

Mean Performance Evaluation and Cluster Analysis in Sunflower (*Helianthus annus* L) Genotypes Tested at Central Highland of Ethiopia

Mohammed Abu

Ethiopian Institute of Agricultural Research, Holeta Agricultural Research Center, Holeta, Ethiopia

Email address:

moabu1440@gmail.com

To cite this article:

Mohammed Abu. Mean Performance Evaluation and Cluster Analysis in Sunflower (*Helianthus annus* L) Genotypes Tested at Central Highland of Ethiopia. *World Journal of Agricultural Science and Technology*. Vol. 1, No. 4, 2023, pp. 122-127.

doi: 10.11648/j.wjast.20230104.17

Received: October 18, 2023; **Accepted:** November 1, 2023; **Published:** November 11, 2023

Abstract: Developing sunflower cultivars with better performance is the aim of the current breeding program. This study was conducted to evaluate sunflower genotypes along with their standard check for their mean performance and genetic diversity following different biometrician techniques. Twenty five sunflower genotypes were evaluated for their performance and variability for yield and yield related traits. It was conducted at two locations namely; Holeta and Adadi using simple lattice design. All recommended packages were followed as per national recommendation. Data were recorded for eleven quantitative traits and subjected to analysis of variance and divergence analysis using a combination of software. The mean performance evaluation indicates that genotype NK-KONDI-SPS-7/-had the highest yield mean and genotype Brazil Long seed PL2-SPS-3/4 recorded the lowest yield mean. Based on relative magnitude of D^2 values the genotypes were grouped in five clusters. cluster I comprised of five genotypes while cluster II, cluster III, cluster IV and cluster V comprised of seven, five, four and four genotypes respectively. The index of genetic diversity shown by the statistical distance indicates cluster- had the highest intra cluster distance and cluster- had the lowest intra cluster distance. The highest inter cluster distance was observed between cluster three and cluster four whereas the lowest inter cluster distance was noticed between cluster one and cluster four.

Keywords: Cluster Analysis, Genetic Divergence, *Helianthus annus* L., Means Performance

1. Introduction

Sunflower (*Helianthus annus* L. 2n=34) is the important oilseed crop in the world. It is an Asteraeae family of helianthus genus that can perform well in different agro ecologies due to its elasticity nature and stress tolerance [1]. oil seed plays an important role in the world economy. Edible oil is one of the most imperative commodities from everyday life of world people. Sunflower is one of the most important oil sources for domestic consumption and cooking in the world [2]. It is an excellent source of vegetable oil and the consumption preference of sunflower oil for the world population is due to its high level of unsaturated fatty acids, high linoleic acid, mid-high oleic acid, good flavor, high spoke point, its light color and high oil content [3]. In addition to edible oil sunflower is a good source of proteins, fiber,

vitamins, minerals and phytochemicals [4]. The requirement of edible oil in Ethiopia is increasing from time to time due to increase in population growth, consumption preference.

The aim of sunflower breeding is to improve it for oil content and seed yield. To improve any crop for any trait desired trait; information on the nature and genetic diversity in the available gene pool is very important. The estimation of genetic diversity can be obtained using different biometrical techniques. Among these the use of cluster analysis, analysis of variance, principal component analysis, variance component estimation and genetic divergence analysis are the most important to be mentioned. In Ethiopia there is deficiency of edible oil which is becoming serious as the country relies on importing the commodity, rapid population increase and higher prices of the product. The country costs huge amount of money in importing edible oil from abroad to meet the oil

requirement. It is found to be important for the country to use its potential to substitute the import with the domestic product by developing superior cultivars. For the development of superior cultivars selection of divergent material is important [5]. Singh et al. also showed the importance of diversity analysis using dendrogram [6]. Any cross between genotypes belonging to the diverse groups will produce better hybrids and recombinants [7]. It needs the evaluation of the germplasm to identify its genetic potential. Hence this study was conducted to evaluate the genotypes for the desirable traits using

divergence analysis and their mean performance.

2. Materials and Methods

2.1. Experimental Materials Used for Study

Twenty five genetic materials of sunflower obtained from Holeta Agriculture research center were used for study (Table 1).

Table 1. Experimental materials used for the study at two location.

| Genotype Code | Genotype Name | Origin | Source | Status |
|---------------|------------------------------|----------|--------|--------------|
| 1 | Adadi-3-SPS-2/4 | India | HARC | PVT |
| 2 | Adadi-3-SPS-5/4 | India | HARC | PVT |
| 3 | Adadi-3-SPS-9/4 | India | HARC | PVT |
| 4 | NK-FERTI-SPS-1/4 | France | HARC | PVT |
| 5 | NK-FERTI-SPS-4/4 | France | HARC | PVT |
| 6 | NK-KONDI-SPS-2/4 | France | HARC | PVT |
| 7 | NK-KONDI-SPS-7/4 | France | HARC | PVT |
| 8 | NK-NEOMA-SPS-2/4 | France | HARC | PVT |
| 9 | Brazil Long seed PL2-SPS-3/4 | Brazil | HARC | PVT |
| 10 | Brazil Long seed PL4-SPS-4/4 | Brazil | HARC | PVT |
| 11 | NK-FERTI-SPS-8/1 | France | HARC | PVT |
| 12 | Brazil Long Seed PL6-SPS-7/4 | Brazil | HARC | PVT |
| 13 | Brazil Long Seed PL9-SPS-4/4 | Brazil | HARC | PVT |
| 14 | H-45-SPS-5/4 | India | HARC | PVT |
| 15 | NK-FERTI-SPS-7/4 | France | HARC | PVT |
| 16 | NK-KONDI-SPS-7/4 | France | HARC | PVT |
| 17 | NK-NEOMA-SPS-7/4 | France | HARC | PVT |
| 18 | VSFH-180-SPS-5/4 | India | HARC | PVT |
| 19 | VSFH-1044-SPS-1/4 | India | HARC | PVT |
| 20 | VSFH-1044-SPS-2/4 | India | HARC | PVT |
| 21 | VSFH-1044-SPS-3/4 | India | HARC | PVT |
| 22 | VSFH-1044-SPS-9/4 | India | HARC | PVT |
| 23 | VSFH-1044-SPS-10/4 | India | HARC | PVT |
| 24 | VSFH-2006-SPS-2/4 | India | HARC | PVT |
| 25 | Oissa | Released | HARC | Breeder seed |

2.2. Experimental Design and Trial Management

The experiment was laid out using simple lattice design at both locations. A total of six rows with 3m length at a space of 0.25 between plants, 0.75cm between rows and 2.5m between blocks were adopted. Data was collected on plot basis for days to 50% flowering and days to maturity, whereas, ten plants were randomly taken for measuring plant height, stem diameter, ray floret number, leaf number, petiole length stem diameter, seed filling percentage and number of seed per plant. Yield per hectare was taken by measuring plot yield and converted to kg/ha. Thousand seed weight was recorded for thousand seeds randomly taken from plot yield and oil content was analyzed for 23g of seeds taken from the plot and oven dried at 78°C for 3hrs. oil yield obtained from oil content and seed yield.

3. Results and Discussion

3.1. Range and Mean Performance

The range and mean values for the twenty five sunflower

genotypes studied in both locations are presented in Table 2. Whereas mean performance of the studied genotypes are shown in appendix Table 2. Yield per hectare ranged from 1319.7 kg to 2846 kg. Forty eight Percent of the genotypes gave above the grand mean (2000 kg/ha). The highest seed yield per hectare was observed for genotype Brazil Long Seed PL9-SPS-4/4 followed by VSFH-1044-SPS-3/4, NK-KONDI-SPS-7/4, and VSFH-1044-SPS-1/4, while the minimum seed yield per hectare was recorded for Brazil long seed PL2-SPS-3-4. Variability manifested by seed yield might be due to genetic variation among the tested materials as well as influence of genotype x location interaction. Number of seed per plant ranged from 771 to 1326. Maximum number of seed per plant was obtained from genotype Adadi-3-SPS-5-4 (1326) followed by genotype NK-NEOMA-SPS-2/4 (1205) while the minimum number of seed per plant was recorded for genotype Brazil Long Seed PL6-SPS-7/4 (771). Oil yield ranged from 39.2 kg to 106.14 kg. The highest oil yield was recorded for genotype VSFH-1044-SPS-3/4 while the minimum was observed for Brazil Long seed PL2-SPS-3/4. Oil content ranged between 27.05% - 40.8%. The highest oil content was obtained from genotype

NK-FERTI-SPS-1/4 (40.8), followed by VSFH-1044-SPS-10/4 (38.8), VSFH-1044-SPS-3/4 (38.1) and NK-NEOMA-SPS-7/4 (38.07). The lowest oil content was recorded for genotype Brazil Long seed PL4-SPS-4/4 (27.05).

The range for yield per plant varied from 39.2 g to 64.35 g. The highest yield per plant was recorded for genotype Adadi-3-SPS-5/4 (64.35 g) where as the lowest yield per plant was obtained from genotype NK-KONDI-SPS-2/4 (39.2g). Phonological traits, days to flowering and days to maturity ranged from 148 to 156, 87 to 103, respectively. Among the tested genotypes, 12% displayed days to maturity lower than the grand mean indicating that those genotypes were early maturing as compared to the others. The highest days to flowering was recorded by genotype NK-NEOMA-SPS-7/4 (103) while the lowest was recorded by genotype VSFH-1044-SPS-9/4 (87). The maximum days to maturity was recorded for genotype NK-KONDI-SPS-7/4. The genotype NK-KONDI-SPS-2/4 was early maturing with the shortest

days to maturity. Plant height ranged between 149cm - 211cm. The maximum plant height was recorded for genotype NK-FERTI-SPS-8/1 (211cm) while the minimum was recorded for genotype Brazil Long Seed PL6-SPS-7/4 (149 cm). The maximum numbers of leaves per plant were observed for genotype Adadi-3-SPS-9/4 (27) followed by genotypes VSFH-1044-SPS-1/4 (26), NK-FERTI-SPS-4/4 (26) and Oissa (26). The minimum leave numbers were obtained from genotype NK-KONDI-SPS-7/4 (21).

Generally, the results obtained from this study indicated that traits which showed wide range would be expected to have variation among the genotypes that could be utilized in breeding program for improvement of the desired traits in sunflower. Jain and Kumar *et al.* were also evaluated sunflower genotypes for their quantitative traits [8, 9]. Sanjay *et al.* also evaluated sunflower genotypes for their performance [10].

Table 2. Mean Performance of 25 Sunflower Genotypes for Fifteen Quantitative traits studied at two location.

| Genotype | RFN | LN | YPP | NSPP | OC | HD | SD | PL |
|------------------------------|--------|--------|-----------|----------|-----------|-----------|----------|-----------|
| Adadi-3-SPS-2/4 | 48-e-f | 23-e-f | 52.5-b-d | 909-g-h | 31.75-j-k | 20-e-f | 2.53-e-f | 13.01f-i |
| Adadi-3-SPS-5/4 | 55-a | 23-e-f | 64.4-a | 1326-a | 30.25-l-k | 23-a | 2.83-b-a | 14.3 c-e |
| Adadi-3-SPS-9/4 | 53-b-a | 27-b-a | 55-b-c | 1053-f-d | 33.05-j-h | 20.2-e-c | 2.5-e-f | 13.65 d-h |
| NK-FERTI-SPS-1/4 | 50-b-a | 26-b-c | 53.3-b-d | 1010-g-h | 40.8-a | 20.75-e-c | 2.6-e-c | 14.65 cd |
| NK-FERTI-SPS-4/4 | 44-h-f | 27-b-a | 52.9-b-d | 999-g-h | 35.6-f-d | 19.2-e-f | 2.63-e-c | 13 f-i |
| NK-KONDI-SPS-2/4 | 46-e-f | 23-e-f | 39.2-f | 854-j-k | 32.9-j-h | 20-e-f | 2.52-e-f | 12.6 i |
| NK-KONDI-SPS-7/4 | 51-b-c | 24-e-f | 51.3-b-d | 1025-g-h | 31.95-j-k | 20.7-e-c | 2.76-b-c | 13.85c-g |
| NK-NEOMA-SPS-2/4 | 50-b-c | 25-e-c | 63.3-a | 1205-b-a | 35.95-f-d | 22.1-b-c | 2.73-e-c | 13.64 d-h |
| Brazil Long seed PL2-SPS-3/4 | 45-e-f | 28-a | 46-e-d | 800-k | 27-j-m | 19.3-e-f | 2.56-e-c | 13.52 d-h |
| Brazil Long seed PL4-SPS-4/4 | 44-h-f | 25-e-c | 54.6-b-c | 788-k | 27.05-m | 19.75-e-f | 2.59-e-c | 13.86 c-g |
| NK-FERTI-SPS-8/1 | 49-e-f | 24-e-f | 57-b-a | 1147-b-d | 34.7-f-h | 21.0-e-c | 2.84-b-a | 16.6 a |
| Brazil Long Seed PL6-SPS-7/4 | 44-h-f | 23-e-f | 54.7-b-c | 771-k | 28.5-l-m | 20.4-e-c | 2.62-e-c | 12.91 g-i |
| Brazil Long Seed PL9-SPS-4/4 | 50-b-c | 25-e-c | 64.3-a | 1018-g-h | 30.02-l-k | 22.7-b-a | 2.56-e-c | 14.21 c-e |
| H-45-SPS-5/4 | 50-b-c | 25-e-c | 51-b-d | 887-j-h | 31.9-j-k | 19.95-e-f | 2.54-e-f | 13.96 c-g |
| NK-FERTI-SPS-7/4 | 50-b-c | 23-e-f | 47.8-e-d | 1149-b-d | 37.3-b-d | 19.85-e-f | 2.54-e-f | 14.14 c-e |
| NK-KONDI-SPS-7/4 | 48-e-f | 22-g-f | 54.43-b-c | 1093-b-d | 32.5-j-k | 22.1-b-c | 2.89-a | 13.3 f-i |
| NK-NEOMA-SPS-7/4 | 50-b-c | 24-e-f | 53.85-b-c | 1138-b-d | 38.1-b-d | 20.55-e-c | 2.74-b-c | 15.23 b |
| VSFH-180-SPS-5/4 | 41-h | 24-e-f | 54.4-b-c | 975-g-h | 35.9-f-d | 21.85-b-c | 2.6-e-c | 13.63 d-h |
| VSFH-1044-SPS-1/4 | 52-b-c | 24-e-f | 55.2-b-c | 1067-b-d | 38.03-b-d | 20.85-e-c | 2.48-f | 13.23 f-i |
| VSFH-1044-SPS-2/4 | 51-b-c | 25-e-c | 53.2-b-d | 1155-b-c | 35.4-f-g | 20.94-e-c | 2.49-f | 12.56 h-i |
| VSFH-1044-SPS-3/4 | 49-e-f | 22-g-f | 51.1-b-d | 1148-b-d | 38.2-b-c | 18.6-f | 2.52-e-f | 14.01 c-e |
| VSFH-1044-SPS-9/4 | 48-e-f | 23-e-f | 43.2-e-f | 861-j-k | 30.3-l-k | 19.15-e-f | 2.44-f | 13 f-i |
| VSFH-1044-SPS-10/4 | 47-e-f | 25-e-c | 54.7-b-c | 1117-b-d | 38.8-b-a | 21.15-e-c | 2.46-f | 14.9 bc |
| VSFH-2006-SPS-2/4 | 49-e-f | 28-a | 43.3-e-f | 911-g-h | 35.2-f-h | 20.4-e-c | 2.54-e-f | 13.6 d-h |
| Oissa (Check) | 47-e-f | 26-b-c | 47.8-e-d | 1010-g-h | 38.0-b-d | 20.1-e-c | 2.62-e-c | 13.8 c-g |
| Mean | 48 | 24 | 52.57 | 1022 | 34 | 20.5 | 2.63 | 14 |
| CV (%) | 8.1 | 5.7 | 10.2 | 10.46 | 5.2 | 5.74 | 6.46 | 7.08 |

Table 2. Continued.

| Genotype | PH | DF | DM | SFP | HSW | YPH | OYPH |
|------------------------------|------------|----------|---------|-----------|----------|----------|---------|
| Adadi-3-SPS-2/4 | 170.5-i | 92-k-i | 150-g-h | 96.75-b-c | 6.55-c-d | 2123-e-f | 62.54ef |
| Adadi-3-SPS-5/4 | 175-h-g | 93-h-i | 152-e-f | 96.05-e-f | 5.57-f-h | 2257-e-f | 64.2 ef |
| Adadi-3-SPS-9/4 | 191.5-d-e | 92-k-i | 152-e-f | 96-e-f | 6.1-f-g | 2228-b-c | 85.13b |
| NK-FERTI-SPS-1/4 | 204.75-b-a | 96-f-g | 153-e-c | 93.4-i-j | 6.3-c-d | 1894-h-j | 71.7c-e |
| NK-FERTI-SPS-4/4 | 203.75-b-c | 98-b-c | 154-b-c | 96.9-b-c | 6.1-f-g | 2128-e-f | 69.9d-f |
| NK-KONDI-SPS-2/4 | 172.75-i | 92-k-i | 148-i | 94.9-e-f | 5.2-j-i | 1571-i-j | 45.1j-m |
| NK-KONDI-SPS-7/4 | 200.5-b-c | 100-b-c | 152-e-f | 95.5-e-f | 5.97-f-g | 1912-h-f | 62.9e-f |
| NK-NEOMA-SPS-2/4 | 185.75-f-g | 96-f-g | 152-e-f | 96.5-e-c | 6.2-f-d | 2200-e-f | 73.94cd |
| Brazil Long seed PL2-SPS-3/4 | 172.0-i | 91.0-k-l | 151-e-h | 94.5-e-f | 6.6-c-b | 1514-i-j | 39.2m |
| Brazil Long seed PL4-SPS-4/4 | 175.3-h-g | 88-n-m | 151-e-h | 97.9-a | 7.83-a | 2171-e-f | 54.3ij |
| NK-FERTI-SPS-8/1 | 211.0-a | 102-a | 155-ba | 97.3-b-a | 5.8-f-g | 2314-edc | 74.52cd |
| Brazil Long Seed PL6-SPS-7/4 | 149.0-j | 88-n-m | 151-e-h | 96.3-e-c | 8.1-a | 1614-hij | 43.5lm |

| Genotype | PH | DF | DM | SFP | HSW | YPH | OYPH |
|------------------------------|--------------|---------|---------|----------|----------|----------|-----------|
| Brazil Long Seed PL9-SPS-4/4 | 189.0-f-e | 91-k-l | 151-e-h | 97.6-a | 7.4-a | 2542-a | 84.54b |
| H-45-SPS-5/4 | 185.75.0-f-g | 97-f-c | 152-e-f | 95.5-e-f | 6.65-b | 1914-h-f | 57.65ij |
| NK-FERTI-SPS-7/4 | 189.5-d-e | 93-h-i | 154-b-c | 92.3-j | 4.83-j | 1542-i-j | 53.32ij |
| NK-KONDI-SPS-7/4 | 200.3-b-c | 102-a | 156-a | 96.3-e-c | 5.83-f-g | 2517-b-a | 88.4b |
| NK-NEOMA-SPS-7/4 | 192.0-d-c | 103-a | 153-e-c | 94.7-e-f | 5.5-f-g | 1722-h-j | 61.62f-i |
| VSFH-180-SPS-5/4 | 177.0-f-g | 92-k-i | 151-e-h | 97.2-b-a | 6.2-f-d | 2428-d-c | 81.1cb |
| VSFH-1044-SPS-1/4 | 170.3-i | 95-h-g | 152-e-f | 96.5-e-c | 6.1-f-g | 2486-b-c | 87.5b |
| VSFH-1044-SPS-2/4 | 177.0-f-g | 94-h-g | 150-g-h | 93.3-i-j | 5.42-j-h | 1800-h-j | 59.6hi |
| VSFH-1044-SPS-3/4 | 174.3-h-i | 89-n-m | 151-e-h | 96.2-e-f | 5.52-f-g | 2522-a | 106.24a |
| VSFH-1044-SPS-9/4 | 177.0-f-g | 87-n | 149-h-i | 93.3-i-j | 5.87-f-g | 1628-h-j | 48.95j-m |
| VSFH-1044-SPS-10/4 | 197.0-b-c | 98-b-c | 153-e-c | 94.5-e-f | 5.6-f-g | 1992-h-f | 77.97 c-e |
| VSFH-2006-SPS-2/4 | 173.0-i | 101-b-a | 155-b-a | 94.1-e-f | 5.32-j-h | 1571-i-j | 52.1i-l |
| Oissa (Check) | 187.0-f-g | 96-f-g | 153-e-c | 94-e-f | 5.45-f-g | 1571-i-j | 56.33ij |
| Mean | 184.03 | 95 | 152 | 95.5 | 6.1 | 2000 | 59.7 |
| CV | 4.6 | 2.34 | 2.59 | 1.54 | 12.01 | 8.95 | 10.3 |

3.2. Cluster Analysis

The D^2 values based on the pooled mean of genotypes resulted in classifying the 25 sunflower genotypes in to five groups (Table 3) (figure I). This indicates the tested sunflower genotypes were moderately divergent. Cluster analysis showed that cluster I comprised of five genotypes (20%), cluster II consisted of seven (28 %) and cluster III had five (20 %) cluster IV and cluster V consisted of four

genotypes each. The genotypes from France and India were distributed over all five clusters, which may suggests that genotypes from these countries were relatively more variable than materials from Brazil. The overlapping of clustering patterns with respect to the genotypes could be explained as lack of differentiation between countries due to gene flow. The present findings indicated that in future sunflower germplasm introduction due emphasis should be given to Indian and Brazilian germplasm.

Table 3. Cluster number and genotypes joined in 25 sunflower genotypes tested for 15 quantitative traits.

| Cluster number | number of genotypes | proportion | name of genotype | Origin |
|----------------|---------------------|------------|------------------------------|----------|
| I | 5 | 0.2 | NK-KONDI-SPS-2/4 | France |
| | | | VSFH-2006-SPS-2/4 | India |
| | | | VSFH-1044-SPS-9/4 | India |
| | | | Brazil Long seed PL2-SPS-4/4 | Brazil |
| II | 7 | 0.28 | Brazil Long Seed PL6-SPS-7/4 | Brazil |
| | | | NK-FERTI-SPS-4/4 | France |
| | | | NK-KONDI-SPS-7/4 | France |
| | | | Adadi-3-SPS-2/4 | India |
| | | | NK-FERTI-SPS-1/4 | France |
| | | | VSFH-1044-SPS-10/4 | India |
| | | | H-45-SPS-5/4 | India |
| III | 5 | 0.2 | Brazil Long seed PL4-SPS-4/4 | Brazil |
| | | | NK-KONDI-SPS-7/4 | France |
| | | | VSFH-1044-SPS-1/4 | India |
| | | | Brazil Long Seed PL9-SPS-4/4 | Brazil |
| | | | VSFH-180-SPS-5/4 | India |
| IV | 4 | 0.16 | VSFH-1044-SPS-3/4 | India |
| | | | NK-NEOMA-SPS-7/4 | France |
| | | | VSFH-1044-SPS-2/4 | India |
| | | | NK-FERTI-SPS-7/4 | France |
| | | | Oissa-SPS-3/4 | Released |
| V | 4 | 0.16 | NK-NEOMA-SPS-2/4 | France |
| | | | Adadi-3-SPS-9/4 | India |
| | | | NK-FERTI-SPS-8/4 | France |
| | | | Adadi-3-SPS-5/4 | India |

The genotypes in cluster I showed highest value for number of leaves per plant and average value for hundred seed weight and seed filling percentage. This cluster has the least values for yield per plant, yield per hectare, Oil yield per hectare, oil content, head diameter, stem diameter and ray floret number. Therefore, selection of these traits could not be Favorable from genotypes of this cluster. The genotypes in this cluster were the shortest and earliest in flowering.

Therefore, selection for genotypes early in flowering and short in height is favorable from genotypes of this cluster. Genotypes in Cluster two were the tallest and showed highest mean value for hundred seed weight.

Highest mean value for seed yield per hectare (2499 kg), oil yield per hectare (87.22) and seed filling percentage (96.76) were observed in cluster three. This indicated that selection can be made for these traits from genotypes of this

cluster. Highest mean value for oil content (37.2) and least mean value for hundred seed weight (5.29) were obtained from genotypes of cluster four whereas, average mean value for the rest of the traits were observed in this cluster. Selection for high oil content from genotypes of this cluster can be an opportunity to improve oil content of sunflower. Genotypes in Cluster five showed maximum mean value for

number of ray floret (52), yield per plant (59.93 g), number of seed per plant (1183), head diameter (21.575) and stem diameter. This implies that selection for these traits from genotypes of this cluster can be effective. Sultana *et al.* also evaluated sunflower germplasm using multivariate analysis [11]. Arshad *et al.* evaluated sunflower germplasm and found genetic diversity for almost all traits in his experiment [12].

Table 4. Cluster means for fifteen quantitative traits of sunflower genotypes studied.

| Traits | I | II | III | IV | V |
|----------------------------|--------|--------|--------|---------|---------|
| Number of ray floret (no) | 46 | 48 | 48 | 49 | 52 |
| Leaf number (no) | 26 | 25 | 24 | 24 | 25 |
| Yield (g) per plant | 45.3 | 52.9 | 55.9 | 50.9 | 59.93 |
| Number of seed/plant (no) | 843 | 977 | 1060 | 1113 | 1183 |
| Yield (kg)/hectare | 1579.6 | 2036.7 | 2499 | 1658.75 | 2249.75 |
| Petiole length (cm) | 12 | 13 | 13.6 | 10.2 | 12.8 |
| Oil content (%) | 30.8 | 33.98 | 34.93 | 37.2 | 33.49 |
| Oil yield (kg) per hectare | 48.66 | 68.9 | 87.22 | 61.63 | 75.32 |
| Head diameter (cm) | 19.85 | 20.21 | 21.22 | 20.36 | 21.575 |
| Stem diameter (cm) | 2.54 | 2.587 | 2.61 | 2.6 | 2.73 |
| Plant height (cm) | 168.75 | 191.1 | 182.18 | 186.4 | 190.8 |
| Days to flowering (days) | 92 | 96 | 94 | 96 | 96 |
| Days to maturity (days) | 151 | 152 | 152 | 152 | 153 |
| Seed filling percent. (%) | 94.6 | 95.8 | 96.76 | 93.57 | 96.5 |
| Hundred seed weight (g) | 6.22 | 6.43 | 6.21 | 5.29 | 5.92 |

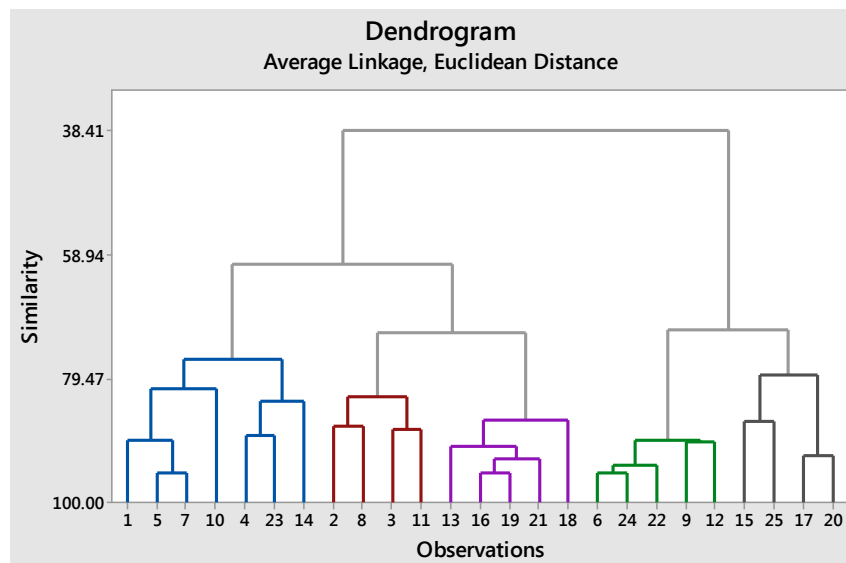


Figure 1. Dendrogram of cluster analysis results.

3.3. Genetic Distance Between Clusters

The generalized squared distance among the clusters based on fourteen quantitative traits were presented in Table 4. The X^2 -test for the five clusters revealed highly significant inter cluster distance for all clusters. This implies there is diversity in the performance of the studied sunflower genotypes. The highest genetic distance was noticed between cluster three and cluster four (352.79) followed by cluster one and cluster three (308.12), cluster four and cluster five (233.94), cluster one and cluster five (206.55), cluster two and cluster three (120.69), cluster two and cluster five (73.67), cluster two and cluster four (68.43), cluster one and cluster two (65.37), cluster three and cluster five (47.75). The minimum inter

cluster distance between cluster was observed between cluster one and cluster four. This indicated that there is less diversity between genotypes of clusters one and cluster four.

Maximum variation is expected from crosses that involve parents from the clusters characterized by high inter cluster distance. Therefore, crossing genotypes selected from, cluster three with cluster four; cluster one with cluster three, cluster four with cluster five, cluster one with cluster five and those from cluster two with cluster three could produce desirable variation as the inter-cluster distance between them were large. However, the selection of genotypes should take into account the advantage of each cluster and each genotype in that cluster depending on the specific objectives of breeding program. From the results of present study the genotype with

highest oil percentage (NK-FERTI-SPS-1/4) found in Custer II should be considered if the objective is to improve oil content. If the objective is to improve seed yield per hectare genotype (VSFH-1044-SPS-3/4) which showed the highest seed yield per hectare in this experiment should be considered in improvement. Shamshad *et al.* studied thirty one germplasm lines of sunflower for yield and yield related traits and the genotypes were grouped into six clusters based on D² analysis indicating the presence of high level of diversity in the genetic material [13]. Tyagi *et al.* studied genetic diversity among 18 sunflower inbred lines and the genotypes were grouped into five clusters based on D² analysis [14].

Table 5. Intra (diagonal) distance and inter cluster (off-diagonal) distance analysis among 25 sunflower genotypes in five clusters.

| Clus | 1 | 2 | 3 | 4 | 5 |
|------|------|---------|----------|----------|----------|
| 1 | 3.22 | 65.37** | 308.12** | 40.85** | 206.55** |
| 2 | | 2.54 | 120.69** | 68.43** | 73.67** |
| 3 | | | 3.218 | 352.79** | 47.75** |
| 4 | | | | 3.66 | 233.94** |
| 5 | | | | | 3.71 |

Whereas, *significant at $p < 0.05$ for $\chi^2 = 23.68$; ** significant at $p < 0.01$ for $\chi^2 = 29.14$

4. Conclusion

From this study the best performing genotypes that can serve as best parents in further breeding program with desirable traits were identified. The presence of moderate level of variation was observed in this experiment. Genotypes were grouped into five clusters using cluster analysis indicating there is variation among the studied genotypes. Crossing between genotypes separated by considerable statistical distance can be helpful in producing superior hybrids or promising recombination in segregating generation.

ORCID

ID: 0000-0003-1730-7829

References

- [1] Khan AK, Iqbal I, Ahmad I, Nawaz H, Nawaz M (2014) Role of proline to induce salinity tolerance in sunflower (*Helianthus annuus* L.). *Sci Tech Dev* 33: 88–93.
- [2] Kholghi, M., Bernousi, I., Darvishzadeh, R. and Pirzad, A. 2011. Correlation and path-coefficient analysis of seed yield and yield related trait in Iranian confectionery sunflower populations. *African Journal of Biotechnology*, 10(61): 13058-13063.
- [3] Hu, J., Seiler, G. and Kole, C., 2010. Genetics, genomics and breeding of sunflower. Routledge, USA, 342.
- [4] Demirer, T., Özer, I., Koçturk, O. M. and Yesilyurt, Er. A. 2004. Effect of Different Leaf Fertilizers on Yield and Quality in Sunflower (*Helianthus annuus* L.). *Pakistan Journal of Biological Sciences* 7(3): 384-388.
- [5] Madhavi Latha, K. (2017). Genetic divergence and association studies in sunflower (*Helianthus annuus* L.). Acharya NG Ranga Agricultural University.
- [6] Singh, N., Choudhury, D. R., Tiwari, G. *et al.* Genetic diversity trend in Indian rice varieties: an analysis using SSR markers. *BMC Genet* 17, 127 (2016). <https://doi.org/10.1186/s12863-016-0437-7>.
- [7] Hussain MM, Rauf S, Riaz MA, Al-Khayri JM, Monneveux P (2017) Determination of drought tolerance related traits in *Helianthus argophyllus*, *Helianthus annuus* and their hybrids. *Breed Sci* 67(3): 257–267.
- [8] Jain, L. K. 2016. Impact assessment of front line demonstrations on green gram in Barmer district of Western Rajasthan. *Journal of Food Legumes*, 29 (3 & 4): 249-252.
- [9] Kumar, S., Tiwari, R. K., Ashthana, R. K. and Kumar, Shailesh, 2018. Evaluation of different cultivars of lentil under clusterfront line demonstration programme in Samastipur District, Bihar. *Journal of Community Mobilization and Sustainable Development*. 13 (2): 271- 274.
- [10] Sanjay Kumar, R. K. Tiwari, Shailesh Kumar, Ranjan Kumar, Sanchita Ghosh, Bharati Upadhaya, Nisha Rani and Vidyapati Choudhary. 2020. Performance Evaluation of Sunflower (*Helianthus annuus* L.) under Cluster Front Line Demonstration Programme in Samastipur District, Bihar, India. *Int. J. Curr. Microbiol. App. Sci.* 9(05): 310-315. doi: <https://doi.org/10.20546/ijcmas.2020.905.033>
- [11] Sultana, T. and A. Ghafoor. 2008. Genetic Diversity in ex-situ Conserved Lens culinaris for Botanical Descriptors, Biochemical and Molecular Markers and Identification of Landraces from Indigenous Genetic Resources of Pakistan. *Journal of Integrative Plant Biology*, 50(4): 484-490.
- [12] Arshad, M., M. K. Ilyas and M. A. Khan. 2007. Genetic divergence and path coefficient analysis for seed yield traits in sunflower (*Helianthus annuus* L.) hybrids. *Pak. J. Bot.*, 39(6): 2009-2015.
- [13] Shamshad M, Dhillon S K, Tyagi V and Akhtar J (2014). Assessment of genetic diversity in sunflower (*Helianthus annuus* L.) germplasm. *Internat J Agric Food Sci Tech* 4: 267-72.
- [14] Tyagi V, Dhillon S K, Bajaj R K and Kaur J (2013) Divergence and association studies in sunflower (*Helianthus annuus* L.). *Helia* 36: 77-94.