for chlorosulfuron herbicide resistant lines has been achieved (Jordan and McHughen, 1986). Furthermore, Ling and Binding (1987) have reported successful plant regeneration from protoplasts of both wild and cultivated species of linseed that may be helpful for the interspecific hybridisation.

Rowland *et al.* (1988a) reported on the field evaluation of a linseed somaclonal variant at the Crop Development Centre, in the University of Saskatchewan (Canada). Their results showed that the error variances for seed yield were homogenous over years and locations. They also indicated that the combined analysis of yield data was significantly ($p<0.01$) different among the cultivars, including the salt tolerant selection (STS) regenerant. This regenerant was found to be significantly different from its parental variety, McGregor. The authors further indicated that STS flowered and matured significantly earlier than McGregor at two locations, and it also had significantly ($p<0.01$) heavier seeds than the parent cultivar. In general, STS was remarkably different from its parent in all investigated characters, according to Rowland *et al.* (1988a). STS was originally regenerated from a single cell colony that survived the saline culture medium. It was tested in both saline and non-saline soils in a glasshouse and found to perform better than its parent, McGregor (McHughen, 1987).

Later on, the STS-II was found to possess high tolerance to other stresses such as heat, and greater ability to germinate under low temperature than McGregor (O'Connor *et al.*, 1991). Moreover it had an extra 5s rDNA repeat that was not found in McGregor (Rowland *et al.*,

1995). Thus STS-II was registered under the variety name of Andro (Rowland *et al.*, 1989) as it had good positive attributes and was best suited to the northern linseed growing areas of Saskatchewan. Following the success of the Andro variety, Rowland and his co-workers (1995) regenerated over 11000 plants from callus cultures of Canadian linseed varieties, and they discovered a large range of variation in the McGregor somaclones. They also estimated the heritability of the somaclonal lines, for important yield components and it ranged from zero for yield to 43% for oil content. Much of the variability was reported stable and had genetic bases from these estimates. The authors further indicated that one regenerant (F86343) out-yielded McGregor consistently over a number of years with up to 18% yield advantage and 5-6 days earlier than its parent (Rowland *et al.*, 1995).

Likewise, Adugna (1993) studied three groups (R_3, R_4 and R_6) of tissue culture derived linseed lines of McGregor, NorLin, STS, Vimy, Dufferin, Rocket, Culbert, and Murray cultivars, which were produced from a callus-based *in vitro* regeneration system. In field trials conducted over two seasons of 1987 and 1988, 724 R_3, 472 R_5 and 62 R_6 regenerant lines were compared with their parental checks for seed yield, oil content, 1000 seed weight, plant height, flowering and maturity dates, flower colours and rust resistance. Significant ($P<0.05$) variability was obtained in seed yield, oil content, fatty acid composition and in earliness. Substantial differences were also reported in plant height, flower colour and rust resistance. Early maturing regenerants were observed to be closely associated with poor seed yield, low oil content, rust susceptibility and light-blue petal colours. Preete (1991) also analysed the molecular changes of 20 regenerants and found nine of these lacked two minor repeat length classes of 18-25s rDNA repeat and one had lost a Bam HI site within the 5s rDNA repeats. However, many of the somaclones had stable fatty acid composition, unlike their variability in yield, days to maturity, seed weight and oil content (Rowland *et al.*, 1995).

2.3.2 Other biotechnological applications

According to McHughen and Holm (1991) linseed has proved to be a crop that can be easily transformed at cellular level using *Agrobacterium tumefaciens* technology. Various genotypes have been transformed with a wide range of *Agrobacterium* strains carrying many different gene constructs (Rowland *et al.*, 1995). Successful transfer of genes for tolerance to three herbicides, namely glyphosate (Jordan and McHughen, 1986), sulfonylurea

(McHughen *et al*., 1986) and phosphyinothicin (Rowland *et al*., 1995) were undertaken at the University of Saskatchewan in Canada. This shows that linseed can be easily transformed with *Agrobacterium tumefaciens* by inserting genes that confer tolerance to three herbicides mentioned above. The sulfonylurea herbicide resistant gene was isolated from *Arabidopsis* and inserted into linseed (McHughen, 1989). Field experiments that have been carried out with these lines carrying a resistance gene for sulfonylurea showed that the materials had a useful level of resistance to this herbicide. The insertion of this foreign gene has not affected the rest of agronomic performance of the transformed lines (McHughen and Holm, 1991).

Moreover, Rowland *et al*. (1995) reported that the two most promising sulfonylurea-resistant lines assessed in registration testing in Canada were not different from their parental variety (Norlin). Based on this successful works of the *Agrobacterium* technique, the authors intended to launch more programmes to further manipulate linseed using genetic engineering. They indicated that additional manipulation of fatty acid profiles would be feasible and important to develop linseed cultivars suitable for cocoa butter, margarine and candy industries. Furthermore, stress tolerant (heat, drought, salinity and cold) genes were suggested to be engineered into linseed cultivars in Canada (Rowland *et al*., 1995).

Attempts have also been made to induce genetic variation in breeding lines through the use of chemical mutagenes such as ethylmethanesulfhonate (EMS), or by radiation (Rowland, 1990; 1994). The basis of the method is to produce a large number of mutants in seeds and to screen for the desired phenotype in the M_2 generation. As the result, single plants may contain many other mutations along with the desired ones; an extensive backcrossing programme using wild-type elite cultivars is then required to obtain plants containing single gene mutations. The potential of this method has recently been demonstrated with the development of low linolenic fatty acid varieties of linseed, referred to as 'Linola'. Linseed used to be an industrial oil crop because of its high linolenic acid, as a drying agent in paints, varnishes, putty, ink, etc. (Murphy, 1994). A decline in the demand for linseed oil during the 1970s the 1980s have led to a search for lower linolenic acid varieties of linseed, which could then be used as a source of edible oils, for which the demand was buoyant (Rowland *et al*., 1995). The lack of low linolenic acid in the available germplasm (Green and Marshall, 1981) led to a chemical mutagenesis whereby Australian and Canadian cultivars were treated with EMS (Green and Marshal, 1984; Rowland and Bhatty, 1990). Two recessive mutants, with low linolenic acid contents of less than 30% were obtained. By crossing these two

mutant lines, a very low linolenic acid double recessive line was produced which contained only 2% of this fatty acid in its seed oil but normal levels of other lipids (Green, 1986a).

A similar methodology was used to reduce the linolenic content of the Canadian cultivar, 'McGregor', from its normal range of 40-60% to about 2% seed oil (Rowland and Bhatty, 1990; Rowland et al., 1995). The results of these two mutation programmes are new 'Linola' linseed lines possessing high (up to 70%) linoleic but very low (2%) linolenic fatty acids in their seed oils. These new varieties can serve as sources of premium grade high polyunsaturated edible oils, which are comparable to the quality oils of sunflower and safflower (Murphy, 1994). The low linolenic mutant of Canada was introduced to Ethiopia in the early 1990s. The necessary selections and crossing with released varieties of Ethiopia were carried out and some of the agronomically promising materials were advanced to the multi-location trials.

Induced mutation requires the screening of hundred thousand plants, relying upon rapid and facile methods, and an extensive backcrossing programme to remove the large numbers of undesirable mutations (Green and Marshal, 1984; Rowland and Bhatty, 1990; Bhatty and Rowland, 1990). Nevertheless, it can produce dramatic results within a few years and it is relatively low technology to be adopted where genetic engineering is not feasible due to the lack of suitable facilities or due to lack of resources, for example in developing countries like Ethiopia. In Table 2.3, the average seed composition of linseed varieties was presented in comparison with that of the mutants in Table 2.4, to demonstrate successful efforts of the recent breeding techniques, including the induced mutations.

Table 2.3. Average whole seed composition of normal (no mutation) linseed varieties in the USA (Carter, 1993).

Component	Percentage	Fatty acid composition	Percentage
Moisture	7.1-8.3	Palmitic (C16:0)	4.6-6.3
Lipids (d.m. basis)	31.9-37.8	Stearic (C18:0)	3.3-6.1
Protein	26.9-31.6	Oleic (C18:1)	19.3-29.4
Total dietary fibre	36.7-46.8	Linoleic (C18:2)	14.0-18.2
Insoluble	30±S.E.	Linolenic (C18:3)	44.6-51.5
Soluble	10±S.E.		

Note: d.m. = dry matter; S.E = Standard error

Table 2.4. Fatty acid composition (%) of mutant lines of Canadian and Australian varieties as compared with their original parents (Green, 1986a; Rowland *et al.*, 1995)

Line	Origin	Palmitic	Strearic	Oleic	linoleic	linolenic
E67	Canada	27.8	1.8	17.5	6.0	42.0
E1747	"	9.5	4.6	15.6	65.3	2.1
E1929	"	9.5	3.4	51.7	16.3	16.2
McGregor (parent)		**9.4**	**5.1**	**18.4**	**14.6**	**49.5**
M1722	Australia	8.4	4.8	35.4	27.8	23.3
M1589	"	7.2	5.0	44.0	24.5	19.1
M Zero	"	9.2	4.7	36.3	48.2	1.6
Glenelg (parent)		**7.0**	**3.7**	**35.1**	**14.1**	**40.1**

Rowland *et al.* (1995) reported that the mutant (E67) which had palmitic acid levels of about 28%, which was three to four times greater than any previously reported amount in linseed (Table 2.4). This mutant also had a significant level of palmitoleic acid (precursor of palmitic acid), which has been reported as trace amount in linseed (Rowland *et al.*, 1995). The

authors indicated that high palmitic-palmitoleic can be crossed with low linolenic character to develop oils suitable for the manufacture of margarine (i.e. 26% palmitic, 3% palmitoleic, 2% stearic, 16% oleic, 51% linoleic and 2% linolenic fatty acid profiles).

2.4. Major agronomic traits of linseed and their response to environments

The major aims of linseed breeding are the improvement of seed yield and oil content as well as protection from yield losses due to lodging and fungal diseases such as wilt (*Fusarium oxysporum* f. lini), powdery mildew (*Odium* spp.), pasmo (*Septoria lini*) and rust (*Melampsora linicola*). Fusarium wilt is the most important disease of linseed in Ethiopia and development of resistant varieties has been one of the major emphasis areas (Adefris *et al.*, 1992). In fact, resistance to wilt has been an essential selection criterion in the breeding of linseed at Holetta Research Centre. Yitbarek (1992) indicated that until 1986 more than 20 lines were identified as resistant to wilt and were submitted to the breeding programme of which some are already released for production. He also indicated over 80 resistant lines and cultivars were identified and promoted to yield trials in 1992. He further indicated that by repeated planting of the surviving plants in wilt-sick plots for over four consecutive seasons, it was possible to increase the resistance of the entries. Spielmeyer and his colleagues (1998) have indicated that two independent genes with additive effects contributed to the resistance response of wilt. On the other hand, rust was reported to be sporadic while pasmo tended to be severe in poorly drained and warmer environments (Yitbarek, 1992; Adefris *et al*, 1992).

According to Kenaschuk (1975), yield improvement of linseed can be achieved by selecting for individual yield components like bolls per plant, seeds per boll and 1000 seed weight. The same author reported that both additive and non-additive genetic effects were significant for yield and its components. Plant density, 1000 seed weight, seeds per boll and bolls per plant need to be considered in cultivar improvement schemes besides tillering and lodging that are much influenced by plant density and nitrogen supply (Luhs and Friedt, 1994). These authors have estimated the yield of modern linseed cultivars up to 3 t ha^{-1} under optimum conditions, indicating that the realisation of this potential is often limited by economic and ecological conditions.

Like other crops, seed yield of linseed was greatly affected by environment. It was particularly sensitive to environmental conditions during the flowering period, especially from the first two to five weeks after flowering (Kenaschuk, 1975). Boll setting, seeds per boll and seed weight were observed to be reduced in the flowers formed later in the season. Very high flower abortions were observed at Holetta when dry spells occur during flowering periods. Large-seeded varieties of linseed were observed to be more sensitive moisture stress than the small-seeded ones (Kenaschuk, 1975). Green and Marshall (1981) have found that larger seeded varieties had higher oil content, palmitic acid, strearic acid and oileic acid but lower linolenic acid than the smaller types.

Besides the moisture stress, temperature was reported to be the most important factor influencing seed weight. High temperature at blooming was found to be deleterious on boll setting, depressing seeds per boll and seed weight. In general, drought and higher temperatures during the sensitive seed-filling periods accelerate maturity, and thus reduce seed size and oil content that normally ranges from about 35-45% depending on variety, seed size, climate and maturity (Luhs and Friedt, 1994). Likewise, Adugna and Adefris (1995) reported that oil content was greater by 3% at cooler testing locality and Green (1986) showed the decline of oil percentage by 4% as temperature increased from 15/10 to 27/22 (day/night) degree centigrade. Moreover, Adugna and Adefris (1995) indicated that the differences among linseed regenerants tested in two diversified environments of Ethiopia have shown significant differences for seed yield, oil content, maturity period, plant height, lodging percentage and disease reactions. They have indicated that the early maturing ones were low in both seed yield and oil contents, and similar results were also reported in Canada (Rowland *et al.*, 1988b).

Likewise, Foster *et al.* (1998) have recently reported that flowering time and plant height were highly heritable while seed and straw weights were moderately inherited. Their quantitative analysis also indicated that dominance gene effects were high for plant height, number of branches, and seed weight. Foster *et al.* (1997) also reported a low level of correlation between most pairs of traits except between height and flowering time, days to maturity and flowering period. From that study, they observed a general lack of correlation between traits, inferring that many traits can be improved independently and may not show a correlated response to selection.

2.5. Association between yield and yield components of linseed

Studies on yield and number of bolls per plant, seed weight and number of seeds per boll have shown positive correlation, the later two factors contributing 75% of the variation in yield (Kenaschuk, 1975). The number of bolls per plant is one of the main criteria used by linseed breeders in selection of superior genotypes. Although seed weight is another important component of yield, large-seeded varieties have not shown any yield advantage over small-seeded varieties. According to Kenaschuk (1975), and Rao and Singh (1985), bolls per plants and seeds per boll were reduced as the seed size increases. Subsequently, small-seeded varieties were reported to be about 10% higher in yield than the large seeded varieties due to the negative association between seed weight and number of seeds per bolls.

2.6. Oil content and oil quality of linseed as influenced by environment

Improvement of oil content and oil quality are the major aims of linseed breeding. Studies have shown that inheritance of oil content was a quantitative character with heritability estimates of 66-80% (Kenaschuk, 1975; Salas and Friedt, 1995; Ntiamoah et al., 1995). The results of these authors demonstrated that strict selection in early generations for oil content was feasible and successful unlike selection for seed yield that has to be done in later generations. Salas and Friedt (1995) estimated the heritability of seed yield to be about 26-41%. As the result, breeding for maximum oil yield of linseed was recommended to be undertaken at two stages, selection at early generation for high oil content and at later generation for seed yield. Higher oil content has been shown to be associated with yellow seed colour though linseed breeders tend to select against it due to the several undesirable characters associated with this trait (Kenaschuk, 1975). Yellow seeded varieties were reported to possess lower germination, higher percentages of seed cracks or splits, lower test weight and significantly lower yielding than the brown-seeded lines. Green and Marshall (1981) and Batta et al. (1985) reported that significant variation of oil content between and within varieties of a diverse collection of linseed in Australia and in India, respectively. In Australia, parent-offspring correlation analysis indicated that a significant proportion of the variation within several varieties was due to genetic heterogeneity. Lines that had up to 46%

oil content were identified as compared to 40% of the standard ones. Likewise, wide variability of 37 to 48% oil content was reported in India (Batta *et al.*, 1985).

High temperature, low soil moisture, low soil fertility and the presence of diseases were also reported to negatively affect oil content and oil quality of linseed (Kenaschuk, 1975; Luhs and Friedt, 1994). Cool climates delay maturity of linseed varieties and provide a longer period for oil and fatty acid synthesis. Warm climate favours the formation of saturated fatty acids, while cold climate favours the formation of unsaturated fatty acids with two or three double bonds. In short, the variability of oil content and oil quality was realised to be affected by low fertility level, drought, high plant density and by the presence of diseases.

2.7. G x E interactions and stability statistics in cultivar assessment programmes

2.7.1 Concepts and importance

Successful cultivars need to possess high performance for yield and other essential agronomic characters. Besides, their superiority should be reliable over a wide range of environmental conditions. The basic cause for differences between genotypes in their yield stability is a wide occurrence of G x E interactions. Such phenotypic stability is often used to refer to fluctuations of yield across the environments. In other words, genotype by environmental interaction is a differential genotypic expression across environments. Genotypes refer to the set of genes possessed by individuals that is important for the expression of the traits under investigation. The environment is usually defined as all non-genetic factors that influence the expression of the traits. It may include all sets of biophysical factors like water, nutrition, temperature, disease etc. that influence the growth and development of the individuals and thereby influence the expression of the traits (Basford and Cooper, 1998).

According to Romagosa and Fox (1993), genotype by environmental interaction reduces association between phenotypic and genotypic values, and may cause selections from one environment to perform poorly in another, forcing plant breeders to examine genotypic adaptation. Its measurement is also important to determine an optimum breeding strategy for

releasing genotypes with adequate adaptation to target environments. It is particularly relevant for countries like Ethiopia that has very diversified agro-ecologies (Appendix 4). Under such conditions the breeders should be able to select desirable cultivars without losing valuable germplasm and other vital resources. Hence, agro-ecological diversity could complicate breeding and testing of improved varieties with adequate adaptation, but it could also permit identification of extreme environmental conditions that might offer selection pressure from different stresses.

The knowledge of genotype by environmental interaction (G x E) can help to reduce the cost of extensive genotype evaluation by eliminating unnecessary testing sites and by fine tuning the breeding programmes (Shafii *et al.*, 1992; Kang and Magari, 1996). The presence of a large G x E interaction may necessitate establishment of additional testing sites, thus increasing the cost of developing commercially important varieties. Thus, G x E interaction relates to sustainable agriculture as it affects efficiency of breeding programmes and allocation of limited resources. According to Kang and Magari (1996), G x E interaction is a major concern in plant breeding since it can reduce progress from selection and it may make cultivar recommendation difficult as it is statistically impossible to interpret the main effects. G x E interaction occurs in both short-term (less than five years testing at a location) and long-term (several years at various locations) crop performance trials.

G x E interaction is considered quantitative (Baker, 1988) if the ranking of genotypes does not change from one environment to another (i.e. non-crossover). Qualitative interactions (crossover) complicate selection and identification of superior cultivars. For variety trials, which are tested in the same locations (L) and genotypes over years (Y), G x E analysis of variance may be partitioned into components due to G x L, G x Y and G x L x Y. If G x L is the important portion of the G x E, then the specific adaptation is exploitable by sub-dividing the regions into homogenous sites that minimise G x E within regions. When G x Y and G x L x Y values dominate, no simplification to sub-divide the testing sites are required.

In general, the common variety testing strategy is to test over a representative range of environments. Therefore, breeders aim to cover a representative sample of spatial and temporal variation. Accumulation of tolerances to a number of stresses is the key to wide adaptation and consequently selection in multiple environments is the best way to breed stable genotypes (Eisemann, 1981; Getinet and Balcha, 1989; Romagosa and Fox, 1993).

They indicated that the success of wheat in combining high yield potential and wide adaptation involved large numbers of crosses, testing advanced lines internationally and continuous alternating selection cycles in various environments. These environments, which differ in altitude, latitude, photoperiod, temperature, rainfall, soil-type and disease situations allowed the expression of high yield potential. Choice of selection sites is particularly relevant in case of production areas with variable levels of abiotic stress. Research stations can be adjusted based on the study of genetic correlations between breeding sites and an extensive, and more commercially representative network of recommendation trials.

Different concepts and definitions of stability have been developed to apply them in the crop breeding programmes and in the evaluation of yield trials (Lin et al., 1986; Becker and Leon 1988; DeLacy et al., 1996). According to Becker and Leon (1988), two different concepts of stability exist, the static and dynamic. Both concepts were said to be useful although their application depends on the traits under consideration. According to the former concept, stable genotypes possess unchanged or constant performance regardless of any variation of the environmental conditions. That means its variance among environments is zero. In contrast, dynamic concept allows a predictable response to environments and a stable genotype has no deviation from this response to environments. The interest of most plant breeders in this regard is to develop well-buffered cultivars. The term stability, thus, refers to the character of a crop that withstands fluctuations of environments. Most breeders are interested to develop cultivars that are stable across a range of environments. In this case environment refers to locations, years or the combination of both. In the earlier years, one of the major concerns of agricultural research has been to develop high yielding crop cultivars. Lately, however, stable and sustainable yields under varying environmental conditions have been gaining importance over increased yields. Stable yield plays a major role in the developing countries such as Ethiopia, where small-scale farmers, particularly those living in marginal areas, are working towards risk-minimisation (Adugna et al., 1996). In such areas, stable yields are the key to sustainable food production. Farmers are basically interested in a constantly superior performance of cultivars on their own farms, specifically adapted to their conditions and needs, and which have a high degree of stability over time (Ceccareli, 1989; 1994). Response to selection is maximised when selection is conducted in the environment where the future varieties will be grown.

DeLacy *et al.* (1996) indicated that many statistical methods have been developed for the analysis of G x E interactions. Nevertheless, better methods that more effectively describe the data for predicting performance to selection (i.e. optimising selection among genotypes) are of greater interest to the breeders. In fact, each analytical alternative seems to have some merit and thus looking into their inter-relationships appears to be a sound approach. The context of G x E interactions in crop production systems and how they are encountered in multi-environment trials are shown in Table 2.5, as summarised by DeLacy and his co-workers (1996). It also shows the objectives of selection in a breeding programme and how G x E influences the selection strategies and the response to selection. Accordingly, phenotypic performance of genotypes in combination with environments can be analysed to quantify the amount of variation attributable to the effects of environment, genotype, and G x E interactions. DeLacy *et al.* (1996) recommended the use of the residual maximum likelihood (REML) analysis of variance and prediction of genotype performance by use of best linear unbiased predictors (BLUPs) to investigate patterns of adaptation of genotypes across environments.

Table 2.5. Consideration for analysis and understanding the form of G x E in terms of their application to selection in plant breeding (DeLacy *et al.*, 1996)

Form of G x E	Model assumptions	Application in plant breeding		Selection strategy
		Analysis method	**Objectives of analysis**	
Non-repeatable	Environment: random Genotype: random	Analysis of variance REML Best linear unbiased Predictors (BLUPs) of G performance	1. Estimate components of variance to determine the relative sizes of sources of variation and estimate heritability. 2. Characterise the form of G x E by examining them for both G & E for: (a) Heterogeneity (HV) + Lack of correlation (this enables calculation of the pooled genetic correlation) (b) Rank change + no rank change partition. (c) The impact of rank change on the composition of the selected group at a defined selection intensity.	Selection for broad adaptation. Decision on sample size (i.e. how test E, replicates and Gs to use)
Mixture of non-repeatable and repeatable	Es: a mixture of random & fixed Genotype: random	Indirect selection Pattern analysis	3. Relationship among Es measured in terms indirect response to selection. 4. Grouping, ordination and partitioning (size & shape) of G x E for individual Es.	Selection for broad and specific adapt. of types of Es.
Mixture of non-repeatable and repeatable	Env'ts: a mixture of Genotypes: a mixture of random & fixed	Pattern analysis	5. Grouping, ordination & partitioning of Gs & Es. 6. Investigation of causes of differences in patterns of adaptation.	Selection for specific adapt. and stability.
Repeatable Genotypes: fixed	Env'ts: fixed Biological model	Pattern analysis	7. Interpretation of causes of G x E interacts.	Decision on breeding and selection strategies. How many & what types of test Es?

Note: RELM = Residual Maximum Likelihood; BLUPs = Best Linear Unbiased Predictors; G = Genotype; E = Environment

2.7.2. Broad versus specific adaptation of genotypes

Generally speaking, the larger the relative size of the interaction components, the more complex the problem of identifying broadly adapted genotypes. Distinguishing and identifying repeatable and non-repeatable interactions (Jalaluddin et al., 1993) is very important. If the interaction is repeatable, specific adaptation strategies should be followed; non-repeatable interactions need to be accommodated by selection for broad adaptation (Basford and Cooper, 1998). According to Romagosa and Fox (1993), if the agronomic stability (well yielding in productive and potential environment) of a genotype prevails over a wide range of environments, it is referred to as having general or wide adaptation. On the contrary, if this manifests over a limited range, that genotype has specific or narrow adaptation.

2.7.3. Analytical approaches to measure stability of genotypes

Lin and his colleagues (1986) have reviewed and classified basic stability parameters into three types. Type one stability is analogous to homeostasis where a genotype is stable if its among-environment variance is small. It is based on deviations from the average cultivar effect whereas in type two, a genotype is considered stable if its response to environment is parallel to the mean response of all genotypes in the trial. The type three stability parameters are derived from the regressions on the environmental index and are measured by the residual mean squares from the regression model. Several authors (Lin et al., 1986; Westcott, 1986; 1987; Shafii et al., 1992) agree that all three concepts have problems in interpretations and usefulness to the breeders.

Type one is often associated with poor response and low yield in environments that are high yielding for other cultivars while type two is highly dependent on cultivars involved in the test which is subsequently used as the environment index although it does not necessarily represent the actual environmental factors. Likewise, type three is generated from regression on environmental index and measures stability due to unpredictable or uncontrollable factors that may not be valid (Lin et al., 1986). Nevertheless, the interpretations and statistics of Eberhart and Russell (1966), that involve both type two and three parameters are commonly

used in studies of many crops (Lin *et al.*, 1986; Westcott, 1987; Becker and Leon, 1988; Romagosa and Fox, 1993).

Becker and Leon (1988) have suggested two different approaches to assess stability. The first was the static, which Lin *et al.* (1986) named as Type 1 statistics. This stability is in the sense of homeostasis, which means maximum stability occurs when the yield of a certain genotype is constant across environments. On the other hand, according to the dynamic concept (Type 2 statistics of Lin *et al.*, 1986), a genotype is regarded as stable if its performance in different environments is close to what can be expected from the potentials of those environments. Maximum stability occurs if the difference between the yield of a genotype and the environmental index (mean of all tested genotypes) is constant across environments. If this difference is not the same in all environments, that genotype is said to interact with environments. Hence, if a breeder prefers the dynamic concept, the goal of breeding stable genotypes may be translated as the goal of minimising G x E interactions. The dynamic approach regards interactions as random unpredictable fluctuations or noise (Becker and Leon, 1988). However, sometimes one may be interested to further analyse the interactions and extract predictable information from it. This leads to the regression approach, which was first suggested by Yates and Cochran (1938) and further elaborated by Finlay and Wilkinson (1963), Eberhart and Russel (1966) and Perkins and Jinks (1968).

According to Romagosa and Fox (1993), there are two major approaches for studying G x E interaction and adaptation. The first one is the parametric (empirical and statistical one), which is more common and involves relating observed genotypic responses, in terms of yield, to a sample of environmental conditions. The second one is the non-parametric (analytical clustering) approach, which defines environments and phenotypes in terms of biotic and abiotic factors. In practice, however, most breeding programmes incorporate some elements of both approaches (Becker and Leon, 1988; Romagosa and Fox, 1993).

Recent developments comprise application of a multiplicative interaction model, which was first introduced by other biometericians, and has been introduced in the agricultural context as Additive Main Effects Multiplicative Interaction, AMMI (Piepho, 1996). These models are appropriate if one is interested in predicting genotypic yields in specific environments, for which yield trials are available. A further advantage of these models is that they may be used for modelling and understanding interaction. However, where there are sufficient funds

and economic justifications are available to breed for a particular environment, stability becomes irrelevant and yield in that environment could be paramount. But if cultivars are being selected for a large group of environments, stability and mean yield across all environments are of major importance and yield for a specific environment is of less importance (Piepho, 1996).

Numerous methods have been proposed (Lin *et al.*, 1986; Becker and Leon, 1988) to analyse G x E interactions or to estimate phenotypic stability and thereby to exploit positive outcomes. However, these authors indicated that parametric and non-parametric methods are the major statistical tools employed to study stability.

2.7.3.1. Parametric approach

According to Huehn (1996), the classical parametric stability statistics include ecovalence, environmental variance, regression coefficient, and sum of squared deviations from regression. Likewise, Lin *et al.* (1986) have described the following nine parametric stability statistics:

1. Environmental variance (variance of genotypes across environments);
2. Coefficient of variability (CV% of each genotype);
3. Mean variance (mean of estimated variance components of G x E for all pairs of genotypes);
4. Variance component for G x E interaction;
5. Wricke's (1962) ecovalence;
6. Shukla's (1972a) stability variance;
7. Finlay and Wilkinson's (1963) regression coefficient;
8. Perkins and Jink's (1968) regression coefficient; and,
9. Eberhart and Russell's (1966) deviation parameter.

According to Becker and Leon (1988), the parametric approach gives only the individual aspects of stability but cannot provide an overall picture of the response. The basic reason for this difficulty is that a genotype's response to environments is multivariate, which parametric

approach tries to transform to a univariate problem via stability index. To escape from this problem a different line of thought has emerged, namely to cluster genotypes according to their responsive structure (i.e. non-parametric method).

Analysis of variance

In a conventional variety assessment trial in which the yield of G genotypes is measured in E environments over R replicates, the classic model to analyse the total yield variation contained in GER observations is the analysis of variance (Fisher, 1918; 1925, cited by Purchase, 1997). After removing the replicate effect when combing data, the G x E observations is partitioned into two sources: (1) additive main effects for genotypes and environments and (2) non-additive effects due to G x E interaction. The analysis of variance of the combined data expresses the observed (Y_{ij}) mean yield of the ith genoype at the jth environment as:

$$Y_{ij} = u + G_i + E_i + GE_{ij} + e_{ij}$$

Where u = overall mean, G_i, E_i and GE_{ij} represent the effect of the genotype, environment and genotype x environment interaction, respectively, and e_{ij} is the average of random errors associated with the rth plot that receives the ith genotype in the jth environment. The non-additive interaction, GE_{ij} implies that an expected value of Y_{ij} depends not only on the levels of G and E separately, but also on the particular combination of levels G and E (Purchase, 1997; Crossa, 1990). According to these authors, the most important limitation in the analysis of variance is that error variances over environments need to be homogeneous to test for genotype differences.

In other words, significant tests from a combined analysis of variance are valid if error terms from different environments are homogenous (Romagosa and Fox, 1993). For a two-factor mixed model (fixed genotypes and random environments), the most commonly used combined analysis of variance is shown in Table 2.6. Means adequately describe the potential of environments and the performance of genotypes in a trial when G x E is not significant. However, when the interaction is significant, main effects should be interpreted with caution and the nature of the interaction, has to be examined, as means often mask cases

where varieties perform well or poorly in sub-sets of sites (Becker and Leon, 1988). In analysis of variance, the magnitude of sums of squares of relevant terms and variance components are used to quantify sources of variation.

Table 2.6. Mixed model (fixed genotype and random environment) analysis of variance for g genotypes at one location with r replications at each site (Romagosa and Fox, 1993).

Source of variation	Degrees of freedom	Mean squares	Expected means	F-ratios
Total	lrg-1			
Environ (E)	l-1	MS1	$V_e + gV_{R(E)} + rgV_E$	MS1/SM2
Rep./E	l(r-1)	MS2	$V_e + gV_{R(E)}$	MS2/MS5
Genotypes (G)	g-1	MS3	$V_e + gV_{GE} + erV_G$	MS3/MS4
G X E	(l-1)(g-1)	MS4	$V_e + gV_{GE}$	MS4/MS5
Error	l(g-1)(r-1)	MS5	V_e	

Note: G/g = Genotype; E = Environment; V = Variance; R = Reps.; l = location; e = error

Likewise, cultivar superiority or performance measure (Lin and Binns, 1988a), are the squares of the differences between an entry mean and the maximum mean at a location, summed and divided by twice the number of locations. Genotypes with the smallest values tend to have larger yields and also be more stable than other genotypes. According to stability variance of Shukla (1972), however, the stability values are estimates of an entry's variance across environments and stable varieties have smaller estimates.

Ecovalence (W$_i$)

Wricke (1962) proposed using the G x E interaction effects for each genotype, squared and summed across all environments, as stability measure. It was found simpler to compute and more directly related to the G x E interactions than other statistics proposed by biometricians (Becker and Leon, 1988). According to these authors, ecovalence measures the contribution of a genotype to G x E interactions and a genotype with zero ecovalence is regarded as stable (i.e. low values indicate high ecovalences). Therefore, Wricke's Ecovalence (1962) are estimates of the G X E interaction effects for each entry, when

squared and summed across all environments, as a measure of stability. As the ecovalence value increases, the genotype's contribution to the total G X E sum of squares also increases.

Regression coefficient (b_i) and deviation mean square (s^2d_i)

Simple linear regression provides a conceptual model for genotypic stability and is the most widely used statistical technique in plant breeding (Romagosa and Fox, 1993). It is also known as the Finlay and Wilkinson (1963) approach. The regression of individual genotype's yields against environment mean yields is determined and preference is explained in terms of main effects multiplied by the regression coefficients of genotypes. The G X E from analysis of variance is partitioned between heterogeneity of regression and deviations from regressions. As already mentioned, the most frequently used method is that involving regression (Becker and Leon, 1988), although opinions vary on the use of the b_i value.

Finlay and Wikilson (1963) defined a genotype with $b_i = 0$ as stable, while Eberhart and Russell (1966) defined a genotype with $b_i = 1$ to be stable. The former was in accordance with the static concept, while the latter was in line with the dynamic concept (Becker and Leon, 1988). These authors have suggested using the ecovalence instead, since it combines b_i and s^2d_i into one parameter. They further emphasised that most biometericians consider b_i not as a measure of stability but as additional information on the average response of a genotype to favourable environments. B_i is usually considered as a response parameter and s^2d_i as stability parameter. This concept is schematically presented in Figure 2.1, as sketched by Becker and Leon (1988). They concluded that the linear regression method will continue to play a vital role in further understanding of G x E interactions because of its simplicity and biological relevance. Thus, the complete ANOVA, with individual stability estimates and departure from linearity, can be computed (Eberhart and Russell, 1966). The deviation sums of squares are the sums of variance due to deviation from regression divided by (S-2), and subtracting pooled error mean square, where S stands for the number of locations for each variety. Varieties with a probability of F at near zero deviate significantly from linearity and thus for the given set of environments, have a less predictable response.

b$_i$ < 1	b$_i$ > 1
High Yield Stability	
s^{2}d$_i$ small	
Adapted to Low Yielding	**Adapted to High Yielding**
Environments	**Environments**
s^{2}d$_i$ large	
Low Yield Stability	
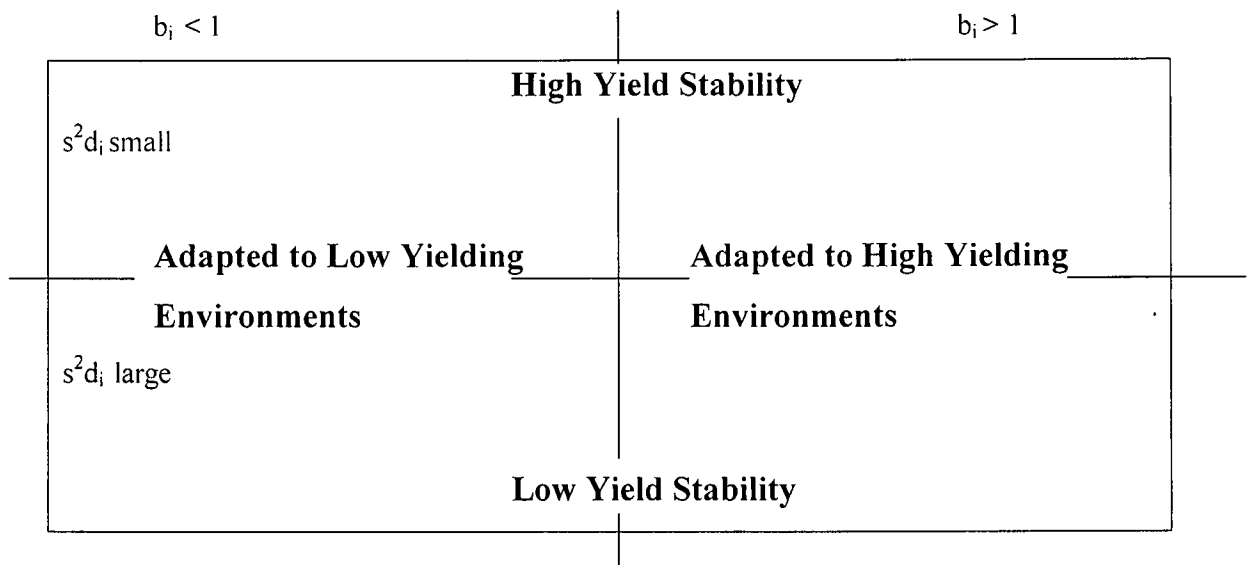
Figure 2.1. Interpretation of the parameters bi and s^{2}d$_i$ of the regression approach (Becker and Leon, 1988)

Coefficient of determination (r$_i^2$)

Pinthus (1973) proposed to use the coefficient of determination instead of deviation mean squares to estimate stability of genotypes, since both are strongly related to each other.

2.7.3.2. Non-parametric approach

This approach groups genotypes according to their similarity of response to a range of environments (Lin *et al.*, 1986). According to Huehn (1990), non-parametric method has the following advantages over the parametric stability statistics:

1. Reduction or avoidance of the bias caused by outliers.
2. No assumptions are needed about the distribution of the phenotypic values.
3. Stability parameters based on ranks are easy to use and to interpret.
4. Additions or deletions of one or few genotypes or another group of the material do not cause much variation of estimates unlike parametric one.

5. For many applications (e.g. selection in breeding and testing programme) the rank orders of the genotypes are the most essential information. Therefore, this method appears the appropriate method.

However, as suggested by Huehn (1990), for an efficient use of stability estimation techniques in practical applications, knowledge on the following aspect are essential: relations between different statistical measures of phenotypic stability (parametric and non-parametric); consistency of relationships among stability parameters; and repeatability of stability parameters. Lin *et al.* (1986) reported that the non-parametric or cluster method has two major sub-divisions, univariate and multivariate stability statistics. They further sub-divided univariate into four, viz. Euclidian distance, standardised distance, dissimilarity index and correlation coefficient. Likewise, the multivariate stability statistics was sub-divided into two, pattern distance and Frechtet distance.

According to Romagosa and Fox (1993), analysis of ranks (stratified ranking) evaluates the proportion of sites where any genotype ranks in the top, middle or bottom third of the entries. A genotype found in the top third of the entries across sites can be considered relatively well adapted. As indicated above, the advantages of non-parametric techniques include: freedom from assumptions concerning additivity of main effects, homogeneity of variances and linear response to increasing environmental yield potentials; insensitivity to error of measurements; and, measurements of adaptation are not unduly affected by genotypic performance in extreme environments. A genotype is considered stable if its ranking is relatively consistent across environments. Clustering environments or grouping genotypes is also possible. Similarly, Huehn (1990) has concluded the following from his investigations on non-parametric measures of stability.

➢ Corrected or transformed data should be used to perform analysis of phenotypic stability, if one wants to estimate the phenotypic stability independent from yield level effects.

➢ For quantitative estimation of phenotypic stability the non-parametric measure (mean rank difference) is preferable, as it is easy to calculate and interpret.

➢ If one is interested in a simultaneous consideration of both stability and yield the non-parametric stability parameter (sum of deviations) can be applied, measuring stability in units of yield by using the original non-corrected yield data.

2.7.3.3 Univariate stability statistics

Becker and Leon (1988) indicated that univariate stability statistics measure uncertainty in respective biometerical analysis. An overview of these most commonly used univariate stability parameters and their underlying stability concepts are presented in Table 2.7, as summarised by Becker and Leon (1988).

Table 2.7. Summary of univariate stability statistics (Becker and Leon, 1988)

Statistics	Symbol	Stability concept
Parametric:		
Environment variance	s^2_{xi}	static
Ecovalence	W_i	dynamic
Regression coefficient	b_i	static/dynamic
Deviation mean square	s^2_{di}	dynamic
Coefficient of determination	r^2_i	dynamic
Non-parametric:		
Mean rank difference	S1	dynamic
Variance of ranks	S2	dynamic

Univariate non-parametric stability statistics have been also proposed, based on rank orders of genotypes and do not need any assumptions about distribution of observed values or variance of homogeneity. These include the stability statistics such as mean rank difference and variance of ranks, which are based on corrected values (i.e. to make linear relationships). As mentioned in the above discussions, they provide a meaningful interpretation of results if ranks are based on corrected values. According to Becker and Leon (1988), they are distribution-free and no assumption on the distribution of values is necessary. As a result, they are said to be less sensitive to errors of measurements than the parametric statistics.

Rank differences (S1) and variances (S2) are non-parametric tests based on ranks of the genotypes across the locations. They give equal weight to each location or environment.

Genotypes with fewer changes in rank are expected to be more stable. The S1 estimates are all possible pair wise rank differences across locations for each genotype. The S1 estimates are simply the variances of the ranks for each genotype across locations (Nassar and Huehn, 1987; Huehn, 1990). For S1, entries may be tested as significantly less stable or more stable than the average stability/instability. For S2, smaller estimates may indicate relative stability. Often, S2 has less power for detecting stability than S1. S1 may lose power when genotypes are similar in their interactions with the environments.

2.7.3.4 Multivariate techniques of stability analysis

Multivariate techniques have been introduced for stability analysis, to provide further information on the real multivariate response of genotypes to environments. According to Becker and Leon (1988), multivariate analysis has three main purposes: to eliminate noise from data pattern, to summarise data and to reveal a structure in the data. Through multivariate analysis, genotypes with similar responses can be clustered, hypothesized and later tested, and their data can easily be summarised and analysed (Crossa, 1990; Purchase, 1997).

The multivariate methods include Multivarate Analysis of Variance (MNOVA), cluster analysis, principal component analysis, geometrical methods, stochastic dominance and methods using external information on environments or genotypes. These techniques may be applied to describe relationships among sites and among genotypes, using yield data from genotype by site matrices generated by breeding program. In clustering, the squared Euclidean distance is often used as a measure of dissimilarity. The output from cluster analysis is displayed as a dendrogram or hierarchical tree. Multivariate methods usually present most of the total variations in a few dimensions, in a dendrogram or scattergram.

Crossa (1990) has distinguished between two groups of multivariate techniques to explain the internal structure of G x E interaction: the ordination and the classification techniques. The ordination techniques include, methods such as principal component analysis, principal coordinates analysis and factor analysis, which assume data to be continuous. They represent data in a low-dimensional space, with similar genotypes and environments near each other,

and dissimilar items further apart. Ordination was reported (Purchase, 1997) to be effective in showing relationships and reducing noise. On the other hand, the classification techniques, like cluster analysis and discriminant analysis seek discontinuities in the data. These methods group similar entities in clusters and summarise redundancies of data effectively.

2.7.3.4.1 Principal Components and coordinates analyses

Principal component analysis (PCA) is one of the most frequently used multivariate techniques (Crossa, 1990; Purchase, 1997). It is used to transform the data from one set of coordinate axes to another, which preserves, as much as possible, the original configuration of the set of points and concentrates most of the data structure in the first principal components axis. Various limitations have been noted for this ordination technique. Crossa (1990) indicated that PCA is a generalisation of linear regression, but that it overcomes the problem of univariate analysis by giving more than one statistic to describe the response pattern of a genotype (Eisemann 1981; cited by Purchase, 1997). Principal coordinates analysis is the generalisation of principal components analysis in which any measure of similarity between individuals can be used. Its purposes and limitations are similar to that of PCA (Crossa, 1990; Purchase, 1997).

2.7.3.4.2 Additive Main Effects and Multiplicative Interaction (AMMI)

The AMMI model is a powerful analytical tool to interpret large genotype x environment x replicate tables without missing values (Crossa et al., 1990). AMMI extracts genotype and environment main effects, then uses Principal Component Analysis (PCA) to explain pattern in the G x E or residual matrix. Zobel et al. (1988) provided a scale for PCA scores, which allows estimation of specific G x E interaction terms. AMMI model combines analysis of variance for the genotype and environment main effects with principal component analysis of the G x E interactions. It has proven useful for understanding complex G x E interactions (Annicchiarico, 1997). The result can be graphed in a very informative biplot that shows both main and interaction effects for both genotypes and environments. It can also partition the data into a pattern-rich model and discard noise rich residual to gain accuracy.

The AMMI model for the average yield (Yge) over replicates of the g genotype in the e environment is:

$$Yge = m + ag + be + S \ln ggn \, den + Qge,$$

Where,

Yge   is the yield of genotype g in environment e;

m   is the grand mean;

ag   are the genotype mean deviations (the genotype means minus the grand mean);

be   are the environment mean deviations;

ln   is the eigenvalue of principal components analysis (PCA) axis n;

ggn and den   are the genotype and environment PCA scores for PCA axis n;

S   is the number of PCA axes retained in the model;

Qge   is the residual.

The AMMI model has been used successfully and extensively over the past few years to analyse and understand various G x E interactions (Gauch and Zobel, 1996; Annicchiarico, 1997; Purchase, 1997). Since AMMI has the biplot feature, genotypes and environments are plotted on the same diagram, facilitating inference about specific interactions of individual genotypes and environments by using the sign and magnitude of PCA1 values. Any genotype with a PCA1 value close to zero shows general adaptation to the tested environments. A large genotypic PCA1 scores reflects more specific adaptation to environments with PCA1 scores of the same sign. AMMI is proved to provide a more adequate biological explanation of G x E than the regression model and it has been found useful when applied to across year analyses with a higher element of unpredictability (Crossa *et al.*, 1990; Yau, 1995; Gauch and Zobel, 1996; Annicchiarico, 1997)

In almost all multi-location yield trials, breeders aim at developing or recommending superior genotypes, but the breeders are often encountered with two basic challenges: interaction and noise (Purchase, 1997). If there were no interactions, one variety would have been good enough all over the world and variety trials would have been conducted only at one location to provide universal results. If there was no noise, results would be exact and there would be no need for replications. But since the practical reality is quite different, two options are available to deal with these problems. The first one targets the genotypes while the second aims at the environment. The first option is to search for high-yielding and widely adapted cultivars that are successful across the growing localities of

interest. The second alternative is to sub-divide the target regions into several relatively homogenous macro-environments. Then, to develop and recommend suitable genotypes for specific regions.

Gauch and Zobel (1996) have noted that AMMI addresses well the challenges of interaction and noise, assisting the crop breeders in the investigation of the G x E interactions. In other words, the AMMI model is helpful in understanding the G x E interactions and in summarising patterns and relationships of genotypes and environments (Crossa, 1990; Purchase, 1997). In the initial analysis of variance, the total variation is partitioned into three sources, namely genotypes, environment and G x E interactions. In this regard, a review of Purchase (1997) revealed very interesting facts. In most yield trials, the proportion of sum of squares due to differences among sites ranged from 80 to 90 per cent and the variation due to G x E interactions is often larger than that of the genotypes. Hence, the AMMI model can produce biplot graphs, which display the variability of genotypes and G x E interactions.

The principal components analysis of AMMI partitions G x E interactions into several orthogonal axes, the interaction principal components analyses (IPCA). Gauch and Zobel (1996) stated that AMMI 1 with IPCA 1 and AMMI 2 with IPCA 1 and IPCA 2 are usually selected and the graphical representation of axes, either as IPCA 1 or IPCA 2 against main effects or IPCA 1 against IPCA 2 is generally informative. Nevertheless, AMMI 3 and higher models, and IPCA 3 and higher axes are generally dominated by noise; have no or little predictive value, no biological interpretability and can thus be discarded (Purchase, 1997). In summary, Gauch and Zobel (1996), Annicchiarico (1997) and Purchase (1997) have concluded that the AMMI model more accurately describes both G x E interaction and stability analysis by means of response patterns which can easily be shown from either the biplot of IPCA1 scores on IPCA2 scores. Consequently, the AMMI technique provides considerably more information in terms of both the stability measures and in describing responses and spatial patterns, classifying genotypic effects and having an inherent predictive value.

2.8. Recent studies of G x E interactions and stability analyses in linseed

A recent study undertaken on linseed regenerants at two locations in Ethiopia has shown that major changes in yield ranks or crossovers for four lines, implying their G x E interaction (Adugna and Adefris, 1995). The authors also reported that four regenerants showed relatively stable yield performance ranging from 1116 to 1143 kg ha^{-1} at both locations. In the same token, genotype x environment interaction of linseed was described (Rowland *et al.*, 1988a) along with environment-evoked heritable changes (genotroph) in some Canadian cultivars. Similarly, Green (1986b) displayed the significant genotype x temperature interaction for 1000 seed weight, oil content and fatty acid composition, indicating temperature-sensitive and stable genotypes of linseed in Australian cultivars.

Mostafa and Ashmawy (1998) evaluated eight genotypes of linseed at three locations in Egypt during the 1996 and 1997 seasons for 17 yield and quality characters. Their report showed that both location and genotype significantly affected straw and seed yields. According to these authors, one genotype (S.296/4) out-yielded the other genotypes in seed yield and its components while three varieties (Giza 7, Giza 8 and 402/I) were found stable across the test environments. Similar studies undertaken in India during the 1989 and 1991 indicated the presence of significant variability among the genotypes and environments (Mahto *et al.*, 1996). They reported the stability of three varieties for seed yield and on other three for days to maturity. Three other varieties were stable for *Fusarium oxysporum* f.sp. lini, while one was stable for blight damage environments, according to these authors. Furthermore, they indicated that one variety performed well under unfavorable conditions, whereas one other variety showed adaptability for most of the characters and environments.

Another study on genotype by environment interaction, stability and genetic diversity in linseed for yield and yield attributes under dryland situation of Birsa Agricultural University, India in 1989-1991 indicated significant G x E for branches/plant and highly significant for plant height, seeds/capsule and capsules/plant (Mahto, 1995). He also identified 12 genotypes on the basis of stability and genetic divergence for yield and yield attributes, while three varieties were found the most stable for most of the characters studied (Mahto *et al.*, 1995).

Mahto *et al.* (1996) studied stability and genetic divergence in linseed under rainfed situation. Their analysis of variance indicated the presence of significant variability among the genotypes for all characters. Of the 26 genotypes, 11 had above average stability and seven of these had high yields (Mahto *et al.*, 1996).

Mishra and Rai (1993) have studied genotype by environment interaction and stability parameters on seed yield and eight quality traits in 10 varieties of linseed and their 45 F_1 hybrids grown under four environments at Ajitmal and Kanpur in India. Stability was shown by T397 variety for seed yield/plant and oil content, R552 for protein content, R17 for palmitic acid content, and K2 for stearic acid content. They also indicated that hybrid T397 X LCK152 was stable for all the measured traits except stearic acid and oleic acid contents.

A study undertaken in Canada to explore the variation in total flavonoid content (antioxidant metabolite) at four locations showed that cultivar, environment and their interaction were highly significant (Oomah *et al.*, 1996). They found that the main effects, cultivar, location and year were dominant, indicating that the relative performance of a cultivar was highly dependent on the environment being considered. From the percentage variance components, environment (year x location) and cultivar accounted for 43% and 39% of the total variation, respectively. Although the between environment items in the analysis was significant, year and location did not account for any variation at all. The cultivar x location interaction showed no variation in total flavonoid content, suggesting that it played no part in the overall variability of total flavonoids in flax, according to Oomah *et al.* (1996).

2.9. Canonical variate and correlation analyses

According to Afifi and Clark (1996), canonical correlation analysis applies to conditions in which regression techniques are appropriate and where there exists more than one dependent variable. These authors indicated that it is especially useful when the dependent variables are moderately interconnected. Manly (1986) and Afifi and Clark (1996) described many good examples of canonical variate analyses and their applications. Similarly, De Lange (1999)

reported that canonical correlation analysis (CANCOR) is used to study linear combinations of two sets of variables, so that the linear combinations (canonical variates) will have maximal correlation. In this case, the best combination of variables could be identified, so that variability of interest, like quality parameters may be predicted for the required variation on site. In this respect, Graybosch *et al.* (1995) used a canonical correlation analysis to verify the degree to which a set of biochemical measurements was related to a set of quality measurements. They were also used to determine the particular components that have been responsible for these correlations.

Similarly, Osborne *et al.* (1993) used canonical variate analysis (linear discriminant analysis) in discriminating quality type breeding materials, where differences between groups were of more importance than that of individual breeding lines. Furthermore, Van Lill *et al.* (1995b) employed canonical variate analysis (CVA) to determine whether groups of variables differ from each other for wheat yield and quality attributes, and they reported good results. CVA is often applied when there is more interest in differences between groups that between individuals (Peterson *et al.*, 1992; Van Lill and Smith, 1997; De Lange, 1999). The variability in a large number of variates is first reduced to a smaller set of variates that account for most of the variability in the in the data set. Then the new sets of variates (canonical variates) are linear combinations of the original measurements. This approach helps to maximise variability between groups of genotypes. The canonical variate analysis, which is sometimes known as discriminant analysis is often used to classify individual genotypes into two or more alternative categories on the basis of a set of measurements. It is also used to identify the variable that contributed more in making the classification by the help of standardised coefficients (Afifi and Clark, 1996). In this discriminant analysis, one needs to know to which population or group the individual belongs to (i.e. dummy or indicator variables). If this is not known, then cluster analysis should be used. In the discriminant function, it is easier to interpret the first canonical variate than the subsequent ones. Moreover, a plot with two values is valuable to illustrate the maximum possible separation among the groups. The advantage of canonical procedure is that it helps to interpret the results when there are two or more groups. When the number of groups is greater than two the investigator may wish to examine the discrimination between the groups taken two at a time. This examination will serve to highlight specific differences between any two groups, and the results may be easier to interpret. Another possibility is to contrast each group with the remaining groups taken together.

CHAPTER 3

MATERIALS AND METHODS

3.1 Plant materials

Eleven entries including six regenerants, two crossed lines and three checks (Norlin, Chilalo and local) were studied (Table 3.1). The tissue culture derived regenerants were introduced from Canada to Ethiopia in 1990 at the R_6 and R_7 stages. The regenerants were originally derived from hypocotyl and callus of three linseed cultivars, namely McGregor, Norlin and Dufferin on modified MS culture medium (Murashige and Skoog, 1962) in the early 1980's at the Crop Development Centre, University of Saskatchewan, Canada (Adugna and Adefris, 1995; Rowland *et al.*, 1995).

Of the 40 regenerants that were initially introduced, those that were agronomically better than the local and standard checks in the preliminary variety evaluations were promoted to multi-location trials in 1995. These materials were also tested for wilt (*Fusarium* spp.) resistance in sick-plots at Holetta Research Centre and they were selected for their resistance or tolerance qualities (Adugna and Adefris, 1995). The regenerants were included in the multi-environment trials (METs) at and above R_{10} stages. The two crossed lines (P13611x10314/B and P13611X10314/D) were the result of crosses made between relatively well-adapted, high yielding and wilt tolerant genotypes at Holetta Research centre during the early 1980s. These parental genotypes were selected out of the collections made by the Plant Genetic Resources Centre of Ethiopia (now Biodiversity and Conservation Institute). The progeny lines were developed by the standard pedigree method. The local check was the cultivar of farmers, which has been under production at each location, while the standard cultivar (Chilalo) was one of the improved varieties released from Holetta centre. Table 3.1, gives a description of these tested materials.

Table 3.1. Description of the test materials, sources and stages at which they were included in the multi-environment trials.

No. Entries	Original source/ description	Stage
1. R11-M20G	Regenerant of McGregor variety from Canada	R11
2. R11-N1266	Regenerant of Norlin variety from Canada	R11
3. R10-N27G	Regenerant of Norlin variety from Canada	R10
4. P13611x10314/B	Cross between high-yielding and wilt resistant varieties	F12
5. R12-N10D	Regenerant from Norlin variety from Canada	R12
6. R12-D33C	Regenerant of Dufferin variety from Canada	R12
7. R12-D24C	Regenerant of Dufferin variety from Canada	R12
8. P13611x10314/D	Cross between high yielding and wilt resistant varieties	F12
9. NORLIN	Norlin (original variety as a check, not regenerant)	
10.CHILALO	Standard check from Holetta	
11.LOCAL CHECK	Farmers' cultivars per location	

3.2 Experimental sites

The experiment was executed at six rainfed locations of Ethiopia from 1996 to 1998. These locations are the principal variety testing sites for many highland crops including linseed. They are believed to represent the major crop growing agro-ecologies of Ethiopia in the highland areas. These localities are situated within the altitudinal ranges of 2200 to 2800 meters above sea level (Table 3.2). More elaborated description of these localities are given in Table 3.2. Holetta, the main testing center, represents the central highlands, while Kulumssa, Bekoji, Asasa and Sinana stand for the south-eastern linseed growing areas of Ethiopia in Oromia Regional State. Similarly, Adet represents the northwest part of the country, in the Amhara Regional State. As indicated in Table 3.2, the experimental locations vary a lot in their edaphic, climatic and biological (weeds, diseases, insects, etc.) and most of them have their own sub-centers for different trials.

Table 3.2. Description of the experimental sites and their overall agro-climatic conditions (Amsal *et al.*, 1997; Asefa *et al.*, 1997).

Trial sites	Altitude (meter)	Annual rainfall (mm)	Temperature (^{0}C) (Min.	Max.)	Soil conditions Classification	Texture
Holetta	2400	1086	8	22	eN	clay
Kulumssa	2200	824	10	25	intergrade*	clay-loam
Bekoji	2800	1000	6	18	eN	clay
Asasa	2360	665	7	23	eN	clay-loam
Adet	2240	1303	8	26	eN	clay
Sinana	2400	851	7	20	pV	clay

Note: eN=eutric Nitosol; pV=pellic vertisol; *=Intergrade between luvic Phaeozem and eutric Nitosol

3.3. Methods

3.3.1. Experimental layout

The experimental layout used was a randomised complete block design (RCBD) with four replications. The plot size was 5 m^2 (i.e. 5 rows 20 cm apart from one another and 5 meters long). The row markers prepared for these purposes were dragged over levelled plots to make the rows at a planting depth of about 2.5 centimetres at Holetta and with the help of marked sticks and strings at the other sites.

3.3.2. Cultural practices

The fields were ploughed by tractors usually from January to March and disc harrowed prior to planting time, which varied from early June at Adet to early July at Sinana depending on the onset of rain. The plots were well pulverised, levelled and made free of clogs and crop residues by manual labour right before planting.

The recommended fertilisers of both nitrogen (N) in the form of urea and phosphorus (P_2O_5) in the form of diammonium phosphate (DAP) were manually drilled and incorporated in the soil both at a rate of 23 kg ha^{-1} at planting. The seeds were also drilled by hand at a rate of 25 kg ha^{-1}. The seeds and fertilisers that were prepared for each plot were divided among the six rows per plot by using the spoons and experienced workers. The trials were sown between early June at Adet and in July at Sinana. Weeds were controlled by hand weeding about 2-3 times as required. Neither herbicides nor insecticides were used in all trials, as there was no need for them. The plots were separately harvested, dried for about 15 to 30 days, threshed and cleaned manually. Seed yield data were taken at about 8% seed moisture level and the plot yield was converted to kilogram per hectare.

3.3.3. Characters measured

Data on seed yield and agronomic traits were taken from the middle four rows of each plot, leaving aside the guard rows on both sides of the plots. Plant height was taken by measuring of five randomly selected plants from the ground level to the top of the plants taken at maturity stage. Days to flowering and maturity were separately recorded when each plot reached about 50% flowering and 75% maturity stages. The days were calculated beginning from the date of sowing. Scores for disease reactions were recorded from the inner four rows at a peak infection period (usually between flowering and maturity stages) for pasmo and powdery mildew on 0-5 point scale (0 = nil; 5 = severe). Fusarium wilt was scored in percentages by counting or estimating the number of infected plants. The same was done for lodging and stand counts at maturity time. These data of wilt, lodging and disease scores were transformed by the square root method before analysis of variance was performed. Oil content was determined by using the Nuclear Magnetic Resonance (NMR) spectrometer. The data of oil content were taken for sampled seeds of each variety over the four replications, instead of for each plot due to shortages of logistics. Subsequently, the oil yield, which was the product of oil content and seed yield, was estimated for the 11 entries. Then, combined analyses were performed using data across locations and years. Moreover, correlations among the yield,

oil content, and other agronomic characters were carried out to determine their associations.

3.3.4. Statistical analyses

The assembled yield and other agronomic data were subjected to statistical analyses using the MSTAT-C (MSTAT-C, 1991) and AGROBASE 98 (Agronomix Software, Inc., 1998) software computer programmes. Analysis of variance was undertaken first for the individual trials. Then combined analysis of variance was performed on the pooled data of the test environments. All the analyses for the stability models and AMMI were performed using AGROBASE 98, while joint linear regression and other similar analyses were computed by employing both software programmes. During the separate trial analysis, data of all the 11 tested entries were used but for the combined, stability and AMMI analyses only 10 entries were considered, as the local check (farmers' varieties) varied from location to location. AMMI's stability value (ASV) was calculated using the formula suggested by Purchase (1997) as shown below. The elaborated reviews of the relevant statistical methods for this study are given in the literature review part (cf. Chapter 2). Spearman's coefficient of rank correlation was computed for each pair of the possible pair-wise comparisons of the seven stability parameters by SAS computer software (SAS Institute, 1996).

$$ASV = \sqrt{\frac{SS\ IPCA1}{SS\ IPCA2} (IPCA1\ score)^2 + (IPCA2\ score)^2}$$

Where,

ASV = AMMI's stability value

SS = Sum of squares

IPCA = Interaction of principal component analysis

Similarly, canonical discriminant analysis was performed using the Statistical Analysis Systems (SAS Institute, 1996) for 11 variables to classify the genotypes and locations. For discriminant analysis of the genotypes, the averages of these 11 variables for each

variety per location (i.e. 60 observations with six classes or frequencies) were used. In the same manner, the averages of the same variates but for each location per year (i.e. 18 observations with three classes) were analysed. In addition, canonical correlation analysis was carried out by using the same SAS programme. However, more relevant data were obtained from the canonical discriminant analysis for this study and its intended purposes. The statistical analyses of variance were generally used to test the significance level of genotypes, locations and G x E interactions for the measured characteristics.

In short, the following statistical analyses were performed to test the significance levels of the measured traits of the entries, locations and their interactions by employing the following statistical procedures:

1. Separate trial analysis for each location and year,
2. Combined analyses across:
    - locations for each year
    - years for each location
    - locations and years

3. Stability analyses by using:
    - Joint regression model (Finlay and Wilkenson, 1963; Eberhart and Russell, 1966)
    - Ecovalence (Wricke, 1962)
    - Stability variance (Shukla, 1972)
    - Cultivar superiority (performance) measure (Lin and Binns, 1988)
    - Variance of ranks (Nassar and Huehn, 1987)

4. Additive Main Effects and Multiplicative Interaction (Zobel *et al.*, 1988)
5. Correlations between measured characters (Van Lill *et al.*, 1995b)
6. Canonical correlation and discririminant analyses (Afifi and Clark, 1996; Van Lill and Smith, 1997)

CHAPTER 4

RESULTS AND DISCUSSION

4.1 Separate analyses of trials

Cropping season of 1996

The separate analysis of variance for the year 1996 indicates highly significant (P<0.01) differences among the entries for seed yield, days to flowering and maturity, plant height, and powdery mildew disease (Table 4.1). However, percentages of lodging, stand count and pasmo were generally non-significant except at few localities, like Asasa and Sinana, where stand percentage and pasmo score were significant, respectively. In fact, there was no incidence of lodging at Sinana, Adet and Asasa during this season and the same was true for pasmo at Adet. In most cases, lodging is associated with high soil fertility, tall plant height, and heavy rainfall accompanied by stormy winds towards the maturity of the crop.

The total variance of seed yield was partitioned among its components and it is summarized in Table 4.1. The result showed that about 65-74% of the total variance was accounted for by genotypes at Asasa, Bekoji and Kulumsa localities. In contrast, 73-81% of the total variance was attributed to blocks at Adet and Holetta, indicating higher heterogeneity in environmental conditions of these testing sites. Hence, closer investigation is required to understand the environmental factors (soils, precipitation, temperature, diseases, etc.) that have major contributions to such variations for corrective measures in the future. As shown in Table 4.2, R10-N27G and Chilalo genotypes were the best yielders across the locations with an average yield of 1736 kg ha^{-1}. Similarly, the two other checks had a yield range of 1302-1599 kg ha^{-1}, the lowest being obtained from the local check. On the other hand, the two crossed lines gave a moderately good mean yield of 1456 kg ha^{-1}. However, four regenerants were found to out-yield these crossed lines, with the yield ranging from 1470 to 1570 kg ha^{-1}. Similarly, the two remaining regenerants (R12-D24C and R12-D33C) gave reasonably good yields, implying the better performance of the regenerants than the crossed lines during the 1996 season. In short, the yield performance of the entries was highly significant and R10-N27G was the top ranking regenerant across the six locations in 1996 (Table 4.2).

Table 4.1. Mean squares of the analysis of variance for eight characters and percent of variance components for yield of 11 linseed entries tested at six locations in Ethiopia, 1996

Location	Source	DF	DM	PH	LP	SP	PM	PS	SY	SY (%)
						Characters				
Bekoji	Block	0.69	3.66	96.93	2.51	1.58	0.38	2.79	24289.77	17.64
	Genotype	15.92**	54.22**	174.31**	0.64	1.62	1.61**	0.50	92463.47**	67.14
	Error	0.59	6.51	10.07	0.77	1.64	0.45	0.27	20964.15	15.22
	CV (%)	0.83	1.63	3.45	29.78	1.29	29.22	26.42	6.67	
Holetta-	Block	6.66	4.02	51.33	1.42	33.06	0.71	0.04	702911.54	73.02
	Genotype	17.46**	0.01*	120.81**	1.09	47.84	0.59**	0.86	176870.57*	18.38
	Error	3.38	3.42	15.68	1.33	31.48	0.16	0.22	82772.14	8.60
	CV (%)	2.21	1.27	5.67	39.82	7.69	32.22	20.01	21.56	
Sinana -	Block	0.52	2.58	11.78	0.0	16.52	0.42	0.02	101908.10	46.50
	Genotype	15.84**	57.56**	56.02	0.0	15.57	0.94**	0.61**	91485.09**	41.10
	Error	4.79	3.34	30.16	0.0	10.27	0.14	0.12	27383.31	12.40
	CV (%)	2.84	1.22	6.71	0.0	3.82	14.75	14.97	11.13	
Adet -	Block	2.121	13.66	54.73	0.0	13.67	0.57	0.0	747501.14	81.25
	Genotype	198.81**	161.41**	364.87**	0.0	16.01	1.14**	0.0	147230.26**	16.00
	Error	2.14	7.13	33.33	0.0	10.78	0.04	0.0	25256.66	2.75
	CV (%)	2.06	1.92	6.43	0.0	3.48	12.83	0.0	12.12	
Kulumsa-	Block	4.27	11.66	25.52	28.29	2.70	0.16	5.80	153833.90	14.57
	Genotype	69.02**	148.99**	83.42**	11.97	8.22	2.77**	0.95	778834.21**	73.78
	Error	1.14	6.54	7.98	8.27	13.44	0.45	0.74	122965.15	11.65
	CV (%)	1.65	1.96	2.76	39.72	3.75	22.76	35.72	22.93	
Asasa -	Block	6.73	11.42	204.39	0.0	68.18	0.75	7.43	37080.07	13.56
	Genotype	143.94**	226.94**	303.62**	0.0	301.82**	1.33**	2.19	179043.07**	65.45
	Error	3.51	12.32	32.34	0.0	98.18	0.20	1.02	57414.55	20.99
	CV (%)	2.78	2.96	6.52	0.0	15.57	28.47	23.08	17.99	

*, ** = Significantly different at 0.05 and 0.01 levels, respectively; 0 = nil or no incidence;

DF = Days to flowering; DM = Days to maturity; PH = Plant height; LP = Lodging percentage; SP = Stand percentage at maturity; PM = Powdery mildew score; PS = Pasmo disease score; SY = Seed yield; SY (%) = Seed yield percent out of total variance.

Table 4.2. Seed yield performance (kg ha^{-1}) of 11 genotypes of linseed varieties tested across six locations in Ethiopia, 1996

No. Genotype	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean	Rank
1. R11-M20G	2331 a	1564 a	1607 abc	1373 bc	1420 bcd	1127 ab	1570	4
2. R11-N1266	2251 ab	928 c	1336 cd	1219 cd	2120 a	1435 a	1548	6
3. R10-N27G	2325 a	1455 ab	1543 abc	1208 cd	2139 a	1615 ab	1714	2
4. P13611x10314B	2134 abc	1574 a	1223 d	1263 bcd	1138 cd	1489 ab	1470	7
5. R12-N10D	2189 abc	1342 abc	1458 bcd	1204 cd	1747 ab	1409 ab	1558	5
6. R12-D33C	2066 bcd	1020 bc	1377 bcd	1482 b	1291 bcd	1435 bc	1445	8
7. R12-D24C	2008 cd	1261 abc	1566 abc	1329 bc	1112 cd	1106 bc	1397	10
8. P13611x10314D	2186 abc	1325 abc	1376 bcd	1289 bcd	1279 bcd	1193 abc	1441	9
9. NORLIN	2185 abc	1314 abc	1491 abcd	1249 bc	2066 a	1291 a	1599	3
10. CHILALO	2362 a	1552 a	1636 ab	1778 a	1631 abc	1591 c	1758	1
11. LOCAL CHECK	1856 d	1342 abc	1741 a	1029 d	881 d	965 d	1302	11
Mean	2172	1334	1487	1311	1529	1332	1528	
SE	72.40	143.85	82.74	74.46	175.33	119.81		
CV %	6.67	21.56	11.13	12.12	22.93	17.99		

Values in columns followed by the same letter are not significantly different at 0.05 probability levels by Duncan's multiple range test.

Cropping season of 1997

The analysis of variance indicated highly significant difference (P<0.01) among the entries for most of the measured traits (Table 4.3). However, the seed yield was significant only at Kulumsa, Bekoji and Adet. In the same manner, the variance component of yield was maximum (72.5%) for the genotypes at Kulumsa, followed by that of Sinana (53.6%) and Bekoji (41.4%). The lowest level, 5-10% of variance component was accounted for by genotypes at Holetta and Asasa, where about 77-90% of the total variability was attributed to the block components. Similarly, the variance component of block was as high as 58% at Adet. These results indicate the substantial variations in environmental conditions of these sites that need further analysis, specifically that of Adet and Holetta testing sites. Westcott (1986) indicated that most of the efforts in series of yield trials are concentrated on measuring the genotypes, while little or none is devoted on measuring environments. Consequently,

detailed and more useful knowledge of G x E interaction is difficult to obtain. Thus more research is needed to analyse environmental (edaphic and climatic) data, to address the G x E interactions and stability studies as mentioned in the 1996 results.

The highest yield of 2059 kg ha^{-1} was recorded from the regenerant R12-D33C at Bekoji site, whereas the lowest (910 kg ha^{-1}) was obtained from R11-M20G at Asasa (Table4.5). Across the localities, however, Chilalo followed by R11-N1266 produced the highest yields of 1523 kg ha^{-1} and 1491 kg ha^{-1}, respectively. All in all, six entries yielded more than the grand mean yield of this season (1411 kg ha^{-1}). Except cultivar Chilalo, all of these entries were the regenerants and their good yield performance of the previous season was also repeated in 1997. All but regenerant R12-D24C showed better yield performance than NorLin (standard check for the regenerants). NorLin yielded 1400 kg ha^{-1} across the six localities.

Like the previous year, the yield variability among the entries was significant (P<0.05) at all sites except at Holetta and Asasa. Although yield variability was not statistically significant, yield difference between the highest and lowest entries was as high as 300 kg ha^{-1} at both localities. Similar to the 1996 data, the two crossed lines were lower in their yield performance than the regenerants and the grand mean, 1411 kg ha^{-1} (Table 4.4). As far as the location means are concerned, Bekoji ranked first with the mean yield of 1835 kg ha^{-1}, as it did during the 1996. The next good yield record was registered from Holetta and Adet within the range of 1419-1568 kg ha^{-1}. These results imply that Bekoji and most of these testing sites have relatively more favorable environments that could enable the exploitation of genetic variation among linseed genotypes and to develop cultivars based on their potentials. However, further studies are required on their detailed climatic and edaphic conditions as indicated in the above discussion. On the other hand, agronomic characters such as, days to flowering, maturity and powdery mildew were significantly (P<0.01) different between the entries as opposed to percentage of lodging, stand count and disease scores, which were generally non-significant except at few localities (Table 4.3), such as Holetta and Bekoji. In a nutshell, Chilalo followed by R11-N1266, R10-N27G and R10-N27G out-yielded the remaining genotypes in 1997.

Table 4.3. Mean squares of the analysis of variance for nine characters and percent of variance components for yield of 11 linseed entries tested at six locations in Ethiopia, 1997

Location	Source	Characters									
		DF	DM	PH	LP	SP	PM	PS	FW	SY	SY %
Bekoji	Block	4.75	50.08	53.18	0.0	16.67	2.42	0.52	0.0	38468	32.91
	Genotype	7.41*	74.36**	20.69	0.0	9.77	4.59**	2.69**	0.0	48400*	41.41
	Error	2.78	7.10	20.72	0.0	12.50	0.79	0.18	0.0	30028	25.68
	CV (%)	1.85	1.66	5.76	0.0	3.63	37.98	14.67	0.0	9.44	
Holetta -	Block	9.11	30.58	211.15	2.273	124.63	0.72	0.45	6.27	498960	89.61
	Genotype	40.57**	105.49**	175.94**	1.02	45.16**	0.57	0.48**	2.84	29075	5.20
	Error	3.06	3.42	34.07	1.02	10.38	0.27	0.10	2.69	28789	5.17
	CV (%)	2.40	2.27	6.05	30.97	3.56	29.36	30.67	15.86	10.82	
Sinana -	Block	1.55	3.49	13.66	964.75	55.30	0.08	0.21	0.0	35998	8.75
	Genotype	61.81**	89.12**	65.26**	1033.25	48.07	1.49**	0.52	0.0	220586	53.59
	Error	0.83	1.79	12.01	754.92	69.89	0.20	0.29	0.0	155014	37.66
	CV (%)	1.24	0.93	3.27	26.54	9.97	19.48	15.84	0.0	30.21	
Adet -	Block	35.42	94.08	24.75	29.27	63.30	1.55	2.84	0.41	44152	58.22
	Genotype	59.35**	222.52**	37.67	41.42	6.64	0.36	0.86	1.91**	72277*	29.19
	Error	12.28	25.92	18.20	71.09	15.19	0.19	0.61	0.16	31165	12.59
	CV (%)	2.06	3.90	4.88	14.22	4.48	19.42	13.56	23.02	12.44	
Kulumsa -	Block	3.17	30.66	57.52	234.33	5.18	0.31	11.16	208.33	24253	10.47
	Genotype	25.92**	111.97**	49.02**	504.05	5.21	1.77**	1.10	116.82	167993**	72.5
	Error	0.99	7.21	7.99	432.43	2.73	0.16	0.54	155.00	39352	16.99
	CV (%)	1.53	2.21	3.17	34.37	1.66	10.78	32.73	24.46	16.00	
Asasa -	Block	2.45	77.11	33.78	294.06	15.66	0.73	1.55	44.69	98133	77.16
	Genotype	42.12**	38.04	23.31	226.34	13.16	0.31	0.26	149.09	80756	10.42
	Error	2.13	22.32	15.31	218.78	15.71	0.40	0.25	116.36	96277	12.42
	CV (%)	2.09	7.25	4.13	25.98	4.06	17.95	20.71	15.11	20.14	

*, ** Significantly different at 0.05 and 0.01 levels, respectively; 0.0 = nil; DF = Days to flowering; DM = Days to maturity; PH = Plant height; LP = Lodging percentage; SP = Stand percentage; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; SY = Seed yield; SY (%) = Seed yield percent out of total variance.

Table 4.4. Seed yield performance (kg ha^{-1}) of 11 genotypes of linseed varieties tested across six locations in Ethiopia, 1997

No. Genotype	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean	Rank
1. R11-M20G	1945 ab	1635 a	1331 ab	1344 bc	1602 a	910 a	1461	4
2. R11-N1266	1831 ab	1608 a	1703 a	1243 c	1297 ab	1265 a	1491	2
3. R10-N27G	1808 ab	1658 a	1466 ab	1407 abc	1043 b	1390 a	1462	3
4. P13611x10314B	1741 b	1543 a	1083 ab	1344 bc	1265 b	1042 a	1336	9
5. R12-N10D	1902 ab	1599 a	1433 ab	1244 c	1215 b	1189 a	1430	6
6. R12-D33C	2059 a	1480 a	1539 ab	1424 abc	1046 b	1126 a	1446	5
7. R12-D24C	1799 ab	1534 a	1038 b	1547 ab	984 b	1014 a	1319	10
8. P13611x10314D	1711 b	1609 a	1143 ab	1365 bc	1302 ab	1141 a	1378	8
9. NORLIN	1672 b	1524 a	1369 ab	1509 abc	1233 b	1094 a	1400	7
10. CHILALO	1868 ab	1670 a	1306 ab	1692 a	1576 a	1026 a	1523	1
11. LOCAL CHECK	1848 ab	1384 a	925 b	1494 abc	1079 b	933 a	1277	11
Mean	1835	1568	1303	1419	1240	1103	1411	
SE	86.64	84.84	196.86	88.27	99.19	155.14		
CV %	9.44	10.82	30.21	16.00	28.14	18.75		

Values in columns followed by the same letter are not significantly different at 0.05 probability levels by Duncan's multiple range test.

Cropping season of 1998

As shown in Table 4.5, the analysis of variance this year also indicated highly significant differences (P<0.01) among the entries for most of the observed traits. The seed yield was significantly different at Bekoji, Holetta, Sinana and Kulumsa. Similarly, the variance component of yield was the highest (65.34%) for the genotypes at Bekoji, followed by that of Asasa and Holetta ranging from 40-43%. On the other hand, about 60-92% of the total variability was attributed to block effects at Sinana, Kulumsa and Adet. These results again indicate the substantial variations in environmental conditions that need detail analysis as stated in the preceding discussion.

The overall yield performance of the 1998 season was very low compared to the previous two seasons (Table 4.6). The grand mean yield was 1150 kg ha^{-1} and it was lower by about 25% than that of 1996. The main reason for this yield decline was poor rainfall distributions encountered during the growing season, especially scarcity of rainfall towards the seed filling stages. Across the locations, however, regenerant R11-M20G ranked first, with a mean yield of 1270 kg ha^{-1} as opposed to P13611x10314B that ranked the lowest (1071 kg ha^{-1}). Generally, seven entries outperformed the grand mean yield (1150 kg ha^{-1}) of which, five were the regenerants, indicating their good performance and adaptability to these test environments.

In contrast to the previous years, the highest location mean yield was registered at Asasa, followed by that of Bekoji, Adet and Kulumsa in this order. Nevertheless, the yield difference among the genotypes was not significant at Asasa unlike at the remaining five localities. Of the 11 tested entries, two regenerants, R11-M20G and R11-N1266 ranked first at Bekoji and Asasa, respectively.

Table 4.8 presents the percentage of variance components for seed yield across six locations during the three years of 1996 and 1998. Much of the variation was accounted for by the blocks, especially at Holetta, Sinana and Adet, indicating the large variability of environmental conditions that needs close follow ups and studies as mentioned in the above discussion. On the other hand, the genotypes had a higher share of the variance component at Bekoji, Kulumsa and Asasa, indicating the suitability of these sites for testing and growing linseed genotypes despite poor distribution of rain in these areas, especially at Asasa where it has been unreliable. In fact, the rainfall distribution during the years of 1997 and 1998 was quite divergent and irregular due to *El Nino* event, unusual oscillation of the tropical Pacific Ocean and the tropical atmosphere on inter-annual time scales (Latif *et al.*, 1997). Adugna *et al.* (1997) assessed the total failure of pulses and oil crops including linseed and the loss was estimated to be 23% in Northwest part of Ethiopia in 1997/98 season.

When an average of the three years is taken into account, about 45% of the total variance was accounted for blocks, while about 39% was attributed to the genotypes and the remaining 16% was for the error variance (Table 4.8). In a nutshell, most of the important source of variation was found to be the environments. This suggests the wide and divergent responses

of the varieties to their environments that could confound the effects of selection unless stability analysis is not undertaken.

With respect to the location mean, the highest seed yield of 2172 kg ha^{-1} was obtained from Bekoji followed by that of Kulumsa (1529 kg ha^{-1}). Only these two sites were found to produce greater than the overall mean yield of 1528 kg ha^{-1}. In general, there was a wide range of seed yield from 620 kg ha^{-1} in 1998 to 2362 kg ha^{-1} in 1996 (i.e. both were recorded from Bekoji), indicating tremendous variations over seasons.

Across the localities, however, Chilalo (standard cultivar) stood first with a mean yield of 1505 kg ha^{-1} over the three years. The next better performing entries were three regenerants, namely R11-M20G, R10-N27G and R11-N1266, yielding within a range of 1414-1455 kg ha^{-1} as indicated in Table 4.7. These performances once again showed the high yielding and good adaptability of these regenerants to the linseed growing environments of Ethiopia although they were out-yielded by the standard variety. Adugna and Adefris (1995) have also reported similar results of linseed regenerants at a relatively cool and wet agro-climatic condition of Holetta and warm and dry areas of Dembi or Debre Zeit.

Table 4.5. Mean squares of the analysis of variance for eight characters and percent of variance components for yield of 11 linseed entries tested at six locations in Ethiopia, 1998

						Characters				
Location	Source	DF	DM	PH	LP	SP	PM	PS	SY	SY (%)
Bekoji	Block	14.63	5.64	53.27	171.90	19.72	0.0	0.40	107014.92	17.01
	Genotype	17.21**	23.11**	25.89*	969.90**	10.57	0.0	0.65**	411041.59**	65.34
	Error	2.30	6.15	8.89	177.92	15.99	0.0	0.18	111013.98	17.65
	CV (%)	1.67	1.38	3.34	15.29	4.11	0.0	24.94	20.66	
Holetta -	Block	2.39	4.18	91.66	0.0	86.36	0.40	0.93	67633.48	45.38
	Genotype	30.92**	52.46**	133.54**	0.0	48.52	0.43	1.15**	59601.90*	40.00
	Error	2.14	2.62	30.43	0.0	30.95	0.20	0.32	21820.35	14.62
	CV (%)	1.84	1.67	6.18	0.0	7.65	27.44	21.65	16.58	
Sinana -	Block	1.61	6.75	58.00	0.0	37.88	1.70	0.21	839991.43	92.00
	Genotype	27.21**	5.19	67.21	0.0	70.46*	1.01**	0.61*	51134.63*	5.60
	Error	4.52	4.37	30.82	0.0	26.21	0.28	0.27	21947.89	2.40
	CV (%)	2.84	1.46	5.98	0.0	6.15	25.32	17.76	14.71	
Adet -	Block	7.48	21.91	162.93	0.0	24.45	0.0	0.0	16423.11	59.96
	Genotype	65.81**	51.41**	243.46*	0.0	18.96	0.0	0.0	49769.63	25.63
	Error	4.14	4.33	88.98	0.0	53.86	0.0	0.0	27983.84	14.41
	CV (%)	2.93	1.65	10.59	0.0	8.03	0.0	0.0	14.13	
Kulumsa-	Block	10.33	23.90	12.63	2467.82	7.54	0.38	0.62	242263.26	59.56
	Genotype	44.77**	69.24**	52.66*	1752.91**	4.14	5.40**	1.59**	120807.22*	29.70
	Error	2.14	6.54	8.38	579.30	4.17	0.43	0.28	43708.88	10.74
	CV (%)	2.19	3.84	3.01	32.93	2.07	21.40	26.24	19.78	
Asasa -	Block	1.05	2.81	15.54	2.33	109.30	1.20	0.11	23789.02	6.17
	Genotype	26.59**	84.16**	57.72	3.02	319.11*	2.11*	0.99	166280.11	43.14
	Error	1.00	12.09	37.84	4.67	112.96	0.74	0.47	195346.10	50.69
	CV (%)	1.39	2.77	7.24	19.10	13.74	23.09	33.01	29.29	

*, ** Significantly different at 0.05 and 0.01 levels, respectively; 0 = nil; DF = Days to flowering; DM = Days to maturity; PH = Plant height; LP = Lodging percentage; SP = Stand percentage; PM = Powdery mildew score; PS = Pasmo disease score; SY = Seed yield; SY (%) = Seed yield percent out of total variance

Table 4.6. Seed yield performance (kg ha^{-1}) of 11 genotypes of linseed varieties tested across six locations in Ethiopia, 1998.

No. Genotype	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean	Rank
1. R11-M20G	1819 a	931 b	1091 abc	1381 a	806 c	1589 a	1270	1
2. R11-N1266	1362 abc	841 b	975 abcd	1103 ab	1282 a	1663 a	1204	4
3. R10-N27G	1085 bcd	818 b	1011 abcd	1134 ab	1236 ab	1846 a	1188	5
4. P13611x10314B	1562 ab	822 b	828 d	1126 ab	778 c	1309 a	1071	8
5. R12-N10D	1252 bc	871 b	1031 abcd	1214 ab	1151 ab	1484 a	1167	7
6. R12-D33C	984 cd	768 b	850 cd	1249 ab	903 bc	1393 a	1024	11
7. R12-D24C	620 ab	1204 a	881 bcd	1213 ab	1070 abc	1168 a	1026	10
8. P13611x10314D	1338 abc	989 b	1052 abcd	1153 ab	1172 ab	1641 a	1224	3
9. NORLIN	1181 bc	810 b	1118 ab	1056 b	1219 ab	1718 a	1184	6
10. CHILALO	1479 abc	924 b	1177 a	1355 a	981 abc	1481 a	1233	2
11. LOCAL CHECK	1067 bcd	825 b	1064 abcd	1040 b	1031 abc	1310 a	1056	9
Mean	1250	891	1007	1184	1057	1509	1150	
SE	166.59	73.86	74.07	104.53	220.99	221.00		
CV %	20.66	16.60	14.70	14.10	19.80	29.29		

Values in columns followed by the same letter are not significantly different at 0.05 probability levels by Duncan's multiple range test.

Table 4.7. Mean seed yield performance (kg ha^{-1}) of 11 genotypes of linseed varieties tested across six locations in Ethiopia, 1996-98.

No. Genotype	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean	Rank
1. R11-M20G	2032	1377	1343	1366	1276	1209	1434	3
2. R11-N1266	1815	1126	1338	1188	1566	1454	1414	4
3. R10-N27G	1739	1311	1340	1250	1473	1617	1455	2
4. P13611x10314B	1812	1313	1044	1245	1060	1280	1293	9
5. R12-N10D	1781	1271	1308	1221	1371	1318	1385	6
6. R12-D33C	1703	1089	1256	1385	1079	1096	1305	8
7. R12-D24C	1476	1333	1162	1363	1056	1096	1247	10
8. P13611x10314D	1745	1308	1190	1269	1251	1325	1348	7
9. NORLIN	1679	1216	1190	1271	1506	1368	1394	5
10. CHILALO	1903	1382	1326	1609	1396	1366	1505	1
11. LOCAL CHECK	1590	1184	1244	1188	997	1069	1212	11
Mean	1752	1264	1266	1205	1277	1315	1363	
LSD 0.05	157.67	143.05	177.07	113.82	177.81	231.43		
SED	94.89	86.07	106.54	68.48	106.99	139.25		
CV (%)	13.26	16.67	20.62	12.86	20.54	25.94		
Repeatability	0.8382	0.8082	0.6566	0.7325	0.7326	0.4859		

Table 4.8. Percentage of variance components (out of total) for seed yield of 11 linseed entries tested over six locations in Ethiopia from 1996 to 1998.

Location	Source	Years 1996	1997	1998	Mean
Bekoji	Block	17.64	32.91	17.01	22.52
	Genotype	67.14	41.41	65.34	57.96
	Error	15.22	25.68	17.65	19.52
	Total	100.00	100.00	100.00	100.00
	CV (%)	6.67	9.44	20.66	
Holetta	Block	73.05	89.61	45.38	69.35
	Genotype	18.35	5.2	40.00	21.19
	Error	8.60	5.17	14.62	9.46
	Total	100.00	100.00	100.00	100.00
	CV (%)	21.56	10.82	16.58	
Sinana	Block	46.62	8.75	92.00	49.12
	Genotype	41.10	53.59	5.60	33.43
	Error	12.40	37.66	2.40	17.45
	Total	100.00	100.00	100.00	100.00
	CV (%)	11.13	30.21	14.71	
Adet	Block	81.25	58.22	59.96	66.48
	Genotype	16.00	29.19	25.63	23.61
	Error	2.75	12.59	14.41	9.92
	Total	100.00	100.00	100.00	100.00
	CV (%)	12.12	12.44	14.13	
Kulumsa	Block	14.57	10.47	59.56	28.20
	Genotype	73.78	72.54	29.70	58.67
	Error	11.65	16.99	10.74	13.13
	Total	100.00	100.00	100.00	100.00
	CV (%)	22.93	16.00	19.78	
Asasa	Block	13.56	77.16	6.17	32.30
	Genotype	65.45	10.42	43.14	39.67
	Error	20.99	12.42	50.69	28.03
	Total	100.00	100.00	100.00	100.00
	CV (%)	17.99	20.14	29.29	
Overall Mean	Block	41.10	46.18	46.68	44.65
	Genotype	46.97	35.40	34.90	39.09
	Error	11.93	18.42	18.42	16.26
	Total	100.00	100.00	100.00	100.00

4.2 Combined analysis of variance across locations

The combined analysis of variance, which was carried out across the six locations for separate year shows highly significant (P<0.01) differences among locations (L), genotypes (G) and L x G interactions for most of the measured traits (Table 4.9). This indicates that there were large differential responses of the entries to the test environments of the six localities for nearly all nine characters under consideration. Nevertheless, Fusarium wilt and stand percentage had lower L x G interactions, when compared with the remaining parameters. The stand count percentage was one of the expected parameters to be consistent across the localities as the same seed rates were used throughout the localities and years from the same seed source of Holetta Research Centre. The possible factors, which may have influenced the stand percentage and other measured traits could be intensities of diseases, rainfall, temperature (Appendices 5-8), and soil related conditions, like soil fertility levels and difference in soil moisture regimes that are caused by poor land levelling.

As presented in Table 4.10 much of the variance components were attributed to the locations, ranging from 76.64 to 84.62% over the three years. Higher variability was realised in 1996 and 1997 than in 1998. The variability accounted for the genotypes was in the range of 3.42-6.96%, with the mean of 5.56%. Similarly, the average genotypic effect (heritability) of the three years was as low as 32.5%. These situations clearly show the high variability in environmental conditions, which complicates the variety selection process and thus necessity of G x E and stability analysis. Under such conditions, the use of AMMI analysis is suggested (Annicchiarico and Perenzin, 1994) to identify major environmental and genotypic factors related to the occurrence of G x L interaction, thereby to support the breeding programme in deciding adaptation areas, choice of varieties and adaptive traits. Zobel et al. (1988) reported that AMMI provides a more appropriate first statistical analysis of yield trials that may have high G x E interaction. Similarly, Abamu and Alluri (1998) indicated that the AMMI offered them a different and useful approach for interpreting the G x E interaction in lowland rice of Nigeria.

As shown in Table 4.10, the mean yield variance component for G x L interaction was 3.96% and it ranged from 3.08% in 1997 to 5.44% in 1998. It was significant (P<0.05) over the three years (Table 4.10). The variance component for locality was found to dominate the other components for seed yield, indicating the existence of large variability among the testing sites.

Among the tested entries, Chilalo significantly ($P<0.05$) out-yielded the other genotypes during the first two years, whereas R11-M20G did the same during the third year of 1998 (Table 4.8). Regarding the average yield across years, Chilalo ranked first, with an average yield of 1505 kg ha^{-1}. The next good yielders were the regenerants (R10-N27G and R11-M20G, with the mean yields of 1455 and 1434 kg ha^{-1}, respectively. In contrast, the crossed lines stood 7th and 9th in the yield ranks. Generally, there were substantial differences in yield among the tested entries across locations during the three years. There were also changes in ranks of the entries from location to location, indicating the G x L interactions.

Table 4.9. Mean squares of the combined analysis of variance for nine characters of 10 linseed entries tested over six locations in Ethiopia, 1996-1998.

		Characters								
Year	Source	DF	DM	PH	LP	SP	PM	PS	FW	SY
1996	Location (5)	4755.9**	8163.9**	4760.11**	12363**	7754.8**	28.27**	34.46**	735.00**	4491077.16**
	R(location(18)	12.20	13.49	143.74	634.10	144.50	0.42	3.10	118.79	286142.72
	Genotype (9)	101.52**	364.21**	230.00**	125.96**	30.61**	2.95**	1.62**	20.19	336119.14**
	LxG (45)	15.26**	26.81**	26.31**	190.14**	29.63**	0.72**	0.50**	20.19	180363.39**
	Residue (162)	2.76	7.02	22.14	16.68	27.25	0.25	0.41	28.21	49640.95
	CV (%)	2.21	1.90	5.31	13.88	6.08	25.90	35.53	30.35	14.37
1997	Location (5)	3115.71**	10456**	3439.51**	11144.4**	1634**	44.82**	47.47**	488.95**	2574366.92**
	Error (18)	65.43	113.84	168.19	2333.84	47.44	0.98	2.54	40.10	206499.23
	Genotype (9)	120.04**	451.81**	57.73**	439.82**	7.50	3.43**	1.75**	21.95	103926.22*
	LxG (45)	23.85**	47.15**	26.95**	303.11**	23.18	1.3**	0.90**	66.87	93596.45*
	Error (162)	3.75	20.83	16.64	24.97	21.74	0.34	0.35	4.85	63751.80
	CV (%)	2.64	3.4	4.40	11.38	5.03	28.71	31.03	18.23	17.72
1998	Location (5)	3550.4**	20981**	488.70	68378**	4706**	56.47**	46.59**	193.7**	2027048.69**
	Error (18)	6.24	11.90	83.31	297.77	117.18	0.47	0.32	3.89	219348.63
	Genotype (9)	151.37**	244.07**	54.93	588.33**	91.21	3.57**	2.65**	12.22**	184272.52**
	LxG (45)	7.18**	13.34**	50.23	473.87**	82.80*	1.14**	0.48*	14.22**	143963.92*
	Error (162)	2.84	5.56	34.33	122.13	38.13	0.27	0.24	5.68	70354.78
	CV (%)	2.22	1.67	6.44	31.16	7.12	37.76	28.6	30.171	22.89

*, ** Significantly different at 0.05 and 0.01 levels, respectively. Numbers in parenthesis stand for the respective degrees of freedom. DF = Days to flowering; DM = Days to maturity; PH = Plant height; LP = Lodging percentage; SP = Stand percentage; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; SY = Seed yield

Table 4.10. Percent (out of total) of variance components for combined analysis of variance (L x G) for seed yield of 10 linseed entries tested across six locations in Ethiopia, 1996-98.

Source	df	Year 1996	1997	1998	Mean
Location	5	84.05	84.62	76.64	81.77
Reps. in location	18	5.36	6.78	8.30	6.81
Genotype	9	6.30	3.42	6.96	5.56
L x G	45	3.35	3.08	5.44	3.96
Residual	162	0.94	2.10	2.66	1.90
Total	239	100.00	100.00	100.00	100.00
CV (%)		14.37	17.72	22.88	18.32
LSD 0.05 for entry		106.40	120.58	126.67	117.88
SE		64.32	72.89	76.57	71.26
Repeatability		0.8281	0.6779	0.6610	0.7223
Heritability		0.443	0.272	0.261	0.325

Table 4.11. Mean yield (kg ha^{-1}) of 10 linseed genotypes tested at six locations in Ethiopia, 1996-98.

		Years			
No. Genotypes	1996	1997	1998	Mean	Rank
1. R11-M20G	1570 d	1461 c	1270 a	1434	3
2. R11-N1266	1548 f	1491 b	1204 d	1414	4
3. R10-N27G	1714 b	1462 c	1188 e	1455	2
4. P13611x10314B	1470 g	1336 h	1071 h	1293	9
5. R12-N10D	1558 e	1430 e	1167 g	1385	6
6. R12-D33C	1445 h	1446 d	1024 k	1305	8
7. R12-D24C	1397 j	1319 i	1026 j	1247	10
8. P13611x10314D	1441 i	1378 g	1224 c	1348	7
9. NORLIN	1599 c	1400 f	1184 f	1394	5
10. CHILALO	1758 a	1523 a	1233 b	1505	1
Mean	1550	1425	1159	1378	
SE	84.59	51.54	54.14		
CV %	14.37	17.72	22.89		

Values in columns followed by the same letter are not significantly different at 0.05 probability levels by Duncan's multiple range test.

4.3 Combined analyses of seed yield across years

Table 4.12 presents the combined analysis of variance and the percentage of these variance components for the seed yields over the three years per location. This combined analysis showed highly significant (P<0.01) differences for years (Y), genotypes (G) and their interactions at Bekoji, Holetta and Kulumsa. However, at Sinana, Adet and Asasa, the Y x G interactions were not significant, indicating more yield stability across the three years at these latter sites than the former ones (i.e. Bekoji, Holetta and Kulumsa). The largest portion of the variance components was accounted for the years or growing seasons. This variability ranged from 50% at Adet to 94% at Bekoji and heritability was also very low for the latter site as the effect of genotype was very small. This large seasonal variability may have been due mainly to the amount and distribution effects of rainfall (Appendices 5-8) among other factors.

The variance due to entries out of the total was in the range of 2.2-19%, the lower limit being recorded at Holetta, while the higher one was for the Adet site (Table 4.12). Likewise, the component of variance for the Y x G interaction was also small (1.4-6.1%); however, it was highly significant (P<0.01) at Bekoji, Holetta, and Kulumsa, suggesting the fluctuations of genotypes across years at these localities. Repeatability of the trials at Bekoji and Holetta was about 85% against the lowest of Asasa (48%). This low repeatability again implies the high level of environmental variation. Similarly, heritability was relatively higher at Holetta followed by that of Adet and Kulumsa as shown in Table 4.9.

The mean seed yield performance of the genotypes at the six locations over the three years is given in Table 4.13. The highest location mean yield of 1769 kg ha^{-1} was obtained from Bekoji, while the remaining five sites yielded in the range of 1268-1339 kg ha^{-1}. At Bekoji, regenerant R11-M20G (2032 kg ha^{-1}) exceeded the other varieties and it was also the most stable at this site as it had relatively the smallest coefficient variability (Francis and Kannenberg, 1978; Lin et al., 1986). In the same manner, R11-N1266 and R10-N27G were the top ranking at Kulumsa and Asasa respectively, whereas Chilalo out-yielded the other entries at Holetta, Sinana and Adet. Further details of yield performance along its coefficient of variation for each locality over the three years are summarised in Table 4.13.

The analysis of variance was found highly significant (P<0.01) for years, genotypes and their interactions at most locations. However, the Y x G interactions was not significant at Sinana,

Adet and Asasa, suggesting their stability over years. The mean yield over three years for each location along with the coefficients of variance was summarised in Table 4.13. At Bekoji, R11-M20G (2032 kg ha^{-1}) exceeded the other varieties followed by Chilalo (1903 kg ha^{-1}) and similar result was obtained at Holetta as well. At Adet and Sinana Chilalo performed very well.

Table 4.12. Mean squares (10^{-3}) of the combined analysis of variance for yield (kg ha^{-1}) of 10 linseed entries tested over three years at six locations in Ethiopia

Source	df	Bekoji	%	Holetta	%	Sinana	%	Adet	%	Kulumsa	%	Asasa	%
Year	2	8879**	94.5	4848**	87	2277**	80	471**	50	3817**	78.7	1704**	72.4
Reps. in year	9	64	0.7	485	8.7	297	10	242	25	175	3.6	229	9.6
Entries	9	255**	2.7	119**	2.2	132*	4.6	179**	19	508**	10.5	230*	9.8
Y x E	18	147**	1.6	79**	1.4	84	3.0	34	3.6	297**	6.1	72	3.1
Residual	81	51	0.5	37	0.7	69	2.4	23	2.4	53	1.1	120	5.1
Total	119	9395		5567		2859		949		4850		2355	
CV (%)		12.79		15.09		20.71		11.58		18.48		25.91	
LSD0.05		153.67		130.42		178.43		103.58		134.61		235.71	
SE		92.36		78.38		107.24		62.25		81.21		141.67	
Repeatability		0.8488		0.8472		0.6400		0.7395		0.7497		0.4752	
Heritability		0.078		0.802		0.525		0.758		0.435		0.230	

*, ** = Significantly different at 0.05 and 0.01 levels, respectively

Table 4.13. Mean yield (kg ha^{-1}), rank and CV (%) of 10 linseed entries tested over three years at six locations in Ethiopia, 1996-98

No. Entries	Bekoji			Holetta			Sinana			Adet			Kulumsa			Asasa		
	Yield	Rank	CV	Yield	Rank	CV	Yield	Rank	CV	Yield	Rank	CV	Yield	Rank	CV	Yield	Rank	CV
1. R11-M20G	2032	1	15.1	1377	2	29.2	1343	2	28.9	1366	3	10.8	1159	7	39.5	1209	9	41.7
2. R11-N1266	1815	3	22.3	1126	9	35.9	1338	4	26.5	1188	10	14.4	1495	1	26.9	1454	2	19.4
3. R10-N27G	1739	7	33.2	1311	5	35.4	1340	3	25.1	1250	7	15.9	1414	3	36.8	1617	1	25.8
4. P13611X10314b	1812	4	16.3	1313	4	36.4	1044	10	25.4	1245	8	13.9	990	10	23.8	1280	8	33.0
5. R12-N10D	1781	5	24.6	1271	7	33.0	1308	6	21.8	1220	9	18.9	1316	4	26.6	1361	5	17.6
6. R12-D33C	1703	8	32.5	1089	10	31.6	1256	7	34.0	1385	2	10.7	1036	9	35.4	1318	7	29.8
7. R12-D24C	1476	10	44.2	1333	3	20.8	1162	9	34.6	1363	4	20.0	1059	8	21.2	1096	10	22.5
8. P13611X10314d	1745	6	26.6	1308	6	28.7	1190	8	32.2	1269	6	14.5	1231	6	22.3	1325	6	39.6
9. NORLIN	1679	9	26.9	1216	8	29.6	1326	5	25.9	1271	5	24.3	1435	2	28.0	1368	3	30.1
10. CHILALO	1903	2	26.7	1382	1	37.5	1373	1	28.5	1609	1	20.7	1292	5	30.3	1366	4	22.9
Mean	1769			1273			1268			1317			1243			1339		

4.4 Combined analysis across locations and years

A better understanding of the relative contribution of cultivars, environment and their interaction as a source of variation could potentially help the breeders to develop cultivars with more stable performance (Basford and Cooper, 1998; De Lange, 1999). In this connection, the results of combined analyses of the measured traits across locations and years (Y x L x G) are given in Tables 4.14 and 4.15. Nearly all the nine traits analysed were highly significant (P<0.01) across the tested years, locations, and genotypes and for their interactions. These significant differences and their interactions imply the fluctuations of entries in their responses to the different environments of locations and years. The significant interactions suggest that some genotypes were not stable.

Moreover, because of such interactions between genotypes and environment, yield of genotypes tested on locations over years vary and this poses difficulties to plant breeders in identifying varieties which consistently give high yields in locations with diverse environmental conditions. Kang and Groman (1989) reported that the G x E interactions significantly reduced a correlation between phenotypic and genotypic values. In other words, G x E interactions of multilocation trials tends to confound varietal selection and make it difficult to evolve varietal recommendations. These conditions imply the need for analysing stability of genotypes across the environments. Pham and Kang (1988) indicated that since G x E interactions minimise the usefulness of genotypes, it is thus imperative that yield levels, adaptation and stability are taken into account in multilocation trials. Furthermore, Crossa (1990) elaborated that only qualitative or crossover interactions are relevant in agriculture, and appropriate statistical analysis is required for quantifying them.

The partitioning of variance components indicated that 54.71% of the total variability was due to the years, 25.60% was because of locations, 13.18% was attributed to their interactions, and the share of genotypes was only 2.62% (Table 4.15). These results revealed that the most important source of variation was environment and these indicated the wide and divergent genetic responses. The major component of environmental variability was the rainfall, which differed greatly across the locations and seasons during the experimental years, along with other edaphic, climatic and biotic factors. The distribution pattern of rain in 1997/98 seasons was quite divergent from the normal in Ethiopia as already stated in the preceding discussion. Tesfaye *et al.* (1998) have reported a similar G x E and stability study, indicating the impacts of

agro-ecological diversity of Ethiopia on the yield performance of tetraploid wheat. In line with these G x E interaction problems, Basford and Cooper (1998) have recently described two major categories of G x E interactions, those with defined causes and undefined ones. They elaborated the importance of the major defined causes as diseases, soil-borne constraints (nutritional deficiencies, toxicities, pathogens, etc.), crop phenology (growth and development patterns in relation to different stresses, drought (time and intensities of water deficits) and poor experimental methods (sub-optimal designs and practices). Similarly, for the undefined causes they emphasised inadequacy of explanations due to lack of environmental data, limited time in detailed investigations and lack of a general framework for analysing G x E interactions. In the final analysis, these authors re-emphasised the need to understand environmental characterisations, repeatability of G x E interactions and effective experimental methods as key issues to be pursued. In earlier studies, Crossa (1990) also recommended that more attention has to paid in collecting, analysing and interpreting the environmental and physiological variables to characterise particular genotypes and geographical regions, thereby to better explain the G x E interactions.

Table 4.14. Mean squares of combined analysis of variance (Y x L x G) for eight characters of 10 linseed entries tested in 18 environments of Ethiopia, 1996-98.

Source	df	Characters DF	DM	PH	LP	SP	PM	PS	FW
Year (Y)	2	435**	328**	1027**	19617**	3441**	29**	14**	494**
Location (L)	5	10740**	35108**	1618**	48405**	9218**	85**	99**	854**
YxL	10	341**	2247**	3535**	3625**	2439**	22**	15**	282**
R (LxY)	54	28**	46**	132**	1089**	103	0.62**	2.00**	54**
Genotype (G)	9	349**	126**	244**	654**	48**	8.06**	5.00**	32.00
YxG	18	12**	107**	49**	250**	41**	0.95**	0.56	11.08
LxG	45	27**	30**	39**	363**	64**	1.61**	0.56**	37.61
YxLxG	90	10**	29**	32**	302**	36**	0.75**	0.66**	31.84
Error	486	3	12	32	18	29	0.29	0.33	9.25
CV (%)		2.36	2.41	5.44	8.35	6.09	20.01	24.48	24.33

*, ** Significantly different at 0.05 and 0.01 levels, respectively. DF = Days to flowering; DM = Days to maturity; PH = Plant height; LP = Lodging percentage; SP = Stand percentage; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt %; R = Replication

Table 4.15. Mean squares and its percentage (out of total) contribution of the combined analysis of variance (Y x L x G) for seed yield of 10 linseed entries tested over 18 environments in Ethiopia, 1996-98.

Source	df	Mean square	%	SE
Year	2	9571062.24**	54.71	15.48
Location	5	4479007.12**	25.60	21.90
YxL	10	2306663.16**	13.18	37.93
R (LxY)	54	237356.37**	1.36	75.85
Genotype	9	458947.47**	2.62	29.65
YxG	18	82618.73	0.47	51.35
LxG	45	178189.44**	1.02	72.62
YxLxG	90	119855.33**	0.69	125.79
Residual	486	61248.64	0.35	-
Total	719	7494945	100.00	-
LSD 0.05 = 67.98	CV (%) = 17.96	Repeatability = 0.7738		

*, ** Significantly different at 0.05 and 0.01 levels

In general, when G x E interaction is due to variation in predictable environmental factors (e.g. soil types, management practices, etc.), the plant breeder may choose to develop different varieties for different environments (regions, soil types, management systems), or develop broadly adapted varieties that will perform reasonably well under a range of conditions. However, when G x E interaction is due to variation in unpredictable environmental factors (e.g. year to year variation in rainfall), the breeder has to try to develop stable varieties that can perform reasonably well under a range of conditions. That is why testing over locations and years becomes important, as we have seen in this trial. If G x E is significant and environmental variation is unpredictable, however, we have to carry out stability analysis to identify stable varieties, using the appropriate analytical methods as we are going to see in the succeeding discussion.

4.5 Stability analyses

4.5.1 Joint regression model

Finlay and Wilkenson (1963) indicated that mean yield of entries across all environments and regression coefficients are important indices of cultivar adaptation. According to them, regression coefficient close to unity indicates average stability and when it is associated with high mean yield, an entry is categorized as possessing general adaptability. Conversely, when it is associated with low mean yield, the entry is said to be poorly adapted to its environments. Similarly, entries with regression coefficients larger than one are regarded as increasingly sensitive to environmental changes (below average stability) and specifically adapted to low-yielding environments (Finlay and Wilkenson, 1963; Purchase, 1997). In contrast, when regression coefficient values are below one, the entries are said to possess average stability, resisting fluctuations of environments and thus specifically adapted to low-yielding environmental conditions. Eberhart and Russell (1966) added one more parameter, deviation from the regression as a measure of stability across environments. Hence, genotypes with high mean yield, regression coefficient equal to unity ($b_i = 1$) and deviation from regression as small as possible ($s^2d_i = 0$) are considered stable.

In accordance with the above concepts and principles, Chilalo, NorLin, and R12-N10D varieties were not significantly different from the coefficient of regression (b=1) and thus had average stability that made them adaptable to diverse environments (i.e. general adaptability). Such high and stable yield performances are desirable attributes of cultivars though it is not always easy to obtain them, particularly where environmental variations are high and unpredictable (Becker and Leon, 1988). These authors indicated that coefficients of regression could be used to describe the general response of genotypes to the environmental conditions, while the deviations from regression measure the yield stability. On the other hand, R12-D24C and P13611x 10314B were found poorly adaptable as they significantly deviated from linearity (Table 4.17). Likewise, R10-N27G and R11-N1266 were adapted to low yielding environments.

The analysis of variance, which was computed according to the joint regression model (Eberhart and Russell, 1966) for seed yield of the 10 linseed entries, is presented in Table 4.16. The result shows highly significant (P<0.01) differences among the genotypes and

significant (P<0.05) difference for genotype by environment interaction. Similarly, the stability parameters are given in Table 4.17, along with the overall mean yield. Chilalo cultivar significantly out-yielded the other entries and it was followed by four other regenerants that yielded 1385-1455 kg ha^{-1}. However, the most stable variety was R12-N10D since its regression coefficient (b_i) was nearly unity and it had the second lowest deviation from regression line (Table 4.18). The coefficient of determination for R12-N10D33 was also high (92.4%) and its coefficient variation was the lowest, confirming the highest stability of this regenerant compared to the others. The next stable genotype was P13611x10314D, one of the crosses developed at Holetta Research Center. It also non-significantly deviated from linearity and had a low coefficient of variation. The simple correlation, which was undertaken among the joint regression stability parameters showed highly significant association between the coefficient of determination and coefficient of regression ($r = 0.726$) and between coefficient of determination and deviation from regression line ($r = - 0.766$). The association among the remaining stability parameters was found weak and non-significant.

Table 4.16. Analysis of variance for stability analysis according to the joint regression model (Eberhart and Russell, 1966).

Source	DF	SS	MS	F-value	Pr>F
Total	719	22256515			
Varieties	9	1032511	114724	3.72**	0.0003
Env.+ in Var.x Env.	170	21224005	124847		
Env. in linear	1	16149878			
Var. x Env. (linear)	9	416385	46265	1.50*	0.0233
Pooled deviation	160	4935470	30847		
Residual	540	10368059	19200		
R-squared = 0.7675	C.V. = 20.38%				

*, ** Significantly different at 0.05 and 0.01 levels

Table 4.17. Mean yield (kg ha^{-1}) and stability parameters of 10 linseed entries tested at 18 environments in Ethiopia, 1996-96.

No. Genotypes	Mean	b_i	s^2d_i	R^2	CV %
		Stability parameters			
1. R11-M20G	1434 abc	1.055**	0.249	0.897	32.3
2. R11-N1266	1414 bc	1.062**	0.399	0.634	29.2
3. R10-N27G	1455 ab	1.145*	0.312	0.605	32.2
4. P13611x10314B	1292 efg	0.956*	0.275	0.855	31.5
5. R12-N10D	1385 bcd	1.002	0.144	0.924	27.2
6. R12-D33C	1305 def	1.056	0.286	0.770	33.3
7. R12-D24C	1247 fg	0.819**	0.335	0.404	31.7
8. P13611x10314D	1348 cde	0.862	0.101	0.962	30.7
9. NORLIN	1394 bcd	1.018	0.243	0.698	29.2
10. CHILALO	1505 a	1.026	0.149	0.843	29.8
Mean	1378	LSD 0.05 = 82.65			

*, ** Significantly different at 0.05 and 0.01 levels; values in columns followed by the same letter are not significantly different at 0.05 probability level according to Duncan's multiple range test

Table 4.18. Simple correlation among the joint regression stability parameters of 10 linseed varieties tested in 18 environments of Ethiopia, 1996-98.

	Regression Coefficient (b_i)	Deviation from regression (s^2d_i)	Coefficient of determination (R^2)	Coefficient of variation (CV)
Mean	0.180	- 0.078	0.257	- 0.306
(b_i)	1.000	- 0.173	0.726**	0.139
(s^2d_i)		1.000	- 0.766**	0.299
(R^2)			1.000	- 0.202
(CV)				1.000

** Significantly correlated at 0.05 and 0.01 levels

4.5.2 Wricke's ecovalence analysis

Wricke's ecovalence (1962) is one the alternative methods frequently used to determine stability of genotypes based on the G x E interaction effects. It indicates the contribution of each genotype to the G x E interaction. Consequently, genotypes with small ecovalence will have small deviations from the mean across environments and thus considered more stable (Purchase, 1997). In other words, according to Wricke (1962), cultivars with the lowest ecovalence contributed the least to the G x E interaction and are thus more stable than the others.

In view of this principle, ecovalence was computed for the 10 entries of linseed and the results are summarised in Table 4.19. According to this result, R11-M20G followed by R11-N1266, R12-N10D and P13611x10314D were the most stable genotypes. The first three genotypes were the regenerants derived from tissue culture of McGregor and NorLin, the fourth being one of the crosses made at Holetta. Likewise, Chilalo, NorLin, R12-D33C and P13611x10314B were categorised as intermediate in stability, in contrast to two regenerants (R10-N27G and D12-D24C) that were found unstable, according to Wricke's (1962) ecovalence.

Table 4.19. Wricke's ecovalence value, overall mean yield (kg ha^{-1}) and their ranks for 10 linseed genotypes tested in 18 environments of Ethiopia, 1996-1998.

No. Variety	Ecovalence	Rank	Mean yield	Rank
1. R11-M20G	21520.40	1	1434	3
2. R11-N1266	25096.90	2	1414	4
3. R10-N27G	619955.59	9	1455	2
4. P13611x10314B	559542.71	8	1292	9
5. R12-N10D	102983.71	3	1385	6
6. R12-D33C	458194.69	7	1305	8
7. D12-D24C	908627.79	10	1247	10
8. P13611x10314D	227054.77	4	1348	7
9. NORLIN	385297.47	6	1394	5
10.CHILALO	365852.22	5	1505	1

4.5.3 Shukla's method of stability variance

Shukla' s stability variance (1972), mean yield and the ranking order of genotypes to these values are given in Table 4.20. According to this stability parameter, entries with minimum stability variance are considered more stable. Hence, R12-N10D, P13611x10314D and Chilalo were the most stable genotypes, while D12-D24C, R11-N1266 and R11-M20G were classified as the least stable ones. It is worth noting that R12-N10D, the regenerant from NorLin cultivar was the most stable genotype as shown above by both ecovalence and stability variance.

Table 4.20. Shukla's stability variance, overall mean yield (kg ha^{-1}) and their ranks for 10 linseed genotypes tested in 18 environments of Ethiopia, 1996-1998.

No. Variety	Stability variance		Overall mean	
	With no covariate	Rank	Yield	Rank
1. R11-M20G	195629.77	8	1434	3
2. R11-N1266	196681.68	9	1414	4
3. R10-N27G	165757.77	7	1455	2
4. P13611x10314B	147989.27	6	1292	9
5. R12-N10D	13707.22	1	1385	6
6. R12-D33C	118181.03	5	1305	8
7. D12-D24C	250661.35	10	1247	10
8. P13611x10314D	50198.70	2	1348	7
9. NORLIN	96740.67	4	1394	5
10.CHILALO	91021.48	3	1505	1

4.5.4 Lin and Binns's cultivar superiority measure

According to Lin and Binns (1988a), the superiority measure (Pi) of cultivars is estimated by the squares of differences between an entry mean and maximum entry mean, summed and divided by twice the number of locations. Cultivars with lowest Pi values are considered the most stable. Table 4.21 presents this cultivar superiority measure (Pi) for seed yield of 10 linseed entries tested in 18 environments of Ethiopia during the periods of 1996-1998. Accordingly, Chilalo, R10-N27G and R11-M20G were the most stable genotypes, whereas D12-D24C and P13611x10314B were the least stable ones. In most case, the ranks of cultivar superiority measure were in harmony with that of the overall mean yield (Table 4.21).

Table 4.21. Lin and Binns's (1988a) cultivar superiority measure (Pi), overall mean yield (kg ha^{-1}) and their ranks for 10 linseed genotypes tested in 18 environments of Ethiopia, 1996-98.

No. Entry	Pi	Rank	Overall mean yield	Rank
1. R11-M20G	50002.39	6	1434	3
2. R11-N1266	47899.24	3	1414	4
3. R10-N27G	45559.23	2	1455	2
4. P13611x10314B	91846.10	9	1292	9
5. R12-N10D	49004.50	5	1385	6
6. R12-D33C	88237.69	8	1305	8
7. D12-D24C	135472.94	10	1247	10
8. P13611x10314D	67136.80	7	1348	7
9. NORLIN	48375.51	4	1394	5
10. CHILALO	27904.67	1	1505	1

4.5.5 Nassar and Huehn's variance of ranks

Table 4.19 presents Nassar and Huehn's (1978) non-parametric measures of stability for seed yield of 10 linseed entries evaluated in 18 environments of Ethiopia. Both S1 (mean absolute rank differences) and S2 (variance of ranks) of the genotypes over the test environments are the measurements of stability (Huehn, 1990). However, the use of S1 was more preferred than S2 for many practical applications. S1 was reported to be easy to calculate, interpret and it has efficient test of significance, according to Huehn (1990).

Since the two overall chi-square stabilities (Z1=24.56 and Z2=19.61) were greater than the tabulated chi-square ($X^2_{0.05, 10}$=18.31), there was evidence for significant differences in stability among the 10 entries. Hence, R12-N10D had the smallest changes in ranks (S1) and thus considered as the most stable regenerant unlike D12-D24C, which was significantly unstable. The next more stable variety was P13611x10314D, followed by Chilalo, which gave the highest yield across the environments (Table 4.19).

Table 4.22. Mean absolute rank difference (S1) and variance of ranks (S2) of Nassar and Huehn, 1987) for seed yield (kg ha^{-1}) of ten linseed entries tested in 18 environments of Ethiopia.

No. Entry	Nassar-Huehn Rank Test					
	S1	Z1	S2	Z2	Overall mean yield	Rank
1. R11-M20G	3.61	0.64	9.21	0.27	1434	3
2. R11-N1266	3.56	0.47	8.92	0.13	1414	4
3. R10-N27G	3.84	2.01	10.28	1.23	1455	2
4. P13611x10314B	3.55	0.42	8.68	0.06	1292	9
5. R12-N10D	1.90	13.29**	2.57	9.55**	1385	6
6. R12-D33C	3.31	0.00	7.87	0.04	1305	8
7. D12-D24C	4.23	5.86*	12.65	5.72**	1247	10
8. P13611x10314D	2.80	1.72	5.40	2.41	1348	7
9. NORLIN	3.43	0.12	8.14	0.00	1394	5
10. CHILALO	3.23	0.04	7.43	0.20	1505	1

Note: Overall chi-square for stability = 24.56, 10 df individual Z1 distributed as single df chi-squares; overall chi-square for stability = 19.61, 10 df individual Z2 distributed as single df chi-squares; *, ** = significantly different at 0.05, and 0.01 probability levels, respectively; tabulated $X^2_{0.05, 10}$=18.31

4.5.6 Additive main effects and multiplicative interaction (AMMI)

The AMMI analysis of variance for seed yield of the 10 linseed entries tested in 18 environments of Ethiopia is given in Table 4.23. The best-fit model was AMMI 2 for this experiment as IPCA 1 and IPCA 2 were highly significant ($P<0.01$). IPCA 1 declared 44.2% of the G x E interaction sum of squares, whereas IPCA 2 declared 25.3%. That means both IPCAs accounted for 69.5% of the total interaction, the remaining 31.5% being the residue or noise, which are not interpretable and thus discarded as described by Purchase (1997).

The IPCA scores of a genotype in the AMMI analysis are reported (Gauch and Zobel, 1988; Purchase, 1997) as indication of the stability of a genotype across environments. The closer the IPCA scores to zero, the more stable the genotypes over their testing environments. Conversely, the higher the IPCA scores (either positive or negative), the more specifically adapted the genotypes are to certain environments. In accordance with this concept, R12-D33C was the most stable regenerant, followed by R12-N10D, P13611x10314D and D12-D24C (i.e. when IPCA 1 score was taken into account). In contrast, R11-N1266 and R10-N27G were adapted to specific environments, like Bekoji and Sinana, where they had the top yields, respectively (cf. Table 4.3). However, when IPCA 2 score was considered, this stability order had a different picture. For example, according to IPCA 2 score, P13611x10314D was the most stable genotype followed by R12-N10D and others. Hence, the other option is to calculate an AMMI stability value (ASV), using the formula indicated in the materials and methods (cf. Chapter 2). This stability value was reported to produce a balanced measurement between the two IPCA scores (Purchase, 1997). According to this stability parameter, N12-N10D was the most stable variety, followed by P13611x10314D, R12-D33C and Chilalo in this listed order (Table 4.24). On the other hand, R11-N1266 and R10-N27G were found unstable, according to these ASV values.

AMMI model has been extensively and successfully used during the past few years to analyse and understand the G x E interactions in various crops (Zobel et al., 1988; Crossa, 1990; Purchase, 1997; Annicchiarico, 1997). Crossa (1990) indicated that the combination of analysis of variance and principal components analysis in the AMMI model, is a valuable approach for understanding G x E interaction and obtaining better yield estimates. Purchase (1997) also found that AMMI model can accurately describe both the G x E interaction and

stability analysis through its response patterns that can be illustrated on biplot or on scatter diagram of IPCA1 scores versus IPCA2 scores.

Table 4.23. Analysis of variance and Gollob tests of interaction principal components in AMMI for the seed yield of 10 linseed entries tested in 18 environments of Ethiopia, 1996-98.

Source	DF	SS	MS	F-value	Pr> F
Total	719	131609207			
Environments	17	64599513	3799971	16.01	0.0000
Reps within Env.	54	12815889	237331		
Genotype	9	4130042	458894	3.46	0.0004
Genotype x Env.	153	20296505	132657	2.17	0.0000
IPCA 1	25	8967622	358705	5.86	0.0000
IPCA 2	23	5140576	223503	3.65	0.0000
Residual	486	29767258	61250		
Pooled error	105	6188307	349971	5.71	

Table 4.24. Mean yield (kg ha^{-1}), rank, IPCA 1 and IPCA 2 scores and an AMMI stability value (ASV) of 10 linseed entries tested in 18 environments of Ethiopia, 1996-98.

No. Genotype	Yield	Rank	IPCA 1 score	IPCA 2 score	ASV	Rank
1. R11-M20G	1434	3	-14.69	-15.75	30.08	8
2. R11-N1266	1414	4	18.93	- 6.76	33.71	10
3. R10-N27G	1455	2	17.70	1.35	30.91	9
4. P13611x10314B	1293	9	-14.42	- 8.04	27.04	6
5. R12-N10D	1385	6	5.50	- 1.07	9.66	1
6. R12-D33C	1305	8	-0.94	10.91	11.04	3
7. D12-D24C	1247	10	-8.96	25.25	29.70	7
8. P13611x10314D	1348	7	-5.61	- 0.37	10.00	2
9. NORLIN	1394	5	12.55	- 2.58	22.05	5
10.CHILALO	1505	1	-10.07	- 2.95	17.81	4

Figure 4.1 shows the AMMI model 2 biplot for 18 environments of Ethiopia. Apparently clear patterns are seen with the higher potential environments predominating in the third quadrant, such as Bekoji 1996, Bekoji 1997 and Holetta 1997, and lower potential environments prevailing in the first quadrant, like Kulumsa 1998, Sinana 1997, Asasa 1998, Asasa 1997, Asasa 1996. Most of these environments were affected by terminal droughts. In the same manner, most of the entries were plotted on less than the average yield of 1378 kg ha^{-1}. In general, ASV, IPCA scores, and locations of genotypes on the biplots indicate that R11-N1266, R10-N27G and Norlin were specifically adapted to low or unfavorable conditions. On the other hand, R12-N10D, P13611x10314D, R12-D33C and Chilalo were relatively the most stable genotypes over the range of environments.

As the IPCA 2 also plays a significant role in the G x E interaction (Purchase, 1997), the IPCA 1 scores were plotted against IPCA 2 scores to further explore stability of the 10 linseed genotypes tested in 18 environments of Ethiopia (Fig.4.2). The closer the genotypes to the center or zero of this figure, the more stable they are. Accordingly, P13611x10314D and R12-N10D were less interactive with the environments and thus more stable than the other genotypes. In addition, the IPCA 2 scores showed that P13611x10314D and R12-N10D were the most stable genotypes over the tested environments (Table 4.24).

IPCA 1 score (-14.7, 25.8)

```
                                          | Kulumsa'96
                                          |
       1ˢᵗ quadrant                       |        2ⁿᵈ quadrant
                                          |
                                          |
                           R11-N1266      |
                            R10-N27G      |
                                          |
                                          |
                           NorLin         |
                                          |
     Kulumsa'98        Sinana'97          |
                                 Asasa'98 |
         Asasa'97                         |
                                          |
                        R12-N10D          |
                                          |
                        Asasa'96          |
                                          |
─────────────────────────────────────────┼──────────────────────────────
   Sinana'98         R12-D33C             |                  Bekoji'96
                                          | Holeta'97
                      Sinana'96           |        Bekoji'97
                                          |
                   PD    Adet'97          |
 Holeta'98       Adet'98                  |
              Kulumsa'97                  |
              DC   Adet'96                |
               Bekoji'98     Chilalo      |
               Holeta'96                  |
       4ᵗʰ quadrant                       |        3ʳᵈ quadrant
              P13..B   R11-M20G           |
```

898   1378   2203.9

Seed yield (kg ha^{-1})
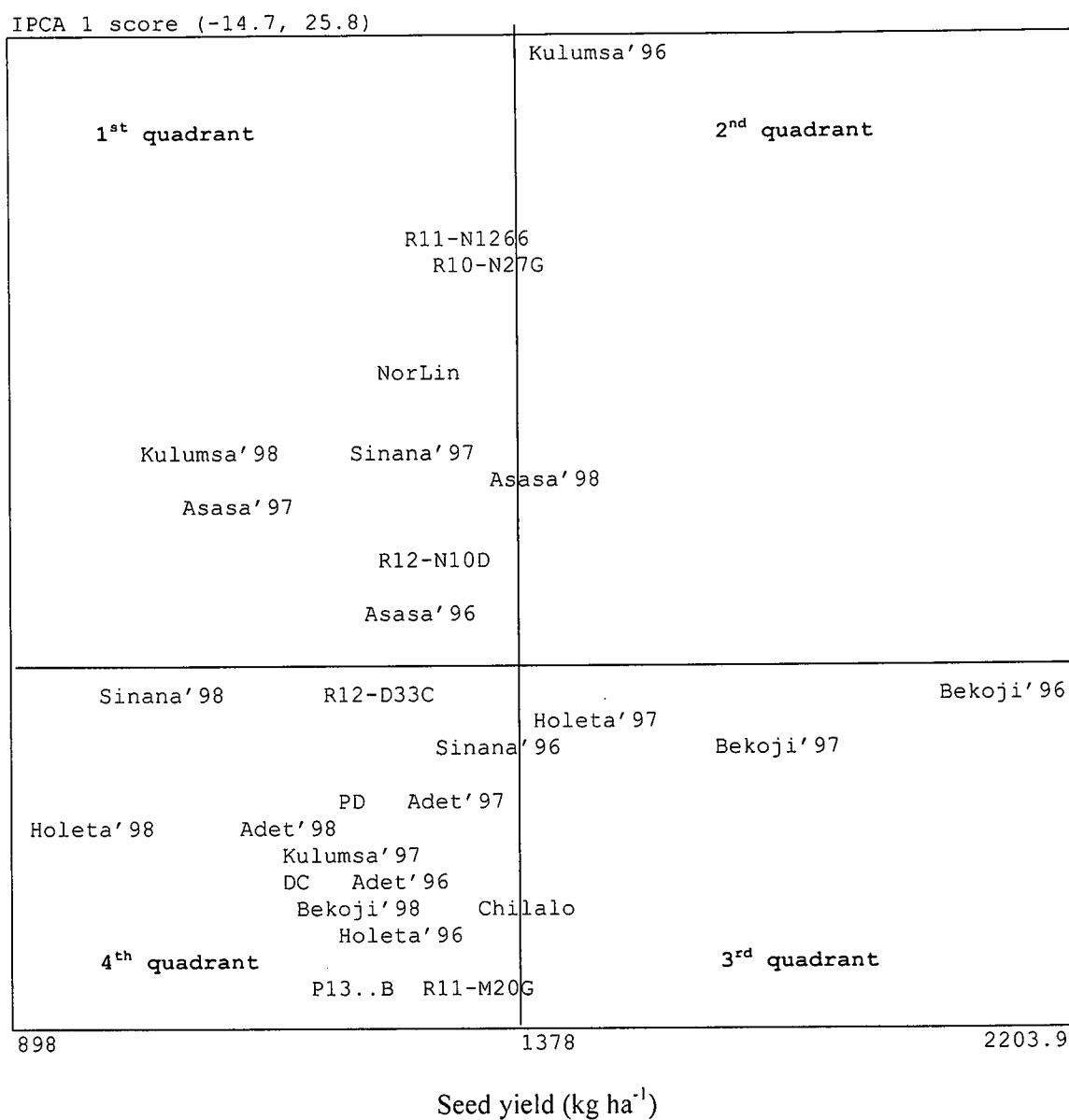
Figure 4.1 AMMI model 1 biplot for seed yield of 10 linseed genotypes tested across 18 environments of Ethiopia, 1996-1998. The first letters of all the genotypes and environments indicate the right spots on the biplots; PD = P13611x1031D, DC = D12-D24C, P13..B = P13611x1031D.

Fig. 4.2 Plotted IPCA1 and IPCA2 scores of 10 linseed genotypes
tested in 18 environments of Ethiopia
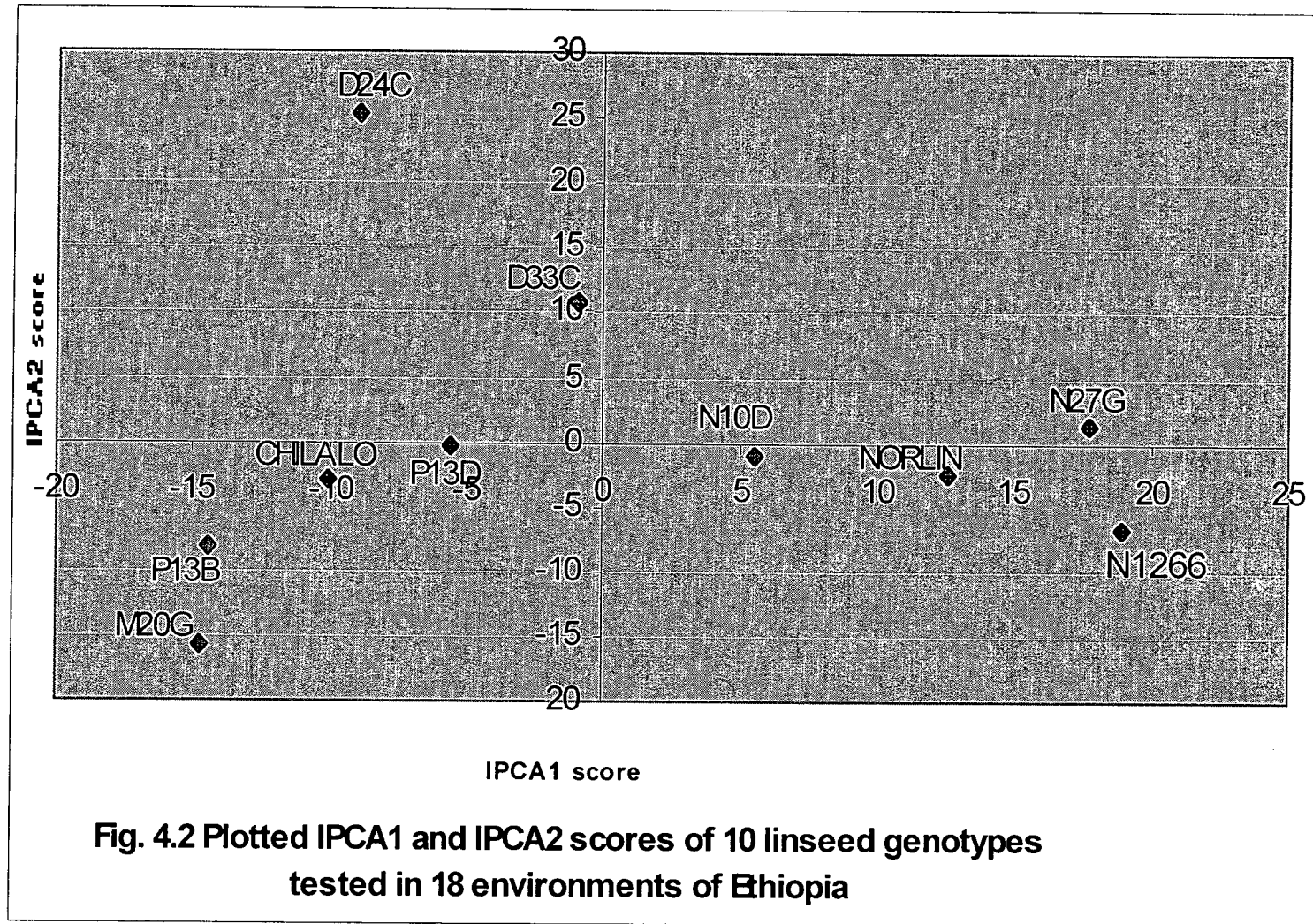
4.6 Comparison of the stability parameters

Table 4.25 shows the summary of seven major stability parameters employed to analyse the seed yield performance of 10 linseed varieties evaluated in 18 environments of Ethiopia. These stability parameters were: coefficient of variation CV% (Francis and Kannenberg, 1978), deviation from regression line S^2di (Eberhart and Russell, 1966), ecovalence Wi (Wricke, 1962), stability variance (Shukla, 1972), cultivar superiority measure Pi (Lin and Binns, 1978), variance of ranks S1 (Nassar and Huehn, 1978) and AMMI's stability value ASV (Gauch and Zobel, 1996; Zobel et al., 1988; Purchase, 1997). The overall mean yield and coefficient of regression (bi) were included to support these stability parameters and for comparison purposes. Leon and Becker (1988) indicated that bi can be used to describe the general response to the goodness of environmental conditions, while s^2di actually measure the yield stability.

As can be seen from Table 4.25, the values of coefficient of variability, Shukla's (1972) stability variance (SV), Nasser and Huehn's (1978) variance of ranks (S1) and AMMI's stability value (ASV) were harmonious in sorting out the most stable regenerant, R12-N10D. Ecovalence and deviation from regression also revealed that this regenerant was among the stable varieties. Only cultivars superiority measure ranked this variety as 5th, categorising it in the intermediate stability group. The same was true to a large extent with the second most stable variety (P13611x10314D). It was picked up as the second stable variety by deviation from regression, stability variance, variance of ranks and AMMI's stability value, while coefficient of variation and ecovalence placed it in 5th and 4th ranks, respectively. Lin and Binns's (1978) cultivar's superiority measure again deviated here, placing it in the 7th position.

As shown in Table 4.25, most of the parameters were also in close harmony in identifying the third (Chilalo) and the fourth (NorLin) stable varieties. It is interesting to note that the most stable regenerant (R12-N10D) was originally derived from NorLin cultivar. Moreover, R10 N27G that became one of the unstable genotype was regenerated from NorLin, and these are some of the examples for the occurrence of somaclonal variations among these tissue culture derived materials. Furthermore, R12-D24C was the most unstable regenerant and it was also the poorest in its seed yield, while R12-D33C was better both in its yield and stability. Both of them were originally derived from the same cutivar, Dufferin.

In general, most of these stability parameters were closely related in sorting out the magnitudes of yield stability of the evaluated linseed genotypes. However, some deviations were also observed especially on ecovalence and cultivars superiority performance. Purchase (1997) also reported similar results on the latter parameter, indicating that it is more of a performance measurement rather than stability over environments. In addition to this, Spearman's rank correlation was computed for these stability parameters and the results are summarised in Table 4.26. There was highly significant ($P<0.01$) rank correlation between AMMI's ASV and S^2di ($r = 0.794$), ASV and S1 ($r = 0.879$), S1 and S^2di ($r = 0.806$), and S1 and SV ($r = 0.770$). Likewise, significant rank correlation ($P<0.05$) was found between ASV and SV ($r = 0.721$), and SV and S^2di ($r = 0.636$). In the same manner, Pham and Kang (1988) reported high rank correlations of S^2di with SV and S1. They also indicated that optimal environments were characterised by relatively low coefficients of variability and vice versa for the poor environment.

In this study, AMMI, Eberhart and Russell's (1966) deviation from regression, Nasser and Huehn's (1978) variance of ranks and Shukla's (1972) stability variance were found important in assessing the stability of linseed genotypes under the tested environment of Ethiopia. Similarly, coefficient of variability and ecovalence were also relatively better than the cultivar superiority measure in identifying stable varieties of linseed. However, the repeatability of different stability parameters has to be compared and the ones with high repeatability should be superior to identify more stable genotypes. Moreover, methods to simultaneously select for high yield and stability are more useful to determine the best genotypes for practical purposes.

In summary, the above stability parameters detected R12-N10D, P13611x10314D and Chilalo as the most stable varieties, while R12-D24C, R10-N27G and P13611x10314B as the unstable ones. The remaining genotypes were intermediate between these two groups. As the result of these analyses, R12-N10D was recommended for national release in Ethiopia as it was tested and adequately demonstrated superiority of yield performance, adaptation and other agronomic traits. Stoskopf, Tomes and Christie (1993) indicated that clear indication of varietal superiority in some specified area or areas, genetic purity to ensure distinctiveness, uniformity and stability (DUS) across sites and years are essential, with a reasonable degree of reliability for licensing new cultivars.

Table 4.25. Mean yield (kg ha^{-1}), various stability measurements and their ranking (R) orders for 10 linseed entries tested in 18 environments of Ethiopia, 1996-98.

No. Genotype	Overall yield				Joint regression			Ecovalence		Stability		S. measure		Variance of ranks		AMMI		
	Yield	R	CV%	R	bi	S^{2}di	R	Wi	R	variance	R	Pi	R	S1	R	ASV	R	Overall R
1. R11-M20G	1434	3	32.3	9	1.055	0.249	5	21520	1	195630	8	50002	6	3.61	8	30.08	8	6
2. R11-N1266	1414	4	29.2	2	1.062	0.399	10	25097	2	196682	9	47899	3	3.56	7	33.71	10	5
3. R10-N27G	1455	2	32.2	8	1.145	0.312	8	619956	9	165758	7	45559	2	3.84	9	30.91	9	8
4. P13611x10314B	1293	9	31.5	6	0.956	0.275	6	559543	8	147989	6	91846	9	3.55	6	27.04	6	9
5. R12-N10D	1385	6	27.2	1	1.002	0.144	2	102984	3	13707	1	49005	5	1.90	1	9.66	1	1
6. R12-D33C	1305	8	33.3	10	1.056	0.286	7	458195	7	118181	5	88238	8	3.31	4	11.04	3	7
7. R12-D24C	1247	10	31.7	7	0.819	0.335	9	908628	10	250661	10	135473	10	4.23	10	29.70	7	10
8. P13611x10314D	1348	7	30.7	5	1.862	0.101	1	227055	4	50199	2	67137	7	2.80	2	10.00	2	3
9. NonLin	1394	5	29.2	2	1.018	0.243	4	385298	6	967441	4	48376	4	3.43	5	22.05	5	4
10.Chilalo	1505	1	29.8	4	1.026	0.149	3	365852	5	91022	3	27905	1	3.23	3	17.81	4	2

Note: R = Rank; CV% = Coefficient of variability; bi = Regression coefficient; S^{2}di = Deviation from regression line; Wi = Wricke's ecovalence; Pi = Cultivars' superiority measure; S1 = variance of ranks; ASV = AMMI Stability Value.

Table 4.26. Spearman's coefficients of rank correlation for eight G x E stability parameters of 10 linseed genotypes evaluated in 18 environments of Ethiopia, 1996-98.

	CV	bi	S^2di	Wi	Sv	Pi	S1	ASV
CV	-	0.189	- 0.424	- 0.321	0.115	0.401	0.492	0.255
bi		-	- 0.042	- 0.321	- 0.212	- 0.418	- 0.115	0.115
S^2di			-	0.370	0.636*	0.115	0.806**	0.794**
Wi				-	0.234	0.333	0.394	0.079
Sv					-	0.055	0.770**	0.721*
Pi						-	0.152	- 0.189
S1							-	0.879**
ASV								-

*, ** = Significantly rank correlated at 0.05 and 0.01 levels, respectively.

4.7 Assessment of oil content and oil yield

The average oil content over the three years of 1996, 1997 and 1998 is given in Table 4.27. Among the localities, Holetta scored the highest oil content of 38.26% as opposed to the lowest 34.99% of Asasa. The remaining four sites yielded within a narrow range 35 to 37%. Of the 11 genotypes, R12-D33C and R12-D24C produced the highest oil content (mean 37.31%) across the localities. Both genotypes were regenerants derived from cultivar Dufferin. R12-D33C had the top oil content of 37.50% and was very consistent in this performance across the sites even at Asasa, where some varieties yielded as low as 33.53% (Table 4.27). The major cause for low oil content at Asasa was terminal drought stress. Kenaschuk (1975) reported that inadequate soil moisture was one of major factors affecting the variability of oil content and oil quality.

The regenerants originated from Dufferin and McGregor were also reported with higher oil contents in previous studies (Adugna and Adefris, 1995). Thus, these genotypes can be used in future breeding programmes to improve the oil contents. R12-N10D, which was the most stable genotype in its seed yield was also good in oil content, producing 36.13% across the sites. Four other varieties (R11-M20G, P13611x10314D, NorLin and Chilalo) also gave comparatively good results.

Similarly, Table 4.28 presents the results of oil yield (kg ha^{-1}) for the 10 varieties across the tested locations. In fact, the oil yield is one of the most important end products obtained from linseed. The oil yield was estimated by multiplying the seed yield data with the oil content. The comparison between the location means depicts that the highest oil yield of 644 kg ha^{-1} was obtained from Bekoji followed by that of Holetta (484 kg ha^{-1}). The remaining four sites, Sinana Adet, Kulumsa, and Asasa had very similar results as shown in Table 4.28.

Table 4.27. Mean oil content (%) of 11 linseed entries tested across six locations in Ethiopia, during the period of 1996 to 1998.

				Locations				
No.	Regenrants	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean
1.	R11-M20G	37.50	39.03	37.10	35.47	36.10	35.53	36.79
2.	R11-N1266	35.90	38.43	35.83	36.17	34.80	33.53	35.78
3.	R10-N27G	34.90	37.90	35.80	36.37	34.70	34.23	35.65
4.	P13611x10314B	36.50	37.43	35.43	35.33	35.07	35.20	35.83
5.	R12-N10D	36.53	38.33	35.90	36.10	35.50	34.40	36.13
6.	R12-D33C	37.93	39.83	38.03	35.60	36.60	37.10	37.50
7.	R12-D24C	37.90	39.37	37.33	35.97	35.73	35.60	37.11
8.	P13611x10314D	36.50	38.13	36.23	36.73	35.87	35.43	36.35
9.	NORLIN	35.87	38.53	35.90	35.80	35.07	35.00	36.03
10.	CHILALO	36.93	38.47	35.40	35.57	35.67	34.83	36.15
11.	LOCAL CHECK	36.17	35.40	33.90	36.10	35.73	34.00	35.49
	Mean	36.60	38.26	36.08	35.99	35.53	34.99	36.25

Among the genotypes, Chilalo produced the highest oil yield of 544 kg ha^{-1} followed by R11-M20G (528 kg ha^{-1}). Likewise, five other entries gave fairly good oil yields of 490-513 kg ha^{-1} against the lowest of 420 kg ha^{-1} of the local check. As far as the relative performance of the genotypes goes, there was a reversal of ranks, indicating high G x E interactions. For example, R11-M20G, which was the top ranking at Bekoji was the second at Holetta and Sinana, fourth at Adet, sixth at Kulumsa and ninth at Asasa. Similarly, Chilalo ranked first at Holetta and Adet but became third, fourth and fifth at Sinana, Kulumsa and Asasa, respectively. The same was true for genotypes that ranked first at Kulumsa and Asasa. These imply that the relative performance of these genotypes in oil yield were highly dependent on the test environments.

The combined analysis of variance across locations was carried out for the oil content and oil yield using the three years data. As shown in Table 4.29, highly significant differences (P<0.01) were found between the genotypes both for oil content and oil yield. Similarly, the share of total variance among its components was computed for both traits. About 57% of the total variation was due to the location effects in oil yield, and it was about 53% for oil content. The genotypes accounted for only about 5% of variability for oil yield and a bit higher for oil content (Table 4.29). These results once again confirm the strong influence of environmental conditions on both characters and breeders need to look into these aspects besides improving the genotypes.

Table 4.28. Mean oil yield (kg ha^{-1}) of 11 linseed entries tested across six locations in Ethiopia, 1996-98.

		Locations						
No.	Regenrants	Bekoji	Holetta	Sinana	Adet	Kulumsa	Asasa	Mean
1.	R11-M20G	763	537	498	471	466	430	528
2.	R11-N1266	653	428	521	414	548	488	509
3.	R10-N27G	610	489	480	436	512	552	513
4.	P13611x10314B	663	483	370	433	374	462	463
5.	R12-N10D	655	484	470	441	488	468	501
6.	R12-D33C	649	436	477	501	396	489	491
7.	R12-D24C	566	526	433	485	377	390	463
8.	P13611x10314D	638	494	431	446	449	469	488
9.	NORLIN	605	465	476	428	533	478	498
10.	CHILALO	705	559	486	538	499	476	544
11.	LOCAL CHECK	577	417	440	361	362	363	420
	Mean	644	484	462	450	455	459	492

Table 4.29. Mean squares of the analysis of variance and percent of variance components for oil content and oil yield combined over six locations, 1996-98.

Source	Degree of freedom	Mean square			
		Oil content (%)		Oil yield	(%)
Location	5	52.34	52.93	224607.15	56.54
Error	18	38.37	38.80	142610.78	35.91
Genotype	9	5.70**	5.76	19677.67**	4.96
LxG	45	1.36	1.38	6102.16	1.54
Error	162	1.12	1.13	4163.28	1.05
CV %		2.92		12.94	

** Significantly different at 0.05 and 0.01 levels

The average data of oil content and oil yield for the genotypes over the three years are shown in Table 4.30. Year to year variation of oil content was in the range of 35 to 37.43%, the highest being recorded in 1996 and the lowest in 1997. During 1997, there was an irregular distribution of rainfall due to *El Nino* effects (unusual disturbance of rainfall due to an irregular phenomenon in Pacific Oceans, whereby a series of events of considerable significance to global weather patterns take place). Of the genotypes, R12-D33C and R12-D24C gave as high as 37.5% oil, while the remaining genotypes yielded 35 to 36.79% across the three years (Table 4.30). Similarly, the highest oil content of 38.9% was obtained from R12-D33 in 1996, while the lowest (33.69%) was recorded from the local check in 1997. This wide variation again indicates the tremendous influences of environmental conditions on the oil contents of linseed.

Like the oil content, the mean oil yield across years was also high in 1996 with an average of 573 kg ha^{-1} and low in 1998 (423 kg ha^{-1}). This low oil yield level was mainly because of the poor seed in 1998 due to erratic distribution of rainfall. With respect to the varieties, Chilalo, R11-M20G, R10-N27G, R11-N1266 and R10-N10D were the best oil yielders, within the range of 501 to 544 kg ha^{-1} over the three years. The highest oil yield, 663 kg ha^{-1} of 1996 was obtained from cultivar Chilalo as opposed to the lowest of 423 kg ha^{-1} of the local check in 1998. These results indicate the high variation from year to year, which are mainly governed by agroclimatic conditions, such as rainfall, temperature, soil and disease related conditions. Kenaschuk (1975) also reported that environmental factors, like temperature, soil moisture, soil fertility and the presence of diseases had a marked influence on oil quantity and quality of linseed.

The combined analyses of variance for oil content and oil yield over three years were carried out and the results are given in Table 4.31. About 56% and 64% of the total variation were attributed to the years for oil content and oil yield, respectively. On the other hand, the genotypes contributed 5.29% of the variability of oil content and 4.11% of the oil yield out of the total variability. These results once again indicate the large role of environmental conditions, especially the climatic factors in influencing the oil content and its subsequent oil yield. Sheppard and Bates (1988) also reported such significant influence of environmental factors on linseed. They demonstrated that yield and responses of linseed to nitrogen were heavily dependent on the weather conditions, especially during the vegetative and ripening phases. They found that over 95% of the seed yield variability were caused by climatic factors.

Table 4.30. Mean oil content and oil yield of 11 linseed entries tested across six sites from 1996 to 1998 in Ethiopia.

No. Regenerants	Oil content (%)				Oil yield (kg ha^{-1})			
	1996	1997	1998	Mean	1996	1997	1998	Mean
1. R11-M20G	38.44	35.25	36.68	36.79	602	509	473	528
2. R11-N1266	37.02	35.00	35.32	35.78	581	511	435	509
3. R10-N27G	36.54	35.41	35.00	35.65	630	486	423	513
4. P13611x10314B	36.84	35.05	35.60	35.83	556	435	398	463
5. R12-N10D	37.48	35.41	35.50	36.13	589	494	420	501
6. R12-D33C	38.90	36.10	37.50	37.50	567	510	396	491
7. R12-D24C	38.88	36.15	36.30	37.11	532	473	384	463
8. P13611x10314D	37.38	35.13	36.54	36.35	542	465	457	488
9. NORLIN	37.52	34.83	35.74	36.03	604	467	423	498
10. CHILALO	37.34	34.77	36.34	36.15	663	500	470	544
11. LOCAL CHECK	37.42	33.69	35.36	35.49	434	454	372	420
Mean	37.43	35.33	35.99	36.25	573	480	423	492

Table 4.31. Mean squares of the analysis of variance and percent of variance components for oil content and oil yield combined over three years, 1996-98.

Source	Degree of freedom	Mean square			
		Oil content (%)		Oil yield	(%)
Year	2	60.16	55.77	308530.35	64.41
Error	9	39.39	36.53	1422189.64	29.71
Genotype	9	5.70**	5.29	19677.67**	4.11
YxG	18	1.45	1.34	3595.71	0.75
Error	81	1.14	1.07	4904.17	1.02
CV %		2.95		14.05	

** Significantly different at 0.05 and 0.01 levels

4.8 Assessment of other agronomic characters and their associations

The summary of oil yield and other measured characteristics across the 18 environments are given in Table 4.32. Oil and seed yields were highest for Chilalo, and lowest for R12-D24C mainly because of its poor seed yield. Nevertheless, the latter variety was one of the best in oil content (37%), similar to R12-D33C. With respect to days to flowering and maturity, on average, the genotypes took 75 days to reach anthesis and 139 days to reach their physiological maturity. This means, the seed filling period was about 64 days. Four varieties reached their flowering stages six days earlier than the late ones that took as long as 79 days. The early flowered entries have also matured earlier than others. They took about 134 days unlike the late maturing ones that took up to 144 days. R11-N1266, R10-N27G, R12-N10D and NorLin were among the early maturing group, while R11-M20G, P13611x10314D and the local checks were late maturing genotypes. It is interesting to see that the most stable variety (R12-N10D) was among the early maturing group.

Regarding the relative tolerance of the genotypes against the major diseases, the two crossed lines were more susceptible to powdery mildew (*Odium spp.*) followed by the local check. On the other hand, R12-D33C, R12-D24C, R11-M20G and Chilalo were relatively resistant to powdery mildew and pasmo (*Septoria lini*) diseases. It is worth noting that these genotypes had higher oil content as well. The infection level of Fusarium wilt (*Fusarium oxysporum* f. lini) was generally low. NorLin, R12-D33C and R12-D24C scored relatively low, showing their good tolerance level.

As to the plant height, except the local check that was 80 centimetres tall, all the remaining entries had similar heights, within the range of 88 to 93 centimetres. On the other hand, lodging percent was relatively higher (20%) for R10-N27G and R12-D24C, unlike Chilalo and P13611x10314D that had a value as low as 12% (Table 4.32). The stand count or plant density was estimated to be between 88 and 90% except for the local check that scored 86% mainly due to its susceptibility to diseases, like Fusarium wilt and pasmo.

Table 4.32. Overall mean of oil yield (kg ha^{-1}) and other agronomic traits of 11 linseed entries tested across 18 environments in Ethiopia, 1996-96.

No. Regenerants	OY	SY	OC	DF	DM	PM	PS	FW	PH	LP	SP
					Characters						
1. R11-M20G	528	1434	36.8	78	144	1.5	1.6	2.5	90	14	88
2. R11-N1266	509	1414	35.8	73	134	1.8	1.9	2.6	91	16	89
3. R10-N27G	513	1455	35.7	73	134	1.9	2.0	3.6	92	20	88
4. P13611x10314B	463	1292	35.8	75	141	2.2	1.4	2.3	90	15	89
5. R12-N10D	501	1385	36.1	73	134	1.8	1.9	2.3	93	19	88
6. R12-D33C	491	1305	37.5	77	140	1.3	1.4	1.4	93	17	88
7. R12-D24C	463	1247	37.1	76	139	1.3	1.4	1.9	92	20	89
8. P13611x10314D	488	1348	36.4	74	142	2.3	1.6	2.3	88	13	88
9. NORLIN	498	1394	36.0	73	135	2.0	2.0	1.2	91	19	88
10.CHILALO	544	1505	36.2	77	139	1.6	1.4	2.3	89	12	90
11.LOCAL CHECK	420	1220	35.5	79	141	2.1	1.6	2.5	80	15	86
Mean	492	1362.8	36.3	75	139	1.8	1.7	2.3	90	16.6	88.3
S.E. (±)	16.7	29.7	0.3	0.2	0.4	0.06	0.07	0.65	0.59	1.58	0.64
C.V. (%)	12.94	18.46	2.92	2.30	2.37	20.7	24.2	24.80	5.52	31.10	6.19

Note: OY = Oil yield; SY = Seed yield; OC = Oil content; DF = Days to flowering; DM = Days to maturity; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; PH = Plant height; LP = Lodging percentage; SP = Stand percentage.

The overall location mean of 11 agronomic traits for the six localities is presented in Table 4.33 to highlight the relative performance of the genotypes across a range of environments. Oil and seed yield were in the top rank at Bekoji and oil content was highest at Holetta. Days to flowering were as early as 65 days at warmer weather of Kulumsa as opposed to 91 days at the cooler site of Bekoji. Likewise, days to maturity were prolonged up to 166 at Bekoji, against the 120 days of Asasa.

Regarding the intensities of diseases, powdery mildew was relatively higher at Kulumsa and Sinana as opposed to that of Bekoji, and a similar trend was noted for pasmo though Adet had the lowest incidence (Table 4.33). Similarly, the scores for Fusarium wilt were negligible at Sinana, Holetta and Adet, unlike at Kulumsa, where a relatively higher score was recorded.

Plant height was maximum at Kulumsa and Sinana (95 cm) and shorter by 10 cm at Holetta. In the associated manner, lodging was also highest at Kulumsa followed by Bekoji. Furthermore, the stand count was very good at Kulumsa unlike that of Holetta and Asasa, where land levelling problem, uneven distribution of rainfall and thus varied soil moisture affected the plant density besides other biotic and abiotic stresses.

Table 4.33. Summary of average oil yield (kg ha^{-1}) and other traits of 11 linseed entries tested across six locations in Ethiopia from 1996 to 1998.

Locations	OY	SY	OC	DF	DM	PM	PS	FW	PH	LP	SP
1. Bekoji	644	1752	36.6	91	166	1.1	1.9	1.5	87	29.2	98
2. Holetta	484	1264	38.3	79	144	1.5	1.5	0.4	85	0.2	79
3. Sinana	462	1266	36.1	77	145	2.3	2.9	0.0	94	10.6	84
4. Adet	455	1305	35.5	70	132	1.6	0.2	0.6	89	1.9	91
5. Kulumsa	459	1276	35.0	65	124	3.2	2.2	7.0	95	50.8	99
6. Asasa	473	1315	36.0	70	120	1.2	1.3	4.1	89	6.7	80
Mean	492	1363	36.3	75	139	1.8	1.7	2.3	90	16.6	88.3
S.E. (±)	65.7	21.9	0.3	0.2	0.3	0.05	0.05	0.5	0.43	1.17	0.48
C.V. (%)	12.94	18.46	2.92	2.30	2.37	20.7	24.2	24.8	5.52	31.10	6.19

Note: OY = Oil yield; SY = Seed yield; OC = Oil content; DF = Days to flowering; DM = Days to maturity; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; PH = Plant height; LP = Lodging percentage; SP = Stand percentage.

The correlation among the 11 measured characters is summarised in Table 4.34. There were highly significant (P<0.01) positive correlations between oil yield and seed yield (r = 0.924), oil yield and plant height (r = 0.585), and oil yield and stand count (r = 0.656). Seed yield was, however, negatively affected by days to flowering and maturity, indicating the poor yielding ability of early maturing varieties. The same was true with seed yield and powdery mildew, and seed yield and lodging percent. Oil content was positively influenced by days to maturity, plant height and stand percentage, implying that late maturing and tall plants positively contribute to the oil content of linseed. Actually, late maturing genotypes have more time to synthesise oils than the early ones.

On the other hand, there was highly significant negative correlation between the oil content and powdery mildews ($r = -0.773$), oil content and Fusarium wilt ($r = -0.644$), oil content and pasmo ($r = -0.511$). This clearly shows the negative effects of these diseases on oil content of linseed. Thus, in order to improve the oil content one may undertake indirect selection through developing resistant varieties against these diseases. The three diseases of linseed were positively but not significantly related with each other, and pasmo was also positively associated with lodging incidences. Days to flowering and maturity were highly and positively correlated ($r = 0.761$) with each other, in contrast to the negative correlation of these characters with most of the measured traits (Table 4.34), indicating the limitations of the early maturing varieties. These include susceptibility to the three diseases, lodging and consequently of poor plant stands. Similarly, lodging was positively associated with plant height, indicating the susceptibility of tall plants to lodging problems.

Table 4.34. Simple correlation among 11 characters of linseed entries tested at six locations in Ethiopia, 1996-1998.

	OY	SY	OC	FD	MD	PM	PS	FW	PH	LP	SP
OY	-	0.924**	0.212	-0.282	- 0.173	- 0.271	0.149	0.033	0.585*	- 0.197	0.656*
SY		-	- 0.123	-0.342	- 0.346	- 0.085	0.407	0.252	0.381	- 0.176	0.478
OC			-	0.247	0.341	- 0.733**	- 0.511	- 0.644**	0.510	0.070	0.289
FD				-	0.761**	- 0.351	- 0.706**	- 0.234	- 0.560*	- 0.473	- 0.257
MD					-	- 0.032	- 0.759**	- 0.335	- 0.437	- 0.651**	- 0.147
PM						-	0.325	0.225	- 0.471	- 0.231	- 0.317
PS							-	0.389	0.181	0.490	- 0.263
FW								-	- 0.126	0.124	- 0.048
PH									-	0.496	0.578*
LP										-	- 0.143

SY = Seed yield; OY = Oil yield; OC = Oil content (%); DF = Days to flowering; DM = Days to maturity; PH = Plant height (in centimetre); LP = Lodging percentage; SP = Stand percentage at maturity; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage

*, ** = Significantly correlated at 0.05 and 0.01 levels, respectively

4.9 Canonical variate analysis of genotypes

The canonical variate analysis, which is sometimes known as discriminant analysis has been used to classify and describe individual genotypes into two or more alternative groups on the basis of a set of measurements (Afifi and Clark, 1996). The extent to which an individual trait contributed to a canonical variate is indicated by the magnitude of its canonical coefficient. Canonical correlation and variate analyses have recently been reported by De Lange (1999) and Mamuya (2000), in the studies of quality characters of small-seeded white beans (*Phaseolus vulgaris* L.) and irrigated spring wheat (*Triticum aestivum* L.), respectively. Their procedures identified linear combinations of variables in one set that are most highly correlated to linear combinations of the second set. As described by De Lange (1999), the analysis of variance (ANOVA) is a univariate technique, whereby one can show statistical evidence for real differences between the genotypes for each variate separately. There were strong evidences (cf. sections 4.1-4.4) of differences between the evaluated linseed genotypes for nearly all the measured traits. Nevertheless, they do not reveal how the genotypes are grouped, or which variates are most important in discriminating between them. Hence, linear discriminant analysis (canonical variate analysis) was used to show these different groups of genotypes and their attributed variates.

In this study, 11 variables (oil yield, seed yield, oil content, agronomic characters and the scores of disease reactions) were analysed for the 10 linseed genotypes evaluated across six locations of Ethiopia. The results indicated that the first two canonical variates (CAN1 and CAN2) altogether accounted for 78.01% of the total variation among the groups of genotypes (Table 4.35). The horizontal separation (CAN1) accounted for 60.63% of the total variation, while the vertical separation (CAN2) attributed only 17.38%. This vertical separation was mainly due to days to flowering, the score of powdery mildew disease and lodging percent as shown by their canonical coefficients (Table 4.37). Similarly, days to flowering and lodging percentage played important roles in the horizontal separation as well.

As indicated in Table 4.37, the horizontal separation contributed a highly significant (P<0.001) share (60.63%) of the total variability. Subsequently, more emphases were given to CAN1 in grouping the 10 linseed genotypes based on their relative values. As presented in Table 4.35, R12-D33C and R12-D24C contrasted the most with the other genotypes, especially with Chilalo and P13611x10314D. This was because of the relatively higher positive CAN1 scores

for R12-D33C and R12-D24C and negative CAN1 scores for Chilalo and P13611x10314D. In the same manner, the groupings of these linseed genotypes are illustrated on a plot of the two canonical variates mean scores (Figure 4.3.). Closer points between the genotypes indicate similarity of genotypes, whereas those further apart suggest dissimilar ones, based on the general performance of the variates employed to distinguish them.

As far as this canonical analysis is considered, R12-D33C and Chilalo varieties were dissimilar from most of other genotypes. As mentioned in the above discussion, days to flowering, percent of lodging, and oil content were mainly responsible for distinguishing R12-D33C, while stand count percentage, days to maturity and oil yield were responsible for identifying Chilalo and other varieties with negative CAN1 values (Table 4.37). Indeed, R12-D33C and Chilalo were dissimilar as they were on the far ends of positive and negative CAN1 values, respectively. On the other hand, P13611x10314D was very similar to Chilalo and the same was true for R11-N1266 and P13611x10314B genotypes. This has shown the close similarity of both the crossed lines (P13611x10314D and P13611x10314B) although Chilalo and R12-N1266 were also classified with this group. In other words, the standard variety (Chilalo), the crossed lines and a regenerant (R12-N1266) were grouped in this category. Such a grouping clearly shows varieties originated from different sources can be clustered in similar groups because of their similar performance in different environments. Likewise, NorLin cultivar was found very similar to R12-N10D (the most stable genotype, seed yield-wise), and it should be noted that R12-N10D was originally derived from the tissue culture of NorLin.

Based on this canonical analysis, the 10 linseed genotypes were generally classified into two major classes; those with above mean CAN1 values (i.e. positive values) and those with below mean values (i.e. negative ones). Among the above average or positive CAN1 values were R12-D33C, R12-D24C and R11-M20G though the latter regenerant was largely deviated from the group due to its lower CAN1 value, which was closer to average or zero. This regenerant was derived from the cultivar McGregor, while the remaining two were initially obtained from Dufferin. These differences and similarities can, therefore, be explained by the original sources of the materials and by various environments in which the genotypes were grown. In fact, the characteristics of genotypes depend on the genetic architecture of cultivars and on environmental factors. Most frequently, breeders exert control on the genetic make-up, but they cannot control the unpredictable environmental factors. However, it is easier to predict the location effects than the year effects (Hosfield, 1984; De Lange, 1999). Thus, more emphases

should be given to understand the localities and their associated agro-climatic conditions in order to improve the crop requirements in addition to modifying the genotypes.

The second group of genotypes that had negative CAN1 values included Chilalo, P13611x10314D, R12-N10D, NorLin, P13611x10314B, R10-N27G and R11-N1266. Nevertheless, R12-N10D and NorLin slightly deviated from this group as they had relatively lower values (Table 4.35). These lower values indicate the closeness of these genotypes to the average values or zero according to their multivariate analysis (Figure 4.3). It also shows the stable performance of genotypes in a range of tested environments. As mentioned in the above discussion, percentage of stand count, days to maturity and oil yield variates have played a large role in discriminating this second group (Table 4.37). In contrast, scores of pasmo and wilt diseases had a minor contribution in distinguishing the cultivars and this could be due to the low incidence of these diseases at some localities during the evaluation seasons. In general, this type of grouping of genotypes has also elucidated the differential response of cultivars in a range of environmental conditions as reported by De Lange (1999) and Mamuya (2000).

Table 4.35. Canonical variate percentage variation and mean scores of the first two canonical variates of the 10 genotypes tested in Ethiopia, 1996-98.

Genotype	CAN1 60.63%	CAN2 17.38%
1. R11-M20G	0.4217	0.0387
2. R11-N1266	-1.1277	-0.8090
3. R10-N27G	-0.7999	-1.0643
4. P13611x10314B	-0.9995	-1.8771
5. R12-N10D	-0.4735	-0.6706
6. R12-D33C	2.9447	0.1500
7. R12-D24C	2.8736	0.4185
8. P13611x10314D	-1.6820	0.8540
9. NORLIN	-0.4094	0.8872
10.CHILALO	-1.6951	0.0928

Table 4.36. Multivariate statistics and F approximations for the canonical discriminant analysis of the 10 genotypes tested in Ethiopia, 1996-98.

Statistic	Value	F	DF	Den DF	Pr > F
Wilks' Lambda	0.04883636	1.5845	99	293.5229	0.0017
Pillai's Trace	2.05414959	1.2905	99	432	0.0453
Hotelling-Lawley Trace	5.16794996	1.9953	99	344	0.0001
Roy's Greatest Root	3.13335640	13.6728	11	48	0.0001

Note: F Statistic for Roy's Greatest Root is an upper bound.

Table 4.37. Pooled within class standardised canonical coefficients, indicating the extent to which each trait contributed to a canonical variate of the 10 genotypes tested in Ethiopia.

Variable	CAN1	CAN2
Oil yield	-0.8839	-0.4912
Seed yield	-0.2975	-1.2361
Oil content	1.5303	-0.1714
Days to flowering	2.5143	3.1818
Days to maturity	-1.0639	-0.8342
Powdery mildew score	-0.3004	1.8371
Pasmo score	-0.0900	-1.0566
Wilt percentage	-0.1103	0.6066
Plant height	1.4042	0.1711
Lodging percent	1.6377	-1.1795
Stand percentage	-1.3879	0.4236

Table 4.38. Mean values of the 10 linseed genotypes for all variates considered in the canonical variate analysis.

No. Genotype	Characters										
	OY	SY	OC	DF	DM	PM	PS	FW	PH	LP	SP
1. R11-M20G	534	1434	36.7	78	144	1.5	1.6	2.5	90	14	88
2. R11-N1266	506	1414	35.8	73	134	1.8	1.9	2.6	91	16	89
3. R10-N27G	520	1455	35.6	73	134	1.9	2.0	3.6	92	20	88
4. P13611x10314B	481	1292	35.9	75	141	2.2	1.4	2.3	90	15	89
5. R12-N10D	507	1385	36.2	73	134	1.8	1.9	2.3	93	19	88
6. R12-D33C	494	1305	37.4	77	140	1.3	1.4	1.4	93	17	88
7. R12-D24C	469	1247	37.1	76	139	1.3	1.4	1.9	92	20	89
8. P13611x10314D	499	1348	36.4	74	142	2.3	1.6	2.3	88	13	88
9. NORLIN	502	1394	36.2	73	135	2.0	2.0	1.2	91	19	88
10.CHILALO	556	1505	36.3	77	139	1.6	1.4	2.3	89	12	90
Mean	498.6	1362.8	36.3	75	139	1.8	1.7	2.3	90	16.6	88.3

Note: OY = Oil yield; SY = Seed yield; OC = Oil content; DF = Days to flowering; DM = Days to maturity; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; PH = Plant height; LP = Lodging percentage; SP = Stand percentage.

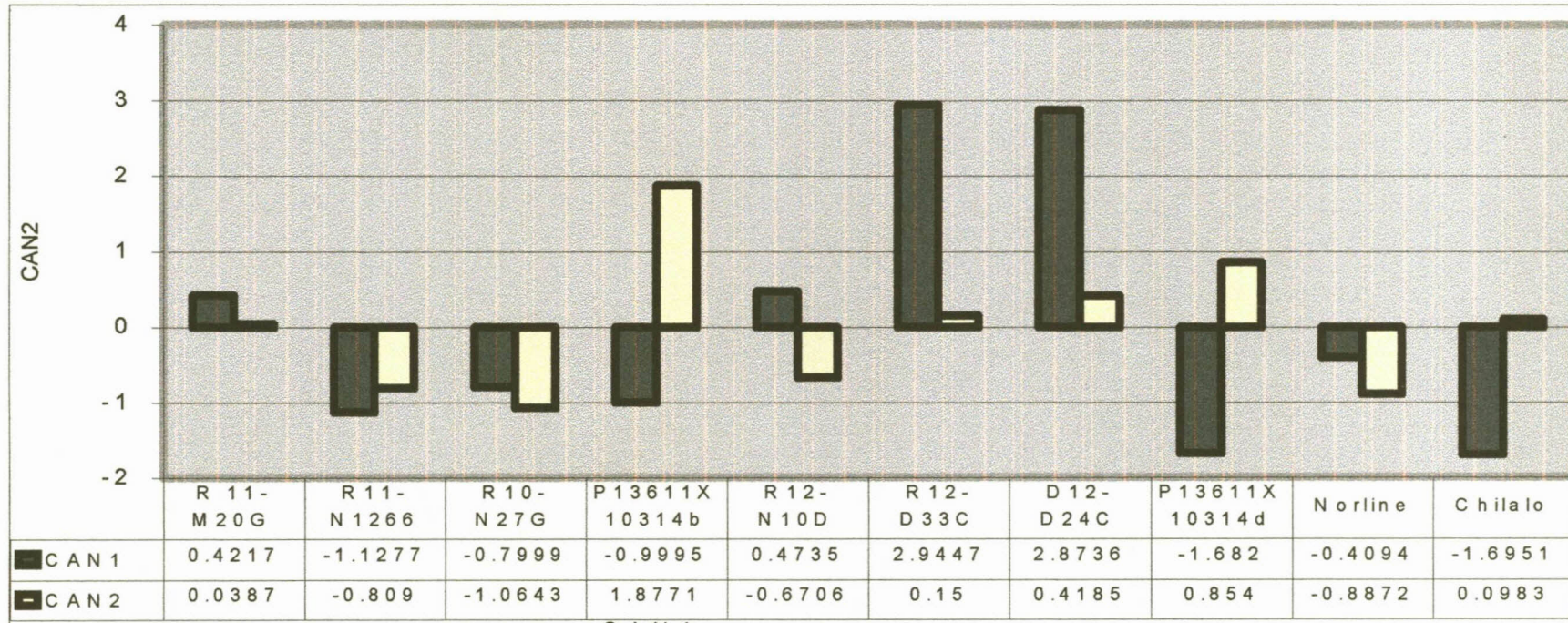|	R 11-M 20G	R 11-N 1266	R 10-N 27G	P 13611X 10314b	R 12-N 10D	R 12-D 33C	D 12-D 24C	P 13611X 10314d	N orline	C hilalo
■ C A N 1	0.4217	-1.1277	-0.7999	-0.9995	0.4735	2.9447	2.8736	-1.682	-0.4094	-1.6951
▬ C A N 2	0.0387	-0.809	-1.0643	1.8771	-0.6706	0.15	0.4185	0.854	-0.8872	0.0983

C A N 1

F ig 4.3. Plot of m ean scores of 10 linseed genotypes, 1996-98

4.10 Canonical variate analysis of locations

The same 11 variates employed to describe the genotypes were also used here to discuss the similarities or differences among the six locations used for the evaluation of linseed genotypes from 1996 to 1998. As shown in Table 4.39, the first two canonical variates (CAN1 and CAN2) together accounted for 96.39% of the total variations among the groups. The horizontal separation (CAN1) significantly (P<0.05) accounted for this variability (Table 4.40) against the vertical one, which was attributed only 4.83%. As a result, CAN1 was mainly considered in classifying these locations.

It is evident from Table 4.39 that Bekoji contrasted the most with other locations because of its highest positive value against the small positive and negative scores of the other sites. This result has confirmed the long-standing truth of Bekoji site that environment of Bekoji has been very good for excellent performance of linseed. The highest seed yield; up to 2.5 t ha^{-1} has been recorded at this site. Bekoji is situated in the South-eastern part of Ethiopia at an elevation of 2800 meters above sea level and it has cooler temperatures (cf. Chapter 3., Table 3.2). As indicated in Table 4.41, Bekoji was dissimilar to most of the other sites based on the seed yield variable. The mean yield obtained from this site was 1752 kg ha^{-1}, exceeding the remaining localities by over 40% (Table 4.42). This analysis has, therefore, displayed the unique environment of Bekoji for linseed production, and it may need special strategy in terms of cultivar development and crop management practices to exploit the existing potentials more effectively. The other variates, which attributed to distinguish this location were oil content, stand percentage, score of pasmo and percent of lodging as shown in Tables 4.41 and 4.42. In short, the unique environment of Bekoji needs special strategy in terms of cultivar development and crop management practices to exploit the existing potentials to their full capacity.

The next different location was Asasa, with its highest negative value (CAN1 = -11.2). As mentioned in the preceding discussion, this site has been known for its unreliable rainfall and terminal drought that occurs most of the time. As far as the CAN1 value goes, Adet site was relatively closer to Asasa (Table 4.39). Further groupings of these locations are illustrated in Figure 4.4. Asasa was dissimilar to most of the other sites based on its oil yield and Fusarium wilt percentage, as indicated in Tables 4.41 and 4.42.

The other different site was Kulumsa and it has shown contrasting negative CAN1 values with Sinana, which had similar values but positive (i.e. both were equally closer to the mean value in different directions). Like Asasa, Kulumsa was discriminated by the oil yield and wilt percentage (Table 4.41). Kulumsa has a relatively warmer climate and fertile soils that are conducive for good crop growth and development, consequently lodging problem has been very high (Table 4.42). Moreover, the environment of Kulumsa was also conducive for the development of wilt, powdery mildew and pasmo diseases as shown in Table 4.42.

On the other hand, Sinana scored positively above but close to the average value (CAN1 = 5.53) and was not similar to the other localities. This result reflects the real circumstances of Sinana. It has a very different agro-ecology, bimodal and erratic rainfall distribution. Subsequently, the area has got two growing seasons per annum, unlike the other research centres. Similarly, Holetta scored a negative value, which is very close to the average value. Thus, it was not grouped with any of the localities though Kulumsa was relatively closer to it. Like the other locations that scored negative CAN1 values, Holetta was discriminated by the oil yield, wilt and other disease scores. These localities are, therefore, appropriate sites to screen for disease resistance and to develop high oil yielding varieties. In summary, this canonical disciminant analysis has confirmed the existence of adequate diversity among these six research centres, and thus adding more sub-centres and testing sites under them are justifiable as far as this study is concerned. However, further analyses and additional studies are needed for wider applications.

Table 4.39. Canonical variate percentage variation and mean scores of the first two canonical variates of six locations in Ethiopia used to test 10 genotypes of linseed during the 1996-98.

	CAN1	CAN2
Genotype	91.56%	4.83%
1. Adet	-9.6251	-0.8645
2. Asasa	-11.2036	-2.0104
3. Bekoji	22.6861	-0.3490
4. Holetta	-1.0489	-2.1694
5. Kulumsa	-6.3349	5.6475
6. Sinana	5.5264	-0.9521

Table 4.40. Multivariate statistics and F approximations for the canonical discriminant analysis of the six locations in Ethiopia used for the test of 10 linseed genotypes, 1996-98.

Statistic	Value	F	DF	Den DF	Pr > F
Wilks' Lambda	0.00001396	2.3802	55	12.84456	0.0450
Pillai's Trace	3.78679337	1.7025	55	30	0.0586
Hotelling-Lawley Trace	219.69469467	1.5978	55	6	0.4614
Roy's Greatest Root	201.14822767	109.7172	11	48	0.0001

Note: F Statistic for Roy's Greatest Root is an upper bound.

Table 4.41. Pooled within class standardised canonical coefficients of the six locations used for to test 10 genotypes of linseed tested, 1996-98

Variable	CAN1	CAN2
Oil yield	-40.8038	-55.1216
Seed yield	42.8387	53.5405
Oil content	5.2655	7.6066
Days to flowering	1.9031	0.4951
Days to maturity	0.3740	-1.3466
Powdery mildew score	-1.1322	0.8839
Pasmo score	3.1721	0.5159
Wilt percentage	-2.8638	-0.5989
Plant height	-1.0873	-1.1127
Lodging percent	2.1835	-1.1127
Stand percentage	3.4035	2.0635

Table 4.42. Mean values of six locations involved in the test of 10 linseed genotypes considered in this canonical variate analysis in Ethiopia from 1996 to 1998.

Locations	OY	SY	OC	DF	DM	PM	PS	FW	PH	LP	SP
						Characters					
1. Bekoji	644	1752	36.6	91	166	1.1	1.9	1.5	87	29.2	98
2. Holetta	484	1264	38.3	79	144	1.5	1.5	0.4	85	0.2	79
3. Sinana	456	1266	36.2	77	145	2.3	2.9	0.0	94	10.6	84
4. Adet	455	1305	35.5	70	132	1.6	0.2	0.6	89	1.9	91
5. Kulumsa	459	1276	35.0	65	124	3.2	2.2	7.0	95	50.8	99
6. Asasa	473	1315	36.0	70	120	1.2	1.3	4.1	89	6.7	80
Mean	499	1363	36.3	75	139	1.8	1.7	2.3	90	16.6	88

Note: OY = Oil yield; SY = Seed yield; OC = Oil content; DF = Days to flowering; DM = Days to maturity; PM = Powdery mildew score; PS = Pasmo disease score; FW = Fusarium wilt percentage; PH = Plant height; LP = Lodging percentage; SP = Stand percentage.

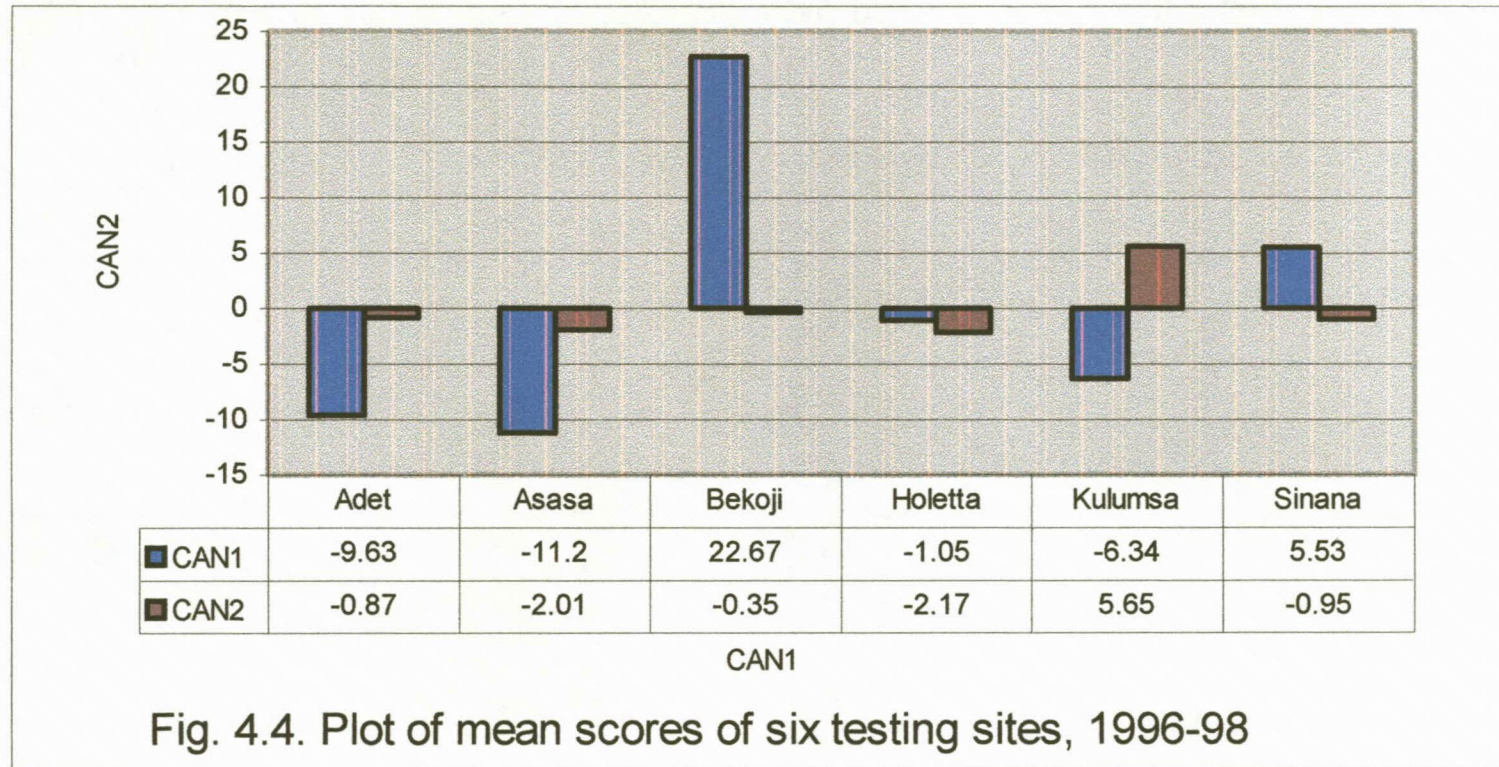|	Adet	Asasa	Bekoji	Holetta	Kulumsa	Sinana
CAN1	-9.63	-11.2	22.67	-1.05	-6.34	5.53
CAN2	-0.87	-2.01	-0.35	-2.17	5.65	-0.95

Fig. 4.4. Plot of mean scores of six testing sites, 1996-98

CHAPTER 5

CONCLUSIONS AND RECOMMENDTIONS

- The standard variety, Chilalo out-yielded all the genotypes, with an average yield of 1505 kg ha^{-1} across locations and years. The next high yielding varieties were three regenerants namely, R11-M20G, R10-N27G and R11-N1266, with the mean yield ranging from 1414 to 1455 kg ha^{-1}. R12-N10D was also the most stable variety with its mean yield of 1385 kg ha^{-1} across locations and years. R11-M20G was already recommended for commercial production in Adet area in 1999. And more promising varieties, like N12-N10D are forthcoming for release or to be used as parents in the future crossing programmes. These results indicated the high potentials and good adaptation of the regenerants to the linseed growing environments of Ethiopia. Moreover, this study and past experience of linseed research showed the tremendous contributions of exotic genotypes in the cultivar development programme of Ethiopia. Therefore, the strategy of introducing exotic materials should be consolidated in addition to utilising the desirable qualities of local germplasm in the breeding programmes.

- The average of separate analyses during the three years showed that 45% of the total variance was accounted for by the blocks; while genotypes contributed 39% and the remaining 16% was due to random errors. Higher levels of variation for blocks were registered at Holetta, Adet and Asasa, indicating more heterogeneous experimental fields, such as poor land levelling and subsequent variability in soil moisture and fertility levels that need close follow ups and corrective measures. On the other hand, the highest seed yield of 2172 kg ha^{-1} was obtained from Bekoji, followed by that of Kulumsa, indicating the good potentials of these sites. Such locations, with unique potentials require special strategies to make use of their full potentials and Bekoji deserves high priority in this regard.

- The combined analyses of variance depicted highly significant (P<0.01) differences among the genotypes (G) for seed yield and other measured traits across locations (L), years (Y) and their interactions. The variance components of seed yield was 55% for

years, 26% for locations, 13% for Y x L interactions, 3% for G x L x Y interactions and 3% for genotypes. These results indicated high differential responses of the genotypes to their growing environments due mainly to the unpredictable climatic factors. These, in turn, suggest the confounding effects of environmental factors on the variety selection processes and, thus, imply the necessity of stability analysis to identify appropriate varieties for their targeted environments. In general, when G x E interaction is due mainly to unpredictable environmental factors (e.g. year to year variation as shown in this study), stable varieties that perform reasonably well under a range of conditions have to be developed. For better description and prediction, however, the environmental variables have to be adequately measured and analysed along with the data of the genotypes, and thus future research should focus in these areas.

• Seven methods of stability analyses were applied to determine the relative stability of 10 linseed genotypes tested across 18 environments of Ethiopia. Francis and Kannenberg's (1978) coefficient of variability, Shukla's (1972) stability variance, Nasser and Huehn's (1978) variance of ranks and AMMI's stability values unanimously detected the most stable genotype, R12-N10D. Wricke's (1962) ecovalence and Eberhart and Russell's (1966) deviation from regression also revealed this genotype as one of the stable varieties, while only Lin and Binns's (1988a) cultivars' superiority measure classified it in the intermediate stability group. The same was true for P13611x10314D variety, which was identified as the second most stable across the tested environments. In other words, these stability parameters identified R12-N10D, P13611x10314D and Chilalo as the most stable varieties in the given order. Consequently, the AMMI model, Eberhart and Russell's (1966) deviation from regression, Nasser and Huehn's (1978) variance of ranks and Shukla's (1972) stability variance were found very important in determining the comparative stability of the tested genotypes in this study. This fact was also reflected by the Spearman's rank correlation that indicated significant correlations among these stability parameters. As AMMI combines the analysis of variance and principal components analysis in one model, it was found useful in describing both the G x E interaction and stability analysis through its response patterns. Since information on G x E interactions and stability of varieties are essential for farmers, breeders and other agricultural experts, the data on stability analyses need to be available to the users whenever new varieties are proposed for commercial release, whether they are recommended for specific or broad adaptations.

- The study of oil content and oil yield revealed that the highest location mean of 38.3% was obtained from Holetta followed by that of Bekoji (36.6%). Among the tested genotypes, R12-D33C and R12-D24C gave the highest average oil percentage of 37.4% across the localities. R12-N10D also had a good oil percentage, like its stability performance in seed yield. Therefore, varieties such as R12-N10D and R12D33C can either be released directly or used in the crossing programme to improve the oil contents. The analyses of variance for both oil content and oil yield across locations and years indicated highly significant differences between the genotypes, indicating the potential for the improvement of oil content. The variance components across locations and years also depicted higher variability for years, locations, and genotypes and for their interactions in this order.

- The assessment of agronomic characters indicated that on average the genotypes took about 75 and 139 days to reach the flowering and maturity stages, respectively. The early flowering entries also matured earlier than others, after 134 days, unlike the late maturing ones, which took up to 144 days. R11-N1266, R10-N27G, R12-N10D and NorLin were among the early maturing group, while R11-M20G, P13611x10314D and the local checks were late maturing. The two crosses were found more susceptible to powdery mildew, while R12-D33C, R12-D24C, R11-M20G and Chilalo were relatively resistant to powdery mildew and pasmo diseases. Hence, these genotypes can be used in the breeding programmes aimed at developing resistant varieties against these diseases.

- The degrees of relationship among the measured characters indicated highly significant positive correlations between oil yield and seed yield, oil yield and plant height, and oil yield and stand count. However, seed yield was negatively affected by days to flowering and maturity, indicating the poor yielding ability of early maturing varieties. The same was true with seed yield and powdery mildew, and seed yield and lodging percent. Similarly, the oil content was positively influenced by days to maturity, plant height and stand percentage, indicating the positive contributions of late maturing and tall plants to the oil content of linseed. On the other hand, a highly significant negative correlation was realised between the oil content and the three diseases of linseed (powdery mildews, Fusarium wilt and pasmo).

- As one of the major outcomes of this study, R12-N10D regenerant is recommended for commercial release in Ethiopia as it fulfils nearly all the desirable qualities of standard linseed varieties, which is required by the variety release system of Ethiopia. Its seed and oil yields were very good and it was the most stable variety of linseed among the tested genotypes by six different stability parameters. It is early maturing and reasonably tolerant to the three major diseases of linseed. It can also be used as parent material in the future crossing programmes.

- The linear discriminant analysis or canonical variate analysis, which was employed to classify and describe the genotypes along with their attributed variates, indicated that the first two canonical variates (CAN1 and CAN2) jointly accounted for 78% of the total variation of the genotypes. The horizontal separation (CAN1) alone accounted for 60.6% of the total variation, while the vertical separation (CAN2) attributed for 17.4%. Hence, horizontal separation was used in classifying the genotypes. Accordingly, R12-D33C and R12-D24C contrasted the most with the other genotypes. P13611x10314D was very similar to Chilalo and the same was true with NorLin and R12-N10D. The 10 linseed genotypes were generally classified into two major categories, the genotypes with above mean values (i.e. positive values) and those with below mean values (i.e. negative ones). R12-D33C, R12-D24C and R11-M20G scored positive values though the latter regenerant was largely deviated from the group and much more closer to the average value. The second group of genotypes that had negative values included Chilalo, P13611x10314D, R12-N10D, NorLin, P13611x10314B, R10-N27G and R11-N1266. However, R12-N10D and NorLin were slightly deviated from this group because of their lower values, which were closer to the average. Percentage of stand count, days to maturity and oil yield played major roles in identifying this second group, while days to flowering, lodging percentage, oil content and plant height played important roles in the separation of the first group.

- The same variates used to describe the genotypes were also applied to explore the similarities and differences of the six test locations. The first two canonical variates together accounted for 96.4% of the total variations among the locations. The horizontal separation significantly (P<0.05) accounted for 91.6% of the variability, while vertical separation was responsible for only 4.8%. Consequently, horizontal separation was used in classifying the locations. Bekoji contrasted the most with other locations and this has

confirmed the long-standing reality of Bekoji. It has been known for producing the highest seed yields, up to 2.5 t ha^{-1}. The canonical variate analysis also proved that Bekoji was dissimilar to most of the other sites because of its seed yield, which was 1752 kg ha^{-1} and exceeded the remaining localities by over 40% during the three years. Bekoji has a cooler climate and very suitable environment for a good performance of linseed. Asasa, with its highest negative value was also different, as it has been known for its unreliable rainfall and terminal drought. It was dissimilar to most of the other sites although it was a bit closer to Adet. Kulumsa showed contrasting negative values with Sinana, being equally closer to the mean value in the opposite directions. It has relatively warmer climate and fertile soils that are conducive for good crop growth and development, often resulting in high percentage of lodging. It was also conducive for the development of wilt, powdery mildew and pasmo diseases and thus can be used as one of the disease screening sites to develop resistant varieties. Sinana scored positively above average and also differed from the other sites. This result again reflects the real environment of Sinana, which has different agro-ecology, bimodal and erratic rainfall distribution, among many others. The area also has two growing seasons per annum, unlike the other research centres. Likewise, Holetta scored a negative value, which was closer to the average value and was ungrouped with any of the localities though Kulumsa was relatively closer to it. Holetta, like the other locations with negative values, was discriminated by the oil yield, wilt and other disease scores, and is appropriate site for screening disease resistant and high oil yielding varieties. This canonical discriminant function has, therefore, found the existence of adequate diversity among these six research centres. Subsequently, opening or adding some more sub-centres and testing sites under them are justifiable to develop either broadly adapted varieties or different varieties for different environments, of course, with additional analyses of the farming systems and feasibility studies.

• Eventually, the canonical variate analysis, which was undertaken to classify and describe the similarities and differences of the genotypes and their test localities by using the measured variables at a time, was found to be a useful and suitable analytical tool to obtain vital information required for developing effective strategy in cultivar development programmes. The knowledge of this analysis helps to reduce cost of extensive evaluation schemes by reducing unnecessary duplications of similar genotypes and testing sites. Conversely, it can assist in identifying diverse testing

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materials and site, and thus can be useful in fine-tuning the breeding programmes. In short, as shown in the above discussion, useful information can be generated by the canonical analysis by providing better classifications of genotypes and sites, showing the relative contribution of the variables to these classifications. However, further studies are required for wider applications and to make use of the method more effectively.

CHAPTER 6

SUMMARY

1. The study was undertaken to assess the comparative performance of six linseed regenerants along with two crosses and three check cultivars across 18 linseed-growing environments of Ethiopia from 1996 to 1998. The seed yield and other agronomically desirable characters were analysed with different statistical procedures to determine the adaptation potential, G x E interactions and seed yield stability performance. The main objective of the study was to understand and describe the genotypes and their growing environments by applying different statistical methods of analyses in order to make useful recommendations for the future. Likewise, contemporary studies on the genotypes, environment and their interactions, and various analytical methods of stability parameters were discussed.

2. Separate and combined analyses of variance across locations and years, seven types of stability parameters, correlation and canonical variate analyses were performed using MSTAT-C, AGROBASE 98 and SAS computer programmes. For the stability analyses, data of 10 varieties evaluated across six locations and three years (excluding the local checks) were analysed by following the procedures of: Francis and Kannenberg (1978) for the coefficient of variation, Finlay and Wilkenson (1963) and Eberhart and Russell (1966) for the joint regression, Wricke (1962) for ecovalence, Shukla (1972) for stability of variance, Lin and Binns (1978) for cultivars' superiority measure, Nassar and Huehn (1978) for variance of ranks and Gauch and Zobel (1988) for AMMI stability model. Comparisons were also made among these different stability measurements. Canonical variate analyses were undertaken on SAS CANDISC programme (SAS Institute, 1982) to classify and describe the genotypes and their test localities.

3. The separate trial analyses for the three years have shown highly significant (P<0.01) differences among the genotypes for seed yield and most of the measured traits. Totally four regenerants outperformed the crosses in 1996 and most of them repeated their performance during the succeeding years. Across locations and years, Chilalo ranked first (1505 kg ha^{-1}), followed by three regenerants (R11-M20G, R10-N27G and R11-N1266), with a yield ranging from 1414-1455 kg ha^{-1}. The high yielding performance of the regenerants indicates

their high potentials and good adaptability to the linseed growing environments of Ethiopia. In fact, R11-M20G was already recommended for commercial production in Adet area in 1999. Among the locations, the highest yield of 2172 kg ha^{-1} was obtained from Bekoji, followed by that of Kulumsa over the years, indicating the good potentials of these sites. The result also showed tremendous yield variations over locations and years, suggesting high G x E interactions. The average of ANOVA components over the three years showed that about 45% of the total variance was accounted for by blocks, 39% by genotypes and the remaining 16% was attributed to random errors. As higher variability for blocks was recorded at Holetta, Adet and Asasa, further analysis of environmental factors (edaphic and climatic) and close supervisions are needed.

4. The combined analysis of variance across locations showed highly significant (P<0.01) difference among the locations (L), genotypes (G) and their interactions for most of the measured traits, indicating high differential responses of the genotypes over the locations, due mainly to edaphic and climatic related factors. About 76-85% of the variance components was also attributed to locations, while the genotypes accounted for only 3-7% (nearly similar to that G x L component) over the three years. These indicate the confounding effects of environmental factors and thus necessity of stability analysis to select appropriate varieties for their required purposes.

5. The combined analysis of variance and the percentage of its components for the seed yield across years per location show highly significant (P<0.01) differences for the years, genotypes and their interactions at Bekoji, Holetta and Kulumsa. In contrast, Y x G interactions were not significant at Sinana, Adet and Asasa, indicating more yield stability over the three years at these sites than the others. The variance components of ANOVA indicate higher variabilty for years or growing seasons, ranging from 50% at Adet to 94% at Bekoji. This large seasonal variability may have been due mainly to the amount and distribution of rainfall, among other factors. Repeatability of the trials at Bekoji and Holetta was about 85% against the lowest of Asasa (48%). This also indicates the high level of environmental variations that needs further diagnosis either to adjust or cope along with them.

6. The combined analysis across locations, years and their interactions reveals highly significant differences (P<0.01) among the genotypes for all the measured traits,

suggesting differential responses of the genotypes to their test environments. As significant G x E interactions tend to confound cultivar selection processes and create difficulties in identifying reliable varieties, stability analysis with appropriate statistical methods are required. The variance components of seed yield were estimated to about 55% for years, 26% for locations, 13% for Y x L interactions, 3% for genotypes and the remaining 3% for the rest of interactions. Most of these interactions were highly significant due mainly to climatic; soil and biotic factors, and more in depth studies are needed for better understanding and further actions. As a general case, however, when G x E interaction is mainly caused by unpredictable environmental factors, such as year to year fluctuations in rainfall (like in this study), the breeder must try to develop stable varieties that can perform relatively good under a range of conditions. But if G x E interaction is due to predictable environmental factors, such as soil types and management practices, the plant breeder can develop either different varieties for different environments or broadly adapted varieties for a range of conditions.

7. The ANOVA of joint regression model for seed yield showed highly significant difference between the genotypes. According to this joint regression, R12-N10D was found the most stable genotype, followed by P13611x10314D and Chilalo (the highest yielder across the environments). All these stable varieties also had higher coefficients of determination, which were significantly correlated with the coefficient of regression and deviation from the regression. NorLin was also non-significantly different from the coefficient of regression and thus had general adaptability to diverse environments. The coefficient of variability also showed similar results.

8. According to Wricke's (1962) ecovalence, R11-M20G followed by R11-N1266, R12-N10D and P13611x10314D were the most stable genotypes. The first three genotypes were the regenerants of tissue culture, whereas the fourth was one of the crosses developed at Holetta Research Center. Chilalo, NorLin, R12-D33C and P13611x10314B were categorised as intermediate in stability, unlike R10-N27G and D12-D24C that were found unstable according to this stability measurement.

9. Shukla' s stability variance (1972) showed that R12-N10D, P13611x10314D and Chilalo were the most stable genotypes, while D12-D24C, R11-N1266 and R11-M20G were classified as the least stable. R12-N10D, the regenerant from NorLin was the most stable

genotype as measured by both ecovalence and stability variance. Join regression was also in close agreement with these results.

10. Lin and Binns's (1988a) cultivars' superiority measure indicated Chilalo, R10-N27G and R11-N1266 were the most stable genotypes, while D12-D24C and P13611x10314B were the least stable. In most cases, ranks of cultivar superiority measure were in harmony with the ranks of varietal mean yield rather than with other stability parameters.

11. Nassar and Huehn's (1978) non-parametric measure of stability revealed that R12-N10D had the smallest changes in ranks and thus was the most stable regenerant unlike D12-D24C, which was significantly unstable. The next more stable varieties were P13611x10314D and Chilalo. This result was in agreement with most of the above stability measurements.

12. Additive main effects and multiplicative interaction's (AMMI) stability value, and scores of the interaction principal component analysis (IPCA) indicated that R12-N10D, P13611x10314D, R12-D33C and Chilalo were relatively the most stable genotypes across the tested environments of Ethiopia. On the other hand, R11-N1266, R10-N27G and Norlin were specifically adapted to low or unfavorable conditions, according to these parameters. AMMI model has been widely and successfully used during the past few years to analyse and understand the G x E interactions and stability in many crops. Since it combines the analysis of variance and principal components analysis in one model, it describes adequately both the G x E interaction and stability analysis through its response patterns.

13. Comparison of the seven stability parameters has shown that the coefficient of variability, Shukla's (1972) stability variance, Nasser and Huehn's (1978) variance of ranks and AMMI's stability value (ASV) were harmonious in detecting the most stable genotype, R12-N10D. Ecovalence and deviation from regression also revealed this genotype as one of the stable varieties and only cultivars superiority measure categorised it in the intermediate stability group. The same was true to with the second most stable variety (P13611x10314D). In general, AMMI, Eberhart and Russell's (1966) deviation from regression, Nasser and Huehn's (1978) variance of ranks and Shukla's (1972) stability variance were found very useful in determining the comparative stability of linseed

genotypes considered in this study. The coefficient of variability and ecovalence were also relatively better than the cultivar's superiority measure. All in all, the seven parameters detected R12-N10D, P13611x10314D and Chilalo as the most stable varieties, and R12-D24C, R10-N27G and P13611x10314B as unstable ones, while the rest were intermediate between these two groups. However, repeatability study is needed to determine the best parameter.

14. The evaluation oil content and oil yield indicated that the highest location mean of 38.26% was obtained from Holetta, followed by that of Bekoji (36.6%). Of the genotypes, R12-D33C and R12-D24C gave the highest of about 37.4% across the localities. R12-N10D was also good in its oil percentage, like its seed yield. These varieties should, therefore, be used in the crossing programme to improve the oil contents. The analyses of variance for both oil content and oil yield across locations and years indicated highly significant difference (P<0.01) between the genotypes. The variance components across locations and years also depicted higher variability for years, locations, and genotypes and for their interactions in this order.

15. The assessment of agronomic characters revealed that the genotypes took 75 and 139 days to reach the flowering and maturity stages, respectively. The early flowered entries have also matured earlier than others after 134 days, unlike the late maturing ones that took up to 144 days. R11-N1266, R10-N27G, R12-N10D and NorLin were among the early maturing group, while R11-M20G, P13611x10314D and the local checks were late maturing. The two crosses were found more susceptible to powdery mildew, while R12-D33C, R12-D24C, R11-M20G and Chilalo were relatively resistant to powdery mildew and pasmo diseases.

16. The correlation among the measured characters showed highly significant (P<0.01) positive correlations between oil yield and seed yield (r = 0.924), oil yield and plant height (r = 0.585), and oil yield and stand count (r = 0.656). Seed yield was, however, negatively affected by days to flowering and maturity, indicating the poor yielding ability of early maturing varieties. The same was true with seed yield and powdery mildew, and seed yield and lodging percent. Oil content was positively influenced by days to maturity, plant height and stand percentage, implying that late maturing and tall plants positively contribute to the oil content of linseed. Highly significant negative correlation was noted between the oil content, and powdery mildews, Fusarium wilt and pasmo, indicating the negative effects of these diseases oil content of linseed.

17. Linear discriminant analysis (canonical variate analysis) was used to classify and compare the 10 genotypes and their attributed variates. The first two canonical variates (CAN1 and CAN2) altogether accounted for 78.01% of the total variation among the groups of genotypes. The horizontal separation (CAN1) was accounted for about 60.63% of the total variation, while the vertical separation (CAN2) attributed for 17.38%. This vertical separation was mainly due to days to flowering, the score of powdery mildew and lodging percent. Days to flowering and lodging percentage played important roles in the horizontal separation as well. Horizontal separation that showed very highly significant contribution in the total variability was used in grouping the genotypes. R12-D33C and R12-D24C contrasted the most with the other genotypes, like P13611x10314D. R12-D33C and Chilalo varieties were also dissimilar with most of other genotypes. P13611x10314D was very similar to Chilalo and the same was true for R11-N1266 and P13611x10314B. NorLin cultivar was very similar to R12-N10D, the most stable variety that deserves a license for commercial production. In general, the 10 linseed genotypes were generally classified into two major categories, the genotypes with above mean values (i.e. positive values) and those with below mean values (i.e. negative ones). R12-D33C, R12-D24C and R11-M20G were among the positive values were though the latter regenerant was largely deviated from the group and much more closer to the average. The second group of genotypes that had negative CAN1 values included Chilalo, P13611x10314D, R12-N10D, NorLin, P13611x10314B, R10-N27G and R11-N1266. Nevertheless, R12-N10D and NorLin were slightly deviated from this group as they had relatively lower values. The percent of stand count, days to maturity and oil yield played major roles in identifying this second group.

18. The same 11 variates employed to describe the genotypes were also used here to explore the similarities and differences of the six locations. The first two canonical variates (CAN1 and CAN2) together accounted for 96.39% of the total variations among the locations. The horizontal separation significantly ($P<0.05$) accounted for 91.56% of the variability, while vertical separation was responsible for 4.83%. Thus, CAN1 was mainly considered in classifying these locations. Bekoji contrasted the most with other locations and has verified the long-standing truth of Bekoji site. It has been very suitable site for good performance of linseed by producing highest seed yield, up to 2.5 t ha^{-1}. Bekoji was dissimilar to most of the other sites based on the seed yield variable. The mean yield obtained from this site was 1752 kg ha^{-1}, exceeding the remaining localities by over 40%. Hence, the environment of Bekoji

needs special strategy in terms of cultivar development and crop management practices to exploit the existing potentials more effectively. The other variates attributed to distinguish this location were oil content, stand percentage, the score of pasmo and percent of lodging and the same was true with Sinana. Asasa, with its highest negative value was also different, as it has been known for its unreliable rainfall and terminal drought. Asasa was dissimilar to most of the other sites based on its oil yield and Fusarium wilt percentage though it was relatively closer to Adet. Kulumsa showed contrasting negative values with Sinana, both being equally closer to the mean value in the opposite directions. Like Asasa, Kulumsa was discriminated by the oil yield and wilt percentage. Kulumsa has a relatively warmer climate and fertile soils that are conducive for good crop growth and development, resulting in high percentage of lodging. It was also conducive for the development of wilt, powdery mildew and pasmo diseases and it can be used as one of disease screening sites. Sinana scored positively above average and differed from the other sites. This result reflects the existing environment of Sinana, as it has a very different agro-ecology, bimodal and erratic rainfall distribution. The area has got two growing seasons per annum, unlike the other research centers. Holetta scored a negative value, which was very closer to the average value and was ungrouped with any of the localities though Kulumsa was relatively closer to it. Holetta, like the other locations with negative values, was discriminated by the oil yield, wilt and other disease scores. These localities are, therefore, considered as proper sites for screening disease resistant and high oil yielding varieties. In short, the canonical discriminant analysis has confirmed the existence of adequate diversity among these six research centers, and opening some more sub-centers and testing sites are justifiable as far as the results of this study are concerned. However, additional studies are required for broader applications and to make use of the canonical discriminant analysis more effectively.

OPSOMMING

1. Die studie is gedoen om die relatiewe prestasie van ses lynsaad regenerante met twee krusings en drie standaard cultivars oor 18 lynsaad produserende omgewings van Etiopië te vergelyk vir 1996-1998. Die saad opbrengs en ander agronomies belangrike eienskappe is geanaliseer met verskillende statistiese prosedures om aanpassings potensiaal, G x E interaksies en saad stabiliteit te vergelyk. Die hoof doel van die studie was om die genotipes te vergelyk en te beskryf in hulle produksie areas met verskillende statistiese analises sodat sinvolle aanbevelings gemaak kan word vir die toekoms. Net so is kontemporêre studies op genotipes, omgewings, en hulle interaksies uitgevoer, en verskillende analitiese metodes van stabilitieits parameters is bespreek.

2. Afsonderlike en gekombineerde analise van variansie is gedoen oor omgewings en jare, sewe tipes stabiliteits parameters, korrelasie en kanoniese variant analise is gedoen met MSTAT-C, AGROBASE 98 en SAS rekenaar pakette. Vir die stabiliteits analises is data van 10 genotipes oor ses lokaliteite en drie jare (uitsluitend plaaslike standaarde) gedoen met die prosedures van : Francis en Kannenberg (1978) vir koeffisiente van variasie, Finlay en Wilkenson (1963) en Eberhardt en Russel (1966) vir gesamentlike regressie, Wricke (1962) vir ekovalensie, Shukla (1972) vir stabiliteit van variansie, Lin en Binns (1978) vir cultivar superioriteit, Nasser en Huehn (1978) vir variansie van rangorde en Gauch en Zobel (1988) vir AMMI stabiliteit. Kanonies variaat analise is gedoen met SAS CANDISC (SAS Instituut, 1982) om genotipes te klassifiseer en te toets in hulle proef omgewings.

3. Die afsonderlike proefanalises vir die drie jare het hoogs betekenisvolle (p<0.01) verskille aangedui tussen genotipes vir saad opbrengs en feitlik alle ander eienskappe. Vier regenerante het beter presteer as kruisings van 1996, en meeste van hulle het dieselfde presteer in opvolgende jare. Oor omgewings en jare het Chilalo die beste presteer (1505 kg ha⁻¹) gevolg deur drie regenerante (R11-M20G, R10-N27G en R11-N1266) met opbrengste wat wissel van 1414-1455 kg ha⁻¹. Die goeie prestasie van regenerante toon hulle goeie potensiaal en goeie aanpassing in lynsaad produksie areas van Etiopië. Vir 'n feit is R11-M20G reeds aanbeveel vir kommersiële produksie in Adet vir 1999. Vir die omgewings is die beste opbrengs van 2172 kg ha⁻¹ aangeteken by Bekoji gevolg deur Kulumsa oor die jare, wat goeie potensiaal aandui vir hierdie omgewings. Die

resultate het geweldige opbrengs variasies aangetoon oor omgewings en jare wat hoë GxE interaksies aangedui het. Die gemiddelde ANOVA komponente oor die drie jaar het aangetoon dat 45% van variasie deur herhalings veroorsaak word, 39% deur genotipes en die orige 16% deur foute. Omdat hoër variasie van herhalings aangedui is by Holetta, Adet en Asasa, is verdere analise van omgewings faktore nodig (edafies en klimatologies) en goeie toesig is nodig.

4.   Die gekombineerde analise van variansie oor omgewings het hoogs betekenisvolle (p>0.01) verskille aangetoon tussen lokaliteite (L), genotipes (G) en hulle interaksie vir meeste van die gemete eienskappe, wat groot differensiële reaksie van genotipes oor omgewings aandui, hoofsaaklik a.g.v. edafiese en klimatologiese faktore. Ongeveer 76-85% van variansie komponente is veroorsaak deur omgewings, terwyl genotipes net 3-7% van variasie bygedra het (ongeveer dieselfde as die GxL komponent) oor die drie jaar. Dit het die baie groot invloed van die omgewing beklemtoon, en die nodigheid van stabiliteits analise om die regte genotipe vir die regte einddoel te kies.

5.   Die gekombineerde analise van variansie en die persentasie van die komponente vir saad opbrengs oor jare per lokaliteit het hoogs betekenisvolle (p>0.01) verskille aangetoon vir genotipes en hulle interaksies by Bekoji, Holetta en Kulumsa. In kontras hiermee was jaar x genotipe interaksie interaksies nie betekenisvol by Sinana, Adet en Asasa, wat meer opbrengs stabiliteit oor die drie jare by hierdie omgewings aantoon. Die variansie komponente van die ANOVA toon hoër variabiliteit vir jare of groei seisoene wat wissel van 50% by Adet tot 94% by Bekoji. Hierdie groot seisoens variabiliteit kan wees a.g.v. die hoeveelheid en verspreiding van reenval, onder ander faktore. Die herhaalbaarheid van van proewe by Bekoji en Holetta was 85% teen die laagste by Asasa (48%). Dit toon ook die hoë vlak van omgewings variasie aan wat verdere diagnose benodig om of aan te pas of dit goed te bestuur.

6.   Die gekombineerde analise oor lokaliteite, jare en hulle interaksies het hoogs betekenisvolle verskille (p>0.01) aangetoon tussen genotipes vir alle gemete eienskappe, wat differensiële respose van genotipes aantoon in hulle toets omgewings. Omdat betekenisvolle GxE interaksies cultivar seleksie bemoeilik, is stabiliteits analises noodsaaklik. Die variansie komponente van van saad opbrengs is bereken op 55% vir jare, 26% vir lokaliteite, 13% vir YxL interaksies en 3% vir genotipes en die orige 3% vir die res van die interaksies. Meeste van

hierdie interaksies was hoogs betekenisvol a.g.v. klimatiese, grond en biotiese faktore, en meer in diepte studies is nodig vir beter begrip hiervan en vir regstellende stappe.

7. Die ANOVA vir die gesamentlike regressie model vir saadopbrengs toon hoogs betekenisvolle verskille tussen genotipes. Volgens die regressie was R12-N10D die mees stabiele genotipe, gevolg deur P13611x10314D en Chilano .(die hoogste produseerder oor alle omgewings). Al hierdie stabiele cultivars het ook hoër koeffisiënte van vasstelling gehad, wat weer sterk gekorreleer was met koeffisiënt van regressie en afwyking van die regressie. NorLin was ook nie betekenisvol verskillend van die koeffisiënt van regressie nie, en het dus algemene aanpasbaarheid gehad oor uiteenlopende omgewings. Die koeffisiënt van variabiliteit het dieselfde resultate getoon.

8. Volgens Wricke (1962) se ekovalensie, was R11-M20G gevolg deur R11-N1266, R12N10D en P13611x10314D die mees stabiele genotipes. Die eerste drie genotipes was regenerante van weefsel kultuur, en die vierde is 'n kruising wat by die Holetta Navorsings Sentrum ontwikkel is. Chilano, .NorLin, R12-D33C en P13611x10314B is geklas as intermediêr stabiel, terwyl R10-N27G en D12-D24C onstabiel geklas is volgens hierdie metode.

9. Shukla se stabiliteits-analise (1972) het getoon dat R12-N10D, P13611x10314D en Chilano die mees stabiele genotipes is, terwyl D12-D24C, R11-N1266 en R11-M20G as onstabiel geklassifiseer is. R12-N10D, die regenerant van NorLin was die mees stabiele genotipe soos gemeet deur beide ekovalensie en stabiliteits variansie. Gesamentlike regressie resultate het ook baie hiermee ooreengestem.

10. Lin en Binns (1988a) se cultivar superioriteits analise het aangetoon dat Chilano, R10-N27G en R11-N1266 die mees stabiele genotipes is terwyl D12-D24C en P13611x10314B die minste stabiel was. In meeste gevalle was die rangordes van cultivars vir superioriteit in harmonie met rangordes van variëteits gemiddelde opbrengste eerder as met ander stabiliteits parameters.

11. Nassar en Huehn (1987) se nie-parametriese meting van stabiliteit het aangetoon dat R12-N10D die kleinste verskil in rangorde toon, en dus die mees stabiel was. Die ander regenerant D12-D24C was onstabiel. Die ander stabiele cultivars was P13611x10314D en Chilano. Die resultate was in ooreenstemming met meeste van die ander stabiliteits analyses.

12. Additiewe hoof effek en veelvoudige interaksies (AMMI) stabiliteits analise en waardes van die interaksie hoof komponent analise (IPCA) het aangetoon dat R12-N10D, P13611x10314D, R12-D33C en Chilano die mees stabiele cultivars was oor die getoetsde omgewings in Etiopië. Aan die ander kant was R11-N1266, R10-N27G en Norlin aangepas vir swak omgewings. Die AMMI model is in die laaste paar jaar baie suksesvol gebruik om GxE interaksies en stabiliteit te analiseer en te verstaan in baie gewasse. Omdat dit die ANOVA en hoof komponent analise kombineer beskryf dit effektief die GxE interaksie en stabiliteit deur respons patrone.

13. Vergelyking van die sewe stabiliteits parameters het getoon dat koeffisiënt van variabiliteit, Shukla (1972) se stabiliteits variansie, Nasse en Huehn (1978) se variansie van rangordes en AMMI se stabiliteits waardes almal dieselfde stabiele cultivar, R12-N10D aangewys het. Ekovalensie en afwyking van regressie het ook hierdie genotipe as een van die stabiele cultivars aangewys, en net cultivar superioriteit het die cultivar as intermediêr stabiel geklas. Dieselfde was waar vir die tweede stabielste cultivar P13611x10314D. Oor die algemeen is AMMI, Eberhart en Russel (1966) se afwyking van regressie, Nasser en Huehn (1978) se variansie in rangordes en Shukla (1972) se stabiliteits variansie baie nuttig gevind om vergelykende stabiliteit te bepaal vir lynsaad cultivars getoets in hierdie studie. Die koeffisiënt van variabiliteit en ekovalensie was relatief beter as die cultivar superioriteits bepaling. In die geheel gesien, het die sewe gemete eienskappe R12-N10D, P13611x10314D en Chilano as stabiel aangetoon, en R12-D24C, R10-N27G en P13611x10314B as onstabiel. Die res was intermediêr tussen hierdie groepe. Herhaalbaarheids studies is nodig om die beste eienskap te bepaal.

14. Die evaluasie van olie inhoud en olie opbrengs het aangetoon dat die hoogste lokaliteits gemiddeld van 38.26% aangetoon is vir Holetta, gevolg deur Bekoji (36.6%). Van die genotipes het het R12-N10D en R12-D24C die meeste olie (37.4%) gegee oor die lokaliteite. R12-N10D het ook goeie olie opbrengs gegee, soos saad opbrengs. Hierdie variëteite kan dus in 'n kruisings program gebruik word om olie opbrengs te verhoog. Die variansie analise vir beide olie opbrengs en inhoud oor lokaiteite en jare het hoogs betekenisvolle verskille (p<0.01) tussen genotipes aangetoon. Variansie komponente oor lokaliteite en jare het

groter variabiliteit aangetoon vir jare, lokaliteite en genotipes en hulle interaksies, in hierdie volgorde.

15. Die bepaling van agronomiese eienskappe het aangetoon dat genotipes 75 en 139 dae gevat het om te blom, en volwassenheid, onderskeidelik, te bereik. Vroeg blommende variëteite was ook vroeg met volwassenheid, na 134 dae, terwyl die later cultivars tot 144 dae gevat het. R11-N1266, R10-N27G, R12-N10D en NorLin was vinnige cutivars, terwyl R11-M20G, P13611x10314D en die plaaslike standaarde langer groeiers was. Die twee kruisings was meer vatbaar vir poeieragtige meeldou, terwyl R12-D33C, R12-D24C, R11-M20G en Chilano relatief weestandbiedend was teen meeldou en pasmo siektes.

16. Die korrelasie tussen gemete eienskappe het hoogs betekenisvolle (p>0.01) positiewe korrelasies getoon tussen olie opbrengs en saad opbrengs (r=0.924), olie opbrengs en plant hoogte (r=0.585) en olie opbrengs en stand (r=0.656). Saad opbrengs was egter negatief beïnvloed deur dae tot blom en volwassenheid, wat aandui dat vinnig groeiende cultivars swak opbrengsvermoë het. Dieselfde was waar vir vir saad opbrengs en poeieragtige meeldou, en saadopbrengs en omval. Hoogs betekenisvolle negatiewe korrelasie is gekry tussen olie inhoud en meeldou, Fusarium verwelking en pasmo, wat aandui dat die siektes die olie inhoud van die lynsaad negatief beïnvloed.

17. Liniêre diskriminante analise (kanoniese variaat analise) is gebruik om 10 genotipeste vergelyk met hulle bydraende variate. The eerste twee kanoniese variate (CAN1 en CAN2) het 78.01% van alle variasie verklaar tussen groepe genotipes. Die horisontale skeiding (CAN1) het 60.63% van variasie verklaar, terwyl vertikale skeiding (CAN2) 17.28% van variasie verklaar het. Vertikale skeiding was hoofsaaklik a.g.v. dae tot blom, poeieragtige meeldou en omval persentasie. Dae tot blom en omval het ook 'n belangrike rol gespeel in horisontale skeiding. Horisontale skeiding wat betekenisvolle bydrae getoon het tot totale variabiliteit is gebruik om genotipes te groepeer. R12-D33C en R12-D24C het die meeste met ander genotipes gekontrasteer soos P13611x10314D. R12-D33C en Chilano was die mees verskillend van ander genotipes. P13611x10314D was baie dieselfde as Chilano en dieselfde was waar vir R11-N1266 en P13611x10314B. NorLin was baie dieselfde as R12-N10D. In die algemeen is die 10 lynsaad cultivars in twee groepe ingedeel, die genotipes met bo gemiddelde waardes (positiewe waardes) en die met onder gemiddelde

waardes (negatiewe waardes). R12-D33C, R12-D24C en R11-M20Ghet positiewe waardes gehad, alhoewel lg. regenerant afgewyk het van die groep, en nader was aan die gemiddeld. Die tweede groep wat negatiewe CAN1 waardes gehad het, het ingesluit Chilano, P13611x10314D, R11-N1266, R12-N10D, NorLin, P13611x10314B, R10N27G en R11-N1266. R12-N10D en NorLin het effens afgewyk van die groep en het relatief lae waardes gehad. Persentasie stand, dae tot volwassenheid, en olie opbrengs het 'n groot rol gespeel om die tweede groep te identifiseer.

18. Dieselfde 11 eienokappe wat gebruik is om die genotipes te beskryf, is ook gebruik om te kyk na ooreenkomste en verskille tusen die ses lokaliteite. Die eerste twee kanoniese (CAN1 en CAN2) het saam 96.39% van variasie verklaar. Horisontale skeiding het betekenisvol (p<0.05) bygedra vir 91.56% van variasie, terwyl vertikale skeiding net 4.83% bygedra het. Dus het CAN1 hoofsaaklik die lokaliteite geklassifiseer. Bekoji het die meeste gekontrasteer met ander lokaliteite, wat bestaande kennis bevestig. Dit is 'n baie geskikte lokaliteit vir verbouiing van lynsaad en opbrengs is soveel as 2.5 t ha^{-1} . Bekoji was dus verksillend van alle lokaliteite vir saad opbrengs. Die gemiddelde opbrengs vir hierdie lokaliteit was 1752kg ha^{-1}, wat meer as 40% van ander lokaliteite se produksie is. Dus sal Bekoji spesiale strategië benodig i.t.v. cultivar ontwikkeling en bestuurs praktyke om die bestaande potensiaal optimal te gebruik. Die ander variate wat hierdie lokaliteit ondeskei het was olie inhoud, stand, pasmo lesings en omval. Dieselfde was waar vir Sinana. Asasa, met die hoogste negatiewe waarde, was ook verskillend omdat dit bekend is vir onbetroubare reenval en terminale droogtes. Asasa het verskil van meeste lokaliteite op grond van olie opbrengs en Fusarium verwelking alhoewel dit relatief nader was aan Adet. Kulumsa het kontrasterende negatiewe waardes gewys met Sinana, waar beide nader was aan die gemiddeld in beide rigtings. Soos Asasa, was Kulumsa gediskrimineer deur olie opbrengs en verwelking. Kulumsa het 'n relatief warmer klimaat en vrugbare gronde wat goed is vir gewas ontwikkeling en groei, wat hoë persentasies omval veroorsaak. Dit was ook voordelig vir verwelking, poeieragtige meeldou en pasmo siekte en kan gebruik word vir siekte evaluasie. Sinana het bo gemiddelde waardes gehad wat verskil het van ander lokaliteite. Hierdie resultate reflekteer die omgewing, omdat dit agro-ekologies verskillend is, bimodaal en onbetroubare reenval het. Hierdie area het ook twee groeiseisoene per jaar wat verskil van ander lokaliteite. Holetta, soos ander lokaliteite met negatiewe waardes, is onderskei met olie opbrengs, verwelk siekte en ander

siekte waardes. In kort het die kanoniese diskriminante analise die bestaan van genoeg variasie aangetoon vir die ses navorsings stasies, meer substasies en toets areas sal ook van nut wees volgens hierdie resultate.

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Appendix 1. Estimates of area ('000 ha), production ('000 tonnes) and yield (kg ha^{-1}) of linseed as compared to noug and Ethiopian mustard in Ethiopia 1987-1997).

	Area			Production			Yield		
Year	Noug	Lin.	Mustard	Noug	Lin.	Mustard	Noug	Lin.	Mustard
1987	124	57	3.3	64	27	1.5	5.2	4.8	4.6
1988	151	60	2.3	51	26	1.5	3.3	4.3	6.6
1989	173	75	2.7	79	36	2.4	4.6	4.8	8.9
1990	155	93	2.2	59	36	1.5	3.9	3.8	7.0
1991	181	83	2.9	62	34	1.6	3.6	4.1	5.5
1992	167	107	2.8	60	38	2.0	3.5	3.6	6.9
1993	150	80	-	42	35	-	2.8	4.3	-
1994	197	115	-	43	55	-	2.3	4.8	-
1995	223	113	14	86	57	57	3.8	5.0	5.0
1996	251	148	21	84	68	68	3.3	4.6	5.6
1997	195	135	13	74	63	8.7	3.8	4.7	5.6

Lin. = Linseed; - = data not available

Sources: Central Statistical Authority, (1987-1997).

Appendix 2. Range of suitable agro-climatic conditions for linseed productions in Ethiopia.

| Factor | Unit | Range of Suitability | | |
		Highly	Moderately	Marginally
Altitude	Meters	2200-2800	1800-2200	1200-1800,2800-3500
Minimum Temperature	^{0}C	6.0-10.0	4.5-6.9	10.0-13.0
Maximum Temperature	^{0}C	18.0-25.0	15.5-18.0	25.0-27.0
Mean Temperature	^{0}C	12.0-17.5	10.0-12.0	20.0-30.0,17.5-20.0
LGP	days	140-204	120-140	90-120
Rainfall	mm	500-700	400-500	300-400,700-1200
Suitable soil types: clay loam (brown/red color); PH = 6.6-7.6				

Source: Getinet and Nigussie 1992;

Appendix 3. Average seed yield and other merits of five released varieties of linseed in Ethiopia, 1976-1996.

Variety	Year of Release	Seed yield	Oil content	Maturity	Origin
Victory	1976	1400	35.3	148	Exotic
CI-1525	1984	1430	38.5	146	Exotic
CI-1652	1984	1360	38.6	146	Exotic
Chilalo	1992	1670	35.2	140	Local
Belay-96	1996	1680	36.3	140	Cross

Appendix 4. Agro-Ecological Zones Map of Ethiopia

Eritrea

Sudan

Sudan

Kenya

Somalia

Somalia

LEGEND

MAJOR AEZ	SUB AEZ	DESCRIPTION
A1		ARID HOT TO WARM LOWLAND PLAINS
	A1-1	Arid hot to warm plains
	A1-3	Arid hot to warm valleys & escarpment
	A1-7	Arid hot to warm mountains
A2		ARID TEPID TO COOL MID HIGHLANDS
	A2-1	Arid tepid to cool plains
	A2-2	Arid tepid to cool mountains
SA1		SEMI-ARID HOT TO WARM LOWLANDS
	SA1-1	Semi-arid hot to warm plains
	SA1-2	Semi-arid hot to warm lakes & rift valleys
	SA1-5	Semi-arid hot to warm mountains & plateau
SA2		SEMI-ARID TEPID COOL MID HIGHLANDS
	SA2-2	Semi-arid tepid to cool lakes & rift valleys
SM1		SUB-MOIST HOT TO WARM LOWLANDS
	SM1-1	Sub-moist hot to warm plains
	SM1-2	Sub-moist hot to warm lakes & plateau
	SM1-3	Sub-moist hot to warm mountains & plateau
	SM1-4	Sub-moist hot to warm gorge
	SM1-7	Sub-moist hot to warm mountains
SM2		SUB-MOIST TEPID TO COOL MID-HIGHLANDS
	SM2-1	Sub-moist tepid to cool plateau
	SM2-2	Sub-moist tepid to cool lakes & plateau
	SM2-5	Sub-moist tepid to cool mountains & plateau
	SM2-7	Sub-moist tepid to cool mountains
SM3		SUB-MOIST COLD TO VERY COLD SUB-AFROALPIN TO AFROALPIN
	SM3-7	Sub-moist cold to very cold mountains
M1		MOIST HOT TO WARM LOWLANDS
	M1-1	Moist hot to warm plains
	M1-2	Moist hot to warm lakes & rift valleys
	M1-3	Moist hot to cool valleys escarpment
	M1-4	Moist hot to warm gorge
	M1-7	Moist hot to warm mountains

MAJOR AEZ	SUB AEZ	DESCRIPTION
M2		MOIST TEPID TO COOL MID HIGHLANDS
	M2-1	Moist tepid to cool plains
	M2-2	Moist tepid to cool lakes & rift valleys
	M2-5	Moist tepid to cool mountains & plateau
	M2-6	Moist tepid to cool plateau
	M2-7	Moist tepid to cool mountains
M3		MOIST COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	M3-7	Moist mountains cold to very cold
SH1		SUB-HUMID HOT TO WARM LOWLANDS
	SH1-1	Sub-humid hot to warm plains
	SH1-2	Sub-humid hot to warm lakes & rift valleys
	SH1-4	Sub-humid hot to warm gorge
	SH1-7	Sub-humid hot to warm mountains
SH2		SUB-HUMID TEPID TO COOL MID HIGHLANDS
	SH2-1	Sub-humid tepid to cool plains
	SH2-2	Sub-humid tepid to cool lakes & rift valleys
	SH2-6	Sub-humid tepid to cool plateau
	SH2-7	Sub-humid tepid to cool mountains
SH3		SUB-HUMID COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	H3-7	Sub-humid cold to very cold mountains
H1		HUMID HOT TO WARM LOWLANDS
	H1-1	Humid hot to warm plains
	H1-2	Humid hot to warm lakes & rift valleys
	H1-7	Humid hot to warm mountains
H2		HUMID TEPID TO COOL MID HIGHLANDS
	H2-2	Humid tepid to cool lakes & rift valleys
	H2-6	Humid tepid to cool plateau
	H2-7	Humid tepid to cool mountains
H3		HUMID COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	H3-7	Humid cold to very cold mountains
Ph1		PER-HUMID HOT TO WARM LOWLANDS
	PH1-5	Per-humid hot to warm mountains & plateau
	Ph1-7	Per-humid hot to warm mountains
Ph2		PER-HUMID TEPID COOL MID HIGHLANDS
	PH2-7	Per-humid tepid to cool mountains

Source: MoA (1998)

Scale 1:2,000,000

LEGEND

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	SM1-7	Sub-moist hot to warm mountains
SM2		SUB-MOIST TEPID TO COOL MID- HIGHLANDS
	SM2-1	Sub-moist tepid to cool plateau
	SM2-2	Sub-moist tepid to cool lakes & plateau
	SM2-5	Sub-moist tepid to cool mountains & plateau
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	M1-2	Moist hot to warm lakes & rift valleys
	M1-3	Moist hot to cool valleys escarpment
	M1-4	Moist hot to warm gorge
	M1-7	Moist hot to warm mountains

MAJOR AEZ	SUB AEZ	DESCRIPTION
M2		MOIST TEPID TO COOL MID HIGHLANDS
	M2-1	Moist tepid to cool plains
	M2-2	Moist tepid to cool lakes & rift valleys
	M2-5	Moist tepid to cool mountains & plateau
	M2-6	Moist tepid to cool plateau
	M2-7	Moist tepid to cool mountains
M3		MOIST COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	M3-7	Moist mountains cold to very cold
SH1		SUB-HUMID HOT TO WARM LOWLANDS
	SH1-1	Sub-humid hot to warm plains
	SH1-2	Sub-humid hot to warm lakes & rift valleys
	SH1-4	Sub-humid hot to warm gorge
	SH1-7	Sub-humid hot to warm mountains
SH2		SUB-HUMID TEPID TO COOL MID HIGHLANDS
	SH2-1	Sub-humid tepid to cool plains
	SH2-2	Sub-humid tepid to cool lakes & rift valleys
	SH2-6	Sub-humid tepid to cool plateau
	SH2-7	Sub-humid tepid to cool mountains
SH3		SUB-HUMID COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	H3-7	Sub-hmid cold to very cold mountains
H1		HUMID HOT TO WARM LOWLANDS
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	H1-7	Humid hot to warm mountains
H2		HUMID TEPID TO COOL MID HIGHLANDS
	H2-2	Humid tepid to cool lakes & rift valleys
	H2-6	Humid tepid to cool plateau
	H2-7	Humid tepid to cool mountains
H3		HUMID COLD TO VERY COLD SUB-AFROALPINE TO AFROALPINE
	H3-7	Humid cold to very cold mountains
Ph1		PER-HUMID HOT TO WARM LOWLANDS
	PH1-5	Per-humid hot to warm mountains & plateau
	Ph1-7	Per-humid hot to warm mountas
Ph2		PER-HUMID TEPID COOL MID HIGHLANDS
	PH2-7	Per-humid tepid to cool mountains

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Appendix 5. Monthly rainfall and temperature of Holetta Research Center, 1996-98.

Fig 1. Monthly total rainfall of Holetta Res. Centre, 1996-98

Fig 2. Monthly mean temperature of Holetta Res. Centre, 1996-98
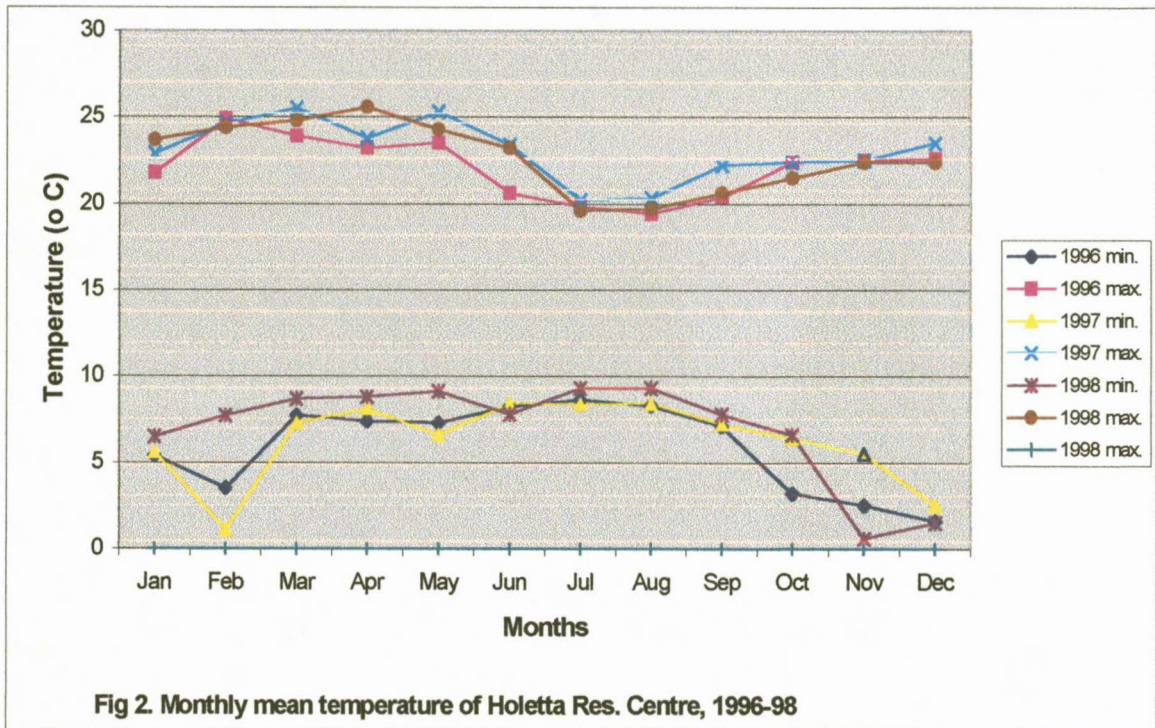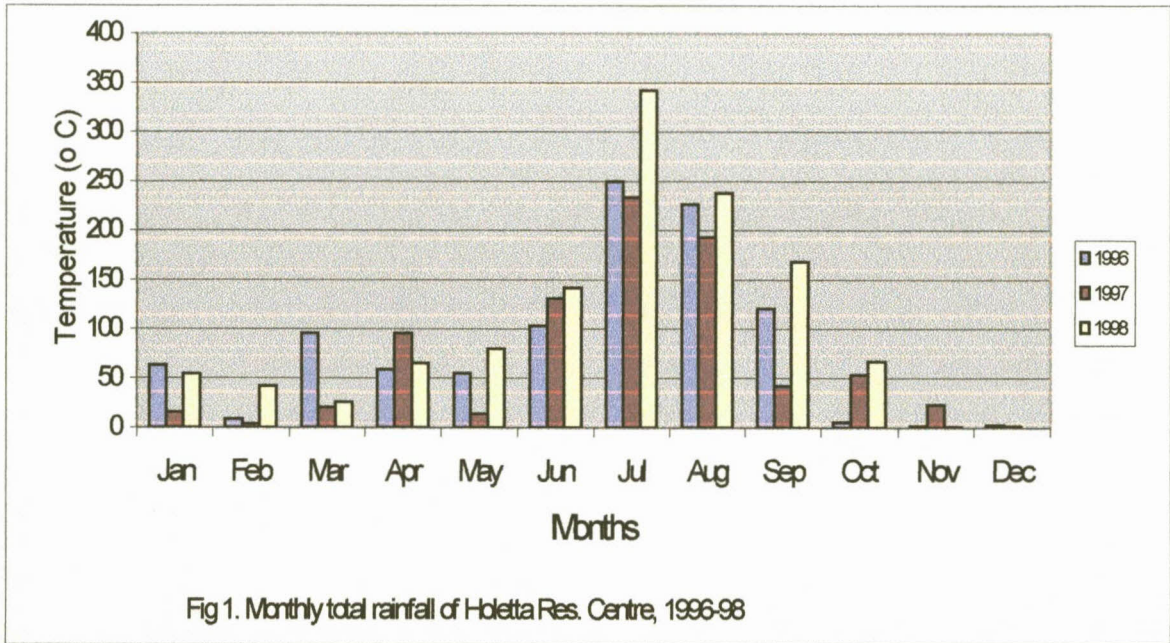
Appendix 6. Agro-climatic data of Holetta Research Centre, 1996-98.

1996	Temp. Min.	Temp. Max.	Rainfall (mm)	Rainy days	Wind sp. (Km/hr)	Soil T 10cm	Soil T 20cm	Soil T 100c	R.H. (%)	Evapor. (mm)
January	5.4	21.8	62.6	9	3.31	17.2	17.2	18.5	58	131
February	3.5	24.9	8.5	6	3.89	18.4	18.1	18.6	39	165.3
March	7.7	23.9	96.1	18	4.3	19.3	19.1	19.3	54	53.88
April	7.4	23.2	58.4	15	3.92	19.2	18.9	19.4	56	136.8
May	7.3	23.5	55.4	12	3.6	19.7	19.8	19.6	56	137.1
June	8.2	20.6	103.8	23	2.37	18.4	18.2	19.3	74	86
July	8.6	19.8	249.8	30	2.31	17.8	17.6	18.7	78	88.8
August	8.3	19.4	226.6	29	2.13	17.6	17.4	18.6	79	81
September	7.1	20.4	120.7	22	2.04	17.4	17.1	18.1	74	88.3
October	3.2	22.4	5.3	1	3.4	18.4	17.2	18.3	48	152.3
November	2.5	22.5	1.4	1	3.12	18.2	17.4	18.4	46	145.7
December	1.6	22.6	2.3	1	3.43	17.3	16.6	18.2	42	164.2
1997										
January	5.6	22.9	15.3	8	3.24	18.3	17.6	18.3	54	131.5
February	1.1	24.6	3.4	1	4.91	20.1	19.1	18.4	34	192.1
March	7.3	25.5	21.1	8	4.38	23.1	21.8	19.2	43	193.9
April	8.1	23.8	95.4	13	4.27	20.3	19.8	19.4	55	145.8
May	6.6	25.3	13.5	6	4.81	21.2	20.7	19.4	42	186
June	8.4	23.4	131	16	3.62	19.6	19.3	19.4	52	132.4
July	8.4	20.2	233.5	30	2.36	17.5	17.3	18.6	77	85.8
August	8.4	20.3	193.2	30	2.2	17.6	17.3	18.3	75	87.28
September	7.2	22.2	42.5	11	2.54	19.2	18.5	18.4	64	114.6
October	6.4	22.4	53.5	11	2.91	19.7	18.7	18.7	59	125.7
November	5.5	22.5	23.6	9	3.51	19.8	19.2	18.8	59	128.8
December	2.5	23.5	2.1	3	3.44	18.6	18.1	18.6	51	147.4
1998										
January	6.5	23.7	54.6	7	3.63	19.5	18.7	18.5	58	139
February	7.7	24.4	42.3	6	3.27	20.7	20.3	19.2	55	135.8
March	8.7	24.8	25.7	8	4.34	21.3	20.8	19.5	54	161.3
April	8.8	25.6	65.7	16	4.25	21.7	21.1	19.9	51	156.3
May	9.1	24.3	80.4	12	3.41	21.2	20.7	19.9	55	137.6
June	7.8	23.2	141.5	25	2.67	19.6	19.7	19.8	66	116.3
July	9.3	19.6	342.1	29	1.93	17.8	17.7	19.1	81	69.14
August	9.3	19.7	238.1	28	1.54	17.8	17.5	18.5	82	68.4
September	7.8	20.6	168.3	25	1.9	17.8	17.4	18.4	75	83.92
October	6.6	21.5	67.4	12	2.08	18.4	17.9	18.4	65	104.7
November	0.6	22.4	0.8	2	2.84	18.9	18.3	18.5	46	142.8
December	1.5	22.4	0	0	3.18	18.1	17.1	18.2	38	158.7

Note: Temp. = Temperature, min. = minimum, max. = maximum; Wind sp. = wind speed at 1 meter height; Soil T = soil temperature at depths of 10, 20 and 100 centimeters; R.H. = Relative humidity (%); Evapo. = Evaporation

Appendix 7. Temperature and rainfall of Adet Research Centre, 1996-98.

Fig 3. Monthly average temperature of Adet Res. Centre, 1996-98

Fig 4. Monthly total rainfall of Adet Res. Centre, 1996-98

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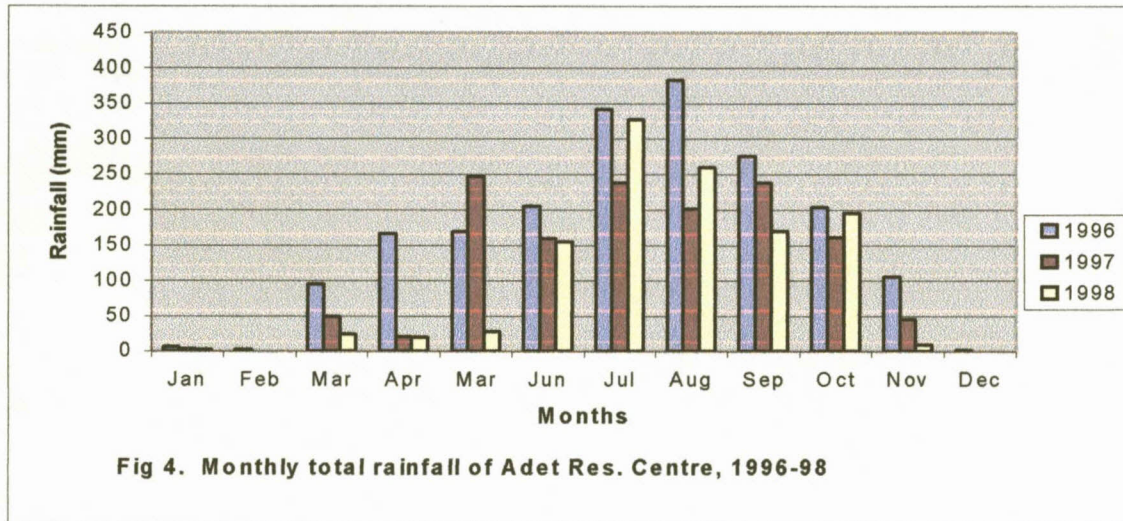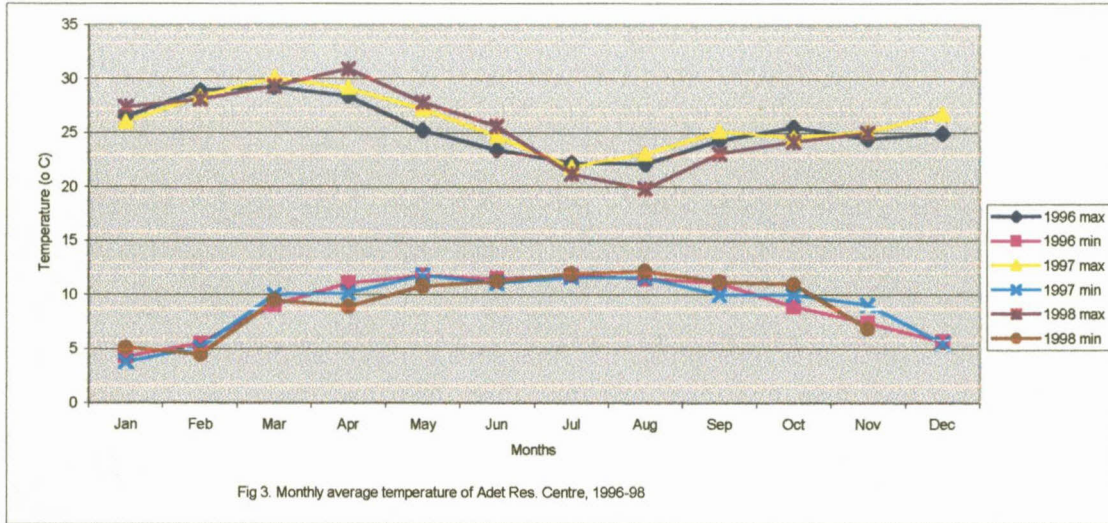
Appendix 8. Monthly total rainfall (mm), average minimum and maximum
temperature (C°) of Asasa, Bekoji and Kulumsa Research Centers, 1996-1998.

	1996			1997			1998		
Asasa	Rainfall	Min.T.	Max.T.	Rainfall	Min.T.	Max.T.	Rainfall	Min.T.	Max.T
January	14.7	-	-	45.6	4.4	22.5	45.6	4.5	22.5
February	6.6	-	-	0.0	1.7	26.5	52.8	4.9	24.3
March	61.6	-	-	65.0	6.7	26.2	23.2	5.6	25.8
April	28.6	-	-	21.4	10.1	23.9	27.3	8.2	25.9
May	109.8	-	-	13.2	7.6	25.9	41.9	7.9	24.0
June	78.0	-	-	107.0	8.0	25.0	102.9	10.0	23.4
July	258.2	9.4	25.0	166.8	10.0	21.2	125.0	10.4	21.6
August	105.4	9.8	22.9	65.9	9.1	21.3	159.5	10.9	21.7
September	45.5	8.9	23.6	13.9	5.5	23.7	61.2	8.8	22.1
October	2.2	2.8	23.3	45.3	5.4	24.1	63.3	8.8	21.5
November	19.4	1.9	23.8	30.3	4.8	22.9	3.1	3.1	22.7
December	6.6	1.5	24.3	0.0	3.4	23.2	0.0	1.6	23.9
Bekoji									
January	58.7	9.1	19.9	74.3	8.6	20.8	73.2	9.6	20.7
February	12.3	9.9	22.5	0.5	8.9	22.4	128.4	10.1	22.0
March	140.2	9.2	21.5	59.9	8.6	23.0	48.0	10.2	21.6
April	55.5	10.3	21.4	133.4	10.0	19.7	91.2	11.2	22.4
May	154.3	10.1	20.9	60.2	9.7	21.4	89.2	10.6	22.7
June	125.1	9.1	19.3	71.3	9.2	21.4	83.2	9.2	21.8
July	158.3	8.8	18.0	180.2	9.0	18.7	229.9	9.7	18.8
August	229.0	8.4	18.0	121.7	11.9	19.1	245.3	9.6	18.7
September	86.1	8.9	19.3	16.4	10.4	19.7	113.2	9.4	20.0
October	35.0	7.5	19.6	-	-	-	116.5	9.2	20.1
November	3.1	7.9	20.7	104.9	9.2	19.7	0.0	7.6	20.7
December	5.9	8.9	20.1	1.0	8.4	20.8	0.0	6.5	21.2
Kulumsa									
January	42.0	10.3	28.6	6.4	10.2	22.9	27.6	10.0	21.3
February	4.3	9.8	25.3	0.0	9.2	23.7	19.8	10.5	24.0
March	133.3	12.0	24.1	218.2	11.2	25.0	148.6	11.4	24.9
April	58.9	12.3	23.6	112.7	11.8	22.9	69.1	11.8	25.0
May	192.9	12.4	23.0	27.5	12.3	24.6	91.7	11.3	24.9
June	126.5	12.2	21.3	115.5	11.2	23.2	96.1	11.4	23.7
July	130.3	12.0	21.2	138.3	11.4	21.4	72.5	10.9	21.3
August	98.5	11.8	20.4	137.6	11.1	21.1	186.6	10.7	20.8
September	88.7	11.1	21.0	61.2	10.7	22.5	119.8	10.2	20.8
October	1.3	10.9	22.6	93.7	11.5	21.5	106.1	10.5	21.8
November	3.5	9.2	22.4	25.7	10.3	21.4	35.0	8.1	21.5
December	0.0	8.2	22.3	0.0	9.2	21.7	0.0	8.5	21.7

- = data not available