GENOTYPE x ENVIRONMENT INTERACTION AND YIELD STABILITY OF WHITE SEEDED SESAME (*Sesamum indicum* L.) GENOTYPES IN NORTHERN ETHIOPIA.

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I hereby certify that I have read and evaluated this Thesis entitled" **Genotype x Environment Interaction and Yield Stability of White Seeded Sesame (*Sesamum indicum* L.) Genotypes in Northern Ethiopia",**I recommend that it be submitted as fulfilling the thesis requirements.

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DEDICATION

I dedicated this thesis tomy late mother Hadash Hans Anbesa

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BIOGRAPHICAL SKETCH

Yirga Belay was born in June 1983 form his father Belay Kindeya and his mother Hadas Hans in Mekelle, capital city of Tigray Region. He attended his elementary school, junior and secondary school at Lachi elementary school, Mekelle junior Secondary School and Atse-Yohannes Preparatory school, respectively. He joined Ambo University in 2003 and graduated with BSc. in Crop Production and Protection in 2006. Soon after graduation from 2007-2011 E.C.,He was employed in Laelay Adiayabo District Office of Agricultural and Rural Development about four years. In 2012 he was employed in Wukro Agricultural TVET College as junior instructor for one year. As of 2013 he is working for Humera Agricultural Research Center as junior researcher. Yirga joined the School of graduate studies of Haramaya University in 2014 to pursue his MSc. study in plant breeding.

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ACRYNOMYS AND ABBREVATIONS

AMMI	Additive Main effect and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	AMMI Stability Value
bi	Regression Coefficient
CSA	Central Statistics Agency
DF	Degree of Freedom
E(Envi)	Environment
G	Genotype
GEI	Genotype x Environment Interaction
GGE	Genotype Main Effects and Genotype x Environment interaction Effects
IPCA	Interaction Principal Component Analysis
IPMS	Improving Productivity and Market Success
LSD	Least Significant Difference
MET	Multi-Environment Trials
MS	Mean Square
OR	Over all Rank
Pi	Cultivar Superiority Performance
RCBD	Randomized Complete Block Design
S^2di	deviation from Regression
Wi	Wricke's Ecovalence
YSI	Yield Stability Index

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ABSTRACT

Sesame is known as queen of oil seed crops, it is mainly grown for its oil of local consumption, sources of incomeand greatcontribution for the national economy Ethiopia. However the productivity and production is low due to environments, GEI, genotypes and management variation. Therefore the experiment was carried out to evaluate Genotype x Environment Interaction for seed yield and oil content of different white seeded sesame genotypes and to identify stable and/or high yielding genotypes and assess their performanceacross locations. Seventeen sesame genotypes were tested at ten environments in northern Ethiopia (Tigray and Amhara) during 2014-2015 main cropping seasons. The experiment was laid out in Randomized Complete Block Designs (RCBD) with three replications across all the environments. Combined analysis of variancerevealed highly significant difference ($p \leq 0.001$) among genotypes (G), environments (E) and genotype x environment interaction (GEI) for seed yield, oil content and yield components. The average seed yield ofsesame genotypes was 649.35kg/ha and 49.9% average mean oil content. Various stability models:AMMI Stability Value (ASV), Yield Stability Index (YSI), cultivar superiority performance (Pi),Wricke's ecovalence(Wi), Regression coefficient (bi) and Devotion from Regression (S^2di) were used to identify stable genotypes. AccordinglyG1, G16 and G7 were the most stable genotypes and accompanied with high mean seed yield and oil content across all locations.On the other hand, G1, G7 and G3 showed, 18.85%, 7.30% and 1.34% yield advantage over the standard check and 34.25%, 22.75% and 16.75% over the local check, respectively. From AMMI analysis, environment, genotype and GEI had 69.73%, 14.68 and 9.58% contribution to the total treatment for seed yield and 61.6%, 6.6% and 13.64% for oil content,respectively. This indicating environment had considerable effect on seed yield and oil content variation among genotypes. Among the stability models(SYI) and (Pi) were highly and positively correlated with mean seed yield, whereas Wi and S^2di were negatively and non-significantly correlated with mean seed yield.The most stable genotypes G1, G7 and G3 had high seed yield and oil content across the testedlocations and will be recommended for wider areas.Genotypes,G4 and G14 had high mean yield and oil content with specific adaptation for Dansha and Sheraro, respectively. The identified genotypes will be promoted to verification trials as per their adaptability.

Key words: AMMI, ASV, GGE bi-plot, Oil content, YSI

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) belongings to the order Tubiflorae, family Pedaliaceae, is an important and ancient oil-yielding crop. It has an edible seed and has high quality oil (Pathak *et al.,* 2014).It is cultivated in tropical and subtropical regions of Asia, Africa and South America (Zhang *et al.,* 2013). It is warm-season annual crop primarily adapted to areas with long growing seasons and well-drained soils (Hansen, 2011).Although, the name of sesame is widely well known in different areas of the world, in different countries and different names; til (Hindi), hu ma (Chinese), sesame (French), goma (Japanese), gergelim (Portuguese) and ajonjoli (Spanish) (Anilakumar *et al.*, 2010).It is also known as benniseed (Africa), benne (Southern United States), gingelly (India), gengelin (Brazil), sim-sim, semsem (Hebrew) and tila (Sanskrit) (Hassan, 2012). In Ethiopia sesame known as *Selit*in AmharicandTigrigna, *Sallet* in Affan Oromo (Seegeler, 1983).

Sesame is the oldest self-pollinating annual oilseed originated in Africa, Ethiopia domesticated over 5000 years ago. Although originated in Africa, it was spread early through West Asia to India, China and Japan which became secondary distribution centers and it is now cultivated in many parts of the world (Yamanura, 2008).

Even though the order of sesame producing countries in the world changed from time to time, Myanmar (0.56ton/ha) was the leading one in 2012 main cropping season followed by India (0.34ton/ha), China (1.31ton/ha), Sudan (0.26ton/ha) and Tanzania (0.67ton/ha),respectively (FAO STAT, 2013). CSA (2015) reported that the average sesame yield in Ethiopia in 2014/2015 main cropping season wasabout 0.7 ton/ha which is above the world the average yield.The average world sesame seed yield productivity was about0.51ton/ha (FAOSTAT, 2014).

Ethiopian sesame is among the highest quality in the world, as seeds are naturally produced at near-organic levels. Seeds produced in Humera and Gonder areas in particular are renowned for their high quality and nutty aroma. It is an important agribusiness sector in Ethiopia and is one of the six priority crops of the Agricultural Growth Programme(AGP) (USAID, 2012). It accounts for 90% of the value of exported oilseeds, estimated at 379 million USD (FAOSTAT, 2012). It is 2nd only to coffee in foreign exchange earnings in Ethiopia (USIAD,

2014). It is the2nd oil seed oil cropinterms of area coverage of 420,494.87ha and the total production 288770 ton/ha next to noug (*Guizotia abyssinica Cass.*) (CSA, 2015). The major sesame regions in Ethiopia are, Tigray (western and north western 36%), Oromia (East Welega 17%) Benishangul Gumuz (Belles valley 15%), Amhara (Metema 31%) are the most sesame producing regions in the country (Adefris *et al*., 2011)

Even though sesame is sources of income for many small scale farmers, investors, traders, exporters and for Ethiopiaeconomic growth. The industrial processing and utilization of sesame have not been fully developed in the country. Thus, the product is locally processed to extract oil and oil cake. The process of oil extraction using local methods in western and north western Tigray are known as *ashera.* Theoil extractedand by product (sesame oil cake) produced by the local process known as*simsim zeyti and Ambas* respectively. The oil cake used as sources of animal feed in the production area (personal communication, 2016).

Sesame seed is branded as the Humera, Gonder and Welega types which are well known in the world market by their white color, sweet taste and aroma. The Humera and Gondar sesame seeds are suitable for bakery and confectionary purposes; on the other hand, the high oil content of the Welega sesame seed gives a major advantage for edible oil production (Yamanura, 2008). The major quality requirements for sesame seed export are thousand seed weight should be greater than 3g, 40-50% oil content, and pearly-white seed color. Regarding quality of sesame seeds, white seeds with a white to golden color, are mainly used in raw form because of their aesthetic value and are mostly priced higher than mixed seeds yellow to dark brown seeds, are generally crushed into oil (Wijnands *et al.,* 2007).

Sesame is an oil seed cropgrown mainly for local consumption and export purposes. It is, used in cooking and salad oils. The oil can be used in the manufacturing of perfumes, pharmaceuticals and insecticides. The meal, left after the oil is used as feed for poultry, livestock and as fertilizer (Khanna, 1991).The seeds also contained significant amount of important minerals with the Potassium concentration being the highest, followed by Phosphorus, Magnesium, Calcium and Sodium (Loumouamou *et al.,* 2010).The chemical composition of sesame shows that the seed is an important source of oil (44-58%), protein (18- 25%), carbohydrate (~13.5%) and ash (~5%) (Borchani *et al*., 2010). It is used for production of margarine, shortening, canned sardine and beef (NAERLS, 2010).

Despite the fact,sesame is highly marketable oil crop and superior sources of income in many sesame growing areas of Ethiopia; its productivity is low and unstable across environments and years due to biotic (weeds, insects and diseases etc.), abiotic factors (soil type, altitude, rail fall distribution and intensity*etc.*Seed shattering at maturity, lack of uniform maturity of capsules, lack of wider adapting cultivars, non-synchronous maturity, poor stand establishment, lack of fertilizer responses and low harvest index *etc.* (Ashri, 1994).

GEI is a challenge for plant breeders and complicates cultivar recommendation because of the inconsistency of best yielding genotypes across cropping environments, however, it may also offer opportunities, of increases yields through growing genotypes specifically adapted to a given area. The main features of quantitative traits are that they are highly influenced by the environment, difficult to understand the genotype-phenotype relationship as compared to qualitative traits. The most commonly used way to evaluate the effect of the uncontrollable environmental factors on crop response is to repeat the experiment at several sites in a single year, or over several crop seasons in a single site, or both (Gauch and Zobel, 1996).The variability in environments such as, location effect, seasonal fluctuations and their interactions highly influences the performance of sesame genotypes in relation to yield potential. When genotypes respond differently to a change in the environment, the phenomenon of genotypes by environment interaction is said to occur. Because of the genotype by environment interaction, the selection of stable genotypes that interact less with the varying environments in which they are to be grown is required (Kumaresan and Nadarajan, 2010).

The effect of GEI becomes more apparent by conducting multi-location and multi-years trials, that have three main objectives: (a) to accurately estimate and predict yield based on limited experimental data; (b) to determine yield stability and the pattern of response of genotypes across environments; and (c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990).

The current sesame production in Ethiopia has many opportunities, such as highly market demand, large area with suitable environments for production (North western and South Western Ethiopia), growing in low moisture areas, presence of genetic diversity to improve the production yield potential and export demandand very competitive world wide(Wijnands

et al., 2007). However, the research attention and breeding programme which has been given to improve its yield and oil content is not comparable with its contribution to Ethiopian economy and no information available on globally demanded white seeded sesame genotypes. Therefore, studyon GEI and due attention for such on the white seeded sesame genotypes will indispensable in Ethiopia. Sufficient GEI studies have been undertaken elsewhere in the world to meet either or all of the objectives, among which Yebio (1993), Kumaresani and Nadarajan (2010), Adebisi (2009), Zenebe and Hussien (2010), Hagos and Fetien (2011), Mirza, *et al.* (2013), Fiseha *et al.*,(2015), Mekonnen*et al.*(2015) and Mohammed *et al.*,(2015). Even all the above studies had undertaken GEI studies on sesame in Ethiopia and the rest of the world,there was no specifically work did on globally preferred white seeded sesame genotypes in Ethiopia. Therefore, this experiment was done(i) to evaluate the GEI for seed yield and oil content of 17 white seeded sesame genotypes and (ii) to identify stable and/or high yielding white seeded sesame genotypes and assess their performance across locations.

2. LITERATURE REVIEW

2.1. Botanical Description and Origin of Sesame

Sesame has been grown for over 7,500 years in Asia and Africa even in very poor growing conditions.Sesame is a broad leaf summer crop similar to cotton, sunflower, soybeans, black-

eyed peas, mung beans, or guar. The fruiting form of sesame is a capsule, often called pods. Some varieties have a single capsule per leaf axil and others have triple capsules per leaf axil. Flowering starts about 35-45 days after planting and flowering stops 75-85 days after planting. The seed is produced in these capsules with about 70 seeds per capsule (Langham *et al.,* 2010). It is an annual self- pollinating plant with an erect, pubescent, branching stem. It is either single stemmed or branched growth habits or two growth characteristics of indeterminate and determinate, reaching up to 2m height. According to Kobayashi *et al.* (1990), 36 species have been identified under the genus Sesamum with three cytogenetic groups 2n = 26, 2n = 32 and 2n = 64 from which the widely cultivated Sesamum indicum is within the first group.

Sesame is ancient crop known and used by man, its center of origin is not clearly known (Jaiwal and Rana, 2003). Since it was growing in India from ancient times and according to different archeological evidences many authors (Bedigian and Harlon, 1986; Brar and Ahuja, 1979; Nayar and Mehar, 1970 cited by Jaiwal and Rana, 2003) believed that sesame was originated in India. Some other scholars also believed that sesame was originated in Africa. On the other hand, Ethiopian sesame researchers, Gemechu and Bulcha (1993) also gave the originality of sesame to Ethiopia based on the assessment of the crop for its diversity and era of cultivation in the country.

2.2. Cultivation and Distribution of Sesame

Sesame grows in tropical to the temperate zones from about 40° N latitude to 40° S latitude. It grows in more than 50 countries in the world (Gulhan *et al.,* 2004). It is a high value oilseed crop grown on 5 million acres (20,000 km) in the world (Mirza, *et al.,* 2013). About 70% of the world's sesame crop is grown in Asia and 26% in Africa Hansen (2011). Sesame is a very rewarding crop due to its low cost of production and high price (Anwar *et al*., 2013). It grows well on stored soil moisture with minimal irrigation and can produce good yields under high temperatures and its grain has a high value Bennet (2011) and Mensah *et al.*(2009) reported that can set seed and yield well under fairly high temperature.Can grow in stored soil moisture without rainfall and irrigation. It grows best on the areas which have an altitude of 500 to 800 meter above sea level and can grow even upto1250 m.a.s.l. Optimum temperature for growth

varies with cultivar in the range 27°C to 35°C. Periods of high temperature above 40°C during flowering reduce capsule and seed development (Nath *et al*., 2000).

Sesame cultivation can be carried out on a wide range of soils but optimum is well drained, loose, fertile and sandy alluvial soils that have a pH value between 5.4 and 6.75. Very low pH values have a drastic effect on growth, whereas some varieties can tolerate a pH value up to 8 (Naturland, 2002). Good drainage is crucial, as sesame is very susceptible to short periods of waterlogging. According to Hansen (2011) the total amount of water required to grow sesame crop ranges from 600 to 1000 mm, depending on the cultivar and the climatic conditions. It can grow in moisture require of 300–400 mm rainfall per season having a very low salt tolerance (Carlsson *et al*., 2008).

The Ethiopian quality sesame varieties are usually known by their brand name. There are three sesame variety types commonly used for commercial production and these are Humera, Gondar and Wollega types. The commercial varieties are suitable for various applications. For instance, the Humera type is appreciated worldwide for its aroma and sweet taste. It is said to be good uniform white seeds, which are quite larger. This makes it very suitable for bakery products. The Gondar type is also suitable for the bakery market. The major competitive advantage of the Wollega type is its high oil content (Wijnands *et al*., 2007).

2.3. Importance of Sesame

Sesame oil is unique among vegetable oils due to the presence of natural antioxidants such as sesamin and sesamolin and their derivatives (sesamol and sesaminol), which provide a significantly long shelf life and stable characteristics. Sesame oil is mostly used for cooking purposes. Sesame oil is also used in soaps, paints, perfumes, pharmaceuticals and insecticides. The cake produced after the extraction of oil from un-hulled seeds is an excellent protein feed for poultry and ruminants (Pathak *et al.,* 2014). Sesame seeds are widely considered to be healthful foods. They are high in energy and contain many health benefiting nutrients, minerals, antioxidants and vitamins that are essential for wellness and have positive effects on human health (Borchani *et al*., 2010). It is also very use full for body as they are digestive, rejuvenative, anti-aging and rich in vitamins E, A and B complex and minerals such as calcium, phosphorus, iron, copper, magnesium, zinc and potassium (Bukya and Vijayakumar,

2013). The fatty acid composition Ethiopian sesame oil linoleic (39.3-59%) and oleic (32.7-53.9%) acid, and palmitic (9-11%) and stearic (5-10%) acid (Geremew *et al*., 2012). The local Ethiopian sesame varieties are a good source of fat and rich in protein, crude fiber, minerals, crude fat, phenols and reducing power values when compared with other world grown sesame varieties (Haftom *et al.*, 2015).

Sesame besides its various advantages it stimulates flora of beneficial soil microbes and reduces the nematode populations, particularly the root knot nematodes (*Meloidogyne arenaria, Meloidogyne incignita*) that attack peanuts and cotton(Langham *et al.*, 2008). It is also an excellent soil builder because of the large amounts of root biomass that are left to decay underground after harvest. The soil is very mellow after sesame cultivation and requires less work to prepare for the next crop in rotation (Haller *et al.*, 1942).

2.4. Sesame Production Constraints

Despite its nutritional and high market value oil crop, research on sesame has been limited worldwide and so that still it has been produced under traditional management practices. Yield of sesame is highly variable depending upon the growing environment, cultural practices and the type of cultivar (Brigham, 1985). The major constraints in sesame production worldwide are lack of widely adapting cultivars, shattering of capsules at maturity, non-synchronous maturity, poor stand establishment, lack of fertilizer responses and low management practices (Ashri, 1994). In the case of Ethiopia lack of improved seed supply and the accompanying extension service for producers is also main problem (Sorsa, 2009). Although, the demand and world price is becoming increasing from time to time sesame producers in the sesame growing areas want to cover almost all of their land year after year with sesame. This mono-cropping practice causes development of diseases, insect pests and weed seeds which results in poor productivity of sesame. So it is important to have a rotation scheme of sesame every three or four year (Getnet *et al*., 1997).

Minot and Sawyer (2013) reported that about 28% production decrement of sesame in Ethiopia is due to insect and diseases. Among the many insect pests affecting sesame production worldwide sesame seed bug (Elasmolomus sordidus), sesame webworm (*Antigastra catalaunalis*), termites, gall midge (*Asphondilia sesami*), green vegetable bug

(*Nezara viridula*), African bollworm (*Helicoverpa armiger*) and jassids (Orosius albicinctus) have been recorded in Ethiopia (Geremew *et al*., 2012) and the first four in their order of priority are common in the western and north western Tigray. In the sesame growing parts of Tigray sesame seed bug (*Elasmolomus sordidus*) caused a weight loss of 94.7% after stored in opened sacks (Muez *et al*., 2008). Weeds are also the major problems in sesame producing areas of western zone Tigray causing a yield reduction up to 86.3% when emerge simultaneously and remained unweeded throughout the entire growing cycle (Mizan, 2011).

2.5. Genotype x Environment Interaction (GEI)

From biological and statistical point of view. Phenotype of an individual plant is a consequence of the interaction between genotype and the environment Baker (2002). An interaction occurs when two genotypes differ in their response to a change in environments. Changes in rank of cultivar through environments indicate GEI and lack of stability in the trait under study GEI reduces correlation between the genotype and the phenotype, hindering evaluation of the genetic potential of the cultivar (Kang and Gorman, 1989).

GEI is the differential response of genotypes evaluated under different environmental conditions. It is a complex phenomenon as it involves environmental (agro-ecological, climatic and agronomic) conditions and all physiological and genetic factors that determine the plant growth and development (Mohammadi *et al.,* 2009).GEIis commonly observed by crop producers and breeders as the differential ranking of cultivar yields among locations or years. Plant breeders conduct METs primarily to identify the superior cultivar for a target region. The targeting of cultivars to specific locations is difficult when GEI is present, since yield is less predictable and cannot be interpreted based only on G and E means (Samonte *et al.,* 2005). When assessing seed yield of a set of cultivars in a METs, changes are commonly observed in the relative yield performance of cultivars with respect to each other across locations. This differential yield response of cultivars from one environment to another is called GEI and can be describedand interpreted by statistical models (Crossa, 1990).

Breeders are primarily concerned with high yielding and stable cultivars as much possible as since cultivar development is a time consuming endeavor. Developed new cultivar should have a stable performance broad adaptation over a wide range of environments in addition to

high yielding potential. Evaluating stability of performance and range of adaptation has become increasingly important for breeding programmes. Hence, if cultivars are being selected for a large group of environments, stability and mean yield across all environments are important than yield for specific environments (Piepho, 1996).Successful cultivars must have good yield and other essential agronomic characters. Besides, their performance should be reliable over a wide range of environmental conditions. The basic cause of differences in stability between genotypes is a wide occurrence of GEI. Therefore, the interplay between genetic and non-genetic effects on development (Comstock and Moll, 1963).

In studying GEIit is important to describe the basic components of phenotypic variability, the genotype, the environment, and the interaction of the genotype and the environment. Genotyperefers to any of pure-line variety, Clone, inbred-line, hybrid variety, open-pollinated variety, Composite variety, Synthetic variety, Elite breeding lines and others on which the breeder collects performance and trait information. Environment refers to the combination of physical attributes of a location and the climatic and other attributes of a specific season (*i.e*. soil type, fertility, topography, temperature, rainfall, pest/disease challenge) that affect the plant growth in the growing season. The genotype and environment interaction refers to the deviation in performance of any attributes of genotypes within the growing environments. The most important thing in GEI is that in the conditions where the different traits under consideration show a change in rank in different environments. Such changes of rank in the genotypes which is called crossover GEI (Becker *Leon* 1988) creates inconvenience in plant breeding.

Information on the adaptation and stability of the genotypes over seasons and over sites is useful for recommending the varieties that should be grown under particular environments and predicting the yield expectations of the test varieties. A Genotype is considered to be the most stable one if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments (Arshad *et al*., 2003). Knowledge of the extent of GEIand stability and performance of genotypes across environments is absolutely essential to the plant breeder;the former will help breeders to decide whether he will aim at widely adapted varieties or specifically adapted ones in recommending the final release (Mosisa, 1999).

2.6. Concepts of Mega-Environment

Mega-environments were first defined as environments with similar “biotic and abiotic stresses, cropping system requirements, consumer preferences, and volume of production” (Braun *et al*., 1996). A cluster of environments or locations which constantly share the same best cultivar(s) are called mega-environments (Yan and Rajcan, 2002). Different environments with similar climatic, edaphic and other characteristics can be described by using different data of the environments and METs data to group under homogenous sub regions. Division of the target environments into meaningful mega-environments and deploying different cultivars for different mega-environments is the only way to utilize positive GEI and avoid negative GEI and sole purpose for GEIanalysis (Yan, *et al.*, 2007).

Annicchiarico and Perenzin (1994) declared that GE interaction in multiple-location and multiple-year trials can be dissected into genotype x location (GL), genotype x year (GY), and genotype x location x year three-way interactions (GLY). Since GEI is almost universal, and as yearly variation is typically largest source of yield variation, it is commonly believed that the greater the number of years a genotype is tested, the more reliable its evaluation will be.

2.7. Stabilityof Genotypic Performance

The knowledge of phenotypic stability is important for the selection of crop varieties as well as for breeding programmes. Yield stability is an interesting feature of today’s plant breeding programmes, owing to the high annual variation in mean yield, especially in the arid and semiarid areas (Mohammadi *et al*., 2012). The varietal stability could be challenged not only due to the change in the test environment but also due to change in growing season per environment (Dagnachew *et al*., 2014).A genotype is stable if at a given location or plant population exhibits very little fluctuation in seed quality from year to year. An ideal sesame selection (genotype) is one that combines high seed quality and stable performance in most of the ecological environments where it is cultivated (Adebisi, 2009).Selection of stable genotype that performs consistently across environments can reduce the magnitude of these interactions. Besides, stability of sesame performance is of special importance under rain-fed

conditions in developing countries where environmental conditions varied considerably and the technologies of modifying the environments are far from adequate (Adebisi, 2004).

The term stability is used to characterize a genotype, which showed a relatively constant yield and independent of changing environmental conditions. On the basis of this idea, genotypes with a minimal variance for yield across different environments are considered stable. This idea of stability may be considered as a biological or static concept of stability (Becker and Leon, 1988). Sesame yield is highly variable depending upon the growing environment, cultural practices and cultivars (Brigham, 1985)

2.8. Stability Analysis Models

Stability is very important for plant breeders to analysis GEI data because it enhances the progress from selection in any one environment (Yau, 1995). Different researchers used different stability models to estimate the stability of genotypes, some of them are:

2.8.1. Wricke's ecovalence (Wi)

Wrick (1962) as cited in Dia (2012) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (Wi) or stability of the i^{th} genotype is its interaction with the environments, squared and summed across environments. Genotypes with a low (Wi) value have smaller deviations from the overall mean across environments and are thus more stable. According to the meaning of ecovalence, the stable genotype possesses a low ecovalence. Hence, genotypes with a low (Wi) value have smaller deviations from the mean across environments and are thus more stable.

2.8.2. Eberhart and Russell's joint regression model

Eberhart and Russell (1966) stressed that the most important stability parameters appeared to be the deviation from linear regression mean square because all types of gene action were involved in this parameter. They use the regression coefficient (bi) and the deviation from regression (S^2di). The (bi) values greater and less than one, if associated with relatively high

mean yield, result in specific adaptation to high yielding (favorable) and low yielding (unfavorable) locations, respectively. Conversely, bi values around one indicate wide adaptation if combined with high mean yield. This model is popular and has been used widely in stability analysis of different crop Firew (2003) in common beans, Adane (2008) in linseed, Yasin and Hussen (2013) in field pea, Wedajo (2014) in pearl millet and Mekonnen*et al*. (2015) in sesame.

2.8.3. Cultivar Performance Measure (Pi)

The method of Lin and Binns (1988) has the great advantage of a directed recommendation of more stable and adapted genotypes, due to the uniqueness of the parameter, the evaluation of genotype performance according to the environmental variation and the fact that the genotypes identified among the most stable and adapted are generally the most productive. The most stable genotype is the one with least deviation from the maximum yield of each environment, *i.e*., with the lowest (Pi) value. It measures mean performance and stability simultaneously. This method was used by Nigussie (2012), Mekonnen*et al.* (2015) and Fiseha *et al*. (2015).

2.8.4. AMMI model

The additive main effects and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach (Gauch, 1988). According to Zobel *et al.* (1988) and Crossa *et al.* (1990), it can be used to analysis METs. The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, AMMI clarifies the GEI and summarizes patterns and relationships of genotypes and environments (Zobel *et al.*, 1988; Crossa *et al.*, 1990). The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five (Zobel *et al.*, 1988; Crossa, 1990).

2.8.5. AMMI Stability Value (ASV)

The ASV is the distance from the coordinate point to the origin in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, *et al*., 1997). Because the IPCA1 score contributes more to the GEI sum of squares, a weighted value is needed. This weight is calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction SS. The genotypes with larger IPCA score, either negative or positive, are the more specifically adapted to certain environments and those with smaller IPCA scores indicate a more stable genotype across environments.

2.8.6. Yield Stability Index (YSI)

Farshadfar *et al*. (2011) developed Yield stability index (YSI) which is similar to genotype selection index developed by Farshadfar (2008) is recommended as a measure of stability.YSI is calculated by summing the rank of mean seed yield across environments and rank of AMMI stability value of genotypes. The lowest ASV takes the rank one, while the highest yield mean takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability. The genotypes with lowest value of this parameter are desirable genotypes with high mean yield and stability.

2.8.7. GGE Bi-plot

GGE bi-plot is a data visualization tool, which graphically displays a GxE interaction ina two way table (Yan, 2000). GGE bi-plot is an effective tool for: 1) mega-environmentanalysis (e.g. “which-won-where” pattern), whereby specific genotypes can berecommended to specific mega-environments (Yan, 2003), 2) genotypeevaluation (the mean performance and stability), and 3) environmental evaluation (thepower to discriminate among genotypes in target environments).Fetien and Bjornstad (2009) in barley; Sabaghnia*et al.* (2013) and Farshadfar*et al*. (2013) in wheat; Munawar*et al.* (2013) and Fiseha*et al*. (2015) in sesame are among the many authors who used GGE bi-plot to identify mega environments, to evaluate the genotypes and to test the environments.

2.9. Genotype x Environment Interaction(GEI) of Sesame in Ethiopia

Sesame yield and oil content are highly variable depending upon the growing environment, cultural practices and cultivars. GEI studies to evaluate sesame genotypes were not practicing for many years ago in Ethiopia. Therefore,inaccessibility of improved, stable and high yieldergenotypes. But some of the few studies are (Yebio, 1993)reported that year and site had significant influence on oil content. There were also significant differences among lines for oil content. The line-site interaction was highly significant difference suggesting that the ranking of the eight lines for oil content across three locations were inconsistent.

Hagos and Fetien(2011)showed that there was significantly among genotypes, environments and GEI and the mean yield of genotypes differed from environment to environment inthirteen sesame genotypes tested across three years and locations from 2006-2008 in Western and North Western lowlands of Tigray.Zenebe and Hussien (2010) revealed that significant different of GEI among 20 sesame genotypes tested across six environments of Southern Ethiopia. They showed the GEI had significant values for all characters, indicating unstable in their expression with change in environment. The oil content of these genotypes also had highly significant difference across locations and seasons. This difference is due to the difference of soil type, rain fall and temperature in the test locations. Mekonnen *et al.*(2015) Reported that there was significant variations among environments and genotypes across all environments in two cropping seasons of twelve sesame genotypes at eight environments in five locations of eastern Amhara Region. The environments had different impacts on the seed yield and oil yield potential of the genotypes Mohammed *et al.*(2015), (Fiseha *et al.* 2015) reported that significance variation among genotypes, environments and GEI components showed highly significant variation for all traits. Thirteen sesame genotypes wereevaluated in three locations in North western andWestern Tigray from 2011-2013 cropping seasons. Environments were the main sources of variation for most of the traits. While, genotypes the main sources of variation for seed yield

3. MATERIALS AND METHODS

3.1. Description of the Study Areas

The experimentwas conducted in Northern Ethiopia; (Tigray and Amhara regional states) and environmentsdescription are presented below (Table 2) and map of test sites in northern Ethiopia presented in(Figure1).

Table 1: Agro-climatic and soil types of six tested locations in Northern Ethiopia

Description	Locations					
	Dansha	Maykadra	Humera	Sheraro	Wargiba	Gendawuha
Altitude(m.a.s.l)	696	646	609	1028	1578	760
Latitude (^{o}N)	13^{o}36'	14^{o}02'	14^{o}15'	14^{o}24'	12° 41'	12^{o}
Longitude (^{o}E)	36^{o}41'	36^{o}35'	36^{o}37'	37^{o}45'	39° 42'	36^{o}
R.F. (mm)	888.4	NA	576.4	1000	750	850-1100
Temp. (^{o}C)	28	NA	18.8-37.6	18.8-34.9	18-25	19.5-35.7
Soil type	Vertisol	Chromic vertisol	Chromic Vertisol	Vertisols	NA	Vertisol

Source: Bereket and Yirgalem (2012)Meteorology data (Dansha, Humera, and Maykadra): IPMS Ethiopia, (2005) (for Gendawuha).
NA=Not Available

Table 2:The Study locations in Northern Ethiopia in 2014-2015 cropping season

				Year	
Location	Region	Zone	District	2014	2015
Humera	Tigray	Western	K/Humera	E1	E2
Dansha	Tigray	Western	Tsegede	E3	E4
Sheraro	Tigray	N/western	T/Adyiabo	E5	E6
Wargiba	Tigray	Southern	R/Azebo	E7	E8
Maykadra	Tigray	Western	K/Humera	-	E9
Gendawuha	Amhara	-	Metema	-	E10

Note: K/Humera=Kafta Humera, T/Adyiabo=Tahtay Adyiabo, R/Azebo=Raya Azebo. E1=Humera, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

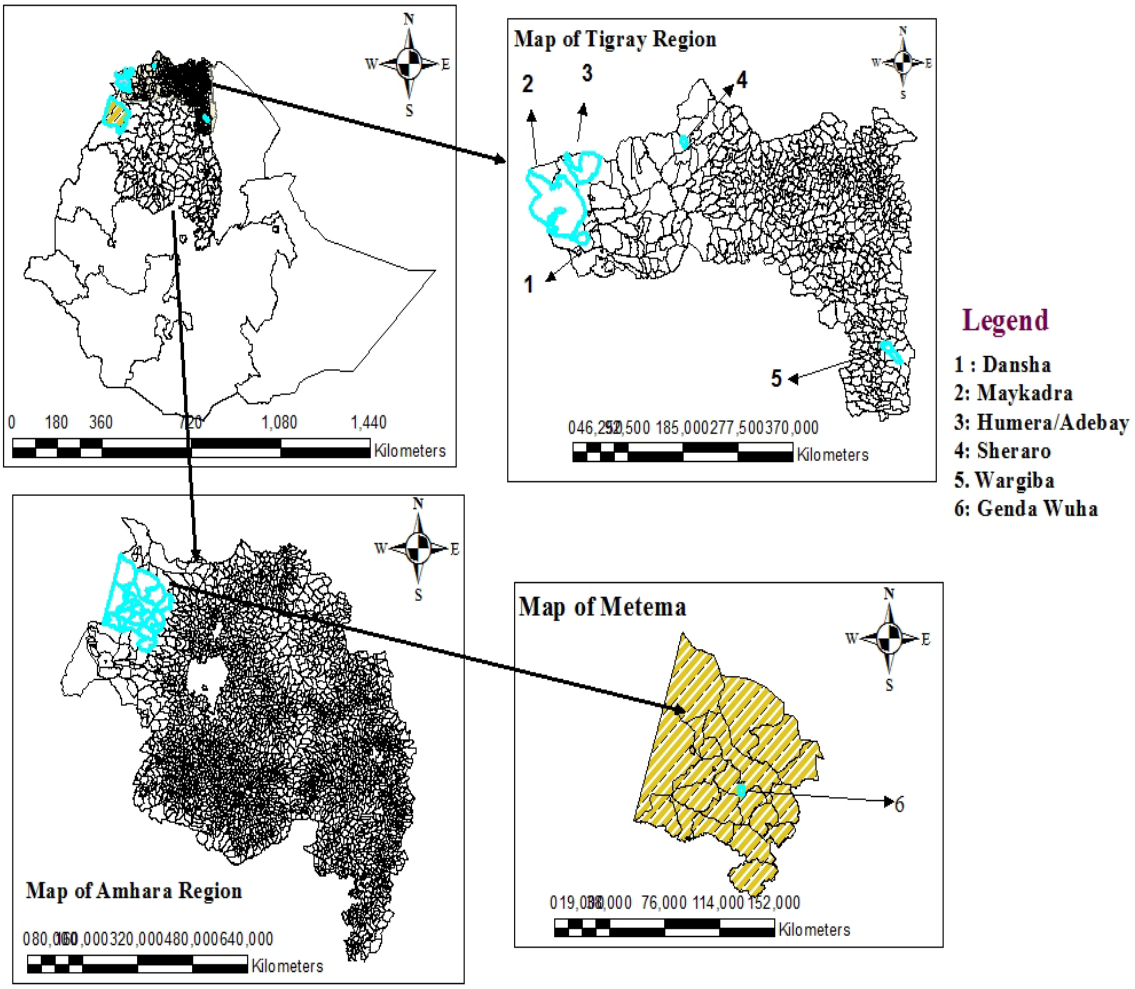

Figure 1: Map of test sites in Northern Ethiopia

3.2. Experimental Genotypes

Seventeen white seeded sesame genotypes (fifteenselected, one standard checks and one local check) were evaluatedin all locations and years. Description of the plant materials is presented in Table 3.

Table 3:Description of genotypes used in the study

Genotype (G)	Code	Status	Sources	Color	Remark
HuRC-4	G1	Advance line	HuARC	White	Collection
Acc202514	G 2	Advance line	HuARC	White	Collection
Land race Gumero	G 3	Advance line	HuARC	White	Collection
Abuseffa	G 4	Advance line	HuARC	White	Collection
HuRC-1	G 5	Advance line	HuARC	White	Collection
Rawyan -2	G 6	Advance line	HuARC	White	Collection
HuRC-3	G 7	Advance line	HuARC	White	Collection
Acc 202300	G 8	Advance line	HuARC	White	Collection
Kefif	G 9	Advance line	HuARC	White	Collection
Acc111824	G 10	Advance line	HuARC	White	Collection
Acc 111518	G 11	Advance line	HuARC	White	Collection
Acc 27913	G 12	Advance line	HuARC	White	Collection
Gumero	G 13	Advance line	HuARC	White	Collection
HuRC-2	G 14	Advance line	HuARC	White	Collection
Acc 227880	G 15	Advance line	HuARC	White	Collection
Setit -1(Standard check)	G 16	Standard check	HuARC	White	Collection
Hirhir (Local check)	G 17	Local check	HuARC	White	Collection

Source: Humera Agricultural research Center (HuARC) Annual report

3.3. Experimental Design and Management

The experiment was laid out in randomized complete block design (RCBD) with three replications in all testing sites. Each genotype was randomly assigned and sown in a plot area of 2m x 5m with 1m between plots and 1.5 m between blocks keeping inter and intra row spacing of 40 cm and 10 cm, respectively. Each plot had a total area of 10 m^2 and total of five rows and 6m^2 net plot area with three harvestable rows. The experimental plots were ploughed two times (first time before sowing and secondly during sowing) to maintain fine seedbed suitable for crop establishment. Each experimental plot received the same rate of DAP (100 kg/ha) and Urea (50 kg/ha) fertilizer and all field managementpractices were done equally and properly as per the recommendations to the study areas.

3.4. Data Collection

From the Centeral three rows ten plants were selected randomly and tagged to collect the agro morphological data such as, plant height, length of capsule bearing zone, number of branches, number of capsules and seeds per capsule. The averages of ten plants were considered for data analysis. Days to 50% flowering and 75% maturity were taken on plot basis. Furthermore, the three experimental rows were harvested, tied in sheaves and were made to stand separately until the capsules opened. After the sheaves have dried out fully and all of the capsules opened, seeds were tipped out onto sturdy cloths or canvases and threshing was accomplished by knocking the sheaves.

Days to 50% flowering (DF): The number of days from emergence to which 50% of the population in each plot had flowered.

Days to 75% maturity (DM): The number of days from emergence to when 75% of the plants in each plot had fully matured.

Plant height (PH) (cm): This growth parameter was measured from ten randomly selected and tagged plants from the harvestable rows of each plot with the help of meter tape from ground surface to the top of the plant.

Length of capsule bearing zone (LCBZ) (cm): A height from the first capsule to tip of the plant, measured using meter tape.

Number of primary branches per plant (NBPP): Branches producing productive capsules were done recorded for randomly selected plants.

Number of capsules (NCPP): The total number of capsules was counted from ten randomly selected plants at maturity.

Seed yield (kg/ha): The total seed yield harvested from the net plot area was weighed using a sensitive balance.

Thousand seed weight (TSW): Weighed in grams of 1000 seed

Number of seeds per capsule (NSPC): Number of seeds per capsule

Oil contents (OC) (%): Oil content was determined by wide line nuclear magnetic resonance (NMR). Seeds were taken from each plot and oven dried at 130 ºC for 2 hours and cooled for 1 hour. A sample of 22 g of oven dried clean seed was used for analysis of oil content by NMR (Newport analyzer) (Newport Pagnell, Bucks, and UK) (Robbelen *et al.*, 1989).

3.5. Data Analysis

Statistical estimations and computations were performed using different statistical softwares. Homogeneity of residual variances was tested prior to a combined analysis over locations in each year as well as over locations and years using Bartlett's test (Steel and Torrie, 1998). Analysis of variance for each environment, combined analysis of variance over environments, AMMI analysis and correlation between different stability parameters were computed using GenStat 16th edition(2009). Coefficient of regression (bi) and deviation from regression (S^2di) stability parameters were also analyzed using Agrobase (2000) software.

3.5.1. Separate and combined ANOVA

As the error variance were homogenous for seed yield and oil content continued to combined analysis of variance from the mean data of all environments to detect the presence of GEI and to partition the variation due to genotype, environment and GEI. The environments (locations and years) in the study were assumed as random effects and the genotype effects were treated as fixed. Moreover, mean comparison using Duncan's Multiple Range Test (DMRT) was performed to explain the significant differences among means of genotypes, years and locations (environments). Unbalanced design ANOVA model were used for combined analysis of variance because of different locations and years in the study. GenStat 16th edition (2009) statistical software was used for most of the statistical analyses. The model employed in the analysis was;

$$Yijk = \mu + Gi + Ej + Bk + GEij + \varepsilon ijk \text{ where:}$$

Yijk is the observed mean of the ith genotype (Gi) in the jth environment (Ej), in the kth block (Bk); μ is the overall mean; Gi is effect of the ith genotype; Ej is effect of the jth environment; Bk is block effect of the ith genotype in the jth environment; GEij is the interaction effects of the ith genotype and the jth environment; and εijk is the error term.

3.5.2. Stability Analysis

Wricke's (1962) ecovalence and Lin and Binns's (1988) cultivar superiority performance were calculated using GenStat 16version software,AMMI stability value (ASV) was calculated in the excel spread sheet using the formula developed by Purchase *et al*. (1997):

$$\mathrm{ASV} = \sqrt{\left[\frac{\mathrm{SS}_{\mathrm{IPCA\ 1}}}{\mathrm{SS}_{\mathrm{IPCA\ 2}}}(\mathrm{IPCA1}_{\mathrm{score}})\right]^2 + (\mathrm{IPCA2}_{\mathrm{score}})^2}$$

Where, ASV= AMMI's stability value, SS=sum of squares, IPCA1=interaction of principal component analysis one, IPCA2 = interaction of principal component analysis two. Similarly Yield stability index (YSI) was also computed by summing up the ranks from ASV and mean seed yield (Farshadfar, *et al*., 2011):

$$\mathrm{YSI} = \mathrm{RASV} + \mathrm{RGY}$$

Where: RASV is rank of AMMI stability value and RGY is rank of mean seed yield to statistically compare the stability analysis procedures used in the study, the Spearman's coefficient of rank correlation (r_s) (Steel and Torrie, 1980) was estimated using SPSS version 16 statistical software.

3.5.3. AMMI Model Analysis

The seed yield data were subjected to AMMI analysis, which combines analysis of variance (ANOVA) with additive and multiplicative parameters in to a single model (Gauch, 1988). After removing the replicate effect when combining the data, the genotypes and environments observations are partioned in to two sources: Additive main effects for genotypes and environments; and Non-additive effects due to genotype by environment interaction. A bi-plot showing the genotype and environmental means against IPCA1 was also performed *via* this model using GenStat (V16). The AMMI model is:

$$\mathrm{Y_{ij}} = \mu + \mathrm{G_i} + \mathrm{E_j} + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \theta_{ij} \quad \text{Where:}$$

$\mathrm{Y_{ij}}$ is the observed mean yield of i^{th} genotype in the j^{th} environment; μ is the grand mean; $\mathrm{G_i}$ is the i^{th} genotypic effect; $\mathrm{E_j}$ is the j^{th} environment effect; λ_k is the eigen value of the principal component analysis (PCA) axis k; α_{ik} and γ_{jk} are the i^{th} genotype j^{th} environment PCA scores

for the PCA axis k; θ_{ij} is the residual; n is the number of PCA axes retained in the model. The number n is judged on the basis of empirical consideration of F-test of significance.

3.5.4. GGE Bi-plot Analysis

GGE bi-plot is able to show the best genotype with the highest yield in a quadrant containing identical locations (Mega-Environments), genotype average performance and stability, ideal genotype and ideal location to increase yield and specific location. Visualization of GGE biplot is very useful to evaluate and find the most stable genotypes (Fashadfar *et al.*, 2013). Genotypes laid in the concentric area are the most stable compared to the genotypes laid outside, even though the environmental effect was very strong (Untung *el al*., 2015).

An ideal genotype is defined as one that is the highest yielding across test environments and absolutely stable in performance (that ranks the highest in all test environments (Farshadfar *et al.*, 2012). Although such an “ideal” genotype may not exist in reality, it could be used as a reference for genotype evaluation (Mitrovic *et al.*, 2012). A genotype is more desirable if it is located closer to “ideal” genotype (Kaya *et al.*, 2006; Mitrovic *et al.*, 2012).

4. RESULTS AND DISCUSSION

4.1. Combined ANOVA and Estimation of Variances Components

Variances of homogeneity from results of the Bartlett test revealed that the mean squares of individual environments were homogenous(Appendix Table 4)for seed yield and oil contents.So, combined analysis of variance could be done. The main effects of environments and genotype and GEI were highly significantat ($p \leq 0.001$) for seed yield, oil content and yield components. The partitioning of sum of squares indicated that environments, GEI and Genotype contributes to 69.73%, 14.68% and 9.58% variation for seed yield and 61.6%, 13.64%) and 6.55% for oil content, respectively.This indicates the big influence of environment on yield performance of sesame genotypes across all locations. Similar result was reported on sesame (Mekonnen*et al.*(2015) and Mohammed *et al.*(2015).

4.2. Mean of Genotypes for Seed Yield AcrossTen Environments

The mean seed yield of the individual environments during 2014-2015 main season are highly significant at ($p \leq 0.001$) and individual mean of environments presented in (Table 4).Overall mean seed yield over ten environments was 649.35 kg/ha and the mean seed yield of genotypes across environments ranged between238.5kg/ha in E2 to 1123.8 kg/haE3. High variationfor seed yield was among genotypes. Therefore, G1 had the highest mean seed yield 867.4kg/ha followed by G7 (792.5), G3 (753.8), G16 (745.1), G14 (723.6), G5 (694.6), G4 (668.6) and G15 (662.9) kg/ha and higher than the nationalaverage of 0.69ton/ha in 2015 cropping season. This figure is also higher than the world average seed yieldobtained in 2014 cropping season0.5 ton/ha. While G8 (441.8) kg/ha was one of the least status of seed yield. Among high yielder genotypes, G1, G7 and G3 showed 18.85%, 7.30% and 1.34% yield advantage over the standard check and 34.25%, 22.75% and 16.75% over the local check,respectively.The yield variation among genotypes indicated that selection should be based on mean performances at the respective environments.Change performance yield with environments was also reported byFiseha *et al.* (2015), Mekonnen*et al.*(2015) and Mohammed *et al.,* (2015) in sesame. Among the tested locations, Dansha, Gendawuha and Sheraro had received optimum rain fall and gavebetter yield. While, Humera, Maykadra and Wargiba gave low yield due low rain fall andhigh moisture stress during 2015 main season.

Table 4:Mean yield (kg/ha)of 17genotypes across10 environments in 2014-2015 main season

	Environments										
G	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Mean
G1	1107.6^{a}	361.7^{ab}	1173^{bcd}	670.5^{ab}	619.8^{bcd}	1325^{a}	844.2^{a}	756^{a}	761.7^{a}	1054.9^{ab}	867.4^{a}
G2	967.7^{bc}	222.5^{cd}	1065^{def}	671.8^{ab}	341.7^{gh}	974^{ef}	385.8^{de}	203.7^{g}	238.9^{h}	761.1^{bc}	583.3^{hi}
G3	1070.9^{ab}	347.8^{b}	1467^{a}	453.5^{cde}	866.1^{a}	1056de	675.9^{ab}	378.3^{de}	446.1^{d}	776.4^{bc}	753.8^{bc}
G4	849.1^{cdefg}	227.2^{cd}	1258^{b}	763.9^{a}	584^{bcde}	1329^{a}	542.3^{bcd}	366.3^{de}	321.9^{f}	445.2^{d}	668.6^{ef}
G5	677.5^{ij}	233.3^{cd}	957^{f}	533.3^{bcd}	716.7^{b}	1183^{bc}	655.9^{b}	714.3^{a}	512.2^{c}	762.6^{bc}	694.6^{de}
G6	983.6^{b}	237.5^{c}	1125^{cd}	338.6^{e}	322.4^{h}	853^{fghi}	461.2^{cde}	481.7^{cd}	345.3^{f}	828.8^{bc}	597.7^{ghi}
G7	837.7^{defgh}	354.7^{b}	1486^{a}	480.2^{cde}	623.8^{bcd}	1158^{bcd}	686.4^{ab}	657.7^{ab}	654.2^{b}	986.4^{ab}	792.5^{b}
G8	611^{ji}	110.6^{e}	492^{g}	354.4^{e}	536.7^{cde}	733^{ik}	469.9^{cde}	288.3^{efg}	177.9^{j}	643.7^{cd}	441.8^{j}
G9	849.2^{cdef}	150de	1094de	354.9^{e}	396.7^{fgh}	882^{fgh}	363.9^{de}	475^{cd}	405.^{8i}	846.5^{abc}	562.1^{i}
G10	632.1^{ijk}	160^{cde}	1075de	550.3^{bc}	366.5^{gh}	855^{fghi}	364.9^{de}	236.7^{fg}	208.9^{e}	834.5^{bc}	548.1^{i}
G11	681.7^{ij}	125^{e}	1132^{cd}	385.4^{de}	550.6^{cde}	1106^{cd}	334.4^{e}	309^{efg}	218.9^{hi}	770.2^{bc}	561.3^{i}
G12	729.3^{fhij}	242.8^{c}	1086de	764.3^{a}	472.2^{efg}	761^{hjik}	393d^{e}	387.7^{de}	325^{f}	1029.8^{ab}	619.1^{fgh}
G13	853.7^{cde}	170^{cde}	1105^{d}	515.4^{cd}	343.4^{gh}	934^{fg}	302.7^{e}	293de	337.2^{f}	863^{abc}	571.8^{hi}
G14	858.9^{cde}	435^{a}	1125^{cd}	467.7^{cde}	504.1^{def}	1250^{ab}	638.5^{bc}	757.3^{a}	265.8^{g}	933.6^{abc}	723.6^{cd}
G15	742.8^{efghi}	233.9^{cd}	987^{fe}	558^{bc}	660.6^{bc}	850^{ghij}	425.2^{de}	348.3^{def}	778.6^{a}	1043.8^{ab}	662.9^{ef}
G16	868.5^{cd}	218.9^{cd}	1246^{b}	522.6^{cd}	663.5^{bc}	1266^{ab}	705.5^{ab}	392de	426.9^{de}	1141·4^{a}	745.1^{bc}
G17	545.9^{k}	223.9^{cd}	1232^{bc}	357.6^{e}	605.6^{bcde}	1203^{bc}	530.3^{bcd}	547^{bc}	449.2^{d}	760.1^{bc}	645.5^{efg}
Mean	815.7	238.5	1123.8	514.3	539.7	1042.24	516.5	446.60	404.38	851.9	649.35
CV%	8	18.7	5.6	15.2	13.3	6.4	19	16.2	3.8	18.3	13.8

G=Genotypes; G1= HuRC-4, G2= Acc202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=, Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7= Wargiba-1, E8= Wargiba-2, E9=Maykadra and E10= Gendawuha

4.3. Mean of Genotypes for Oil Content (%)Across Six Environments

The mean performance of genotypes for oil content across the tested environments during 2015 main season were highly significance difference across six locations at ($p \leq 0.001$) indicated in Table5. Genotype variation for mean oil content across locations givesa chance to select genotypes having better oil contentfor sesame growing areas in northern Ethiopia.

The major requirements for sesame export are pearly white seed color and 40-50% oil content. All the genotypes in this study had full filled the export requirements. Grand mean oil content of the genotypes over six environments was 49.9% and the mean oil content ranged between 49% in G5 to 51.9% in G12 across the tested locations. Nine genotypes gave mean oil content greater than grand mean oil content, while eight genotypes gave less than the grand mean. Highest oil content was obtained from G12 and the lowest from G5 (Table 5).

The oil content percentage was variedamong genotypes and is consistent with the previous finding:Zenebe and Hussein (2010)45.9-52-5% 24-58%, Alege and Mustapha (2013) 38-57% Yahaya *et al.* (2014), 45.2-52.7% Mohammed *et al.* (2015) and 46.4%-53.4% Mekonnen*et al.* (2015). Hence, variation exist among genotypes indicated that oil content was highly affect by environments (rain fall, altitude, soil type, temperature *etc*.). Gendawuha (52.5%) gave the highest mean oil content followed by Sheraro (50.99% and Dansha (50.6%)which received optimum rainfall in the 2015 main cropping season resulted high oil content.

Locations faced to moisture stress gave low oil content: Humera (48.2%) followed by Wargiba (48.5%) and Maykadra (48.61%).Sesame oil content varied greatly across seasons and environments.This result is in agreement withZenebe and Hussein (2010) andMekonnen*et al.* (2015).To improve the oil content of sesame genotypes, selection should be based on high seed yield with relatively high oil content or cross breeding of high seed yielder with high oil content genotypes.

Table 5:Mean oil content (%) of 17 genotypes across six locations during 2015 main season

	Environments						
G	E2	E4	E6	E8	E9	E10	Mean
G1	47.18^{d}	50.91^{bcd}	50.49^{ab}	48.2	47.7^{efg}	51.83^{bcde}	49.4^{fgh}
G2	48.52^{abcd}	50.27^{cdef}	50.77^{ab}	48.37	49.54^{bc}	53.74^{ab}	50.2^{abcdef}
G3	48.87^{ab}	52.03^{ab}	49.18^{b}	48.08	49.78^{b}	52.64^{abcd}	50.10^{bcdef}
G4	48.5^{abcd}	51.36^{abc}	50.51^{ab}	48.74	50.27^{ab}	52.16^{bcde}	50.26^{abcde}
G5	47.34^{d}	49.58^{ef}	50.31^{ab}	47.92	47.63^{efg}	51.37^{de}	49.03^{h}
G6	47.19^{d}	49.82^{def}	52.09^{ab}	48.67	46.9^{fg}	50.49^{e}	49.18^{gh}
G7	47.67^{bcd}	51.21^{bc}	51.81^{ab}	49.59	49.5^{bc}	52.33^{abcde}	50.35^{abcd}
G8	48.8^{abc}	49.34^{f}	51.26^{ab}	48.63	47.54^{efg}	51.42^{cde}	49.54^{defgh}
G9	49.33^{a}	49.28^{f}	52.62^{a}	48.13	46.79^{g}	51.87^{bcde}	49.67^{cdefgh}
G10	49^{ab}	50.7$_{cde}$	49.91^{ab}	48	47.63^{efg}	52.17^{bcde}	49.57^{defgh}
G11	48.13^{abcd}	49.47^{ef}	50.2^{ab}	48.59	47.82^{def}	52.58^{abcde}	49.46^{efgh}
G12	48.93^{ab}	52.52^{a}	51.7^{ab}	47.68	50.79^{a}	54.24^{a}	51^{a}
G13	47.32^{d}	50.46^{cdef}	51.78^{ab}	48.43	47.53^{efg}	52.3^{abcde}	49.67^{cdefgh}
G14	48.32^{abcd}	51.33^{abc}	52.03^{ab}	48.29	49.79^{b}	53.68^{ab}	50.6^{ab}
G15	48.4^{abcd}	51.29^{abc}	50.11^{ab}	49.1	50.11^{ab}	53.39^{abc}	50.4^{abc}
G16	48.56^{abcd}	50.92^{bcd}	51.43^{ab}	48.47	48.26^{de}	54.17^{a}	50.3^{abcd}
G17	47.42^{cd}	50.2^{cdef}	50.7^{ab}	49.87	48.73^{cd}	52.77^{abcd}	49.95^{bcdefg}
Mean	48.20	50.6	50.99	48.5	48.61	52.5	49.9
CV%	1.5	1.3	3.1	2.8	1.1	1.9	1.95

Values connected with the same letters in a column were not significantly different; G=Genotype, CV%= Coefficient of variability, E2= (Humera-2), E4= (Dansha-2), E6 = (Sheraro-2), E8= (Wargiba-2), E9= (Maykadra), E10= (Gendawuha),

4.4. Seed Yield related traits

G1 was the earliest flowering (41.17) and early maturing (76.9). G4 (86.43) followed by G13 (86.17), G3 (85.73) and G9 (85.13) were the late maturing. G3 (103.89) and G14 (103.41) were the tallest genotypes. G10 (94.25) and G13 (94.01) were with shortest plant stature. The highest number of branches and number of capsules were recorded from G1. G6, G7, G10 and G14 were recorded the highest thousand seed weight (TSW) above the standard requirement of 3.0g and fulfill the standard requirement of international sesame oilseed market (Table 6).GEI is important contribution for variation of yield related traits among genotypes across testing environments. This is in line with Hagos and Fetien (2011) and Yahaya (2014) in sesame.Early maturing genotypes are important for moisture stress areas. Whereaslate maturing are for high rain fall areas. Genotypes had high number of branches, number of seeds and thousand seed yield weight are important for increasing yieldof sesame genotypes.

Table 6:Mean performance of 17 genotypesfor different traits over all locations

G.	DF	DM	LCBZ	NBPP	NCPP	PH	SPC	TWT
G1	41.17^{i}	76.9^{h}	54.5^{a}	3.21^{cdef}	37.25^{b}	101.35^{bcd}	69.33^{abcd}	2.701cd
G2	46.03^{de}	81.63^{de}	48.31^{f}	3.38^{abcd}	28.85^{f}	97.52^{f}	68.77^{abcd}	2.643cde
G3	47.87^{bc}	85.73^{ab}	51.4^{d}	3.63^{a}	31.43^{de}	103.89^{a}	66.2cd	2.848abc
G4	49.87^{a}	86.43^{a}	51.87^{cd}	3.35^{bcde}	35.77^{c}	97.17^{f}	68.99^{abcd}	2.899abc
G5	44.17^{fg}	79.13^{fg}	52c^{d}	3.09^{efgh}	31.59^{de}	103.39^{ab}	71.2^{ab}	2.45de
G6	48.17^{b}	83.83^{bc}	49.21^{ef}	2.85^{hi}	32.03^{d}	100.33^{de}	69.36^{abcd}	3.043ab
G7	43.2^{gh}	79.8^{ef}	52.89^{bc}	3.12^{defgh}	27.73^{f}	100.36^{de}	67.6^{bcd}	3.11a
G8	46.63^{d}	83.83^{bc}	48.24^{f}	3.02^{fghi}	30.95^{de}	98.15e^{f}	69.97^{abc}	2.459de
G9	50.37^{a}	85.13^{abc}	43.39^{g}	3.57^{ab}	28.5^{f}	101.42^{bcd}	71.05^{ab}	2.383de
G10	48.17^{b}	81.03^{ef}	40.45^{h}	2.93^{ghi}	25.04^{g}	94.25^{g}	72.18^{ab}	3.058ab
G11	47.9^{bc}	84.93^{abc}	40.09^{h}	2.82^{i}	26.04^{g}	97.33^{f}	70.2^{abc}	2.899abc
G12	46.63^{d}	81e^{f}	49.86^{e}	3.19^{cdefg}	36.13^{c}	88.79^{h}	66.16^{cd}	2.778bc
G13	50.1^{a}	86.17^{a}	41.25^{h}	2.81^{i}	23.17^{h}	94.01^{g}	72.47^{a}	2.938abc
G14	45.13^{ef}	80.3e^{f}	53.57^{ab}	3.4^{abc}	35.14^{c}	103.41^{ab}	69.43^{abcd}	3.085ab
G15	46.57^{d}	83.43^{cd}	52.37^{bcd}	3.51^{ab}	38.81^{a}	98.65e^{f}	66.03^{cd}	2.683cd
G16	43.17^{gh}	77.83^{gh}	49.97^{e}	3.21^{cdef}	30.5^{e}	100.5^{cde}	64.98^{d}	2.935abc
G17	42.73^{h}	80.1^{ef}	52.44^{bcd}	3.44^{abc}	32.03^{d}	102.82^{abc}	70.53^{abc}	2.922abc
Mean	46.36	82.19	48.93	3.21	31.23	99.02	69.09	2.81
CV%	4.7	4.3	5.2	14.5	7.3	4.3	11	18.1

G= Genotype, DF =days to flowering, DM=days to maturity, PH= plant height, LCBZ= length of capsule bearing zone, NBPP =number of branches per plant, NCPP= number of capsules per plant, SPC =seeds per capsule, TSW= thousand seed weight, SY= seed yield

4.5. Sesame Seed Yield Stability Using Different Stability Parameters

4.5.1. Wricke's (Wi) Ecovalence Analysis

According to Wricke's (Wi) Ecovalence model shown in Table 7,G11, G9, G13, G10 and G1 were the most stable ranked 1st, 2nd, 3rd, 4th and 5thfor seedyield and 4th, 16th, 7th, 2nd and 3rd formean oil content respectively.While, G4, G3 and G8, were unstable ranked 17th, 14th and 15th for seed yield and 13th, 15th and 19thfor oil content, respectively (**Table 7**).This result is in accordance with Alberts (2004) in common bean.

Table 7:Wricke's ecovalence value of seed and oil yields for 17 sesame genotypes

G	SY	R	Wi	R	OC	R	Wi	R
G1	867.4	1	110047	5	49.8	12	0.93	3
G2	583.3	12	163463	10	50.2	6	2.84	10
G3	753.8	3	233791	14	50.1	9	6.81	15
G4	668.6	7	341095	17	50.26	7	3.57	13
G5	694.6	6	188863	12	49.03	17	0.31	1
G6	597.7	11	123724	8	49.18	16	8.19	17
G7	792.5	2	115774	7	50.35	5	1.60	6
G8	441.8	17	269022	15	49.5	15	2.26	9
G9	562.1	14	67623	2	49.67	14	7.05	16
G10	548.1	16	73381	4	49.57	13	0.91	2
G11	561.3	15	67254	1	49.4	11	1.47	4
G12	619.1	10	202390	13	51	1	6.36	14
G13	571.8	13	70485	3	49.67	10	1.75	7
G14	723.6	5	169296	11	50.6	2	1.51	5
G15	662.9	8	270511	16	50.4	4	3.14	11
G16	745.1	4	114803	6	50.3	3	3.54	12
G17	645.5	9	160177	9	49.95	8	1.96	8

*, ** significance at 5% and 1%, respectivelyG =genotype, SY= seed yield, R = rank, Wi=, Oc =oil content, OR = over all rank

4.5.2. Eberhart and Russell's Linear Regression Model

According to coefficient of regression estimated value, G17, G1, G5, G9 and G7 had near to unity and considered as stable genotypes, while G15, G16, G14, G13, G12, G11,G8, G6, andG4 had greater than unity estimated value and consideredas unstable for seed yield. G1, G2, G3, G4, G5, G6, G7, G8, G9, G13 and G15 were near to unity regression coefficient and the most stable for oil content. G16, G17, G14, G10, G11 and G12 had greater than unity were unstable (**Table8**). This result is in line with Firew(2003) in common bean and Mekonnen*et al.*(2015) in sesame.

Table 8:Eberhart and Russell (1966) stability value of seed and oil content of sesame genotypes

G	SY	R	bi	R	S^2di	R	OC	R	bi	R	S^2di	R
G1	867.4	1	0.89	4	20758.74	14	49.8	12	0.82	2	1.28	12
G2	583.3	12	1.02	8	12142.36	8	50.2	6	0.73	1	0.15	8
G3	753.8	3	0.57	1	12680.67	9	50.1	9	0.93	8	-0.33	1
G4	668.6	7	1.13	14	37759.30	17	50.26	7	0.93	8	1.28	13
G5	694.6	6	0.97	7	5791.59	5	49.03	17	0.93	8	0.15	8
G6	597.7	11	1.11	15	4391.77	2	49.18	16	0.82	3	0.28	9
G7	792.5	2	0.93	5	10043.85	6	50.35	5	0.99	10	1.96	14
G8	441.8	17	1.05	9	16486.66	12	49.5	15	0.90	5	0.20	9
G9	562.1	14	0.76	3	14783.53	10	49.67	14	0.96	9	-0.04	5
G10	548.1	16	0.99	6	17843.66	13	49.57	13	1.24	15	0.95	11
G11	561.3	15	1.09	12	10382.49	7	49.4	11	1.20	13	0.01	6
G12	619.1	10	1.09	11	16406.79	11	51	1	1.21	14	-0.10	4
G13	571.8	13	1.08	10	4500.34	3	49.67	10	0.91	4	0.39	10
G14	723.6	5	1.24	17	5354.35	4	50.6	2	1.32	16	-0.19	2
G15	662.9	8	1.20	16	1419.28	1	50.4	4	0.95	6	0.30	10
G16	745.1	4	1.13	13	24115.89	15	50.3	3	1.07	11	-0.11	3
G17	645.5	9	0.75	2	24593.31	16	49.95	8	1.07	12	0.13	7

*, ** significance at 5% and 1%, respectively. G =Genotype, SY=Seed yield, OC= oil content, bi=coefficient of regression, S^2di =deviation from regression, OC=Oil content

4.5.3. Cultivar Superiority Measure (Pi) of Lin and Binns Model

The ranks of the Pi measure for mean seed and oil content are given in Table 9. According to the (Pi) G1, G7, G3 and G16 were ranked 1st, 2nd, 4th, and 3rd for mean seed yield and11th, 4th, 9th, 5rdfor meanoil content, respectively (Table 9).This result is in harmony with Lin and Binns (1988) in bean and Molla (2010) in finger millet.

Table 9:Seed yield, Oil content and their Cultivar superiority Value (Pi)

G	SY	R	Pi	R	OC	R	Pi	R
G1	867.4	1	9036	1	49.8	12	2.57	11
G2	583.3	12	80169	13	50.2	6	1.07	6
G3	753.8	3	29813	4	50.1	9	1.79	9
G4	668.6	7	58946	9	50.26	7	1.34	7
G5	694.6	6	42711	6	49.03	17	3.69	16
G6	597.7	11	69822	11	49.18	16	4.37	17
G7	792.5	2	16102	2	50.35	5	0.95	4
G8	441.8	17	146926	17	49.5	15	3.22	14
G9	562.1	14	80574	15	49.67	14	3.4	15
G10	548.1	16	86227	16	49.57	13	2.73	13
G11	561.3	15	80386	14	49.4	11	2.6	12
G12	619.1	10	68775	10	51	1	0.47	1
G13	571.8	13	77593	12	49.67	10	2.1	10
G14	723.6	5	38301	5	50.6	2	0.49	2
G15	662.9	8	54425	8	50.4	4	0.86	3
G16	745.1	4	27076	3	50.3	3	1.03	5
G17	645.5	9	53505	7	49.95	8	1.47	8

*, ** significance at 5% and 1%, respectively. G =Genotype, SY= Seed yield, R = Rank, Pi= Cultivar Superiority Measure, OC =Oil content

4.5.4.AMMI Analysis

The AMMI analysis of variance of ten environments for seed yield and six locations for oil contentare presented in (Table 10 and 11) respectively.Showed highly significance variation at ($P \leq 0.001$) among genotypes, environments and GEIforseed yield and oil content.

High environmental variations and differential response of genotypes to the variable environments leading to inconsistency ranking of genotypes. From the total variation, 69.73%, 14.68%, 9.58% were explained by environments, GEI and genotypes for seed

yieldand 61.6%, 13.64%) and 6.55%) for oil content,respectively.The result is agreed with the previous findings Yebio (1993), Mohammed (2015) and Mekonnen et al. (2015) in sesame.

This showed that the significances influence of environments on yield and oil content performance of sesame genotypes in different locations of northern Ethiopia indicating the need to test sesame genotypes under various environments. The presence of significant GEI, suggested the need to developing genotypes that would have low G x EI for the target area. The four IPCAs were highly significant leading to a cumulative 99.8% variation and the rest 2.62% was contributed due to noisefor seed yield and three IPCs significance leading to a cumulative contribution of 83.7% variation and the rest due to noise for oil content. Thus, the AMMI with only the two interaction principal component axes was the best predicative model for both seed yield and oil content.This is in harmony with Zobel *et al*. (1988) and Annicciarico (2002). The further interaction principal component axes captured mostly noise and did not help to predict validation observations. Hence, the interaction of the 17 genotypes with ten environments was best predicted by the two interaction principal components.

Table 10: AMMI's ANOVA for seed yield (kg/ha) of 17 genotypes during 2014-2015

Source of variation	df.	SS.	MS.	Sum of squares Total V.E	% explained GEIE	GEI Cmu.
Genotypes	16	5367408	335463**	9.58		
Environments	9	39066091	4340677**	69.73		
Block within Envi.	20	1306032	65302**	2.33		
Interactions	144	8225103	57119**	14.68		
IPCA 1	24	4234567	87589**		51.56	51.48
IPCA 2	22	1849997	84091**		22.49	73.97
IPCA 3	20	1250159	62508**		15.2	89.17
IPCA 4	18	1121227	62290**		10.63	99.8
Residuals	8	78316	4789^{ns}			
Total	281	62498900	5099828			

** Significance at($p \leq 0.001$) respectively. Block =replication within environments. Total V.E. =Total variation explained, GEIE. =GEI explained and GEI cum. = GEI cumulative, SS= Sums of squares and MS=Means of squares.

Table 11:AMMI's ANOVA for oil content (%) of 17 genotypes during 2104 main season

Sources of Variation	df.	SS.	MS.	Sum of squares Explained (%)		
				Total V.E.	GEI E.	GEI cum.
Genotypes	16	82.4	5.15**	6.55		
Environments	5	775.5	155.1**	61.6		
Block with En.	12	18.9	1.57ns	1.50		
Interactions	80	171.7	2.15**	13.64		
IPCA 1	20	90.6	4.53**		52.77	52.77
IPCA 2	18	30.3	1.69**		17.65	70.42
IPCA 3	16	22.9	1.43*		13.34	83.75
IPCA 4	14	18	1.28^{ns}		10.48	94.24
Residuals	12	9.9	0.82^{ns}		5.766	100
Total	193	1220.2	173.72			

ns=, *, ** indicated no significant and significant, ($p \leq 0.05$)($p \leq 0.001$) respectively.Block =replication within environments. Total V.E. =Total variation explained, GEIE. =GEI explained and GEI coum. = GEI cumulative, SS= Sums of squares and MS=Means of squares.

Nine high yielder genotypes:G15, G1, G16, G3, G4, G5, G14, G17 and G7 were gave seed yieldabove grand meanin the favorable environments, while eight genotypes G12, G8, G10, G2, G13, G6, G9 and G11were gave seed yield below the grand meanand low yield in the unfavorable environments (Figure2). Stable genotypeswere adaptive to wider areas and give consistency mean yield across the test locations. G1, G7, G2, G3, G6, G9 and G16 werefound nearly closer to the origin and the most stable with little responsive to the GEI.Genotypes far from the origin are sensitive to environmental changes. Hence, G4, G10, G8, G11, G12,G13,G17, G15 and G14were the unstable. In contrast,G1, G7, G 16 and G3were the most stable in the favorable environments. G8 and G11 were unstable with low yield in the unfavorable environments. Therefore, genotypes with high yield and wider stability performanceare the most desirable for wider area.

Environmentssuitable to sesame production are classified according their position found in the quadrant (Figure 2). Environments on 1st and 2nd quadrant,E1, E3, E6, and E10 were favorable.Whereas, E9, E4, E2, E5, E8 and E7 in 3rd and 4th quadrant of the graphwere considered as unfavorable environments

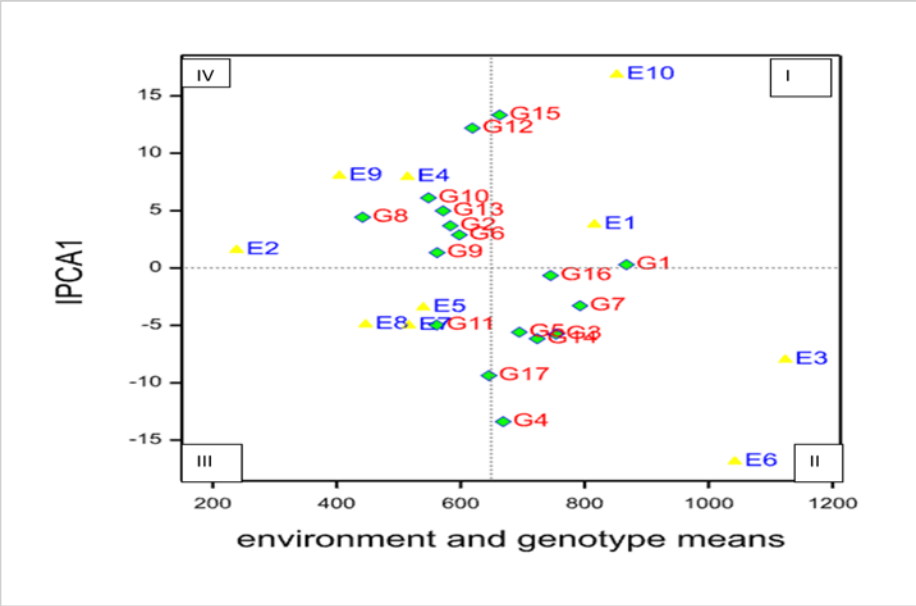

Figure2:AMMI1bi-plot showing Genotype and Environment means seed yield againstIPCA1.

G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. Environments: E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2,E5=Sheraro-1,E6=Sheraro-2,E7=Wargiba-1,E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

E10, E4 and E6 were favorable environments, while E2, E9 and E8 were unfavorable environments for mean oil content. Due to environmental factors the oil content varied among genotypes. Hence, G1, G5, G6, G8, G9, G10, G11 and G3 had low mean oil content in the unfavorable environments and G1, G5, G10 and G11 were the most stable found close to the origin. Whereas, G2, G4, G7, G12, G13, G14, G15, G16 and G17 were in the favorable environments and G17, G16, G7 and G14 were the most stable.Therefore, the oil content of sesame was high at higher altitude and high rain fall areas, whereas decreased at low altitude environment and low rainfall areas. Hence, improving the oil content selection should be based on high seed yield with relatively high oil content genotypes or cross breeding of high seed yielder with high oil content genotype. This is in harmony with the result of Zenebe and Hussien (2010) and Mekonnen*et al. (*2015) in sesame.

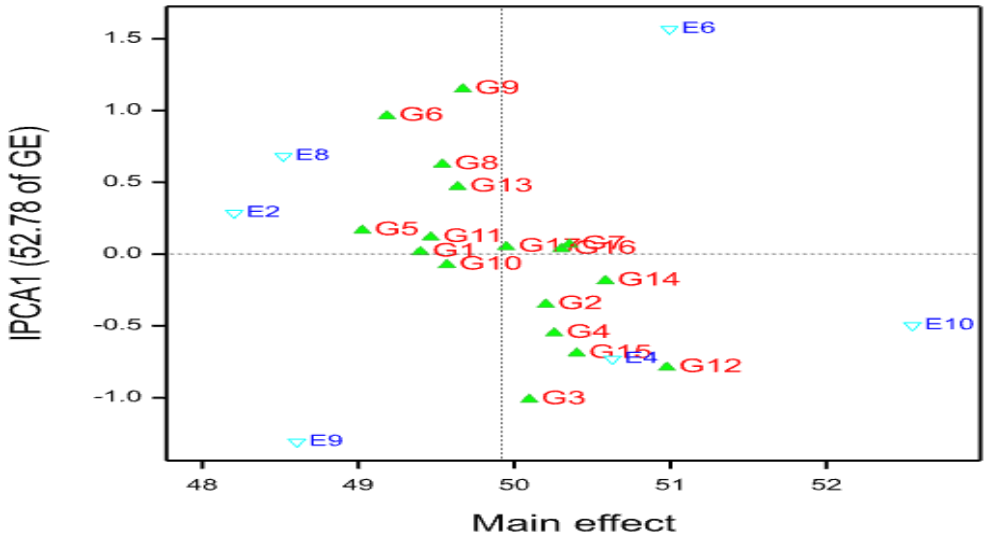

Figure 3: AMMI1 showing Genotype and Environment means for oil content (%) in 2015 G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir.E2=humera-2, E4=Dansha-2, E6=Sheraro-2, E8=Wargiba-2,E9=Maykadra, E10=Gendawuha.

4.5.5. AMMI Stability Value (ASV)

AMMI stability value statistic (ASV)was developed by Purchase to quantify and rank the genotypes on the basis of their yield stability. Genotypes with least ASV scores are the most stable, on the other hand,genotypes with high ASV score are unstable Purchase (2000).According to this model, G16, G9, G7, G3, and G1were the most stable followed by G9, G7,G6 and G1. G4 wasunstable followed by G15, G5, and G12 andG8 (Table 12). Similar results were reported by Abdurahman (2009) in maize, Muez *et al.* (2014) in barelyand Fiseha *et al*. (2015) in sesame.

4.5.6. Yield Stability Index (YSI)

Genotypes with lowest estimated value are desirable and considered as the most stable.Based on YSI, G1, G3, G7 and G16 were the most stable. Conversely, G8, G15, G4 and G12 were the most unstable indicated (Table 12). Similar results were reported by Olayiwola and Ariyo(2013)in okra and Mohammed (2015) insesame.

Table 12: Seed yield, AMMI Stability Value (ASV), IPCA1 and IPCA2 scores

G	SY	R^y	IPCA1	IPCA2	ASV	R^a	YSI(R^y+ R^a)	R
G1	867.4	1	0.28663	-5.81703	5.826141	5	6	2
G2	583.3	12	3.67765	10.87913	11.65413	11	23	8
G3	753.8	3	-5.76472	7.55516	9.999435	10	13	3
G4	668.6	7	-13.3909	7.88498	17.13767	17	24	9
G5	694.6	6	-5.59487	-13.3887	14.82141	15	21	6
G6	597.7	11	2.88248	3.61228	4.876118	4	15	4
G7	792.5	2	-3.2911	-0.31103	3.752583	3	5	1
G8	441.8	17	4.41429	-12.4188	13.39347	13	30	10
G9	562.1	14	1.33789	2.53944	2.959711	2	16	5
G10	548.1	16	6.11223	2.81746	7.495031	7	23	8
G11	561.3	15	-4.97112	2.51615	6.183731	6	21	6
G12	619.1	10	12.18338	3.27089	14.22511	14	24	9
G13	571.8	13	4.97666	6.81876	8.858564	9	22	7
G14	723.6	5	-6.16104	-4.41624	8.277322	8	13	3
G15	662.9	8	13.3302	-6.17663	16.35802	16	24	9
G16	745.1	4	-0.6543	0.25334	0.785457	1	5	1
G17	645.5	9	-9.37341	-5.61922	12.04239	12	21	6

R^a = Rank by ASV, R^y = Rank by seed yield, YSI =yield stability index

Positive and negative environmental index (EI) showed favorable and unfavorable environments respectively. Based on the Environmental Index (Table 13) four environments, E1, E3, E6, E10 for seed yield andE4, E6 and E10 for oil content had positive environmental index in the favorable environments, while E2, E4, E5, E8, E9 for seed yield and E2, E8 and E9 had negative environmental index in the unfavorable environments.The current result is in agreement with the previous findingsofMekonnen*et al.*(2015) in sesame, Wedajo (2014) in finger millet and Fiseha *et al.* (2015) in sesame.

Table 13:IPCAs and Environmental Index (EI)of environments seed yield and oil content

Envi.	Seed yield				Oil content			
	IPCA1	IPCA2	SY	EI	IPCA1	IPCA2	OC	EI
E1	0.3093	0.454	815.9	196.8	-	-	-	-
E2	-1.003	-1.193	238.	-410	0.29	-1.11	48.21	-1.71
E3	0.688	1.497	1124	475.4	-	-	-	-
E4	-0.457	0.187	514	-148	-0.73	0.29	50.63	0.71
E5	-0.085	0.251	539.7	-109	-	-	-	-
E6	1.8944	-1.145	1042	393.2	1.57	0.04	50.99	1.07
E7	-0.631	1.394	516.4	-128	-	-	-	-
E8	-0.843	0.177	446.6	-214	0.68	1.04	48.52	-1.39
E9	-1.054	-1.276	404.4	-262	-1.31	0.472	48.61	-1.31
E10	1.1827	-0.345	851.9	204.7	-0.50	-0.74	52.55	2.63

Envi=environment, EI= environmental index, SY=seed yield, OC = oil content, IPCAI=Interaction principal component analysis one, IPCA2=Interaction principal component analysis two.E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

4.6. Comparison and Correlation of Stability Parameters

4.6.1. Overall Ranking of Genotypes Using Various Stability Models

Even though, the stability ranking of the genotypes were varied among the stability parameters for seed yield and oil content,G1, G7 and G3 including the released variety (G16) and local check (G17) were found the most stableandranked 1^{st}, 2^{nd}, 3^{rd}, $4^{th}$and 9^{th}. While, G4, G8 and G15 were unstable and7^{th}, 17^{th} and $8^{th}$for seed yield, respectively (Table 14).

According to those models, the oil content were also varied from one environment to another. G2, G15 and G16 were the most stableand ranked 6^{th}, 3^{rd} and 4^{th}. On contrary, G6, G10 and G9 were the most unstableand ranked16^{th},14^{th} and 13^{th}formean oil content across the tested locations, respectively(Table15).

Table 14: Ranking of seed yield of sesame genotypes based on the various stability parameters

G	SY	R	YSI	R	ASV	R	Wi	R	Pi	R	bi	R	S^2di	R	OR.
G1	867.4	1	6	2	5.8	5	110047	5	9036	1	0.76	6	14783.53	10	1
G2	583.3	12	23	8	11.7	11	163463	10	80169	13	1.24	16	5354.35	4	15
G3	753.8	3	13	3	10	10	233791	14	29813	4	0.89	5	20758.74	14	5
G4	668.6	7	24	9	17.1	17	341095	17	58946	9	1.11	12	4391.77	2	16
G5	694.6	6	21	6	14.8	15	188863	12	42711	6	1.09	11	10382.49	7	13
G6	597.7	11	15	4	4.9	4	123724	8	69822	11	1.13	13	37759.30	17	10
G7	792.5	2	5	1	3.8	3	115774	7	16102	2	1.08	9	4500.33	3	3
G8	441.8	17	30	10	13.	13	269022	15	146926	17	0.97	3	5791.59	5	17
G9	562.1	14	16	5	2.9	2	67623	2	80574	15	1.2	15	1419.28	1	11
G10	548.1	16	23	8	7.5	7	73381	4	86227	16	0.93	4	10043.85	6	9
G11	561.3	15	21	6	6.2	6	67254	1	80386	14	1.13	13	24115.89	16	12
G12	619.1	10	24	9	14.	14	202390	13	68775	10	0.57	17	12680.67	9	8
G13	571.8	13	22	7	8.9	9	70485	3	77593	12	1.05	8	16486.66	12	7
G14	723.6	5	13	3	8.3	8	169296	11	38301	5	1.09	10	16406.79	11	6
G15	662.9	8	24	9	16.4	16	270511	16	54425	8	1.02	1	12142.36	8	14
G16	745.1	4	5	1	0.8	1	114803	6	27076	3	0.99	2	17843.66	13	2
G17	645.5	9	21	6	12.0	12	160177	9	53505	7	0.75	7	24593.31	15	4

Note: ASV=AMMI stability value, YSI=yield stability index, bi = Eberhart and Russell's (1966) regression coefficient, R= Rank, OR. = Overall rank, Pi = Lin and Binns (1988) cultivar performance measure, S^2di = Eberhart and Russell's (1966) deviation from Regression, SY= Seed yield (kg/ ha) and Wi = Wricke's (1962) Ecovalenc.

Table 15:Ranking of oil content based on the various stability parameters

G	OC.	R	Wi	R	Pi	R	bi	R	S^2di	R	OR.
G1	49.4	12	0.93	3	2.57	11	0.819	2	1.28	12	6
G2	50.2	6	2.84	10	1.07	6	0.732	1	0.15	8	1
G3	50.1	9	6.81	15	1.79	9	0.93	8	-0.33	1	7
G4	50.26	7	3.57	13	1.34	7	0.93	7	1.28	13	9
G5	49.03	17	0.31	1	3.69	16	0.93	9	0.15	8	11
G6	49.18	16	8.19	17	4.37	17	0.82	3	0.28	9	15
G7	50.35	5	1.60	6	0.95	4	0.99	11	1.96	14	6
G8	49.5	15	2.26	9	3.22	14	0.903	5	0.20	9	12
G9	49.67	14	7.05	16	3.40	15	0.96	10	-0.04	5	14
G10	49.57	13	0.91	2	2.73	13	1.24	16	0.95	11	13
G11	49.4	11	1.47	4	2.60	12	1.20	14	0.01	6	10
G12	51	1	6.36	14	0.47	1	1.21	15	-0.10	4	4
G13	49.67	10	1.75	7	2.1	10	0.91	4	0.39	10	9
G14	50.6	2	1.51	5	0.49	2	1.32	17	-0.19	2	5
G15	50.4	4	3.14	11	0.86	3	0.95	6	0.30	10	2
G16	50.3	3	3.54	12	1.03	5	1.07	12	-0.11	3	3
G17	49.95	8	1.96	8	1.47	8	1.07	13	0.13	7	10

OC= oil content, bi = Eberhart and Russell's (1966) regression coefficient, R= Rank, OR. = Overall rank, Pi = Lin and Binns (1988) cultivar performance measure, S^2di = Eberhart and Russell's (1966) deviation from Regression and Wi = Wricke's (1962) Ecovalenc.

4.6.2. Correlation of Stability Parameters

Correlation of stability parameters described (Table 16), SYI (r=0.65) and Pi (r=0.92) were significantly and positively correlated with SY. Wi (r=0.78) were significantly and positively correlated with ASV and YSI.Indicated they can measure similar aspects of stability. This is similar with the finding of Chemeda *et al.* (2014) and Fiseha *et al.* (2015). $S^2di$was negative and none significantly correlation with Wi, ASV, Pi and bi stability parameters. The negative and non- significance and correlation of S^2di with Wi, ASV,Pi and bi indicated separate use of the stability parameters to measure biological stability of stability. Similar results were reported by Farshadfar and Rozgard(2014). The AMMI stability parameter (ASV,r=0.09), Wi (r=-0.24), bi(r=0.27) and S^2di(r=0.1) were non- significantly correlated with seed yield. This non-significant correlation among seed yield and stability parameters indicated thatinformation cannot be collected from average yield alone (Duarte and Zimermann(1995)

Table 16:Spearman's rank correlation for stability parameters of sesame seed yield

	SY	ASV	Wi	Pi	bi	S^2di	YSI
SY	1						
ASV	0.09^{ns}	1					
Wi	-0.24^{ns}	0.784**	1				
Pi	0.92**	-0.07^{ns}	-0.22^{ns}	1			
bi	0.27^{ns}	-0.15^{ns}	-0.16^{ns}	0.4^{ns}	1		
S^2di	-0.1^{ns}	-0.19^{ns}	-0.21^{ns}	-0.27^{ns}	-0.28^{ns}	1	
YSI	0.65**	0.77**	0.45^{ns}	0.57*	0.001^{ns}	-0.33^{ns}	1

ns,*,**=non significant, significant at ($p \leq 0.05$) and significant at ($p \leq 0.001$) respectively

4.7. GGE Bi-plot for Evaluation of Environments and Genotypes

GGE bi-plot was determined using GenStat software version 16 for both seed yield and oil content. From this study G1 (HuRc-4) was the "ideal" genotype and the highestmean seed yield. G1 considered the most stable across variable environments. Genotypes closer to the ideal genotype were the stable ones, while genotypes far from the ideal genotypes were the unstable. Genotype is more desirable if it is located closer to the ideal genotype. Similar result was reported by (Kaya *et al.*, 2006; Mitrovic *et al.*, 2012; Farshadfar *et al.*, 2012). G7, G3, G5, G16, G17 and G14 were plotted to the ideal genotype considered as desirable genotypes, whileG15 and G4 were high yielding genotypes associated withgenotypic instability (Figure 4).

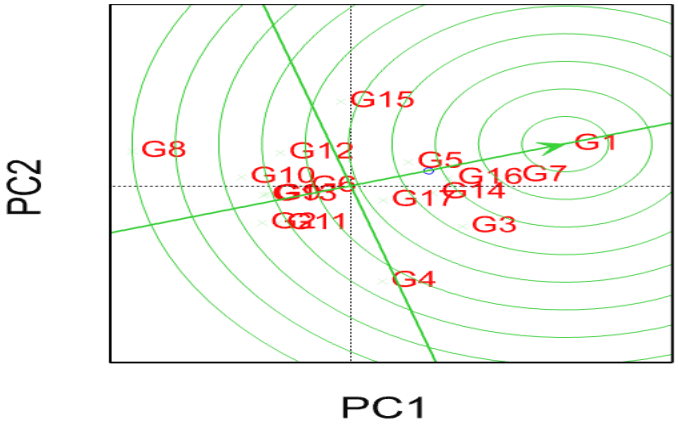

Figure 4: GGE-bi-plot showing the "ideal" genotype.
G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir.

E1(Humera -1) had the longest vector with small IPCA, which fell into the center of concentric circles was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. The concentric circles on the biplot help to visualize the length of the environment vectors, which are proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments (Asnake *et al*., 2013). An environment is more desirable and discriminating when located closer to the center circle or to an ideal environment (Naroui *et al*.,2013). E2, E4, E5, E7 and E8 were closer to the ideal environment and considered as stable. E3, E10, E6, E4 and E9 were far from the ideal environment and considered as unstable (Figure 5). This result in line with Yan *et al*.(2000), Yan and Rajcan(2002) and Yan *et al*.(2007) and Fiseha *etal*.(2015).

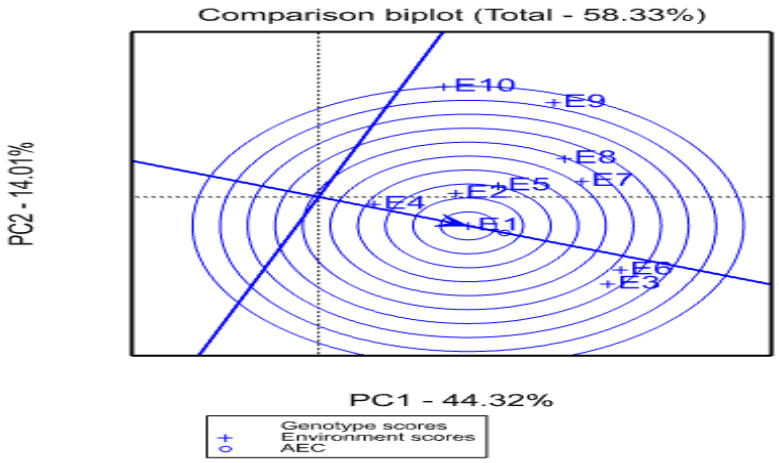

Figure 5: GGE-biplot based on the ranking of environments relative to an ideal environment E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

The mean oil content of genotypes were inconsistent across locations due to environmental factors. G12 was ideal genotype for oil content and G14, G16, G7, G2 and G5 were stable, while G3 had high oil content and unstable. E10 was the ideal environment followed by E4 and E9 and the most stable for oil content. On the other hand, E2, E6 and E8 were plottedfar from the ideal environment considered as unstable and unfavorable environments (Figure 6).

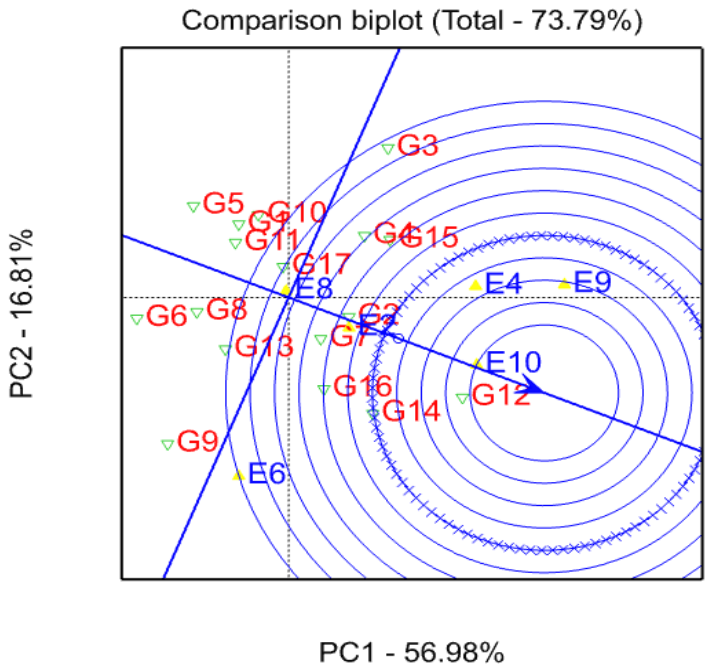

Figure 6: GGE-biplot based on the ranking of environments and genotypes for oil content relative to an ideal environment and ideal genotype.

E2=humera-2,E4=Dansha-2,E6=Sheraro-2, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha.G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. Environments: E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1,E6=Sheraro-2,E7=Wargiba-1,E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

4.7.1. 'Which-Won-Where' Pattern and Mega-environment Identification

The ten environments fell into six sectors with different winner genotypes and the bi-plot showed that four vertex genotypes, G4, G15, G1 and G8.From winner genotypes except G8 were high yieldingin favorable environments. The GGE biplotidentified three different sesame growing mega-environments. The first environment containing the highest yielding environment (E3) in Dansha area with a vertex genotype G4; the second environment containing the higher yielding environment (E6) in Sheraro area with winner genotype G3; and third environment includes medium E1 and E10 to low yielding E2, E4, E5, E7, E8 and E9 environments, respectively with the winner genotype G1 (Figure 7).

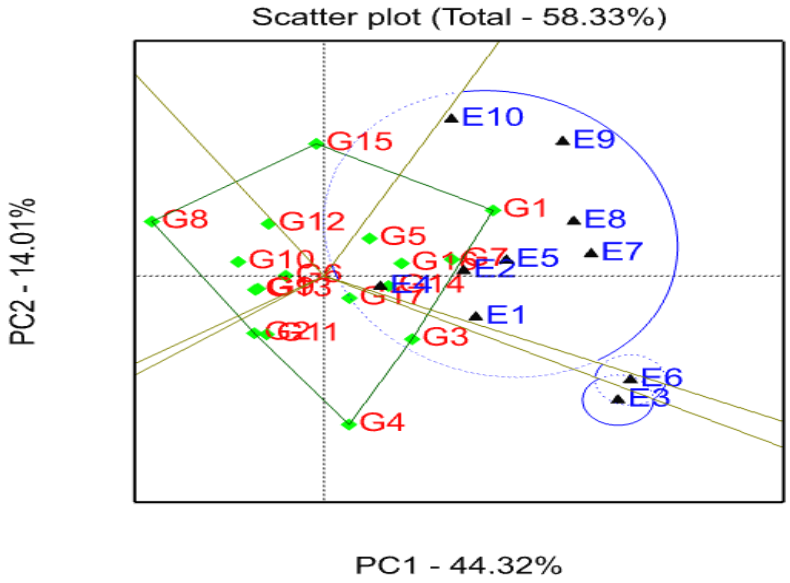

Figure 7**:**Which-Won-Where View of GGE bi-plot genotypes and environments of yield. G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir.E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1,E6=Sheraro-2,E7=Wargiba-1,E8=Wargiba-2,E9=Maykadra, E10=Gendawuha.

According the GGE bi-plot six sections with five vertex genotypes G3, G5, G6, G12 and G9 and identified three different sesame growing mega-environments for oil content:The first environment containing G12, G7 and G2in the mega-environment group of E2 (Humera-2), E4 (Dansha) and E10 (Gendawuha). The second environment E6 (Sheraro-2)containing G9 and third environment E8 (Wargiba), containingG17 presented in(Figure 8).

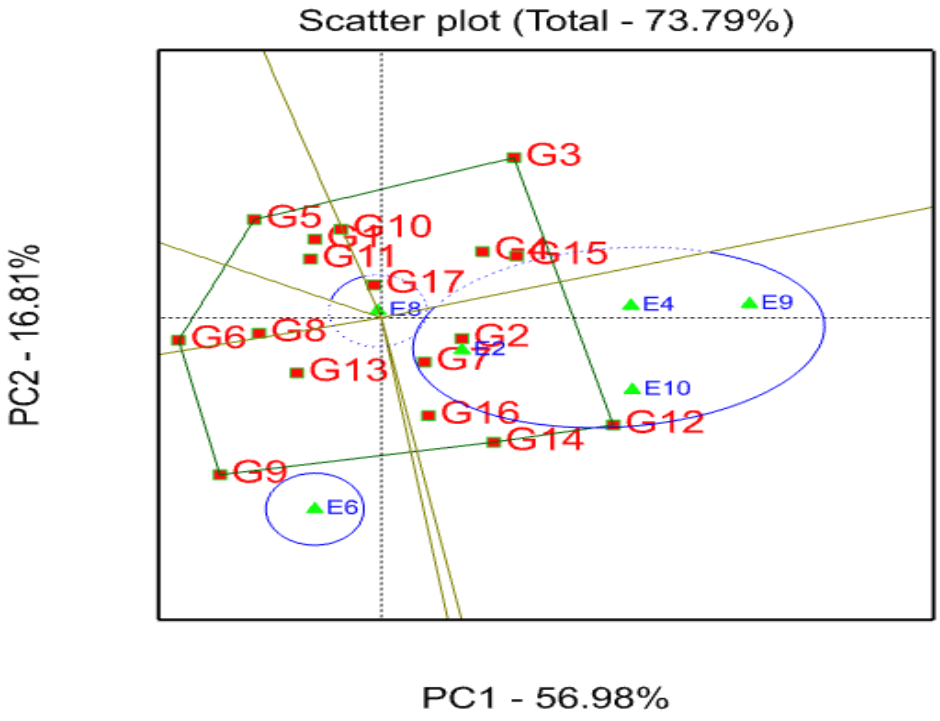

Figure 8**:** The environment-vector view of the GGE bi-plot to show similarities of oil content. E2 =Humera-2, E4=Dansha-2, E6=Sheraro-2, E8=Wargiba-2, E9 =Maykadra, E10 =Gendawuha. G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir

5. SUMMARYAND CONCLUSION

Sesame is known as queen of oil seed crops, it is mainly grown for its oil of local consumption, sources of income and great contribution for Ethiopia economy. However, the productivity and production is low due to environmental factors, genotypes and GEI. Therefore, the experiment was carried out to evaluate GEI for seed yield and oil content of different white seeded sesame genotypes and to identify stable and/or high yielding genotypes and assess their performance across locations. Seventeen sesame genotypes were tested at ten environments in Northern Ethiopia (Tigray and Amhara regional states) during 2014-2015 main cropping seasons. The experiment was laid out in Randomized Complete Block Designs (RCBD) with three replications across all environments.

The results of the study indicated that there were significant differences among genotypes, environments and GEI. The significance effect of and GEI on yield that suggested the need to assess the stability of genotypes overall environments.Bases on the combined analysis of variance over locations the mean seed yield of environments ranged from 110.6 kg/ha in E2 (humera-2) to 1486 kg/ha in E3 (Dansha-1).The highest yield was obtained from G1, while the lowest was from G8 kg/ha. Setit-1 (released variety) (745.1 kg/ha) and Hirhir (local variety) (645 kg/ha) were beaten by G1 (867.4), G7 (792.5) and G3 (753.8) kg/ha in this study respectively. Moreover, G1, G7, and G3 had 18.85%, 7.30% and 1.34% yield advantage over the standard check, and 34.25%, 22.75% and 16.75% over the local check, respectively.

All the genotypes had given better oil content and they have white seed color. The grand mean oil content over six environments was 49.9% and the mean oil content ranged between 49% in G5 to 51.86% in G12 across the tested locations in 2015 main cropping season. The highest oil content was recorded from G12 51% followed by G2 50.2%, G3 50.10%, G4 50.26%, G7 50.35%, G8 50%, G9 50%, G10 50%, G13 50%, G14 50.6%, G15 50.4%, G16 50%, G17 50% and G1 49.9%. However, G5 (49%), G6 (49.2%) and G11 (49.5%) had similar oil content to the grand mean. G2, G14, G15 and G16 were the most stable and ranked $6^{th,}$ 3^{rd} and 4^{th}. Conversely, G6, G10 and G9 were unstable and ranked 16^{th}, 14^{th} and 13^{th} for mean oil content across the tested locations respectively.

Various stability models were used in measurement of genotype stability such as AMMI model, AMMI Stability Value (ASV), Yield Stability Index (YSI), GGE bi-plot, coefficient of regression (bi), deviation from regression (S^2di), cultivar superiority performance (Pi) and Wricke's (Wi) Ecovalence. AMMI model were used to identify potential and poor environments, evaluation of genotype performance and identification of genotype and environment stability and identification of genotype interaction. GGE biplot were used to identify mega environments, genotype and environment evaluation, stability of genotypes and identification of ideal genotype and environments. Even though the genotypes showed inconsistency ranking in the stability measurements, G1, G3, G7 and G16 were high yielding and the most stable for seed yield and oil content. G9, G2 and G6 were low yielding and stable in the unfavorable environments. G15, G1, G7, G14, G5, G16, G3, G17 and G4 yielded above grand mean seed yield in the favorable environments. Whereas, G12, G8, G10, G2, G13, G6, G9 and G11 yielded below the grand mean in the unfavorable environments.

Combined analysis of variance indicated that significant ($p \leq 0.001$) variations of genotypes, environments and GEI, suggesting the high environmental variations and differential response of genotypes to the variable environments thus leading to inconsistency ranking of genotypes.The large sum square and highly significant of environment indicated that the environments were diverse and causing most of the variation in seed yield, oil content and yield components. 69.73%, 14.68% and 9.58% and 61.5%13.64% and 9.58% and 6.55% of variationwas explained by environments, GEI and genotypes explaining for seed yield and oil content, respectively. This indicate the existence of a considerable amount of differential response among the genotypes to the changes of growing environments and the differential discriminating ability of the tested environments.

According to the GGE bi-plot different sesame growing environments grouped into three: The first environment containing the favorable environment Dansha area with a vertex G4; the second environment containing the favorable environment Sheraro area with winner G3; and third environment includes medium to low environments E2(Humera-2), E4(Dansha-2), E5(Sheraro-1), E7(Wargiba-1), E8(Wargiba-2) and E9(Maykadra).G1 (HuRC-4) identified as an "ideal" genotype because it fell into the center of concentric circles. E1(Humera-1) also identified as an ideal environment because it had the longest vector with small IPCA, which

fell into the center of concentric circles, the most representative of the overall environments and the most powerful to discriminate genotypes. E1 (Humera-1), E3 (Dansha-1), E6 (Sheraro-2) and E10 (Gendawuha) considered as favorable, while E2 (Humera-2), E4 (Dansha-2), E5 (Sheraro-1), E7 (Wargiba-1), E8 (Wargiba-2) and E9 (Maykadra) were unfavorable environments. According to the GGE biplot three different sesame growing mega-environments for oil content production were identified: The 1st environment containing G12, G7 and G2 in the mega-environment group of Humera, Dansha and Gendawuha. The 2nd environment, Sheraro containing G9 and the 3rdenvironment Wargiba, containing G17.

There were inconsistencies with the univariate stability parameters being considered, which created uncertainty to select or recommend the stable genotypes. However, the multivariate approach, AMMI model and GGE biplot were better for partitioning the GEI into the causes of variation and the best multivariate models in this study. According to different stability models, G1, G7, and G3 were high yielder and the most stable both in terms of seed yield and oil content. Moreover, showed yield advantage over the standard and local check. Hence, G1, G7 and G3 will be recommended for wider environments and G14and G4 forfavorable environments Sheraro and Dansha, respectively.

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7. APPENDICES

Appendix Table 1Annual Rain fallof the test locations from 2005-2015

Year	Humera	Dansha	Sheraro	Wargiba	Maykadra	Gendawuha
2005	NA	374.8	NA	NA	NA	NA
2006	NA	1082.2	NA	NA	NA	NA
2007	469.8	1300	835.6	NA	NA	NA
2008	803.9	989.7	504.6	NA	NA	NA
2009	480.9	761.8	606.3	NA	NA	NA
2010	693.4	1634	776.7	NA	NA	NA
2011	434.1	76.4	427.7	NA	NA	NA
2012	588.6	1072.9	610.3	NA	808.7	NA
2013	471.8	769	350	NA	514	NA
2014	746.7	1024.3	550	NA	374.1	NA
2015	456.3	578.7	310	NA	333.1	NA

NA=Not available

Appendix Table 2: Combined ANOVA for seed yield (kg/ha) of 17 sesame genotypes

Sources of variation	df	SS.	MS.
Rep	20	641291.	320645.
Genotype	16	5367408	335463**
Location	5	14530872	2906174**
Year	1	3624459	3624459**
Genotype x Location	80	5200223	65003**
Genotype x Year	16	770108	48132**
Location x Year	5	20910760	6970253**
Genotype x Location x Year	80	2254772	46974**
Residual	304	1367169	9903
Total	529	56025771	110070

**=highly significance at ($p \leq 0.001$)

Appendix Table 3:Combined ANOVA for oil content (%) of 17 sesame genotypes

Sources of variation	df	SS.	MS.
Rep	12	0.696	0.348
Genotype	16	82.4	5.15**
Location	5	775.5	155.1**
Genotype x Location	80	171.69	2.15**
Residual	202	228.715	1.132
Total	315	1258.996	163.88

Appendix Table 4:Mean sum squares of combined ANOVA yield related traits

Traits	Sources of variation				
	Rep(20)	Genotype(16)	Environment(9)	GEI(144)	Errors (338)
SY	320645^{ns}	335463**	4340677**	57119**	8065
OC	2.5^{ns}	7.4**	163**	2.0**	1.21
DF	2.282^{ns}	226.1**	1461.7**	40.1**	4.704
DM	49.5^{ns}	267**	1105**	49**	12.57
LCBZ	9.64^{ns}	673**	12982**	105**	6.442
NBPP	0.027^{ns}	2.088**	182.6**	0.665**	0.2174
NCPP	3.747^{ns}	583.66**	10684.8**	124.08**	5.242
SPC	307^{ns}	148**	28388**	155**	57.81
TSW	0.1446^{ns}	1.366**	3.8347**	0.2479**	0.1344
PH	13.6^{ns}	478**	48572**	156**	17.76

ns, ** significant and ns= non significance at ($p \leq 0.001$)

Appendix Table 5:Response of agronomic traits of sesame genotype in respective environment

	E1							E2						
G.	DF	DM	PH	LCBZ	NBPP	NCPP	SY	DF	DM	PH	LCBZ	NBPP	NCPP	SY
G1	41.0	74.0	116.5	69.6	2.6	45.9	1107.6	36.7	75.0	68.5	35.5	1.7	25.0	361.7
G2	55.0	84.0	116.3	68.5	2.5	26.7	967.7	42.0	73.0	67.8	37.9	2.0	21.0	222.5
G3	47.3	88.3	117.3	66.5	2.7	32.3	1070.9	45.7	81.0	64.3	35.5	1.6	18.7	347.8
G4	55.0	94.0	100.7	66.3	2.1	33.4	849.1	55.0	87.7	67.5	36.2	2.2	23.1	227.2
G5	44.3	71.3	122.8	71.1	2.2	22.9	677.5	43.7	80.0	48.0	36.0	1.7	19.2	233.3
G6	45.3	83.0	105.7	53.0	2.0	26.0	983.6	54.0	84.3	69.6	36.9	1.9	22.7	237.5
G7	44.0	77.3	116.1	69.3	3.4	24.0	837.7	35.7	77.0	61.2	34.5	1.5	19.0	354.7
G8	52.7	88.3	102.8	63.6	2.6	40.1	611.0	54.0	88.3	67.1	36.9	2.5	21.1	110.6
G9	56.0	87.3	112.5	42.6	3.1	29.2	849.2	46.0	87.0	71.3	34.9	2.6	13.9	150.0
G10	43.3	80.7	105.1	43.5	1.7	38.2	632.1	43.3	75.7	64.3	32.2	2.2	11.6	160.0
G11	43.0	84.3	96.7	41.7	1.1	42.3	681.7	43.0	81.7	73.3	30.9	1.7	15.9	125.0
G12	50.0	86.0	96.1	62.6	2.4	29.5	729.3	47.7	77.0	62.2	37.1	2.5	30.8	242.8
G13	45.3	93.3	107.7	50.1	2.0	40.3	853.7	48.7	79.3	70.3	34.0	1.7	14.8	170.0
G14	56.0	81.3	106.4	54.0	3.0	30.6	858.9	36.0	75.7	63.9	34.3	1.9	20.9	435.0
G15	42.0	88.0	85.9	56.9	2.0	39.7	742.8	48.0	85.0	69.0	33.6	2.9	30.6	233.9
G16	43.7	76.0	102.8	59.1	2.1	41.8	868.5	42.0	74.7	62.9	32.9	1.3	20.3	218.9
G17	42.7	75.0	117.9	65.7	2.9	33.5	545.9	41.3	75.3	60.7	32.5	2.3	16.3	223.9
Mean	47.5	83.1	107.7	59.1	2.4	33.9	**815.7**	44.9	79.9	65.4	34.8	2.0	20.3	**238.5**
CV%	4.0	3.1	6.1	11.4	8.7	4.1	8.0	3.2	2.9	9.6	19.6	13.2	14.0	18.7

Appendix Table 2 continued-----

	E3							E4						
G.	DF	DM	PH	LCBZ	NBPP	NCPP	SY	DF	DM	PH	LCBZ	NBPP	NCPP	SY
G1	45.3	126.2	75.0	59.2	2.7	40.5	1173.0	39.3	77.0	80.8	40.2	2.5	20.5	670.5
G2	51.0	119.0	90.7	49.5	2.2	27.2	1065.0	50.0	81.7	66.3	21.9	2.4	7.7	671.8
G3	52.7	133.0	88.0	48.7	3.4	36.0	1467.0	52.7	83.0	93.2	44.1	3.2	17.7	453.5
G4	52.0	123.7	87.0	49.5	2.5	37.9	1258.0	52.7	89.0	82.9	41.1	2.7	19.3	763.9
G5	49.3	134.6	75.7	55.3	1.9	37.9	957.0	41.0	83.3	96.1	48.4	3.2	23.7	533.3
G6	50.7	143.7	82.3	54.9	2.1	43.2	1125.0	50.0	85.3	78.9	34.6	2.1	13.5	338.6
G7	48.7	133.7	81.0	57.0	2.4	34.4	1486.0	43.3	82.0	88.4	44.7	2.4	17.3	480.2
G8	48.7	117.5	87.0	44.5	1.3	24.8	492.0	52.0	84.0	77.3	39.1	1.6	14.7	354.4
G9	51.0	130.1	81.3	43.5	3.0	24.5	1094.0	41.7	90.0	87.7	34.7	2.5	14.9	354.9
10	51.0	120.3	78.0	39.3	1.7	19.0	1075.0	46.7	89.7	65.4	30.2	2.0	13.2	550.3
G11	50.7	128.6	88.7	45.6	1.3	21.0	1132.0	47.3	85.7	87.1	29.5	1.7	11.0	385.4
G12	50.7	116.7	74.3	55.3	3.4	48.7	1086.0	46.0	81.3	63.5	30.9	1.8	13.1	764.3
G13	50.0	122.5	86.7	40.4	1.4	18.5	1105.0	51.7	90.0	78.0	29.2	2.5	12.8	515.4
G14	51.7	133.1	76.3	44.4	2.7	32.7	1125.0	43.7	82.0	97.1	43.1	2.4	18.5	467.7
G15	49.0	142.4	83.0	52.5	2.5	44.9	987.0	51.3	84.3	77.4	35.2	2.3	14.3	558.0
G16	45.0	134.7	80.0	52.8	1.8	27.5	1246.0	38.0	76.3	85.5	31.7	2.9	11.6	522.6
G17	45.3	130.1	77.0	45.1	2.6	28.6	1232.0	38.0	79.3	78.3	38.8	2.2	16.5	357.6
Mean	49.6	128.8	81.9	49.3	2.3	32.2	**1123.8**	46.2	83.8	81.4	36.3	2.4	15.3	**514.3**
CV%	2.8	2.7	7.0	14.5	9.4	3.3	5.6	3.0	2.7	4.9	10.3	7.9	3.5	15.2

DF=days to flowering, DM=days to maturity, PH plant height, LCBZ= length of capsule bearing zone, NBPP number of branches per plant, NCPP =number of capsules per plant, SY= seed yield OC= oil content

Appendix Table 2 continued-----

	E5							E6						
G.	DF	DM	PH	LCBZ	NBPP	NCPP	SY	DF	DM	PH	LCBZ	NBPP	NCPP	SY
G1	44.3	90.0	114.0	66.1	3.0	49.3	619.8	34.3	66.0	132.8	76.5	7.2	43.3	1325.0
G2	42.7	89.7	105.2	52.4	3.2	33.9	341.7	35.3	72.0	134.9	80.0	7.1	44.3	974.0
G3	43.3	90.0	109.8	52.7	3.5	32.9	866.1	33.7	79.0	132.5	70.1	7.3	45.9	1056.0
G4	42.3	89.3	95.1	53.6	3.3	37.7	584.0	39.0	70.3	125.9	69.7	7.3	41.9	1329.0
G5	43.7	90.0	110.5	56.1	2.2	31.6	716.7	38.0	72.3	137.5	68.5	7.1	42.4	1183.0
G6	45.0	90.3	106.5	58.7	2.3	35.9	322.4	36.7	76.0	130.1	73.3	7.5	40.4	853.0
G7	43.3	92.0	96.8	54.3	2.6	29.5	623.8	36.0	70.0	130.5	78.1	7.0	36.2	1158.0
G8	44.0	89.0	97.3	53.8	2.1	26.1	536.7	34.7	69.7	127.3	71.9	7.5	42.7	733.0
G9	46.0	91.7	92.4	40.5	2.9	25.6	396.7	39.3	73.0	129.0	68.1	7.5	39.5	882.0
10	44.3	92.0	92.6	42.8	1.7	21.7	366.5	40.7	77.3	124.4	67.3	7.5	38.5	855.0
G11	45.3	92.0	88.3	40.5	1.9	18.7	550.6	37.0	75.0	120.2	61.4	7.5	46.6	1106.0
G12	42.7	89.7	93.5	52.3	2.8	36.5	472.2	36.0	70.0	120.3	72.7	7.4	45.9	761.0
G13	45.3	92.0	84.1	35.9	1.5	17.4	343.4	36.7	71.3	127.6	64.3	7.4	39.0	934.0
G14	43.7	90.3	100.1	54.7	2.1	27.7	504.1	35.0	72.3	125.6	86.3	7.1	47.4	1250.0
G15	43.3	89.0	92.5	60.1	3.7	39.4	660.6	35.0	70.3	137.1	83.9	7.1	49.9	850.0
G16	44.0	92.7	106.5	60.6	3.3	33.2	663.5	35.0	75.3	124.6	70.8	7.5	39.2	1266.0
G17	43.7	92.3	102.9	52.3	2.6	31.0	605.6	35.0	72.0	126.9	79.5	7.1	39.7	1203.0
Mean	43.9	90.7	99.3	52.2	2.6	31.1	**539.7**	36.3	72.5	128.7	73.1	7.3.00	42.5	**1042.2**
CV%	2.6	0.9	6.0	13.8	9.6	4.1	12.2	11.5	8.7	2.8	5.8	4.4	1.7	6.4

Appendix Table 2 continued…

	E7							E8						
G.	DF	DM	PH	LCBZ	NBPP	NCPP	SY	DF	DM	PH	LCBZ	NBPP	NCPP	SY
G1	53.7	72.7	72.9	44.0	4.8	74.4	844.2	42.7	90.3	66.0	34.5	3.5	19.0	756.0
G2	54.0	84.3	80.1	29.0	6.5	49.9	385.8	49.0	84.3	53.4	23.0	3.7	14.5	203.7
G3	56.0	85.3	83.6	43.7	6.3	46.5	675.9	51.3	85.3	62.5	29.3	3.5	20.1	378.3
G4	54.0	84.0	77.5	41.0	5.1	80.2	542.3	54.0	92.0	58.5	21.3	3.5	12.1	366.3
G5	55.0	76.0	83.3	39.0	5.2	56.7	655.9	40.0	79.0	65.9	32.7	3.1	17.9	714.3
G6	53.7	79.3	64.4	36.7	4.7	65.7	461.2	52.7	87.0	69.5	32.5	3.5	18.2	481.7
G7	54.0	77.7	69.7	33.7	5.3	43.9	686.4	46.3	80.0	76.8	35.4	3.6	13.7	657.7
G8	55.0	81.7	93.5	32.3	5.5	68.5	469.9	50.7	79.0	74.1	36.5	4.2	18.1	288.3
G9	63.7	84.0	86.0	42.0	5.9	60.1	363.0	56.0	89.7	75.8	46.1	3.6	25.0	475.0
10	65.0	73.7	75.7	28.0	5.7	52.7	364.9	55.3	79.0	67.5	27.3	2.8	12.2	236.7
G11	64.0	76.7	81.0	29.0	6.1	39.9	334.4	47.0	87.3	67.9	27.4	3.4	14.3	309.0
G12	54.0	83.0	63.5	33.7	4.8	60.8	393.0	53.0	86.0	60.9	31.5	2.5	14.0	387.7
G13	65.7	88.0	72.7	35.0	5.7	29.5	302.7	62.3	89.0	59.0	32.1	3.0	11.8	293.0
G14	56.3	76.7	88.9	45.3	6.2	84.1	638.5	50.0	88.0	82.0	48.7	4.8	27.7	757.3
G15	54.0	80.3	87.1	39.3	6.0	67.0	425.2	52.3	82.7	79.3	42.6	3.8	26.7	348.3
G16	53.7	72.7	74.8	36.0	5.5	59.1	705.5	44.3	83.3	76.0	36.7	3.9	16.1	392.0
G17	54.7	74.3	77.7	45.0	5.9	53.9	530.3	43.0	91.3	90.1	48.7	3.8	27.9	547.0
Mean	56.8	79.4	78.4	37.2	5.6	58.4	**516.4**	50.0	85.5	69.7	34.5	3.5	18.2	**446.6**
CV%	2.8	5.8	4.8	20.2	3.2	1.6	19.0	3.2	6.4	5.7	8.7	5.8	2.5	16.2

DF=days to flowering, DM=days to maturity, PH plant height, LCBZ= length of capsule bearing zone, NBPP number of branches per plant, NCPP =number of capsules per plant, SY= seed yield OC= oil content

Appendix Table 2 continued---

	E9							E10						
G.	DF	DM	PH	LCBZ	NBPP	NCPP	SY	DF	DM	PH	LCBZ	NBPP	NCPP	SY
G1	38.3	74.0	71.5	38.9	1.5	17.8	761.7	36.0	75.0	164.2	80.5	2.7	36.9	1054.9
G2	38.0	75.0	77.1	38.9	0.9	15.0	238.9	43.3	81.7	155.0	82.0	3.4	48.4	761.1
G3	44.7	87.3	79.0	43.7	1.2	22.8	446.1	46.0	90.0	163.7	79.8	3.5	41.3	776.4
G4	47.0	82.0	76.7	41.4	1.1	16.4	321.9	48.0	89.0	163.0	98.6	3.6	55.6	445.2
G5	41.0	81.7	81.7	42.8	0.7	18.1	512.2	45.7	82.0	153.5	70.2	3.6	45.4	762.6
G6	43.7	80.7	69.1	35.6	0.3	11.0	345.3	50.0	90.0	165.7	75.9	2.3	43.7	828.8
G7	40.7	86.0	69.5	40.9	0.3	13.6	654.2	40.0	75.0	160.9	80.9	2.9	45.7	986.4
G8	42.7	83.3	68.9	37.5	0.3	13.0	177.9	42.3	88.0	155.8	66.2	2.7	40.4	643.7
G9	48.0	87.3	76.5	26.0	0.9	13.9	208.9	45.7	80.0	152.9	55.4	4.3	38.5	846.5
10	43.7	87.3	73.9	29.5	0.8	10.4	405.8	42.7	77.0	153.4	64.5	2.6	32.9	834.5
G11	51.0	90.0	76.3	26.6	0.7	8.9	218.9	50.7	88.0	153.9	68.3	3.0	41.7	770.2
G12	37.7	75.7	69.5	42.7	1.2	19.3	325.0	51.0	87.0	141.7	79.9	3.1	62.7	1029.8
G13	51.0	87.3	71.5	25.4	0.1	7.1	337.2	44.3	84.7	146.7	66.1	2.8	40.4	863.0
G14	41.0	82.0	76.7	37.9	0.5	13.3	265.8	38.0	78.3	160.3	87.1	3.3	48.5	933.6
G15	45.0	87.0	64.2	36.1	1.4	19.4	778.6	45.7	84.7	151.6	83.5	3.5	56.3	1043.8
G16	42.0	77.0	70.9	38.9	0.8	14.5	426.9	44.0	70.3	166.3	80.1	2.9	45.7	1141.4
G17	44.0	88.7	81.7	41.4	1.3	20.0	449.2	39.7	75.7	161.8	75.5	3.7	49.0	760.1
Mean	43.5	83.1	73.8	36.7	0.8	15.0	**404.4**	44.3	82.1	157.1	76.1	3.2	45.5	**851.9**
CV%	4.3	3.0	2.6	18.9	11.2	3.3	3.8	5.2	2.2	2.4	6.8	5.0	2.2	18.3

DF=days to flowering, DM=days to maturity, PH plant height, LCBZ= length of capsule bearing zone, NBPP number of branches per plant, NCPP =number of capsules per plant, SY= seed yield OC= oil content

Appendix Table 6: Mean squares of different traits across environments

Envi.	S of Va	df	DF	DM	PH	LCBZ	NBPP	NCPP	SPC	TWT	SY
Humera-1	rep	2	5.804	36.51	38.56	19.53	0.06118	4.493	21.8	0.01882	18687
	genotype	16	1409.29	2131.69	4540.09	4781.11	15.6451	2383.98	1091.32	6.20157	1225935
	Residual	32	115.529	213.49	610.51	410.68	2.34549	281.58	1164.68	2.54784	136257
	total	50	1530.63	2381.69	5189.16	5211.32	18.0518	2670.05	2277.8	8.76824	1380879
Humera-2	rep	2	1.098	6.627	206.24	25.08	0.8722	9.959	358.4	0.8506	2962
	genotype	16	1710.71	1214.04	1614.11	184.99	9.1969	1325.21	4097.5	8.5616	384656
	Residual	32	64.235	169.373	2694.62	356.92	4.9678	230.121	8101.6	9.1761	63880
	total	50	1776.04	1390.04	4514.96	566.99	15.0369	1565.29	12557.4	18.5882	451499
Dansha-1	rep	2	2.98	0.118	59.69	19.75	0.0953	28.215	149.69	1.0169	129129
	genotype	16	265.843	1363.96	3169.28	1722.91	21.2208	4112.44	2936.61	2.4016	2248859
	Residual	32	59.686	157.216	588.2	376.97	3.518	294.392	2174.92	6.0831	125639
	total	50	328.51	1521.29	3817.17	2119.64	24.8341	4435.05	5261.22	9.5016	2503627
Dansha-2	rep	2	3.569	54.471	17.658	6.887	0.17294	12.067	89.99	0.4804	7967
	genotype	16	1343.37	853.176	4807.61	2330.7	11.0518	737.123	1803.22	8.8333	923168
	Residual	32	61.098	161.529	261.915	100.893	1.92706	47.159	919.61	4.0196	195513
	total	50	1408.04	1069.18	5087.19	2438.48	13.1518	796.35	2812.82	13.3333	1126648

Continued…

Sheraro-2	rep	2	5.804	36.51	38.56	19.53	0.06118	4.493	205.18	0.2592	18687
	genotype	16	1409.29	2131.69	4540.09	4781.11	15.6451	2383.98	683.29	4.3137	1225935
	Residual	32	115.529	213.49	610.51	410.68	2.34549	281.58	1650.82	3.8875	136257
	total	50	1530.63	2381.69	5189.16	5211.32	18.0518	2670.05	2539.29	8.4604	1380879
Wargiba-1	rep	2	206.24	36.51	38.56	19.53	0.06118	4.493	11.277	0.2651	18687
	genotype	16	1614.11	2131.69	4540.09	4781.11	15.6451	2383.98	1808.01	6.19843	1225935
	Residual	32	2694.62	213.49	610.51	410.68	2.34549	281.58	264.216	2.44157	136257
	total	50	4514.96	2381.69	5189.16	5211.32	18.0518	2670.05	2083.51	8.9051	1380879
Wargiba-2	rep	2	1.098	36.51	38.56	19.53	0.06118	4.493	2.38	0.1945	18687
	genotype	16	1710.71	2131.69	4540.09	4781.11	15.6451	2383.98	4929.98	6.9051	1225935
	Residual	32	64.235	213.49	610.51	410.68	2.34549	281.58	739.33	4.0255	136257
	total	50	1776.04	2381.69	5189.16	5211.32	18.0518	2670.05	5671.69	11.1251	1380879
Maykadra	rep	2	5.804	36.51	38.56	19.53	0.06118	4.493	115.7	4.3726	18687
	genotype	16	1409.29	2131.69	4540.09	4781.11	15.6451	2383.98	339.34	4.1835	1225935
	Residual	32	115.529	213.49	610.51	410.68	2.34549	281.58	709.72	5.4406	136257
	total	50	1530.63	2381.69	5189.16	5211.32	18.0518	2670.05	1164.75	13.545	1380879
Gendawuha	rep	2	5.804	36.51	38.56	19.53	0.06118	4.493	95.68	0.18855	18687
	genotype	16	1409.29	2131.69	4540.09	4781.11	15.6451	2383.98	3133.66	6.30464	1225935
	Residual	32	115.529	213.49	610.51	410.68	2.34549	281.58	1773.33	1.60492	136257
	total	50	1530.63	2381.69		5211.32	18.0518	2670.05	5002.68	8.09811	1380879

Appendix Table 7:Mean seed yield, oil content and yield components across ten environments

Envi.	DF	DM	PH	LCBZ	NBPP	NCPP	SPC	TSW	SY	OC
E1	48.08^{b}	83.08^{c}	107.60^{c}	59.06^{c}	2.38^{ef}	33.91^{c}	59.86^{e}	2.91^{c}	845.13^{c}	-
E2	44.86^{cd}	79.86^{de}	65.40 ^{h}	34.81^{f}	2.01^{g}	20.28^{d}	43.81^{g}	2.64^{e}	238.51^{f}	48.21^{c}
E3	49.57^{b}	81.88^{cd}	128.82^{b}	49.26^{e}	2.28^{f}	32.19^{c}	71.98^{bc}	3.08^{ab}	1123.79^{a}	-
E4	46.20^{c}	83.76^{bc}	81.42^{e}	36.32^{f}	2.38^{f}	15.30^{ef}	65.66^{d}	2.83^{cd}	500.08^{d}	50.6^{b}
E5	43.94^{d}	90.71^{a}	99.30^{d}	52.20^{d}	2.64^{e}	31.07^{c}	53.33^{f}	3.09^{ab}	539.67^{d}	-
E6	36.31^{e}	72.47^{f}	128.66^{b}	73.09^{b}	5.30^{a}	42.52^{b}	73.88^{b}	3.12^{a}	1041.54^{b}	50.99^{b}
E7	56.84^{a}	79.43^{e}	78.39^{e}	37.22^{f}	2.30^{g}	12.41^{g}	61.05^{e}	2.94^{bc}	520.39^{d}	-
E8	50.00^{b}	85.49^{b}	69.72^{g}	34.48^{f}	2.50^{g}	18.19^{de}	54.52^{f}	2.69^{de}	434.84^{e}	48.5^{c}
E9	43.49^{d}	83.08^{c}	73.81^{f}	36.72^{f}	0.83^{h}	14.97^{f}	59.5^{e}	2.21^{f}	386.76^{e}	48.61^{c}
E10	44.29^{cd}	82.14^{cd}	157.08^{a}	76.14^{a}	3.16^{d}	45.48^{b}	69.26^{c}	2.71^{de}	853.04^{c}	52.54^{a}

G= Genotype, DF =days to flowering, DM=days to maturity, PH= plant height, LCBZ= length of capsule bearing zone, NBPP =number of branches per plant, NCPP= number of capsules per plant, SPC =seeds per capsule, TSW= thousand seed weight, SY= seed yield. OC=oil content. E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=, Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7= Wargiba-1, E8= Wargiba-2, E9=Maykadra and E10= Gendawuha