GENETIC VARIABILITY AND ASSOCIATIONS OF TRAITS IN INDIGINEOUS AND EXOTIC SESAME (*Sesamum indicum L.*) GENOTYPES AT WERER, ETHIOPIA

MSc. THESIS

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GENETIC VARIABILITY AND ASSOCIATIONS OF TRAITS IN INDIGINEOUS AND EXOTIC SESAME (*Sesamum indicum* L.) GENOTYPES AT WERER, NORTH-EASTERN-ETHIOPIA

By

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A Thesis

Submitted to School of Graduate Studies, College of Agriculture and Veterinary Medicine, Department of Horticulture and Plant Science, in Partial fulfillment for the Requirement of Master of Science in Agriculture (Plant Breeding)

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DEDICATION

I dedicated this manuscript to my family and my best friends who supported and shared impressive pain in my life during my M.Sc. study.

STATEMENT OF THE AUTHOR

By my signature below, I declare and confirm that this thesis is my work and all sources of materials used for this thesis has been acknowledged. I have followed all proper and technical principles of scholarships in the research, data collection, data analysis and accomplishment of this thesis. This thesis has been submitted in partial fulfillment of the requirements for MSc Degree at the Jimma University and is deposited at the University Library to be made available to borrowers under the rules of the Library. I declare that this thesis is not submitted to any other institution anywhere for the award of academic degree, diploma or certificate.

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Graduate Studies (Plant Breeding)

BIOGRAPHICAL SKETCH

The author was born on October, 1989 in Meskan Woreda, Guragae zone of Southern Nations Nationalities of Peoples Regional State; from his father Ato Hassen Shammoro and his mother W/ro Fatima Woledea. He attended his elementary Schools at Meskan Koto; secondary and preparatory Schools at Butajira. After the completion of his preparatory School, he joined Haramaya University in 2008 for his BSc. study in school of plant science.

Soon after his graduation in May 2010, he was employed by Butajira Municipality Green Development Processes and Environmental Protection as expert from April 2011 to May 2014, and then after he joined Ethiopian Institute of Agricultural Research and served for two years as a junior low land oil crop breeder in oil crop improvement program till 2016. Then after, he joined Jimma University for M.Sc. degree study in plant breeding in 2016.

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LIST OF ACRONYMS AND ABBREVIATIONS

ANOVA	Analysis of Variance
CCC	Cubic Clustering Criterion
CSA	Central Statistical Agency
D^2	Squared Distance
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistics
GA	Genetic Advance
GAIN	Global Agricultural Information Network
GAM	Genetic Advance as a Percent of Mean
GCV	Genotypic Coefficient of Variation
h^2b	Broad Sense Heritability
IPGRI	International Plant Genetic Resource Institute
PC	Principal Component
PCA	Principal Component Analysis
PCV	Phenotypic Coefficient of Variation
PSF	Pseudo F
PST^2	Pseudo t^2
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis System
WARC	Werer Agricultural Research Center

TABLE OF CONTENTS

Content **Page**

LIST OF TABLES

Page

LIST OF APPENDIX

GENETIC VARIABILITY AND ASSOCIATIONS OF TRAITS IN INDIGINEOUS AND EXOTIC SESAME (*Sesamum indicum L.*) GENOTYPES AT WERER, NORTH-EASTERN-ETHIOPIA

ABSTRACT

In Ethiopia the productivity of sesame is low and below the world avergae. This low productivity is attributed to certain yield constraints mainly lack of high yielding improved variety. Understanding of genetic variability and association of characters becomes essential. Therefore, this study was conducted to estimate the extent of genetic variation and association among yield and 19 yield components. A total of 100 sesame genotypes were evaluated in 10x10 triple lattice design at Werer from 2017 to 2018 for two cropping seasons. The combined analysis of variance over the two seasons showed that the genotypes differed significantly for all the characters studied. Higher phenotypic (PCV) and genotypic (GCV) coefficients of variation were observed for shattering resistance, whereas plant height, number of capsule per plant, harvest index and seed yield showed medium PCV and GCV values; it indicating weak influence of environment. High heritability values coupled with moderate to high genetic advance as a percent of mean (GAM) were observed for shattering resistance, plant height, capsule per plant, harvest index and seed yield; this implies that the experssion of the charactrs geverned by additive gene acction. Seed yield showed positive and significant correlation with length of capsule bearing zone, length of first capsule, capsule length, capsule per main axis number of capsule per plant, harvest index and oil content. This signfied that the improvement of one traits will simultaneously improve the other. Path coefficient analysis revealed capsule per main axis, capsule per plant and harvest index had positive direct effect on seed yield.The D^2 analysis exhibited that 100 sesame genotypes grouped into seven clusters. This makes the genotypes to become moderately divergent. Principal component analysis revealed that seven principal components have accounted for 78.67% of the total variation. The present study revealed that to increase sesame seed yield, the genotypes should possess more number of capsules per main axis, capsule per plant and high harvest index. This study suggested these characters were important yield contributing traits and selection based on these characters would be most effective. However, in order to give confirmative result further studies should be conducted at multiple locations.The present study was based on morphological traits only. Hence, supporting the assessment of sesame genetic resources with molecular markers and high throughout molecular data for marker assisted breeding should be considered in the future.

Key Words*: Oil crop***,** *Sesame, Variability, Heritability, Genetic Advance, Character Association, Clustering and Principal Component.*

1. INTRODUCTION

Sesame (*Sesamum indicum L.*) belongs to the genus *Sesamum* in the *Pedaliaceae* family (Asheri, 1998). *Sesamum indicum L.* has two alternative centers of origin; Ethiopia and India (Bedigian 2015).There are about 36 species of sesame; the most cultivated one is S*esamum indicum (*Kobayashi, 1990*).* The cultivated species of sesame is diploid species with chromosome number of 2n=2x=26 (Morinaga *et al*., 1929) and which is normally a self-pollinated species; but 2 to 48% natural outcrossing might occur depending on the activity of pollinating agents (Daniel and Parzies, 2011).

Sesame (*Sesamum indicum L.*) has been domesticated, consumed and cultivated for over 3000 years (Ashri, 1994). It is the most important oil crop successfully grown in tropical and sub-tropical climates (Daniel and Parzies, 2011; and Weiss, 1983). Seeds of sesame are used as ingredients in many food items; a major part of the product is processed into cooking oil and meal. The seed is also used in the preparation of different foods like *wet*, a source for porridge, appetizers, flavoring, sweets and beverages (Adefris *et al.*, 2011 and Daniel, 2017). It is an excellent sources of vegetable oil and is designated as "queen of oil seeds" containing high oil content (44-58%) with 83-90% unsaturated fatty acids, (18-25%) proteins, (11-13%) carbohydrate and (3-4%) mineral. The oil has primary demand in the food industry because of its excellent cooking quality, flavor and stability. The oil cake rich in calcium is used as animal feed. It is also a good source of lignans such as sesamin, sesamol and sesamolin with remarkable oxidation resistance and thereby a long shelf life (Nupur *et al*., 2010).

Globally, sesame is grown by more than 78 counties across all habitable continents covering a total area of about 11.3 million hectares with a global production of about 6.9 million metric tons. The world largest volume of sesame production is concentrated in India, Myanmar, Tanzania, Nigeria, Burkina Faso, China and Ethiopia and contributing 51% of the world total sesame production. Likewise, sesame cultivated by 29 countries in Africa on a total land of 6.8 million hectare which a total production of 3.4 million ton (FAOSTAT, 2017).

Ethiopia is the top seven in the world and the fourth in Africa in sesame production (FAOSTAT, 2017). According to CSA (2017) the major sesame growing regions in Ethiopia are Amhara, Tigray, Oromia and Benshungul Gumze. The average sesame productivity in Ethiopia is very

low (0.793 ton ha^{-1}) compared to the world average 2.0 ton ha^{-1}. Productivity of Sesame is constrained by many factors such as indeterminate flowering nature, shattering of capsules at maturity, insects, diseases, weeds (grass family) and abiotic stresses (drought, salinity and heat) (Geremew *et al.*, 2012).

Future production of sesame in Ethiopia is very promising due to its economic value and export potential. Eventhough there is a huge genetic potential of the crop as center of diversity; yield of sesame is very low. In order to initiate appropriate breeding procedure for crop improvement and developing genotypes with high productivity, information on genetic variability and association between yield and yield related characters is a pre requisite (Kumar *et al*., 2010). The effectiveness of selection for genetic improvement in yield and yield contributing characters depends on genetic variability present in gene pool and the extent of its heritability.

Different researchers have studied the genetic variability and associated characters in sesame (Endale *et al*., 2011; Yirgalem *et al*., 2012; Gadisa *et al.*, 2015; Mohammed *et al*., 2015 and Desawi *et al*., 2017). For instance, Desawi *et al.* (2017) reported high phenotypic and genotypic coefficients of variations for number of capsule per plant and seed yield, moderate phenotypic and genotypic coefficients of variations for plant height and number of seed per capsule at Humera in Northern part of Ethiopia. Mohammed *et al*. (2015) reported that seed yield had positive and significant correlation with number of capsule per plant, seed per capsule, harvest index and 1000 seed weight; and number of capsules per plant had maximum positive and direct effect on seed yield per plant followed by harvest index.

In order to increase sesame production and productivity in Ethiopia research efforts are aimed at supplying farmers with improved varieties. Under Ethiopian sesame improvement project, large numbers of sesame genotypes were introduced by FAO (Food and Agricultural Organization) to Ethiopia. Little is known about traits in these sesame genotypes. Hence the present study was conducted with the following objectives.

1. To estimate the level of phenotypic and genotypic variability among sesame genotypes at Werer
2. To estimate association among seed yield and yield related traits
3. To estimate the level of genetic divergence among the genotypes

2. LITERATURE REVIEW

2.1. Taxonomy of Sesame

The genus *Sesamum* comprises consists of 36 species of which 22 species originated in Africa, five in Asia, seven in Africa and Asia, and one each in Crete and Brazil (Kobayashi *et al.*, 1990). There are three cytogenetic group of which 2n = 2x=26 comprised of the cultivated *S. indicum* followed by with *S. alatum, S. capense, S. schenckii*, *S. malabaricum*; 2n=32 contained *S. prostratum, S. laciniatum, S. angolense, S. angustifolium*; *latifolium*, whereas *S. radiatum, S. occidentale and S. schinzianum* belong to 2n=64. *Sesamum indicum L.* is the most cultivated spp. The existence of different chromosome numbers contributes to the restriction of cross compatibility among the species. As a result, it has been challenging to transfer desired traits like drought tolerance, and resistance to diseases and pests from wild relatives into cultivated sesame (Carlsson *et al.*, 2009).

2.2. Importance of Sesame

The seed of sesame is mainly used for confectionary consumption whole in different forms and also processed for oil extraction at household and industry levels (Geremew *et al*., 2012 and Daniel, 2017). According to GAIN (2016) sesame is the single largest exported oilseed in Ethiopia and an important source of foreign exchange. About 95 % of exports are in the form of unrefined seeds, leaving prospect for value-addition prior to distribution. Ethiopia is the second largest sesame exporter after India and 5 % direct uses. The oil is primary demand in the food industry because of its excellent cooking quality, flavor, and stability (Adefris *et al.*, 2011 and Daniel, 2017). The major importers of Ethiopian sesame are China, Israel, Turkey, and Middle East countries (Wijnands *et al*., 2009). There are two Ethiopian trademark concerning sesame seed color in international market namely Wellega type which comprises of uniform, white in color and high oil content mainly oil purposes; and Humera type uniform whitish seeded known for its aroma and sweet taste in the global market exported for confectionary market where white seeded types are more preferred (GAIN, 2016).

Nutritionally, sesame seed contains 34 to 63% oil content and 25% protein (Toan, 2016). The composition of oil is mainly four fatty acids, stearic, palmitic, oleic and linoleic), while other fatty acids appear in very small amounts (Ashri, 1998). According to Were *et al.* (2006b) in Sesame the oleic acid level ranges from 32.7 to 58.2% and linoleic acid from 27.3 to 59%, whereas palmitic and stearic acids ranges from 7.2 to 9.6% and 3.7 to 5.6%. Oleic and linoleic acids are the major essential fatty acid (Kamaleldin *et al.*, 1994).

2.3. Production Status of Sesame in Ethiopia

Sesame production in Ethiopia is predominantly grown by smallholder and some commercial farmers. According to CSA (2017) 804,752 hectare of land is covered by oil crops and 839, 202.19 metric ton of oil seeds are produced. Sesame is cultivated on 42% of the total land covered by oil crops contributing 32% of the total oil seed produced in Ethiopia. Major sesame growing areas in Ethiopia are; Amhara (North Gondar, North and South Wollo), Tigary (Western and North West Tigary), Oromia (East Welega and Horoguduru); and Benshungul Gumze Region (Metekel, Kemashi and Asosa) (GAIN, 2016).

The total cultivated area at national level has 337,926.82 hectare with considerable difference across regions. Similarly, sesame production has a total of 267,866.55 tons; and productivity 0.793 ton per hectare (CSA 2017). Accordingly in each major sesame producer regions are 48.2% Amhara, 32.0% Tigray, 10.0% Oromia and 8.6 % Benshungul Gumze respectively recorded in terms of area. Similarly, in terms of production, 54.7% Amhara, 26.2% Tigary, 10.4% Oromia and 8.5% Benshungul Gumze regions (CSA, 2017).

According to National Sesame Sector Development Strategy, the climate and geographies in some locations in the eastern half and southern parts of the country in Afar, Somali, and SNNP regions are conducive to growing sesame. Commercial and small-scale production in these areas has already underway. The question of how much production will increase as these new areas arise on line will depend to the large extent on international sesame prices and the trade off with other crops. Additional utilization of new technologies and improved inputs would also have a wonderful boost to annual sesame production. Affording to industry sources, these modifications could increase yields by more than double their current level of 0.793 tons per hectare (GAIN, 2016).

2.4. Sesame Breeding, Achievements and Strategy in Ethiopia

Sesame enhancement research in Ethiopia was started in the late l960s by Institute of Agricultural Research (IAR), known at present as the Ethiopian Institute of Agricultural Research (EIAR) at Werer Agricultural Research Center (WARC) under irrigation system using landraces and exotic genotypes. Since then, three phases of Sesame improvement efforts can be seen.

During the first phase breeding material were collected, introduced, characterized followed by evaluation for detecting appropriate and best adaptable sesame cultivars for the prospective areas. In the second phase the major effort to incorporate desirable traits by crossing program into the already pre-existing breeding methods. The crossing program was aimed to generate new working materials to achieve market oriented white seed coat, earliness, seed retention, high yield and bacterial blight resistance. Nevertheless, enhancement for non-shattering types was not successful at all (Daniel, 2017).

Sesame improvement efforts in the Ethiopia contributed to the release of eleven varieties of sesame have been released from Werer Agricultural Research Center from 1976 to 2016 (T-85, Kelafo-74, E, S, Mehado-80, Abasena, Aregene, Adi, Serkamo, Tate and Ado). Besides WARC, two varieties each from Gode, two varieties from Haromaya University, and one variety each from Assosa, Pawe and Gonder, and three varieties from Humera (Humera-1, Setit-1, and Setit-2), three from Bako and Sirinka Agricultural Research Centers were released from 2007 to 2016. Out of twenty seven varieties, two variety (Humera-1 and Setit-1) are extensively grown by farmers in Humera and Metema areas, while Adi and Abasena, are grown in irrigated and in areas of optimum rainfall.

Current strategic directions of sesame breeding programmes are: (i) enrichment of cultivar adapted to agro ecology base (ii) increase market value in terms of good quality components; and (iii) extension of sesame into new potential areas. Nevertheless, there is lack of strong breeding program in all regions in Ethiopia (EIAR, 2016).

The main goals of sesame enhancement in Ethiopia is to improve outstanding cultivar based on the concern of stakeholders and growers higher yields, partial/non shattering, determinate flowering, insects (webworm, gall midge, termites, seed bug) and diseases resistance (bacterial blight, phayllody, Fusarium wilt, Powdery mildew) and abiotic stress tolerance; for processors: more uniform maturity; and for the consumer: improved nutritional value of with seed of preferred oil, shape, size, texture, color and flavor (Daniel, 2017).

2.5. Phenotypic and Genotypic Variations in Sesame

Variability is the existence of dissimilarities between individuals due to differences in their genetic structure or environment in which they are innovative (Allard, 1999). All the variability existing in biological systems can be accredited to heritable and/or observable; they have grown (Welsh, 1981 and Allard, 1999).

According to Allard and Hansche (1964) advancement in plant breeding is subject to on variability for the reason that superior genotypes obviously cannot be designated from the same populations. Achievement in improving adaptation requires that the population under selection be genetically dissimilar. Opening a breeding program with any crop, evidence on the nature and extent of genetic variation within the species for traits of agronomic importance greatly aids in formulating a comprehensive crop breeding program and to develop better varieties (Baltensperger and Kalton, 1958).

Phenotypic dissimilarity is the observable that holds both heritable and environmental variation; and thus changes under different environmental conditions. Such variation is measured in terms of phenotypic variance. To advance improved varieties, the plant breeder begins his/her remark on the measurement of the phenotype. For plant, breeding to be effective, there must be observable deviation of the desired trait and some of the variation must be inherited from parent to offspring (Stockpot *et al*., 1999). All phenotypic coefficient of variation is greater than the genotypic coefficient of variation in general (Ghimiray and Sarkar 2002 and Dinesh *et al.*, 2010).

The development of an effective sesame improvement program is dependent up on the existence of genetic variability. The more diverse the parents that make the population the

better the probabilities of better spectrum of variability. The basic idea of study of variation is it's partitioning into components attributed to the different roots. The relative magnitude of these components determines the heritable properties of the population. Genetic variability is crucial to the plant breeder because proper management of this variation can produce permanent gain in the performance of the plant (Welsh, 1990).

Eventhough some environmental variations can be reduced by appropriate experimentation, their total removal is impossible because environmental variation contains the not-heritable difference and much of these are left from experimental control (Gomez and Gomez, 1984). Welsh (1990) stated that environment is the sum total of all things to which the organism is exposed, as a result, environmental deviations consistencies on fertility level of plots, moisture content of the soil, and periodic instabilities give to the component of variation.

Genetic variability studies for agronomic characters are the key components of improvement program for widening the gene pool of sesame. Chavan and Chopde (1982) reported high variation for capsule per plant, primary branches per plant, plant to first branch and capsules on the main stem. Fayan *et al*. (1991) reported in sesame high genetic variation for number of capsules per plant, length of fruiting sections and seed yield per plant but lower variation was reported for plant height and 1000 seed weight on 36 released varieties of sesame. Banerjee (2006) reported genetic variability on some physiological traits was studied in a population of thirty genotypes of sesame and high phenotypic and genotypic coefficients of variability was revealed for days to flowering and oil yield, while it was moderate for days to maturity and low for oil content. The highest GCV was recorded for seed yield per plant followed by number of capsules per plant, plant height, 1000 seed weight and number of seeds per capsule (Khan *et al*., 2001). Ahadu (2008) reported that PCV and GCV values for days to 50% flowering, capsule filling period and plant height were medium and days to maturity, 1000 seed weight and oil content had low PCV values. The high GCV value of characters suggest that the possibility of improving these trait through selection.

Mohammed *et al.* (2015) showed high phenotypic coefficients of variation and medium genotypic coefficients of variation values for primary branch per plant (28.91 and 14.06%), number of capsule per plant (22.81 and14.42%) and seed yield $kgha^{-1}$(28.42 and 17.13%); and

medium PCV and low GCV for number of seed per capsule (10.93 and 7.16%), capsule length (10.82 and 2.17%), pant height (10.05 and 6.54%) and 100 seed weight (16.76 and 9.73%), while low phenotypic coefficients of variation and genotypic coefficients of variation values was recorded for days to 50% flowering (5.12 and 3.16%), days to maturity (2.61 and 1.59%), harvest index (6.81 and 9.92 %) and oil content (5.08 and 3.27%) from 81 sesame genotypes. Gadisa *et al.* (2015) reported high values for GCV and PCV for number of primary branch (49.32 and 45.89%), biomass yield(21.88 and 20.52%) and harvest index (29.4 and 27.2%); and medium PCV and GCV were obtained for capsule per plant(10.80 and 10.38%) and seed yield (18.31 and 18.30%), whereas medium PCV and low GCV for 1000 seed weight, while low PCV and GCV for days to 50 % flowering (8.64 and 8.42%), days to maturity (6.63 and 6.48%), capsule filling period (8.23 and 7.81%) and plant height (6.27 and 6.14%).

Yirgalem *et al.* (2012) reported that low difference between PCV and GCV for days to 50 % of flowering, date of maturity and oil content while high in case of capsule length and biomass yield. High difference between PCV and GCV shows high influence of the environment on the characters whereas low difference shows low influence of the environment on the characters.

2.6. Heritability in Sesame

The proportion of genotypic variance to phenotypic variance is called heritability; the range to which the variability of a trait is passed to the offspring (Allard, 1999). Heritability assessments deliver a clue of the expected response to selection in segregating population. As of interest to the plant breeders, mainly as a measure of the value of selection for particular characters and as index of transmissibility in conjunction with genetic advance reveals the amount of heritable variation in the population and also the resultant effect for selecting the best individuals can be anticipated (Johnson *et al.*,1955).

If heritability is high it indicates that the genotype play more important role than the environment in determining the phenotype. Normally, heritability values for quantitative characters are low due to large environmental effect but also with the nature of the test population (Briggs and Knowles, 1987). It is observable that alteration due to environment

may have a tendency to obscure genotypic variations. The larger the fraction of the total variability that is due to the environment, the more difficult it will be to select for inherited dissimilarities. On the other hand, if environmental deviation is small in relation to heritable differences, selection will be efficient because the characters to be selected will be transmitted to offspring (Briggs and Knowles, 1987). If genetic difference in offspring is great in relation to the environmental variation then heritability will be high while it is small in relation to the environmental variation, at that point heritability will be little (Mittal and Sethi, 2004).

Heritability can be either broad sense or narrow sense. Broad sense heritability is the relative magnitude of genotypic and phenotypic variance (VG/VP) for the characters including additive, dominance and epistasis (multi-genic interaction), where individuals are directly affected by their parents phenotype. It is used as a predictive role in selection procedures (Allard, 1960). This gives an idea of the total variation power to genotypic effects, which are exploitable portion of variation. Narrow sense heritability is the proportion of additive and phenotypic variance (VA/VP), and it expresses the extent to which phenotypes are determined by the genes transmitted by the parents to progenies' (Falconer, 1989).

A large number of studies have been conducted for yield and yield related characters to estimate heritability in sesame. According to Hamid *et al.* (2003) high heritability estimates were recorded for days to 50 % flowering, days to maturity and 1000 seed weight. Ahadu (2008) reported high heritability for days to maturity, whereas low for number of capsules per plant, seed and biomass yield per ha, and moderate for characters such as days to 50% flowering, plant height, capsule filling period, number of primary branches per plant and harvesting index. Yirgalem *et al.* (2012) conveyed high heritability for days to 50% flowering (98.8%), date of maturity (96.7%), capsule filling period (89.5%), plant height (84.70%), number of primary branch (97.1%), number of seed per capsule (90.10%), oil content (93.70%), seed yield (87.81%), harvest index (72.90%) and 1000 seed weight (78.20%), while medium heritability for biomass yield (45.7%), and low heritability for capsule per plant (16.1%).

Gadisa *et al.* (2015) reported high estimates of heritability values for days to 50% flowering (94.99%), date of maturity (95.32%), date of capsule filling period (90.08%), number of primary branch (86.59%), capsule per plant (92.49%), seed yield per (99.81%), biomass yield

(87.92%) and harvest index (85.71%), while low heritability estimated for 1000 seed weight (45.21%). In addition Desawi *et al.* (2017) also reported high heritability values for days to 50% flowering (90.04%), date of maturity (76.97%), date of capsule filling period (65.07%), capsule per plant (92.72%), length of capsule bearing zone (70.92%), plant height (80.78%), number of capsule per plant (92.72%), number of seed per capsule (61.95%), oil content (73.13%) and yield per plant (66.47%), while low heritability for number of primary branch (38.59%) and 1000 seed weight (26.45%).

2.7. Genetic Advance in Sesame

Genetic advance stated in proportion of mean showed a wide range of variations across the environments. According to Burton and Devane (1953) genetic advance tell us the clue estimate of the expected gain for a particular character through selection. Once heritability estimates are accessible for a trait in a particular population, expected can be made of the amount of breeding value anticipated for a given selection power. Genetic advance under selection refers to improvement of characters in genotypic value for the new population compared with the base population after one cycle of selection at a given selection intensity (Singh, 2001). Mostly, large heritability values showed relative simplicity with which selection can be made based on observable characters; however, their practical function in crop upgrading is further enhanced if accompanied by concurrently high GA estimates (Johnson *et al*., 1955). The genetic advance under selection will depend on the amount of genetic variability; the magnitude of the effects of environmental and interaction components of the variability in hiding the genetic expression, and the strength of selection that is competent (Allard, 1999).

Johnson *et al*. (1955) and Allard (1990) advised that heritability is not enough in forecasting the success of selection without genetic advance. Assessments of heritability in combination with genetic advance will help to know the nature of gene action affecting the character and also indicates the scope of genetic improvement for the characters through selection. High Heritability coupled with high genetic advance exhibited by the characters, controlled by additive gene action, (Singh *et al*., 2001) and improves through selection. Thus, selection for the character having high heritability associated with high genetic advance leads to

accumulate more additive genes. It can enhance the opportunity for further improvement of their performance. Therefore, heritability in conjunction with genetic advance would give a more reliable index of better selection value (Akinwal *et al.,* 2011). Those traits possessing low genetic advance with high heritability indicates the presence of non-additive gene action, as a result simple selection procedure in early segregating generations will not be effective for screening of the desirable traits (Chand *et al*., 2008).In sesame high heritability coupled with high expected genetic advance was observed for capsules per plant, primary branches and capsules on main shoot, while highest heritability with moderate genetic advance for days to 50 % flowering reported by (Chavan and Chopde, 1982).

High heritability coupled with high genetic advance was observed for seed oil content, number of capsules per plant and seed yield (Siva *et al.,* 2013). Yirgalem *et al*. (2012) reported high heritability coupled with genetic advanced as percent mean for days to 50% flowering (34.88%), capsule filling period (35.9%), plant height (35.43%), primary branch per plant (74.95%), number of seed per capsule per plant (52.65%), 1000 seed weigh (20.74%) and seed yield (113.87%); high heritability with moderate GAM for days to maturity (16.39%), while high heritability coupled with low GAM for oil content (9.06%).

Further, Mohammed *et al.* (2015) reported moderate estimates of heritability coupled with moderate to high genetic advance over mean was recorded for seed yield (24.62%), number of capsules (18.77%), biomass yield (18.34%), and 1000 seed weight (11.64%) indicating that these characters are controlled by additive gene action and phenotypic selection for these characters will be effective. However, low genetic advance as percent of mean for day to 50% flowering (4.02%), days to maturity (2.0%), capsule length (0.9%), number of seed per capsule (9.66%), plant height (8.04%), harvest index (9.62%) and oil content (4.34%). Moreover, Gadisa *et al.* (2015) reported high heritability coupled with high genetic advance as percent of mean values for capsule per plant (20.57%), seed yield per plant (37.66%), biomass yield (39.63%) and harvest index (51.91%), whereas high heritability coupled with moderate genetic advance as percent of mean for days to flowering (16.91%), days to maturity (13.02%), days to capsule filling period (15.27%), plant height (12.4%) and number of primary branch (12.4%).

2.8. Association Studies in Sesame

2.8.1. Correlation coefficient

Correlation coefficient is the measure of the level for linear association between two characters (Gomez and Gomez, 1984). It is simply measures the common association without concern to causality (Dewey and Lu, 1959). There are three types of correlations phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of observable values or phenotypic correlation. The phenotypic correlation measures the extent to which the two observed characters are linearly interconnected. Genetic correlation is the association of breeding values of the two traits (Falconer, 1989). The inherited roots of correlation are mainly pleiotropic effects of genes affecting diverse characters (additive genetic variance). Pleiotropic is the property of a gene whereby it affects two or more characters, therefore the genes segregating it cause simultaneous variation in the two characters it affects (Falconer and Mackay, 1996).

Correlation is helpful in determining the component characters of a complex trait like yield. The practical value of selecting for a given character as a means of improving another depends on the extent to which improvement in major characters is assisted by selection for the indicators. Such improvement depends not only on the genotypic correlation but also on phenotypic correlation (Johnson *et al*., 1955b). According to Sidwell *et al*. (1967) the components should be should be highly heritable, genotypic governed or have innately positive association physiologically related in a positive manner.

Falconer (1989) and Rangaswamy (1995) suggested significant correlation coefficients among various characters may occur from pleotropic effects of genes or from linkage effects. Generally, negative correlation between two traits implies selection for improving one trait will leads to decrease in the other trait, whereas for positive correlation, simultaneous improvements of both traits could be achieved.

In sesame, seed yield had positive and significant genotypic correlation with days maturity, capsule filling period, number of capsules per plant and biomass yield; while negative and significant genotypic correlation with oil content and plant height (Ahadu,

2008). Fazal *et al*. (2010) reported that days to maturity, number of capsules per plant, 1000 seed weight, plant height and capsule had a significantly positive genotypic correlation with seed yield, number of primary branches and number of seeds per capsule showed positive and non-significant with seed yield and a significantly negative correlation with days to 50% flowering. Moreover, Mohammed *et al*. (2015) also reported primary branch per plant (rp= 0.31*, rg= 0.27**), number of capsule per plant(rp= 0.83**, rg= 0.79**), number of seed per capsule (rp= 0.52**, rg= 0.48**), plant height (rp= 0.42**, rg= 0.28**), biomass yield (rp= 0.98**, rg= 1.00**), harvest index(rp= 0.96**, rg= 0.94**) and 1000 seed weight positive (rp= 0.65**, rg= 0.6**) and significantly associated with seed yield at both phenotypic and genotypic level.

Prithvras *et al. (*2015) found seed yield had positive and significant relationship for plant height (rp= 0.7405**, rg= 0.8882**), primary branch per plant (rp= 0.1319*, rg= 0.8086**), number of capsule per main stem (rp= 0.2586**, r= 0.3221**), number of capsule per plant (rp= 0.6917**, rg= 0.7507**), capsule length(rp= 0.2174**, rg= 0.3902**), capsule width(rp= 0.2567**, rg= 0.4739**), number of seed per capsule (rp= 0.2568**, rg= 0.2658**), 1000 seed weight (rp= 0.2826**, rg= 0.2989**) and oil content (rp= 0.1486*, rg= 0.1635*), at phenotypic and genotypic level.

Furthermore, Desawi *et al.* (2017) conveyed seed yield had positively and significantly associated with phenotypic level for length of capsule bearing zone (rp= 0.426**), number of capsule per plant (rp= 0.440**) and primary branch per plant (rp= 0.334**), whereas seed yield had positive and significant with genotypic level for length of capsule bearing zone (rg= 0.490**), primary branch per plant (rg= 0.355**), capsule length (rg= 0.547**), number of seed per capsule (rg= 0.275*) and 1000 seed weight (rg= 0.554**), while date of maturity(rg= -0.440**), plant height (rg= -0.98**) and number of capsule per plant (rg= -0.485**) had negative and significant associated with seed yield at genotypic level.

2.8.2. Path-coefficient analysis

Seed yield is composed of a number of components. Choice for yield should also take into concern all the significantly correlated characters in the positive direction. However, correlation coefficient does not give a complete picture of the relative direct and indirect

influence of each component on seed yield is possible through the path coefficient analysis (Woldemariam, 1985).

Path coefficient analysis is a statistical tool developed by Wright (1921) intended the method for path analysis for the purpose of clarification of a system of correlation coefficients in terms of path causation. Path coefficients differ from correlation coefficients in that they may exceed by +1or -1 in absolute value as there is no restriction on the relative amounts of the differences of an effect and a cause. To improve grain yield via selection of its components path coefficient analysis is a convenient tool for thoughtful grain yield formation and provides valuable extra information about the characters (Garcia *et al*., 2003).

Mohammed *et al*. (2015) stated the number of capsules per plant (0.98) had maximum positive direct effect on seed yield per plant followed by harvest index (0.35). Moreover, Desawi *et al.* (2017) found that the length of capsule bearing zone had maximum positive and direct effect on seed yield (0.735) followed by 1000 seed weight (0.612), number of capsule per plant (0.326), date of maturity (0.279) and number of seed per capsule (0.239), while on capsule length (-1.005), plant height (-1.135), capsule filling period (-1.09) and date of flowering(-0.481) direct and negative effect on seed yield at genotypic level. Yirgalem *et al. (*2012) reported that had positive and direct effect on seed yield observed on days for 50% flowering (0.995), 1000 seed weight (0.265), biomass yield (0.343), capsules per plant (0.236) and capsule filling period (0.997), while days to maturity (-0.998) had negative and direct effect on seed yield of sesame.

2.9. Cluster and Divergence Analysis in Sesame

2.9.1. Cluster analysis

Cluster analysis is a process assemblage of multivariate method, whose primary purpose is to group individuals based on measured variables into a number of different groups such that similar subjects are located in the same group. Accordingly, if the classification is successful, individuals within a cluster shall be closer when plotted geometrically and different clusters shall be farther apart as suggested by Hair *et al*. (1995).

There are broadly two types of clustering methods, distance based and model based methods. In distance based methods, a pair wise distance matrix is used as input for clustering analysis. The result can be visualized as tree or dendrogram in which cluster may be identified. In Model based methods, observations from each cluster are assumed to be random from some parametric model and inference about parameter corresponding to each cluster and cluster membership of each individual are performed jointly using maximum-likelihood or Bayesian methods (Johnson and Wichern, 1992).

Additional key aspect in cluster analysis is determining the optimal number of clusters or number of acceptable clusters. In essence, this involves deciding where to "cut" a dendrogram to find the true or natural groups. An acceptable cluster is defined as a group of two or more genotypes within genetic distance less than the overall mean genetic distance and between cluster distance greater than their within a cluster distance of the two cluster involved. The resulting clusters of individuals should then exhibit high internal (within cluster) homogeneity and high external (between clusters) heterogeneity. Cubic clustering criterion (CCC), pseudo F (PSF), and pseudo t^2 (PST^2) statistics were used in determining the number of clusters in the data. That is, local peaks of the CCC and pseudo F statistic combined with a small value of the pseudo t^2 statistic and a larger pseudo t2 for the next cluster fusion (Mohammadi and Prasanna, 2003). Fazal *et al*. (2011) clustered 105 sesame accessions which were collected from Pakistan and found high variation and finally grouped into seven clusters. Furthermore, Spandana *et al*. (2011) studied 60 sesame accessions which were collected from India and found high variation and finally grouped into eight clusters. Prithvras *et al. (*2015) studied 131 genotypes of sesame in India for assessments of natural genetic diversity in multivariate analysis in squared distance concerning thirteen important characters viz. (days to 50% flowering, days to maturity, plant height, height to first capsule, number of branches per plant, number of capsule on main stem, number of capsules per plant, capsule length, capsule width, number of seeds per capsule, 1000 seed, oil content and seed yield per plant) distributed in 10 cluster. The maximum number of genotypes were grouped in cluster I (87) followed by cluster III (18), Cluster II (13) and VI (7), and the remaining clusters (IV, V, VII, VIII, IX and X) were all solitary single genotype for each. Some genotypes from different origins were

grouped into the same clusters as a result there is absence of relationship between genetic diversity and geographic diversity.

Moreover, Mohammed *et al.* (2015) in sesame to attain maximum heterosis under breeding program crossing of genotypes with maximum distance between them resulted in high yield determined genetic divergence of 81 sesame genotypes for seed yield and attributing traits and categorized the genotypes into seven clusters. The maximum genotypes lay in cluster III (22) followed by cluster II (19), V (14), I (10), IV (9), VI (5) and VII (2). Collecting of genotypes in the same region grouped in to different cluster, hence clustering was not associated with geographical distribution rather genotypes mainly grouped regarding their morphological characters.

2.9.2. Genetic divergence analysis

Genetic diversity is usually thought of as the amount of genetic variability among individuals of a variety, or population of species (Brown, 1983). The pattern and level of genetic diversity in a given crop gen pool can be measured interms of genetic distances. Genetic distances measures the average genetic deviation among cultivars or populations (Souza and Sorrels, 1991). Moll *et al*. (1965) defined genetic divergence of two varieties as a function of their ancestry, geographic separation and adaptation to different environments.

A genetic distance measure based on multiple characters is given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for quantitative characters. Information on the extent of genetic diversity amongst the breeding materials is very important in the crosses between groups with maximum genetic divergence would be more responsive for improvements they are likely to produce desirable recombination and segregation in their progenies after hybridization (Reddy, 1988). For instance, scholars were suggested Geographic diversity as index of genetic diversity in crop plants. However, it was pointed out that there were no close correspondence between geographic diversity and genetic diversity in some crops. According to Chandel and Joshi (1983), sesame collection from different geographical region of complex atmosphere are normally anticipated to accumulate considerable inherent diversity; nevertheless, the distribution of strains in diverse clusters did not follow definite pattern with respect to geographical origins. Kumar *et al.* (2010) reported 146 sesame genotypes of Indian

and exotic origin, based on the D^2 analysis those accessions was grouped into 13 clusters and the clustering was not in harmony with physical origin. Akbar *et al.* (2011) evaluated 105 genotypes accessions and reported that plant height, days to maturity, capsules per plant and seed yield per plant was the major determinants of the genetic diversity in the collection. Cluster analysis was done and all the accessions were clustered into seven groups. Clustering was not associated with the geographical distribution instead accessions was mainly grouped due to their morphological differences.

Tripathi *et al.* (2014) estimated genetic divergence using D^2 values the genotypes lines were grouped into eleven different clusters 100 sesame accessions collected from diverse ecologies of India. Clustering was not associated with the geographical distribution instead accessions were mainly grouped due to their morphological differences. Maximum inter cluster distance was observed between cluster VI and XI (134.72) followed by clusters V and XI (124.23) while, lowest divergence was noticed between cluster IV and V (9.37). Prithvras *et al. (*2015) reported the inter cluster distance value exhibited a wide range from 36.90 (between cluster VII and VIII) to 327.84 cluster (between clusters X and IV) suggesting the presence of considerable amount of diversity among the cluster. The relative divergence of cluster from each (inter cluster divergence) indicated high order of divergence between cluster X and IV (327.54) followed by cluster III and IV (261.9). The selection of parents from such clusters for hybridization program help to achieve novel recombination. Mohammed *et al.* (2015) reported the inter cluster distance ranges from 14.98 between cluster (II and IV) to 570.34 (V and VII). The maximum genetic distance was obtained between cluster V and VII (570.34) and cluster III and VII (447.17) implies that superior hybrids/recombinants will be realized by crossing the lines of this cluster in appropriate crossing design.

2.10. Principal Component Analysis in Sesame

Principal component analysis (PCA) is one of the multivariate statistical procedures which are a powerful tool for examining and summarizing fundamental trends in complex data structures (Legendre and Legendre, 1998). PCA reflects the importance of the major contributor to the total variation at each alignment for differentiation (Sharma, 1998). The PCA generates three important products, the eigenvalues, eigenvectors and scores, the

dominant modes representing the most important characteristics from the original data. PCA can be used to drive a two dimensional scatter plot of individuals, such that the geometrical distance among individuals in the plot reflect the genetic distances among them with minimal alteration. Aggregates of individuals in such a plot will reveal sets of genetically similar individuals (Warburton and Crossa, 2000).

According to Chahal and Gosal (2002), characters with largest absolute values closer to unity within the first principal component influence the clustering more than those with lower absolute values closer to zero. The reduction is achieved by linear transformation of the original variables into a new set of uncorrelated variables known as principal components (PCs). The first step in PCA is to calculate Eigen values, which define the amount of total variation that is displayed on the PC axes. The first PC summarizes most of the variability present in the original data relative to all the remaining PCs. The second PC explains most of the variability not summarized by the first PC and uncorrelated with the first and so on (Jollife, 1986). Ahadu (2008) employed PCA for detecting variation in 64 sesame accessions which were collected from Ethiopia and reported that four of principal components (PCs) explained about 75.6 % of the total variation among 81 accessions of sesame. Shim *et al*. (2009) also reported that the first four principal components (PCs) elucidated around 83.7 % of the entire dissimilarity among 18 accessions of sesame. Furthermore, Fazal *et al*. (2010) reported that the four principal components (PCs) explained about 63.63% of the total variation among 105 accessions of sesame. Similarly, Seymus *et al.* (2011) reported that the seven principal components (PCs) explained about 69.9 % of the total variation among 103 accessions of sesame.

3. MATERIALS AND METHODS

3.1. Description of the Experimental Site

A field experiment was carried out at Werer Agricultural Research Center. Werer is located 90^0 27 N and 40^0 15 E in north eastern part of Ethiopia about 280 km from Addis Ababa. The altitude of Werer is 740 meter above sea level. Fourteen years climatic data showed that the average maximum and minimum temperatures at Werer station are 34^0c and 19^0c, and the average rainfall in the area is about 571 mm annually and it is erratic bi-modal (with higher rains from June-Septembers and small rains from February-April) and the main water source for crop production in the region is irrigation water from Awash river. The rainy seasons are not sufficient for crop production. The soil in Werer station is predominantly vertisol with pH of 8.5; the porosity and bulk density (0-25cm depth) of 49.06 % and 1.35 gm/cm^2 (WARC, 2012).

3.2. Genetic Materials

Out of 1000 local collections and 400 introduced genotypes, a total of 100 sesame genotypes were randomly taken and considered in this study. The genetic material consists of one standard (Adi) and one local check, 71 genotypes collected from major sesame growing regions of Ethiopia and 27 introduced genotypes from FAO. List of sesame genotypes, origin and seed source are given in Table 1.

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Table 1. Description of genetic material

No	Name of genotypes	Origin	Seed source	No	Name of genotypes	Origin	Seed source
1	Acc- 00019	ET	WARC	51	EW - 020 (1)-sel-2	ET	WARC
2	Acc- 00065	ET	WARC	52	G - 03 – 1	ET	WARC
3	Acc - 024 - sel- 1	ET	WARC	53	Hihir Baker sel- 1	ET	WARC
4	Acc - 024 sel- 3	ET	WARC	54	Hirhir Adi Gosh sel-4	ET	WARC
5	Acc- 044-sel-1	ET	WARC	55	Hirhir humera sel- 6	ET	WARC
6	Acc - 111 - 848 – 1	ET	WARC	56	Hirhir Kebebew early sel-1	ET	WARC
7	Acc - 202 – 363	ET	WARC	57	K-74 X C22 (71-2)-3	ET	WARC
8	Acc - 202 - 374 – 2	ET	WARC	58	M - 80 # 402 – 2	ET	WARC
9	Acc - 203 – 187	ET	WARC	59	NN – 0021	ET	WARC
10	Acc - 205 – 180	ET	WARC	60	NN - 0029 (2)	ET	WARC
11	Acc - 205 – 344	ET	WARC	61	NN - 0036 – 1	ET	WARC
12	Acc - 205 - 374 – 1	ET	WARC	62	NN – 0052	ET	WARC
13	Acc - 205 - 374 – 2	ET	WARC	63	NN – 0054	ET	WARC
14	Acc - 211 – 015	ET	WARC	64	NN - 0068 - 2	ET	WARC
15	Acc - BG – 001	ET	WARC	65	NN - 0108 – 2	ET	WARC
16	Acc - BG - 001(3)	ET	WARC	66	NN - 0129-2	ET	WARC
17	Acc - BG – 003	ET	WARC	67	NN - 0183 – 3	ET	WARC
18	Acc - BG – 009	ET	WARC	68	NN - 088 – 2	ET	WARC
19	Acc - EW – 006	ET	WARC	69	Tejahir-2Late ginwuha-sel-1	ET	WARC
20	Acc - EW - 009(5)	ET	WARC	70	Tejareb-2 Late gindwuha	ET	WARC
21	Acc - EW - 011(1)	ET	WARC	71	W – 118	ET	WARC
22	Acc - EW - 012 (7)	ET	WARC	72	Acc - 203 - 336 – 2	(Zimbabwe)FAO	WARC
23	Acc - EW - 017(6)	ET	WARC	73	Acc - 203 - 336 - 4	(Zimbabwe)FAO	WARC
24	Acc - EW - 025(1)	ET	WARC	74	Acc - 203 – 612	(Zimbabwe)FAO	WARC

Table 1 . (*continue*)

No	Name of genotypes	Origin	Seed source	No	Name of genotypes	Origin	Seed source
25	Acc - GA - 005(1)	ET	WARC	75	Acc - 203 - 623-sel-1	(Zimbabwe)FAO	WARC
26	Acc - No – 024	ET	WARC	76	Acc - 203 – 630	(Zimbabwe)FAO	WARC
27	Acc - No – 044	ET	WARC	77	Acc - 210 - 986 – 1	(Sudan)FAO	WARC
28	Acc - No – 045	ET	WARC	78	Acc - 210 - 991 – 4	(Sudan)FAO	WARC
29	Acc - No – 049	ET	WARC	79	BAR – 0004	(Somalia)FAO	WARC
30	Acc - No – 05	ET	WARC	80	BAR – 002	(Somalia)FAO	WARC
31	Acc - No 04 + 06 + 07	ET	WARC	81	Bering bowng	FAO	WARC
32	Acc - NS - 007(2)	ET	WARC	82	China FAO (ACC-68-542)	(China)FAO	WARC
33	Acc - WW - 001 (4)	ET	WARC	83	Clusu - Acc- 2	(Philipins)FAO	WARC
34	Acc - WW - 001(6)	ET	WARC	84	HB - 22 - FAM (1- 4)	(Egypt)FAO	WARC
35	Acc - WW - 003(4)	ET	WARC	85	HB - 38 FAM - 2 BAR Grey	(Egypt)FAO	WARC
36	Acc # 033	ET	WARC	86	HB - 49 FAM - 2 – 2	(Egypt)FAO	WARC
37	Acc -111- 524 – 1	ET	WARC	87	JAPAN-651	(Japans)FAO	WARC
38	Acc -111- 821	ET	WARC	88	SPS - SIK - # 811	(Kenya)FAO	WARC
39	AW – 001	ET	WARC	89	SSBS - (9 - 2) -3	(Kenya)FAO	WARC
40	AW – 007	ET	WARC	90	Tmax	(Israel)FAO	WARC
41	BACKO-MW-42	ET	WARC	91	Unknown - sel- 3	FAO	WARC
42	Banja Gobate sel- 4	ET	WARC	92	Unknown Nguara sel-9	FAO	WARC
43	BCS - 001 (1)	ET	WARC	93	Unkown Kaja sel- 4	FAO	WARC
44	BCS – 033	ET	WARC	94	USR - 82 # 171 NS	FAO	WARC
45	Bounja – filwuha sel- 2	ET	WARC	95	Venezuela – 1	(Venzula)FAO	WARC
46	Bounja – filwuha sel- 6	ET	WARC	96	Win black (Tall) – 2	FAO	WARC
47	Bounja – filwuha sel- 8	ET	WARC	97	X - 30/40 # 403	(Israel)FAO	WARC
48	Bounja - fiyel kolet sel- 4	ET	WARC	98	Ying White – 2	(China)FAO	WARC
49	EW - 017(1)	ET	WARC	99	Local check	check	WARC
50	EW - 017(5) x NS - 001 # 48	ET	WARC	100	Adi	check	WARC

WARC=Werer Agricultural Research center, ET=Ethiopia collection; FAO=Food and Agricultural Organization

3.3. Experimental Design and Trial Management

The experiment was conducted from 2017 to 2018 in two cropping seasons. The experiment was laid out in 10 x 10 triple lattice design with three replications. Each plot was 4 m long, and 1.2 m wide, which consisted of 3 rows with a spacing of 40 cm between rows and 0.4m between plots. Sowing was done by hand drilling. Thinning was carried out after 21 days, and plant to plant distance was kept at 10 cm. Other agronomic practices such as irrigation and weeding were applied as per the research recommendation (WARC, 2012).

3.4. Data Collected

Data were collected for each experimental unit on plant and plot basis by using IPGRI descriptor (IPGRI, 2004).

On plot basis

Days to flower initiation: the number of days from emergency to a stage when the plants in a plot at least one flower could be initiated.

Days to 50% flowering: the number of days from emergence to a stage when 50 % of the plants in a plot produced flower.

Capsule filling period: the number of days from 50 % flowering to physiological maturity that capsule of two-third of the plant turns from green to yellow color

Days to maturity: the numbers of days from emergence to a stage when the plants in a plot produced 90 % matured capsules of two third capsules were changed from green to yellowish.

1000 seed weight (g): measured weight in grams of 1000 seeds taken randomly from bulked seed from each plot

Biomass yield per hectare (ton): the total above ground biomass harvested from central one row and weighing in gram after sun dried; then converted in to tons per hectare.

Harvest index (%): the ratio of dry seed yield to biomass yield calculated to Baydar (2005) as follows

$$HI = \frac{\text{Dry Seed yield x 100}}{\text{total dry weight}}$$

Seed yield per hectare (kgha^{-1}): taken by weighting seed yield in gram obtained from a central row of each experimental plot; and converted into seed yield kilo gram per hectare at 7 % moisture content

Oil content (%): oil content was determined by wide line nuclear magnetic resonance (NMR). Bulk seeds were taken from each plot and oven dried at 130°C for 2hr and cooled in desiccators for 1hr. 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, 1989).

On plant basis

Data were collected from five randomly taken plants per plot of experimental unit.

Plant height (cm): plant height was measured in centimeter from the ground level to the tip of the plant at maturity and averaged.

Length of capsule bearing zone (cm): length of capsule bearing zone measured from the starting point of first capsule to tip of the plant and averaged.

Length of first capsule (cm): five capsules were taken randomly within a plot; first capsule was measured from the base of the capsule to the tip and averaged.

Capsule length (cm): five capsules were taken randomly within a plot in five plants from the middle part of capsule bearing zone; measured the length capsule at maturity and averaged.

Capsule width (cm): average width of five capsules was taken randomly within a plot in five plants from the middle part of capsule bearing zone.

Capsule thickness (cm): five capsules were taken randomly within a plot in five plants from the middle part of capsule bearing zone from different plant and measured the thickness and averaged.

Number of primary branches per plant: the number of branches originated from the main stem of five randomly taken plants and averaged.

Number of capsules per main axis: The number of capsules could be obtained from middle part of capsule bearing zone in main stem from of five randomly taken plants at harvest.

Number of capsules per plant: The number of capsules was harvested from five different randomly selected plants.

Number of seed per capsule: Ten capsules were randomly taken within a plot in middle part of five capsule bearing zone in main stem, then count the seed and were taken in count averaged number of seed per capsule.

Estimating the level of Shattering resistance (%): $ISR = RW * 100/TSW.$; RW= retained seed weigh and TSW= total seed weight

3.5. Data Analysis

All data were subjected to analysis using SAS software 9.3 (SAS, 2014)

3.5.1. Analysis of variance (ANOVA)

Data were checked for the normality assumption and all the data met the normality assumption except for number of capsule per plant, seed per capsule, number of capsule per main axis, date of capsule filling period, length of capsule bearing zone, primary branch per plant and harvest index. Square root and Arc sin transformation methods were used as per the standard procedure set by Gomez and Gomez (1984) in order to normalize the distribution. The analysis variances for each seasons were generated. The ANOVA model for individual season was:

$$Pijk = \mu + gi + bk(j) + rj + eijk$$

Where, P_{ijk} = phenotypic value of i^{th} genotype under j^{th} replication and k^{th} incomplete block within replication j; μ =grand mean; gi= the effect of i^{th} genotype; $b_{k(j)}$ = the effect of incomplete block k within replication j; r_j=the effect of replication j; and e_{ijk}= the residual or effect of random error.

Table 2. Analysis of variance skeleton for individual season analysis in triple lattice design

Source of Variation	Degree of Freedom(df)	Sum of Square(SS)	Mean square MS=ss/df	Computed F
Replication	R-1	SSR	MSR	MSR/ MSE
Treatment				
- (Unadj.)	k^2-1	SSG(unadj)	MSG	MSG/MSE
-(Adj.)	K^2-1	SSG(adj)	MSG	MSG/ MSE
Block within replication (Adj.)	R(K-1)	SSB(adj)	MSB	MSB/ MSE
Error				
Intra block	(k-1)(Rk-k-1)	SSE	MSE	
RCBD	(k-1)(k^2-1)	SSE	MSE	
Total	(RK^2-1)	TSS		

df= degree of freedom, R = the replication number, G = number of genotypes and K = the block size, SSR and MSR = sum square and mean square of replication, SSG and MSG = sum square and mean square of genotypes, SSB and MSB = sum square and mean square of block, SSE and MSE = sum square and mean square of intera block and RCBD error and TSS = total sum of square.

Homogeneity test for the error variance of two seasons were done separately. For combined analysis of variance over seasons, the homogeneity of error variance was tested by using F-max test as suggested by Hartley (1950), which is based on the ratio of the larger mean square of error (MSE) to the smaller mean square of error from the separate analysis of variance given by the formula: $\text{Fmax} = (\text{Largest MSE})/(\text{Smallest MSE})$. Then the test showed all the characters non-significant met the homogeneity assumption and data were combined.

Therefore, combined analysis was computed based on general leaner model (GLM) procedures using SAS statistical package. Mean separation among treatment means was done using LSD (least significant difference) at 5 % probability level. The combined analysis of variance over two seasons was carried out according to the following model:

$$Pijks = \mu + gi + bk(j)(s) + rj(s) + Ss + (gs)is + eijks$$

Where, P_{ijks}= phenotypic value of i^{th} genotype under j^{th} replication at s^{th} season and k^{th} incomplete block within replication j and season s; μ= grand mean; g_i = the effect of i^{th} genotype; $b_{k(j)(s)}$ = the effect of incomplete blocks within replication j and season s; $r_{j(s)}$ = the effect of replication j within season s; S_s= the effect of season; $(gs)_{is}$ = the interaction effects between genotype and season; and e_{ijks} = the residual error.

Table 3. Analysis of variance skeleton for combined analysis over season in lattice design

Sources of variation	Df	MS	F-value	Expected Mean Square(EMS)
Season	S-1	MSS	MS_S/MS_E	$\sigma^2e+ R \sigma^2gs + G \sigma^2s$
Replication (R)	R-1	MSR	MS_R/MS_E	$\sigma^2e + G\sigma^2 r$
Within replication (B)	R(K-1)	MSB	MSB/MS_e	$\sigma^2e + R\sigma^2gs+ R \sigma^2g$
Genotype (G)	G-1	MSG	MS_G/MS_E	$\sigma^2e + R\sigma^2gs+ RS \sigma^2g$
Genotype x season	(G-1)(S-1)	MSG x S	$MS_{G\ x\ S}/ MS_E$	$\sigma^2e^2+ R\sigma^2gs$
Error	SG(R-1)-(RK-1)	MSE		σ^2e

Where: R = number of replication, G=number of genotypes, DF= degree of freedom, K = block, MSS=mean squares of season, MSR = mean squares of replication, MSG = mean squares of genotypes; MSB = mean squares of blocks within replication, $MS_{G\ x\ S}$ = mean square of genotype by season; MSE = mean squares of intra-block error, σg^2 = genotypic variance, σe^2 = environmental variance, σs^2 = season variance, σr^2 = replication variance, and σgs^2 = genotype x season interaction.

3.5.2. Estimation of Genetic Parameters

3.5.2.1. Phenotypic and genotypic variances and coefficients of variation

Estimates of variance components were computed using the formula suggested by Burton and De Vane (1953) as follows.

1) Phenotypic variance $(\sigma^2p) = \sigma^2g + \sigma^2gS/S + \sigma^2e/SR = MSG/RS$

Where : σ^2p=Phenotypic variance, σ^2g=Genotypic variance, σ^2gs=genotype by season variance, σ^2e= Environmental variance, R=number of replication, S= number of season and MSG=mean square of genotype

2) Genotype variance $(\sigma^2g) = (MSG - MSGxS/RS)$

Where: σ^2g = genotypic variance, MSG = mean square of genotype, MSG x S = mean square genotype by season, R= number of replication and S= number of season.

3) Genotype x season interaction variance $(\sigma^2gs) = (MSGxS - MSE/R)$

Where: σ^2gs= genotype by environment interaction variance, MSGxS= genotype by environmental interaction, MSE=mean square of error and R=number of replication.

4) Environmental variance (mean square error) $(\sigma^2e) = MSE$

5) Phenotypic and genotypic coefficient of variations were estimated using the methods suggested by Singh and Chaudhury (1985) as follows

Phenotypic coefficients of variation (PCV) $= \frac{\sqrt{\sigma^2 p}}{\bar{x}} x100$

Genotypic coefficients of variation (GCV) $= \frac{\sqrt{\sigma^2 g}}{\bar{x}} x100$

Where: $\sigma^2 p$ = Phenotypic variation; $\sigma^2 g$ = Genotypic variation and

$\bar{x}$ = Grand mean of the trait under consideration.

Sivasubramaniam and Menon (1973) classified PCV and GCV values greater than 20 % as high, less than 10 % as low, and values between 10 % and 20 % as moderate:

3.5.2.2. Broad Sense Heritability ($h^2 b$)

Heritability in broad sense for all traits were calculated using the formula given by Falconer (1989) and Johnson *et al.*,(1955) and classified as low (below 30 %), medium (30-60 %) and high (above 60 %)

$$\text{Heritability}(h^2 b) = \frac{\sigma^2 g}{\sigma^2 p} \text{ x } 100$$

Where: $h^2 b$ = heritability in broad sense, $\sigma^2 p$ = Phenotypic variance and $\sigma^2 g$ = Genotypic variance

3.5.2.3. Estimation of genetic advance

Anticipated genetic advance for each character at 5 % selection intensity was calculated using the procedure designated by Allard (1999):

$$GA = \frac{k * \sigma ph * h^2 b}{100}$$

Where; GA= expected genetic advance, K= constant (selection differential where K=2.063 at 5% selection intensity), σph = phenotypic variance, $h^2 b$ = heritability in broad sense.

Genetic advance as percent of mean (GAM) was calculated as described by Johnson *et al.* (1955) and classified as low (<10 %), moderate (10-20 %) and high (>20 %):

$$GAM = \frac{GA}{\bar{x}} \text{ X } 100$$

Where: GAM=genetic advance as percent of mean, GA=genetic advance under selection, $\bar{X}$= mean of the population in which selection is effective.

3.6. Association of Characters

3.6.1. Estimation of correlation coefficients

The correlation coefficients among all possible trait combinations at phenotypic (rp) and genotypic (rg) levels were estimated according to Miller *et al.* (1958) as follows:-

Phenotypic covariance $(\sigma p_{xy}) = \sigma g_{xy} + \frac{\sigma_{e\,xy}}{r}$

Genotypic covariance $(\sigma g_{xy}) = \frac{MSPg - MSPe}{r}$

Where, MSPe =mean square of cross product for error, MSPg= mean square of cross products for genotypes, $\sigma^{e}xy$ environmental covariance between x and y, and r=number of replications.

Phenotypic correlation (rp), the observable correlation between two variables, which includes both genotype and environmental components between two variables was be estimated using the formula suggested by Johnson *et al.* (1955) and Singh and Chaudhury (1996) as follows:-

Phenotypic correlation coefficient **(**$rpxy) = (pcovx.y)/(\sqrt{\sigma^2}px.\sigma^2py)$,

Genotypic correlation coefficient$(rgxy) = (gcovx.y)/(\sqrt{\sigma^2}gx.\sigma^2gy)$

Where: rp_{xy} and rg_{xy} are phenotypic and genotypic correlation coefficients, respectively; pcovx.y and gcovx.y are phenotypic and genotypic covariance between variables x and y, respectively; σ^2px and σ^2gx are phenotypic and genotypic variances for variable x; and σ^2py and σ^2gy are phenotypic and genotypic variances for the variable y.

Test of significance of correlation were tested by using "r" tabulated value at n-2 degree of freedom, at 5% and 1% probability level, where n is the number of observation as suggested by Fisher and Yates (1963).

3.6.2. Path Coefficients Analysis:

Path coefficient analysis was conducted as recommended by Wright (1921) and operated out by Dewey and Lu, (1959) using the phenotypic as well as genotypic correlation coefficients to governed the direct and indirect effects of yield components on seed yield based on the following relationship:

$$rij = Pij + \Sigma rikpkj;$$

Where: rij=mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient, Pij=Component of the direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient, Σrikpkj=Summation of components of indirect effect of a given independent trait (i) on the given dependent trait (j) by all other independent traits (k).

Whereas the contribution of the remaining unknown characters measured residual effect estimated as follows:

Residual effect $=\sqrt{1-R^2}$; Where: - $R^2 = \Sigma p_{ij} r_{ij}$

Where, R^2 is the residual factor, P_{ij} is the direct effect of yield by i^{th} characters, and r_{ij} is the correlation of yield with the i^{th} characters.

3.6.3. Cluster analysis

Clustering of genotypes in different sets was carried out by average linkage clustering method. The proper numbers of clusters were determined by following the approach suggested by Copper and Milligan (1988) by looking into three statistics namely Pseudo F, Pseudo t^2 and cubic clustering criteria. The points where local peaks of the CCC and pseudo F-statistic join with small values of the pseudo-t^2 statistic followed by a larger pseudo-t^2 for the next cluster fashion.

3.6.4. Genetic divergence analysis

A measure of a group distance based on multiple traits was given by generalized Mahalanobis D^2 statistics (Mahalanobis, 1936) for quantitative characters in matrix notation, the distance between any two groups was estimated from the following relationship:

$$D^2_{ij} = (X_i - X_j)\, S^{-1}(X_i - X_j):$$

Where: D^2_{ij} = the squared distance between case i and j; X_i and X_j = vectors of the values of cases i^{th} and j^{th} genotypes; S^{-1} = the inverse of pooled variance covariance matrix within groups.

Testing the significance of the squared distance values obtained for a pair of clusters was taken as the calculated value of χ^2 (chi-square) and tested against the tabulated χ^2 values at p-

1 degree of freedom at 1% and 5% probability level, where P = number of characters used for clustering genotypes (Singh and Chaudhury, 1985).

3.6.5. Principal component analysis

Principal components (PCs) with eigen value greater than 1.0 had been used as criteria to determine the number of PCs as suggested by Kaiser (1960). The general formula to compute the scores on the first component extracted in a principal component analysis is:-

$$PC_1=b_{11}(X_1) +b_{12}+\ldots b_{1p} (X_p)$$

Where: PC1 = the subject's score on principal component 1 (the first component extracted); b1p = the regression coefficient (or weight) for observed variable p, as used in creating principal component 1; Xp = the subject's score on observed variable p.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance (ANOVA)

Mean squares of the 20 characters from analysis of variance (ANOVA) at individual seasons and combined over the two seasons are presented in Appendix 1 and 2. Analysis of variance at season one and season two revealed that all the characters were significantly different ($p<0.01$) for all traits.

Combined analysis of variance (ANOVA) across seasons for the different characters is presented in Table 4. Mean square due to genotype showed highly significant differences ($P<0.01$) for all traits, indicating that presence of genotypic variation among the tested sesame genotypes. This finding is in line with Yirgalem *et al.* (2012) who reported highly significant differences among 81 sesame accessions for days to 50% flowering, days to maturity, capsule filling period, plant height, number of capsules per plant, number of primary branches per plant, capsule length, number of seeds per capsule, 1000 seed weight, harvest index, biomass yield, oil content and seed yield per hectare. Moreover, Gadisa *et al.* (2015) reported highly significant differences in 64 sesame populations for days to 50 % flowering, days to maturity, plant height, capsule filling period, number of primary branches, number of branches per plant, number of capsules per plant, biological yield, seed yield, harvest index and thousand seed yield.

The mean squares due to genotype x season interaction effects were highly significant ($P<0.01$) for all traits except capsule width and number of capsule per main axis. It indicates differential performance of genotypes across season. Mohammed *et al.* (2015) reported highly significant differences between variety, environment and genotype by season interaction suggesting differential response of variety across testing environment. The mean square due to seasons showed highly significant difference ($P<0.01$) for most of the traits except for length of first capsule, capsule length and thickness. These results indicated that the phenotypic expression of the characters were different at across seasons. This finding is in line with Hagos *et al.* (2011) and Fiseha *et al*. (2014) who reported significant season effect for 13 sesame genotypes tested across three years.

Table 4. Mean squares of combined analysis of variance for 20 traits of 100 sesame accession evaluated in 2017 and 2018 growing season

Traits	MSG (Df =99)	MSG x season (Df =99)	MS. season (Df =1)	MS. error (Df =369)	CV (%)
DFI	20.104**	4.224**	337.500**	2.643	4.301
DF	51.060**	6.883**	4113.402**	2.711	3.826
$DCFP	25.156**	10.261**	165.375**	2.453	3.135
DM	309.912**	67.793**	20265.282**	26.059	4.855
PLH	1414.643**	486.548**	23826.602**	64.438	7.148
$LCBZ	58.412**	9.514**	3710.107**	3.099	3.609
LFC	0.089**	0.041**	0.002^{ns}	0.027	6.716
CL	0.116**	0.041**	0.002^{ns}	0.024	6.243
CW	0.007**	0.004^{ns}	0.402**	0.003	7.206
CTK	0.004**	0.002**	0.002^{ns}	0.001	6.928
#PBPP	0.074**	0.046**	0.954**	0.024	8.199
$CPMA	22.505**	3.830^{ns}	1117.935**	3.243	6.680
$CPP	121.981**	24.303**	2009.340**	5.827	5.623
$SPC	31.235**	11.610**	58.907**	6.522	5.191
ISR	26.743**	1.824**	29.748**	0.548	16.434
BY	2.271**	1.202**	11.946**	0.253	9.801
$HI	39.622**	4.237**	581.544**	2.254	6.650
TSW	0.541**	0.086**	0.173**	0.031	5.198
OL	19.071**	4.675**	9.627*	2.102	2.876
YLD	227063.000**	30710.500**	188219.050**	9243.730	9.862

Df=degree of freedom, ns=non significant, MS = mean square, G = genotypes, CV = coefficient of variation, *= Significant at ($p< 0.05$),$**= significant\ at$ ($p < 0.01$),DFI = days to flower initation, DF= days to 50 % flowering, DCFP = days to capsule filing period, DM = days to physiologically maturity, PLH = plant height(cm), LCBZ = length of capsule filing zone(cm), LFC = length of first capsule(cm), CL = capsule length(cm), CW = capsule width (cm), CTK = capsule thickness (cm), PBPP = primary branch per plant, CPMA = capsule per main axis, CPP = capsule per plant, SPC = seed per capsule, ISR = percent of inverted shattering resistance (%),BY = biomass yield per hectare (ton), HI = harvest index (%), TSW = 1000 seed weight (g), OL = oil content (%) and YLD = yield $kgha^{-1}$; $ = indicates characters based on arcsine transformed data and, # = indicates characters based on square root transformed data.

4.2. Mean and Range of Yield and Major Yield related Traits

Estimated range, mean and standard deviation of 20 characters are presented in Table 5. The mean performance of 100 sesame genotypes for 20 characters is given in Appendix 4. The mean sesame seed yield ranged from 507 to 1391 $Kgha^{-1}$. More than 50% of the genotypes gave mean seed yield above the grand mean (975 $kgha^{-1}$) and 15% of the genotypes gave mean seed yield greater than standard check Adi. The maximum mean yield was observed from the top five genotypes Acc-203-336-4 (1391 $Kgha^{-1}$) followed by Hirhirbaker sel-1(1389 $Kgha^{-1}$), Acc-111-524-1(1382 $Kgha^{-1}$), Tmax (1378 $Kgha^{-1}$), SPS SIK-#811(1345 $Kgha^{-1}$) which were above the standard check Adi (1236 $Kgha^{-1}$), while the lowest yield was harvested from Acc-No-044 (507$Kgha^{-1}$) which gave mean seed yield below the local check (1101$kgha^{-1}$) (Appendix 4). There is wide mean range between genotypes regarding seed yield. This indicated that variation in existing genotypes due to diverse source of materials tested that differ in their genetic makeup as well as influence of environments. This finding in general agrees with Yirgalem *et al.* (2012) who reported that sesame genotype display tremendous levels of variation in see yield due to diversity of genetic and environmental factors.

Oil content widely ranged from 42 to 55 %. Based on mean performance, 9 % of the genotypes gave above the standard check, whereas 70 % of the genotypes gave above the grand the mean. The highest oil content was recorded in genotypes: SPS-SIK-#811 (55%) followed by Acc-BG-003 (53%), Acc-203-612 (53%), Acc-211-015 (53%), Acc-211-015 (53%) and Adi (52%), while the lowest oil content was observed in Acc-WW-001(4) (42%) which was also below the local check (47%) in Appendix 4. Genotype SPS-SIK-#811 could be one of the potential genotypes possible to advance for the future improvement program having both high yielder and oil content.

Harvest index ranged from 14 to 29 %. The highest harvest index was recorded in genotypes BCS-001(1) (29%), NN-0036-1 (28%), NN-0183-3 (28%), Bounja-fiyel kolet sel-4 (28%), BAR-002 (28%), Acc-203-336-4 (28%) and Adi (25%).While the lowest harvest index was recorded in Acc-No-044 (14%). Relatively, genotypes that exhibited the highest harvest index also gave the highest seed yield per hectare (Appendix 4). Gadisa *et al.* (2015) reported that the high yielding potential of genotypes is associated with increased harvest index. The

highest number of capsule per plant was recorded in genotypes HB-22-FAM-(1-4) (60) followed by Tmax (55), Unknown-sel-3 (53), NN-088-2 (52), Bounja Gobate sel-4 (52) and standard check Adi (46); while the lowest number of capsule per plant was recorded in G-03-1 (33).

Days to 50 % flowering ranged from 39 to 53 days. Among the test genotypes, 57 % showed days to 50 % of flowering lower than the grand mean, indicating there were early flowering compared to other. This finding similar with Desawi *et al.* (2017) who reported a wide range of 40 to 56 for days to 50 % flowering. Days to maturity ranged from 95 to 126 days. Among the tested genotypes 53 % showed days to maturity lower than the grand mean, indicating there were early maturing compared to other. These early maturing genotypes could be promising genotypes for short rainy agro ecology, while the late maturing types of genotypes are for long rainy area. Gadisa *et al.* (2015) reported a wide range of 116 to 146 days for date of maturity.

Shattering ranged from 1.39 to 11.88. The highest pod shattering resistance was recorded in Acc-00019 (12%), Bounja-filwuha sel-6 (10.8%), NN-0036-1(10.4%), Acc-203-630 (10.1%), HB-38-FAM-2 BAR Grey (9.5%); while the lowest was displayed in Acc-111-821(1.8%). According to WARC (2012) pod shattering resistance is classified as supper shattering <10%, shattering 10 to 50%, non-shattering 50-80 %, and direct combine >80 % and indehiscent accessions retained all the seed. Based on this delineation, 96 % of the genotypes studied were grouped under supper shattering and 4% of the genotypes were grouped under shattering type. Similarly, Langham (2001) reported that sesame accession collected from different countries of the world were shattering type.

Table 5. Estimates of ranges, mean, standard deviation (SD), Variance components, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2b), expected genetic advance (GA) and genetic advance as percent of the mean (GAM) for 20 characters combined over the two seasons.

Traits	Range		Mean ±SD	σ^2e	σ^2p	σ^2g	PCV (%)	GCV (%)	h^2b (%)	GA	GAM (%)
	Min	Max									
DFI	33.759	43.881	37.8±1.63	2.6428	3.3507	2.6467	4.84	4.30	78.99	2.98	7.89
DF	38.549	53.673	43.0±1.65	2.7112	8.5101	7.3628	6.78	6.30	86.52	5.21	12.10
DCFP	46.3(52)	56.6(69)	50.0(58)±1.57	2.4534	4.1927	2.4827	4.10	3.15	59.21	2.50	5.01
DM	94.555	127.07	105±5.10	26.0587	51.6520	40.3531	6.84	6.04	78.12	11.58	11.03
PLH	84.099	152.08	112±8.03	64.4379	235.7738	154.6825	13.67	11.07	65.61	20.78	18.56
LCBZ	40.9(43)	56.8(68)	48.8(56)±1.76	3.0988	9.7353	8.1496	6.40	5.85	83.71	5.39	11.05
LFC	2.104	2.727	2.43±0.16	0.0265	0.0149	0.0081	5.02	3.71	54.50	0.14	5.64
CL	2.184	2.898	2.49±0.16	0.0241	0.0193	0.0124	5.58	4.47	64.42	0.18	7.41
CW	0.682	0.8487	0.76±0.05	0.0030	0.0012	0.0005	4.48	3.01	45.18	0.03	4.18
CTK	0.451	0.613	0.51±0.04	0.0013	0.0007	0.0004	5.24	3.93	56.23	0.03	6.08
PBPP	1.57(2)	2.26(5)	1.91(4)±0.16	0.0245	0.0124	0.0047	5.83	3.60	38.14	0.09	4.59
CPMA	22.0(15)	32.6(26)	27(20)±1.80	3.2426	3.7509	3.1126	7.19	6.54	82.98	3.32	12.30
CPP	32.524(28)	60.26(74)	42.95(46)±2.41	5.8273	20.3301	16.2796	10.50	9.39	80.08	7.45	17.35
SPC	42.99(48)	54.30(67)	49.19(57)±2.55	6.5222	5.2059	3.2708	4.64	3.67	62.83	2.96	6.01
ISR	1.3874	11.882	4.50±0.74	0.5480	4.4571	4.1531	46.87	45.24	93.18	4.06	90.10
BY	3.6192	6.7627	5.13±0.50	0.2532	0.3786	0.1783	11.98	8.22	47.10	0.60	11.64
HI	14.26(6)	29.323(24)	22.57(15)±1.50	2.2544	6.6037	5.8975	11.38	10.75	89.31	4.73	20.97
TSW	2.5612	4.0769	3.41±0.18	0.0314	0.0901	0.0758	8.80	8.07	84.10	0.52	15.27
OL	42.232	55.398	50.4±1.45	2.1015	3.1784	2.3992	3.54	3.07	75.48	2.78	5.51
YLD	506.92	1391	975±96.14	9243.7300	37843.8333	32725.4133	19.95	18.56	86.47	347.05	35.60

() = represents non transformed data, DFI=days to flower initiation, DF= days to 50 % flowering, DCFP= days to capsule filling period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield $kgha^{-1}$

4.3. Estimates of Genetic Parameters

4.3.1. Estimates of variance components and coefficients of variation

Estimates of phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) are given in Tables 5. The phenotypic coefficient of variation ranged from 3.54 % for oil content to 46.87% for percent of shattering resistance. At the same time the genotypic coefficients of variation ranged from 3.07 % for oil content to 45.43 % for percent of shattering resistance. In this study, the GCV values were lower than that of PCV indicating that the environment had an important role in the expression of these characters. Commonly quantitative characters or agronomic traits are highly affected by the environment. According to Sivasubramaniam and Menon (1973) PCV and GCV values greater than 20 % are regarded as high, whereas values less than 10% are considered to be low, and values between 10% and 20% are moderate. Based on this delineation shattering resistance had high PCV and GCV values (46.87, 45.4 %); whereas, plant height (13.67, 11.07 %), harvest index (11.38, 10.8%) and seed yield per hectare (19.95, 18.56%) had moderate PCV and GCV values. It indicates the phenotypic expression of the characters would be a good indication of genetic potential, and the diverse genotypes can provide materials for a sound breeding program. This result was in agreement with Gadisa *et al.* (2015) who reported medium PCV and GCV values for seed yield, while high PCV and GCV value for on harvest index in sesame genotypes.

Medium PCV and low GCV was recorded for number of capsule per plant (10.50, 9.39%) and biomass yield (11.98, 8.22%), indicating that these trait phenotypically varies, but there is influence of the environment. Low PCV and GCV values were recorded for days to flower initation, days to 50 % flowering, days to capsule filling period, days to maturity, primary branch per plant, length of capsule bearing zone, length of first capsule, capsule length, capsule width, capsule thickness, number capsule per main axis, number of seed per capsule and oil content. This implies that high influenced of environment. These low value indicates that the need for variability either by hybridization or mutation strategies. This finding is in line with Gadisa *et al.* (2015) who reported low PCV and GCV values for days to 50 % flowering, days to capsule filling period, days to maturity and oil content. Similarly,

Mohammed *et al.* (2015) found low PCV and GCV values for days to 50% flowering, days to maturity, primary branch per plant and oil content.

In this study the PCV values was found to be greater than its corresponding estimates of GCV for all traits, indicating the involvement of the environment in the expression of these traits; however, the difference between PCV and GCV values was small for most of the studied characters signifying minimal environmental effects on these characters. Singh *et al.* (2000) shown that the phenotypic coefficients of variation was higher than the genotypic coefficient of variation for all similar characters.

4.3.2. Estimates of broad sense heritability (h^2b)

Heritability ranged from 38.14% for primary branch per plant to 93.18% for percentage of shattering resistance (Table 5). Desawi *et al.* (2017) reported heritability values ranged from 0.03% for capsule length to 92.72% for number of capsule per plant. The reason for this deviating from my result is due to the nature of testing material and environment considered.

According to Johnson *et al*. (1955) h^2b was classified as low (below 30%), medium (30-60) and high (above 60%). Based on this benchmark, the characters days to flower initiation (78.99%), days to 50 % flowering (86.52%), maturity date (78.12%), plant height (65.77%), length of capsule bearing zone (83.71%), capsule length (64.42%), number of capsule per main axis (82.98%), number of capsule per plant (80.08%), number of seed per capsule (62.83%), percentage of shattering resistance (93.18%), harvest index (89.31%), 1000 seed weight (84.10%), oil content (75.48%) and seed yield per hectare (86.47%) had high heritability. This indicates the effect of genetic variation in the inheritance of the traits and it gives an opportunity for sesame breeder to exploit there traits by selecting on the bases of phenotypic performance. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. Hamid *et al.* (2003) obtained high heritability estimates for days to 50 % flowering, days to maturity and 1000 seed weight. Similarly, Prithviraj *et al.* (2015) obtained high heritability for days to 50 % flowering, days to maturity, plant height, number of capsules on main axis, number of capsules per plant, number of seeds per capsule, seed yield, 1000 seed weight and oil content.

Medium heritability was obtained for date of capsule filling period (59.21%), length of first capsule (54.50%), capsule width (45.18%), capsule thickness (56.23%), biomass yield (47.10%) and primary branch per plant (35.48%). Medium heritability implies great role of environment on the expression of these characters. Prithviraj *et al.* (2015) obtained medium heritability for length of first capsule, capsule width and primary branch per plant.

4.3.3. Estimates of genetic advance

Estimates of genetic gain for seed yield at WARC 347.05 $kgha^{-1}$ (Table 5) indicating that whenever selecting the best 5% high yielding genotypes as parents, mean seed yield of progenies could be improved from 975 to 1322.05 $kgha^{-1}$ over the base population.

Percent of shattering (90.10 %) had high GAM followed by seed yield per hectare (35.60 %) and harvest index (20.97 %), whereas days to 50 % flowering (12.10 %), date of maturity (11.02 %), plant height (18.51 %), length of capsule bearing zone (11.05 %), number of capsule per main axis (12.30 %), number of capsule per plant (17.35 %), biomass yield (11.64 %) and 1000 seed weight (15.27 %) had moderate GAM. This implies the weak influence of environment in expression of the characters. Selection based of traits with a relatively high as well as moderate genetic advance as percent of mean will result in the improvement of the performance of the genotypes for the traits.

According to Johnson *et al.* (1955) high heritability estimates along with high GAM is usually more helpful in predicting of gain under selection than heritability estimates alone. In this study, high heritability coupled with high genetic advance as percent of mean was obtained for percent of shattering resistance, harvest index and seed yield, whereas high heritability coupled with moderate genetic advance as percent of mean was obtained for days to 50 % flowering, date of maturity, plant height, length of capsule bearing zone, number of capsule per main axis, number of capsule per plant and 1000 seed weight and signifying the greater role of additive gene action for the inheritance of these character and selection will be effective. This finding is in line with Banergee and Kole (2006) who obtained moderate to high estimates of heritability accompanied by moderate to high GAM for plant height, capsules per plant, seed yield and 1000 seed weight. Gawali *et al.* (2007) evaluated 50 genotypes and found high heritability coupled with GAM in seed yield, moderate heritability

coupled with moderate GAM number of capsules per plant and 1000 seed weight. Similarly, Parameshwarappa *et al.* (2009) evaluated 146 genotypes and obtained high heritability coupled with high GAM for seed yield, whereas high heritability with moderate GAM was obtained for days to 50 % flowering, plant height and days to maturity.

Seed per capsule, days to flower initation, capsule length and oil content had high heritability coupled with low GAM. This implies weak influence of environment but prevalence of non-additive gene action indicating simple selection will be less effective. Hence, heterosis breeding or hybridization followed by repeated selection (recurrent selection) would be recommended for the improvement of such traits. This finding is similar to the finding of Banerjee *et al.* (2006) and Padmavathi (2007) who reported that oil content had higher heritability values together with low GAM.

Traits with relatively medium heritability coupled with low GAM include days to capsule filling period, length of first capsule, width and thickness, primary branch and biomass yield recorded. For these traits breeder may not benefits from selection as well as hybridization based on the above mention traits due to high involvement of environment. Hence, it is better to create variation by hybridization and mutation rather than selection.

Relatively medium PCV and GCV, high heritability coupled with moderate GAM was obtained for plant height, harvest index and seed yield per hectare, while all for variance components high value was recorded for percent of shattering resistance. This implies the genetic expression of genotype and transmissibility of the trait from parent to offspring.

4.4. Correlation Coefficient Analysis

4.4.1. Phenotypic and genotypic correlation coefficient of seed yield with other characters

Phenotypic (rp) and genotypic (rg) correlation estimates between the various characters are presented in Tables 6 and 7, respectively. The phenotypic correlation ranged from 0.056 for number of seed per capsule to 0.574 for harvest index. Seed yield showed positive and significant phenotypic association with length of capsule bearing zone (rp= 0.265**), length of first capsule (rp= 0.243**), capsule length (rp= 0.225**), number of capsule per main axis

(rp= 0.489**), number of capsule per plant (rp = 0.491**), harvest index (rp= 0.574**), 1000 seed weight (rp= 0.214 **) and oil content (rp= 0.226**). This signified that the improvement of one trait will simultaneously improve the other. Ahadu (2008) and Fazal *et al.* (2011) reported that number of capsules per plant had significant positive correlation with seed yield. This finding also agrees with the findings of Yirgalem *et al.* (2012) who reported that seed yield had positive significant associated with harvest index. Moreover, according to Mohammed *et al.* (2015) number of capsule per plant, harvest index and 1000 seed weight had positively and significantly associated with seed yield. Furthermore, Prithvras *et al.* (2015) reported that seed yield had positively and significantly associated with number of capsule per main stem, number of capsule per plant, capsule length, 1000 seed weight and oil content.

On the other hand, seed yield showed negative and significant phenotypic correlation with date of flower initiation (rp = -0.241**), date of 50 % flowering (rp= -0.277**), date of maturity (rp= -0.249**), percent of shattering resistance (rp= -0.219**) and biomass yield (rp= -0.146*), which implies separate improvement is recommended. The other remaining characters had non-significant association with yield.

The genotypic correlation ranged from 0.031 for number of seed per capsule to 0.600 for harvest index (Table 7). Seed yield showed positive and significant genotypic association with length of capsule bearing zone (rg = 0.250*), length of first capsule (rg = 0.259**), capsule length (rg = 0.238*), number of capsule per main axis (rg = 0.511**), number of capsule per plant (rg = 0.503**), harvest index (rg = 0.600**) and oil content (rg = 0.221*), indicating the existence of pleiotropic as one of the genetic causes for correlation. The positive and significant correlation between seed yield and the above mentioned traits signified that the improvement of one trait will simultaneously improve the other. This finding is similar with the result of Prithvras *et al.* (2015) who reported that seed yield had positive and significant relationship with number of capsule per main stem, number of capsule per plant, capsule length and oil content at genotypic level. Mothilal and Manoharan (2006) reported seed yield had positive and significant correlation with capsules on main stem. Engin *et al.* (2010) considered 345 accessions in his study and found that the number of capsules per plant had significant and positive association with seed yield. Furthermore, Desawi *et al.* (2017)

reported that seed yield had positive and significant association with length of capsule bearing zone, capsule length and number of capsule per plant.

On the other hand, seed yield showed negative and significant genotypic correlation with date of flower initation (rg = -0.244*), date of 50 % flowering (rg = -0.281**), date of maturity (rg = -0.281**) and percent of shattering resistance (rg = -0.242*). This indicates that the improvements of one character leads to decrease the other, as a result independent improvement of the character must be followed. It had non-significant association with the rest of the characters. Similarly, Engin *et al.* (2010) reported that maturity date, days to flower initiation and days to 50 % flowering showed negative correlation with seed yield. Akbar *et al.* (2011) also obtained that maturity date, days to flower initiation and days to 50 % flowering showed negative correlation with seed yield.

4.4.2. Phenotypic correlation coefficient among seed yield related traits

Date of flower initation and date of 50 % flowering showed positive and significant correlation with date of maturity, plant height, primary branch per plant, percent of shattering resistance and biomass yield. This indicates the possibility of simultaneous improvement of these traits. This finding is in line with Yirgalem *et al*. (2012) who reported that day to 50 % flowering, days to maturity and plant height had positive and significant association with biomass and primary branch per plant. Date of flower initation and date of 50 % flowering showed negative and significant correlation with capsule length, capsule per main axis, harvest index, 1000 seed weight and oil content.

Maturity date had positive and significance associated with plant height, length of capsule bearing zone, primary branch per plant, percent of shattering resistance and biomass yield, whereas it had negative and highly significance relationship with harvest index and 1000 seed weight and significant with oil content. Its association the other remaining characters were non-significant; which indicates the longer plant, longer capsule bearing zone and larger biomass and this type of genotypes have late maturing types. In this study those traits which had positive and significant association with plant height were length of capsule bearing zone, primary branch per plant, capsule per main axis, capsule per plant, percent of shattering resistance, biomass yield and capsule per plant; while it had negative and significant

associated with harvest index and 1000 seed weight. This result was in line with Yirgalem *et al.* (2012) who stated that plant height was positively and significantly associated with length of capsule bearing zone, primary branch per plant, capsule per plant, and biomass yield; but negative and significant with harvest index and 1000 seed weight.

Length of capsule bearing zone had positive and significant correlation with length of first capsule, capsule length, capsule per main axis, capsule per plant, biomass yield and oil content. This finding was in line with Desawi *et al.* (2017) who suggested that length of capsule bearing zone had positive and significant associated with number of capsule per plant, capsule length and oil content.

Capsule per plant had positive and significant association with biomass, harvest index and oil content, while negative and significant association with percentage of shattering resistance. Number of seed per capsule had positive and highly significant associated with oil content, while negative and significant relationships with 1000 seed weight. It had non-significant association with rest of the traits.

Percentages of shattering resistance had significant positive associated with biomass yield, while it had negative and significance relationship with harvest index and oil content. Those traits which had negative and significant relationship with biomass yield were harvest index and 1000 seed weight. Harvest index had positively and significantly associated with 1000 seed weight and oil content.

Table 6. Phenotypic correlation coefficient for studied quantitative traits studied

Traits	DFI	DF	DCF	MD	PLH	LCBZ	LFC	CL	CW	CTK	BPP	CPMA
DFI		0.801**	0.159**	0.617**	0.453**	0.010	-0.150**	-0.162**	0.059	0.072	0.215**	-0.187**
DF			0.268**	0.806**	0.627**	0.069	-0.119*	-0.121*	0.061	0.084	0.210**	-0.162**
DCF				0.716**	0.459**	0.225**	-0.053	-0.034	0.132*	0.210**	0.101	0.047
MD					0.695**	0.179**	-0.125*	-0.114*	0.082	0.149*	0.198**	-0.059
PLH						0.557**	0.098	0.074	0.044	0.181*	0.262**	0.213**
LCBZ							0.317**	0.345*	0.055	0.248**	0.058	0.588**
LFC								0.772**	-0.089	0.034	0.043	0.412**
CL									-0.016	0.097	-0.083	0.425**
CW										0.546**	0.037	-0.064
CTK											0.012	0.134*
BPP												0.064
CPMA												
CPP												
SPC												
ISR												
BY												
HI												
TSW												
OL												
YLD												

Table.6 (Continue)

Traits	CPP	SPC	ISR	BY	HI	TSW	OL	YLD
DFI	-0.109	0.068	0.227**	0.347 **	-0.426**	-0.362**	-0.155**	-0.241**
DF	-0.128*	-0.047	0.307**	0.490**	-0.578**	-0.410**	-0.116*	-0.277**
DCF	0.049	-0.077	0.190**	0.191**	-0.274**	0.045	-0.084	-0.104
MD	-0.055	-0.062	0.293**	0.440**	-0.541**	-0.243**	-0.125*	-0.249**
PLH	0.134*	0.032	0.176**	0.531**	-0.417**	-0.221**	0.093	-0.100
LCBZ	0.413**	0.059	-0.109	0.265	0.058	0.038	0.352**	0.265**
LFC	0.237**	0.261**	-0.191**	0.007	0.093	-0.014	0.348**	0.243**
CL	0.178**	0.250**	-0.196**	-0.006	0.105	0.034	0.335**	0.225**
CW	-0.076	-0.050	0.011	0.011	0.030	0.203**	-0.121*	-0.069
CTK	0.090	-0.049	-0.062	0.207**	0.028	0.045	0.102	-0.064
PBPP	0.272**	0.001	0.112	0.211**	0.070	0.067	-0.064	0.106
CPMA	0.719**	0.157**	-0.240**	0.103	0.275**	-0.033	0.370**	0.489**
CPP		0.109	-0.216**	0.116*	0.294**	-0.082	0.226**	0.491**
SPC			-0.019	0.066	-0.039	-0.148*	0.196**	0.056
ISR				0.141	-0.212**	0.009	-0.305**	-0.219**
BY					-0.317**	-0.222**	0.106	-0.146*
HI						0.547**	0.193**	0.574**
TSW							-0.030	0.214**
OL								0.226**
YLD								1

*= Significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF= days to 50 % flowering, DCF= days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%),BY=biomass yield per hectare (ton), HI=harvest index (%),TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield $kgha^{-1}$

4.4.3. Genotypic Correlation coefficient among yield related traits

Genotypic (rg) correlation estimates between the various characters are presented in Tables 7. Date of flower initation and date of 50 % flowering showed positive and significant correlation with date of capsule filling period, date of maturity, plant height, primary branch per plant, percent of shattering resistance and biomass yield; whereas, it had negative and significant correlation with harvest index, 1000 seed weight, number of capsule per main axis, number of capsule per plant and oil content at genotypic level. This indicates late flowering genotypes have longer capsule filling period and date of maturity; tallest plant have numbers of primary branch and large biomass yield the reverse is true for early flowering, capsule filling and early maturing type have short in plant, higher harvest index and 1000 seed weight becomes we have get higher yielder. In short the tallest and late maturing type have long capsule filling period. This is in agreement with the result of Yirgalem *et al.* (2012) who reported that days to 50% flowering had positive and significant association with plant height, days to maturity, biomass yield per hectare and number of primary branches per plant.

Date of maturity had positive and significant association with plant height, percent of shattering resistance, biomass yield, primary branch per plant, capsule thickness; whereas, it had negative and significant relationship with harvest index and 1000 seed weight. This indicates those genotypes with longer date of maturity have taller plant height, more branches, higher biomass yield and lower harvest index. Plant height had positive and significant association with length of capsule bearing zone, capsule thickness, branch per plant, biomass yield and capsule per main axis; while it had negative and significant correlation with harvest index and 1000 seed weight and had non-significant association with the other traits at genotypic level. This indicates that the taller the plant the longer capsule bearing zone and have more primary branch consequently large biomass yield. Capsule per main axis and capsule per plant showed positive and significant associate with harvest index and oil content. Seed per capsule revealed that positive and significant association with oil content. However, negative and significant relationship with 1000 seed weight at genotypic level. These indicates more number of seed per capsule reduce thickness of the seed. This result agrees with the result of Desawi *et al.* (2017) who reported that the number of seed per capsule had

positive and significantly associated oil content, while negative and significantly with 1000 seed weight.

Harvest index had positive and significant association with 1000 seed weight; this implies the larger biomass is the lower the harvest index. This result is agreement with Yirgalem *et al.* (2012) report that harvest index had negative and significant correlation with biomass yield per hectare.

Table 7. Genotypic correlation coefficient for studied quantitative traits

Traits	DFI	DF	DCF	MD	PLH	LCBZ	LFC	CL	CW	CTK	PBPP	CPMA
DFI		0.869**	0.246**	0.747**	0.569**	0.031	-0.197	-0.202*	0.017	0.027	0.278**	-0.171
DF			0.355**	0.890**	0.711**	0.089	-0.149	-0.139	0.039	0.078	0.280**	-0.151
DCF				0.735**	0.503**	0.237*	-0.073	-0.073	0.237*	0.288**	0.111	0.021
MD					0.769**	0.192	-0.148	-0.143	0.149	0.203*	0.262**	-0.089
PLH						0.562**	0.079	0.046	0.068	0.272**	0.309**	0.205*
LCBZ							0.357**	0.364**	0.107	0.362**	0.036	0.632**
LFC								0.875**	-0.217*	0.067	-0.148	0.448**
CL									-0.103	0.140	-0.255*	0.437**
CW										0.571**	0.004	-0.047
CTK											0.016	0.246*
PBPP												-0.045
CPMA												
CPP												
SPC												
ISR												
BY												
HI												
TSW												
OL												
YLD												

Table 7 (continue)

Traits	CPP	SPC	ISR	BY	HI	TSW	OL	YLD
DFI	-0.111	0.115	0.261**	0.439**	-0.488**	-0.385**	-0.152	-0.244*
DF	-0.134	-0.034	0.328**	0.556**	-0.621**	-0.432**	-0.115	-0.281**
DCF	0.046	-0.138	0.215*	0.230*	-0.351**	-0.016	-0.156	-0.148
MD	-0.064	-0.086	0.323**	0.515**	-0.626**	-0.328**	-0.158	-0.281**
PLH	0.128	0.001	0.185	0.600**	-0.485**	-0.299**	0.070	-0.150
LCBZ	0.421**	0.026	-0.118	0.306**	0.046	-0.002	0.364**	0.250*
LFC	0.231*	0.311**	-0.250*	0.044	0.060	-0.061	0.409**	0.259**
CL	0.154	0.311**	-0.238*	-0.002	0.080	0.008	0.374**	0.238*
CW	-0.091	-0.015	0.019	0.002	0.047	0.351**	-0.177	-0.074
CTK	0.139	0.014	-0.088	0.258*	0.037	0.114	0.173	-0.039
PBPP	0.293**	-0.036	0.131	0.271**	0.033	0.044	-0.107	0.086
CPMA	0.772**	0.151	-0.280**	0.115	0.275**	-0.103	0.408**	0.511**
CPP		0.115	-0.232*	0.126	0.305**	-0.118	0.238*	0.503**
SPC			-0.024	0.104	-0.061	-0.233*	0.222*	0.031
ISR				0.153	-0.231*	0.009	-0.345**	-0.242*
BY					-0.374**	-0.280**	0.126	-0.181
HI						0.581**	0.175	0.600**
TSW							-0.093	0.191
OL								0.221*
YLD								1

*= Significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF= days to 50 % flowering, DCF= days to capsule filing period, DM=days to physiologically mature, PLH=plant height (cm), LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%), BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield $kgha^{-1}$

4.5. Path Coefficient Analysis

4.5.1. Phenotypic path coefficient analysis

In the current study, traits that showed significant correlation with grain yield (kgha^{-1}) were advanced to path coefficient analysis at phenotypic levels. Phenotypic path coefficient analysis between yield and yield related traits is presented in Table 8.

Harvest index had the highest direct (0.491) on seed yield with positive and highly significant association (0.574**). The magnitude of the direct effect was almost equivalent to that of phenotypic correlation coefficient. This justifies that the correlation explains the true association and direct selection through harvest index would be effective in improving seed yield of sesame.

Biomass yield had negative direct effect on seed yield with negative and significant association. The indirect effects through other traits were negligible. Therefore, the phenotypic correlation with seed yield was largely due to the direct effects.

Capsule per plant and capsule per main axis had positive direct effects. The phenotypic correlations they had with seed yield were significant and positive. Their indirect effect via other traits was mostly positive and negligible. Hence, their positive correlation with seed yield was mainly due to their direct effect.

Days to 50 % flowering positive direct effects, however the phenotypic correlation of days to 50 % flowering was negative and significant; while the indirect effect of via other traits negligible. This finding is similar with Mohammed *et al.* (2015) who reported that number of capsules per plant had maximum positive direct effect on seed yield followed by harvest index. The path analysis revealed the residual value of 0.717 which means the characters in the path analysis expressed the variability in grain yield by 28.3%.

Table 8. Phenotypic path coefficient analysis indicating the direct (**diagonal**) and indirect (off diagonal) effect of the characters

YLD	DFF	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	BY	HI	TSW	OL	rp
DFI	**-0.076**	0.170	-0.017	0.000	-0.011	0.000	-0.031	-0.024	-0.009	-0.037	-0.209	0.001	0.002	-0.241**
DF	-0.061	**0.213**	-0.022	0.003	-0.009	0.000	-0.027	-0.028	-0.012	-0.052	-0.284	0.001	0.001	-0.277**
MD	-0.047	0.171	**-0.027**	0.008	-0.009	0.000	-0.010	-0.012	-0.011	-0.047	-0.266	0.000	0.001	-0.249**
LCBZ	-0.001	0.015	-0.005	**0.047**	0.023	-0.001	0.098	0.089	0.004	-0.028	0.028	0.000	-0.004	0.265**
LFC	0.011	-0.025	0.003	0.015	**0.073**	-0.002	0.068	0.051	0.007	-0.001	0.046	0.000	-0.003	0.243**
CL	0.012	-0.026	0.003	0.016	0.056	**-0.003**	0.071	0.039	0.007	0.001	0.052	0.000	-0.003	0.225**
CPMA	0.014	-0.034	0.002	0.028	0.030	-0.001	**0.166**	0.155	0.009	-0.011	0.135	0.000	-0.004	0.489**
CPP	0.008	-0.027	0.001	0.019	0.017	0.000	0.119	**0.216**	0.008	-0.012	0.144	0.000	-0.002	0.491**
ISR	-0.017	0.065	-0.008	-0.005	-0.014	0.001	-0.040	-0.047	**-0.038**	-0.015	-0.104	0.000	0.003	-0.219**
BY	-0.026	0.104	-0.012	0.012	0.001	0.000	0.017	0.025	-0.005	**-0.106**	-0.155	0.000	-0.001	-0.146*
HI	0.032	-0.123	0.015	0.003	0.007	0.000	0.046	0.064	0.008	0.034	**0.491**	-0.001	-0.002	0.574**
TSW	0.027	-0.087	0.007	0.002	-0.001	0.000	-0.006	-0.018	0.000	0.023	0.268	**-0.001**	0.000	0.214**
OL	0.012	-0.025	0.003	0.016	0.025	-0.001	0.062	0.049	0.011	-0.011	0.095	0.000	**-0.010**	0.226**

Residual=0.717, *=significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF=days to 50 % flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone(cm), LFC=length of first capsule(cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=% inverted shattering resistance (%),BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%), YLD=yield $kgha^{-1}$ and rp = phenotypic correlation value

4.5.2. Genotypic path coefficient analysis

In the current study, traits that showed significant correlation with grain yield ($kgha^{-1}$) were advanced to path coefficient analysis at genotypic level. Genotypic path coefficient analysis between yield and yield related traits are given in Table 9.

Harvest index had a positive direct effect (0.593) on seed yield which was almost equivalent to the correlation coefficient (0.600**). This suggests the true relationship and direct selection through this character will be effective. Date of flower initation had negative direct effect. The correlation coefficient with seed yield was negative and significant. The indirect effects via other traits were negligible. Hence, the genotypic correlation with seed yield was largely due to the direct effect.

Capsule per main axis, capsule per plant and length of first capsule had positive direct effects. The genotypic correlations they had with seed yield were significant and positive. Their indirect effects via other traits were mostly positive and negligible. Hence, their positive correlation with seed yield was mainly due to their direct effect. This finding is similar with Mohammed *et al.* (2015) who reported that number of capsules per plant had maximum positive direct effect on seed yield followed by harvest index. The genotypic path coefficient analysis exhibited the residual value of 0.688, indicating that the characters in the path analysis expressed the variability in seed yield by 31.20%, the remaining 68.8% the contribution of other characters are not considered in the path analysis and environmental factor.

Table 9. Genotypic Path coefficient analysis indicating the direct (**diagonal**) and indirect (off diagonal) effect of the characters

YLD	DFI	DF	MD	LCBZ	LFC	CL	CPMA	CPP	ISR	HI	OL	rg
DFI	**-0.090**	0.237	-0.016	-0.001	-0.029	0.004	-0.037	-0.018	-0.014	-0.289	0.009	-0.244*
DF	-0.078	**0.272**	-0.019	-0.003	-0.022	0.003	-0.033	-0.022	-0.018	-0.368	0.007	-0.281**
MD	-0.067	0.242	**-0.022**	-0.006	-0.022	0.003	-0.019	-0.010	-0.018	-0.371	0.009	-0.281**
LCBZ	-0.003	0.024	-0.004	**-0.030**	0.053	-0.008	0.138	0.068	0.006	0.027	-0.021	0.250*
LFC	0.018	-0.041	0.003	-0.011	**0.148**	-0.019	0.098	0.037	0.014	0.036	-0.024	0.259**
CL	0.018	-0.038	0.003	-0.011	0.130	**-0.022**	0.095	0.025	0.013	0.047	-0.022	0.238*
CPMA	0.015	-0.041	0.002	-0.019	0.066	-0.009	**0.218**	0.125	0.015	0.163	-0.024	0.511**
CPP	0.010	-0.037	0.001	-0.012	0.034	-0.003	0.168	**0.162**	0.013	0.181	-0.014	0.503**
ISR	-0.024	0.089	-0.007	0.003	-0.037	0.005	-0.061	-0.038	**-0.055**	-0.137	0.020	-0.242*
HI	0.044	-0.169	0.014	-0.001	0.009	-0.002	0.060	0.049	0.013	**0.593**	-0.010	0.600**
OL	0.014	-0.031	0.003	-0.011	0.061	-0.008	0.089	0.039	0.019	0.104	**-0.058**	0.221*

Residual=0.688, *= significant at $p \leq 0.05$, ** highly significant at $p \leq 0.01$, DFI=days to flower initation, DF= days to 50 % flowering, DM=days to physiologically mature, LCBZ=length of capsule filing zone (cm), LFC=length of first capsule (cm), CL=capsule length (cm), CPMA=capsule per main axis, CPP=capsule per plant, ISR=percent of inverted shattering resistance (%), HI=harvest index(%), OL=oil content (%),YLD=yield $kgha^{-1}$ and rg = genotypic correlation value

4.6. Multivariate Analysis

4.6.1. Cluster analysis

The D^2 values based on the pooled mean of genotypes resulted in classifying the 100 sesame genotypes into seven clusters (Table 10) (Appendix 1). This showed that the tested sesame genotypes were moderately divergent. There was statistically approved difference between most of the clusters.

Cluster III contained the maximum number of sesame genotypes 28 (28%), followed by cluster I 21 (21%), cluster V 15 (15%), cluster IV 13 (13%) and cluster II 12 (12%) genotypes. It also comprising two checks (standard check Adi inter in to cluster IV and local check in cluster III). In contrast cluster VI and VII the smallest number of genotypes 9 (9%) and 2 (2%), respectively.

The introduced (exotic) genotypes were almost distributed in all clusters except cluster VII, indicating the existence of genotypes from the same origin might have different genetic background. The first cluster consists of twenty one genotypes; out of which fifteen genotypes were Ethiopian collections, while six were introduced (Ying White–2, China FAO (ACC-68-542), HB-49FAM-2–2, Acc-203–630, Acc-210-991–4 and Acc-203-336–2). The second cluster comprised of twelve genotypes, nine of them originated from Ethiopia and the rest are introduced materials (Acc-210-986–1, HB-22-FAM (1-4), HB-38FAM-2 BAR Grey). The third cluster consisted of twenty eight sesame genotypes, twenty two of them originated from Ethiopia including the local check and six exotic materials (Unknown Nguara sel-9, BAR–002, Unknown-sel–3, Bering bowng, USR-82 # 171 NS and Venzula–1). The fourth cluster holds thirteen genotypes out of these materials nine of them were Ethiopian collection and one standard check (Adi), whereas three were exotic materials viz Acc-203–612, Acc-203–623 and Unkown Kaja sel–4. Cluster five consists of fifteen genotypes out of which ten were from local collection and five were from introduced materials namely JAPAN-651, BAR–0004, Win black (Tall)–2, SSBS-(9-2)-3 and Acc-203–623. Cluster six comprises nine sesame genotypes; five of them local collection and four of them introduced (SPS-SIK- # 811, Tmax, Acc-203-336–4 and X-30/40 # 403) and the last cluster contained only two sesame genotypes originated from Ethiopia.

Genotypes from Ethiopia appeared in all clusters, although the majority of its genotypes appeared in cluster I and cluster III. In addition, the genotypes from Ethiopia were distributed in cluster VII different clusters which suggested that the genotypes from Ethiopia were relatively more variable. Regarding FAO genotypes, they were distributed in out of VII clusters, probably reflecting less variation among genotypes.

The overlapping of clusters patterns with respect to genotypes could be explained as lack of differentiation among the FAO and Ethiopia genotypes, probably arising partly due to gene flow (Alarmelu and Ramanathan, 1998). In general, it might be possible to state that genotypes from Ethiopia were relatively more variable in their clustering pattern compared to those from the FAO (Table 10).This indicated that in the future sesame genotypes exploitation endeavors, due emphasis must be given to the major sesame producing regions as Ethiopia is the center of origin for sesame (Vavilov, 1926)

Table 10. Distribution of the 100 sesame genotypes into different clusters at Werer.

Cluster	Number of Genotypes	Proportion	Name of genotypes
Cluster I	21	21 %	Acc–00065, W–118, Acc-No 04 + 06 + 07, Ying White–2, Acc-No–05, Acc-EW–006, Acc-BG–001, NN–0054, AW–001, EW-017(1), Acc-WW-001(6), Acc-024-sel–1, Acc–044, Acc-No–049, BACKO-MW–42, China FAO (ACC- 68-542), Acc-203-336–2, HB-49 FAM-2–2, Acc-20–630, Acc-210-991–4 and EW-17(5) x NS-001 # 48,
Cluster II	12	12 %	Acc-211–015,Acc-EW-012(7),Acc-210-986–1,Acc-205–344,NN–0021,HB-38 FAM-2 BAR Grey, Acc-WW-003(4),Acc-BG–003, Tejareb-2 Late gindwuha, Acc-No–024, HB-22-FAM (-4) and Acc-No-045
Cluster III	28	28 %	Local check, NN-0068-2, Acc-BG–009, Acc-111-848–1, Acc-EW-017(6), Unknown Nguara sel-9, Acc-EW-025(1), BAR–002, NN-0029 (2), Unknown-sel–3, Acc-205–180, Acc-202-374–2, BCS-033, NN-0036–1, NN–0052, Bering bowng, NN-0108–2, EW-020(1), Hirhir Adi Gosh sel-4, Acc–00019,USR-82 # 171 NS, Hirhir Humera sel-6, Venzula–1, Acc-203–187, M-80 # 402–2, Acc-BG-001(3), Acc-024 sel–3 and K-74 X C_{22}(71-2)-3
Cluster IV	13	13 %	Adi, Banja Gobate sel–4, Bounja-filwuha sel–8, BCS-001 (1), Acc-203–612, Acc # 033, Acc-205-374–2, Tejahir-2 Late ginwuha-sel-1, Hirhir Kebebew early sel-1, Acc-EW-009(5), Acc-203–623, Bounja-fiyel kolet sel–4 and Unkown Kaja sel- 4
Cluster V	15	15 %	G-03–1, Bounja-filwuha sel–2, Bounja-filwuha sel–6, Win black (Tall)–2, SSBS-(9 -2)-3, BA–0004, Acc-111-821, AW–007, Acc-GA-005(1), Clusu-Acc–2, Acc-202–363, NN-0129-2, JAPAN-651, Acc-NS-007(2) and Acc-WW-001 (4)
Cluster VI	9	9 %	NN-088–2, Acc-EW-011(1), SPS-SIK- # 811, NN-0183–3, Tmax, Acc-203-336-4, X-30/40 # 403, Acc-111-524–1 and Hirhir Baker sel–1
Cluster VII	2	2 %	Acc-205-374–1 and Acc-No–044

4.6.2. Cluster performance

Mean value of the 20 characters for each cluster group is presented in Tables 11. Cluster I had characterized by moderate in magnitude. Cluster II had the maximum cluster mean values for thick capsule (0.53 cm), number of seed per capsule (50.18) and biomass yield (5.44 ton). Cluster III had moderate in magnitude. Cluster IV had mean values of the shortest plant height (104.65cm), few numbers of primary branch (1.85), minimum biomass yield (4.76 ton) and high oil content (51.18). Cluster V was categorized by the shortest (2.38 cm) and widest capsule (0.77 cm), while the remaining traits were moderate.

Cluster VI had the earliest flower initation (36.59 days), shortest date of 50 % flowering (41.40 days), shortest date of capsule filling period (49.22 days), the earliest maturity genotypes (101.08 days), the longest capsule bearing zone (50.37 cm) and capsule length (2.56 cm), heaviest harvest index (25.08 %) and 1000 seed weight (3.50g); and the highest number of capsule per main axis (28.76) and capsule per plant (47.14), the highest seed yield $kgha^{-1}$ (1348.14kg).

Cluster VII had late flower initation (42.27 days), the longest date of 50 % flowering (51.19 days) and capsule filling period (53.12 days); late maturing type (124.00 days), the tallest plant (128.00 cm), the shortest capsule bearing zone (41.52 cm) and length (2.35 cm); narrowest capsule (0.48cm), most branched (2.09), minimum number of capsule per main stem (35.48) and capsule per plant (46.62); the highest percentages of shattering resistance (6.97 %) and biomass yield (5.36 ton); the lowest harvest index (16.48 %), 1000 seed weight (2.91 g), oil content (49.27) and seed yield (520.13 kg) while the remaining traits were moderate in amount.

Table 11. Cluster means value of 20 characters of 100 sesame genotypes

Traits	cluster-I	cluster-II	cluster-III	cluster-IV	cluster-V	cluster-VI	cluster-VII
DFI	37.87	38.13	37.64	37.39	38.23	36.59*	42.27**
DF	42.90	43.87	42.61	42.15	44.01	41.40*	51.19**
DCFP	50.09	50.03	50.01	49.48	50.05	49.22*	53.12**
MD	105.10	106.59	104.73	102.79	106.77	101.08*	124.46**
PLH	112.58	118.46	110.10	104.65*	116.20	111.34	128.00**
LCBZ	48.50	49.91	48.56	49.18	48.35	50.37**	41.52*
LFC	2.42	2.46	2.41	2.45	2.38*	2.51**	2.385
CL	2.48	2.51	2.47	2.54	2.46	2.56**	2.35*
CW	0.76	0.76	0.75	0.76	0.77**	0.74	0.72*
CTK	0.51	0.53**	0.52	0.51	0.52	0.50	0.48*
PBPP	1.90	1.89	1.93	1.85*	1.88	1.95	2.09*
CPMA	26.47	27.56	26.95	28.20	25.66	28.76**	21.97*
CPP	42.06	43.23	43.67	44.86	39.35	47.14**	35.48*
SPC	49.56	50.18**	49.09	49.29	48.55	48.88	46.62*
ISR	4.91	4.52	4.69	3.86	4.86	2.74*	6.97**
BY	5.15	5.44**	5.11	4.76*	5.24	5.10	5.36
HI	21.62	22.05	23.65	24.09	20.34	25.08**	16.48*
TSW	3.36	3.35	3.48	3.46	3.37	3.50**	2.91*
OL	50.19**	51.09	50.26	51.18**	49.65	50.84	49.27*
YLD	821.80	927.31	1052.42	1218.94	707.70	1348.14**	520.13*

**= highest value, *= lowest value, DFI=days to flower initation, DF= days to 50 % flowering, DCF= days to capsule filing period, DM=days to physiologically mature, PLH=plant height(cm), LCBZ=length of capsule filing zone(cm), LFC=length of first capsule (cm), CL=capsule length (cm), CW=capsule width (cm), CTK=capsule thickness (cm), PBPP= primary branch per plant, CPMA=capsule per main axis, CPP=capsule per plant, SPC=seed per capsule, ISR=percent of inverted shattering resistance (%),BY=biomass yield per hectare (ton), HI=harvest index (%), TSW=1000 seed weight (g), OL=oil content (%) and YLD=yield kgha^{-1}

4.6.3. Genetic distance (genetic divergence) analysis

The generalized divergence as measured by Mahalanobis D^2 statistics showed genetic distance and significant variation ($p<0.01$ and $p<0.05$) among the seven clusters (Table 12). Generally, this study revealed that the genotypes included in this study are moderately divergent. The chi-square test showed highly significant differences between clusters except between clusters I and cluster II, cluster II and cluster III; cluster I and cluster V; and cluster IV and VI. The result showed that the inter cluster distances were larger than the intra cluster distances for all circumstances, signifying broader diversity among the genotypes of different groups. The maximum squared inter cluster distance was found between cluster VI and VII (D^2 =1012) followed by IV and VII (D^2 =764.8), V and VI (D^2 =507.4), III and VII (D^2 = 474). The minimum squared distance was found between cluster II and cluster III (D^2 =21). Minimum inter cluster indicates that genotypes in these clusters were not genetically diverse or there was little genetic diversity between the clusters. This signifies that crossing of genotypes from these three clusters might not give high heterotic value in F_1 and narrow range of variability in the segregating F_2 population. Maximum genetic recombination is expected from the parents selected from divergent clusters. Therefore, maximum recombination and segregation of progenies is expected from crosses involving parents selected from cluster six and seven followed by cluster four and seven, cluster five and six, cluster three and seven.

The maximum and minimum intera cluster distance was observed for cluster VII (7.8) and cluster II (2.5). This indicates genotypes in cluster VII were more divergent than genotypes any other cluster. However, the selection of parents should also consider the special advantages of each cluster and each genotype within a cluster depending on the definite purposes of hybridization as suggested by Singh, (1990) and Chahal and Gosal (2002).

In addition, Alarmelu and Ramanathan (1998) and Mohammed *et al*. (2015) suggested that hybridization should be done between diverse genotypes to produce promising breeding material. Not only the existence of higher genetic diversity but also parents should express the optimum level of the entire desired component traits for accumulating yield, resilient to biotic and abiotic environmental stresses and achieve quality concerning required in the target area as suggested by Wallace and Yan (1998).

Table 12. Inter and Intra (bolded along diagonal) generalized distance (D^2) among clusters

Cluster	I	II	III	IV	V	VI	VII
I	**3.1**	21.5^{ns}	69.0**	205.7**	21.2^{ns}	343.3**	207.6**
II		**4.2**	21.0^{ns}	109.4**	70.5**	213.3**	328.4**
III			**2.5**	42.8**	152.2**	111.9**	474.0**
IV				**4.1**	335.9**	25.9^{ns}	764.8**
V					**3.8**	507.4**	121.4**
VI						**4.8**	1012.0**
VII							**7.8**

** = significant, X^2 = 30.14 at 5% & 36.19 at 1% probability level, respectively, ns= non-significant and bold number represent intra-cluster distance

4.6.4. Principal component analysis

The first seven principal components with eigenvalues greater than one accounted for 78.67 % of the total variation (Table 13). The first principal component (PC1) accounted for 26.00 % of the variability and the major attributing characters include date of flower initation, date of 50% flowering, date of capsule filling period, maturity date, capsule length, capsule width, capsule per main axis, seed per capsule, shattering resistance, biomass yield per hectare and oil content. Likewise, 17.84 % of the total variability among genotypes accounted for the second principal component analysis originated maturity date, plant height, length of capsule bearing zone, length of first capsule, capsule width, primary branch per plant, and capsule per main axis, shattering resistance and 1000 seed weight. Similarly, the third principal component (PC3) which accounted for 10.73 % of the total variability among genotypes was attributed to discriminatory traits like date of 50 % flowering, capsule length, capsule width, capsule per plant, shattering resistance, harvest index and seed yield.

The 4th principal component (PC4) accounted for 7.76 % of the total variation capsule thickness, primary branch, capsule per main axis, 1000 seed weight and seed yield the main contributing characters. The fifth principal component (PC5) accounted for 6.01% of the variability among genotypes and contributed by length of capsule bearing zone, capsule length, capsule width, seed per capsule, 1000 seed weight and seed yield; the sixth principal component (PC6) explained 5.49 % of the total variability with capsule thickness, capsule per plant, percentage of shattering resistance and harvest index were the main contributor to PC6. In the same way, 7th principal components (PC7) mainly originated from capsule thickness, number of capsule per plant and seed yield accounted for 4.85 %. Of all quantitative traits

evaluated, capsule width, percent of inverted shattering resistance and yield contributed to the variations in four principal components out of the seven principal components (Table 13).

Generally, the principal component analysis indicated the existence of variation in the studied genotypes. This suggests opportunities for genetic improvement through selection directly from the accessions and/or selection of diverse parents for hybridization programme and conservation of genotypes for future utilization. In line with the present findings, Fazal *et al*. (2011) stated that the four principal components (PCs) described about 63.63% of the total variation among 105 accessions of sesame. Moreover, Shim *et al*. (2009) also reported that the first four principal components (PCs) explained 83.7 % of the total variation.

Table 13. Eigen vector and Eigen value of the first seven principal components (PCs) for 20 characters of 100 sesame genotypes.

Traits	PCA1	PCA2	PCA3	PCA4	PCA5	PCA6	PCA7
Date of flower initation	0.881	0.044	-0.268	-0.022	0.091	-0.075	-0.168
Date of 50 % flowering	0.553	0.073	0.589	0.211	-0.252	-0.113	0.098
Date of capsule filing period	0.940	0.038	0.102	0.109	-0.073	-0.098	-0.056
Maturity date	0.817	0.348	0.018	0.120	-0.098	-0.007	-0.174
Plant height (cm)	0.272	0.751	0.299	0.041	-0.116	0.043	-0.202
Length of capsule b/ng zone(cm)	-0.278	0.785	-0.008	-0.018	-0.326	0.081	0.106
Length of 1^{st} capsule (cm)	-0.206	0.789	0.068	-0.148	-0.272	0.006	0.216
Capsule length(cm)	0.418	-0.035	0.599	0.202	0.310	0.073	0.288
Capsule width (cm)	0.341	0.430	0.554	0.036	0.412	0.019	-0.054
Capsule thickness(cm)	-0.032	-0.164	-0.232	0.672	-0.040	0.368	-0.314
Primary branch per plant	-0.211	0.773	-0.112	0.312	0.101	-0.268	0.021
Capsule per main axis	-0.348	0.455	-0.275	0.606	0.150	-0.152	0.020
Capsule per plant	0.032	0.271	-0.339	-0.037	-0.021	0.630	0.461
Number of seed per capsule	0.428	-0.254	0.047	0.218	-0.563	0.170	0.178
% of Inverted Shattering resistance	0.529	0.370	-0.318	0.037	0.100	0.354	-0.152
Biomass yield per hectare(ton)	-0.819	-0.083	0.128	0.253	0.198	0.125	-0.143
Harvest index (%)	-0.285	-0.298	0.604	0.294	0.034	0.408	-0.064
100 seed weight (g)	-0.162	0.593	0.063	-0.423	0.375	0.262	-0.103
Oil content (%)	-0.591	0.268	-0.034	0.185	-0.238	-0.141	-0.229
Yield ($kgha^{-1}$)	0.258	-0.036	-0.332	0.401	0.313	-0.226	0.530
Eigen value :-	5.460	3.746	2.252	1.629	1.262	1.153	1.019
% of total variance	26.000	17.840	10.730	7.760	6.010	5.490	4.850
% of Cumulative variance	26.000	43.840	54.560	62.320	68.330	73.820	78.670

5. SUMMARY AND CONCLUSION

The progress of crop improvement program depends on the choice of material, the extent of variability present and the knowledge of quantitative characters with grain yield and among themselves. The present study comprises 100 sesame genotypes that were evaluated at two seasons at Werer with the objective of assessing the genetic variability and associations of characters.

The combined analysis of variance revealed genotypes were highly significant different for all the character studied, indicates the existence of variation among the tested genotypes

The wide ranges of mean values were observed for most of the characters showing the existence of variations among the tested genotypes. The estimates of phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients of variation (GCV) for most of the characters, indicating the presence of slight environmental influence on the phenotypic expression of the characters. High phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) value were recorded for percentage of shattering resistance, whereas medium PCV and GCV were recorded for plant height, harvest index and seed yield; it indicating weak influence of environment. The lowest PCV and GCV vales were recorded for days to flower initation, days to 50% flowering, days to capsule filling period, days to maturity, primary branch per plant, length of capsule bearing zone, length of first capsule, capsule length, capsule width, capsule thickness, number capsule per main axis, number of seed per capsule and oil content. This implies substantial environmental influence on the expression of the characters and the need for creation of variability either by hybridization or mutation.

Heritability estimates were high for days to flower initiation, days to 50 % flowering, maturity date, length of capsule bearing zone, plant height, number of capsule per main axis, number of capsule per plant, shattering resistance, harvest index, 1000 seed weight, seed yield per hectare, number of seed per capsule, capsule length and oil content.

High heritability estimate coupled with high genetic advance as a precent of mean (GAM) were recorded for precent of shattering resistances, harvest index and seed yield; this implies

that the expression of the characters governed by additive gene action. High heritability estimates coupled with moderate GAM were observed for date of 50 % flowering, date of maturity, plant height, length of capsule bearing zone, number of capsule per main axis, capsule per plant and 1000 seed weight; it indicates both additive and non-additive genes governed the expression of these characters; as a result these characters important for selection and also possible to exercise hybridization followed by selection. However, high heritability estimates coupled with low GAM were recorded for days to flower initiation, capsule length, number of seed per capsule and oil content, it indicating the expression of the characters are mainly governed by non-additive gene. Hence, it is better to improve by hybridization followed by recurrent selection. Moderate values of heritability coupled with low GAM was recorded for date of capsule filling period, length of first capsule, capsule width, thickness, biomass yield and primary branch per plant; implies that the expression of these characters influenced by non-additive gene action and substantial influence of environment in the expression of these characters. Therefore, selection based on these characters might be not effective.

Seed yield had positive and significant phenotypic and genotypic associations with length of capsule bearing zone, length of first capsule, capsule length, number of capsule per main axis, number of capsule per plant, harvest index and oil content. By selecting for these traits, there is a possibility to increase seed yield of sesame.

Path coefficient analysis revealed that harvest index had the highest positive direct effect on seed yield. Moreover, capsule per plant and capsule per main axis also had positive correlation with seed yield. In the process of selection, these characters could be used for indirect selection.

The cluster analysis based on D^2 analysis of pooled mean of genotypes classified the 100 genotypes into seven clusters, which makes them to be moderately divergent. There was statistically significant difference between most of the clusters. The narrow range for the mean of the 20 characters among clusters also suggests the genotypes were not highly divergent. The probably reason behind is their being from one source and the narrow genetic base of the crop.

Principal component analysis of the characters revealed that the first seven principal components (PC1 to PC7) with Eigen values greater than one accounted for 78.67 % of the total variation. The first Principal component (PC1) contributed 26.00% of the total variation, and the remaining contributed 17.84%, 10.73%, 7.76%, 6.01%, 5.49% and 4.85% of the total variation, as a result PC indicating that there is genetic variation in the studied genotypes.

The following conclusions can be drawn from the present study:
There were differences in the performance of the genotypes as there were statistically supported significant differences among genotypes for all of the 20 characters and relatively wide range of the mean values for most of the characters. Harvest index, capsule per plant and capsule per main axis as they showed medium genotypic coefficients of variation, medium to high heritability, relatively better GA (%) and positive correlation coefficient and direct effect on seed yield.

Harvest index, capsule per main stem and capsule per plant had maximum positive direct effect on seed yield with positive and significant correlation coefficient. These will be useful traits for indirect selection to increase seed yield in sesame.

However, in order to give confirmative result further studies should be conducted at multiple locations. The present study was based on morphological traits only. Hence, supporting the assessment of sesame genetic resources with molecular markers and high throughout molecular data for marker assisted breeding should be considered in the future.

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APPENDIX

Appendix 1. Dendrogram showing the clusters of 100 sesame genotypes evaluated using 20 quantitative traits at Werer.

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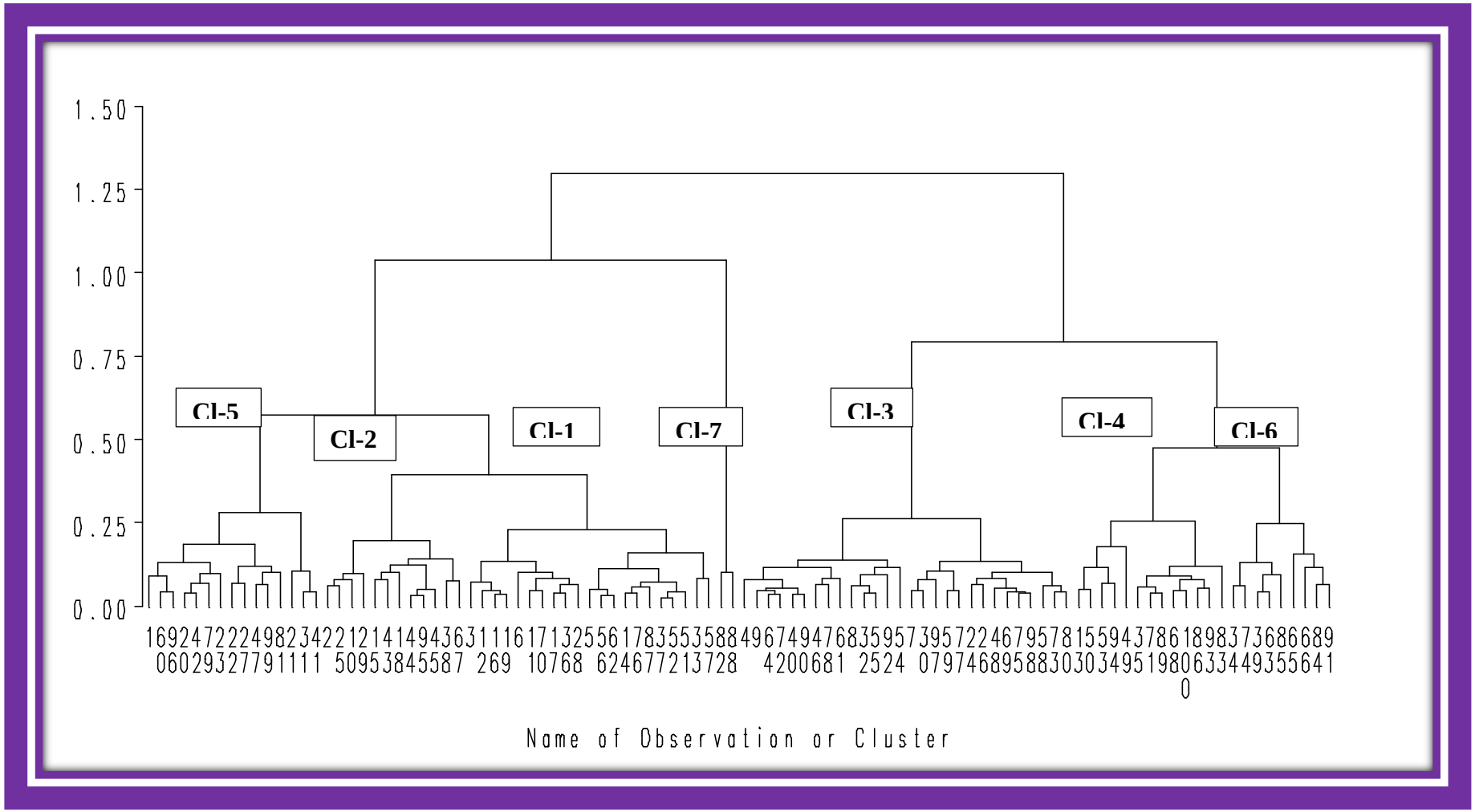
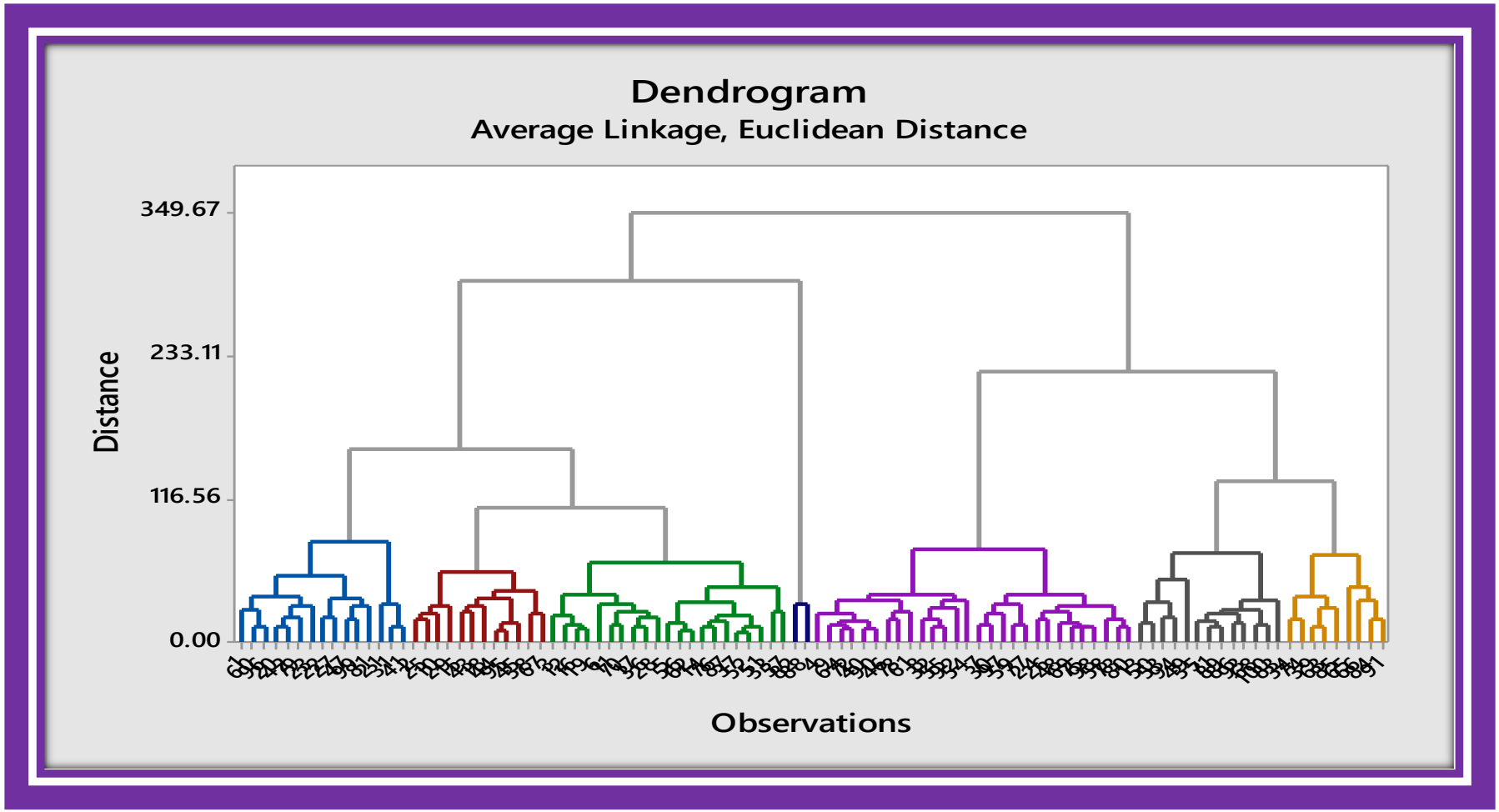
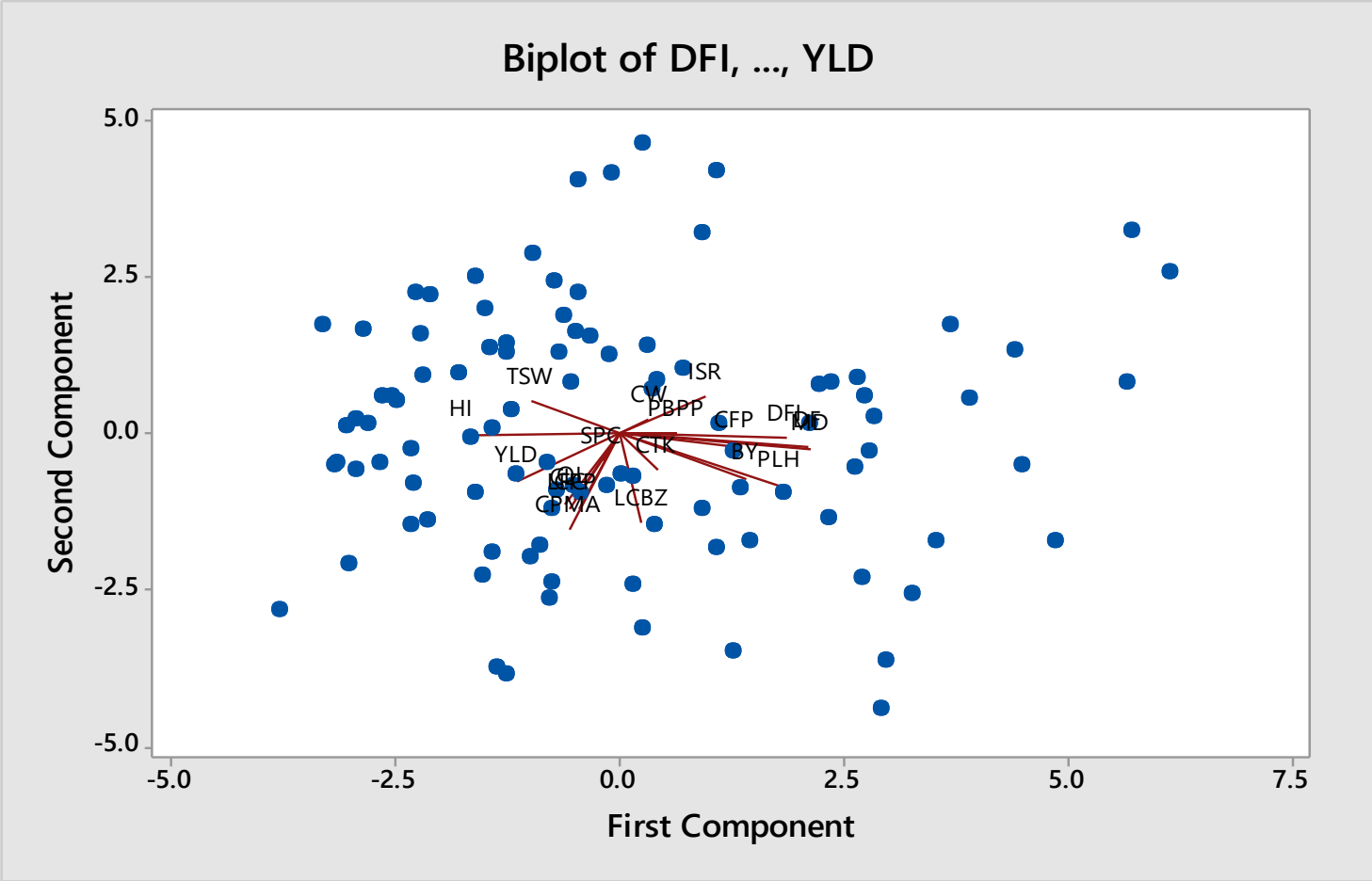
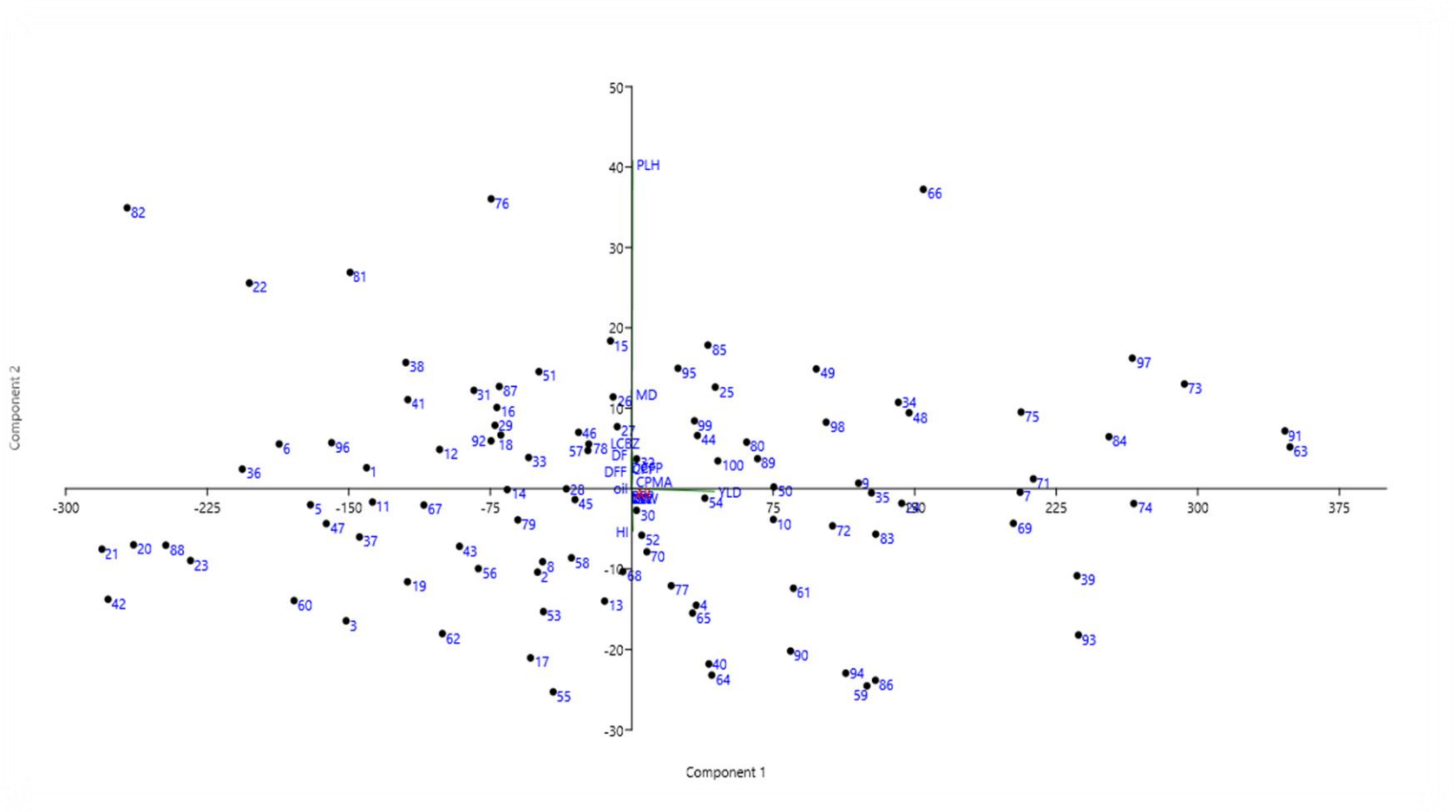



Dendrogram
Average Linkage, Euclidean Distance
349.67
233.11
116.56
0.00
Distance
Observations


Biplot of DFI, ..., YLD
Second Component
First Component
5.0
2.5
0.0
-2.5
-5.0
-5.0
-2.5
0.0
2.5
5.0
7.5
TSW
ISR
CW
PBPP
HI
CFP
DFL
SPG
CTK
YLD
BY
PLH
LCBZ
GPM
A



Appendix 8: Biplot scores of the first two principal components