DIVERSITY ANALYSIS OF SUNFLOWER GERMPLASMS FOR YIELD AND YIELD CONTRIBUTING CHARACTERS

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You’ve been a blessing and inspiration from the start, I love you son with all my heart.

&

Thank you for all you have taught me, My respected Co-supervisor.

DEDICATED TO-

MY BELOVED SON
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MY RESPECTED CO-SUPERVISOR

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CERTIFICATE

This is to certify that the thesis entitled, "**DIVERSITY ANALYSIS OF SUNFLOWER GERMPLASMS FOR YIELD AND YIELD CONTRIBUTING CHARACTERS**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGROFORESTRY AND ENVIRONMENTAL SCIENCE**, embodies the result of a piece of bona fide research work carried out by **LUBABA NISHAT** Registration No. **18-09095** under my supervision and my guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: December, 2020
Dhaka, Bangladesh

Dr. Md. Kausar Hossain
Professor
Supervisor

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- Author

DIVERSITY ANALYSIS OF SUNFLOWER GERMPLASMS FOR YIELD AND YIELD CONTRIBUTING CHARACTERS

ABSTRACT

Twenty-two sunflower germplasms along with two released varieties were evaluated at the research field of ORC, BARI, Gazipur during rabi season 2018-19 to study the diversity among the genotypes for yield and yield contributing characters. In this study analysis of variance, mean performance of sunflower genotypes, character association, direct and indirect effects of yield contributing characters on seed yield and cluster dendrogram for higher seed yield was performed. The main objective of this study was to analyze and evaluate sunflower lines/genotypes morphologically and find out desired lines/genotype with high yield potential in combination with good agronomic traits which could be used for developing high yielding sunflower variety. In this study, the studied parameters were days to 50% flowering, days to maturity, plant height (cm), stem diameter (cm), head diameter (cm), number of seed/head, 1000 seed weight (g), yield/head (g) and yield/plot (g). The analysis of variance showed that the treatment effects were highly significant for most of the characters which indicates that there were marked variations among the sunflower accessions for the studied characters. The mean performances indicated that the genotype GP04011 and GP01009 (59.22 cm and 63.82cm) respectively, were dwarf type while genotype GP04015 (2.22 cm) produced thick stem. The genotype MiniatureP1 produced wider heads of 17.95 cm. Highest number of seeds per head was produced by the genotype BD9385 (256 seeds) and both the genotype GP04016 and GP04018 produced maximum 1000-seed weight (78.54g). The genotype BHACPS2 (Check-2) gave highest yield/head (29.24 g) and produced higher yield 725.15g. Among the studied traits, character association were observed highly significant and positive correlation for the character days to 50% flowering with stem diameter (0.58**), plant height with stem diameter (0.55**) and head diameter (0.62**), stem diameter with head diameter, head diameter with yield/head, number of seed/ head with yield/head and plot yield, yield/head with plot yield were found in this study. Direct and indirect effects showed that days to 50% flowering and yield/head exhibited higher direct effects on sunflower seed yield. Moreover, plant height, head diameter, number of seed/head and 1000-seed weight also had direct effect on sunflower yield which might be a good indicator for seed yield. Based on quantitative traits, all sunflower accessions by cluster analysis were divided into 2 groups which were group A (4 accessions) and group B again divided into 4 sub-groups (I, II, III and IV). A large number of accessions were placed in sub-group II and III (6 accessions) followed by sub-group I and IV (3 accessions). The genotypes which fall in same group were more closely related. On the other hand, the genotypes were more distantly related which were fall in another group. In this study, no single accessions were categorized as promising for all the characters but different accessions were found promising for different characters. The present study showed that the accessions (BARISurjamukhi-2 (Check-1), BHACPS2 (Check-2), GP04023, BD9385, MiniatureP1) produced high yield in sunflower. So, these genotypes would use to develop desirable high yielding sunflower variety.

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ABBREVIATIONS AND ACCORONYMS

AEZ = Agro-ecological Zone
Agric. = Agricultural
ANOVA = Analysis of Variance
Appl. = Applied
BARI = Bangladesh Agricultural Research Institute
Biol. = Biology
Bot. = Botany
CV = Coefficient of variance
Environ. = Environment
et al. = And others
Exp. = Experiment
g = Gram
i.e. = That is
J. = Journal
Kg = Kilogram
mm = Millimeter
Pak. = Pakistan
RCBD = Randomized Complete Blocked Design
Res. = Research
SAU = Sher-e-Bangla Agricultural University
Sci. = Science
Spp. = Species
Technol. = Technology
DAE = Days after emergence
ORC = Oilseed Research Center
LSD = Least significant difference

CHAPTER I

INTRODUCTION

Bangladesh is vulnerable to multiple climate change hazards. Southwestern coastal region of Bangladesh is highly susceptible due to rising salinity with increasing temperature. Besides, in our northern areas drought become a common phenomenon due to high temperature and low rainfall. Cultivation of crops is seriously hampered in these regions because most of the crops are not suitable to grow in saline or drought condition. Therefore, introduction of saline and drought tolerant crops in the southwestern and northern regions of our country is a sustainable alternative to cope up such vulnerable situations successfully (Afjal *et al*., 2012). Sunflower (*Helianthus annuus L.*) is a day and thermo-neutral, an annual, erect, broadleaf plant with strong taproot and prolific lateral spreading of surface root. It belongs to the family Asteraceae. The *Helianthus* genus contains 65 different species where 14 are annual plants (Andrew *et al*., 2013). Sunflower can be grown both in Rabi and Kharif seasons in anywhere in our country. It tolerates different levels of pH (5.7-8.0), salinity (8-12 ds/m) (Miller, 1995) as well as medium level of drought (Oliveira *et al*, 2004; Baloğlu *et al*., 2012).

Sunflowers originated in North America approximately 5,000 years ago as flour and oil seed crop (Eric, 1997). In the late 1800s the sunflower was introduced in Russian Federation as an oil seed crop where Russian farmers made significant improvements in the sunflower cultivation techniques. Nowadays sunflower as an oilseed crop has rivaled that of soybean for its 6-fold production potentiality (Putnam *et al*., 1990). One kg of sunflower seeds yields 500 to 600 g of oil which is more than that of any other oilseeds (Anon., 2015). Ukraine, the Russia, Argentina, Turkey, France, Hungary, and Spain are the largest producers of sunflower oil.

Sunflower is the world‘s fourth largest oil-seed crop where it contributes about 13% of the world edible oil production with high value (Gabagamb *et al.*, 2010). The demand of sunflower oil is increasing day by day. Sunflower oil contains low cholesterol. It is good for health. Sunflower oil is mainly a triglyceride. Sunflower vegetable oil contains high level of unsaturated fatty acids and free from toxic constituents namely Trans fatty acid. Sunflower seed contains up to 90% unsaturated fatty acids (combined oleic and linoleic), and approximately 10% saturated fatty acids (palmitic and stearic).

Sunflower is a minor oil seed crop in Bangladesh. Since 1975 farmers are cultivating sunflower in small scale. In our country, mainly sunflower is cultivated by imported hybrid seed. The imported seed is expensive and increase the cost of production. Most of the growers cannot afford to purchase hybrid seed every year, because its yield reduces up to 50% in next generations and also have acclimatization issues in local climatic conditions. Therefore, there is huge demand to develop high yield potential local variety with better performance (Muhammad *et al.*, 2012).

Germplasm diversity is one of the criteria of parent selection for developing high yielding varieties. Studies on genetic divergence are important to obtain high yield cultivars (Luciene *et al.,* 2010). Due to its high economic importance, the developments of suitable variety are required with superior yield and quality traits. Presence/existence of ample amount of diversity is prerequisite before embarking any variety development. Information of variability is useful to formulate selection criteria for improvement of seed yield and its component traits (Singh, 2019).

An imperative aspect of Sunflower cultivation is the lodging tendency due to its tall appearance. Availability of sunflower germplasms in our country is limited. To grow sunflower in wind prone saline area we need dwarf high yielding sunflower variety. To develop high yielding dwarf variety, variation in sunflower lines is a pre-requisite (Sultan *et. al*., 2013). In sunflower line/genotype characterization is mainly done based on morphological traits as these are easy to record and require less technical hands and labor. Seed yield traits to identify the best genotypes on the basis of result for future exploitation.

Therefore, this study was under taken to analyze and investigate the variation present in the sunflower lines or genotype of Oilseed Research Centre, BARI, through agro-morphological characterization, which could be used to develop high yield potential sunflower variety.

Objectives:

1. To analyze and evaluate 22 sunflower lines/genotypes morphologically.
2. To find out desired genotype with high yield potential in combination with good agronomic traits for developing high yielding sunflower variety.

CHAPTER II

REVIEW OF LITERATURE

Sunflower

Sunflowers are botanically classified as *Helianthus annuus L*. Sunflower belongs to the family Compositae and imperative member of Asteraceae family originated from temperate and tropical regions cultivated widely and more drought tolerant than the other grain crop. Sunflower genus Helianthus comes from two Greek words “helios” meaning sun and “anthos” meaning flower which has the same meaning as Sunflower. Due to its tendency to reposition itself to face the sun, it is called as sunflower. In general, it’s an annual plant which possesses a large inflorescence (flowering head), and its name is derived from the flower's shape and image. Sunflower plant is an annual herb, with a rough, hairy stem, broad, coarsely toothed, rough leaves and circular heads of flowers. It is normally three to twelve feet high, three to twelve inches long, three to six inches wide in wild specimens and a foot or more in cultivation (Khaleghizadeh, 2011). The genus Helianthus’s basic chromosome number is 17. Diploid, tetraploid and hexaploid species are known (Duane *et al*., 2007).

In Bangladesh, Sunflower is recently introduced an oil seed crop. In future, Sunflower a good source of high-quality edible oil and gaining popularity among farmers because of its easy extraction method. They are large plant and are grown throughout the world because of their relatively short growing season (Anon., 2005-06). Usually, in country like Bangladesh when there is late rain or floods, sowing of oil seeds like mustard and sesame are deferred, hampering production. Under such conditions, sunflower can be stand as a good substitute to fill up this gap of production (Habib *et al*., 2017).

Sunflower seed is mainly used for the manufacturing of sunflower oil and oilcake. In the world, about 11% of crude vegetable oil production is supplied by sunflower (Sema K. 2017). Ukraine, Russia, European Union and Argentina are the major sunflower producing countries. Almost half of the world sunflower seeds are produced in Ukraine and Russia. According to FAO Statistics in 2018, the total production of sunflower is approximately 51.95 million metric tons and the area under its cultivation was 26.67 million hectares in the world. According to Food and Agricultural Organization (FAO), in current world, sunflower ranges second subsequent to soybean as an oil crop.

History and origin of sunflower

The sunflower was firstly originated from North America. The plant was cultivated by natives in present-day Arizona and New Mexico about 3000 B.C (NSA, 2013). Sunflower was domesticated once in eastern North America and second domestication center in southern Mexico. In around 1500, this exotic North American plant was taken to Europe by Spanish explorers. Throughout Western Europe, the plant became widespread mainly as an ornamental, but some uses as medicinal. An English patent was granted for squeezing oil from sunflower seed in 1716. After that Sunflower became very popular as a cultivated plant in the 18th century. After 1830, the manufacture of sunflower oil was done on a commercial scale. In early 19th century, Russian farmers were growing more than two million acres of sunflower. In that time two specific types had been identified oil type for oil production and another a large variety for direct human consumption. A successful breeding program was developed by V. S. Pustovoit at Krasnodar. By late 19th century, Russian sunflower seed was found its way into the US. In 1880, seed companies were advertising 'Mammoth

Russian' sunflower seed in catalogues. In 1970, nearly 100 years later, this particular seed name was still being offered in the US. The first official government sunflower breeding program was started in 1930.

Area and production of sunflower in the world

Nowadays, Sunflower production has distributed almost worldwide mainly temperate and subtropical regions. Global production of sunflower grew steadily in last 25 years (PSD-USDA, 2011). Within 2050, FAO expects a total world output close to 60 million tons. The four largest producers (Ukraine, Russia, Argentina and European Union) account for 70% of global volume, with an exponential growth of production in the last ten years in the Black Sea region.

According to FAOSTAT-2018, Ukraine had the highest production volume of sunflower seeds of any country in the world in 2018. During that time period, Ukraine produced around 14.16 million metric tons of sunflower seeds or 27% of the world total. Russia Federation and Argentina ranked second and third place with 12.75 and 3.53 million metric tons of sunflower seeds, respectively. The total sunflower seed production is reaching ca. 51.95 millions of tons (FAOSTAT, 2018).

Uses of Sunflower

Sunflower (*Helianthus annuus L.*) is that the world‘s fourth largest oil-seed crop which seeds are used as food and dried stalk as fuel. Sunflower-seed oil is employed for cooking, salad dressings, and manufacturing of margarine (Kunduraci et al., 2010). It is used commonly within the manufacture of soaps and detergents. Sunflower-seed oil used as a pesticide carrier, and within the production of agrichemicals, surfactants, adhesives, fabric softeners, lubricants and coatings has been explored. In some countries the seed cake that's left after the oil extraction is employed as livestock feed. Sunflower is also used in making dyes for the textile industry, body painting, certain paints, varnishes and plastics because of good semidrying properties without color modification associated with oils high in linolenic acid. Due to high nutritional value and lack of anti-nutritional factors, Sunflower meal is a good source of protein for human consumption (Fozia *et al.*, 2008). Sunflower meal is higher in fiber, lower in lysine and has a lower energy value but higher in methionine than soybean meal. Sunflower meal has protein percentage ranges from 28% for non-dehulled seeds to 42% for completely dehulled seeds.

Fatty Acid composition of Sunflower oil

Sunflower is an important crop that seed contains 40-50% oil (Ali *et al.,* 2007). Its oil is very stable as it has lesser degree of hydrogenation when kept for long period for storage (Gomes *et al.,* 2013). Its oil is considered as good quality oil from health point of view, due to presence of polyunsaturated fatty acids which are known to reduce the risk of cardiac related problems (Monotti, 2004). Its oil is premium due to its good taste, high smoke point, dietary quality, lack of linolenic acid and high level of unsaturated fatty acids (Joksimovic *et al.,* 2006) Its oil is also enriched with vitamin A, D, E and K and is free from any type of toxic elements (George *et al.,* 1993). It is also a great source of phosphorus, nicotinic acid and calcium (Thomas *et al.,* 2010). Sunflower achene contains 35% of high protein meal from one hundred pounds (Michael and Jeri, 2004).

Economic importance of sunflower

Sunflower is considered as an attractive crop which provides quick returns of the farmers because it is salt tolerant and has seemingly high yields. Currently, at a global level, oil plants are highly valued by farmers because the products resulting from their processing are demanded and used in several sectors of activity. There is a worldwide increase in the production of oilseeds which directly contributes to increased attractiveness for oilseed crops. Sunflower (*Helianthus annuus L.)* is part of the oil plant category. Sunflower is a short duration crop (95-120 days) so it fits well in any cropping pattern. It holds great importance and has tremendous position because of its photo-insensitivity and wider adaptability. The sunflower fruit (achenele) contains 50% oil, which on the one hand is highlighted by remarkable food properties and, on the other hand, a high degree of conservatism.

Area and production of sunflower in Bangladesh

Bangladesh started to cultivate sunflower since 1975 but on a small scale. Sunflower is categorized as a low to medium drought sensitive crop; the cultivation of sunflower is suitable in the coastal environment because of its high yield and extensive adaptability. Sunflower is being harvested in sixteen districts of Bangladesh and the average production is about 1.2t/ha. Sunflower cultivation is gaining popularity in Barguna. The total area of sunflower cultivation is 3425 acre which is 0.28% of total oilseed production area with a total production of 1913 metric tons in 2016-2017. It can be possible to increase the production of edible oil by expanding sunflower growing area. (Mohammad *et al.*, 2019).

In Bangladesh, the consumption of edible oil is around 1029 thousands MT per year. In present situation, the values of imported edible oil and oilseeds were 1574 USD and 354 USD in 2017-18 (Bangladesh Bank, 2017). By boosting up the production of sunflower, a huge amount of import expenditure on edible oil and oilseeds can be reduced.

Diversity analysis

Diversity analysis is one of the criteria of parent selection for developing high yielding varieties.

Sanju *et al*. (2018) analysed significant differences among the 116 genotypes for all the 12 traits to indicate the existence of genetic variability. These 116 restorer line was grouped into twenty three clusters. Greater genetic divergence was found between X and XXIII clusters and X and XXI clusters that suggest the genotypes of these clusters may be exploited to explore the fullest range of variability for the character (s) and to realize good recombinant lines. Characters like seed filling percentage, oil content, days to 50% flowering, seed yield per plant, head diameter, hull content, leaf lamina width, leaf lamina length, volume weight and test weight contributed more to the total divergence.

Arshad *et al.*, (2018) was carried out twenty four sunflower hybrids for different agronomic traits. Cluster analysis indicates the degree of genetic diversity. Hybrids in Cluster II and IV with high seed yield and oil content was selected as desirable hybrids and suggested to exploit further under diverse environments.

Rama *et al.* (2014) studied the genetic divergence of 38 sunflower genotypes. The genotype was grouped into 13 clusters, among which the cluster IX with 9 genotypes was the largest. This was followed by cluster X with 5 genotypes. Maximum inter cluster distance was recorded between cluster XII and XIII (39.58) followed by clusters II and XII (38.18). Hence hybridizing between these divergent groups may lead to higher variation in segregating population. The study revealed that the characters *viz*., 50% flowering followed by seed yield (35.00%) contributed more to the total genetic divergence in the genotypes.

Chandirakala and Manivannan (2014) studied genetic divergence of 38 sunflower genotypes. The genotype was grouped into 13 clusters, among which the cluster IX with 9 genotypes was the largest. This was followed by cluster X with 5 genotypes. Maximum inter cluster distance was recorded between cluster XII and XIII (39.58) followed by clusters II and XII (38.18). In this study, the genotypes *viz.,* GMU 322, COSF3B and COSF4B in the cluster II, the genotypes *viz.*, GMU 503, GMU 1074, GMU 1108 in the cluster XII and the genotype COSF1B in the cluster XIII are widely divergent and the genotypes of these clusters to get more heterosis among the hybrids.

Tyagi *et al.* (2013) studied the genetic diversity among 18 sunflower inberd lines involving alloplasmic cms lines, conventional cms and restorer lines (petiolaris source) using twenty traits. Analysis assigned the test accessions into five clusters in which the highest inter cluster distance was observed between clusters II and V followed by clusters II and III, clusters II and IV and clusters I and V. Minimum diversity was observed between the members of cluster IV and III. The inter-cluster distances were larger than intra-cluster distances indicating wider genetic diversity between genotypes of the clusters with respect to the traits considered.

Ibrar *et al.* (2018) studied 97 sunflower accessions using hierarchical clustering and grouped them into two main groups. The Group-I contained 43 accessions. This cluster was sub-divided into three classes, wherein group I-A had 15 genotypes, group

II-B contained 17 genotypes while the group I-C had 11 genotypes clustered together. The other main cluster contains total of 53 genotypes. This group was also sub-divided into three smaller classes based on the magnitude of difference in the seed protein banding patterns of sunflower. The group II-A had 10 genotypes, while the second group II-B contained 19 sunflower lines. The third group designated as group II-C showed 24 sunflower genotypes clustered together closely.

Srinivas *et al*. (2006) studied genetic divergence in 45 sunflower genotypes. The genotype was grouped into nine clusters. Days to maturity, 100 seed weight, oil content and total dry matter contributed maximum towards total genetic divergence.

Thirumala Rao *et al*. (2005) evaluated 94 sunflower genotypes for genetic divergence and revealed that the genotypes were grouped into 10 clusters. Mean values of clusters for seed yield and yield components indicated the existence of considerable distance for all characters in various genotypes. The genotypes exhibited random pattern of distribution into various clusters, indicating that genetic diversity and geographical diversity are not related. Among the characters, number of filled seeds had the maximum contribution to genetic divergence. In order to assess the genetic divergence, 102 sunflower genotypes were grouped into 12 clusters (Vishnuvardhan Reddy *et al*., 2005). Seed yield per plant contributed maximum divergence (40.2 %) followed by number of leaves per plant (25.8 %) and 100 seed weight (17.0 %).

Mohan and Seetharam (2005) assessed genetic divergence in 137 sunflower lines and the lines were grouped into 6 clusters. Cluster I had maximum number (130) of lines. Highest intercluster distance was observed between II and IV followed by IV and V. Clusters with highest mean values for various characters were mainly due to five characters *viz.*, head diameter, plant height, seed length, oil content and days to 50 per cent flowering.

Reddy and Devasenamma (2004) evaluated 58 inbreds and 3 control cultivars to study genetic divergence. Analysis of variance showed significant differences among the inbreds for all the traits examined. The 61 genotypes were grouped into 19 clusters. Genotypes in cluster V and XVII recorded the highest seed yield and number of days to maturity. The genotypes in cluster X recorded the highest oil content. The character, 100-seed weight contributed the high percentage (35 %) to the divergence in the genotypes.

Reddy *et al*. (2004) studied genetic divergence in 79 sunflower genotypes for selection of appropriate material in various breeding programmes. Genotypes were grouped into seven clusters, cluster I had the highest number of entries, followed by cluster II with 5 entries, whereas clusters III, IV, V and VI were formed with solitary entry. Intercluster distance was maximum between cluster IV and VI (D = 63.20) followed by cluster III and VI (D = 58.14).

Komuraiah *et al*. (2004) evaluated 101 genotypes for genetic divergence and the genotypes were grouped into 10 clusters. The number of filled seeds per head contributed highest towards genetic divergence followed by plant height, number of unfillled seeds per head, days to maturity, oil content, seed yield, days to 50 per cent flowering, number of leaves and head diameter.

Rama *et al.* (2003) was evaluated eleven characters in 85 sunflower genotypes consisting of 80 inbreds and five check cultivars. The genotype was grouped into fifteen clusters. Based on the inter cluster distance and cluster mean for various characters, potential lines was identified from clusters III, IV, VI, VIII, XI, XII and XIV for crossing program. In this study indicates that the inclusion of GP-347, GP-1341 (cluster III), 300-B, ARM-244, aRM-248 (cluster IV), HAR-5 (cluster VI), 853-

B (cluster VIII), GP-913 (cluster XI), GP-507 (cluster XII) and GP-831 (cluster XIV) in future breeding programs could result in the development of superior sunflower cultivars.

Manivannan *et al*. (2003) studied genetic divergence in 62 genotypes of sunflower and were grouped into 17 clusters based on their genetic diversity. Among the twelve characters studied, plant height, number of chaff seeds per head, seed yield per plant and head diameter showed the highest contribution towards total divergence. The clusters V, XV and XVII showed superior mean performance and high inter cluster distance.

Subramanyam *et al*. (2003) determined the extent of genetic divergence with respect to eleven characters in 85 sunflower genotypes. Univariate and multivariate analysis of variance revealed the presence of significant differences among the genotypes. It indicated the presence of substantial genetic diversity. The genotypes were grouped into fifteen clusters. Among the characteristics, the number of filled seeds per head, test weight, kernel: hull ratio and seed yield per plant exhibited high contribution towards genetic divergence.

Ravi (2001) evaluated 66 sunflower genotypes for genetic divergence and grouped them into nine clusters. The characters seed yield, total dry matter, seed set per cent under self-pollination and plant height contributed maximum towards genetic divergence. Teklewold *et al.* (2000) analysed the extent of genetic divergence in 144 sunflower genotypes consisting of 66 germplasm accessions, 75 inbred lines and three checks for 16 characters. They have observed highest genetic divergence among the inbred lines than in the germplasm accessions.

Association analysis

Association analysis is an important approach in a variety development. It gives an idea about relationship among the various characters and determines the component characters, on which selection can be based for genetic improvement in the seed yield. Effectiveness of selection process affected by the degree of association. The degree of association between independent and dependent variables was suggested by Galton 1888, its theory was developed by Pearson (1904) and their mathematical utilization at phenotypic, genotypic and environmental levels was described by Searle (1961).

Correlation analysis

Seed yield is a complex character and it depends upon the expression and interaction of number of yield component characters. Therefore, attention has to be bestowed for direct and indirect methods of selection for seed yield. Correlation coefficient is a measure which determines the relationship between two variables and helps in selection of superior plants or lines for the improvement of a particular character. It is very important to define the traits that directly affect to the seed yield.

For efficient selection, Abrar *et al*. 2010 studied that programmed interrelationship between yield and its components was inevitable and mutual association of plant characters, which was determined by correlation coefficient. In other word, correlation coefficient was used to find out the degree (strength), mutual relationship between various plant characters and the component character on which selection could be relied upon the genetic improvement of yield.

Arshad *et al.*, (2018) was carried out twenty four sunflower hybrids for different agronomic traits using RCBD design. In this study both positive and negative correlations was found to be between different traits. Days to flower initiation (DFI), days to flower completion (DFC) and days to maturity (DM) contribute positively and highly significantly with plant height (PH) for both genotypic and phenotypic level. Correlation between plant height and oil content was found to be highly significant and positive. Seed yield had positive association but non-significant with DFI, PH 100SW, HD and OC percentage while negative association with DFC and DM. DFI, DFC, HD, 100 SW and OC percentage contribute positively toward seed yield.

Vikas *et al.* (2015) was evaluated 143 sunflower germplasm accessions for yield and yield contributing characters to study the extent of variation for different quantitative traits. Highest phenotypic and genotypic coefficients of variation was recorded for seed yield per plant (53.4 % and 46.9% respectively) followed by head diameter, test weight, plant height, volume weight and oil content. High heritability was noticed for all the traits studied. High heritability coupled with high genetic advance over mean was recorded for seed yield per plant (77 and 65.1) followed by head diameter, test weight and plant height. It was noticed that sunflower germplasm accessions exhibited wide range of variability for all the morphological characters studied.

Purwati and Herwati (2016) observed that 33 sunflower germplasm accessions were characterized. These results indicated that on the base of their qualitative morphological characters, sunflower accessions possessed high diversity. The seed size and seed thickness showed significant positive correlation with 100 seeds weight.

Amin *et al*. (2016) conducted an experiment to determine correlation among many important traits of sunflower. The results revealed that plant height had positive and significant relation with leaf area, stem diameter, head diameter, 100-achene weight and achene yield per plant. Days to maturity correlated significantly and negatively with number of achenes per head. Leaf area had significant and positive association with stem diameter, capitulum diameter, 100-achene weight and yield of seeds per plant. Harvest index and weight of 100 seeds also correlated significantly and positively with yield of seeds per plant.

Baloch *et al.* (2016) conducted an experiment on 18 genotypes of sunflower to evaluate heritability and phenotypic correlation. Significant differences were observed for all studied traits. The results showed that traits like head diameter, plant height, seed per plant and seed index were significantly and positively associated with seed yield per plant. High broad sense heritability was observed for all studied traits excluding head diameter that showed moderate heritability. Results depicted that genotypes with high value of these characters may be preferred in selection for enhancement of sunflower yield.

Biljana *et al.* (2014) evaluated 20 sunflower varieties to study the character associations and reported that 1000 seed weight was obtained highly positive and significant correlation with seed yield and grain width. On the other hand, 1000 seed weight showed negative and significant correlation with oil content.

Mehmet *et al.* (2014) evaluated 8 open-pollinated confectionary sunflower populations and two open-pollinated confectionary sunflower cultivars used as control varieties during two growing seasons. The results for the individual years and the combined data for both years revealed that there were significant positive correlations between the seed yield and the plant height, head diameter, 1000-seed weight and crude protein yield. The crude protein yield was also positively and significantly correlated with the 1000-seed weight and the seed yield, but the correlations with the plant height, head diameter, kernel ratio and crude protein ratio were not significant.

Tyagi *et al.* (2013) evaluated 18 sunflower inbred lines to study the character associations and reported that grain yield an important character showed highly significant positive correlation with days to 50% flowering, days to maturity, plant height, chlorophyll content, oil content, and biological yield at both genotypic and phenotypic levels. Highly significant negative association was recorded between oleic acid and linolenic acid.

Zia *et al.* (2013) conducted an experiment to check the correlation among various yield related traits like head diameter, percent filled achene, 100 achene weight, achene yield per plant, plant height, harvest index, oleic acid, linoleic acid, oil content, stearic acid and palmitic acid. There were significant and positive correlation of capitulum diameter, 100-seed weight and harvest index with yield per plant.

Ravi *et al.* (2006) evaluated 63 inbred lines to study the character associations and path analysis and reported that number of filled seeds per head, seed set percentage under self-pollination and head diameter had strong positive association with seed yield.

Sridhar *et al.* (2005) evaluated 44 genotypes of sunflower to study the character association and path analysis and reported that head diameter, number of leaves per plant, number of filled seeds per head, seed filling percentage and 100 seed weight were positively correlated with seed yield.

Vidhyavathi *et al.* (2005) studied correlation by evaluating 29 sunflower genotypes. Correlation analysis revealed that head diameter and plant height had significant positive correlation with seed yield.

Mohan *et al.* (2005) evaluated 20 sunflower hybrids lines to study the character associations reported that days to maturity had positive correlation with head diameter but negative association with seed yield. However, seed yield had highly positive genotypic correlation with oil contents but non-significant with 100 seed weight. Oil contents had negative association with days to flower initiation, completion and plant height but significantly positive correlation with seed yield.

Nehru and Manjunath (2003) studied correlation and path analysis in sunflower genotypes and revealed that seed yield was positively associated with growth and yield components.

Ravi (2001) studied character associations in 66 sunflower germplasm accessions and indicated that the characters number of filled seeds per head; seed set per cent under open pollination had showed significant positive correlation with seed yield per plant. While head diameter, harvest index and seed set per cent recorded positive association with seed yield under self-pollination. Ayub Khan (2001) also observed that days to 50 per cent flowering, number of seeds per capitulum, 100 seed weight, head diameter and days to maturity were positively correlated with seed yield.

Teklewold *et al.* (2000) studied inter relationships of 12 physio-morphological characters on 144 sunflower genotypes including 75 inbred lines. The study revealed that the characters viz., plant height, head diameter, number of filled seeds, 100 seed weight and harvest index were positively correlated with seed yield.

Path coefficient analysis

Path-coefficient analysis is simply a standardized partial regression coefficient and as such measures the direct and indirect effect for one variable upon another and permits the separation of the correlation coefficient into components of direct and indirect effect (Dewey and Lu, 1959). Using path coefficient analysis, it is easy to determine, which yield component is influencing the yield substantially. Having this information, selection can then be based on that criterion thus making great progress possible through selection in limited time. The advantage of path analysis is that it permits the partitioning of the correlation coefficient into its components one component being the path coefficient (or standardized regression partial regression coefficient) that measures the direct effect of a predictor variable upon its response variable through other predictor variables. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959).

Biljana *et al.* (2014) evaluated 20 sunflower varieties to study the character associations and path analysis. This trait expressed the biggest positive direct effect on seed yield. Indirect positive effect on seed yield was obtained for oleic acid content and the highest negative indirect effect was determined for oil content.

Mehmet *et al.* (2014) evaluated eight open-pollinated confectionary sunflower populations and two open-pollinated confectionary sunflower cultivars used as control varieties during two growing seasons. The path coefficients from path analysis indicated that the seed yield had the maximum positive direct effect on the crude protein yield, followed by the crude protein ratio. The greatest positive indirect effects on the crude protein yield were attributed to the 1000-seed weight, plant height and head diameter through their effects on seed yield.

Rigon *et al.* (2014) studied path coefficients in eight sunflower hybrids. The experiment was conducted in two different locations and correlations were same in both environments. 1000 seed weight and head diameter were significantly correlated with sunflower yield. Numbers of achene per head were significantly associated with productivity but was indirectly affected by primary components and it was an undesirable character for selection.

Tyagi *et al.* (2013) evaluated 18 sunflower inbred lines to study path coefficient analysis. Path coefficient analysis revealed direct positive effect of no. of leaves per plant, 100 seed weight, chlorophyll content, leaf area, leaf area index, oil content, biological yield and harvest index on grain yield.

Zia *et al.* (2013) conducted an experiment to check the correlation among various yield related traits like head diameter, percent filled achene, 100 achene weight, achene yield per plant, plant height, harvest index, oleic acid, linoleic acid, oil content, stearic acid and palmitic acid. Path coefficient analysis revealed that there were high direct effects of 100 achene weight, capitulum diameter and harvest index. Achene yield per plant were highly contributed by harvest index, head diameter, percent filled achene and head diameter.

Martin *et al.* (2012) conducted path coefficient analysis on six sunflower cultivars and used spatial distribution of 40 and 60 cm between rows. They examine various traits that influence the 100 seed weight and seed yield. Regression analysis was also carried out to get the 100 seed weight and seed yield. They reveal in their results that spatial distribution had no effects on seed yield. On the other hand characters like number of plants and stem diameter at 15 days had direct effect on grain yield. Seed yield was indirectly affected by stem diameter and plant stature both at 15 days. Plant stature at 90 days had negative effect on 100 seed weight.

Muhammad *et al.* (2007) evaluated 20 sunflower hybrids lines to study the path analysis. The direct effects of days to flower initiation, plant height and head diameter were positive while remaining characters exhibited negative direct effects. The highest direct effect was exhibited by days to flower initiation and plant height. Head diameter had also positive direct effect on seed yield.

Ravi *et al.* (2006) evaluated 63 inbred lines to study the character associations and path analysis. Path coefficient analysis revealed that number of filled seeds per plant had higher direct effect on seed yield.

Vidhyavathi *et al.* (2005) studied path analysis by evaluating 29 sunflower genotypes. Path analysis indicated that plant height and head diameter had high and medium positive direct effects on seed yield, respectively.

Madhavilatha *et al.* (2004) studied the magnitude of association of yield and yield component characters and to ascertain the relative contribution of direct and indirect effects of the components towards yield. Path analysis indicated that preference should be given to number of seeds per plant and head diameter, followed by number of leaves per plant, plant height, 100 seed weight and oil per cent, because of their positive direct influence on seed yield.

Nehru and Manjunath *et al.* (2003) studied path analysis showed maximum direct effect of number of filled seeds per head followed by test weight and seed yield per plant, while seed yield had maximum direct effect on oil yield. Studies on path analysis in 45 sunflower genotypes (Gill *et al.*, 2003) revealed that selection for any trait would influence oil yield per plant through seed yield per plant.

Thirumala Rao *et al*. (2002) studied 94 sunflower genotypes for character associations and path analysis and reported that there was positive association of characters viz., days to maturity, plant height, and number of leaves, head diameter, number of filled seeds per head, test weight and oil content with seed yield.

Ravi *et al.* (2001) studied character associations in 66 sunflower germplasm accessions and indicated that filled seeds per head, total dry matter per plant and harvest index had positive direct effect on seed yield. Ayub Khan *et al.* (2001) reported that number of seeds per capitulum, 100 seed weight and head diameter had positive direct effect on seed yield, while 50 per cent flowering had negative direct effect on seed yield.

CHAPTER III

MATERIALS AND METHODS

This study was under taken to analyze the divergence among the sunflower germplasms/lines collected by Oilseed Research Centre (ORC), Bangladesh Agricultural Research Institute (BARI) for yield and different yield contributing characters. The experiment was conducted during rabi season of 2018-19. The details of experimental site, materials and method followed for conducting the experiment were as follows:

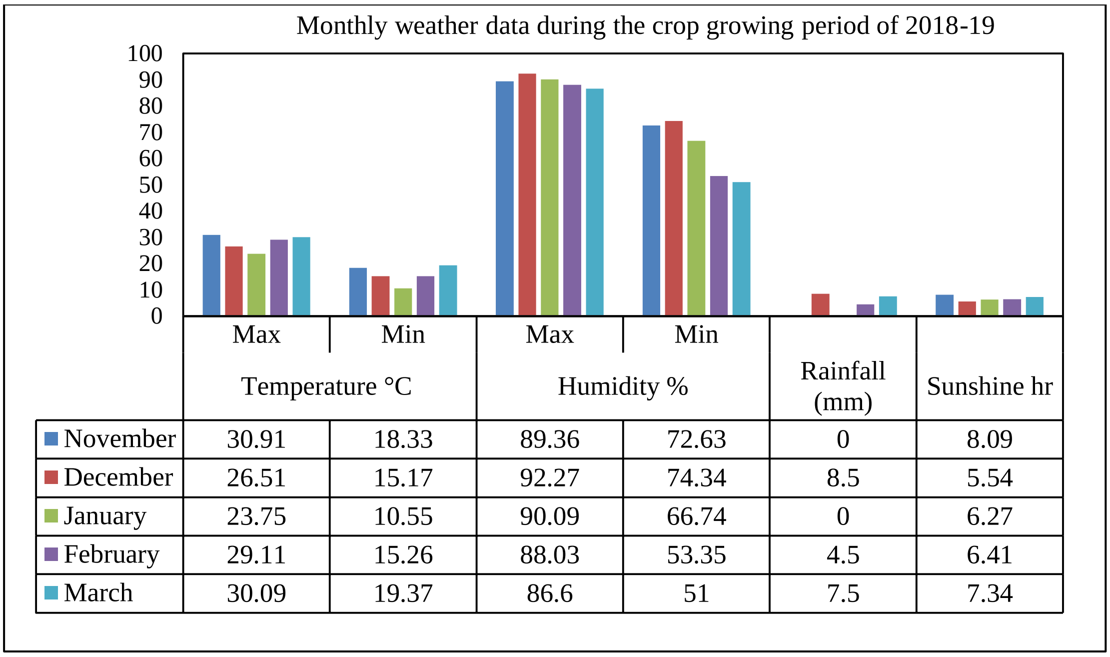
3.1 Experimental site

The present research work was carried out at the research field of ORC, BARI, Gazipur during the period of rabi season, 2018-2019.

3.2 Soil and Climate

Soil condition of the experimental plot was texturally clay loam having soil p^H 6.2 and land type was medium high, which belongs to the Chhiata series of the gray terrace soils (*Aeric Albaquept*) (Huq and Shoaib, 2013), under the agroecological zone of Modhupur Tract (AEZ-28).

The meteorological information regarding the average maximum and minimum temperature, average maximum and minimum relative humidity, sunshine hour and total rainfall received at the experimental site during the crop growth period of 2018-19 is presented in Figure 1.



	Temperature °C		Humidity %		Rainfall (mm)	Sunshine hr
	Max	Min	Max	Min		
🟦 November	30.91	18.33	89.36	72.63	0	8.09
🟥 December	26.51	15.17	92.27	74.34	8.5	5.54
🟩 January	23.75	10.55	90.09	66.74	0	6.27
🟪 February	29.11	15.26	88.03	53.35	4.5	6.41
🟦 March	30.09	19.37	86.6	51	7.5	7.34

Figure 1. Monthly average maximum and minimum temperature (°C), average maximum and minimum relative humidity (%), rainfall (mm) and sunshine (hr) during the crop growing period of 2018-19

3.3 Plant Materials

In this study a total of 22 sunflower genotypes including a released variety BARI Surjamukhi-2 and sunflower advanced line BHACPS2 were used as check to determine the divergency among the materials. All the genotypes were collected from ORC, BARI.

3.4 Methods

3.4.1 Land preparation and fertilization

The experimental plot was prepared by ploughing with tractor and power tiller followed by harrowing and laddering. After ploughing and cross laddering all the stubbles and uprooted weeds were removed from the field. The field was fertilized with following fertilizers:

Table 1: Rates of fertilizers and manures (kg/ha) applied

Name of fertilizer	Rate (kg/ha)
Urea	200
TSP	180
MP	170
Gypsum	170
Zinc sulfate	10
Boric acid	12
Magnesium sulfate	100

All amounts of other fertilizers and half of the urea were applied at the time of final land preparation. The remaining half of the urea was applied as top dress twice in equal amount at 25 and 50 days after emergence (DAE).

3.4.2 Sowing of seed and experimental design

Before sowing, to protect the seeds from soil and seed borne diseases, seeds were treated with Vitavex-200 @ 3 g/kg seed. Twenty-two genotype of sunflower were grown at the research field of ORC, BARI Gazipur on 19 November 2018 in an augmented design (Federrer, 1956).

Following the design, the experimental field was divided into equal four blocks. Each block was received a total of five new entry and two checks. The entries were assigned randomly in each plot. The layout of the experimental field was as follows:

	B-1		**B-2**		**B-3**		**B-4**	
	BARI Surjamukhi-2		GP01009		GP04015		GP04016	
	GP01005		BHAC-SH-S7-04016		BARI Surjamukhi-2		GP04024	
	MiniatureP1		BHACPS2		GP04018		BHACPS2	
	GP04017		BARI Surjamukhi-2		BHAC-SH-S7-04038		GP04011	
	BHACPS2		GP04028		BD9360		BD931	
	BHAC-SH-S7-04032		SUN-W-S7-101		BHACPS2		GP04019	
	GP04023		GP01004		BD9385		BARI Surjamukhi-2	

Figure-2. Layout of the experimental field using Augmented design (Federrer, 1956)

Seeds of each entry were sown in 2 rows x 4 m long plot, keeping 50 cm inter-row spacing with 25-30 cm between plants. Three to four seeds were sown per hill to facilitate better emergence and to maintain uniform stand.

3.4.3 Intercultural Operations

Thinning of excess seedling keeping one healthy seedling/hill was done within 15-20 DAE. Weeding was done as and when necessary to keep the crop free from weeds. Three times irrigation at 25, 50 and 70 days after emergence were applied during the growing period. Other intercultural operations and appropriate pest control practices were followed to grow a healthy crop.

3.4.4 Data collection

At maturity, 10 randomly selected competitive plants were used for recording data. Among the characters days to 50 % flowering, days to maturity, plant height (cm), stem diameter (cm) and head diameter (cm) were recorded from the standing plants in the field. The other characters were recorded in the laboratory after harvest. The observations on days to 50% flowering and days to maturity were recorded on plot basis. The characters were:

Days to 50% flowering (DF 50%): It was recorded from date of sowing when till approximately 50% of the flower buds per plot bloomed in each entry.

Days to maturity (DM): It was recorded from sowing to full maturity when the back side of the heads turned brown and the number of days required from the date of sowing to the date when 80% heads were matured.

Plant height (PH cm): The plant height was measured from the ground level to the point of attachment of disk with stem in cm at physiological maturity.

Head diameter (HD cm): Sunflower head diameter was recorded in centimeter with a graduated ruler from one edge of the head to the other at physiological maturity.

Stem diameter (SD cm): Stem diameter (cm) of plants was measured with a slide caliper by taking the reading in the cervical region of the plant at maturity.

No. of seed/head: Heads of selected plants in each entry were harvested, dried and threshed individually. The fully matured ripen achenes were considered as seed whereas shriveled, partially filled and damaged achenes were considered as non-seed. The seed from one head was counted and considered as number of seeds/head.

Seed yield/plant (g): All the matured seeds produced by a head were weighed by the help of an electrical balance in gram and that was considered as seed yield/plant.

1000 seed weight (g): 1000 seeds were counted and weighed using an electrical balance in gram from each genotype.

Yield/plot (g): Plot yield was recorded on a plot basis adjusted to 10% seed moisture by weighing seed which had been dried in the sun for 5-6 days.

3.4.5 Statistical Analysis:

The mean data of different characters were used for statistical analysis. The data were subjected to analysis of variance (ANOVA) and tested for significance using the least significant difference (LSD), path co-efficient analysis and cluster analysis were performed by R Software (R Core Team. 2017). Correlation coefficient was performed by Statistical Tool for Agricultural Research (STAR) software.

CHAPTER IV

RESULT AND DISCUSSION

The assessment of divergency for quantitative characters, estimates of character associations, direct and indirect effects of yield contributing characters with seed yield are important for initiating any high yielding variety development. Information obtained by evaluating the sunflower germplasms along with cluster analysis helps to identify diverse genotypes for their further use. Therefore, to assess the divergency among the sunflower germplasms/lines, this study was conducted at the research field of ORC, BARI during rabi season 2018-19.

To find out distinctiveness among sunflower genotypes quantitative characters have been used. Quantitative characters are considered as morphological markers in the identification of germplasm accessions of sunflower. In the present investigation, among the quantitative characters observed, days to 50% flowering, days to maturity, plant height (cm), head diameter (cm), stem diameter (cm), number of seed/ head, 1000 seed weight (g), yield/head (g), and plot yield. The data were statistically analyzed and subsequently obtained results are illustrated below under the following heads:

4.1 Analysis of variance

4.2 Mean performance of sunflower genotypes

4.3 Character associations

4.4 Direct and indirect effects of yield contributing characters on seed yield

4.5 Cluster dendrogram analysis

Table 2: Analysis of variance for nine quantitative traits in 22 genotypes of sunflower

Source of Variation	**DF**	**DM**	**PH**	**SD**	**HD**	**SH**	**SW**	**YHG**	**PYG**
Block (Adjusted)	3.00^{ns}	3.00^{ns}	9.81^{ns}	0.00^{ns}	0.12^{ns}	42.2^{ns}	11.88^{**}	0.00^{ns}	258^{ns}
Treatment (Adjusted)	19.78^{ns}	107^{**}	621.35^{**}	0.08^{*}	6.13^{*}	5422.4^{**}	255.38^{***}	84.31^{*}	80345^{*}
Residual	5.58	1.05	11.13	0.00	0.34	106.0	0.10	3.60	3983

Note: * significant at $p \leq 0.05$, ** significant at $p \leq 0.01$, ns: non-significant

DF: Days to 50% flowering (cm), DM: Days to maturity (cm), PH: Plant Height (cm), SD: Stem Diameter (cm), HD: Head Diameter (cm), SH: No. Seed /head (cm), SW: 1000-seed weight (cm), YHG: yield/head (g), PYG: plot yield (g)

4.1 Analysis of Variance

Mean squares of the nine characters from analysis of variance (ANOVA) are presented in Table 2. The analysis of variance showed that the adjusted block effects were non-significant for most of the traits indicating homogeneity of the experimental blocks. The ANOVA also revealed that the adjusted treatment effects were highly significant for all the characters except for the character days to flowering. This result indicates that there were marked variations among the sunflower accessions for the studied characters. Therefore, these sunflower accessions could be a suitable source for the development of superior sunflower variety. From the ANOVA, Arshad *et.al*.(2018) also found significant differences for yield and other yield contributing characters except for days to flower initiation among some sunflower hybrids.

4.2 Mean Performance of Sunflower Accessions

Mean performances of 22 sunflower genotypes for nine different agro-morphological traits are presented in Table 3a and 3b.

Days to 50% flowering

Days to 50% flowering ranged from 63 to 79. From the result it was found that the genotype MiniatureP1 took long time for days to 50% flowering (79 days) which was closely followed by GP04016 and GP04023 (78 days). On the other hand, the genotype GP04017 took lesser time for days to 50% flowering (63 days) which was closer to the genotype BHAC-SH-S7-04032 (65 days) as compared to the rest of the genotypes (Table 2a). Onemli and Gucer (2010) reported significant differences for flowering time in sunflower genotypes. Highly significant differences were also reported in days to flowering in sunflower by Siddiqi *et. al*. (2012).

Days to maturity

From the mean performance significant variations were observed among the genotypes for days to maturity. The genotype BD931 took maximum days (109 days) to mature which was statistically similar with the genotypes GP04018, GP04028 and MiniatureP1 as they took 109 days to mature which indicates that these are long maturing genotypes. On the other hand, from the result it was found that the genotype GP04024 took least number of days (98 days) to mature among the tested genotypes. The genotypes GP01009, GP04011 and GP04017 ranked second and the genotypes GP01004, GP01005 and GP04023 ranked third for taking a total number of days for maturity of 100 and 101 days, respectively (Table 3a). Days to maturity are important characters in sunflowers for selecting genotypes. The genotypes took around 100 days to mature considered as early maturing genotypes. Therefore, these genotypes could be considered as early genotypes among the genotypes studied. Time of flowering character was important for selection of early maturity accessions. Accessions with time of flowering less than 60 days after planting indicated as early maturity accessions. Highly significant differences were reported for days to maturity in sunflower by Siddiqi *et. al*. (2012), Purwati *et.al*. (2016). Machikowa *et al*. (2005) who reported that maturity time and time to flowering were closely related to yield and yield components. Maturity time might be changed due to the influence of environmental factors (Dhillion *et al.* (2009).

Plant Height

In case of plant height, the genotype MiniatureP1 produced taller plants of 143.37cm, which was closely followed by SUN-W-S7-101 (139.37cm); while short stature plants of 59.22 cm were observed in the genotype GP04011, which was statistically similar to GP01009 (63.82cm) (Table 3a)

Table 3a: Mean Performance of 22 Sunflower Accessions for nine different agro-morphological traits

Entry	**DF**	**DM**	**PH**	**SD**	**HD**
BARISurjamukhi-2 (Check-1)	76	108^{abc}	136.00^{ab}	1.81^{bc}	15.15^{b}
BHACPS2 (Check-2)	70	102^{efg}	66.74 ^{j}	1.53^{defgh}	12.55^{def}
GP01004	72	101^{efg}	87.82^{efgh}	1.59^{cdefg}	12.35^{def}
GP01005	74	101^{efg}	85.62^{fghi}	1.51^{defgh}	11.75^{def}
GP01009	71	100^{fg}	63.82 ^{j}	1.21 ^{hi}	8.55^{ghi}
GP04011	71	100^{fg}	59.22 ^{j}	1.43^{defghi}	10.75^{efghi}
GP04015	76	104^{bcdef}	91.22^{defg}	2.22^{a}	14.10^{bcd}
GP04016	78	104b^{bcdefg}	83.41^{fghi}	1.69^{bcde}	11.75^{defg}
GP04017	63	100^{fg}	67.62^{ij}	1.13^{i}	7.75^{i}
GP04018	69	109^{abc}	71.22^{hij}	1.33^{fghi}	9.75^{fghi}
GP04019	75	102^{defg}	84.62^{fghi}	1.29^{ghi}	8.15^{hi}
GP04023	78	101^{efg}	83.82^{efg}	1.53^{cdefgh}	8.55^{hi}
GP04024	68	98^{g}	95.77^{def}	1.23 ^{hi}	8.05 ^{i}
GP04028	77	109^{ab}	85.17^{fghi}	1.67^{cdef}	10.85^{efgh}
BD9385	74	102^{efg}	109.57^{cd}	1.77^{bcd}	12.05^{def}
BD9360	75	105^{bcdef}	104.97^{de}	1.80^{bc}	14.25^{bcd}
BD931	75	110^{a}	73.17^{ghij}	1.19^{hi}	10.00^{fghi}
BHAC-SH-S7-04032	65	107^{abcd}	134.17^{ab}	1.39^{efghi}	13.75^{bcde}
BHAC-SH-S7-04038	68	106^{abcde}	124.37^{bc}	1.43^{defghi}	12.75^{cdef}
BHAC-SH-S7-04016	67	102^{efg}	134.37^{ab}	1.47^{defghi}	13.35^{bcde}
SUN-W-S7-101	71	103^{cdefg}	139.37^{ab}	1.49^{defgh}	14.95^{bc}
MiniatureP1	79	109^{ab}	143.37^{a}	2.03^{ab}	17.95^{a}

Note: The figures with common letters are statistically identical

DF: Days to 50% flowering (cm), DM: Days to maturity (cm), PH: Plant Height (cm), SD: Stem Diameter (cm), HD: Head Diameter (cm)

Short type plants have some advantages like these were not easy to damage by wind flow and easier to harvest. Therefore, these genotypes could be used to develop short stature sunflower variety. Significant differences in plant height of various sunflower lines and hybrids were also reported by Encheva *et al*. (2008), Onemli and Gucer (2010), Siddiqi *et. al*. (2012).

Stem Diameter

Stem diameter is an important trait for sunflower and was most affected by environment as compared to other characters. Thick stem sunflower had advantages over thin stem sunflower as it prevents lodging in windy areas. For the trait of stem diameter, the sunflower genotype GP04015 produced thicker stem of 2.22 cm, which was closely followed by MiniatureP1 (2.03cm); while the thinner stem of 1.13 cm was observed in the genotype GP04017, which was statistically similar to the genotype BD931 (1.19cm). The genotypes found with thick stem in this study could be used in developing lodging resistant sunflower variety (Table 3a).

Head Diameter

Head diameter is an important character in sunflower as bigger headed sunflower could lead to higher seed yield. From the mean performance it was found that the genotype MiniatureP1 produced wider heads of 17.95 cm, while smaller heads of 7.75 cm was produced by the genotype GP04017(Table 3a). Danish *et.al.* (2018) was reported differences in head diameter in the sunflower accessions ranged from 8.6 to 23.75. Therefore, the genotypes produced wider head in this study would be a potential genotype for developing high yielding sunflower variety.

Table 3b: Mean Performance of 22 Sunflower Accessions for nine different agro-morphological traits

Entry	**SH**	**SW**	**YHG**	**PYG**
BARISurjamukhi-2 (Check-1)	215^{abc}	63.75^{d}	19.20^{b}	778.45^{a}
BHACPS2 (Check-2)	233^{ab}	60.33^{f}	29.24^{a}	725.15^{a}
GP01004	117^{fgh}	58.21^{g}	11.03^{bcdef}	260.93^{def}
GP01005	104^{fghi}	63.21^{de}	8.23^{cdef}	338.13^{bcdef}
GP01009	61^{i}	58.21^{g}	5.23^{def}	270.13^{cdef}
GP04011	113^{fghi}	63.21^{de}	9.63^{cdef}	164.53^{ef}
GP04015	118^{fgh}	78.21^{a}	13.43^{bcd}	114.53^{ef}
GP04016	73^{hi}	78.54^{a}	11.00^{bcdef}	314.80^{cdef}
GP04017	186^{cde}	53.54^{h}	8.80^{cdef}	177.60^{ef}
GP04018	154^{def}	78.54^{a}	11.00^{bcdef}	219.80^{ef}
GP04019	59^{i}	53.54^{h}	4.40^{df}	143.20^{ef}
GP04023	204^{abcd}	68.54^{b}	13.0^{bcde}	621.80^{ab}
GP04024	97^{ghi}	3.99^{l}	5.76^{def}	131.70^{ef}
GP04028	81^{ghi}	3.79^{l}	5.56^{def}	97.50^{f}
BD9385	256^{a}	16.29^{k}	18.06^{bc}	615.00^{abc}
BD9360	228^{abc}	18.69^{j}	20.46^{b}	382.40^{bcde}
BD931	69^{hi}	1.69^{m}	3.46^{df}	230.40^{def}
BHAC-SH-S7-04032	116^{fghi}	66.71^{c}	2.58^{ef}	221.40^{ef}
BHAC-SH-S7-04038	206^{abcd}	61.71^{e}	8.38^{cdef}	212.20^{ef}
BHAC-SH-S7-04016	192^{bcd}	61.71^{e}	8.18^{cdef}	382.0^{bcdef}
SUN-W-S7-101	133^{efg}	61.71^{e}	6.38^{def}	350.20^{bcdef}
MiniatureP1	90^{ghi}	51.71^{i}	4.98^{def}	528.80^{abcd}

Note: The figures with common letters are statistically identical

SH: No. Seed /head (cm), SW: 1000-seed weight (cm), YHG: yield/head (g), PYG: plot yield (g)

Number of Seeds /head

Number of seeds per head also an important character in sunflower selection. From the result, the highest number of seeds per head was produced by the genotype BD9385 (256 seeds) followed by BHACPS2 and BD9360 having 233 and 228 seeds per head, respectively. Whereas the genotype GP04019 produced lower number of seeds per head (60 seeds) followed by the genotype GP1009 (61 seeds/head) (Table 3b). Variation in number of seeds per head was also reported in exotic sunflower hybrids by Iqbal *et al*. (2018).

1000-Seeds weight

1000-Seed weight is the most important yield attributes in sunflower. Accessions which have high seed weight are categorized as potential accessions. The genotype GP04016 and GP04018 produce maximum 1000-seed weight (78.54g) which was statistically similar to GP04015 (78.21 g), whereas the genotype BD931 gave minimum seed weight (1.69 g), which was statistically identical with GP04028 (3.79 g) and GP04024 (3.99 g) (Table 3b). Significant variations for 1000-seed weight in sunflower germplasm also reported by (Dehkhoda *et al*. 2013; Rafiei *et al*. 2013; Ion *et al*. 2015).

Yield/head

Yield/head is the most important yield attribute and it was significantly different among the sunflower germplasms. The genotype BHACPS2 (Check-2) gave higher yield/head (29.24 g) however, the genotype BHAC-SH-S7-04032 gave the lower yield/head (2.58 g) (Table 3b).

Plot yield

Plot yield showed significant difference among the sunflower germplasm. The check variety BARISurjamukhi-2 and check line BHACPS2 produced maximum yield 778.45g and 725.15g, respectively followed by the genotype GP04023 (621g) and BD9385 (615g). On the otherhand, the genotype GP04028 produced minimum yield (97.50g), which was statistically identical with the GP04015 (114.53g) (Table 3b).

Table 4. Correlations among different morphological characteristics of 22 sunflower accessions

Characters	**DF**	**DM**	**PH**	**SD**	**HD**	**SH**	**SW**	**YHG**	**PYG**
DF	1	0.05^{ns}	0.23^{ns}	0.58**	0.19^{ns}	-0.22^{ns}	-0.29^{ns}	0.02^{ns}	0.27^{ns}
DM		1	0.14^{ns}	-0.11^{ns}	-0.07^{ns}	0.30^{ns}	-0.35^{ns}	0.26^{ns}	0.24^{ns}
PH			1	0.55**	0.62**	0.25^{ns}	-0.08^{ns}	0.25^{ns}	0.372^{ns}
SD				1	0.76**	0.15^{ns}	0.17^{ns}	0.40^{ns}	0.32^{ns}
HD					1	0.18^{ns}	0.26^{ns}	0.46*	0.37^{ns}
SH						1	0.08^{ns}	0.83**	0.62**
SW							1	0.16^{ns}	0.12^{ns}
YHG								1	0.73**
PYG									1

Note: * significant at $p \leq 0.05$, ** significant at $p \leq 0.01$, ns: non-significant

DF: Days to 50% flowering (cm), DM: Days to maturity (cm), PH: Plant Height (cm), SD: Stem Diameter (cm), HD: Head Diameter (cm), SH: No. Seed /head (cm), SW: 1000-seed weight (cm), YHG: yield/head (g), PYG: plot yield (g)

4.3 Character associations

Character association is very important to define the different traits that are affected to the seed yield. The closeness of two important variables can be determined by correlation coefficient on which selection criteria could be reliably established. Correlation coefficient helps to identify the traits that are useful to determine the component character on which selection can be maid (Jockovic *et al*. 2012). In the present study both positive and negative correlations were found between different traits that are presented in Table 4.

Days to 50% flowering

Highly significant and positive correlation of days to 50% flowering with stem diameter ($r = 0.58; p \leq 0.01$) was found which suggested that if days to flowering increased then stem diameter will be increased. Negative and non-significant correlations between days to 50% flowering and number of seed /head ($r = -0.22$), 1000-seed weight ($r = -0.29$) was obtained from this study. While, non-significant but possitive correlations of the days to 50% flowering with days to maturity ($r = 0.05$), plant height ($r = 0.23$), head diameter ($r = 0.19$), yield/head ($r = 0.02$), plot yield ($r = 0.27$) were found. Farhatullah *et al*., (2006) reported highly significant correlation of days to 50% flowering with days to maturity and plant height and a non-significant but positive correlation of days to 50% flowering with head diameter and yield per head. Manivannan *et al*. (2005) reported significantly positive association of days to 50% flowering with head diameter.

Days to maturity

Days to maturity showed both positive and non-significant correlation with plant height ($r = 0.14$), number of seed/head ($r = 0.30$), yield/head ($r = 0.26$), plot yield ($r =$

0.24) but negative correlation with stem diameter (r = -0.11), head diameter (r = -0.07) and 1000-seed weight (r =-0.35) (Table 4). Amin *et al*. (2016) reported that days to maturity correlated significantly and negatively with number of achene's per head.

Plant height

Highly significant and positive correlation of plant height with stem diameter (r = 0.55; p ≤ 0.01) and head diameter (r = 0.62; p ≤ 0.01) was recorded. Plant height was positively and non-significantly correlated with number of seed/head, yield/head and plot yield but negatively correlated with 1000-seed weight (Table 4). Farhatullah *et al*. (2006) had reported highly significant correlation of plant height with head diameter in sunflower. Amin *et al*. (2016) reported that plant height had positive and significant relation with stem diameter, head diameter, 100-achene weight and achene yield per plant.

Stem diameter

Positive and highly significant correlation between stem diameter with head diameter (r = 0.76; p ≤ 0.01) was recorded. Stem diameter also showed positive and non-significant correlation with number of seed/head, 1000-seed weight, yield/head and plot yield. Mudassar *et al*., (2013) reported that stem diameter exhibited positive and significant correlation with head diameter in sunflower.

Head diameter

Head diameter showed positive and significant correlation with yield/head (r = 0.46; p ≤ 0.01). Head diameter exerted non-significant positive correlation with number of seed/head (r =0.18), 1000-seed weight (r =0.26), plot yield (r =0.37). Positive and significant correlation between head diameter and yield/head in sunflower hybrid was reported by Farhatullah *et al*., (2006). Khan *et al* (2003), Ozer *et al.* (2003) and Sridhar *et al*. (2005) have reported that head diameter had positive and significant correlations with achene yield. Mudassar *et al.,(*2013) reported that head diameter had significant association with whorls per head.

Number of seed/head

Number of seed/head showed positive and highly significant correlation with yield/head (r= 0.83; $p \leq 0.01$) and plot yield (r = 0.62; $p \leq 0.01$) but non-significant positive correlation with 1000-seed weight. The positive correlation of seed/head with yield/head and plot yield might imply that the sunflower yield will be increased if number of seed/head increased. Therefore, this character is most important in selection of high yielding sunflower line. Farhatullah *et al*., (2006) and Hladni *et al*. (2010) also reported a positive and significant correlation between seed/head and yield in sunflower.

1000-seed weight

1000-seed weight showed positive and non-significant correlation with yield/head and plot yield. Many researchers have reported significant and positive correlation between 1000-seed weight and seed yield (Rigon *et al.* (2014), Joksimović et al. (2004), Kaya et al. (2009), Mijić et al. (2009) and Anandhan et al. (2010).

Yield/head

Yield/head showed positive and highly significant correlation with plot yield (r= 0.73; $p \leq 0.01$). This indicates that strong association of these characters with plot yield could be fruitfully exploited for enhancing the yield potential in sunflower. This also indicated that simultaneous selection for these characters might bring an improvement in plot yield. Similar results were also reported by Nehru and Manjunath (2003) and Prasad *et al*. (2006).

Table 5. Direct and indirect effects of different characteristics on seed yield of sunflower accession

Characters	DF	DM	PH	SD	HD	SH	SW	YHG	Correlation
DF	**0.787**	-0.002	0.063	-0.470	0.057	-0.084	-0.09	0.01	0.27^{ns}
DM	0.039	**-0.037**	0.038	0.089	-0.02	0.114	-0.11	0.125	0.24^{ns}
PH	0.181	-0.005	**0.272**	-0.446	0.177	0.095	-0.025	0.121	0.37^{ns}
SD	0.456	0.004	0.150	**-0.811**	0.217	0.057	0.053	0.193	0.32^{ns}
HD	0.157	0.003	0.169	-0.616	**0.285**	0.069	0.081	0.222	0.37^{ns}
SH	-0.173	-0.011	0.068	-0.122	0.051	**0.381**	0.025	0.401	0.61**
SW	-0.228	0.013	-0.022	-0.138	0.074	0.03	**0.313**	0.077	0.12^{ns}
YHG	0.015	-0.010	0.068	-0.324	0.131	0.316	0.050	**0.483**	0.73**

Note: **Bold: Direct effect, Normal: Indirect effect**

*significant at $p \leq 0.05$, **significant at $p \leq 0.01$, ns: non-significant
DF: Days to 50% flowering (cm), DM: Days to maturity (cm), PH: Plant Height (cm), SD: Stem Diameter (cm), HD: Head Diameter (cm), SH: No. Seed /head (cm), SW: 1000-seed weight (cm), YHG: yield/head (g)

4.4 Direct and indirect effects of different characteristics on seed yield of sunflower accessions

The direct and indirect contribution of various independent characters on a dependent character can be determined by using path coefficient analysis. Path coefficient analysis is supportive in partitioning the correlation into direct and indirect effects so that relative contribution of each component character to the yield could be evaluated (Singh and Narayanam, 2007). In this study direct and indirect effects of different characters like days to flowering, days to maturity, plant height, stem diameter, head diameter, number of seed/head, 1000-seed weight and yield/head on plot yield was studied through path coefficient analysis as shown in Table 5.

Days to flowering

The path analysis revealed that, the character days to flowering had the maximum direct effect (0.787) on plot yield. It had positive but indirect effect on plot yield through plant height, head diameter, and yield/head (0.063, 0.057 and 0.01 respectively) while negative indirect effect via days to maturity, stem diameter, seeds per head and 1000-seed weight (-0.002, -0.470, -0.084 and -0.09), respectively. Arshad *et.al*. (2018) also reported positive direct effect of days to flowering on sunflower yield.

Days to maturity

Days to maturity had negative direct effect (-0.037) on seed yield, while positive indirect effect via days to flowering, plant height, stem diameter, seeds per head and yield/head (0.039, 0.038, 0.089, 0.114 and 0.125 respectively) and negative indirect effect through head diameter and 1000-seed weight (-0.02 and -0.11) respectively. Tyagi *et al*., (2013) reported negative direct effect of Days to maturity on seed yield in sunflower.

Plant height

Path coefficient analysis revealed that plant height had positive direct effect (0.272) on seed yield, while positive indirect effect via, days to flowering, head diameter, seeds per head and yield/head (0.181, 0.177, 0.095, and 0.121 respectively). Plant height had negative indirect effect through days to maturity, stem diameter, 1000-seed weight (-0.005, -0.446, and -0.025) respectively. Farhatullah *et al.*, (2006), Machikowa and Saetang (2008), Arshad *et.al*. (2018) observed direct effect of plant height on sunflower yield.

Stem diameter

Stem diameter had negative direct effect (-0.811) on seed yield, while positive indirect effect via days to flowering (0.456), days to maturity (0.004), plant height (0.150), head diameter (0.217), seeds per head (0.057), 1000-seed weight (0.053) and yield/head (0.193) respectively on seed yield. These results did not agree with the report by (Machikowa and Saetang, 2008; Kaya *et al.*, 2007; Hladni *et al.*, 2006) who found high positive direct effect of stem diameter on sunflower seed yield.

Head diameter

For the trait, head diameter had positive direct effect (0.285) on seed yield, while positive indirect effect via days to flowering, days to maturity, Plant height, seeds per head, 1000-seed weight and yield/head on seed yield. Farhatullah *et al.*, (2006), Machikowa and Saetang, (2008), Kholghi *et al.*, (2011), and Arshad *et.al*. (2018) also reported positive direct effect of head diameter on seed yield in sunflower.

Seeds per head

Seeds per head had positive direct effect on seed yield and positive indirect effect through plant height, head diameter, 1000-seed weight and yield/head (0.068, 0.051, 0.025 and 0.401 respectively) while negative indirect effects via days to flowering, days to maturity, stem diameter (-0.173, -0.011, and -0.122 respectively) on seed yield of sunflower. Farhatullah *et al*. (2006), Machikowa and Saetang, (2008), Hladni *et al*. (2010), Abrar *et al*. (2010) and Kholghi *et al.* (2011), also found positive direct effect of number of seed per head in sunflower.

1000-seed weight

The direct effect of 1000-seed weight on seed yield was positive (0.313), while it was also showed positive indirect effect through days to maturity, head diameter, seeds per head and yield/head (0.013, 0.074, 0.03 and 0.077 respectively). For the trait, negative indirect effect through days to flowering, plant height, and stem diameter (-0.228, -0.022, and -0.138 respectively). Positive direct effect of seed weight on seed yield in sunflower was reported by Farhatullah *et al*., (2006), Hladni *et al*. (2010), Kholghi et al., (2011), though a negative direct effect of seed weight on seed yield was noticed in sunflower by many researcher (Machikowa and Saetang, 2008, Arshad *et.al*. 2018).

Yield/head

Yield/head had positive direct effect (0.483) on seed yield and positive indirect effect through days to flowering, plant height, head diameter, seeds per head, and 1000-seed weight (0.015, 0.068, 0.131, 0.316 and 0.050 respectively) on seed yield of sunflower.

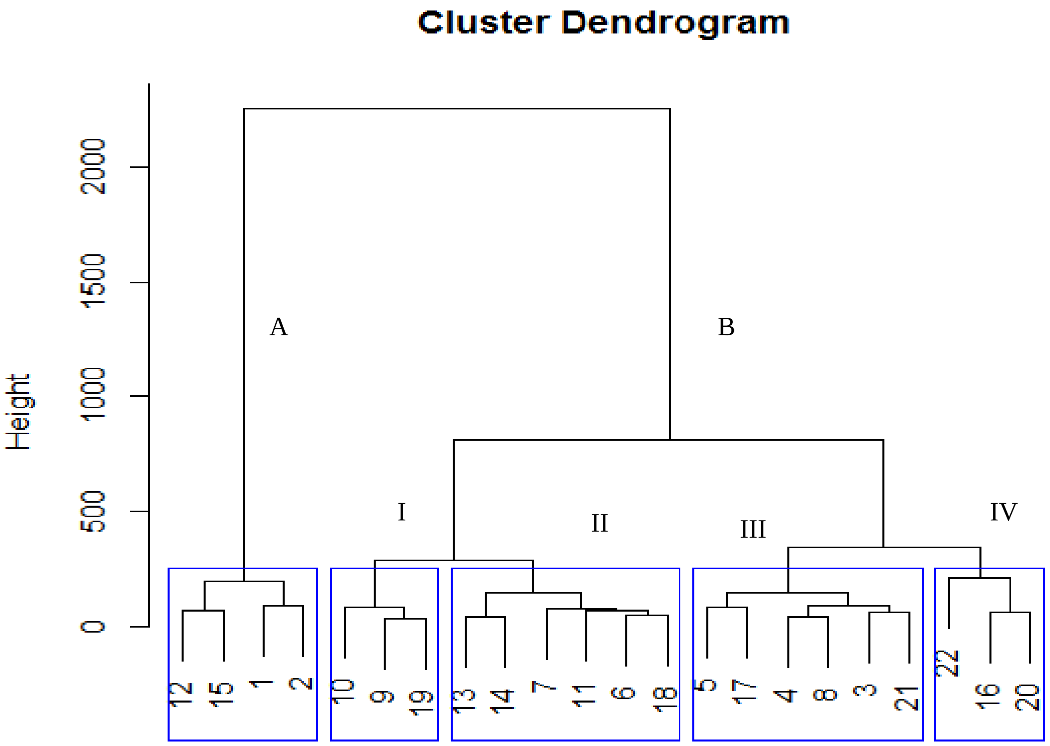


Figure-3. Cluster Dendrogram of 22 sunflower accessions used for morphological analysis

4.5 Cluster analysis

The 22 sunflower accessions were classified in to main two groups by cluster analysis (Figure 3). Hierarchical clustering indicates the degree of diversity among the lines and this information can be efficiently used in selection of lines for varietal development (Sultana *et al.,* 2006). A superior hybrid could be developed by combining two genetically diverse parents. Thus, cluster analysis could provide useful information about the variability of the lines under study. The germplasm that show a divergency along with better performance for yield and yield contributing traits might be used in sunflower varietal improvement program (Nasreen *et al.,* 2011).

The results of cluster dendrogram revealed that genotypes exhibited considerable variation, although some exceptions existed (Figure 3). All sunflower accessions by cluster analysis were divided into 2 groups (Group A & B) based on quantitative traits. The first group A consisted of four genotypes viz: 12 (GP04023), 15 (BD9385), 1(BARISurjamukhi-2), and 2(BHACPS2). The second group B again sub-divided into four subgroups of I-IV. The first subgroup I consisted of three genotypes as 10 (GP04018), 9(GP04017), and 19(BHAC-SH-S7-04038). The second subgroup II consisted of six genotypes as 13(GP04024), 14(GP04028), 7(GP04015), 11(GP04019), 6(GP04011), 18(BHAC-SH-S7-04032) respectively. The subgroup III contained genotypes of 5(GP01009), 17(BD931), 4(GP01005), 8(GP04016), 3(GP01004), 21(SUN-W-S7-101) and the subgroup IV contained of 22(MiniatureP1), 16(BD9360) and 20 (BHAC-SH-S7-04016) sunflower accessions. Genotypes in same group were more closely related to one another than the genotypes in the anothert groups. Similarly, the accessions in group A were more distantly related compare to the accessions in group B. From the Figure 3 it was found that the group A contained four accessions. Highest number of sunflower accessions were fall in sub-group II and

III (6 accessions), while the subgroup I and IV contained least number (3 accessions) of sunflower accessions.

Table 6: Grouping of 22 sunflower accessions as promising for different characters

Accessions	**Promising sunflower accessions**
Days to 50% flowering (<65 days)	GP04017, BHAC-SH-S7-04032
Days to maturity (<101 days)	GP01004, GP01005, GP01009, GP04011, GP04017, GP04023, GP04024
Plant Height (< 90cm)	BHACPS2 (Check-2), GP01004, GP01005, GP01009, GP04011, GP04016, GP04017, GP04018, GP04019, GP04023, GP04028, BD931
1000-seed weight (>60 g)	BARI Surjamukhi-2 (Check-1), BHACPS2 (Check-2), GP01005, GP01011, GP04015, GP04016, GP04018, GP04023, BHAC-SH-S7-04032, BHAC-SH-S7-04038, BHAC-SH-S7-04016, SUN-W-S7-101

4.5.1 Grouping of 22 sunflower accessions as promising for different characters

In this study none of the accessions have performed better for all the characters studied but some of the accessions were found to be promising for different characters (Table 6). The accession which took less number of days for flowering (GP04017, BHAC-SH-S7-04032) and maturity (GP01004, GP01005, GP01009, GP04011, GP04017, GP04023, GP04024) could be considered as early maturing genotype. Plant height is an important phenomenon for developing dwarf variety for wind prone area. Therefore, the accessions were found less plant height (BHACPS2 (Check-2), GP01004, GP01005, GP01009, GP04011, GP04016, GP04017, GP04018, GP04019, GP04023, GP04028, BD931) could be used for dwarf trait. Seed weight also an important yield contributing traits in sunflower, therefore accessions showing higher 1000-seed weight (BARISurjamukhi-2 (Check-1), BHACPS2 (Check-2), GP01005, GP01011, GP04015, GP04016, GP04018, GP04023, BHAC-SH-S7-04032, BHAC-SH-S7-04038, BHAC-SH-S7-04016, SUN-W-S7-101) might be used for developing high yielding sunflower variety. These accessions could be used as a base material to develop desirable variety. Besides, a gene pool also can be developed by combining all the accessions with desired traits. Rully and Anik (2016), Vivek *et al.* (2019) also found different sunflower accessions promising for different characters.

CHAPTER V

SUMMARY AND CONCLUSION

5.1 Summary

A total of 22 sunflower germplasms including two checks were grown at the research field of ORC, BARI, Gazipur during rabi season 2018-19 with the objective to find out the divergency among the genotypes. The experiment was conducted following Augmented design, with two check (BARI surjamukhi-2 and BHAC-PS-2). In order to find accessions with desired characters analysis of variance, mean performance of sunflower genotypes, character associations, direct and indirect effects of yield contributing characters on seed yield, cluster dandogram analysis were studied and the results are summarized as below:

The Analysis of variance showed that the adjusted treatment effects were highly significant for most of the characters which might implies the existence of significant variability among the accessions for the characters studied.

The mean performances recorded for various traits indicated a lot of variation for the studied traits in the present material. Days to flowering ranged from 63 to 79 days and the genotype GP04017 was the early flowering genotype (63 days to 50% flowering). Days to maturity ranged from 98 to 109 days and the genotype GP04024 took least number of days (98 days). Therefore, these genotypes might be considered as early maturing sunflower genotype. The genotype GP04011 and GP01009 was the dwarf (59.22 cm and 63.82cm, respectively) stature accessions among the tested materials. The sunflower genotype GP04015 produced thick stem plant of 2.22 cm. Dwarf type and thick stem plants have some importance as these were not easy to damage by wind flow and easier to harvest. Therefore, these genotypes could be selected for dwarfism and thick stem. The genotype MiniatureP1 produced wider head (17.95 cm), the highest number of seeds per head was found to be produced by the genotype BD9385 (256 seeds). The genotype GP04016 and GP04018 produced maximum 1000-seed weight (78.54g). The genotype BHACPS2 (Check-2) gave highest yield/head (29.24 g) and produced higher yield 725.15g. Therefore, the genotype MiniatureP1, BD9385, GP04016, GP04018 and BHACPS2 could be selected as high yield potential sunflower accessions.

Character association between seed yield and morphological traits are effectively studied by the simple correlation coefficient analysis. Character association studies revealed that days to 50% flowering had highly significant and positive correlation with stem diameter ($r = 0.5841$; $p \leq 0.01$). Days to maturity showed positive and non-significant correlation with plant height ($r = 0.1414$), number of seed /head ($r = 0.3034$), yield/head ($r = 0.2565$), Plot yield ($r = 0.2407$). Plant height showed positive and highly significant correlation with stem diameter ($r = 0.5527$; $p \leq 0.01$) and head diameter ($r = 0.6182$; $p \leq 0.01$). Highly significant and positive correlation between stem diameter with head diameter, head diameter with yield/head, number of seed/head with yield/head and plot yield was found in this study. Seed weight showed positive and non-significant correlation with yield/head and plot yield. Yield/head showed positive and highly significant correlation with plot yield. In this study, significant associations were found between plot yield with number of seed/head and yield/head. This experiment, suggested that the selection for yield of sunflower, it should be made through the selection for number of seed/head and yield/head.

Correlations of different independent characters on dependent character were partitioned into direct and indirect effects to investigate the selection criteria in sunflower. The partitioning of these correlations showed that days to 50% flowering and yield/head exhibited high direct effects on sunflower seed yield. Besides, from this study plant height, head diameter, number of seed/head and 1000-seed weight also had direct effect on sunflower yield which might be a good indicator for seed yield. Therefore, beside selection for yield per seed which are practicing in most of the crops, this study showed that selection for yield in sunflower may be done through these traits.

Cluster analysis was also used to identify the diverse accessions. Based on quantitative traits, all sunflower accessions by cluster analysis were divided into 2 groups which are group A and group B. The group B again divided into four sub-groups such as: I, II, III and IV. Group A were found to be consisted four genotypes (GP04023, BD9385, BARISurjamukhi-2, and BHACPS2). The sub group II and III were contained maximum 6 number of genotypes which are (GP04024, GP04028, GP04015, GP04019, GP04011, BHAC-SH-S7-04032) and (GP01009, BD931, GP01005, GP04016, GP01004, SUN-W-S7-101), respectively. On the other hand, both the sub-group I and IV consisted three genotypes of (GP04018, GP04017, BHAC-SH-S7-04038) and (MiniatureP1, BD9360 and BHAC-SH-S7-04016), respectively. The genotypes which fall in same group were more closely related, but the genotypes were more distantly related which are fall in another group. Therefore, more heterotic sunflower variety could be developed by using the genotypes from different group.

In this study, no single accessions were found as promising for all the characters but different accessions were found promising for different characters. Two accession (GP04017, BHAC-SH-S7-04032) and seven accession (GP01004, GP01005, GP01009, GP04011, GP04017, GP04023, GP04024) were found early maturing as they took least number of days to 50% flowering (<65 days) and maturity (<101 days), respectively. The accessions BHACPS2 (Check-2), GP01004, GP01005, GP01009, GP04011, GP04016, GP04017, GP04018, GP04019, GP04023, GP04028, BD931) were identified as short stature plants with plant height less than 90 cm. The accessions BARISurjamukhi-2 (Check-1), BHACPS2 (Check-2), GP01005, GP01011, GP04015, GP04016, GP04018, GP04023, BHAC-SH-S7-04032, BHAC-SH-S7-04038, BHAC-SH-S7-04016, and SUN-W-S7-101) produced higher 1000-seed weight (>60 g). Therefore, these accessions could be used to develop desirable variety of early maturing, dwarf and high yielding sunflower variety.

5.2 Conclusion

A field study was conducted to analyze the divergence for yield and yield contributing characters of 22 sunflower germplasms including two checks at the research field of ORC, BARI, Gazipur during rabi season 2018-19. Analysis of variance showed that the adjusted treatment effects were highly significant for all the characters except for the character days to flowering which indicates that there were marked variations among the sunflower accessions for the studied characters. The mean performances indicated that GP04017 and GP04024 respectively considered as early flowering and early maturing genotypes. The genotypes GP04011 and GP01009 were dwarf types in nature whereas genotype GP04015 produced thick stem. The sunflower genotype MiniatureP1, BD9385, GP04016, GP04018 and BHACPS2 having high yield potentiality. In this study, highly significant and positive correlation was found for days to flowering with stem diameter, plant height with stem diameter and head diameter, stem diameter with head diameter, head diameter with yield/head, number of seed/ head with yield/head and plot yield, yield/head with plot yield, plot yield with the number of seed/head and yield/head except for days to maturity and seed weight. The positive direct effect with days to flowering, plant height, head diameter, no. seed /head, 1000-seed weight, yield/head and negative direct effect days to maturity, stem diameter on seed yield were observed. The cluster analysis enables the selection of genotypes with desirable traits. Cluster analysis divided into two groups (A and B) and group B again divided into four sub-groups (I, II, III and IV). The highest seed yield was recorded from group A and contained 4 genotypes. Sub-group II and III were contained a maximum of 6 number genotypes and both the sub-group I and IV consisted of three genotypes. The selection of these traits would be more effective to bring about simultaneous improvement for yield in sunflower.

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APPENDICES

Appendices I and II: Analysis of variance for nine quantitative traits in 22 genotypes of sunflower & Mean Performance of 22 Sunflower Accessions for nine different agro-morphological traits

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block df
1   101     1  BARISurjamukhi2     1 77
2   102     2          BHACPS2     1 67
3   103     3          GP01004     1 72
4   104     4          GP01005     1 74
5   105     5          GP01009     1 71
6   106     6          GP04011     1 71
7   107     7          GP04015     1 76
8   108     8  BARISurjamukhi2     1 74
9   109     9          BHACPS2     2 72
10  110    10          GP04016     2 78
11  111    11          GP04017     2 63
12  112    12          GP04018     2 69
13  113    13          GP04019     2 75
14  114    14          GP04023     2 78
15  115    15  BARISurjamukhi2     2 74
16  116    16          BHACPS2     3 72
17  117    17          GP04024     3 70
18  118    18          GP04028     3 79
19  119    19           BD9385     3 76
20  120    20           BD9360     3 77
21  121    21            BD931     3 77
22  122    22  BARISurjamukhi2     3 77
23  123    23          BHACPS2     4 70
24  124    24 BHAC-SH-S7-04032     4 62
25  125    25 BHAC-SH-S7-04038     4 65
26  126    26 BHAC-SH-S7-04016     4 64
27  127    27      SUN-W-S7-101     4 68
28  128    28       MiniatureP1     4 76
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "df"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(df~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: df
            Df Sum Sq Mean Sq F value  Pr(>F)
block.unadj  3 209.57  69.857 12.5117 0.03341 *
trt.adj     21 415.39  19.781  3.5428 0.16240
Residuals    3  16.75   5.583
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(df~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: df
          Df Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 615.96 29.3316  5.2534 0.09822 .
block.adj  3   9.00  3.0000  0.5373 0.68867
Residuals  3  16.75  5.5833
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> model<- DAU.test(Block,Name.,df,method="lsd",group=TRUE)
```

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block  dm
1   101     1  BARISurjamukhi2     1 107
2   102     2          BHACPS2     1 101
3   103     3          GP01004     1  72
4   104     4          GP01005     1  74
5   105     5          GP01009     1  71
6   106     6          GP04011     1  71
7   107     7          GP04015     1  76
8   108     8  BARISurjamukhi2     1 108
9   109     9          BHACPS2     2 103
10  110    10          GP04016     2 105
11  111    11          GP04017     2 101
12  112    12          GP04018     2 110
13  113    13          GP04019     2 104
14  114    14          GP04023     2 102
15  115    15  BARISurjamukhi2     2 110
16  116    16          BHACPS2     3 103
17  117    17          GP04024     3  98
18  118    18          GP04028     3 109
19  119    19           BD9385     3 102
20  120    20           BD9360     3 105
21  121    21            BD931     3 110
22  122    22  BARISurjamukhi2     3 107
23  123    23          BHACPS2     4 102
24  124    24 BHAC-SH-S7-04032     4 104
25  125    25 BHAC-SH-S7-04038     4 103
26  126    26 BHAC-SH-S7-04016     4  99
27  127    27     SUN-W-S7-101     4 100
28  128    28      MiniatureP1     4 106
> attach(d)
> names(d)
[1] "Plot"  "Entry" "Name." "Block" "dm"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
```

```
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(dm~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: dm
            Df  Sum Sq Mean Sq F value    Pr(>F)
block.unadj  3 2123.92  707.97  674.26 9.671e-05 ***
trt.adj     21 2249.04  107.10  102.00  0.001375 **
Residuals    3    3.15    1.05
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(dfm~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
Error in eval(predvars, data, env) : object 'dfm' not found
> anova(model2)
Analysis of Variance Table

Response: dm
          Df Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 615.96 29.3316  5.2534 0.09822 .
block.adj  3   9.00  3.0000  0.5373 0.68867
Residuals  3  16.75  5.5833
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> model<- DAU.test(Block,Name.,dm,method="lsd",group=TRUE)
> print(model$groups)
                        dm groups
BD931            110.12500      a
GP04028          109.12500     ab
MiniatureP1      109.12500     ab
GP04018          108.62500    abc
BARISurjamukhi2  108.00000    abc
BHAC-SH-S7-04032 107.12500   abcd
BHAC-SH-S7-04038 106.12500  abcde
BD9360           105.12500  bcdef
GP04016          103.62500  bdefg
SUN-W-S7-101     103.12500  cdefg
GP04019          102.62500   defg
BHACPS2          102.25000    efg
BD9385           102.12500    efg
BHAC-SH-S7-04016 102.12500    efg
GP04023          100.62500    efg
GP04017           99.62500     fg
GP04024           98.12500      g
GP04015           75.79167      h
GP01005           73.79167     hi
GP01004           71.79167     hi
GP01009           70.79167      i
GP04011           70.79167      i
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block   phcm
1   101     1  BARISurjamukhi2     1 131.00
```

```
2   102     2           BHACPS2     1  68.44
3   103     3           GP01004     1  97.60
4   104     4           GP01005     1  95.40
5   105     5           GP01009     1  73.60
6   106     6           GP04011     1  69.00
7   107     7           GP04015     1 101.00
8   108     8   BARISurjamukhi2     1 134.00
9   109     9           BHACPS2     2  66.70
10  110    10           GP04016     2  85.40
11  111    11           GP04017     2  69.60
12  112    12           GP04018     2  73.20
13  113    13           GP04019     2  86.60
14  114    14           GP04023     2  85.80
15  115    15   BARISurjamukhi2     2 140.00
16  116    16           BHACPS2     3  67.40
17  117    17           GP04024     3  97.60
18  118    18           GP04028     3  87.00
19  119    19            BD9385     3 111.40
20  120    20            BD9360     3 106.80
21  121    21             BD931     3  75.00
22  122    22   BARISurjamukhi2     3 139.00
23  123    23           BHACPS2     4  64.40
24  124    24 BHAC-SH-S7-04032     4  97.20
25  125    25 BHAC-SH-S7-04038     4  87.40
26  126    26 BHAC-SH-S7-04016     4  97.40
27  127    27      SUN-W-S7-101     4 102.40
28  128    28       MiniatureP1     4 106.40
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "phcm"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(phcm~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: phcm
            Df  Sum Sq Mean Sq F value   Pr(>F)
block.unadj  3   510.5  170.18  15.295 0.025328 *
trt.adj     21 13048.4  621.35  55.844 0.003366 **
Residuals    3    33.4   11.13
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(phcm~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: phcm
          Df  Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 13529.5  644.26 57.9036 0.00319 **
block.adj  3    29.4    9.81  0.8815 0.54007
```

```
Residuals  3    33.4   11.13
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> model<- DAU.test(Block,Name.,phcm,method="lsd",group=TRUE)
> print(model$groups)
                      phcm groups
MiniatureP1      143.36750      a
SUN-W-S7-101     139.36750     ab
BARISurjamukhi2  136.00000     ab
BHAC-SH-S7-04016 134.36750     ab
BHAC-SH-S7-04032 134.16750     ab
BHAC-SH-S7-04038 124.36750     bc
BD9385           109.56750     cd
BD9360           104.96750     de
GP04024           95.76750    def
GP04015           91.22083   defg
GP01004           87.82083   efgh
GP01005           85.62083   fghi
GP04028           85.16750   fghi
GP04019           84.61750   fghi
GP04023           83.81750   fghi
GP04016           83.41750   fghi
BD931             73.16750   ghij
GP04018           71.21750    hij
GP04017           67.61750     ij
BHACPS2           66.73500      j
GP01009           63.82083      j
GP04011           59.22083      j
```

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block sdcm
1   101     1  BARISurjamukhi2     1 1.80
2   102     2          BHACPS2     1 1.46
3   103     3          GP01004     1 1.62
4   104     4          GP01005     1 1.54
5   105     5          GP01009     1 1.24
6   106     6          GP04011     1 1.46
7   107     7          GP04015     1 2.25
8   108     8  BARISurjamukhi2     1 1.82
9   109     9          BHACPS2     2 1.59
10  110    10          GP04016     2 1.70
11  111    11          GP04017     2 1.14
12  112    12          GP04018     2 1.34
13  113    13          GP04019     2 1.30
14  114    14          GP04023     2 1.54
15  115    15  BARISurjamukhi2     2 1.76
16  116    16          BHACPS2     3 1.48
17  117    17          GP04024     3 1.22
18  118    18          GP04028     3 1.66
19  119    19           BD9385     3 1.76
20  120    20           BD9360     3 1.80
21  121    21            BD931     3 1.18
22  122    22  BARISurjamukhi2     3 1.84
23  123    23          BHACPS2     4 1.58
24  124    24 BHAC-SH-S7-04032     4 1.30
```

```
25  125    25 BHAC-SH-S7-04038     4 1.34
26  126    26 BHAC-SH-S7-04016     4 1.38
27  127    27     SUN-W-S7-101     4 1.40
28  128    28      MiniatureP1     4 1.94
> attach(d)
> names(d)
[1] "Plot"  "Entry" "Name." "Block" "sdcm"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(sdcm~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: sdcm
            Df  Sum Sq  Mean Sq F value  Pr(>F)
block.unadj  3 0.13363 0.044542  11.030 0.03966 *
trt.adj     21 1.70440 0.081162  20.098 0.01509 *
Residuals    3 0.01212 0.004038
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(sdcm~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: sdcm
          Df  Sum Sq  Mean Sq F value  Pr(>F)
trt.unadj 21 1.83317 0.087294 21.6163 0.01358 *
block.adj  3 0.00486 0.001620  0.4012 0.76356
Residuals  3 0.01211 0.004038
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> model<- DAU.test(Block,Name.,sdcm,method="lsd",group=TRUE)
> print(model$groups)
                     sdcm groups
GP04015          2.222917      a
MiniatureP1      2.026250     ab
BD9360           1.806250     bc
BARISurjamukhi2  1.805000     bc
BD9385           1.766250    bcd
GP04016          1.691250   bcde
GP04028          1.666250   cdef
GP01004          1.592917  cdefg
GP04023          1.531250 cdefgh
BHACPS2          1.527500  defgh
GP01005          1.512917  defgh
SUN-W-S7-101     1.486250  defgh
BHAC-SH-S7-04016 1.466250 defghi
GP04011          1.432917 defghi
BHAC-SH-S7-04038 1.426250 defghi
BHAC-SH-S7-04032 1.386250  efghi
GP04018          1.331250   fghi
GP04019          1.291250    ghi
```

```
GP04024          1.226250     hi
GP01009          1.212917     hi
BD931            1.186250     hi
GP04017          1.131250      i
```

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block  hdcm
1   101     1  BARISurjamukhi2     1 15.00
2   102     2          BHACPS2     1 13.10
3   103     3          GP01004     1 13.00
4   104     4          GP01005     1 12.40
5   105     5          GP01009     1  9.20
6   106     6          GP04011     1 11.40
7   107     7          GP04015     1 14.75
8   108     8  BARISurjamukhi2     1 15.40
9   109     9          BHACPS2     2 13.00
10  110    10          GP04016     2 11.80
11  111    11          GP04017     2  7.80
12  112    12          GP04018     2  9.80
13  113    13          GP04019     2  8.20
14  114    14          GP04023     2  8.60
15  115    15  BARISurjamukhi2     2 14.80
16  116    16          BHACPS2     3 11.80
17  117    17          GP04024     3  7.80
18  118    18          GP04028     3 10.60
19  119    19           BD9385     3 11.80
20  120    20           BD9360     3 14.00
21  121    21            BD931     3  9.80
22  122    22  BARISurjamukhi2     3 15.40
23  123    23          BHACPS2     4 12.30
24  124    24 BHAC-SH-S7-04032     4 12.20
25  125    25 BHAC-SH-S7-04038     4 11.20
26  126    26 BHAC-SH-S7-04016     4 11.80
27  127    27      SUN-W-S7-101     4 13.40
28  128    28       MiniatureP1     4 16.40
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "hdcm"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(hdcm~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: hdcm
            Df  Sum Sq Mean Sq F value  Pr(>F)
block.unadj  3  28.575  9.5250  27.636 0.01096 *
trt.adj     21 128.633  6.1254  17.772 0.01803 *
Residuals    3   1.034  0.3447
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(hdcm~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: hdcm
          Df  Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 156.842  7.4687  21.669 0.01353 *
block.adj  3   0.366  0.1220   0.354 0.79180
Residuals  3   1.034  0.3447
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> model<- DAU.test(Block,Name.,hdcm,method="lsd",group=TRUE)
> print(model$groups)
                  hdcm groups
MiniatureP1      17.95      a
BARISurjamukhi2  15.15      b
SUN-W-S7-101     14.95     bc
BD9360           14.25    bcd
GP04015          14.10    bcd
BHAC-SH-S7-04032 13.75   bcde
BHAC-SH-S7-04016 13.35   bcde
BHAC-SH-S7-04038 12.75   cdef
BHACPS2          12.55    def
GP01004          12.35    def
BD9385           12.05    def
GP01005          11.75    def
GP04016          11.75   defg
GP04028          10.85   efgh
GP04011          10.75  efghi
BD931            10.05   fghi
GP04018           9.75   fghi
GP01009           8.55    ghi
GP04023           8.55     hi
GP04019           8.15     hi
GP04024           8.05      i
GP04017           7.75      i
```

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block  sh
1   101     1  BARISurjamukhi2     1 214
2   102     2          BHACPS2     1 228
3   103     3          GP01004     1 114
4   104     4          GP01005     1 101
5   105     5          GP01009     1  58
6   106     6          GP04011     1 110
7   107     7          GP04015     1 115
8   108     8  BARISurjamukhi2     1 222
9   109     9          BHACPS2     2 249
10  110    10          GP04016     2  79
11  111    11          GP04017     2 192
12  112    12          GP04018     2 160
13  113    13          GP04019     2  65
```

```
14  114    14          GP04023     2 210
15  115    15  BARISurjamukhi2     2 210
16  116    16          BHACPS2     3 224
17  117    17          GP04024     3  92
18  118    18          GP04028     3  76
19  119    19           BD9385     3 251
20  120    20           BD9360     3 223
21  121    21            BD931     3  64
22  122    22  BARISurjamukhi2     3 213
23  123    23          BHACPS2     4 231
24  124    24 BHAC-SH-S7-04032     4 123
25  125    25 BHAC-SH-S7-04038     4 213
26  126    26 BHAC-SH-S7-04016     4 199
27  127    27      SUN-W-S7-101     4 140
28  128    28       MiniatureP1     4  97
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "sh"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(sh~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: sh
            Df Sum Sq Mean Sq F value   Pr(>F)
block.unadj  3   2412   803.9  7.5842 0.065089 .
trt.adj     21 113869  5422.4 51.1543 0.003833 **
Residuals    3    318   106.0
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(sh~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: sh
          Df Sum Sq Mean Sq F value   Pr(>F)
trt.unadj 21 116154  5531.2 52.1808 0.003722 **
block.adj  3    127    42.2  0.3986 0.765069
Residuals  3    318   106.0
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> model<- DAU.test(Block,Name.,sh,method="lsd",group=TRUE)
> print(model$groups)
                        sh groups
BD9385           256.37500      a
BHACPS2          233.00000     ab
BD9360           228.37500    abc
BARISurjamukhi2  214.75000    abc
BHAC-SH-S7-04038 205.87500   abcd
GP04023          204.37500   abcd
```

```
BHAC-SH-S7-04016 191.87500    bcd
GP04017          186.37500    cde
GP04018          154.37500    def
SUN-W-S7-101     132.87500    efg
GP04015          117.54167    fgh
GP01004          116.54167    fgh
BHAC-SH-S7-04032 115.87500   fghi
GP04011          112.54167   fghi
GP01005          103.54167   fghi
GP04024           97.37500    ghi
MiniatureP1       89.87500    ghi
GP04028           81.37500    ghi
GP04016           73.37500     hi
BD931             69.37500     hi
GP01009           60.54167      i
GP04019           59.37500      i


> d<-read.table('clipboard',header=T)
> d
   Plot Entry             Name. Block    sw
1   101     1  BARISurjamukhi2     1 65.00
2   102     2          BHACPS2     1 61.50
3   103     3          GP01004     1 60.00
4   104     4          GP01005     1 65.00
5   105     5          GP01009     1 60.00
6   106     6          GP04011     1 65.00
7   107     7          GP04015     1 80.00
8   108     8  BARISurjamukhi2     1 65.00
9   109     9          BHACPS2     2 57.00
10  110    10          GP04016     2 75.00
11  111    11          GP04017     2 50.00
12  112    12          GP04018     2 75.00
13  113    13          GP04019     2 50.00
14  114    14          GP04023     2 65.00
15  115    15  BARISurjamukhi2     2 60.00
16  116    16          BHACPS2     3 62.50
17  117    17          GP04024     3  5.70
18  118    18          GP04028     3  5.50
19  119    19           BD9385     3 18.00
20  120    20           BD9360     3 20.40
21  121    21            BD931     3  3.40
22  122    22  BARISurjamukhi2     3 65.00
23  123    23          BHACPS2     4 60.33
24  124    24 BHAC-SH-S7-04032     4 65.00
25  125    25 BHAC-SH-S7-04038     4 60.00
26  126    26 BHAC-SH-S7-04016     4 60.00
27  127    27      SUN-W-S7-101     4 60.00
28  128    28       MiniatureP1     4 50.00
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "sw"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(sw~ block.unadj + trt.adj)
```

```
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: sw
            Df Sum Sq Mean Sq F value    Pr(>F)    
block.unadj  3 7135.4 2378.47 24818.8 4.342e-07 ***
trt.adj     21 5363.0  255.38  2664.8 1.040e-05 ***
Residuals    3    0.3    0.10                      
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(sw~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: sw
          Df  Sum Sq Mean Sq F value    Pr(>F)    
trt.unadj 21 12462.8  593.46 6192.67 2.935e-06 ***
block.adj  3    35.6   11.88  123.93  0.001213 ** 
Residuals  3     0.3    0.10                      
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> model<- DAU.test(Block,Name.,sw,method="lsd",group=TRUE)
> print(model$groups)
                      sw groups
GP04016          78.54125      a
GP04018          78.54125      a
GP04015          78.20792      a
GP04023          68.54125      b
BHAC-SH-S7-04032 66.71125      c
BARISurjamukhi2  63.75000      d
GP01005          63.20792     de
GP04011          63.20792     de
BHAC-SH-S7-04016 61.71125      e
BHAC-SH-S7-04038 61.71125      e
SUN-W-S7-101     61.71125      e
BHACPS2          60.33250      f
GP01004          58.20792      g
GP01009          58.20792      g
GP04017          53.54125      h
GP04019          53.54125      h
MiniatureP1      51.71125      i
BD9360           18.69125      j
BD9385           16.29125      k
GP04024           3.99125      l
GP04028           3.79125      l
BD931             1.69125      m
```

```
> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block   yhg
1   101     1  BARISurjamukhi2     1 19.40
2   102     2          BHACPS2     1 30.56
3   103     3          GP01004     1  9.40
4   104     4          GP01005     1  6.60
5   105     5          GP01009     1  3.60
6   106     6          GP04011     1  8.00
7   107     7          GP04015     1 11.80
8   108     8  BARISurjamukhi2     1 17.80
9   109     9          BHACPS2     2 27.44
10  110    10          GP04016     2 11.00
11  111    11          GP04017     2  8.80
12  112    12          GP04018     2 11.00
13  113    13          GP04019     2  4.40
14  114    14          GP04023     2 13.00
15  115    15  BARISurjamukhi2     2 21.00
16  116    16          BHACPS2     3 29.72
17  117    17          GP04024     3  5.70
18  118    18          GP04028     3  5.50
19  119    19           BD9385     3 18.00
20  120    20           BD9360     3 20.40
21  121    21            BD931     3  3.40
22  122    22  BARISurjamukhi2     3 18.60
23  123    23          BHACPS2     4 29.24
24  124    24 BHAC-SH-S7-04032     4  7.60
25  125    25 BHAC-SH-S7-04038     4 13.40
26  126    26 BHAC-SH-S7-04016     4 13.20
27  127    27     SUN-W-S7-101     4 11.40
28  128    28      MiniatureP1     4 10.00
> attach(d)

> names(d)
[1] "Plot"  "Entry" "Name." "Block" "yhg"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(yhg~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: yhg
            Df  Sum Sq Mean Sq F value  Pr(>F)
block.unadj  3    4.74   1.579  0.4385 0.74203
trt.adj     21 1770.62  84.315 23.4197 0.01208 *
Residuals    3   10.80   3.600
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(yhg~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
```

```
Analysis of Variance Table

Response: yhg
          Df  Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 1775.34  84.540 23.4821 0.01204 *
block.adj  3    0.01   0.004  0.0011 0.99994
Residuals  3   10.80   3.600
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> model<- DAU.test(Block,Name.,yhg,method="lsd",group=TRUE)
> print(model$groups)
                       yhg groups
BHACPS2          29.240000      a
BD9360           20.460000      b
BARISurjamukhi2  19.200000      b
BD9385           18.060000     bc
GP04015          13.433333    bcd
GP04023          13.000000   bcde
GP01004          11.033333  bcdef
GP04016          11.000000  bcdef
GP04018          11.000000  bcdef
GP04011           9.633333   cdef
GP04017           8.800000   cdef
BHAC-SH-S7-04038  8.380000   cdef
GP01005           8.233333   cdef
BHAC-SH-S7-04016  8.180000   cdef
SUN-W-S7-101      6.380000    def
GP04024           5.760000    def
GP04028           5.560000    def
GP01009           5.233333    def
MiniatureP1       4.980000    def
GP04019           4.400000     df
BD931             3.460000     df
BHAC-SH-S7-04032  2.580000     ef


> d<-read.table('clipboard',header=T)
> d
   Plot Entry            Name. Block   pyg
1   101     1  BARISurjamukhi2     1 759.4
2   102     2          BHACPS2     1 786.6
3   103     3          GP01004     1 264.4
4   104     4          GP01005     1 341.6
5   105     5          GP01009     1 273.6
6   106     6          GP04011     1 168.0
7   107     7          GP04015     1 118.0
8   108     8  BARISurjamukhi2     1 719.8
9   109     9          BHACPS2     2 720.0
10  110    10          GP04016     2 331.0
11  111    11          GP04017     2 193.8
12  112    12          GP04018     2 236.0
13  113    13          GP04019     2 159.4
14  114    14          GP04023     2 638.0
15  115    15  BARISurjamukhi2     2 816.0
16  116    16          BHACPS2     3 681.0
17  117    17          GP04024     3 129.7
18  118    18          GP04028     3  95.5
19  119    19           BD9385     3 613.0
```

```
20  120    20           BD9360     3 380.4
21  121    21            BD931     3 228.4
22  122    22  BARISurjamukhi2     3 818.6
23  123    23          BHACPS2     4 713.0
24  124    24 BHAC-SH-S7-04032     4 182.6
25  125    25 BHAC-SH-S7-04038     4 173.4
26  126    26 BHAC-SH-S7-04016     4 343.2
27  127    27     SUN-W-S7-101     4 311.4
28  128    28      MiniatureP1     4 490.0
> attach(d)
> names(d)
[1] "Plot"  "Entry" "Name." "Block" "pyg"
> block.unadj <- as.factor(Block)
> trt.adj <- as.factor(Name.)
> block.adj <- as.factor(Block)
> trt.unadj <- as.factor(Name.)
> modelo1 <- formula(pyg~ block.unadj + trt.adj)
> model1 <- lm(modelo1)
> anova(model1)
Analysis of Variance Table

Response: pyg
            Df  Sum Sq Mean Sq F value  Pr(>F)
block.unadj  3   19490    6497  1.6312 0.34877
trt.adj     21 1687243   80345 20.1721 0.01501 *
Residuals    3   11949    3983
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
> glerror <- df.residual(model1)
> MSerror <- deviance(model1)/glerror
> modelo2 <- formula(pyg~ trt.unadj + block.adj)
> model2 <- lm(modelo2)
> anova(model2)
Analysis of Variance Table

Response: pyg
          Df  Sum Sq Mean Sq F value  Pr(>F)
trt.unadj 21 1705958   81236 20.3959 0.01477 *
block.adj  3     775     258  0.0649 0.97494
Residuals  3   11949    3983
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

> model<- DAU.test(Block,Name.,pyg,method="lsd",group=TRUE)
> print(model$groups)
                trt mean.adj     M
1  BARISurjamukhi2  778.4500     a
2  BHACPS2          725.1500     a
3  GP04023          621.8000    ab
4  BD9385           615.0000   abc
5  MiniatureP1      528.8000  abcd
6  BD9360           382.4000  bcde
7  BHAC-SH-S7-04016 382.0000 bcdef
8  SUN-W-S7-101     350.2000 bcdef
9  GP01005          338.1333 bcdef
10 GP04016          314.8000  cdef
11 GP01009          270.1333  cdef
12 GP01004          260.9333   def
```

```
13 BD931             230.4000   def
14 BHAC-SH-S7-04032 221.4000    ef
15 GP04018          219.8000    ef
16 BHAC-SH-S7-04038 212.2000    ef
17 GP04017          177.6000    ef
18 GP04011          164.5333    ef
19 GP04019          143.2000    ef
20 GP04024          131.7000    ef
21 GP04015          114.5333    ef
22 GP04028           97.5000     f
```

Appendices **III:** Correlations among different morphological characteristics of 22 sunflower accessions

CORRELATION ANALYSIS (By Statistical Tool for Agricultural Research (STAR))

Pearson's product-moment correlation, Prob > |r|

```
                       df        dm      phcm      sdcm      hdcm        sh        sw       yhg
pyg

df     coef        1.0000    0.0519    0.2310    0.5841    0.1972   -0.2203   -0.2897    0.0239
0.2701

       p-value               0.8185    0.3010    0.0043    0.3790    0.3246    0.1910    0.9158
0.2241

       n               22        22        22        22        22        22        22        22
22

dm     coef        0.0519    1.0000    0.1414   -0.1146   -0.0747    0.3034   -0.3536    0.2565
0.2407

       p-value     0.8185              0.5303    0.6116    0.7411    0.1699    0.1065    0.2491
0.2806

       n               22        22        22        22        22        22        22        22
22

phcm   coef        0.2310    0.1414    1.0000    0.5527    0.6182    0.2482   -0.0752    0.2461
0.3718

       p-value     0.3010    0.5303              0.0076    0.0022    0.2654    0.7394    0.2696
0.0884

       n               22        22        22        22        22        22        22        22
22

sdcm   coef        0.5841   -0.1146    0.5527    1.0000    0.7636    0.1468    0.1664    0.4034
0.3244

       p-value     0.0043    0.6116    0.0076              0.0000    0.5145    0.4592    0.0626
0.1407

       n               22        22        22        22        22        22        22        22
22

hdcm   coef        0.1972   -0.0747    0.6182    0.7636    1.0000    0.1827    0.2608    0.4553
0.3737

       p-value     0.3790    0.7411    0.0022    0.0000              0.4157    0.2412    0.0332
0.0867

       n               22        22        22        22        22        22        22        22
22

sh     coef       -0.2203    0.3034    0.2482    0.1468    0.1827    1.0000    0.0850    0.8280
0.6168

       p-value     0.3246    0.1699    0.2654    0.5145    0.4157              0.7069    0.0000
0.0022

       n               22        22        22        22        22        22        22        22
22

sw     coef       -0.2897   -0.3536   -0.0752    0.1664    0.2608    0.0850    1.0000    0.1553
0.1241
```

```
       p-value     0.1910    0.1065    0.7394    0.4592    0.2412    0.7069              0.4901
0.5821

       n               22        22        22        22        22        22        22        22
22

yhg    coef        0.0239    0.2565    0.2461    0.4034    0.4553    0.8280    0.1553    1.0000
0.7339

       p-value     0.9158    0.2491    0.2696    0.0626    0.0332    0.0000    0.4901
0.0001

       n               22        22        22        22        22        22        22        22
22

pyg    coef        0.2701    0.2407    0.3718    0.3244    0.3737    0.6168    0.1241    0.7339
1.0000

       p-value     0.2241    0.2806    0.0884    0.1407    0.0867    0.0022    0.5821    0.0001

       n               22        22        22        22        22        22        22        22
22
```

Appendices IV: Direct and indirect effects of different characteristics on seed yield of sunflower accession

```
> W=read.table('clipboard',header=T)
> W
      df     dm    phcm   sdcm  hdcm  sh      sw   yhg    pyg
1  75.50 108.00 136.000 1.8050 15.15 215 63.7500 19.20 778.45
2  70.25 102.25  66.735 1.5275 12.55 233 60.3325 29.24 725.15
3  72.00  72.00  97.600 1.6200 13.00 114 60.0000  9.40 264.40
4  74.00  74.00  95.400 1.5400 12.40 101 65.0000  6.60 341.60
5  71.00  71.00  73.600 1.2400  9.20  58 60.0000  3.60 273.60
6  71.00  71.00  69.000 1.4600 11.40 110 65.0000  8.00 168.00
7  76.00  76.00 101.000 2.2500 14.75 115 80.0000 11.80 118.00
8  78.00 105.00  85.400 1.7000 11.80  79 75.0000 11.00 331.00
9  63.00 101.00  69.600 1.1400  7.80 192 50.0000  8.80 193.80
10 69.00 110.00  73.200 1.3400  9.80 160 75.0000 11.00 236.00
11 75.00 104.00  86.600 1.3000  8.20  65 50.0000  4.40 159.40
12 78.00 102.00  85.800 1.5400  8.60 210 65.0000 13.00 638.00
13 70.00  98.00  97.600 1.2200  7.80  92  5.7000  5.70 129.70
14 79.00 109.00  87.000 1.6600 10.60  76  5.5000  5.50  95.50
15 76.00 102.00 111.400 1.7600 11.80 251 18.0000 18.00 613.00
16 77.00 105.00 106.800 1.8000 14.00 223 20.4000 20.40 380.40
17 77.00 110.00  75.000 1.1800  9.80  64  3.4000  3.40 228.40
18 62.00 104.00  97.200 1.3000 12.20 123 65.0000  7.60 182.60
19 65.00 103.00  87.400 1.3400 11.20 213 60.0000 13.40 173.40
20 64.00  99.00  97.400 1.3800 11.80 199 60.0000 13.20 343.20
21 68.00 100.00 102.400 1.4000 13.40 140 60.0000 11.40 311.40
22 76.00 106.00 106.400 1.9400 16.40  97 50.0000 10.00 490.00
> library(agricolae)
> y=W$pyg
> x=W[,c(1,2,3,4,5,6,7,8)]
> cor.y=correlation(y,x)$correlation
> cor.y
    df   dm phcm sdcm hdcm   sh   sw  yhg
y 0.27 0.24 0.37 0.32 0.37 0.62 0.12 0.73
> cor.x=correlation(x)$correlation
> cor.x
        df    dm  phcm  sdcm  hdcm    sh    sw  yhg
df    1.00  0.05  0.23  0.58  0.20 -0.22 -0.29 0.02
dm    0.05  1.00  0.14 -0.11 -0.07  0.30 -0.35 0.26
phcm  0.23  0.14  1.00  0.55  0.62  0.25 -0.08 0.25
sdcm  0.58 -0.11  0.55  1.00  0.76  0.15  0.17 0.40
hdcm  0.20 -0.07  0.62  0.76  1.00  0.18  0.26 0.46
sh   -0.22  0.30  0.25  0.15  0.18  1.00  0.08 0.83
sw   -0.29 -0.35 -0.08  0.17  0.26  0.08  1.00 0.16
yhg   0.02  0.26  0.25  0.40  0.46  0.83  0.16 1.00
```

```
> path.analysis(cor.x,cor.y)
Direct(Diagonal) and indirect effect path coefficients
=======================================================
              df           dm        phcm        sdcm        hdcm
sh
df    0.78724426 -0.001839065  0.06261493 -0.47013604  0.05705360 -
0.08377471
dm    0.03936221 -0.036781306  0.03811344  0.08916373 -0.01996876
0.11423825
phcm  0.18106618 -0.005149383  0.27223883 -0.44581866  0.17686616
0.09519854
sdcm  0.45660167  0.004045944  0.14973136 -0.81057939  0.21680368
0.05711912
hdcm  0.15744885  0.002574691  0.16878808 -0.61604033  0.28526800
0.06854295
sh   -0.17319374 -0.011034392  0.06805971 -0.12158691  0.05134824
0.38079415
sw   -0.22830084  0.012873457 -0.02177911 -0.13779850  0.07416968
0.03046353
yhg   0.01574489 -0.009563140  0.06805971 -0.32423175  0.13122328
0.31605915
              sw         yhg
df   -0.09081503 0.009652061
dm   -0.10960435 0.125476787
phcm -0.02505242 0.120650757
sdcm  0.05323640 0.193041211
hdcm  0.08142037 0.221997393
sh    0.02505242 0.400560513
sw    0.31315529 0.077216485
yhg   0.05010485 0.482603028

Residual Effect^2 =  0.2234082
> Residualeffect=sqrt(0.2234082)
> Residualeffect
[1] 0.4726608
>
```

Appendices **V:** Cluster Dandrogram of 22 sunflower accessions

```
> library(ggplot2)
> library(ggfortify)
Error in library(ggfortify) : there is no package called
‘ggfortify’
> library(devtools)
Error in library(devtools) : there is no package called
‘devtools’
> library(plyr)
>  library(scales)
> library(grid)
> d<-read.table('clipboard',header=T)
> d
      df     dm    phcm   sdcm  hdcm  sh      sw   yhg    pyg
1  75.50 108.00 136.000 1.8050 15.15 215 63.7500 19.20 778.45
2  70.25 102.25  66.735 1.5275 12.55 233 60.3325 29.24 725.15
3  72.00  72.00  97.600 1.6200 13.00 114 60.0000  9.40 264.40
4  74.00  74.00  95.400 1.5400 12.40 101 65.0000  6.60 341.60
5  71.00  71.00  73.600 1.2400  9.20  58 60.0000  3.60 273.60
6  71.00  71.00  69.000 1.4600 11.40 110 65.0000  8.00 168.00
7  76.00  76.00 101.000 2.2500 14.75 115 80.0000 11.80 118.00
8  78.00 105.00  85.400 1.7000 11.80  79 75.0000 11.00 331.00
9  63.00 101.00  69.600 1.1400  7.80 192 50.0000  8.80 193.80
10 69.00 110.00  73.200 1.3400  9.80 160 75.0000 11.00 236.00
11 75.00 104.00  86.600 1.3000  8.20  65 50.0000  4.40 159.40
12 78.00 102.00  85.800 1.5400  8.60 210 65.0000 13.00 638.00
13 70.00  98.00  97.600 1.2200  7.80  92  5.7000  5.70 129.70
14 79.00 109.00  87.000 1.6600 10.60  76  5.5000  5.50  95.50
15 76.00 102.00 111.400 1.7600 11.80 251 18.0000 18.00 613.00
16 77.00 105.00 106.800 1.8000 14.00 223 20.4000 20.40 380.40
17 77.00 110.00  75.000 1.1800  9.80  64  3.4000  3.40 228.40
18 62.00 104.00  97.200 1.3000 12.20 123 65.0000  7.60 182.60
19 65.00 103.00  87.400 1.3400 11.20 213 60.0000 13.40 173.40
20 64.00  99.00  97.400 1.3800 11.80 199 60.0000 13.20 343.20
21 68.00 100.00 102.400 1.4000 13.40 140 60.0000 11.40 311.40
22 76.00 106.00 106.400 1.9400 16.40  97 50.0000 10.00 490.00
> attach(d)
> names(d)
[1] "df"   "dm"   "phcm" "sdcm" "hdcm" "sh"   "sw"   "yhg"  "pyg"
> str(d)
'data.frame':   22 obs. of  9 variables:
 $ df  : num  75.5 70.2 72 74 71 ...
 $ dm  : num  108 102 72 74 71 ...
 $ phcm: num  136 66.7 97.6 95.4 73.6 ...
 $ sdcm: num  1.8 1.53 1.62 1.54 1.24 ...
 $ hdcm: num  15.2 12.6 13 12.4 9.2 ...
 $ sh  : int  215 233 114 101 58 110 115 79 192 160 ...
 $ sw  : num  63.8 60.3 60 65 60 ...
 $ yhg : num  19.2 29.2 9.4 6.6 3.6 ...
 $ pyg : num  778 725 264 342 274 ...
> d <- na.omit(d)
> id <- scale(d[, 2:9])
> d <- dist(d, method = "euclidean")
> fit <- hclust(d, method="ward.D")
> plot(fit)
> groups <- cutree(fit, k=5)
> rect.hclust(fit, k=5, border="blue")>
```