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# Investigation of genetic divergence in local sunflower hybrids and inbred lines by applying morphological markers

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**Key words:** Sunflower, *Helianthus annuus* L, Genetic diversity, Cluster analysis, Principle component analysis.

## Abstract

Knowledge of genetic diversity is the basic requisite for any plant breeding program. Seventeen sunflower hybrids and fifteen inbred lines including ten Cytoplasmic male sterile lines and five restorer lines were evaluated at the experimental area of National Agriculture Research centre, Islamabad, Pakistan during autumn-2011. The objective of study was to investigate the genetic diversity, categorize the proficient cross combiners and approximate characters association among sunflower hybrids and inbred lines. Data was estimated on i.e. flower initiation days, full flowering days, full developmental days, height of plant, disk diameter, stem thickness, leaves per plant, hundred achenes weight, achenes yield and oil content percentage. The maximum achenes yield was contributed by Hysun-33 2119 kg ha$^{-1}$followed by SMH-0924 and SMH-0925, SMH-1028 and SMH-0926 were suggested as potential significant hybrids for future breeding plans to incorporate maximum achenes yield and oil content percentage. The CMS-11, CMS-25 and CMS-10 were long statured with vigorous stem and all the restorers were early maturing recommended for including in hybridization program to generate high heterotic factions. Cluster diagram based on euclidean dissimilarity matrix grouped hybrids as well as inbred lines in four groups. The group I and IV consist of four whereas group II and group III have three and five hybrids respectively. All the restores were clustered in III and IV and CMS in I and II groups respectively. According to principle component analysis the first two components contribute 64% and 89% in total variation in hybrids as well as in inbred lines respectively.

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## Introduction

Pakistan has always been challenging, constant scarcity of edible oil and large amount of edible oil provisions are met through import escalating at the rate of 12.5% per annum constantly. Local production meets only 30-35% of edible oil requirements. The gap between consumption and production can be avoided by developing hybrids with high edible oil percentages, early maturity and disease resistance. Presently, sunflower becomes a significant crash crop of country and its area has been increased up to 300614 hectares with the production of 404391 tones (Anonymous 2012).

Sunflower (Helianthus annuus L.) is very imperative member of Asteraceae family originated from temperate and tropical regions cultivated widely and more drought tolerant than any other grain crop. It was introduced in 1960s and ranks second after cotton in area and production in Pakistan (Arshad *et al*., 2012). All over the country crop is grown with 100 percent imported hybrid seed. The imported seed is much expensive and boost up the cost of production. Most of growers cannot afford to purchase hybrid seed every year, because its yield reduced up to 50 % in next generations and also have acclimatization issues in local climatic conditions. Therefore; there is big demand of time to develop local hybrids with higher yield potential and better adoptability (Muhammad *et al*., 2012).

Yield is the combination of numerous organized aspects which are exceptionally influenced by environmental instabilities. It is highly recommended to explore configuration of yield via breeding approaches. The investigation of diverse traits and their association is significant for direct and indirect genetic advancement of crop. The knowledge of the genetic associations among lines can be applied to exploit maximum potential of crop predominantly functional in developing crosses and to identify the particular heterotic fractions, and in accurate estimation with regard to plant varietal conservation. Study of genetic diversity is the practice by which variant individuals or groups of individuals or populations are recognized. (Mudassar *et al*., 2013).

Principle component analysis (PCA) is an appropriate technique; cluster analysis principal component analysis and path coefficient analysis are contemporary mainly very popular advances applied by sunflower researchers for assessment of genetic diversity and for scrutinizing genetic traits and revealed significant consistency regarding conventional breeding procedures. (Mohammadi and Prasanna 2003; Shankar *et al*., 2006; Arshad *et al*., 2007; Hidyatullah *et al*., 2008; Rehman *et al*., 2013; Ghaffoor 2009). Keeping in view the significance of technique the current investigation was designed with the target to approximate the genetic diversity and character association among sunflower lines and hybrids by applying cluster and principle component analysis. Extensive manuscripts pertaining to genetic diversity and character association in sunflower has been produced earlier by other researchers (Maryyum *et al*., 2011; Presotto *et al*., 2009; Darvishzadeh *et al*., 2011; Amjad *et al*., 2013).

## Material and methods

The study was conducted in National Agriculture Research centre (NARC), Islamabad, Pakistan during autumn 2011. 10-CMS (Cytoplasmic male sterile lines), 5-Restorers lines along with 17 hybrids were evaluated to explored the genetic diversity regarding numerous agronomic traits. The experimental material CMSHA-03, CMSHA-10, CMSHA-11, CMSHA-18, CMSHA-24 CMSHA-25, CMSHA-54, CMSHA-56, CMSHA-99, CMSHA-103, RHP-73, RHP-42, RHP-46, RHP-73, RHP-77, SMH-1107, SMH-106, SMH-1109, SMH-1030, SMH-1018, SMH-1007, SMH-1019, SMH-1028, SMH-0933, SMH-1105, SMH-0924, SMH-0920, SMH-0951, SMH-0926, SMH-0945 and SMH-0925 were the NARC (National Agricultural Research Centre), Islamabad locally developed lines and hybrids two imported check hybrids i.e. Hysun-33 (Australia) and NKS-278 (USA) were collected from ICI, Pak seed Pvt. Ltd and Syngenta, Pak seed Ltd. Lahore. The hybrids were replicated using Randomized Complete Block Design (RCBD). Each investigational division holds 5m long

4 rows with row to row spacing of 75cm and plant-to-plant 25cm respectively. 3-4 seeds to maintain optimum population per plot were sown on ridges to a depth of 2-3 cm. All other suggested practices were adopted during whole growth period. Optimum fertilizers (120 Kg ha-1 Nitrogen, 60 Kgha-1 Phosphorus) were applied following seed bed preparation and flowering. At maturity ten plants were picked erratically from each division in the central two rows. Observations were carried out regarding:

1) Flower initiation Days (FID)

Flower initiation days were calculated from the date of cultivation to 50 percent blooming of flower buds per plot.

2) Full Flowering Days (FFD)

The days to full flowering were calculated from the date of cultivation to 90 percent of blooming.

3) Full development Days (FDD)

Days to full development were estimated from the date of planting following back of the disk turn yellow and bracts were turn brownish in color.

4) Leaves per plant

Leaves of 10 randomly selected plants were counted after attaining of maximum leaves.

5) Height of plant (cm)

At full development of crop 10 plants were selected randomly and height was recorded from ground level to the point of attachment of disk with the stem.

6) Disk length (cm)

Length of disk of randomly selected plants was measured from one edge of the disc to the other.

7) Thickness of stem (mm)

The random plants per plot were selected for recoding thickness of stem from bottom, middle and top of the plant.

8) Weight of 1000 achenes (g)

Weight of 1000 achenes was recorded in grams on electric balance from achenes of the selected plants after threshing them manually.

9) Achenes yield (kg/ha).

The yield data was calculated at eight percent moisture level by applying formula:

Achenes yield at 8% = plot achenes yield at harvest x moisture factor

$$\text{Moisture factor} = \frac{\text{Dry wt. of achenes sample (with paper bag)}}{\text{Fresh wt. of achenes sample (with paper bag)}}$$

10) Oil percentage (%)

Oil percentage was determined by using nuclear magnetic resonance (NMR). (Bruker Mini-Spec 10).

*Statistical analysis*

Data collected from experiment was analyzed statistically to calculate independently descriptive statistics using computer software MSTAT-C mean association among treatments were estimated using least significant difference (LSD) test at P=0.05 for yield and yield components. The cluster analysis was conducted for presenting genotypes assortment by constructing diversity tree with the help of computer software 'STATISTICA' for windows by applying WARD's method (Sneath and Shokal 1973) mathematical analysis and simple statistics was calculated by using principal component analysis by utilizing computer software 'Past' for Windows.

## Result and discussion

The Range, mean values, coefficient of variation and least significant differences regarding morphological characters are presented in (Table. 1, Table. 2, Table. 3 and Table. 4). The CMS and restorer lines were evaluated only for few characters during initial developmental phases.

*Flowering and Maturity Traits*

The highly significant differences were observed among sunflower hybrids and inbred lines at (P <0.05) indicates the diverse nature of hybrids. The analysis of the variance reveals the presence of highly significant genetic variation for flower initiation days, full flowering days and full developmental days among sunflower lines and hybrids. The coefficient of variation for days to full development was very low 1.98 (Table. 3). The early flowering hybrids and inbred lines also took minimum days to flower completion. Association pertaining to maturity and yield in sunflower have also been elucidated by other researchers (Ghaffari *et al.*, 2011).

*Height of plant (cm)*

The hybrids and inbred lines regarding height of plant were significantly ($P<0.05$) different from each other. Coefficient of variation was low for height of plant 5.86 in sunflower hybrids where as maximum in inbred lines indicates the heritability among hybrids was minimum for height of plant and have maximum environmental influence. These outcomes were supported by (Mazher 2005).

**Table 1.**Name, origin, source, character mean for morphological traits in 15 Sunflower inbred lines.

| *S.No* | *Lines* | *Origin* | *Source* | *FID* | *FFD* | *HP* | *L/P* | *ST* |
|---|---|---|---|---|---|---|---|---|
| 1 | CMSHA-11 | Pakistan | NARC,ISLAMABAD | 53 | 61 | 120 | 28 | 14.84 |
| 2 | CMSHA-54 | Pakistan | NARC,ISLAMABAD | 52 | 60 | 105 | 28 | 8.84 |
| 3 | CMSHA-103 | Pakistan | NARC,ISLAMABAD | 50 | 59 | 74 | 28 | 11.21 |
| 4 | CMSHA-18 | Pakistan | NARC,ISLAMABAD | 53 | 61 | 118 | 27 | 14.16 |
| 5 | CMSHA-25 | Pakistan | NARC,ISLAMABAD | 52 | 60 | 111 | 27 | 11.72 |
| 6 | CMSHA-56 | Pakistan | NARC,ISLAMABAD | 51 | 59 | 81 | 26 | 27.8 |
| 7 | CMSHA-03 | Pakistan | NARC,ISLAMABAD | 54 | 61 | 111 | 25 | 8.43 |
| 8 | CMSHA-10 | Pakistan | NARC,ISLAMABAD | 53 | 61 | 122 | 25 | 11.39 |
| 9 | CMSHA-24 | Pakistan | NARC,ISLAMABAD | 52 | 61 | 118 | 25 | 8.67 |
| 10 | CMSHA-99 | Pakistan | NARC,ISLAMABAD | 50 | 59 | 78 | 21 | 13 |
| 11 | RHP-71 | Pakistan | NARC,ISLAMABAD | 50 | 59 | 66 | 24 | 9.82 |
| 12 | RHP-42 | Pakistan | NARC,ISLAMABAD | 48 | 59 | 61 | 24 | 8.49 |
| 13 | RHP-77 | Pakistan | NARC,ISLAMABAD | 47 | 57 | 57 | 24 | 8.13 |
| 14 | RHP-46 | Pakistan | NARC,ISLAMABAD | 59 | 60 | 20 | 8.42 | 8.42 |
| 15 | RHP-73 | Pakistan | NARC,ISLAMABAD | 59 | 59 | 20 | 8.13 | 14.84 |

FID; Flower initiation days FFD; Full flowering days HP; Height of plant (cm). L/P; Leaves per plant ST; Stem thickness (mm).

**Table 2.** Name, origin, source, character mean for morphological traits in 17 sunflower Hybrids.

| *S.No* | *Hybrids* | *Origin* | *Source* | *FID* | *FFD* | *FDD* | *HP* | *DD* | *ST* | *NL* | *100AW* | *AY* | *OC%* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | Hysun-33 | Australia | ICI Pakistan seed (Pvt.); Ltd. Lahore | 54 | 59 | 89 | 156 | 15.6 | 17.4 | 31 | 5.38 | 2119 | 37 |
| 2 | SMH-0920 | Pakistan | NARC, ISLAMABAD | 53 | 62 | 91 | 156 | 16.6 | 20.7 | 33 | 4.42 | 1629 | 34.1 |
| 3 | SMH-0924 | Pakistan | NARC, ISLAMABAD | 53 | 61 | 91 | 146 | 18.1 | 20.5 | 29 | 4.38 | 2028 | 34.3 |
| 4 | SMH-0925 | Pakistan | NARC, ISLAMABAD | 52 | 62 | 92 | 157 | 17.1 | 19.2 | 32 | 5.45 | 1906 | 33.1 |
| 5 | SMH-0926 | Pakistan | NARC, ISLAMABAD | 52 | 59 | 89 | 139 | 17.3 | 13.6 | 30 | 4.76 | 1820 | 35.5 |
| 6 | SMH-0933 | Pakistan | NARC, ISLAMABAD | 49 | 54 | 86 | 128 | 14.9 | 19.4 | 30 | 4.62 | 1386 | 33.8 |
| 7 | SMH-0945 | Pakistan | NARC, ISLAMABAD | 48 | 55 | 88 | 119 | 14.5 | 17 | 33 | 5.43 | 1251 | 33.2 |
| 8 | SMH-0951 | Pakistan | NARC, ISLAMABAD | 48 | 55 | 85 | 117 | 15 | 16.2 | 29 | 4.77 | 1389 | 34.8 |
| 9 | SMH-1005 | Pakistan | NARC, ISLAMABAD | 47 | 53 | 88 | 140 | 15.6 | 19.1 | 30 | 4.5 | 1670 | 33.5 |
| 10 | SMH-1007 | Pakistan | NARC, ISLAMABAD | 47 | 51 | 86 | 141 | 13 | 18.4 | 31 | 5.61 | 1557 | 32.4 |
| 11 | SMH-1018 | Pakistan | NARC, ISLAMABAD | 46 | 51 | 87 | 120 | 12.2 | 17.5 | 30 | 4.51 | 1550 | 35 |
| 12 | SMH-1019 | Pakistan | NARC, ISLAMABAD | 45 | 51 | 88 | 138 | 18.9 | 19.8 | 25 | 4.7 | 1789 | 32.1 |
| 13 | SMH-1028 | Pakistan | NARC, ISLAMABAD | 44 | 50 | 87 | 118 | 12.4 | 19.2 | 26 | 4.68 | 1919 | 35.6 |

FID; Flower initiation days FFD; Full flowering days FDD ; Full development daysHP; Height of plant (cm) DD; Disk diameter (cm) ST; Stem thickness (mm) NL; Number of leaves per plant 100AW; 100 Achenes weight (g), AY; Achenes yield (Kg $ha^{-1}$) OC%: Oil content %.

*Disk diameter (mm)*

The coefficient of variation regarding disk diameter were significantly diverse among sunflower hybrids and inbred lines. The maximum disk diameter was recorded in local hybrids SMH-1019 and SMH-0925. The coefficient of variation was low for disk diameter (Table. 3). The significant divergence among various hybrids was also reported by (Nouman 2009).

*Stem thickness (mm)*

The data presented in (Table .3 and Table. 4) reveals highly significant differences among sunflower hybrids and inbred lines at ($P < 0.05$). The maximum stem thickness was observed in local hybrids SMH-0920, SMH-0924 and CMSHA-011. The coefficient of variation was maximum in sunflower hybrids as well as in inbred lines 15.20 and 28.95 respectively.

*Leaves per plant*

The sunflower hybrids and inbred lines vary significantly for the number of leaves per plant. (Table. 3 and Table. 4). The maximum leaves were recorded in SMH-0920, SMH-0945 and CMS HA-011. The coefficient of variation was low for number of leaves per plant 4.52.

**Table 3.** Name, origin, source, character mean for morphological traits in 17 sunflower Hybrids (Contd).

| *S.No* | *Hybrids* | *Origin* | *Source* | *FID* | *FFD* | *FDD* | *HP* | *DD* | *ST* | *NL* | *100AW* | *AY* | *OC%* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 14 | SMH-1030 | Pakistan | NARC, ISLAMABAD | 43 | 50 | 86 | 114 | 12.4 | 19.5 | 30 | 5.09 | 1343 | 32.5 |
| 15 | SMH-1106 | Pakistan | NARC, ISLAMABAD | 42 | 48 | 83 | 131 | 13.2 | 15 | 29 | 5.22 | 1299 | 33.3 |
| 16 | SMH-1109 | Pakistan | NARC, ISLAMABAD | 39 | 45 | 84 | 121 | 14.1 | 17.8 | 28 | 4.72 | 1437 | 34 |
| 17 | NKS-278 | USA | Syngenta Pakistan seeds Pvt. Ltd; Lahore | | | | Did not Germinate | | | | | | |

**Table 4.**Range, analysis of variance for morphological traits in sunflower hybrids.

| *Variables* | *FID* | *FFD* | *FDD* | *HP* | *DD* | *ST* | *L/P* | *100AW* | *AY* | *OC%* |
|---|---|---|---|---|---|---|---|---|---|---|
| Character range | 39-54 | 45-59 | 84-89 | 121-156 | 14.1-15.6 | 17.4-17.8 | 28-31 | 4.72-5.38 | 1437-2119 | 34.04-36.97 |
| MS (varieties) | $65.33^{**}$ | $68.25^{**}$ | $1.18^{**}$ | $288.58^{**}$ | $0.983^{**}$ | $15.021^{**}$ | $4.188^{**}$ | $0.249^{**}$ | $317782.938^{**}$ | $4.442^{**}$ |
| MS(Rep) | $57.68^{**}$ | $84.30^{**}$ | $17.81^{**}$ | $658.34^{**}$ | $37.46^{**}$ | $11.067^{**}$ | $12.689^{**}$ | $0.5^{ns}$ | $224555.88^{**}$ | $5.222^{**}$ |
| MS (Error) | 6.53 | 8.94 | 2.99 | 61.47 | 2.85 | 7.62 | 1.81 | 0.4 | 180550 | 5.91 |
| CV | 5.38 | 5.52 | 1.98 | 5.86 | 10.08 | 15.2 | 4.52 | 2.97 | 26.06 | 7.15 |
| LSD(0.05) | 4.26 | 2.88 | 13.07 | 4.6 | 2.78 | 4.6 | 2.24 | 708.5 | 1.06 | 4.05 |

*: Significant at 0.01 level

**: Significant at the 0.05 level

FID; Flower initiation days FFD; Full flowering days FDD ; Full development daysHP; Height of plant (cm) DD; Disk diameter (cm) ST; stem thickness L/P; Leaves per plant, 100AW; 100 Achenes weight (g) AY; Achenes yield (Kg $ha^{-1}$) OC%; Oil content percentage.

*Hundred Achenes weight*

The maximum 100 achenes weight was recorded in Hysun-33 and SMH-1030 followed by SMH-1007, SMH-1018, SMH-1028 and SMH-1106. The coefficient of variation was maximum 12.97 for 100 achnes weight.

*Achenes yield (kg/ha).*

The results regarding achenes yield were significant among sunflower hybrids at ($p<0.05$) (Table. 3). The coefficient of variation for achenes yield was maximum 26.00. These conclusions are in accord with (Bakhat *et al.*, 2006) also accounts significant divergence for achenes yield in sunflower hybrids.

**Table 5.**Range, analysis of variance for morphological traits in 15 sunflower inbred lines.

| Variables | FID | FFD | HP | L/P | ST |
|---|---|---|---|---|---|
| Character range | 47-53 | 59-61 | 59-120 | 20-28 | 8.13-27.8 |
| MS (Varieties) | $3.2^{**}$ | $5.689^{**}$ | $51.2^{**}$ | $0.356^{**}$ | $2.763^{**}$ |
| MS(REP) | $8.571^{**}$ | $4.879^{**}$ | $1232.99^{**}$ | $13.127^{**}$ | $47.415^{**}$ |
| MS(ERROR) | 5.057 | 2.641 | 341.533 | 3.784 | 12.229 |
| LSD (0.05) | 3.76 | 2.718 | 30.91 | 3.253 | 4.603 |

*: Significant at 0.01 level

**: Significant at the 0.05 level

FID; Flower initiation days FFD; Full flowering days HP; Height of plant (cm) L/P; Leaves per plant ST; Stem thickness (mm).

**Table 6.** Principal components based on quantitative traits in 17 sunflower hybrids.

| *PC* | *1* | *2* | *3* | *4* | *5* | *6* |
|---|---|---|---|---|---|---|
| Eigen value | 4.74866 | 1.75386 | 1.43907 | 0.843716 | 0.696356 | 0.266364 |
| % variance | 47.487 | 17.539 | 14.391 | 8.4372 | 6.9636 | 2.6636 |
| Traits | Eigen vector | | | | | |
| Flower initiation days | 0.9276 | 0.2087 | -0.1324 | -0.1376 | -0.05487 | 0.06569 |
| Full flowering days | 0.9404 | 0.1897 | -0.03248 | -0.1645 | -0.1152 | 0.1278 |
| Full development days | 0.9305 | -0.04683 | 0.1575 | -0.07642 | 0.07847 | 0.1975 |
| Height of plant | 0.8513 | 0.08409 | 0.1359 | 0.285 | 0.04824 | -0.4042 |
| Disk Length | 0.7358 | -0.2921 | 0.1707 | 0.2428 | -0.5063 | 0.03244 |
| Stem thickness | 0.2776 | -0.432 | 0.6717 | -0.2459 | 0.4471 | -0.00034 |
| Number of leaves | 0.3901 | 0.8085 | 0.1323 | -0.3797 | 0.03554 | -0.1172 |
| 100 achenes weight | -0.08415 | 0.7605 | 0.09848 | 0.5502 | 0.2566 | 0.1577 |
| Achenes Yield | 0.7383 | -0.3902 | -0.2646 | 0.3361 | 0.3222 | 0.03844 |
| Oil content percentage | 0.3008 | -0.09463 | -0.8942 | -0.1772 | 0.2108 | -0.04642 |

*Achenes oil content percentage (%)*

Data regarding oil content percentage in sunflower hybrids reveals highly significant differences among hybrids for oil content percentage. The maximum oil contents were recorded in check hybrid Hysun-33 followed by SMH-1028, SMH-0926 and SMH-1018.The coefficient of variation was low for oil content percentage 7.15. (Table. 3).

**Table 7.**Principal components based on quantitative traits in 15 sunflower inbred lines.

| *PC* | *1* | *2* | *3* | *4* | *5* |
|---|---|---|---|---|---|
| Eigen value | 3.14005 | 1.68895 | 0.104465 | 0.049604 | 0.016929 |
| % variance | 62.801 | 33.779 | 2.0893 | 0.99207 | 0.33858 |
| Flower initiation days | -0.4382 | 0.4735 | 0.2303 | -0.3428 | -0.6428 |
| Full flowering days | 0.09192 | 0.7479 | -0.3672 | 0.541 | 0.0682 |
| Height of plant | 0.4554 | 0.4377 | 0.1203 | -0.6516 | 0.4025 |
| Leaves per plant | 0.5467 | 0.04015 | 0.698 | 0.3614 | -0.2858 |
| Stem thickness | -0.5415 | 0.1524 | 0.5572 | 0.1862 | 0.5817 |

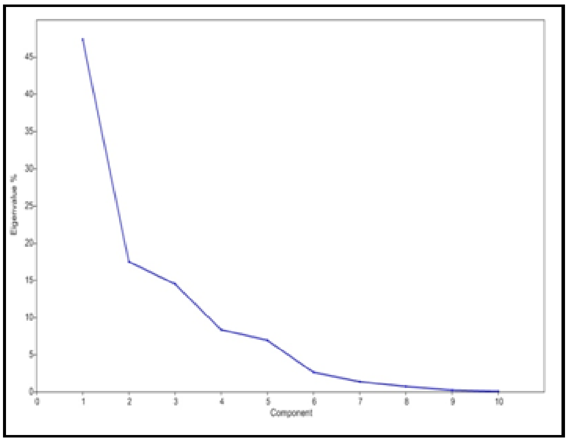

**Fig. 1.** Scree plot diagram regarding morphological traits in 17 sunflower hybrids.

*Principle component analysis*

The results regarding PCA revealed that according to Joliffe cut off 0.7 six principal components with >0.7 eigen value contributed maximum total variation among all the hybrids. The total variation is partitioned into six components in hybrids and three components in inbred lines (Table 5 and Table 6). The scree plot (Fig. 1) confirms our results. The graphical line representing the eigen values become straighter after six components in hybrids and after third in inbred lines. It was observed that the first two PCs contributed maximum in hybrids and in inbred lines by contributing 47.417 %, 17.525%, 73.701% and 16.155% total divergence respectively. The characters which add utmost contribution in PC1 were i.e. days to flower initiation, full flowering days and height of plant in both hybrids and inbred lines whereas, all other characters in this PC1 add not utmost contribution and scattered among other PCs. Therefore; this section can presents a significant assortment of genotypes by considering flowering and height of plant. Second component has utmost weight of leave per plant, stem girth and 100 achenes weight. Finally, the former with maximum contribution in overall variance and significant association with others might be almost functional in alignment and identification of advanced genotypes. The genotypes may respond in diverse manner to these characters which elucidate their respective scores and proficient traits regarding assortment of sunflower hybrids and inbred lines. The biplot obtained from first two components almost confirmed the cluster analysis grouped. The first group includes four hybrids i.e. SMH-0925, Hysun-33, SMH-0926 and SMH-0920. The group II includes three hybrids i.e. SMH-1005, SMH-0924 and SMH-1019. The third group includes five hybrids i.e. SMH-0945, SMH-1007, SMH-0951, SMH-1030 and SMH-1106. The fourth group includes three hybrids i.e. SMH-1018, SMH-1028 and SMH-1109 whereas, in case of inbred lines cluster I include five lines i.e. CMSHA-11, CMSHA-54, CMSHA25, CMSHA-103 and CMSHA-56 group II include four lines i.e. CMSHA-18, CMSHA-03, CMSHA-10 and CMSHA-24 group III include three i.e. RHP-77, RHP-42 and RHP-74 and group IV include three restorers i.e. RHP-46, RHP-73 and RHP-99 respectively. PCA or factor analysis due to its significance also suggested by other sunflower researchers in conventional breeding for genetic divergence, germplasm assortment and cultivar development. (Ghaffoor and Arshad 2008; Sultana and Ghaffoor 2008; Ghaffari 2004). Multivariate analysis has also been frequently applied in other crop species for diversity analysis such as wheat (Triticum spp.) and peanut (Arachis hypogaea L.). (Hailu *et al.*, 2006; Upadhyaya *et al.*, 2009).

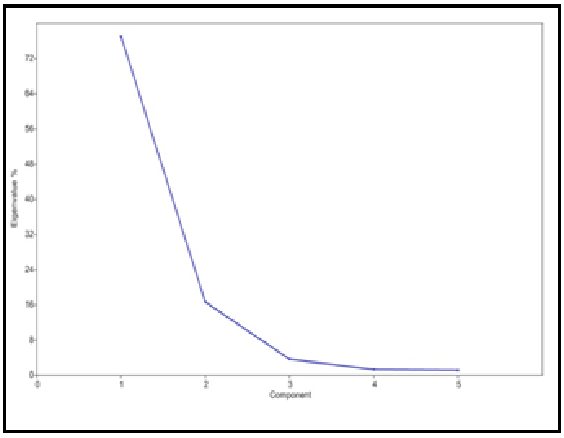

**Fig. 2.** Scree plot diagram for morphological traits in 15 sunflower inbred lines.

*Cluster analysis*

Information regarding extent and pattern of genetic diversity can be valuable in any crop breeding program for assessment of genetic variability in cultivars (Reddy *et al.*, 2004). The hybrids dendrogram based on euclidean dissimilarity revealed two main clusters at linkage distance 720 which were again divided into four main sub clusters at linkage distance 240. The cluster I consist of two hybrids (Hysun-33 and SMH-0924), four are in cluster II (SMH-0925, SMH-1028, SMH-0926 and SMH-1019) and also four in cluster III (SMH-1007, SMH-1018, SMH-0920 and SMH-1005) and six in cluster IV (SMH-0945, SMH-1030, SMH-1106, SMH-1109, SMH-0933 and SMH-0951). Any accomplishment in hybridization program frequently based on the assortment of parents encompasses utmost diversity for various factors. The hybrids grouped in cluster I were late flowering, late maturing with maximum height, number of leaves, maximum yield and oil contents percentage that can be desirable for further cultivation on the basis of high oil content percentage. While hybrids grouped in cluster II were also late flowering, late maturing, medium height, disk diameter, number of leaves per plant, achenes yield and oil content percentage (Fig. 5) and the hybrids in cluster III has moderate flowering days, moderate maturity days, medium height, maximum number of leaves and medium disk diameter. Whereas, in cluster IV the hybrids were early flowering early maturity, short statures with minimum disk diameter. The Dendogram based on inbred lines revealed two main clusters at linkage distance 40 which were again grouped into four main sub clusters at linkage distance 20. The cluster I include only one inbred line CMS-11, cluster II include six inbred lines i.e. CMS-54, CMS-25, CMS-03, CMS-10, CMS-18 and CMS-24 cluster III include three i.e. CMS-103, CMS-56 and CMS-99 whereas, in cluster IV five RHP-71, RHP-46, RHP-73, RHP-42 and RHP-77 respectively. The CMS included in cluster I were late flowering with maximum height, leaves per plant and stem thickness. While included in cluster II were also late flowering, tall with maximum number of leaves and vigorous stem whereas, in cluster III were with moderate flowering and height of plant all the restorers grouped in one cluster IV were early flowering, short stature with maximum stem thickness (Fig. 6). It is highly suggested to make crosses among CMS in cluster I with restorers incluster IV to incorporate early maturity.

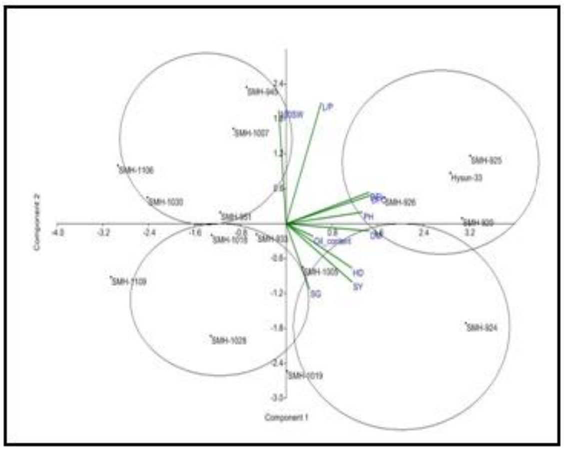

**Fig. 3.** Scattered diagram for 17 sunflower hybrids based on morphological traits.

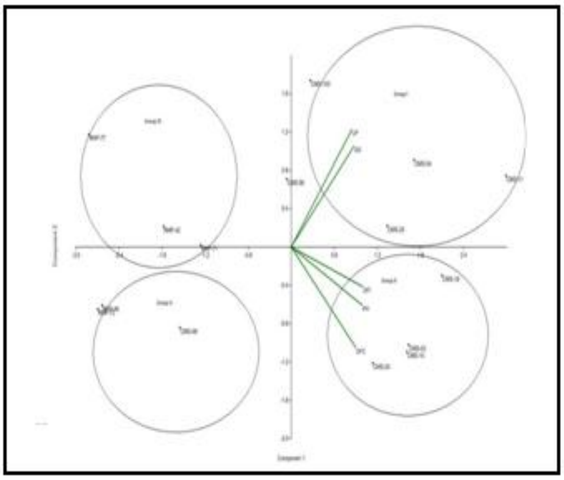

**Fig. 4.** Scattered diagram for 15 sunflower inbred lines based on morphological traits.

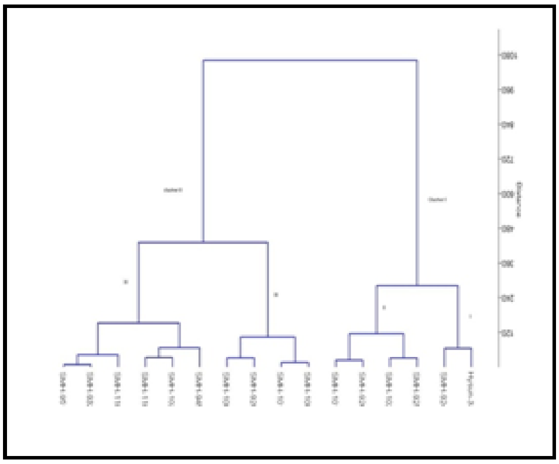

**Fig. 5.** Cluster diagram of 17 sunflower hybrids based on quantitative traits.

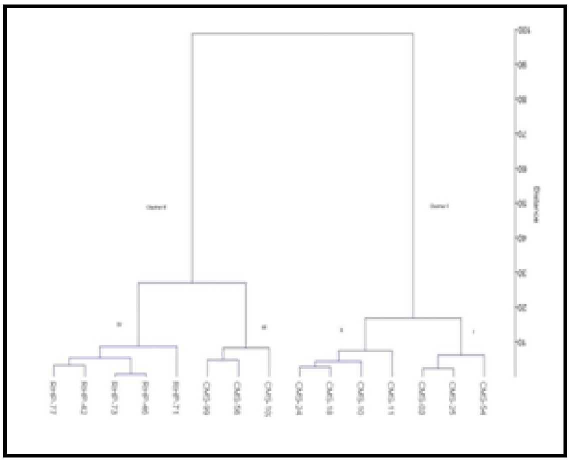

**Fig. 6.** Cluster diagram of 15 sunflower inbred lines based on quantitative traits.

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**Conclusion**

It can be recapitulated from this project that 17 sunflower hybrids and 15 sunflower inbred lines including 10 CMS and 5 restorers exposed marked divergence and substantiate roughly 93% and 64% of whole genetic variation by first two principle components The first component has significant association with flowering, maturity and yield can be employed in well-organized manner in rapid assortment and preference of genetic material in initial developmental phases. Biplot drawn by considering first two components revealed that the cluster analysis assembles crosses and the hybrids with maximum genetic distance expected to generate new groups to exploit high heterosis.

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