

**STUDIES ON CHARACTERISATION AND EVALUATION
OF SUNFLOWER (*Helianthus annuus* L.) GENOTYPES**

By
B. SAINARAYANA
B.Sc.(Ag.)

**THESIS SUBMITTED TO THE
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COLLEGE OF AGRICULTURE
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RAJENDRANAGAR, HYDERABAD - 500 030**

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CERTIFICATE

Mr. B. SAINARAYANA has satisfactorily prosecuted the course of research and that the thesis entitled "**STUDIES ON CHARACTERISATION AND EVALUATION OF SUNFLOWER (*Helianthus annuus* L.) GENOTYPES**" submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any university.

Date :
Place : Hyderabad

(Dr. D. LOKANADHA REDDY)
Major Advisor

CERTIFICATE

This is to certify that the thesis entitled “**STUDIES ON CHARACTERISATION AND EVALUATION OF SUNFLOWER (*Helianthus annuus* L.) GENOTYPES**” submitted in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the **Acharya N.G. Ranga Agricultural University, Hyderabad**, is a record of the bonafide research work carried out by **Mr. B. SAINARAYANA** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee.

No part of the thesis has been submitted for any other degree or diploma. The published part has been fully acknowledged. All the assistance and help received during the course of investigation have been duly acknowledged by the author of the thesis.

(Dr. D. LOKANADHA REDDY)

Chairman of the Advisory Committee

Thesis approved by the Student’s Advisory Committee

Chairman : **(Dr. D. LOKANADHA REDDY)** _____

Senior Scientist
National Seed Project
Rajendranagar, Hyderabad.

Member : **(Dr. A. VISHNUVARDHAN REDDY)** _____

Senior Scientist (Plant Breeding)
Directorate of Oilseeds Research
Rajendranagar, Hyderabad.

Member : **(Dr. A. SIVA SANKAR)** _____

Associate Professor
Department of Plant Physiology
College of Agriculture
Rajendranagar, Hyderabad.

DECLARATION

I, **B. SAINARAYANA** hereby declare that the thesis entitled “**STUDIES ON CHARACTERISATION AND EVALUATION OF SUNFLOWER (*Helianthus annuus* L.)**” submitted to the Acharya N.G. Ranga Agricultural University for the degree of **MASTER OF SCIENCE IN AGRICULTURE** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that any material contained in the thesis has not been published earlier in any manner.

Date :
SAINARAYANA)

(B.

Place: Hyderabad

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LIST OF SYMBOLS AND ABBREVIATIONS

%	: Per cent
σ^2_g	: Genotypic variance
σ^2_p	: Phenotypic variance
ANOVA	: Analysis of variance
bi	: Regression coefficient
C.D.	: Critical difference
C.V.	: Coefficient of variation
cm	: centimetre
d.f.	: Degrees of Freedom
D ²	: Genetic distance
DOR	: Directorate of Oilseeds Research
<i>et al.</i>	: and others
Fig.	: Figure
g	: gram
GA	: Genetic advance
GCV	: Genotypic coefficient variation
GS	: Genetic advance under selection
h ²	: Heritability in broad sense
ha	: hectare
i.e.	: which is to say in other words
kg ha ⁻¹	: kilogram per hectare
kg	: kilogram
m	: metre
m.ha	: million hectare
m.t	: million tonnes
mg	: milligram
MSS	: Mean Sum of Squares
No.	: Number
OP	: Open pollination
PCV	: Phenotypic coefficient of variation
RBD	: Randomized Block Design
S.Ed.	: Standard error of deviation
SE	: Standard Error
S ² di	: Deviation from regression coefficient
<i>viz.</i>	: namely

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ABSTRACT

The present investigation was conducted to characterise and evaluate fifty germplasm lines along with two checks, Morden and DRSF-108 at the College Farm, College of Agriculture and Directorate of Oilseeds Research, Rajendranagar, Hyderabad during late *kharif* 2005, early *rabi* 2005-06 and *rabi* 2006.

The overall perusal of results revealed that genotypes for the documentation of characterization, important characters like, hypocotyl anthocyanin colouration, leaf fineness of serration, angle of lateral veins, petiole pigmentation; anthocyanin colouration of disc flower stigma, number of leaves on main stem, head shape of grain side, seed shape and seed colour which exhibited high amount of variability were found useful.

High heritability coupled with high genetic advance was recorded in the traits, plant height, stem diameter, filled seeds per head, total seeds per head, and seed yield per plant and hence the breeder can fix or pyramidise the genes since the gain in selection will be in desirable direction.

Based on Mahalanobis D^2 analysis the fifty two genotypes were grouped into eight clusters. Greater genetic divergence found between clusters V and VII

could be exploited in the hybridization programme for obtaining segregants with high yield potential.

Correlation studies revealed that seed yield was positively associated with days to maturity, plant height, stem diameter, number of filled seeds per head, total number of seeds per head, filling seed percentage and oil content while days to 50 per cent flowering, number of unfilled seeds per head and hull content recorded negative association with seed yield.

Number of days to maturity, plant height, filled seeds per head and total number of seeds per head recorded significant positive direct effect on seed yield while days to 50 per cent flowering, stem diameter, unfilled seed per head and oil content recorded significant negative effect on seed yield.

Stability analysis was carried out based on Eberhart and Russel (1966) and the results revealed that the out of twelve quantitative characters studied, four characters viz., days to 50 per cent flowering, days to maturity, number of filled seeds per head and seed yield per plant recorded significant GE interaction. Genotypes GMU-284, 286, 289, 293, 297 and 252 adjudged as the best under wide environmental situation. It clearly indicates, that these have high buffering gene action under tailored environmental situations. Genotypes, GMU-242, 268, 276, 289, 298 and 300 will perform better even under abiotic situations i.e. poor environments when compared to other genotypes. Genotypes, GMU-281 and 292 were exhibit their fullest potential under favourable environments.

CHAPTER I

INTRODUCTION

Oil seeds play an important role and occupy pride place in Indian economy. The requirement of edible oils in India is increasing day by day due to increase in population and demand of oils for domestic and industrial purposes.

Sunflower, emerged as an admirable crop for its quality oil in the oilseed scenario of India. The introduction of sunflower 'a crop of all seasons' in India was taken up in view of its various advantages viz., Photo and thermoinsensitivity, short duration, high yield and better quality of oil with low cholesterol content. However, the productivity is rather low because of both physiological and material constraints.

In India, it has been cultivated in 2.0 million hectares with 0.99 million tonnes production and a productivity of 496 kg/ha in the year 2004-05 (Hegde and Damodaram, 2005). Due to tremendous increase in human population, the demand for edible oils has been increased considerably.

Intensive crop improvement programme has resulted in development of diverse germplasm lines and inbreds in sunflower. Many of them are in seed production chain. During hybrid seed production cycle, strict attention is to be given to the maintenance of genetic purity of germplasm lines and inbreds to harness full dividends of high yielding hybrids. To achieve this objective, crop

descriptors/characteristics are required by seed certification agencies and also by seed testing labs in order to determine the genetic purity of hybrid seed and to remove off-types from seed crop. Morphological characterisation of seed, seedling and plant would generally be considered for varietal identification.

The yield levels in sunflower has been stagnated over a decade. There is a need to study the gentic variability of the sunflower lines for physiological and yield attributes, so as to incorporate these traits in future breeding programme. The knowledge on the nature and extent of genetic variability present in any crop species plays an important role in framing a successful breeding programme. It has been well established that greater the genetic variability in the plant population grater will be the chance of obtaining the desirable gene recombinants with high heterotic effect. In this context, Mahalanobis's D^2 statistic is an effective tool in quantifying the degree of divergence at genetic level and it also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). In addition to genetic divergence and characterisation, stability of genotypes must be studied over environments to identify the right genotypes for any environment.

Keeping the above aspects in view, the present study was carried out with the following objectives.

1. Morphological characterisation
2. Genetic diversity and Stability over environments

CHAPTER II

REVIEW OF LITERATURE

A brief review of literature pertaining to the present study characterisation and evaluation of sunflower (*Helianthus annuus* L.) genotypes is presented in this chapter under relevant headings.

- 2.1 Morphological Characterisation
- 2.2 Variability, Heritability, Genetic advance and *per se* performance
- 2.3 Genetic Divergence
- 2.4 Correlations and Path Analysis
- 2.5 Stability Over Environments

2.1 MORPHOLOGICAL CHARACTERISATION

Intensive crop improvement programme has resulted in development of diverse germplasm lines and inbreds in sunflower and many of them are in seed production chain. During hybrid seed production cycle, strict attention is to be given to the maintenance of genetic purity of germplasm lines and inbreds to harness full dividends of high yielding hybrids. To achieve this objective, crop descriptors/characteristics are required by seed certification agencies and also by seed testing labs in order to determine the genetic purity of hybrid seed and to remove off-types from seed crop. Morphological characterisation of seed, seedling and plant would generally be considered for varietal identification. Initially, the work on sunflower was conducted on morphological

characterisation taking UPOV guidelines as basis and in later stages as National Test Guidelines for DUS of sunflower. Some of the research findings on characterisation using morphological characters are reviewed below:

Jagdish *et al.* (1994) studied key diagnostic characters under field and laboratory conditions in order to distinguish sunflower parental lines and hybrids based on branching nature, plant height, seed colour, shape, etc. and found that characters, seed colour, shape and number of leaves on main stem varied with genotypes studied

Suma and Virupakshappa (1994) characterized and evaluated 196 accessions of sunflower germplasm and reported that out of 196, 157 had medium petiole length, 115 had strong vigour, 58 had high branching, 73 had head inclination and 116 had 10 per cent bending.

Anita (1995) classified sunflower genotypes using seed characters *viz.*, seed shape, colour, 100-seed weight, seed size and plant characters like leaf shape, colour, margin, stem pubescence, branching, number of nodes, number of branches per plant, petiole colour, pubescence, length of the petiole, plant height and head diameter.

Rajendra Prasad *et al.* (2003) characterized ten hybrids of sunflower along with parental lines using morphological characters *viz.*, leaf size, leaf colour, leaf angle between lower part of petiole and stem, hairiness on leaf, petiole pigmentation, stem pigmentation, ray flower colour, shape, disk flower

colour, bract shape, plant height, seed size, seed shape, seed length and seed base colour.

Rajeswari (2004) characterized and evaluated 16 genotypes of sunflower using 10 morphological characters viz., leaf size, leaf colour, leaf angle between lower part of petiole and stem, petiole pigmentation, ray flower colour, disc flower colour, branching, type of branching, seed shape, seed base colour and eight yield contributing characters viz., plant height, days to 50 per cent flowering, days to maturity, head diameter, number of filled seeds per head, 100 seed weight (g), seed yield/plant (g) and oil content.

2.2 VARIABILITY, HERITABILITY, GENETIC ADVANCE AND *PER SE* PERFORMANCE

Success in plant breeding primarily depends on the nature and magnitude of variation present in the germplasm. Variability is the most significant feature of any population. Genetic variability in population is the prerequisite for response to selection in any crop improvement programme.

Heritability in broad sense measures the relative amount of heritable portion of variability. In addition, genetic advance under selection gives an idea about how much of genetic gain is attainable due to selection. Hence, the estimates of genetic variability, heritability and genetic advance are of immense value in identifying the superior genotypes.

It is also necessary to study the *per se* performance of genotypes for selection of superior genotypes for future breeding programme. The study and utilization of existing variability becomes highly essential to a plant breeder, so that, proper breeding method can be employed.

Lush (1949) proposed that heritability (narrow sense) as the ratio of additive variance to total variance. Johnson *et al.* (1955) reported that values of heritability along with the estimates as genetic gain are more useful than heritability alone in predicting the effect of selection trait(s) for crop improvement.

Klocozowski (1975) observed high genetic advance for plant height, achene weight and achene yield and low genetic advance for seed yield with 30 per cent selection intensity. Srivastava and Mishra (1976) observed high heritability for seed yield per plant, 100-seed weight and stem girth. Low estimates of heritability was recorded for plant height and head diameter.

Singh *et al.* (1977) indicated high heritability for 1000-seed weight and seed filling per cent and low heritability for oil content. They also reported that highest expected genetic gain for seed yield followed by 1000-seed weight, oil content and seed filling per cent. High heritability (broad sense) for stem diameter and moderate heritability for seed yield and head diameter were noticed by Pathak (1978).

Shinde *et al.* (1983) studied 123 varieties of sunflower and noticed high variability for seed yield/plant, head diameter and 1000-seed weight and high heritability estimates for plant height, head diameter and seed yield per plant. They also indicated that seed yield per plant and percentage of filled seeds showed higher estimates of genetic advance.

Sheriff *et al.* (1985) observed high phenotypic variance than genotypic variance and moderate GCV coupled with moderate heritability estimates for seed yield, plant height, seeds/capitulum and dry matter. They also revealed low expected genetic gain for these characters indicating high GCV or heritability need not necessarily be reflected as high genetic gain. Singh and Yadava (1986) recorded high heritability estimates for characters like yield, filled seeds/plant, 100-seed weight and head diameter.

A range of variation in respect to characters viz., plant height (50-175 cm), 100-seed weight (2.5-6.64 g), seed yield (4.15 - 40.63 g) and oil content (23.8 - 42.4%) was observed by Virupakshappa and Sindagi (1987). Gangappa (1991) indicated high heritability and high expected genetic advance for total head weight and seed yield and high PCV and GCV for dry leaf weight/plant, seed yield/plant, dry stem weight and 100-seed weight, whereas, high genotypic and phenotypic variances for plant height, oil content and achene yield was observed by Muhammad *et al.* (1992). They reported high heritability and genetic advance for oil content and achene yield while high heritability and low genetic advance for plant height and capitulum diameter.

Suma and Virupakshappa (1994) while evaluating 196 accessions of sunflower observed high variability coupled with high heritability and genetic advance as per cent of mean for seed yield, oil yield and 100-seed weight and low variability for days to 50 per cent flowering, seed filling per cent and oil content. They also reported moderate heritability and genetic gain for oil content. Rukminidevi (1994) reported that seed yield, 100-seed weight, diameter of the head, days to maturity and plant height had high heritability.

Perumal and Rajasekharan (1994) reported low variability for days to 50 per cent flowering and days to maturity, moderate heritability for plant height, 100-seed weight, stem thickness and head diameter and high variability for seed yield. They also reported high heritability coupled with low genetic advance as per cent of mean for days to 50 per cent flowering, days to maturity, stem thickness and 100-seed weight and high heritability coupled with high genetic advance as per cent of mean for seed yield and plant height.

Satisha (1995) reported that characters like oil content, test weight, seed filling per cent and number of filled seeds/plant recorded high heritability estimates while test weight, seed yield and plant height recorded high genetic advance. Kshirsagar *et al.* (1995) found high heritability estimates for plant height and 100-seed weight and moderate heritability for seed yield.

Narsaiah (1995) studied 70 genotypes and observed high variability for seed yield/plant followed by number of seeds/capitulum and plant height. High heritability for plant height followed by seed yield was noticed and high genetic

advance as per cent of mean for seed yield/plant and number of seeds/capitulum was observed.

Sarvanan *et al.* (1996) studied 40 sunflower hybrids and observed moderate variability for head diameter, plant height, stem thickness and 100-seed weight and low variability for days to 50 per cent flowering and maturity.

Patil *et al.* (1996a) reported high heritability coupled with low genetic advance as per cent of mean for plant height and oil content. They also noticed high genetic advance for head weight, seed yield, oil yield/plant and number of seeds/head.

Chikkadevaiah *et al.* (1998) evaluated 52 germplasm accessions of sunflower and reported high variability for seed yield, head diameter and filled seeds/plant and high heritability estimates for days to 50 per cent flowering, leaves/plant and seed oil content.

Rukminidevi *et al.* (1999) studied 35 sunflower genotypes and reported that days to 50 per cent flowering and days to maturity showed low variability coupled with high heritability and low genetic advance as per cent of mean. They also reported that high variability with high heritability and high genetic advance as per cent of mean for plant height, seeds/capitulum and yield/plant, whereas high heritability and low genetic advance were observed for oil content.

Teklewold *et al.* (1999) reported high PCV and GCV values for oil yield (61.09 and 57.82), seed yield/plant (58.24 and 56.83), number of filled seeds (41.73 and 34.37), 100 seed weight (33.01 and 29.34), plant height (21.03 and 19.00) and head diameter (21.51 and 18.96). They also found high heritability estimates coupled with high genetic advance for seed yield and oil content.

Ashok *et al.* (2000a) reported high range for phenotypic and genotypic coefficient of variation for seed yield. Days to 50 per cent flowering, plant height, stem diameter, capitulum diameter showed moderate PCV and GCV and low variability was recorded for days to maturity and oil content. They reported high heritability for plant height, days to 50 per cent flowering, days to maturity, capitulum diameter, 100-seed weight, seed yield and oil content. A combination of high heritability and genetic advance was noticed for days to 50 per cent flowering, plant height, capitulum diameter, 100-seed weight and seed yield.

Manjula and Seetharam (2000) evaluated 32 inbred lines along with checks to assess yield and yield attributes from the interspecific cross, *Helianthus annuus* var. Morden x *Helianthus argophyllus* (2n=34) and reported that lines HAM 184 (91%), HAM 192 (40%) and HAM 195 (41.9%) had highest oil per cent. These lines with desirable characters could be used in population improvement or in synthesis of hybrids.

Ojha and Roy (2001) studied ten characters in sunflower for estimation of genetic components of variance and heritability. Results showed high genetic

variance for yield/plant and plant height and low genetic variance for oil content. Khan (2001) observed high heritability values for days to 50 per cent flowering, 100 seed weight, days to maturity and oil content. In contrast to this, low heritability values were recorded for number of seeds/capitulum.

Ravi (2001) evaluated 66 genotypes and reported high variability coupled with high heritability and genetic advance as per cent of mean for 100 seed weight, leaf area index, total dry matter/plant and number of filled seeds as well as unfilled seeds/plant. Low variability coupled with high heritability and low genetic advance as per cent of mean was observed for days to maturity.

Komaraiah (2002) recorded high heritability values for all yield component traits. High heritability coupled with high genetic advance was noticed for number of filled seeds, seed yield, test weight and plant height.

Sujatha *et al.* (2002) studied 51 inbreds and three control genotypes of sunflower. They showed significant differences for 15 quantitative characters. The range of variation was the highest for per cent autogamy followed by plant height and oil yield, whereas, it was the lowest for number of days to 50 per cent flowering. Rao *et al.* (2003) studied 11 characters in 82 genotypes of sunflower for genetic variability, character association and path coefficient. The highest phenotypic and genotypic coefficient of variation were recorded for number of filled seeds/head (48.127 and 47.776, respectively), seed yield (45.723 and 45.522), plant height (21.069 and 20.581) and test weight (20.227 and 20.099).

Rao *et al.* (2003) studied 82 sunflower genotypes and reported that correlation studies showed the presence of significant positive association of seed yield with the number of filled seeds per head, test weight, head diameter, stem girth, number of leaves per plant and plant height. In contrast, seed yield was negatively-associated with oil content. Path analysis indicated that the number of filled seeds per head, test weight and head diameter had maximum direct effects on seed yield. It was clearly understood that the seed yield per plant in sunflower could be increased by increasing the number of filled seeds per head, test weight and head diameter.

Rajeswari (2004) evaluated ten diverse CMS lines, four inbreds and two checks, CMS 234 and Morden for yield and yield attributes and reported high heritability and moderate genetic advance as per cent of mean for days to 50 per cent flowering. High heritability coupled with low genetic advance as per cent of mean for days to maturity, and high heritability coupled with high genetic advance as per cent of mean for traits viz., plant height, head diameter, number of filled seeds/head, 100 seed weight and seed yield/plant were observed.

2.3 GENETIC DIVERGENCE

For estimation of degree of genetic divergence in germplasm collection of various crops, multivariate analysis using D^2 statistics has been found to be a potential biometrical tool (Rao, 1952; Singh and Gupta, 1968). The utility of multivariate analysis and use of generalized distance (D^2) could be used as a

quantitative measure of genetic divergence was illustrated in crop plants and other biological populations (Singh and Gupta, 1968). The importance of D^2 statistics as a powerful tool in measuring the divergence has been widely used by various workers in wide range of economically important crops.

A study conducted by Anand and Chandra (1980) on genetic diversity, using 30 cultivars of sunflower from 6 different geographic regions of the world enabled them to group the genotypes into 9 clusters. The maximum distance was found between IX and III cluster and the minimum between II and V cluster. All the clusters were lying near to each other. Four clusters contributing about 75.8 per cent. Number of leaves, 1000-seed weight, head diameter, stem girth at the middle contributing 6.9, 5.1, 4.8, 4.6 and 2.1 per cent respectively to genetic diversity. The clustering pattern of cultivars revealed that there was no relation between genetic diversity and geographic origin.

Yadav *et al.* (1988) studied 36 sunflower genotypes for their genetic divergence and grouped them into 9 clusters. The maximum distance was observed between the cluster II and IX. Their studies revealed that there was appreciable variation among 100-seed weight, seed yield per plant and oil content.

Marinkovic *et al.* (1992) observed diversity for 1000-seed weight husk and kernel percentage and oil content in seed of 178 varietal populations using cluster analysis with euclidean distance as matrix distance. They grouped the genotypes into 9 clusters. Genotypes included in clusters III and IV were

characterized by having higher kernel percentage and oil content and 1000 - seed weight, were recommended for use in breeding programme.

Haile (1994) studied 20 genotypes of sunflower from seven different geographic origins which were grouped into 8 clusters in which clusters of maximum and minimum number of entries were four and one respectively. He reported that there was no association between geographic origin and divergence.

Muppidathi *et al.* (1995) evaluated 121 inbreds of sunflower for their genetic divergence and the inbreds were grouped into 9 clusters based on D^2 analysis. The grouping of inbreds within clusters was not related to their geographic origin. Seed yield, head diameter and self fertility percentage contributed most towards total genetic divergence.

Narsaiah (1995) studied 64 sunflower genotypes for their genetic divergence using D^2 analysis and grouped them into 8 clusters. Results indicated that the crosses between genotypes of cluster VI and VII may exhibit high heterosis as well as higher level of production, as they were highly divergent from each other and recorded high mean values for characters like seed yield, plant height, number of seeds per capitulum and stem diameter. Among the characters studied, plant height showed maximum genetic divergence.

Sankarapandian *et al.* (1996) studied genetic divergence in 54 genotypes of sunflower by D^2 analysis for a set of divergent characters. The genotypes were grouped into seven clusters. Based on the intercluster distance and cluster mean for various traits, potential parents were identified from clusters VII, VI and V. Head diameter, seed yield and days to 50 per cent flowering contributed more towards genetic divergence.

Cronn *et al.* (1997) evaluated 146 germplasm accessions of 32 wild and 101 domesticated sunflower including 36 accessions of elite hybrids, using allozyme analysis for genetic divergence. Results showed that wild sunflower exhibits geographically structured genetic variation, as samples from the great plain region of the Central United States were genetically divergent from accessions from California and South Western United States.

Venkateswara Rao (1999) studied 82 genotypes of sunflower and grouped them into 10 clusters based on D^2 values. Among them, cluster VII was found to be largest group having 19 genotypes. Higher divergence observed between cluster II and VII while, lowest was noticed between cluster I and III.

A study conducted by Sridhar (1999) on 41 sunflower genotypes for genetic divergence using D^2 analysis enabled him to group them into 9 clusters. Twenty seven genotypes representing different eco-geographical regions were grouped into one cluster which indicated that there was no relation between genetic divergence and geographical origin. The traits, oil content, total number of seeds per head, total dry matter per plant, days to maturity and days to

flowering contributed maximum towards genetic divergence in both D^2 and canonical analysis.

Teklewold *et al.* (2000) evaluated 144 sunflower genotypes consisting of 66 germplasm accessions, 75 inbred lines and three controls. Mahalanobis D^2 statistics indicated the presence of substantial genetic diversity. Higher D^2 values were observed among the inbred lines than in germplasm accessions. Clustering of the genotypes resulted in the formation of 7 and 14 clusters in the germplasm accessions and inbred lines respectively. They reported that factors other than geographic origin appeared to be a potent source of genetic diversity. The intercluster distance showed that clusters II and V among the germplasm accessions and clusters XI and XIII among the inbred lines, were most divergent.

Manjula *et al.* (2001) assessed genetic diversity in 46 non-oilseed sunflower genotypes for 14 traits by adopting D^2 analysis. Oil content and plant height exhibited maximum contribution towards genetic divergence. The genotypes were grouped into 11 clusters. The contribution of oil content towards genetic divergence in 46 genotypes was confirmed when D^2 analysis was performed for seed characteristics such as test weight, volume weight, hull content, kernel recovery, oil and protein content.

Ravi (2001) evaluated 66 sunflower genotypes for their genetic divergence using D^2 analysis 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.

Sujatha *et al.* (2002) studied genetic divergence in 51 sunflower inbreds along with 3 checks using the Mahalanobis D^2 statistics and grouped them into 8 clusters which were not related to their geographic origin. Stem girth and seed yield per plant contributed the most to total genetic divergence. Highest inter cluster distance was observed between the inbreds grouped in clusters I and V.

Subramanyam *et al.* (2003) studied genetic divergence with respect to eleven characters in 85 sunflower genotypes consisting of 80 inbreds and 5 cultivars as checks. Mahalanobis D^2 statistics indicated the presence of substantial genetic diversity. The genotypes were grouped into 15 clusters. Among the investigated characters, the number of filled seeds per head, test weight, kernel to hull ratio and seed yield per plant exhibited high contribution towards genetic divergence.

Maivannan *et al.* (2003) in his experiment sixty two genotypes of sunflower were clustered into seventeen clusters based on their genetic diversity during *kharif* 2000. 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 intercluster distance. Hence, genotypes of these clusters, namely TNAUSUF 6/8 and No. 61/7 (cluster V);

TNHAP 179 (cluster XV); and 1149-2-1 (cluster XVII), were selected for intermating among themselves to produce wider segregation.

Roy and Ali (2003) reported that D2 analysis of 18 sunflower hybrids grown in Pantnagar, Uttar Pradesh, India in 2000, resulted in 8 clusters. Cluster one consisted of 7 hybrids, 4 other clusters contained 2 hybrids each, whereas the rest contained one hybrid each. All the hybrid cultivars within a cluster can be inter crossed and the resulting population (intra-cluster crosses) can be used for starting recurrent selection for achieving short term objectives, whereas the population cross of hybrids from different clusters can be used as broad base population for achieving long term objectives. Cluster numbers IV, V, III, VII and VIII showed the highest inter-cluster distance and thus, inter crosses are expected to generate higher variation of non-additive type. Cluster number V showed the maximum divergence from other clusters. It contained 2 hybrids which showed susceptibility to charcoal rot (Macrophomina phaseoli [M. phaseolina]). Among the characters studied days to 50 % flowering (41.83%) and days to maturity (19.61%) contributed the maximum 19.61 %, respectively to the genetic diversity, followed by a contribution of yield per plot 14.4%

Komaraiah *et al.* (2004) evaluated 101 sunflower genotypes for their genetic divergence using D² analysis and grouped them into 10 clusters. The number of filled seeds per head contributed highest towards genetic divergence followed by plant height, number of unfilled seeds, days to maturity, oil

content, seed yield, days to 50 per cent flowering, number of leaves and head diameter.

Reddy *et al.* (2004) studied genetic divergence using Mahalanobis generalized divergence in 79 newly developed sunflower genotypes for selection of appropriate material in various breeding programmes. Observations were recorded for seven characters and the genotypes were grouped into seven clusters. Cluster I had the highest number of entries (69), followed by cluster II with 5 entries, whereas clusters III, IV, V, VI, VII and were formed with solitary entry. Intercluster distance was maximum between cluster IV and VI followed by cluster III and VI.

Reddy and Devasenamma (2004) evaluated 58 inbreds and 3 control (KBSH-1, MFSH-17 and Surya) cultivars using the Mahalanobis D^2 analysis. Analysis of variance showed significant difference among the inbreds for all the traits examined. The 61 genotypes were grouped into 19 clusters. Genotypes in cluster XVII recorded the highest seed yield and number of days to maturity. Whereas, genotypes in cluster X recorded the highest oil content. The trait, 100-seed weight contributed the most (35 %) to the divergence in the genotypes.

Reddy *et al.* (2004) conducted experiment on sixty nine newly developed sunflower genotypes and one open pollinated cultivar (Morden) to determine the magnitude of genetic divergence. Data were recorded on days to 50 per cent flowering, days to maturity, plant height, number of leaves per plant, head diameter, 100 seed weight, number of seeds per head, oil percentage, seed

filling percentage and seed yield per plant. The analysis of variance revealed a wide range of variability and significant differences among all the genotypes for all the characters studied. The genotypes were grouped into 12 clusters, of which cluster I contained 59 genotypes while the remaining 11 clusters had one genotype each. The average intra and intercluster D values among the 12 clusters showed that the maximum intracluster D values were recorded by cluster I, while the other clusters had zero values. Intercluster D value was minimum between cluster II and V (13.29) indicating a close relationship and similarity for most of the characters. The maximum intercluster D value (108.91) found between cluster VII and XII was followed by cluster XI and XII (102.75), cluster III and XII (94.13), cluster VI and XII (92.53) and cluster II and XII (91.67) suggesting more diversity among the genotypes for the characters studied. N-NDOL-87 (cluster VI) showed superiority for plant height and number of seeds per head. Acc-1439 (cluster II), M-1005 (cluster IV) and Acc 1464 (cluster IX) were earliest to reach 50 % flowering stage. N-NDOL-1 (cluster X) was late in maturity and had high oil percentage, while EC 376211 (cluster VII) showed maximum mean value for 100 seed weight, head diameter and seed yield per plant. DSI-74 (cluster V) showed maximum mean value for number of leaves per plant, while DSI-23 (cluster VIII) had maximum mean value for seed filling percentage.

Mohan and Seetharam (2005) assessed genetic divergence in 137 sunflower lines and the lines were segregated into 6 clusters. Cluster I had

maximum number (137) of lines. Highest intercluster distance was observed between II and IV followed by IV and V and IV and I. Clusters with highest mean values for various economic characters and the diversity among the lines was mainly due to five characters viz., head diameter, plant height, seed length, oil content and days to 50 per cent flowering.

Thirumala Rao *et al.* (2005) evaluated 94 sunflower genotypes to and grouped into 10 clusters based on D values. 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.

2.4 CORRELATIONS AND PATH ANALYSIS

Yield is a complex character and 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 aids in selection of superior plants or lines for the improvement of particular character. Path coefficient analysis gives aides the information on direct and indirect effects of characters on seed yield and it is useful to find out the direct and indirect causes of association. It also helps in examining the relative contribution of direct and indirect effects of individual

variables. Hence, path coefficient analysis is of much importance in the breeding programme.

Natali and Shaikh (1970) reported that the number of flowers were positively correlated with seed yield, while head diameter was negatively correlated with seed yield. A positive correlation was observed between plant height of parental lines and the corresponding hybrids (Stayanova *et al.*, 1971).

Kovacik and Skaloud (1972) reported positive correlation of seed yield with head diameter, seed number and plant height. Fick *et al.* (1974) observed that seed oil content had a positive correlation with days to 50 per cent flowering, plant height and test weight but negatively correlated with seed weight of inbred lines. Chandra and Anand (1977) observed positive correlation of seed yield with plant height, head diameter and 100 seed weight. Zali *et al.* (1977) reported that a positive correlation existed between oil per cent and characters like plant height and number of seeds but it was negatively correlated with seed yield, head diameter and number of leaves per plant.

Giriraj *et al.* (1979) evaluated 362 lines and observed that seed yield had strong positive correlation with plant height, head diameter and 100 seed weight.

Lakshmanaiah (1980) observed a positive correlation between yield and characters like head diameter, 100 seed weight, seed number per capitulum, plant height and oil content. Path coefficient analysis, reported that among the

component characters, head diameter, exhibited maximum positive direct effect and also indirect effect via seed weight, plant height, seed filling and oil content on yield.

Sheriff *et al.* (1987) noticed that seed yield was positively associated with plant height, number of leaves, head diameter and number of seeds per head. Further, they found that head diameter and number of seeds per head had high positive direct effects on seed yield per plant.

Sudha Rani (1992) reported that seed yield was positively correlated with plant height, number of leaves per plant and number of filled seeds per head. Results also indicated positive direct effect of plant height, number of leaves per plant and 100 seed weight on seed yield. However, days to 50 per cent flowering had negative direct effect on seed yield.

Chaudary and Anand (1993) reported positive direct effects of days to flowering and plant height on seed yield, while other traits influenced seed yield indirectly. Sixty three sunflower genotypes were evaluated by Punia and Gill, 1994 and reported that seed yield per plant was significantly correlated with number of seeds per head, head diameter, 100 seed weight, percentage of filled seeds and plant height. They also indicated that number of seeds per head, 100 seed weight and head diameter were the most important traits for seed yield.

Rukmini Devi (1994) reported that seed yield was positively correlated with days to maturity, plant height and number of leaves per plant. Path analysis

indicated the direct positive effect of head diameter and number of seeds per head on seed yield per plant.

Suma and Virupakshappa (1994) evaluated 196 sunflower accessions and indicated that seed yield was positively correlated with number of filled seeds per plant, test weight and seed filling percentage. Plant height was positively correlated with all yield component characters except seed filling percentage. Oil per cent was negatively correlated with seed yield at genotypic level. They also reported that number of filled seeds had more direct effect on seed yield, whereas the remaining characters had high positive indirect effect on seed yield. Seed yield had the highest direct effect on oil yield followed by seed filling percentage, oil content and head diameter.

Narasaiah (1995) reported that the correlation between seed yield and other characters viz., plant height, number of leaves per plant, head diameter, days to maturity, number of seeds per head and test weight showed a positive significant association. The path analysis revealed high magnitude of positive direct effects of number of seeds per capitulum followed by 100 seed weight, number of leaves per plant, capitulum diameter and days to maturity, while the characters, plant height and oil per cent exhibited positive direct association with seed yield.

Patil *et al.* (1996b) reported that growth and yield components were positively associated with seed yield. Among yield components, correlation of number of seeds per head was maximum followed by head weight and further

noticed that direct effect was maximum for number of seeds per head followed by 100 seed weight in respect of both seed yield and oil yield.

Forty seven sunflower genotypes were evaluated (Doddamani *et al.*, 1997) and reported that head diameter, 100 seed weight showed significant positive correlation with seed yield. Their findings also indicated head diameter had positive direct effect on seed yield.

Eva and Andrei (1997) conducted experiment on sunflower (*Helianthus annuus*) hybrids Turbo, Florom-350, Super, Select, HS-PI-692 and lines LC-304-A and LC-1183-C (parental varieties of HS-PI6-92) and evaluated for leaves/plant, green leaves/plant, yellow and old leaves/plant, active leaf area, leaf area index, light interception and stem height and diameter. Coefficients of variation were $< 10\%$ for the majority of characters in both years, indicating homogeneity and phenotypical stability of the studied material. There were positive correlations between all studied characters, except for yellow and old leaves/plant.

Sinha *et al.* (1998) evaluated 24 hybrids of sunflower and reported that seed yield had significant positive correlation with stem girth, head diameter, number of leaves per plant, number of seeds per head and 100 seed weight and also observed positive direct effect of 100 seed weight and number of filled seeds on seed yield per plant.

Nirmala *et al.* (1999) conducted experiment to study genotypic and phenotypic correlations among seed yield and 10 component characters in 65

genotypes (15 parents and 50 crosses) of sunflower (*Helianthus annuus* L.). Pooled analysis of parents and crosses revealed that head diameter, leaves per plant, hundred seed weight and stem girth had significant and positive correlations with yield. Head diameter, stem girth, hundred seed weight, number of leaves and oil content had significant and positive intercorrelation among themselves. Head diameter, days to first flowering and number of leaves influenced the yield directly. Improvement of this crop through the component traits is significant.

Venkateshwar Rao (1999) reported the characters viz., plant height, days to 50 per cent flowering, days to maturity, stem girth and number of filled seeds per head had significant positive association with seed yield per plant. Number of filled seeds per head recorded highest positive direct effect on seed yield followed by test weight and head diameter.

Ashok *et al.* (2000) conducted an experiment with 40 sunflower hybrids during the *kharif* season showed that yield per plant was positively and significantly correlated with days to maturity (0.804), plant height (0.858), diameter of stem (0.824) and diameter of capitulum (0.806). These characters also showed the highest direct effects on yield. Percentage of oil content and 100-seed weight though positively correlated with yield, but showed negative direct effects. Days to 50 per cent flowering was negatively correlated and showed negative direct effects on yield. Harvest index showed positive direct effects on yield, but was negatively correlated with yield. The narrow

differences between genotypic and phenotypic values indicate that the environment does not play a major role in the relationship among traits.

Teklewold *et al.* (2000) studied 12-physiomorphological characters with 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. They also reported that number of filled seeds, oil content and 100 seed weight had significant positive direct effect on seed yield.

Ravi (2001) studied character association in 66 sunflower germplasm accessions and indicated the characters, filled seeds per head, seed set per cent under open pollination 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. Also indicated that filled seeds per head, total dry matter per plant and harvest index had positive direct effect on seed yield.

Ayub Khan (2001) observed that days to 50 per cent flowering, number of seeds per capitulum, 100 seed weight, head diameter and maturity were positively correlated with seed yield and also 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 the high negative direct effect on seed yield.

Chikkadevaiah *et al.* (2002) studied fifty one sunflower inbreds along with three control genotypes (GAUSUF-7, TNAUSUF-15 and KBSH-1) were evaluated during summer. Correlation studies revealed that seed yield was positively and significantly associated with seed volume weight, hull percent, percent autogamy, days to 50 percent flowering and oil yield. Oil content was positively associated with plant height, number of leaves per plant, seed volume weight, hull percentage, head diameter, percent autogamy, days to 50 percent flowering, 100-seed weight, seed yield and oil yield. Path coefficient analysis for seed yield at phenotypic level showed that the direct effect was highest for oil yield followed by 100-seed weight. The highest indirect effect for seed yield and oil content was minimum through oil yield, and yield per plant, respectively.

Nehru and Manjulatha (2003) studied correlation and path analysis in sunflower genotypes and revealed that seed yield was positively associated with growth and yield components. Path coefficient analysis showed maximum direct effect for number of seeds per head followed by test weight and seed yield per plant, while seed yield had maximum direct effect on oil yield.

Gill *et al.* (2003) conducted path coefficient analysis on 45 sunflower genotypes and revealed that selection for any trait would influence oil yield per plant through seed yield per plant.

Madhavilatha *et al.* (2004) conducted an experiment to study the magnitude of association of yield and yield contributing 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 percentage, because of their positive direct influence on seed yield.

Manivannan *et al.* (2005) conducted experiment on 82 sunflower genotypes to determine the correlation between yield and its component characters (days to 50 % flowering, plant height, head diameter, number of filled seeds per head, number of chaff seeds per head, total number of seeds per head, seed filling percentage, 100-seed weight, seed volume per 100 ml and oil content). Seed yield had a significant positive association with head diameter and a significant negative association with oil content. Plant height had significant negative correlation with oil content but significant positive association with head diameter. Number of filled seeds per head had significant positive association with total number of seeds per head. Seed filling and number of chaff seeds per head had significant negative association with seed yield. Hundred-seed weight had significant positive association with seed volume. Seed volume had significant positive association with oil content.

Sridhar *et al.* (2005) evaluated 44 genotypes of sunflower and showed that yield per plant was head diameter, number of leaves per plant was positively number of filled seeds per head, seed filling percentage and 100 seed weight.

Vidhyavathi *et al.* (2005) studied correlation and path analysis to evaluate character association in 29 sunflower genotypes. Correlation analysis revealed that seed yield per plant had significant and positive correlation with head diameter and plant height. Path analysis indicated that plant height and head diameter had high and medium positive direct effects on seed yield, respectively.

Ravi *et al.* (2006) evaluated 63 inbred lines to study the character associations and path analysis and reported that filled seeds per plant and seed set percentage under self pollination and head diameter yield per plant had strong positive association with seed yield. Path coefficient analysis revealed that filled seeds per plant had higher direct effect on seed yield.

2.5 GENOTYPE, ENVIRONMENT INTERACTION AND STABILITY ANALYSIS

The phenotypic performance of a genotype is not necessarily be the same under diverse agro ecological conditions and all the genotypes may not reach the same level of phenotypic expression under all environmental conditions. Some genotypes may fare well in some environment but not so well in other. This is indicative of the phenomenon of Genotype x Environment interaction (G x E). The G x E interaction implies differential behavior of genotypes under varied environments.

The phenotype is the product of the genotype, environment and genotype, environment interaction. At times a potential genotype may fail to

reach an optimum phenotypic expression due to decrease in correlation between the genotype and environment and as a consequence of the interactions between the genotype and the environment.

The interaction between the genotype and the environment indicates the objectives of the plant breeder to select genotypes either for limited conditions or for a wide range of environments. In case the breeder desires to evolve genotypes to a very narrow range of agro-ecological situations, the study of genotype environment interactions will be beneficial and some important landmarks are presented here.

Yates and Cochran (1938) sub-divided genotype x environment interaction into linear and non-linear components. Sprague and Federer (1951), in an analysis of maize data obtained over many environments presented evidence that double crosses interact with environments less than the single crosses. Johnson *et al.* (1955) analysed the G x E interactions using ANOVA. Wricke (1962) developed environmental covalence with genotypes. Comstock and Mill (1963) also analysed the G x E interactions using ANOVA.

Finlay and Wilkinson (1963) using regression analysis first proposed the analysis of Genotype x Environment interaction at phenotypic level. Allard (1960), Allard and Bradshaw (1964) and quoted the term stability as "well buffered" capacity of genotypes. Allard and Bradshaw (1964) stated that the nature of Genotype x Environment interactions were extremely complex. Eberhart and Russel (1966) made a slight improvement over Finley and

Wilkinson's Model (1963), which includes three parameters namely genotypic mean, regression and deviation from linearity. Despite the development of several models, the one developed by Eberhart and Russel (1966) is being used widely and is considered to be a standard method. Perkins and Jinks (1968) proposed the analysis of Genotype x Environment interaction at genotypic level. Eberhart and Russel (1969) proved that G x E interactions usually exist, irrespective of the fact whether the varieties are pure lines, single crosses / double crosses, hybrids, test crosses and segregating populations or any other material with which the breeder may be working.

Genotype and Environment Interaction in Sunflower

The reviews pertaining to the Genotype and Environment interaction in sunflower are presented here under. Taranchunk (1951) was the first to report that seed yield of sunflower could be increased by appropriate cultural conditions. Habura (1958) reported that oil content was more influenced by environmental conditions than the proportion of seeds per head. A significant influence of the environment on 1000 seed weight, per cent normal seeds per head and oil content was noticed by Pinthus (1963). Sharma and Chide (1979) in their study on the stability of yield in sunflower observed that the differences in stability among the genotypes were mainly due to linear regression. Mean performance of the genotypes was found to be inversely proportional to their stability and the strain EC 68415 exhibited high mean specificity towards most unfavorable environments.

Seetharam *et al.* (1980), while testing eight indigenously developed hybrids along with EC 68415 over three years observed that the hybrids manifested greater specificity of adaptability to favorable environments. They also identified BSH I and BSH 2 as the most desirable hybrids in terms of mean seed yield and oil content.

Sivaram (1981) found a significant linear genotype x environment interaction for all traits studied. Roath and Miller (1982) studied the environmental effect on seed set in sunflower and concluded that environment affected seed set considerably.

George (1983) studied G x E interaction for seed and oil yield on sunflower and suggested that differences due to interaction of location with genotypes were substantially relative to those among genotypic means. Habeebulla *et al.* (1983) reported that the highest seed yield, oil yield and oil percentage were obtained with February sowing and concluded that seed yield and oil content were positively correlated with maximum temperature and bright sunshine hours during the flowering phase.

Pathak and Dixit (1984) evaluated five popular sunflower varieties over five seasons under semi-arid conditions of Rajasthan and indicated significant differences due to genotypes and environments. Significant genotype x environment interaction variance indicated differential performance of the genotypes in varied environments. The genotype, EC 68415, in addition to

producing the highest mean yield also exhibited specific adaptation to favorable environments.

Sen *et al.* (1985) observed significant differences among seven sunflower varieties tested over five seasons for yield stability. The linear component of variety x environment interaction was also significant for seed yield.

Chaudhary and Anand (1988) reported that variety x season interaction in sunflower revealed significant differences among varieties for all characters, except dry matter of seedlings in the rainy season. The combined analysis during different seasons showed highly significant differences between genotypes for all the characters except fresh and dry matter weight of the seedlings and protein content. Seasonal effect was also significant for all these characters except oil content. The performance of different varieties; or the characters showing non-significant G x E interaction varied from season to season. A variety performing well in a season was relatively better in other season.

Sreedhar (1989) analysed five sunflower genotypes for stability over five seasons at Hyderabad and reported that with the exception of one genotype, rest of the four genotypes registered a significant deviation from regression (s^2d_i) for yield per plant indicating an element of unpredictability associated with each of them.

Velazquez *et al.* (1990) evaluated thirty genotypes at three locations in Mexico and indicated the significance of genotype x environment interaction for seed yield, oil content, oil yield, kernel and hull percentage and 1000 seed weight. They further reported that a few genotypes were stable and one hybrid, although unstable gave the highest seed and oil yield.

Nora Mancuso (1992) evaluated sunflower cultivars, open pollinated varieties and hybrids over fourteen environments and reported that the highest yield in seed and oil was reached by the hybrid, which showed average stability in all environments.

Shinde *et al.* (1992) evaluated 15 sunflower genotypes across three seasons (*kharif*, *rabi* and summer) and indicated significant environmental effects and genotype x environment interaction for all the characters studied. *Kharif* was found to be favorable environment for stem girth, head diameter, number of filled seeds, yield per plant and oil per cent, while *rabi* for days to 50 per cent flowering and days to maturity and summer for plant height and number of leaves per plant.

Virupakshappa (1991) studied 24 hybrids developed by crossing 4 cytoplasmic male sterile lines with 6 testers over three environments, namely rainy, post-rainy and summer. Three hybrids (CMS 234 x NDRLOS 6, CMS851 - x RHA 296 and CMS 234 x RHA 296) recorded a high mean yield over three seasons and were considered stable considering the stability parameters namely regression coefficient and mean square deviation.

Madrap *et al.* (1994) observed that the hybrids performed well during *rabi* and summer seasons than *kharif*. Subba Rao (1994) reported 19 hybrids had high mean and average stability over environments. In a stability study involving two sets of eight cultivars tested over four and eight locations respectively Xanthopoulos (1994) indicated that only two hybrids were stable across the environments. Further, he observed that most varieties expressed linear response to the environmental effects.

Ilyas Ahmad (1995) studied 127 entries and reported that 16 hybrids for seed yield, 48 for seed set, 18 for head diameter, 45 for oil percent as stable genotypes as per Eberhart and Russel Model and further stated that stable hybrids identified by Shukla's method (1972) were more or less similar to Eberhart and Russel (1966).

Pillai *et al.* (1995), while evaluating 21 hybrids identified five hybrids to be stable for seed yield, head diameter and plant height. Uma *et al.* (1995) evaluated 12 sunflower hybrids and varieties in saline environments and indicated non-significant genotype x environment interaction for seed yield. MSFH -17 was found to be more stable with high mean yield and average response to environmental changes.

Muppidathi *et al.* (1996) observed differential behavior of 11 sunflower hybrids across four seasons. Genotype x environment interaction was highly significant for plant height, head diameter, days to maturity and seed yield.

Regression analysis revealed that head diameter was the most important component.

Dhanraj (1997) reported differential response of the genotypes for changes in the environment in respect of all characters, except for stem diameter and 100 seed weight. He further reported the existence of significant differences among the chosen environments in respect of all characters except for stem diameter, 100 seed weight, harvest index and seed yield per plant indicating the stability of these four characters across the environments. In contrast to these, days to 50 per cent flowering, plant height and number of filled seeds per capitulum were greatly affected by changes in the environments.

Kandalkar (1997) evaluated 15 open pollinated sunflower genotypes at four different dates of sowing under two locations in Madhya Pradesh and observed significant mean square differences due to genotypes and genotype x environment interaction for seed yield. Regression coefficient indicated, Latur 9917 and Surya to be the most suitable genotypes for favorable environment. Late maturing genotypes expressed average response and stability under different sowing dates with higher yield performances.

Laishram and Singh (1997) in their study conducted at three locations at Imphal reported significant genotype x environment interaction for plant height, days to flowering, days to maturity, head diameter, test weight, seed yield and oil content in eleven sunflower genotypes. They further observed that both linear and non-linear components were significant for all characters except plant

height, for which only linear components were significant. The cultivar Morden was the most unstable for most of the characters whereas, IET 23 was the most stable and recommended for Manipur.

Sharma *et al.* (1997) evaluated nine genotypes of sunflower under six sowing dates for eight yield components and revealed the superiority of February sowing where as the October sown crop recorded the lowest yields. They further reported that Cultivar 14 was the most stable for seed yield, test weight and head diameter.

Swathi *et al.* (1997) from a study of 15 sunflower genotypes in four environments reported that, NK212, NSH 70, NSH 45 and Euroflor recorded high mean yields and regression coefficients near to unity. Whereas the genotypes NSH 64, NSH 84, and Hysum 33, NK 265 and NK 177 were adaptable to favourable and poor environments respectively.

Baljit Singh *et al.*, (1999) from a stability study of 25 inbreds and 25 hybrids of sunflower grown during spring and *kharif* seasons reported that G x E interaction was significant for all characters except for days to maturity of hybrids.

Lakshaman (1999) reported significant differences between genotypes and also environments for all the characters except 100-seed weight. The mean sum of squares due to pooled deviation were found to be highly significant for

all the seven characters indicating predominance of unpredictable portion of G x E interaction.

Prusti *et al.* (1999) reported that G x E linear component was significant for volume weight and for the remaining characters like seed yield, days to flowering, days to maturity and head diameter, the non linear component was highly significant. Hybrids PAC 36 and SSFH-1 recorded high adaptability.

Shashikala (1999) reported that each genotype differed significantly from one another for all the characters. In respect of environments also significant differences were observed for all the characters except for number of unfilled seeds per capitulum, 100 seed weight and oil per cent. The mean squares due to genotypes and environments were highly significant indicating that the differences among the genotypes and environments were real. The genotype x environment interaction was also highly significant when tested against pooled error for all the characters except for stem girth, which revealed differential behaviour of genotypes to varying environments.

Halaswamy *et al.* (2000) evaluated twenty seven genotypes (14 three-way cross hybrids, ten single cross hybrids and three controls) were evaluated in four different environments during 1996-97. Genotype environment interactions were significant for the six characters (days to maturity, head diameter, number of filled seeds, seed yield, oil content and oil yield). The variance due to genotype environment interaction was not significant for the characters except seed filling and seed yield. The highest number of genotypes

(16 of 27) showed their stability for seed yield. Among the hybrids, 3 three-way cross hybrids viz. (234A x 207B) x 6D-1, (851A x 207B) x RHA 274 and (338A x 300B) x RHA-274 and two single cross hybrids (338A x 6D-1 and 851A x RHA274) were stable for most of the characters.

Subbalakshmi *et al.* (2001) in their study at four locations with 19 hybrids reported that the hybrids and environments differed and interacted significantly. The hybrids, New Bhavani, SH 187 and Jwalamukhi recorded high mean and stability for oil and seed yield and recommended for all environments due to their average responsiveness and the hybrid MSFH 17 to highly favourable environment due to above average responsiveness to environment.

Vega-Aj-de-la *et al.* (2001) evaluated a reference set of 10 sunflower hybrids (Contiflor 15, Aguara, GV23105, GV25015, GV25086, TC 2001, GV23146, GV22510, Contiflor 9 and Morgan 734 in 21 subtropical (northern), temperate (central), and managed environments of Argentina, during the 1996/97-98/99 seasons, to identify patterns of genotype-by-environment interaction and opportunities for indirect selection. Pattern analyses showed that the average genotypic discrimination effects of the central and northern regions for oil yield were strongly orthogonal. Pattern analyses of physiological determinants and components of yield revealed the existence of different specific genotype responses to specific environmental challenges within the same genotype group.

Kaya and Atakisi (2002) conducted experiment on 25 sunflower hybrids in 3 locations. The best hybrid was 2453-A x 2644-R, recording the highest average seed and oil yields, followed by 2453-A x R-01001 and HA-89-A x R-01001. In addition, 2453-A x 2644-R showed the best for flowering date, head diameter and hectolitre weight. HA-89-A x R-01001 showed the best for physiological maturity, head diameter and hectolitre weight, while 2453-A x R-1001 showed the best for flowering date, plant height and head diameter. However, BAH4-A x 2644-R, 2453-A x 25711R, 0704-A x 2644-R and HA89-A x 2280-R were the most stable in terms of flowering date BAH4-A x 2644-R, BAH8-A x 2280-R, 0704-A x 2644-R and 0704-A x 2284-R were the most stable in terms of physiological maturity; BAH8-A x 2644-R, BAH8-A x 2284-R and BAH8-A x 25711R were the most stable in terms of plant height; BAH8-A x 25711R, HA89-A x R-1001, BAH8-A x 2284-R and HA89-A x 2280-R were the most stable in terms of head diameter; BAH8-A x R-1001, BAH8-A x 25711R and BAH8-A x 2644-R were the most stable for 1000-seed weight.

Kumar *et al.* (2002) carried out yield stability analysis with 5 elite sunflower by hybrids (NDSH3, NDSH5, NDSH15, NDSH6 and NDSH18) grown during summer, *rabi* and *kharif*. The results revealed significantly genotypic differences in response to environments, as the genotype mean squares when tested against pooled deviation and pooled error were significant. This indicates the genetic control of response to environments and independent

nature of genetic systems in controlling stability parameters. None of the genotypes exhibited ideal stability values. NDSH15 was suitable to more favourable environments due to high mean performance, high b_i and non significant S^2_{di} values. NDSH18 with non significant regression coefficient was non-responsive to environmental fluctuations and was relatively stable due to its low deviation from regression.

Rukmini (2002) reported that genotypes and environments showed significant differences for all characters. G x E interaction was linear for flowering, days to maturity and seed weight. The non-linear component was important for head diameter and unfilled seeds. She further reported that linear and non-linear components were equally important for rest of the characters. *Rabi* sowing was found to be favourable for the expression of important characters.

Pawan Kumar *et al.* (2003) conducted experiment with twenty five open pollinated cultivars of sunflower (*H. annuus*) in *kharif* (1998 and 1999) and *rabi* (1998/99 and 1999/2000) seasons, i.e. under four environments. Significant difference was observed for 1000-seed weight and seed yield per plant due to genotype (G), environment (E), and G x E interaction. Environment responded linearly to cultivars for both traits. EC 376166, EC 376167, EC 376199 and EC 394663 had higher mean value for 1000-seed weight and their performance was consistent in all environment. Similarly EC 68414-S1, EC 376183, EC 376199, EC 376212, EC 376220, EC 376234, EC 394663, EC 399280 and LC 009 had

higher mean value for seed yield per plant and non significant regression and deviation from regression. EC 376199 and EC 394663 consistently performed better for both traits.

Murali *et al.* (2004) conducted experiment with 8 sunflower hybrids during the *kharif*, *rabi* and summer seasons of 1995 to evaluate their adaptability to the crop growing conditions in the dry zone of Andhra Pradesh, India. Genotype x environment interaction was significant for number of days to 50 per cent flowering, number of days to maturity, plant height, test weight and seed yield. Both linear and non-linear components were important for all the characters. Hybrids RSFH15 and RSFH 21 were suitable for cultivation during the *kharif* and *rabi* seasons, whereas RSFH 9, RSFH 20 and RSFH 30 were suitable for cultivation in summer. None of the hybrids showed stable performance in all the seasons. Further efforts are required to improve the stability of sunflower across different crop growing seasons.

Shankar Goud and Sarala (2004) reported that both linear and non-linear components of G x E interactions were significant for all characters studied and observed that high yielding hybrids were found to be less stable.

Reddy *et al.* (2004b) evaluated the cytoplasmic male sterile lines of sunflower, i.e. CMS 234A with PET-1 cytoplasm, DCMS 6 with PET-2 cytoplasm, DCMS 1 with GIG-1 cytoplasm, DCMS 4 with PEF-1 cytoplasm and DCMS 3 with ANL-2 cytoplasm were grown at 2-month intervals from June 1999 to April to identify the most stable sources among the newly developed

cytoplasmic sources. ANL-2 was unstable as it produced fertile pollen to a maximum of 9.7 % during April followed by 9.2, 8.8, 6.2 and 5.8 per cent during June, February, August and December, respectively, whereas no fertile pollen was produced during October. Similarly, PEF-1 produced fertile pollen upto 6.2 % during April followed by 5.6, 4.0 and 2.3 % during February, June and August, respectively, while no fertile pollen was produced during October and December. GIG-1 produced fertile pollen upto 0.8 % during April followed by 0.6 and 0.3 % during February and June, respectively, whereas it did not produce fertile pollen during August, October and December. PET-1 and PET-2 did not produce fertile pollen in all planting dates and were regarded as stable sources. Pollen and seed fertility was highest in the April sown crop. High maximum temperature and marginally low relative humidity prevailed during March, April, May and June indicating that the effect of high temperature and low relative humidity were the causes for breakdown of male sterility in sunflower.

Kll and Altunbay (2005) conducted experiment in Turkey to determine the response of sunflower oilseed (P 6480) and confection cultivars (Inegol) to different sowing dates during 2001. Days to maturity, plant height, head diameter, total number of seeds per head, seed setting efficiency, 1000-seed weight, seed yield, hull ratio and seed oil content of oilseed and confection sunflower cultivars were significantly affected by the different sowing dates. The oilseed sunflower cultivar recorded higher head diameter, total number of

seeds per head, seed setting efficiency, seed yield and oil content than confection sunflower cultivar.

Dani and Pepo (2005) studied the yield potential utilization of sunflower hybrids (54 In 20901; 44 in 2002 and 2003) in terms of yield combined with yield stability, the best hybrids in the very early, early, middle and confectionary groups were LG 5385 Altesse RM, Lympil and IS 8004, respectively.

CHAPTER III

MATERIAL AND METHODS

The experiment, studies on characterisation and evaluation of sunflower (*Helianthus annuus* L.) genotypes was conducted at College farm, College of Agriculture and Directorate of Oil Seeds Research, Rajendranagar, Hyderabad in three seasons late *Kharif*, 2005, early *Rabi* 2005-06 and *Rabi* 2006. The studies were programmed to evaluate the sunflower genotypes for their morphological characterisation, genetic divergence and stability over environments under field situations.

3.1 CHARACTERISATION AND EVALUATION OF SUNFLOWER GENOTYPES

3.1.1 Material

Fifty germplasm lines and two checks (DRSF-108, Morden) of sunflower used for characterisation and evaluation, were obtained from Directorate of Oilseeds Research (DOR), Rajendranagar, Hyderabad. The list of fifty two genotypes are presented in Table 1.

Fifty two germplasm lines were characterized for morphological traits and evaluated for variability, heritability, genetic advance and *per se* performance genetic diversity, correlation and path analysis and stability over environments along with their respective checks, DRSF-108 and Morden during

late *Kharif* 2005 at the Directorate of Oilseeds Research, Rajendranagar, Hyderabad.

3.1.2 Methods

Fifty germplasm lines along with two checks, DRSF-108 and Morden were planted during late *Kharif* 2005 at Directorate of Oilseeds Research, Rajendranagar, Hyderabad. Each line was sown in three rows of 4.5 m length (with a spacing of 60 x 30 cm) in two replications. Two to three seeds per hill were sown to facilitate better emergence thinning is done by retaining healthy seedlings and to provide uniform plant stand.

3.1.3 Crop management

Recommended package of practices were adopted to raise a healthy crop. Necessary prophylactic measures were taken to safeguard the crop from pests and diseases.

3.1.4 Observations recorded

Observations were recorded on eleven morphological characters and eleven yield contributing characters.

3.1.4.1 Morphological characters

Morphological characters were recorded as per National Test Guidelines for DUS. Visual assessment was done by taking observation of group of plants or parts of plants. The number of aberrant plants or parts of plants should not exceed 5 per cent in the genotypes.

3.1.4.1.1 Hypocotyl anthocyanin colouration

It was observed during seedling emergence stage and grouped as absent, medium and strong.

3.1.4.1.2 Leaf shape

It was observed visually and grouped as oblong, lanceolate, triangular, cordate, rounded and ovate.

3.1.4.1.3 Leaf colour

It was observed visually at flowering and grouped as green, medium green and dark green.

3.1.4.1.4 Leaf size

The leaf length and width from central third portion of the plant selected at flowering stage was measured in centimeters and leaf size was calculated and grouped as very small, small, medium, large and very large.

3.1.4.1.5 Leaf fineness of serration(Leaf margin)

It was observed at flowering stage and grouped as fine, medium and coarse.

3.1.4.1.6 Leaf : angle of lateral veins

Observed at flowering stage as acute, right angle or nearly right angle and obtuse.

3.1.4.1.7 Leaf base

Visually observed at flowering stage as auriculate, acute and obtuse.

3.1.4.1.8 Leaf ; petiole pigmentation

Leaf petiole pigmentation was observed visually at flowering as absent and present.

3.1.4.1.9 Leaf ; hairiness

Leaf hairiness visually observed using hand lense at flowering stage as absent, sparse and dense.

3.1.4.1.10 Stem : number of leaves on main stem

Number of leaves on main stem were counted at flowering and classified as low (< 21), medium (21-25) and high (> 25).

3.1.4.1.11 Stem pubescence

Stem pubescence at the top visually observed using hand lense at flowering as absent, medium and strong.

3.1.4.1.12 Stem pigmentation

Stem pigmentation visually observed at flowering as present or absent.

3.1.4.1.13 Ray flower colour

Ray flower colour visually observed at flowering as ivory, pale yellow, yellow, orange, purple, red brown and multicoloured.

3.1.4.1.14 Ray flower : Shape of ray flowers

Shape of ray flowers observed at flowering as elongated, ovoid and rounded.

3.1.4.1.15 Disk flower colour

It was visually observed at flowering stage and grouped as yellow, red and purple.

3.1.4.1.16 Disk flower : anthocyanin colouration of stigma

Anthocyanin colouration of stigma at flowering was observed under microscope at flowering and genotypes were categorized as absent or present.

3.1.4.1.17 Pollen colour

It was visually observed at flowering stage and grouped as white and purple.

3.1.4.1.18 Plant branching

It was observed visually at harvest / maturity stage and indicated as absent or present.

3.1.4.1.19 Head attitude (at maturity)

It was visually observed at harvest maturity stage and indicated as horizontal, inclined, vertical, half-turned down and turned down.

3.1.4.1.20 Bract shape

Bract shape visually observed as elongated and rounded and ovate at seed setting stage.

3.1.4.1.21 Head shape of grain side

It was visually observed at harvest maturity stage and indicated as concave, flat, convex and misshapen.

3.1.4.1.22 Seed base colour

It was recorded visually after harvest as white, grey, brown and black.

3.1.4.1.23 Seed shape

It was observed after harvest and classified as ovoid, elongate, ovoid elongate, ovoid wide and rounded.

3.1.4.2 Yield contributing characters

Data were recorded for the following eleven yield contributing traits on five randomly selected plants per entry in each replication and the averages were computed in three seasons i.e. late *Kharif* 2005, early *Rabi* 2005 and *Rabi* 2006.

3.1.4.2.1 Days to 50 per cent flowering

Number of days from the date of sowing to the day on which flowers in 50 per cent of plants open were recorded.

3.1.4.2.2 Days to maturity

Number of days from the date of sowing to the day on which back of capitulum in 50 per cent of plants in a line turned to lemon yellow colour were recorded.

3.1.4.2.3 Plant height (cm)

The height from the scar of the cotyledonary leaves to the top of the peduncle of the capitulum was measured in centimeters at the time of harvest.

3.1.4.2.4 Stem diameter (cm)

Stem diameter was measured in cm at one third height of the plant from ground level with the help of vernier calipers

3.1.4.2.5 Number of filled seeds per head

Number of filled seeds per head were counted manually for five plants and mean was computed.

3.1.4.2.6 Number of unfilled seeds per head

Number of unfilled seeds per head were counted manually for five plants and mean was computed.

3.1.4.2.7 Total number of seeds per head

Total number of seeds per head were calculated from number of filled seeds and unfilled seeds of the head.

3.1.4.2.8 Seed filling per cent

Seed filling per cent was estimated by the formula

$$\text{Seed filling per cent} = \frac{\text{Number of filled seeds}}{\text{Total number of filled and unfilled seeds}} \times 100$$

3.1.4.2.9 100-seed weight (g)

One hundred filled seeds were selected randomly, weighed and the weight was recorded in grams.

3.1.4.2.10 Seed yield per plant (g)

The total weight of filled seeds per plant was recorded in grams.

3.1.4.2.11 Oil content (%)

The seed oil content was determined through non-destructive method by utilizing Nuclear Magnetic Resonance (NMR) technique in the laboratory of National Seed Project (NSP), Rajendranagar, Hyderabad.

3.1.4.2.12 Hull content (%)

Sample of 100 seed from each genotype were dehulled and hull percentage was calculated by the formula :

$$\text{Hull content (\%)} = \frac{\text{Weight of hull}}{\text{Weight of seeds}} \times 100$$

3.2 STATISTICAL ANALYSIS

The data recorded on twelve yield contributing traits were subjected to the statistical analysis

3.2.1 Analysis of variance

RBD Analysis

The design adopted was Randomized Block Design (RBD) with two replications. The analysis of variance was carried out by the method adopted by Panse and Sukhatme (1985).

$$Y_{ij} = \mu + g_i + v_j + e_{ij}$$

Where

Y_{ij} = Phenotypic observation in i^{th} genotype and j^{th} replication

μ = General mean

v_j = True effect of j^{th} genotype

e_i = Random error

The analysis of variance (ANOVA) was carried out for each character as indicated below :

Source of variation	df	MS	F-ratio
Replications (r)	(r-1)	Mr	Mr / Me
Treatments (t)	(t-1)	Mt	Mt / Me
Error (e)	(r-1) (t-1)	Me	
Total	(rt-1)		

Where r = Number of replications

t = Number of treatments (genotypes)

Mr = Mean sum of squares of replications

Mt = Mean sum of squares of treatments

Me = Mean sum of squares error

d.f. = Degrees of freedom

MS = Mean sum of squares

The significance of mean sum of squares for each character were tested against the corresponding error degree of freedom using 'F' test (Fisher and Yates, 1963).

Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV)

These were computed according to Burton (1952)

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

Categorisation of the range of variation was followed as proposed by Sivasubramanian and Menon (1973).

Less than 10% : Low

10 to 20% : Moderate

More than 20% : High

Heritability in broad sense [$h^2(b)$]

Heritability in broad sense was estimated as per Allard (1960)

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

As suggested by Johnson *et al.* (1955), $h^2(b)$ estimates were categorized as:

Low : 0-30 %

Medium : 31-60%

High : 61 % and above

Genetic advance (GA)

Genetic advance was estimated as per the formula proposed by Lush (1949) and Johnson *et al.* (1955).

$$GA = K. \sigma_p.h^2(b)$$

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06 (Lush, 1949)

$h^2(b)$ = Heritability in broad sense

σ_p = Phenotypic standard deviation

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\text{Grand mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (1955).

Low : Less than 10%

Moderate : 10-20 %

High : More than 20 %

3.3 GENETIC DIVERGENCE

3.3.1 Mahalanobis's generalized distance (D^2)

Genetic diversity among genotypes can be better estimated using D^2 statistics given by Mahalanobis (1936).

3.3.2 Test of significance

Variances were calculated for all the 12 quantitative characters studied and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1985). After testing the difference between genotypes for each of the character, a simultaneous test of significance for differences in the mean values for a number of correlated variables with regard to pooled effect of 12 characters was carried out using 'V' statistic, which in turn utilizes Wilk's Criterion (Wilk, 1932). The sum of squares and sum of products of error and error + variety variance – covariance matrix were used for this purpose. The estimation of Wilk's criterion was done by using the following relationship.

$$\Lambda = \frac{W}{S}$$

Where,

Λ = Wilk's criterion

W = Determinant of error matrix and

S = Determinant of error + variety matrix

The significance of Λ was tested by V (stat)

$$V(\text{stat}) = -m \log_e \Lambda = -\left(n - \frac{p + q + 1}{2}\right) \log_e \Lambda$$

Where,

$$m = -(p+q+1)/2$$

p = number of characters (or) variable observations

q = number of genotypes -1 (or) degrees of freedom for population

n = degrees of freedom for error + genotypes at base of natural log = 2.7183

V(stat) is distributed as χ^2 and pq degrees of freedom

3.3.3 Transformation of correlated variables

Transformation was done by using pivotal condensation transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values because of computation of D^2 values because of computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e. $\sum di^2$.

3.3.4 Computation of D^2 values

The D^2 value between i^{th} and j^{th} genotypes for 'p' character was calculated as :

$$D^2_{ij} = \sum_t^p (y_{it} - y_{jt})^2$$

Where,

$$\begin{aligned} y_{it} &= \text{uncorrelated mean value of the } i^{\text{th}} \text{ genotype for } t \text{ character} \\ y_{jt} &= \text{uncorrelation mean value of } j^{\text{th}} \text{ genotype for } t \text{ character} \\ D^2_{ij} &= D^2 \text{ between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ genotype} \end{aligned}$$

Testing the significance of D^2 values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against tabulated χ^2 at p degrees of freedom where, 'p' is the number of characters considered.

3.3.5 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all the combinations for each genotype were arranged in the increasing order of their magnitude (Singh and Chaudhary, 1985). To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value

from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.3.6 Intra and inter cluster distance

3.3.6.1 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D_i^2/n$. Where ' ΣD_i^2 ' was the sum of distance between all possible combinations and 'n' is the number of genotypes included in a cluster.

3.3.6.2 Average inter cluster distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between the two clusters as the sum of D^2 value between the number one cluster to each of the members of other cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D values (inter cluster distance), the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

3.3.6.3 Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically by using D^2 values.

3.3.6.4 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = y_{it} - y_{jt}$). Rank I was given to the highest mean difference and rank 'p' to the lowest difference, p is the total number of characters considered. Percentage contribution of each character (X) towards genetic divergence was calculated using the following formula:

$$X = \frac{N \times 100}{M}$$

Where,

X = per cent contribution of character

N = number of genotype combinations where the characters ranked first

M = all possible combinations of genotypes considered

3.4 CANONICAL ANALYSIS

The **canonical vector** or roots were calculated to represent the genotypes in two dimensional graphical form (Rao, 1952). The steps involved are as follows:

3.4.1 Calculation of sum of squares and sum of products

The correlated standard means were transformed into the uncorrelated standardized variables. For each character and combination of characters, sum of squares and sum of products were computed using the transferred variables to obtain the matrix of variables and co-variance (matrix A). From matrix A, matrix $(A)^p$ were derived, where 'p' is the number of characters.

3.4.2 Calculation of first vector

The approximation of trial vector was obtained by getting the column totals of matrix $(A)^p$ and then by dividing each of the column totals by the highest quantity among them. The canonical variables were determined by interaction starting with trial vector. The highest element in this vector was found and the vector and the procedure was repeated till the elements of the two approximation vectors were same. The vectors were then standardized by dividing them by correlated sum of squares of these vectors. The first root A, was calculated as the p^{th} root of the highest column total of the last approximation.

3.4.3 Calculation of second vector

For getting the second vector $\wedge^2$, the original $(A)^p$ matrix was transformed and represented $(B)^p$. In $(B)^p$ each $(i, j)^{\text{th}}$ element was calculated as follows:

$$(i, j)^{\text{th}} \text{ element} = (A)^p - \lambda X_j^{\text{th}} \text{ element } X_j^{\text{th}} \text{ element of the first vector.}$$

The procedure followed in case of matrix 'A' was repeated to obtain the second canonical root.

3.4.4 Estimation of Z values

From the values of $y_1, y_2, \dots, y_{ij}$ the mean values of characters considered Z_1, Z_2 and Z_3 were calculated as :

$$Z_1 = (y) (V_1); Z_2 = (y) (V_2)$$

(Y) = mean transformed value

V_1, V_2 = the first and second vector, respectively

The mean values of Z_1 and Z_2 for each genotype were represented in a 2- dimensional diagram.

3.4.5 Contribution of vectors towards divergence

Total contribution of all the vectors was given by the sum of diagonal elements in matrix A.

$$\text{Per cent contribution of vector '1' } (X_1) = \frac{\lambda_1 \times 100}{\text{Total variance of all the variables (Characters)}}$$

$$\text{Per cent contribution of vector '2' } (X_2) = \frac{\lambda_2 \times 100}{\text{Total variance of all the variables (Characters)}}$$

Where,

λ s are cononical roots

3.5 GENOTYPE ENVIRONMENT AND STABILITY ANALYSIS

Stability analysis

Eberhart and Russell (1966) model was followed

- Overall mean of each genotype over the range of environments.
- The regression of each genotype on the environmental index and
- A function of the squared deviation from this regression were estimated.

The model proposed by Eberhart and Russell (1966) is as follows.

$$Y_{ij} = \mu_i + b_i I_j + a_{ij}$$

Where I varies from 1-67 (for single crosses) and 1 to 53 for three way crosses.

j varies from 1-4 (single crosses) and 1 to 3 (for three way crosses).

Y_{ij} = means of I^{th} genotype in J^{th} environment.

μ = Mean of all genotypes in all environments.

b_i = regression coefficient of i^{th} genotype on the environmental index, which measures the response of this genotype to varying environments.

I_j = The environmental index which is defined as the deviations of the mean of all genotypes at a given location from the overall mean.

a_{ij} = the deviation from the regression of the i^{th} genotype at j^{th} environment.

3.5.1 Analysis of variance for stability

The analysis of variance for stability as proposed by Eberhart and Russel (1966) is as follows.

Source	d.f.	S.S.	M.S.
Total	ge-1	$\sum_i \sum_j Y_{ij}^2 - CF$	
Genotype	g-1	$1/e \sum_i Y_i - C.F$	MS ₁
Environment + (G x E)	g(e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_i^2 / e$	
Environment	1	$1/g (\sum_j I_j Y_j)^2 / \sum_j I_j^2$	
G x E (linear)	g-1	$\sum_i [(\sum_j Y_{ij} I_j^2) / \sum_j I_j] - \text{Env. Linear SS}$	MS ₂
Pooled deviation	G(e-2)	$\sum_i \sum_j S_{ij}^2$	MS ₃
Deviation due to genotype	e-2	$\sum_j Y_{ij}^2 - (Y_i^2 / e) / (\sum_j I_j Y_j)^2 / (\sum_j I_j^2 - ((\sum_j \sigma^2 I_j)$	MS ₃₋₁
Genotypes	e-2	$(\sum_j Y_{gi}^{2/e}) ((\sum Y_{gi}^{2/e}) (\sum_j I_j^2 g) = S_{gi}^2$	MS _{3-g}
Pooled error	e(r-1) (g-1)		

G = genotype; e = environment; r = replication

3.5.2 Estimation of stability parameters

The regression coefficient b_i and S^2_d were estimated as follows.

a. Regression coefficient

$$B_i = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

Where,

$\sum_j Y_{ij} I_j$ – the sum of products of environmental index (I_j) with corresponding mean of that genotype at each environment (Y_{ij}).

$\sum_j I_j^2$ = the sum of squares of the environmental index I_j

b) Mean square deviations (s^2_d) from linear regression

$$S^2_d = \frac{\sum_j \sigma_{ij}}{e-2} - S^2_e / r$$

Where,

$$\sum_j \sigma^2_{ij} = \sum_j y^2_{ij} - \frac{Y^2_i}{g} - \frac{(\sum_j Y_{ij} I_j)^2}{\sum_j I_j^2}$$

= Variance due to deviation from regression for a genotype

$$\sum_j y^2_{ij} = Y^2_{I/g} = \text{Variance due to dependent variable}$$

$$\sum_j Y_{ij} I_j^2 / \sum_j I_j^2 = \text{Variance due to regression}$$

S^2_e = the estimate of the pooled error, e = number of environments, n = number of replications

The various computational steps involved in the estimations are as follows :

3.5.3 Computation of environmental index (I_j)

$$I_j = \sum_j Y_{ij}/g - \sum_j \sum_j Y_{ij}/ge$$

$$= \frac{\text{Total of all the genotypes at the } j\text{th environment}}{\text{Number of genotypes}} - \frac{\text{Grand total}}{\text{Total No. of observations}}$$

Computation of regression coefficient (b_i) for each genotype :

- a. for each value of the regression coefficient, $-\sum_j I_j^2$ is common.

b. $\sum_j Y_{ij} I_j$ for each genotype is the sum of products of environmental index (I_j) with the corresponding mean (X) of that genotype in each environment and can be obtained in the following manner.

$$(x) (I_j) = (\sum_j Y_{ij} I_j) = (s),$$

Where,

(x) = matrix of means, (I_j) = vector for environmental index

(s) = vector for sum of products : i.e. $(\sum_j Y_{ij} I_j)$

Computation of $S^2 d_i$

It is possible to partition the variance of a dependent variable (Y) in any regression analysis into two parts, the one that explains the linearity between dependent and independent variables (variance due to regression) whereas the other explains the variance due to deviations from linearity $\sigma^2 Y = \sigma^2_{\text{regression}} + \sigma^2_{\text{deviation from the regression}}$. The variance of mean over different locations with regard to individual genotype may be obtained in the following way $\sigma^2 g_i = \sum_j Y^2_{ij} - (Y^2_i / g)$

variance due to deviations from regression.

$$\sum_j \sigma^2_{2ij} \text{ for a genotype will be } \sum_j \sigma^2_{ij} = [(\sum_j Y^2_{ij}) - Y^2_i / g - (\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j]$$

Where,

$[(\sum_j Y^2_{ij}) - Y^2_i / g]$ = variance due to dependent variable and

$(\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j$ = variance due to regression

$$(\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j = ((\sum_j Y_{ij} I_j) (\sum_j Y_{ij} I_j)) / \sum_j I^2_j = b_i \sum_j Y_{ij} I_j$$

The stability parameter (σ^2_d) for each entry can be computed from the values of $\sum_j \sigma^2_{ij}$ as follows $(\sigma^2_d) = \{\sum_j \sigma^2_{ij}/(e-2)\} - (S^2_e/r)$

Mean square deviation = (Deviation from regression/degrees of freedom for environment) – (pooled error/No of replications). $(\sum_j \sum_j Y^2_{ij}) - (\sum_j Y^2_{i/e})$

ss due to environment + (G x E) = $(\sum_j \sum_j Y^2_{ij}) - (\sum_j Y^2_{i/e})$

ss due to linear environment = $(1/g) / [(\sum_j Y_j I_j)^2 / (\sum_j I^2_j)]$

ss due to genotype x environment linear = $\sum_j [(\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j] - SS$

where, $(\sum_j Y_{ij} I_j)^2 / \sum_j I^2_j = b_i \sum_j Y_{ij} I_j$ for each entry/variety

Tests of significance

The following test of significance were carried out

1. F test was used to test the significance of difference among genotype means i.e. $H_0 = \mu_1 = \mu_2 = F = \text{Mean square due to genotype}/\text{MS due to pooled deviation MS1}/\text{MS3}$.
2. F test was used to test that the genotypes did not differ due to regression on environmental index, that is $H_0 = b_1 = b_2 = b_3 \dots$

$F = \text{MS due to genotype x Environment (linear)}/\text{MS due to pooled deviation} = \text{MS2}/\text{MS3}$

3. Individual deviation from linear regression was tested as follows :

$$F = [(\sum_j \sigma^2_{ij})/(E-2) / E_j I^2_{j,p} = 0.05 \text{ at } (g-2) \text{ degrees of freedom}$$

Stability of parents

A genotype with unit regression coefficient ($b=1$) and the deviation not significantly differing from zero ($S^2d = 0$) was taken to be stable genotype with unit response.

$$SEb = \frac{\text{Mean and standard error of 'b' mean of } b = \Sigma_i b_i / g}{\sqrt{S \text{ due to pooled deviation} / \Sigma_j I^2 j}}$$

Table 1 : Details of experimental material of sunflower genotypes

S. No.	Genotype	S. No.	Genotype
1.	GMU-208	26.	GMU-273
2.	GMU-212	27.	GMU-274
3.	GMU-214	28.	GMU-275
4.	GMU-218	29.	GMU-276
5.	GMU-223	30.	GMU-277
6.	GMU-224	31.	GMU-278
7.	GMU-225	32.	GMU-279
8.	GMU-226	33.	GMU-280
9.	GMU-228	34.	GMU-281
10.	GMU-238	35.	GMU-282
11.	GMU-239	36.	GMU-284
12.	GMU-242	37.	GMU-285
13.	GMU-244	38.	GMU-286
14.	GMU-248	39.	GMU-287
15.	GMU-252	40.	GMU-288
16.	GMU-254	41.	GMU-289
17.	GMU-257	42.	GMU-290
18.	GMU-258	43.	GMU-291
19.	GMU-260	44.	GMU-292
20.	GMU-261	45.	GMU-293
21.	GMU-262	46.	GMU-294
22.	GMU-265	47.	GMU-296
23.	GMU-267	48.	GMU-297
24.	GMU-268	49.	GMU-298
25.	GMU-270	50.	GMU-300
			Checks
		51.	DRSF-108
		52.	Morden

CHAPTER IV

RESULTS

In the present study 50 genotypes of sunflower were characterized and evaluated along with their respective checks, Morden, DRSF-108. The data was recorded on twelve quantitative characters over the seasons. Results were presented for the pooled mean values over the environments.

The results are presented under the following headings.

- 4.1 Characterisation
- 4.2 Variability, heritability, genetic advance as per cent of mean and *per se* performance
- 4.3 Genetic diversity
- 4.4 Correlation coefficient analysis
- 4.5 Path analysis
- 4.6 Stability analysis over environments

4.1 CHARACTERISATION

Fifty genotypes along with two checks (Morden and DRSF-108) were characterized based on their morphological characters. Characterisation was done based on DUS guidelines and IBPGR (Table 2)

Genotypes were grouped based on their morphological characters under the following headings (Table 3)

4.1.1 Hypocotyl anthocyanin colouration

Sixteen genotypes were grouped with anthocyanin colouration. Among them ten genotypes (GMU-218, 226, 228, 244, 252, 262, 268, 273, 276 and 278) were with medium anthocyanin and 6 genotypes (GMU-242, 258, 274, 285, 289 and 297) with strong anthocyanin colouration. In the remaining genotypes the anthocyanin colouration is absent.

4.1.2 Leaf size

Leaf was divided into three size groups, small leaf size was observed in genotypes, GMU-238 and 273, medium leaf size was recorded in genotypes, GMU-223, 239, 242, 254, 279 and 296 and the remaining genotypes were with large leaf size.

4.1.3 Leaf shape

Leaf shape was divided into three groups. Genotypes, GMU-260, 273 and 300 were round in leaf shape, genotypes GMU-223 and 274 were triangle in leaf shape and the remaining genotypes were with cordate leaf shape.

4.1.4 Leaf colour

Leaf colour was divided into two groups. Most of the genotypes have leaf colour dark green except GMU-248, 273 and DRSF-108 (Green).

4.1.5 Fineness of Leaf serration (leaf margin)

Leaf serration was partitioned into three groups i.e. fine, coarse, very coarse, genotype GMU-296 was fine, Genotypes GMU-212, 218, 226, 244,

261, 267, 268, 270, 276, 278, 279, 282, 285, 286, 287, 288, 289, 293, 298, 300 and Morden were with very coarse leaf margin and remaining were with coarse margin.

4.1.6 Leaf : Angle of lateral veins

Genotypes were divided into three groups based on the angle of lateral veins in leaf. Genotypes, GMU-214, 223, 228, 238, 260, 268, 274, 277, 281, 282, 290, 291, 294, 296 and DRSF-108 had acute angle. GMU-248, 257, 273 and 300 genotypes were with obtuse vein angle and the remaining were with right angle.

4.1.7 Leaf : Hairyness

Leaf hairyness divided the genotypes into two groups, sparse and dense. Six genotypes viz., GMU-208, 248, 273, 280, 289 and 294 were with sparse hairyness and the remaining were with dense leaf hairyness.

4.1.8 Leaf base

Auriculate leaf base was observed in all the genotypes except in GMU-223 and 225 which possessed acute leaf base.

4.1.9 Petiole pigmentation

Genotypes were classified into two groups, based on the presence or absence of the petiole pigmentation. Genotypes GMU-225, 248, 254, 258, 275, 285, 292, 293 and 294 were with the presence of petiole pigmentation and remaining were devoid of petiole pigmentation

4.1.10 Number of leaves on main stem

Low number of leaves was recorded in GMU-208, 218, 242 and 258. Fifteen genotypes were with medium number of leaves and remaining genotypes were with high number of leaves on main stem.

4.1.11 Stem pubescence

All the genotypes were with the dense stem pubescence.

4.1.12 Stem pigmentation

Stem pigmentation was observed in GMU-248 only. All the other genotypes showed absence of stem pigmentation.

4.1.13 Ray flower colour

All the genotypes were with yellow ray flower colour.

4.1.14 Ray flower shape

All the genotypes were with elongate ray flower shape except genotypes GMU-281 and 291 and 300, which had ovate ray flower.

4.1.15 Disc flower colour

Disc flower colour divided the genotypes into two groups (purple and yellow). Genotypes GMU-248, 280, 281, 282, 292 and 296 were with purple disc flower and the remaining genotypes were with yellow colour.

4.1.16 Anthocyanin colouration of disc flower stigma

Genotypes were classified, based on the presence or absence of anthocyanin colour in disc flower stigma genotypes GMU-226, 238, 242, 244, 248, 252, 258, 265, 270, 276, 227, 279, 280, 282, 285, 286, 290, 292, 296, 298 and Morden were devoid of anthocyanin colour and the remaining genotypes were with anthocyanin colouration.

4.1.17 Pollen colour

Genotypes GMU-218 and 248 were with white colour pollen and remaining genotypes were with purple pollen.

4.1.18 Plant branching

Genotypes GMU – 214, 248, 282 and 294 were with the branches and the remaining were unbranched.

4.1.19 Head attitude

Head attitude was divided into four groups based on their head inclination at the time of harvest. Genotype GMU-212 with half turned head, genotypes GMU-291 and 292 were with turned head, genotype, GMU-298 and Morden with vertical head and 47 genotypes exhibited turned down head attitude.

4.1.20 Shape of bracts

Bracts shape was divided into two groups viz., Elongate and round. Genotypes GMU-226, 248, 262, 265, 267, 268, 276, 281, 293, 296 and DRSF-108 were with elongate bracts while the remaining were with round bracts..

4.1.21 Head shape of grain side

Head shape of grain side divided the genotypes into three groups. Genotypes, GMU-224, 228, 238, 257, 258, 261, 262, 265, 267, 268, 273, 274, 275, 276, 277, 280, 286, 287, 289, 290, 293, 296, 298, 300 and DRSF-108 were with flat head, GMU-226, 242, 248, 252, 270, 278, 282 and 294 were with concave head and the remaining genotypes were with convex head.

4.1.22 Seed shape

Seed shape divided the genotypes into 5 groups. Genotypes GMU-208, 218, 238, 239, 242, 265, 275 and 298 were elongate in seed shape. GMU-254 and 260, Elongate slender. Genotypes GMU-223, 226, 228, 248, 257, 258, 261, 268, 274, 277, 278, 280, 288, 291, 300 and DRSF-108 were round in shape. Genotypes, GMU-270, 276, 282, 284, 286 and Morden were ovoid elongate, genotype GMU-267 was ovoid long seed shape and the remaining genotypes were with ovoid seeds.

4.1.23 Seed base colour

Genotypes were divided into three groups based on seed base color. Genotypes GMU-242, 248, 262 and 288 had brown colour, genotypes

GMU-212, 225, 238, 258, 265, 279, 285, 296 and 298 were with grey colour and in remaining genotypes the seed base in black colour.

4.2 ANALYSIS OF VARIANCE FOR YIELD AND YIELD CONTRIBUTING CHARACTERS

Analysis of variance for yield and yield contributing characters is presented in Table 4. The mean sum of squares for genotypes were found to be significant for all the traits studied.

4.2.1 Variability, heritability and genetic advance as per cent of mean

The phenotypic and genotypic coefficients of variation, heritability in broad sense, genetic advance and genetic advance as per cent of mean were calculated for yield and yield contributing characters and presented in Table 5.

4.2.1.1 Days to 50 per cent flowering

Days to 50 per cent flowering recorded a GCV of 5.29 per cent and PCV of 6.53 per cent. Heritability and genetic advance as per cent of mean were 65.79 and 8.84 respectively.

4.2.1.2 Days to maturity

Days to maturity showed GCV (2.13), PCV (3.07), heritability (48.01) and genetic advance (3.04) as per cent of mean.

4.2.1.3 Plant height (cm)

GCV and PCV for the plant height were 12.28 and 14.34. Heritability and genetic advance as per cent of mean were 73.36 and 21.67 per cent, respectively.

4.2.1.4 Stem diameter (cm)

GCV and PCV for the Stem diameter recorded a GCV of 25.97 and PCV of 30.89 per cent. Heritability and genetic advance as per cent of mean were 70.89 and 45.04 respectively.

4.2.1.5 Number of filled seeds per head

For this character GCV and PCV values were 35.55 and 37.42. Heritability and genetic advance as per cent of mean were 90.24 and 69.56 respectively.

4.2.1.6 Number of unfilled seeds per head

GCV and PCV for number of unfilled seeds were 19.22 and 32.44 per cent. Heritability and genetic advance as per cent of mean were 35.10 and 23.46 respectively.

4.2.1.7 Total number of seeds per head

Total number of seeds had 27.38 per cent of GCV and 29.82 per cent of PCV with heritability and genetic advance as per cent of mean as 84.33 and 51.80 respectively.

4.2.1.8 Filling seed percentage

GCV and PCV values for filling seed percentage were 9.42 and 13.81. Heritability and genetic advance as per cent of mean were 45.56 and 13.25 respectively.

4.2.1.9 100-seed weight (g)

GCV, PCV, heritability and genetic advance as per cent of mean were 11.67, 15.52, 50.62 and 18.08 per cent respectively.

4.2.1.10 Seed yield per plant (g)

Seed yield per plant recorded GCV, PCV, heritability and genetic advance as 44.81, 48.31, 86.04 and 85.63 per cent, respectively.

4.2.1.11 Oil content (%)

GCV and PCV for oil content were 9.83, 14.74. Heritability and genetic advance as per cent of mean were 44.51 per cent and 13.52 per cent, respectively.

4.2.1.12 Hull content (%)

For the character hull content, GCV and PCV were 9.26 and 22.82 per cent, respectively with 16.49 per cent heritability and 7.75 per cent genetic advance as per cent of mean.

4.2.2 *Per se* performance

Per se performance of genotypes was estimated by comparing their mean performance in three seasons with checks, Morden and DRSF-108 (Table 6).

4.2.2.1 Days to 50 per cent flowering

The genotypes took 58 days to 50 per cent flowering with a range of 52 (GMU-293) to 64 (GMU-292) days. Checks, Morden and DRSF-108 took 48.50 and 54.33 days to 50 per cent flowering respectively.

No genotype was found earlier in flowering than Morden, but 5 genotypes were earlier to DRSF-108 in flowering.

4.2.2.2 Days to maturity

The mean values ranged from 89.83 (GMU-238) to 96.33 (GMU-273) days with a mean of 92.76 days. Mean values of checks, Morden (83 days) and DRSF-108 (92.66 days).

All genotypes were late in maturity when compared to check, Morden, while 21 genotypes were earlier in maturity than DRSF-108.

4.2.2.3 Plant height (cm)

Plant height ranged from 103.64 (GMU 298) to 171.53 cm (GMU 214) with a mean of 139.69 cm. Checks, Morden, DRSF-108 recorded 116.66 and 147.33 cm respectively.

Five genotypes showed superior performance in negative direction when compared with check, Morden while 32 genotypes registered shorter plant height than check DRSF 108.

4.2.2.4 Stem diameter (cm)

Stem diameter ranged from 1.62 cm (GMU-228) to 4.41 (GMU 284) cm with a grand mean of 2.28. Checks, Morden and DRSF-108 registered mean stem diameter of 2.48 cm and 2.22 cm respectively.

Seventeen genotypes were thicker than the check DRSF-108 while Ten were thicker than check, Morden.

4.2.2.5 Number of unfilled seeds/head

Mean values for the character unfilled seeds/head ranged from 99.66 (GMU 294) to 259.33 (GMU 274). Twenty six and Twenty eight genotypes recorded superior performance in negative direction over the two checks, Morden (173) and DRSF-108 (165.66) respectively.

4.2.2.6 Number of filled seeds/head

GMU 252, 273, 274, 281, 291 and 292 exhibited above mean performance over two checks, Morden (474.33) and DRSF-108 (532.99). Range for the filled seeds per head was between GMU-273 (190.00) and GMU-298 (599.44).

4.2.2.7 Total number of seeds per head

Total number of seeds per head ranged from 306.25 (GMU-294) to 817.37 (GMU-273). Genotypes 757.53 (GMU-274) 731.68 (GMU-291), 699.00 (GMU-292) recorded high mean performance over two checks, Morden (648) and DRSF-108 (692).

4.2.2.8 Filling seed percentage

Mean values for genotypes ranged from 51.44 (GMU-244) to 77.23 (GMU-286) with an average mean seed filling per cent of 64.84. The mean values for checks were 73.25 (Morden) and 76.92 (DRSF-108).

Seven genotypes out of fifty showed superior mean performance in desirable direction over check, Morden while one genotype was superior to check DRSF-108.

4.2.2.9 100-seed weight (g)

Mean values for germplasm lines ranged from 3.56 g (GMU-223) to 5.47 g (GMU-291) with an average test weight of 4.16 g. The mean values of checks were 4.10 g (Morden) and 4.28 g (DRSF-108).

Fifteen and thirteen genotypes out of fifty showed higher test weight which is in desirable direction over checks, Morden and DRSF-108 respectively.

4.2.2.10 Seed yield per plant (g)

Seed yield per plant was ranged from 5.57 g (GMU-278) to 26.67 g (GMU-291) with mean seed yield of 11.90 g per plant. The checks recorded 19.36 g (Morden) and 21.36 g (DRSF-108) of seed yield per plant.

Four genotypes showed superior mean performance over Morden and three over DRSF-108.

4.2.2.11 Oil content (%)

Oil content ranged from 22.57 per cent (GMU-282) to 33.55 per cent (GMU-243) with an average oil content of 26.46 per cent. The oil content was 32.66 per cent in Morden and 35.33 per cent in DRSF-108.

Two genotypes showed higher oil content than check, Morden while none of the tested genotypes were found superior over check DRSF-108.

4.2.2.12 Hull content (%)

Hull content ranged from 16.06 per cent (GMU-276) to 28.51 per cent (GMU-289) with an average of 23.42 per cent.

Nineteen and twelve genotypes showed superior mean performance in desirable negative direction over checks, Morden and DRSF-108, respectively.

4.3 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistics for yield and its contributing characters.

4.3.1 Test with Wilk's criteria

The Wilk's criteria obtained was used in calculation of 'V' statistics. The "V" statistic has showed highly significant difference among the genotypes for the aggregate effect of all the characters indicating existence of considerable divergence among the genotypes.

4.3.2 Mahalanobis's generalized distance D^2

In order to assess the genetic diversity among the 52 genotypes, D^2 statistics was carried out following the procedure given by Rao (1952). Since all the twelve variables were correlated, they were transformed into uncorrelated linear combination through Pivotal condensation method.

4.3.3 Grouping of genotypes into various clusters

Fifty two genotypes were grouped into 8 clusters based on D^2 values such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of different clusters is given in Table 7 Out of 8 clusters formed, cluster VII and I were the largest groups comprising 19 and 9 genotypes each followed by cluster VIII with 7 genotypes. Cluster V was the smallest group and contain only one genotype.

4.3.4 Average inter and intra cluster distance

The average intra and inter cluster D values are presented in Table 8. Intra cluster D values ranged from zero (cluster V) to 36.40 (Cluster IV).

The inter cluster D values of the 8 clusters, indicated that the highest divergence occurred between cluster IV and V (538.98) followed by cluster V and VII (448.24), cluster V and VIII (446.70) and cluster V and VI (438.41), while lowest divergence was noticed between cluster VI and VIII (22.76) followed by cluster VI and VIII (24.13).

4.3.5 Cluster means of the characters

The cluster means for each of twelve characters are presented in Table 9. From the data it can be seen that considerable differences existed for all the characters studied. The data indicated that the cluster mean for days to 50 per cent flowering ranged from Cluster IV (51.41 days) to Cluster III

(60.26 days). Early maturity was recorded in genotypes of Cluster IV (87.83 days), whereas, genotypes of Cluster III were late to maturity (94.93) days. Dwarf plant height was recorded in Cluster VI (125.64 cm) where as tall height was recorded in Cluster V (171.53 cm). Highest mean value for number of unfilled seeds per head was recorded in cluster II (211.64) and lowest value in cluster VII (154.166). Cluster IV recorded the highest mean value for number of filled seeds per head (659.82) while cluster VII recorded the lowest value (235.79). Seed filling percentage ranged from 60.46 per cent (Cluster VIII) to 75.98 per cent in Cluster IV. Highest 100 seed weight was recorded in Cluster VIII (5.04) and the value was lowest for Cluster VI (3.84). Seed yield per plant was highest in Cluster IV (24.18 g) and lowest in Cluster VII (7.53 g). Highest cluster mean of 34.00 per cent for oil content was recorded in Cluster IV and lowest mean value in Cluster V (24.802). Highest stem diameter was recorded in cluster V (4.13) and lowest in cluster VI (1.86). For total number of seed per head, the highest and lowest values recorded by Cluster III (700.02) and Cluster VII (389.96) respectively. Highest cluster mean for hull content was recorded in cluster II (24.94) and lowest in cluster VIII (18.64).

4.3.6 Relative contribution of characters towards diversity

The number of times that each of 12 characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 10.

Among all the characters, number of filled seeds per head contributed maximum to genetic diversity (42.01 %) followed by plant height (13.65 %), test weight (11.61 %), stem diameter (10.03 %) and days to 50 per cent flowering (9.20%). The remaining characters contributed very less to diversity. Seed yield per plant contributed the least (0.23 %).

4.3.6 Canonical analysis

Canonical analysis was carried out in 52 genotypes as per the method suggested by Rao (1952). The values of 5 canonical roots and percentage of variation observed by them are furnished in Table 11.

The first canonical root accounted for 40.07 per cent of total variability, while second canonical root accounted for 24.42 per cent of total variability. The third, fourth and fifth root accounted for 10.10, 8.38 and 4.27 per cent, respectively. The 5 canonical roots were responsible for 87.25 per cent of total variability, hence the canonical means were obtained in three dimensions.

The sum of the values of the 5 canonical roots was 242.59 of which root `1' had a value of 111.42, root `2' value was 67.90, root `3' a value of 28.09. The root `4' a value of 23.3 and root `5' a value of 11.87.

For the five canonical vectors, the amount of contribution towards diversity was presented in Table 12.

In the first vector (Z1), plant height (0.324), stem diameter (0.212), number of unfilled seeds per head (0.101), number of filled seeds per head

(0.80), total number of seeds per head (0.229), test weight (0.163), seed yield per plant (0.240), oil content (0.058) and hull content (0.065) contributed positively towards diversity while the remaining characters contributed negatively towards diversity.

In the second vector (Z2) number of unfilled seeds per head (0.032), number of filled seeds per head (0.304), test weight (0.066), seed yield per plant (0.070), oil content (0.071) and hull content (0.039) contributed positively towards diversity. The remaining characters contributed negatively towards diversity.

In the third vector (Z3), days to 50 per cent flowering (0.014), days to maturity (0.127), plant height (0.447) and stem diameter (0.6290), unfilled seeds per head (0.030), filling seed per cent (0.290), and hull content (0.044) contributed positively towards diversity, while the remaining characters contributed negatively towards diversity.

In the fourth vector (Z4), stem diameter (0.217), unfilled seeds per head (0.0052), total seeds (0.12), oil content (0.012) and hull content (0.065) positively contributed to diversity, while the remaining characters contributed negatively to diversity.

In the vector (Z5) days to 50 per cent flowering (0.356), unfilled seeds per head (0.152), filled seeds per head (0.341), total seeds per head (0.106), filling seed per cent (0.180), oil content (0.200) and hull content (0.087)

contributed positively towards diversity while remaining five characters contributed negatively towards diversity.

Days to 50 per cent flowering Z1, Z2 and Z4, days to maturity in Z1, Z2 and Z4 and Z5, plant height in Z2, Z4 and Z5 and stem diameter in Z2 and Z5, number of filled seeds per head in Vector three (Z₃) and vector four (Z₄), total seeds per head in Vector two (Z₂) and three (Z₃), filling seed per cent in Z1, Z2 and Z4. Test weight in Z3, Z4 and Z5, seed yield per plant in Z3, Z4, Z5, oil content in Z3 contributed negatively towards diversity.

4.4 CORRELATION COEFFICIENT

The phenotypic and genotypic correlations among the yield and yield component characters in sunflower are presented in Table 13. In the general values for genotypic correlations were higher than that of phenotypic correlations.

The yield component characters were found to be significantly and positively associated with seed yield per plant. Number filled seeds per head (0.91 / 0.96), total number of seeds per head (0.83 / 0.93), seed filling per cent (0.56 / 0.76), test weight (0.40 / 0.45), oil content (0.9 / 0.29) and days to maturity (0.10 / 0.14), plant height (0.34 / 0.45) and stem diameter (0.24 / 0.31) showed positive correlation while characters, days to 50 per cent flowering, number of unfilled seeds per head, hull content showed significant but negative phenotypic and genotypic correlation with seed yield.

However, the inter character association was presented here under :

4.4.1 Days to 50 per cent flowering

Days to 50 per cent flowering registered significant positive phenotypic and genotypic correlations with days to maturity (0.36 / 0.55) and plant height (0.20 / 0.25) while genotypic correlation alone was significant with test weight.

4.4.2 Days to maturity

Days to maturity exhibited significant phenotypic and genotypic positive correlation with plant height (0.28 / 0.36) and stem diameter (0.12 / 0.15) while genotypic positive correlation was recorded in unfilled seeds per head (0.13), total number of seeds per head (0.7) test weight (0.19) and hull content (0.16)

4.4.3 Plant height (cm)

Plant height recorded significant phenotypic and genotypic correlations with stem diameter (0.47/0.66), number of filled seeds per head (0.35 / 0.43), total number of seeds/ head (0.33 / 0.42), filling seed per cent (0.31 / 0.53), while genotypic positive correlation was significant in unfilled seeds per head (0.12) and hull content (0.16).

4.4.4 Stem diameter (cm)

Stem diameter recorded phenotypic and genotypic significant positive correlation with unfilled seeds/ head (0.14 / 0.37), number of filled seeds per head (0.34 / 0.37), total number of seeds (0.34 / 0.45) and filling seed per cent (0.20 / 0.30), while genotypic correlation was significant with hull content

(0.23). However, test weight (-0.14) was negatively correlated with stem diameter.

4.4.5 Number of unfilled seeds per head

Number of unfilled seeds per head registered significant phenotypic and genotypic positive correlations with number of filled seeds per head (0.29 / 0.51), total number of seeds (0.61 / 0.68) and oil content (0.13 / 0.41) while genotypic positive correlation was significant with hull content (0.13).

4.4.6 Number of filled seeds per head

Number of filled seeds per head significantly and positively correlated with total number of seeds (0.93 / 0.97), filling seed per cent (0.61 / 0.79), test weight (0.13 / 0.20), oil content (0.22 / 0.34).

4.4.7 Total number of seeds per head

Total number of seeds was phenotypically and genotypically significant and positively correlated with filling seed per cent (0.30 / 0.67), oil content (0.22 / 0.38), while genotypically correlated with test weight (0.17).

4.4.8 Filling seed per cent

Filling seed per cent was phenotypically and genotypically positively correlated with test weight (0.12 / 0.12).

4.4.9 100 seed weight (g)

Test weight was negatively significant and phenotypically and genotypically correlated with hull content (-0.29 / -0.82).

4.4.10 Seed yield per plant (g)

Seed yield showed positive phenotypic and genotypic significant correlation with filled seeds (0.91 / 0.96), total number of seeds (0.83 / 0.93), filling seed per cent (0.56 / 0.76), test weight (0.41 / 0.45), oil content (0.18 / 0.29), days to maturity (0.10 / 0.14), plant height (0.34 / 0.45), stem diameter (0.24 / 0.31) and unfilled seeds per head (0.23 / 0.46).

4.4.11 Oil content (%)

Oil content was phenotypically and genotypically negatively correlated with hull content (-0.17 / -0.27).

4.4.12 Hull content (%)

Hull content recorded negative and significant phenotypic and genotypic correlations with 100 seed weight (-0.29 / -0.87), while genotypically significantly correlated with days to maturity (0.16), plant height (0.16), stem diameter (0.24) and number of unfilled seeds per head (0.14).

4.5 PATH COEFFICIENT ANALYSIS

Based on the data recorded on 52 genotypes of sunflower in the present investigation, the genotypic and phenotypic correlations were estimated to determine direct and indirect effects of yield components on seed yield. The results are presented in Table 14.

Among all the characters, number of filled seeds per head (0.77 / 0.94), total number of seeds (0.11 / 0.30), test weight (0.30 / 0.14), days to maturity

(0.03 / 0.10) and plant height (0.02 / 0.13) showed positive direct effect on seed yield. Number of unfilled seeds per head, oil content, days to 50 per cent flowering and stem diameter exhibited direct negative effect on seed yield.

4.5.1 Days to 50 per cent flowering

Negative direct effect on yield (-0.01 / -0.074) was exhibited by days to 50 per cent flowering but indirectly contributed through plant height (0.00 / 0.02) and negatively through days to maturity (-0.04).

4.5.2 Days to maturity

Days to maturity had direct phenotypic and genotypic effect (0.10 / 0.13) on seed yield. It indirectly contributed to yield through days to 50 per cent flowering (0.01 / 0.05) and stem diameter (0.01 / 0.01) and genotypically contributed through number of unfilled seeds, total number of seeds and hull content.

4.5.3 Plant height (cm)

Plant height had direct positive effect (0.021 / 0.13) on seed yield. It indirectly contributed to yield through number of unfilled seeds (0.00 / 0.01), number of filled seeds (0.00 / 0.05), total seeds per head (0.00 / 0.05), filling seed per cent (0.00 / 0.07), hull content (0.00 / 0.02), oil content (0.00 / 0.01), days to 50 per cent flowering (0.00 / 0.04), days to maturity (0.01 / 0.05) and stem diameter (0.01 / 0.90).

4.5.4 Stem diameter (cm)

Stem diameter had negative direct effect (-0.02 / -0.89) on seed yield. It also indirectly contributed to yield through test weight (0.00 / 0.13). It indirectly positively influenced through 100 seed weight (0.01 / 0.00) and negatively through remaining all characters.

4.5.5 Number of unfilled seeds per head

Number of unfilled seeds per head had direct negative effect (-0.03 / -0.18) on seed yield per plant. It also indirectly contributed to yield through filling seed per cent (0.01 / 0.01) and negatively influenced through remaining all characters.

4.5.6 Number of filled seeds per head

Number of filled seeds per head had direct positive effect (0.77 / 0.94) on yield. It also indirectly contributed to seed yield through unfilled seeds per head (0.22 / 0.48), total number of seeds (0.71 / 0.91), filling seed per cent (0.47 / 0.74), test weight (0.09 / 0.18), oil content per cent (0.16 / 0.32), days to maturity (0.04 / 0.03), plant height (0.27 / 0.40) and stem diameter (0.23 / 0.35).

4.5.7 Total number of seeds per head

Total number of seeds per head had direct effect (0.10 / 0.30) on seed yield. It also indirectly influenced the yield through plant height (0.03 / 0.12) and stem diameter (0.03 / 0.13) unfilled seeds per head (0.06 / 0.20), filled seeds per head (0.10 / 0.29), filling seed per cent (0.03 / 0.20), test weight

(0.09 / 0.18) and oil content (0.02 / 0.11) and negatively influenced through days to 50 per cent flowering and hull content.

4.5.8 Filling seed per cent

Filling seed per cent had direct negative genotypic effect (-0.27) on seed yield. It positively influenced through number of filled seeds per head.

4.5.9 100-seed weight (g)

Test weight had direct positive effect (0.30 / 0.14) on seed yield. It also indirectly influenced seed yield through filled seeds (0.03 / 0.03), total seeds (0.02 / 0.02), filling seed per cent (0.03 / 0.02), days to 50 per cent flowering (0.02 / 0.02), days to maturity (0.02 / 0.02) and plant height (0.02 / 0.01).

4.5.10 Oil content (%)

Oil content had direct negative effect (-0.012) / -0.08) on seed yield and indirectly negatively influenced through all characters except days to 50 per cent flowering (0.00 / 0.01).

4.5.11 Hull content (%)

Hull content had direct phenotypic positive (0.033) and genotypic negative effect on yield. Indirectly through oil content (0.01 / 0.00) and negatively influenced through remaining all characters.

4.6 STABILITY ANALYSIS

Data was recorded from twelve characters from the three seasons and the stability analysis was made based on the Eberhart and Russel (1966) model. Results were presented here under by the following headings.

1. Analysis of variance.
2. Environmental indices
3. Stability parameters

4.6.1 Pooled analysis of variance

Fifty genotypes along with two checks, Morden and DRSF-108 were subjected to pooled analysis of variance for twelve characters.

The analysis revealed that the genotypes and environments were significant for all the twelve characters, indicating the diversity among the genotypes and environments studied (Table 15). The G and E interactions were significant for four characters viz., days to 50 per cent flowering, days to maturity, number of filled seeds per head and seed yield per plant implying differential behavior of genotypes under three seasons for these characters. The GE interactions for the remaining characters were found to be non-significant. Therefore, further analysis of stability was not carried out for remaining characters.

Partitioning of sum of squares into that of varieties, environment + (Genotypes + environment) and pooled error revealed that mean squares due to environment + (genotypes + environment) were significant for all the four

characters viz., days to 50 per cent flowering, days to maturity, a number of filled seeds per head and seed yield per plant reemphasizing the existence of GE interactions for these characters. Sum of squares due to $E + (G \times E)$ was further partitioned into that of environment (Linear), Genotype x Environment linear and pooled deviation. Significant variation due to environment (linear) the four characters viz., days to 50 per cent flowering, days to maturity, number of filled seeds per head and seed yield per plant revealing the linear contribution of environmental effects and additive environment variance on these characters. The linear component of GE non significant for the four characters suggesting that the genotypes did not differ for their linear response to environments.

The mean sum of squares for pooled deviation were significant for the four characteristics indicating the non-linear response and unpredictable nature of the genotypes by significantly differing for stability.

Since, further stability analysis was not carried out for all the traits viz., plant height, stem diameter, number of unfilled seeds per head, number of filled seeds per head, total number of seeds, seed filling per cent, 100 seed weight, oil content and hull content, judgment of the promising varieties is done based on their pooled mean performance only.

For the trait plant height, genotypes GMU-248, 260, 287, 296 and 298 recorded shorter plant height than check, Morden and thirty two genotypes recorded shorter plant height than DRSF-108. Among the genotype GMU-298 was shortest genotype.

Genotypes GMU-208, 214, 224, 252, 267, 273, 274, 282, 284 and 285 recorded thicker stem than check, Morden and seventeen genotypes were thicker than check DRSF-108. Among these genotypes GMU-284 recorded highest stem diameter.

In case of unfilled seeds per head, twenty six genotypes recorded less number of unfilled seeds per head than DRSF-108 and twenty eight genotypes were recorded less than Morden. Genotype, GMU-294 recorded least number of unfilled seeds per head.

Genotypes GMU-252, 273, 274, 291 and 292 recorded high total number of seeds per head than check, Morden and four genotypes were higher than DRSF-108 and the genotype, and the GMU-273 recorded highest number of seeds per head.

Only genotype i.e. GMU-268 recorded high seed filling per cent than check DRSF-108 and seven genotypes recorded high seed filling per cent than check, Morden.

Thirteen genotypes recorded high test weight when compared to check, DRSF-108 and Fifteen genotypes than check, Morden while GMU-294 recorded highest test weight.

For the trait, oil content two genotypes were with high oil content than check, Morden while none of the genotype was recorded high oil content than check DRSF-108.

Nineteen genotypes recorded less hull content than check, Morden and twelve genotypes recorded less hull content than check DRSF-108 while genotype GMU-276 recorded least hull content.

4.6.2 Environmental indices

Late *kharif* was considered to be the best season for the character, days to 50 per cent flowering while early *rabi* was best for the remaining three characters viz., days to maturity, number of unfilled seeds per head and seed yield per plant (Table 16).

4.6.3 Stability parameters

Stability parameters were presented for the characters with significant GE interaction (Table 17)

4.6.3.1 Days to 50 per cent flowering

Out of fifty two genotypes evaluated twenty nine genotypes recorded non significant deviation from regression (S^2_{di}) values i.e. the genotypes are statistically within the range of 'minimum deviation from regression' and whose performance can be predicted. Genotypes GMU-284, 286, 289, 293 and 297 were early in flowering when compared to check, DRSF-108 and these are stable across the seasons. Genotypes GMU-274, 284, 291 and 292 recorded long duration and exhibited the more than the average stability ($b_i < 1$) and hence adaptable for poor environments. Genotypes GMU-225, 276 and 297 recorded long duration and GMU-289 recorded shorter duration than check

DRSF-108 and exhibited less than the average stability ($b_i > 1$) and are adaptable to favourable environments.

4.6.3.2 Days to maturity

For the trait, days to maturity, thirty nine genotypes recorded non – significant deviation from regression values, it indicates that the genotypes were within the range of ‘minimum deviation from the regression’ and whose performance can be predicted. Genotypes GMU-218, 228, 238, 239, 244, 248, 254, 258, 265, 267, 270, 275, 285, 294, 297 and 300 matured earlier than check DRSF-108 they were stable performance over the environments ($b_i=1$).

Genotype GMU-286 earlier to mature than check DRSF-108 and exhibited more than the average stability and adopted to poor environments ($b_i < 1$). Genotypes GMU-242 and 289 were early in maturity than check DRSF-108 and genotypes GMU-262 and 281 were late in maturity and exhibited less than the average stability and adoptable to favorable environments ($b_i > 1$).

4.6.3.3 Number of filled seeds per head

Out of fifty two genotypes, thirty six genotypes recorded non-significant deviation from regression and they are in the range of minimum deviation from regression, whose performance can be predicted. Genotypes GMU-252, 251 recorded high number of filled seeds than check, Morden and these are stable across the seasons ($b_i = 1$).

Genotypes GMU-212, 225, 270 and 294 were with less number of filled seeds per head than check, Morden and DRSF-108 and exhibited more than the average stability and adoptable to poor environments ($b_i < 1$).

Genotypes, GMU-281 and 282 recorded high number of filled seeds per head than check, Morden and the genotypes, GMU-277 and 290 recorded less than the checks, Morden and DRSF-108 exhibited less than the average stability and adaptable to favourable environments.

4.6.3.4 Seed yields per plant

Out of fifty two genotypes, forty four genotypes recorded non-significant deviation from regression and they are in the range of 'minimum deviation from regression' and whose performance can be predicted. Among them GMU-291 recorded highest seed yield and adaptable to all seasons.

Genotypes GMU-268, 276 and 300 recorded low seed yield while GMU-273 recorded high seed yield than checks, Morden and DRSF-108 and exhibited more than the average stability and adopted to poor environments.

Genotypes GMU-238, 248, 281 and 291 recorded low yield and exhibited less than the average stability and adoptable for favourable environments.

Table 2 : Morphological characterisation of sunflower genotypes

Geno- types	Hypo- cotyl anthoc yanin color	Leafss ha-pe	leaf size	Leaf colour	Serra- tion	angle of veins	Hairy- ness	leaf base	Patiole pigmen- tation	No.of leaves	stem pubes- cence	stem pig- men- tation	Rayfl- ower colour	Rayfl- ower shape	discflo- wer colour	Anthoc ya0nin colo-ur of disc flower stigma	Pollen colour	plant bran- ching	head atti- tude	head shape of grain side	Shape of bracts	Seed base colour	Seed shape
208	A	C	L	DG	C	RA	S	AU	A	16.6	D	A	Y	E	Y	P	Y	A	TD	V	R	B	E
212	A	C	L	DG	VC	RA	D	AU	A	24.6	D	A	Y	E	Y	P	Y	A	HT	V	R	G	O
214	A	C	L	DG	C	A	D	AU	A	25.3	D	A	Y	E	Y	P	Y	BE	TD	V	R	B	O
218	M	C	L	DG	VC	RA	D	AU	A	13.0	D	A	Y	E	Y	P	W	A	TD	V	R	B	E
223	A	T	M	DG	C	A	D	A	A	24.0	D	A	Y	E	Y	P	Y	A	TD	V	R	B	R
224	A	C	L	DG	C	RA	D	AU	A	23.0	D	A	Y	E	Y	P	Y	A	TD	F	R	B	O
225	A	C	L	DG	C	RA	D	A	P	23.0	D	A	Y	E	Y	P	Y	A	TD	V	R	G	O
226	M	C	L	DG	VC	RA	D	AU	A	23.0	D	A	Y	E	Y	A	Y	A	TD	C	E	B	R
228	M	C	L	DG	C	A	D	AU	A	25.6	D	A	Y	E	Y	P	Y	A	TD	F	R	B	R
238	A	C	S	DG	C	A	D	AU	A	25.3	D	A	Y	E	Y	A	Y	A	TD	F	R	G	E
239	A	C	M	DG	C	RA	D	AU	A	27.0	D	A	Y	E	Y	P	Y	A	TD	V	R	B	E
242	S	C	M	DG	C	RA	D	AU	A	19.8	D	A	Y	E	Y	A	Y	A	TD	C	R	BR	E
244	M	C	L	DG	VC	RA	D	AU	A	28.0	D	A	Y	E	Y	A	Y	A	TD	V	R	B	R
248	A	C	L	G	C	O	S	AU	P	21.6	D	P	Y	E	P	P	W	BE	TD	C	E	BR	R
252	M	C	L	DG	C	RA	D	AU	A	33.0	D	A	Y	E	Y	A	Y	A	TD	C	R	B	O
254	A	C	M	DG	C	RA	D	AU	P	21.6	D	A	Y	E	Y	A	Y	A	TD	V	R	B	ES
257	A	C	L	DG	C	O	D	AU	A	25.3	D	A	Y	E	Y	P	Y	A	TD	F	R	B	R
258	S	C	L	DG	C	RA	D	AU	P	20.0	D	A	Y	E	Y	A	Y	A	TD	F	R	G	R
260	A	R	L	DG	C	A	D	AU	A	20.3	D	A	Y	E	Y	P	Y	A	TD	V	R	B	ES
261	A	C	L	DG	VC	RA	D	AU	A	29.6	D	A	Y	E	Y	P	Y	A	TD	F	R	B	R
262	M	C	L	DG	C	RA	D	AU	A	28.0	D	A	Y	E	Y	P	Y	A	TD	F	E	BR	O
265	A	C	L	DG	C	RA	D	AU	A	22.0	D	A	Y	E	Y	A	Y	A	TD	F	E	G	E
267	A	C	L	DG	VC	RA	D	AU	A	24.5	D	A	Y	E	Y	P	Y	A	TD	F	E	B	OL
268	M	C	L	DG	VC	A	D	AU	A	29.0	D	A	Y	E	Y	P	Y	A	TD	F	E	B	R
270	A	C	L	DG	VC	RA	D	AU	A	27.5	D	A	Y	E	Y	A	Y	A	TD	C	R	B	OE
273	M	R	S	G	F	O	S	AU	A	35.6	D	A	Y	E	Y	P	Y	A	TD	F	R	B	O
274	S	T	L	DG	C	A	D	AU	A	26.0	D	A	Y	E	Y	P	Y	A	TD	F	R	B	R
275	A	C	L	DG	C	RA	D	AU	P	25.2	D	A	Y	E	Y	P	Y	A	TD	F	R	B	E
276	M	C	L	DG	VC	RA	D	AU	A	20.6	D	A	Y	E	Y	A	Y	A	TD	F	E	B	OE
277	A	C	L	DG	C	A	D	AU	A	28.0	D	A	Y	E	Y	A	Y	A	TD	F	R	B	R
278	M	C	L	DG	VC	RA	D	AU	A	29.0	D	A	Y	E	Y	P	Y	A	TD	V	R	B	R
279	A	C	M	DG	VC	RA	D	AU	A	25.0	D	A	Y	E	Y	A	Y	A	TD	C	R	G	O
280	A	C	L	DG	C	RA	S	AU	A	28.0	D	A	Y	E	P	A	Y	A	TD	F	R	B	R

Table 2 : Morphological characterisation of sunflower genotypes

Genotypes	Hypocotyl anthocyanin color	Leaf shape	leaf size	Leaf colour	Serration	angle of veins	Hairiness	leaf base	Petiole pigmentation	No. of leaves	stem pubescence	stem pigmentation	Rayflower colour	Rayflower shape	discflower colour	Anthocyanin colour of disc flower stigma	Pollen colour	plant branching	head attitude	head shape of grain side	Shape of bracts	Seed base colour	Seed shape
281	A	C	L	DG	C	A	D	AU	A	28.0	D	A	Y	O	P	P	Y	A	TD	V	E	B	O
282	A	C	L	DG	VC	A	D	AU	A	25.0	D	A	Y	E	Y	A	Y	BE	TD	C	R	B	OE
284	A	C	L	DG	C	RA	D	AU	A	31.0	D	A	Y	E	Y	P	Y	A	TD	V	R	B	OE
285	P	C	L	DG	VC	RA	D	AU	P	29.1	D	A	Y	E	Y	A	Y	A	TD	V	R	G	O
286	A	C	L	DG	VC	RA	D	AU	A	23.6	D	A	Y	E	Y	A	Y	A	TD	F	R	B	OE
287	A	C	L	DG	VC	RA	D	AU	A	24.0	D	A	Y	E	Y	P	Y	A	TD	F	R	B	O
288	A	C	L	DG	VC	RA	D	AU	A	26.0	D	A	Y	E	Y	P	Y	A	TD	V	R	BR	R
289	S	C	L	DG	VC	RA	S	AU	A	25.0	D	A	Y	E	Y	P	Y	A	TD	F	R	B	O
290	A	C	L	DG	C	A	D	AU	A	26.5	D	A	Y	E	Y	A	Y	A	TD	F	R	B	O
291	A	C	L	DG	C	A	D	AU	A	22.3	D	A	Y	O	Y	P	Y	A	T	V	R	B	R
292	A	C	L	DG	C	RA	D	AU	P	27.3	D	A	Y	E	P	A	Y	A	T	V	R	BR	O
293	A	C	L	DG	VC	RA	D	AU	P	26.9	D	A	Y	E	Y	P	Y	A	TD	F	E	B	O
294	A	C	L	DG	C	A	S	AU	P	26.0	D	A	Y	E	Y	P	Y	BE	TD	C	R	B	O
296	A	L	M	DG	M	A	D	AU	A	23.0	D	A	Y	E	P	A	Y	A	TD	F	E	G	O
297	S	C	L	DG	C	RA	D	AU	A	25.0	D	A	Y	E	Y	P	Y	A	TD	V	R	B	O
298	A	C	L	DG	VC	RA	D	AU	A	22.6	D	A	Y	E	Y	A	Y	A	V	F	R	G	E
300	A	R	L	DG	VC	O	D	AU	A	27.1	D	A	Y	O	Y	A	Y	A	TD	F	R	B	R
MOD	A	C	L	DG	VC	RA	D	AU	A	32	D	A	Y	E	Y	A	Y	A	V	V	R	B	OE
DR	A	C	L	G	C	A	D	AU	A	30	D	A	Y	E	Y	P	Y	A	TD	V	E	B	R

Hypocotyl Anthocyanin colouration : A = Absent; M = Medium; S = Strong

Leaf size : S = Small; M = Medium; L = Large . **Angle of lateral veins**:RA=Right angles;A= Acute;O=Obtuse

Leaf shape : C = Cordate; R = Round; L = Lanceolate; T = Triangle; **Serration** : C = Coarse; F = Flat; VC = Very coarse

Hairiness : S = Sparse; D = Dense; **Leaf base** : AU= Auriculate; A = Acute

Petiole pigmentation : A = Absent; P = Present; **Stem pigmentation** : A = Absent; P = Present

Number of leaves on main stem :L=Low ;M=Medium ;H=High **Disc flower colour** :P=Putple;Y=Yellow ;

Ray flower shape : E = Elongate ; O = Ovoid **Anthocyanin colouration disc flower** : A = Absent; P = Present

Pollen colour : Y = Yellow ; W = White **Type of branching** : A = Absent; BE = Branching entire

Head shape at grain side : V = Convex; C = Concave; F = Flat **Head attitude** : HT = Half turned; TD : Turned down; V = Vertical; T = Turned

Bract shape: R=Round;E=Elongate : **Seed color** : B = Black; Br = Brown; G = Grey

Seed shape : R = Round; O = Ovoid; OE = Ovoid elongate; OL = Ovoid long; ES : Elongated slender

Table 3 : Grouping of different genotypes based on morphological characterisation

Leaf size			
Very large	Medium	Small	Large
GMU-225, 270, 277, 278, 297, Morden	GMU-223, 242, 254, 279, 296, 239, 279	GMU-238,273	Remaining all
Leaf shape			
Round	Triangular	cordate	
GMU-260,273,300	GMU-223,274	Remaining all	
Leaf color			
Green	Dark green		
GMU-248,273,DRSF-108	Remaining all		
Leaf fineness of serration			
Fine	very coarse	coarse	
GMU-273	GMU-212, 218,226, 244,261,267,268,270, 276,278,279,282,285,286,287,288, 289, 293, 298, 300, MORDEN	Remaining all	
Leaf angle of viens			
acute	obtuse	right angles	
GMU-214, 223, 228, 238, 260, 268, 274, 277, 281,282,290,291	GMU-248, 257, 273	Remaining all	
Leaf hairyness			
sparse	dense		
GMU-208, 248, 273, 280, 289, 294	Remaining all		
Shape of leaf base			
acute	auriculate		
GMU-223, 225.	Remaining all		
petiole pigmentaion			
presant	absent		
GMU-214, 225, 248, 254, 258, 275, 292, 293,294	Remaining all		
Stem pubescence			
all are with dense pubescence			
Number of leaves on main stem			
Low	Medium	High	
GMU-208, 218, 242, 258	GMU-212, 223, 224, 226, 248, 254, 260, 265, 267, 276, 279, 286, 287, 289, 291	Remaining all	
Ray flower shape			
ovate	elongated		
GMU-281,291, 300	Remaining all		

Ray flower color			
all are yellow			
Disc flower color			
Purple	Yellow		
GMU-244, 248, 280, 281,282,292,296	Remaining all		
Anthocyanin coloration of disc flower			
Absent	Present		
GMU-226,242,248,252,254, 258,265,270,276,277, 280, 282,285,286,290, 298, Morden	Remaining all		
Pollen color			
White	purple		
GMU-218, 248	Remaining all		
Shape of bracts			
elongate	round		
GMU-226,248,262,265,267, 268,276,281,293,296, DRSF-108	Remaining all		
Branching habit			
present	absent		
GMU-214, 248, 282,294			
Head attitude			
Half turned	turned	vertical	turned down
GMU-212	GMU-291,292	GMU-298,morden	Remaining all
head shape of grean side			
flat	convex	concave	
GMU-224, 228, 238, 257, 258, 261, 262, 265,267,268,273,274, 275, 276, 277,280,286,287,289, 290, 293, 296,298,300	Remaining all	GMU-226, 242, 248, 252, 270, 278, 282, 294	
Seed shape			
elongated	elongate slender	ovate	ovate long
GMU-208,218,238,239,242, 265,275,298	GMU-254,260,	GMU-214, 212, 224, 225, 252, 262, 273, 279,281,285,287,289, 290,292,293, 294,296	GMU-267
Ovate elongate	Round		
GMU-270,276,282,284,286	GMU-223,226,228,244,248,257, 258,261,268,274,277, 278,280,288,291,300, DRSF-108		
Seed base color			
brown	black	gray	
GMU-242,248,288,262,292	Remaining all	GMU-212, 225, 238, 265, 279, 285,296, 298, 258	

Table 4 : Analysis of variance for yield and yield attributing characters

Characters	Replications	Treatments	Pooled error
Days to 50% Flowering	0.869	30.911 **	0.986
Days to Maturity	4.705	13.828 **	1.375
Plant Height (cm)	33.076	937.007 **	50.758
Stem Diameter (cm)	0.019	1.122 **	0.023
Unfilled seeds / head	564.749	4401.271 *	155.345
Filled seeds / head	383.517	42261.050 **	321.357
Total seeds / head	1348.22	59644.330 **	581.443
filling seed %	10.442	133.600 **	3.888
Test weight (g)	0.036	0.797 **	0.096
Seed yield / plant (gm)	1.868	87.559 **	1.592
Oil content %	0.084	24.561 **	1.831
Hull content %	2.052	26.063**	2.3
d.f.	3	51	153

Table 5 : Estimates of variability, heritability, genetic advance as per cent of mean for yield and yield contributing characters of sunflower genotypes

S.No	Character	gcv	pcv	Herita- bility	Genetic advance as % of mean
1	Days to 50% Flowering	5.29	6.53	65.79	8.84
2	Days to Maturity	2.13	3.07	48.01	3.04
3	Plant Height (cm)	12.28	14.34	73.36	21.67
4	Stem Diameter(cm)	25.97	30.84	70.89	45.04
5	Unfilled Seeds/Head	19.22	32.44	35.10	23.46
6	Filled Seeds/Head	35.55	37.42	90.24	69.56
7	Total Seeds/Head	27.32	29.82	84.33	51.80
8	Filled Seed %	9.42	13.81	45.56	13.25
9	100 seed weight (g)	11.67	15.52	56.56	18.08
10	seed yield/plant(g)	44.81	48.34	86.04	85.63
11	Oil Content %	9.83	14.74	44.51	13.52
12	Hull Content %	9.26	22.82	16.49	7.75

Table 6a : Mean performance of 52 genotypes over 3 seasons

	Genotypes	Days to 50 % flowering				Days to maturity			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
1	GMU-208	60.50	62.50	59.50	60.83	96.50	95.50	94.50	95.50
2	GMU-212	58.50	54.50	58.50	57.17	95.50	90.50	91.00	92.33
3	GMU-214	61.50	57.50	60.50	59.83	94.50	92.50	92.00	93.00
4	GMU-218	64.50	52.00	52.50	56.33	92.50	95.50	90.50	92.83
5	GMU-223	64.50	62.00	62.50	63.00	93.00	94.00	90.00	92.33
6	GMU-224	61.50	60.50	60.00	60.67	95.00	96.50	94.50	95.33
7	GMU-225	60.00	55.50	53.50	56.33	94.00	94.50	92.00	93.50
8	GMU-226	62.00	58.50	57.00	59.17	95.00	94.00	92.50	93.83
9	GMU-228	64.50	58.00	59.50	60.67	91.00	94.50	88.00	91.17
10	GMU-238	58.50	59.00	55.50	57.67	90.00	93.50	86.00	89.83
11	GMU-239	55.00	62.00	54.50	57.17	91.00	95.50	89.00	91.83
12	GMU-242	56.50	62.00	52.50	57.00	90.00	93.50	86.50	90.00
13	GMU-244	60.00	57.00	57.00	58.00	90.50	92.00	89.50	90.67
14	GMU-248	63.00	52.00	58.50	57.83	91.50	92.50	89.50	91.17
15	GMU-252	66.00	61.50	58.50	62.00	97.00	96.50	94.00	95.83
16	GMU-254	63.50	60.00	57.50	60.33	90.50	93.50	90.00	91.33
17	GMU-257	66.00	62.50	61.00	63.17	94.00	96.50	92.50	94.33
18	GMU-258	64.00	61.50	60.50	62.00	90.00	96.50	88.50	91.67
19	GMU-260	56.50	57.50	54.00	56.00	91.50	96.50	91.50	93.17
20	GMU-261	59.00	55.00	57.50	57.17	93.50	95.50	94.00	94.33
21	GMU-262	62.00	54.50	58.00	58.17	95.50	95.50	94.00	95.00
22	GMU-265	60.00	56.00	56.50	57.50	90.00	93.00	87.50	90.17
23	GMU-267	61.00	60.00	54.50	58.50	92.50	93.00	89.50	91.67
24	GMU-268	60.00	59.00	56.50	58.50	92.50	92.00	95.50	93.33
25	GMU-270	62.50	54.00	57.00	57.83	95.00	92.00	91.00	92.67
26	GMU-273	56.50	53.50	56.00	55.33	96.00	96.50	96.50	96.33
27	GMU-274	64.00	62.50	60.50	62.33	96.00	97.00	95.00	96.00
28	GMU-275	59.50	57.50	55.00	57.33	89.50	92.50	89.50	90.50
29	GMU-276	61.00	58.00	56.50	58.50	91.50	96.00	92.50	93.33
30	GMU-277	58.50	60.00	58.50	59.00	92.00	96.50	90.00	92.83
31	GMU-278	63.00	66.00	62.50	63.83	95.50	97.50	93.50	95.50
32	GMU-279	62.00	59.50	58.50	60.00	94.50	96.00	90.00	93.50
33	GMU-280	62.50	59.50	56.00	59.33	92.00	96.50	90.50	93.00
34	GMU-281	66.50	62.50	58.00	62.33	94.50	96.50	91.50	94.17
35	GMU-282	58.50	57.00	56.00	57.17	92.00	96.50	89.50	92.67
36	GMU-284	55.50	53.00	51.00	53.17	93.00	94.50	91.00	92.83
37	GMU-285	60.00	59.50	58.50	59.33	93.50	96.50	90.00	93.33
38	GMU-286	55.50	54.00	52.00	53.83	90.50	92.50	91.00	91.33
39	GMU-287	60.00	54.50	52.50	55.67	91.00	96.50	91.50	93.00
40	GMU-288	56.50	55.50	54.50	55.50	96.00	92.50	92.00	93.50
41	GMU-289	56.50	52.50	50.50	53.17	92.50	95.50	89.50	92.50
42	GMU-290	56.50	53.50	57.50	55.83	95.00	92.50	91.00	92.83
43	GMU-291	61.00	61.00	61.00	61.00	96.50	96.50	95.50	96.17
44	GMU-292	64.50	64.00	64.00	64.17	93.50	95.50	95.00	94.67
45	GMU-293	54.00	52.50	50.00	52.17	95.50	92.00	91.50	93.00
46	GMU-294	58.50	59.50	54.00	57.33	93.00	90.00	90.00	91.00
47	GMU-296	59.00	59.50	54.50	57.67	96.50	90.50	93.50	93.50
48	GMU-297	55.50	52.50	53.50	53.83	94.00	93.00	90.50	92.50
49	GMU-298	66.50	60.00	62.50	63.00	97.50	91.00	89.50	92.67

	Genotypes	Days to 50 % flowering				Days to maturity			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
50	GMU-300	59.00	55.50	58.00	57.50	89.50	93.50	88.50	90.50
	CHECKS								
1	Morden	48.50	50.50	46.50	48.50	81.00	85.50	82.50	83.00
2	DRSF-108	54.00	56.50	52.50	54.33	92.00	94.50	91.50	92.67
	Mean	60.08	57.78	56.61	58.15	93.00	94.21	91.08	92.76
	C. V.	2.25	2.64	2.35	3.82	1.60	1.97	1.77	2.22
	SE of Difference	1.35	1.52	1.33	0.91	1.48	1.86	1.61	0.84
	CD 95%	2.71	3.06	2.67	2.53	2.98	3.73	3.24	2.34
	CD 99%	3.61	4.08	3.56	3.33	3.97	4.97	4.31	3.08

Table 6b : Mean performance of 52 genotypes over 3 seasons

	Genotypes	Plant height (cm)				Stem diameter			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
1	GMU-208	169.50	163.50	163.00	165.33	3.28	3.41	2.97	3.22
2	GMU-212	123.40	140.63	120.13	128.05	2.03	2.00	1.88	1.97
3	GMU-214	170.63	171.61	172.38	171.54	4.34	4.57	3.50	4.13
4	GMU-218	120.45	140.75	112.33	124.51	2.18	2.16	1.41	1.92
5	GMU-223	138.38	155.93	132.30	142.20	2.00	2.06	1.49	1.85
6	GMU-224	153.30	168.28	161.00	160.86	3.22	3.26	2.72	3.07
7	GMU-225	127.73	151.24	132.42	137.13	2.15	2.00	2.15	2.10
8	GMU-226	129.90	150.13	120.55	133.53	1.68	2.92	2.16	2.25
9	GMU-228	136.15	153.58	130.78	140.17	1.58	2.02	1.27	1.62
10	GMU-238	170.83	171.40	163.33	168.52	2.17	3.32	1.69	2.39
11	GMU-239	138.56	160.13	121.63	140.10	1.48	2.72	1.46	1.89
12	GMU-242	132.47	149.63	106.20	129.43	1.41	2.73	1.40	1.85
13	GMU-244	118.23	142.33	119.74	126.76	2.11	2.26	1.86	2.07
14	GMU-248	111.78	130.73	100.78	114.43	1.63	2.00	2.02	1.88
15	GMU-252	158.67	158.93	155.68	157.76	3.41	3.51	3.58	3.50
16	GMU-254	140.60	151.08	130.80	140.82	2.06	3.22	2.00	2.43
17	GMU-257	140.23	169.65	132.46	147.45	2.00	3.13	1.42	2.18
18	GMU-258	120.80	137.79	122.36	126.98	1.75	2.08	2.17	2.00
19	GMU-260	108.20	129.63	104.15	113.99	1.47	2.02	2.19	1.89
20	GMU-261	117.95	131.66	114.03	121.21	1.86	2.08	1.81	1.91
21	GMU-262	127.06	150.86	131.60	136.51	1.70	2.15	1.69	1.85
22	GMU-265	122.94	142.11	113.96	126.34	2.03	2.69	2.52	2.41
23	GMU-267	166.55	173.50	149.83	163.29	3.38	3.69	2.62	3.23
24	GMU-268	159.90	169.58	158.00	162.49	2.36	2.65	2.42	2.48
25	GMU-270	132.30	143.95	119.63	131.96	2.10	1.52	1.64	1.75
26	GMU-273	164.00	170.78	157.50	164.09	2.48	3.64	2.50	2.87
27	GMU-274	159.00	159.58	163.40	160.66	3.51	3.88	3.41	3.60
28	GMU-275	132.50	147.50	127.58	135.86	1.84	2.23	1.68	1.91
29	GMU-276	113.50	132.46	121.03	122.33	2.39	2.29	1.42	2.03
30	GMU-277	151.48	167.50	152.68	157.22	1.96	3.40	1.62	2.32
31	GMU-278	139.33	156.27	122.31	139.30	1.89	1.29	2.13	1.77
32	GMU-279	107.00	138.00	113.15	119.38	1.72	1.70	2.14	1.85
33	GMU-280	142.38	159.87	128.83	143.69	1.81	2.08	1.38	1.76
34	GMU-281	146.63	159.00	139.00	148.21	1.46	2.13	1.38	1.66
35	GMU-282	150.50	161.50	136.75	149.58	2.18	3.05	2.40	2.54
36	GMU-284	169.80	176.75	160.50	169.02	4.40	4.13	4.73	4.42
37	GMU-285	157.25	159.00	140.63	152.29	2.01	3.49	2.76	2.75
38	GMU-286	129.15	145.75	131.78	135.56	1.73	2.19	1.99	1.97
39	GMU-287	109.93	120.13	111.00	113.68	1.80	2.00	2.00	1.93
40	GMU-288	127.50	142.65	117.18	129.11	1.31	2.76	1.17	1.75
41	GMU-289	113.80	131.50	117.08	120.79	1.58	3.00	1.83	2.14
42	GMU-290	172.00	163.00	171.50	168.83	1.78	2.04	2.40	2.07
43	GMU-291	151.50	160.50	168.00	160.00	1.80	2.09	2.01	1.97
44	GMU-292	160.67	157.33	141.18	153.06	1.33	2.78	1.75	1.95
45	GMU-293	140.00	132.43	124.50	132.31	2.03	2.48	1.72	2.08
46	GMU-294	124.15	145.88	129.73	133.25	1.92	2.40	2.33	2.21
47	GMU-296	102.70	116.88	121.00	113.53	1.92	2.32	1.41	1.88
48	GMU-297	109.75	125.65	138.70	124.70	1.87	2.20	2.53	2.20
49	GMU-298	99.30	112.16	99.45	103.64	1.27	2.57	2.03	1.96
50	GMU-300	138.93	147.30	130.50	138.91	2.00	3.21	2.00	2.40

	Genotypes	Plant height (cm)				Stem diameter			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
	CHECKS								
1	Morden	105.00	119.50	125.50	116.67	2.28	2.72	2.46	2.48
2	DRSF-108	142.00	157.50	142.50	147.33	1.98	2.24	2.46	2.23
	Mean	136.47	149.52	133.11	139.70	2.11	2.62	2.11	2.28
	C. V.	7.27	5.07	9.16	7.40	6.37	9.58	11.14	16.64
	SE of Difference	9.92	7.59	12.19	4.22	0.13	0.25	0.24	0.15
	CD 95%	19.91	15.23	24.48	11.76	0.27	0.50	0.47	0.43
	CD 99%	26.54	20.30	32.62	15.50	0.36	0.67	0.63	0.57

Table 6c : Mean performance of 52 genotypes over 3 seasons

	Genotypes	Number of unfilled seeds / head				Number of filled seeds / head			
		Late kharif	Early rabi	Rabi	Pooled Mean	Late kharif	Early rabi	Rabi	Pooled Mean
1	GMU-208	209.50	150.00	128.80	162.77	339.83	359.79	333.63	344.42
2	GMU-212	127.00	288.00	160.00	191.67	326.71	336.24	314.51	325.82
3	GMU-214	199.50	201.66	150.65	183.94	339.83	359.79	333.63	344.42
4	GMU-218	169.00	139.28	254.50	187.59	248.50	287.00	234.83	256.78
5	GMU-223	158.80	111.30	138.56	136.22	253.83	261.67	289.00	268.17
6	GMU-224	162.33	251.66	329.30	247.76	392.00	382.00	351.50	375.17
7	GMU-225	111.50	139.77	210.62	153.96	225.25	248.69	287.26	253.73
8	GMU-226	172.29	161.73	167.30	167.10	252.33	273.66	210.30	245.43
9	GMU-228	109.65	161.15	91.80	120.87	224.67	232.82	240.67	232.72
10	GMU-238	166.50	152.75	115.48	144.91	409.05	531.93	370.00	436.99
11	GMU-239	58.00	161.95	119.94	113.30	216.69	221.00	163.50	200.40
12	GMU-242	129.42	117.40	281.97	176.26	337.17	390.80	304.00	343.99
13	GMU-244	173.67	200.00	155.55	176.40	246.50	219.70	119.13	195.11
14	GMU-248	250.30	110.54	238.77	199.87	347.51	449.00	305.50	367.34
15	GMU-252	157.65	139.45	250.62	182.57	494.27	515.95	491.50	500.57
16	GMU-254	244.09	141.03	359.77	248.30	363.31	346.95	347.00	352.42
17	GMU-257	166.13	200.50	93.08	153.23	277.20	232.51	210.64	240.12
18	GMU-258	161.50	181.18	141.98	161.55	250.50	450.50	240.64	313.88
19	GMU-260	124.99	106.50	93.63	108.37	221.92	225.25	202.26	216.48
20	GMU-261	160.77	153.16	115.27	143.07	332.66	294.42	232.53	286.54
21	GMU-262	151.21	161.50	153.75	155.49	407.50	374.28	400.63	394.13
22	GMU-265	113.00	138.28	192.90	148.06	274.50	263.45	245.50	261.15
23	GMU-267	117.82	165.33	252.50	178.55	283.50	310.15	248.30	280.65
24	GMU-268	39.96	195.94	201.85	145.91	478.77	487.28	430.94	465.66
25	GMU-270	259.76	125.47	262.80	216.01	348.00	354.67	344.00	348.89
26	GMU-273	263.13	160.50	230.25	217.96	653.50	610.25	534.50	599.42
27	GMU-274	223.33	252.93	301.75	259.34	456.17	528.00	510.50	498.22
28	GMU-275	200.15	231.63	118.70	183.49	249.16	272.00	240.86	254.01
29	GMU-276	129.40	152.79	121.80	134.66	237.50	254.00	270.50	254.00
30	GMU-277	172.30	105.78	189.00	155.69	325.83	390.50	253.50	323.28
31	GMU-278	179.40	154.32	114.95	149.56	163.50	264.00	221.63	216.38
32	GMU-279	253.77	252.45	206.67	237.63	278.00	293.66	259.67	277.11
33	GMU-280	122.87	207.00	190.50	173.46	178.33	220.50	188.00	195.61
34	GMU-281	120.63	152.50	206.50	159.88	502.50	518.33	420.00	480.27
35	GMU-282	112.50	102.50	187.50	134.17	391.00	352.50	353.50	365.67
36	GMU-284	208.15	207.15	163.75	193.02	441.50	453.00	391.25	428.58
37	GMU-285	256.50	253.00	197.00	235.50	321.00	349.75	312.00	327.58
38	GMU-286	139.40	202.60	134.15	158.72	309.00	219.90	213.15	247.35
39	GMU-287	208.25	310.50	145.25	221.33	263.90	273.90	260.50	266.10
40	GMU-288	151.00	113.35	129.95	131.43	282.65	219.50	210.25	237.47
41	GMU-289	153.50	162.55	175.50	163.85	220.65	242.28	251.50	238.14
42	GMU-290	114.50	120.50	119.00	118.00	222.15	301.00	206.50	243.22
43	GMU-291	235.85	194.15	154.50	194.83	508.25	612.80	489.50	536.85
44	GMU-292	217.50	193.00	251.75	220.75	460.85	561.16	413.80	478.60
45	GMU-293	172.40	252.35	273.00	232.58	272.35	198.36	228.00	232.90
46	GMU-294	89.00	87.45	122.55	99.67	207.65	219.23	192.90	206.59
47	GMU-296	157.75	155.55	197.50	170.27	392.80	401.03	221.25	338.36
48	GMU-297	173.50	115.65	201.80	163.65	271.40	232.17	196.00	233.19
49	GMU-298	139.30	192.80	160.15	164.08	195.88	221.30	155.50	190.89
50	GMU-300	135.50	178.25	177.00	163.58	314.40	389.50	393.00	365.63

	Genotypes	Number of unfilled seeds / head				Number of filled seeds / head			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
	CHECKS								
1	Morden	1455.50	192.00	171.50	173.00	482.25	502.00	439.75	474.33
2	DRSF-108	164.50	260.50	192.00	165.66	533.35	515.62	547.75	532.29
	Mean	165.07	174.22	183.37	174.22	332.37	354.10	306.19	330.88
	C. V.	12.43	9.39	8.50	26.14	5.57	6.20	10.85	11.69
	SE of Difference	20.52	16.36	15.59	18.59	18.52	21.96	33.21	15.80
	CD 95%	41.20	32.85	31.30	51.77	37.18	44.08	66.68	43.99
	CD 99%	54.91	43.78	41.72	68.23	49.55	58.75	88.87	57.98

Table 6d : Mean performance of 52 genotypes over 3 seasons

	Genotypes	Total number of seeds / head				Filling seed per cent			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
1	GMU-208	549.33	509.79	462.43	507.18	61.82	70.59	72.26	68.22
2	GMU-212	453.71	624.24	474.51	517.48	72.01	53.76	66.30	64.02
3	GMU-214	679.67	653.76	561.73	631.72	70.63	69.16	73.19	70.99
4	GMU-218	417.50	426.28	489.33	444.37	59.52	67.33	47.97	58.27
5	GMU-223	412.63	372.96	427.56	404.38	61.53	70.18	67.60	66.43
6	GMU-224	554.33	633.66	680.80	622.93	74.75	60.24	51.43	62.14
7	GMU-225	336.75	388.46	497.88	407.70	66.96	63.99	57.62	62.86
8	GMU-226	424.62	435.39	377.60	412.53	59.43	62.85	55.72	59.33
9	GMU-228	334.32	393.97	332.47	353.58	67.23	59.10	72.38	66.23
10	GMU-238	575.55	684.68	485.48	581.90	71.93	77.69	76.29	75.30
11	GMU-239	274.69	382.95	283.44	313.69	78.90	57.68	57.69	64.75
12	GMU-242	466.58	508.20	585.97	520.25	72.27	76.91	51.88	67.02
13	GMU-244	420.17	419.70	274.67	371.51	58.65	52.32	43.36	51.44
14	GMU-248	597.81	559.54	544.27	567.20	58.12	80.26	56.14	64.84
15	GMU-252	651.91	655.40	742.12	683.14	75.81	78.73	66.23	73.59
16	GMU-254	607.40	487.98	706.77	600.71	59.83	71.11	49.09	60.01
17	GMU-257	443.32	433.01	303.72	393.35	63.55	53.65	69.38	62.19
18	GMU-258	412.00	631.68	382.62	475.43	61.52	71.14	62.81	65.15
19	GMU-260	346.91	331.75	295.89	324.85	64.01	67.88	68.25	66.71
20	GMU-261	493.43	447.57	347.80	429.60	67.41	65.78	66.54	66.57
21	GMU-262	558.71	535.78	554.38	549.62	72.73	69.81	72.27	71.60
22	GMU-265	387.50	401.73	438.40	409.21	70.86	65.58	56.00	64.15
23	GMU-267	401.32	475.48	500.80	459.20	70.60	65.24	49.57	61.80
24	GMU-268	518.72	683.21	632.79	611.57	92.30	71.32	68.07	77.23
25	GMU-270	607.76	480.13	606.80	564.90	57.27	73.79	56.34	62.47
26	GMU-273	916.63	770.75	764.75	817.38	71.31	79.18	70.17	73.55
27	GMU-274	679.50	780.93	812.25	757.56	67.15	67.47	62.73	65.78
28	GMU-275	449.31	503.63	359.56	437.50	55.45	54.68	66.99	59.04
29	GMU-276	366.90	406.79	392.30	388.66	64.77	62.44	68.96	65.39
30	GMU-277	498.13	496.28	442.50	478.97	65.42	78.49	57.28	67.06
31	GMU-278	342.90	418.31	336.58	365.93	47.64	63.84	65.76	59.08
32	GMU-279	531.77	546.11	466.33	514.73	52.28	53.77	55.70	53.92
33	GMU-280	301.20	427.50	378.50	369.07	59.29	51.55	49.71	53.52
34	GMU-281	623.13	670.83	626.50	640.15	80.62	77.27	67.04	74.98
35	GMU-282	503.50	455.00	541.00	499.83	77.66	77.47	65.40	73.51
36	GMU-284	649.65	660.15	555.00	621.60	68.00	68.63	70.48	69.03
37	GMU-285	577.50	602.75	509.00	563.08	55.59	58.03	61.29	58.30
38	GMU-286	448.40	422.50	347.30	406.07	68.79	52.05	60.91	60.58
39	GMU-287	472.15	584.40	405.75	487.43	55.92	46.87	64.22	55.67
40	GMU-288	433.65	332.85	340.20	368.90	65.17	65.96	61.82	64.32
41	GMU-289	374.15	404.83	427.00	401.99	58.97	59.84	58.62	59.14
42	GMU-290	336.65	421.50	325.50	361.22	65.97	71.41	63.52	66.96
43	GMU-291	744.10	806.95	644.00	731.68	68.31	75.94	76.01	73.42
44	GMU-292	678.35	754.16	665.55	699.35	67.93	74.41	62.18	68.17
45	GMU-293	444.75	450.71	501.00	465.49	61.24	43.86	45.47	50.19
46	GMU-294	296.65	306.68	315.45	306.26	69.73	71.53	61.26	67.51
47	GMU-296	550.55	556.58	418.75	508.63	71.36	72.13	52.85	65.45
48	GMU-297	444.90	347.82	397.80	396.84	61.01	66.74	49.22	58.99
49	GMU-298	335.18	414.10	315.65	354.98	58.30	53.44	49.19	53.64
50	GMU-300	449.90	567.75	570.00	529.22	69.88	68.63	69.05	69.18

	Genotypes	Total number of seeds / head				Filling seed per cent			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
	CHECKS								
1	Morden	640.50	694.00	611.50	648.00	75.29	72.33	71.91	73.25
2	DRSF-108	657.85	736.12	684.75	692.00	81.07	70.04	79.95	76.92
	Mean	500.14	530.09	491.05	507.09	66.40	66.15	61.97	64.84
	C. V.	5.77	5.18	8.88	11.80	4.98	3.66	4.13	10.10
	SE of Difference	28.88	27.47	43.59	24.44	3.30	2.42	2.56	2.67
	CD 95%	57.98	55.15	87.51	68.05	6.63	4.86	5.14	7.45
	CD 99%	77.27	73.50	116.64	89.68	8.84	6.48	6.85	9.82

Table 6e : Mean performance of 52 genotypes over 3 seasons

	Genotypes	100 seed weight (g)				Seed yield per plant (g)			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
1	GMU-208	3.61	4.00	3.98	3.86	10.65	11.88	12.44	11.65
2	GMU-212	3.60	3.48	3.85	3.64	11.06	8.85	8.45	9.45
3	GMU-214	3.69	4.23	4.17	4.03	12.13	13.41	11.78	12.44
4	GMU-218	5.05	5.07	5.00	5.04	9.88	12.62	10.60	11.03
5	GMU-223	3.51	3.94	3.26	3.57	7.40	8.47	7.76	7.87
6	GMU-224	4.14	3.97	4.11	4.07	15.47	14.27	11.87	13.87
7	GMU-225	4.92	5.09	5.21	5.07	8.09	9.90	13.48	10.49
8	GMU-226	3.17	4.30	3.47	3.64	8.26	9.80	6.02	8.02
9	GMU-228	5.21	4.90	5.10	5.07	10.07	9.25	9.86	9.72
10	GMU-238	3.91	3.66	4.05	3.87	14.66	16.94	14.62	15.40
11	GMU-239	4.09	3.62	4.11	3.94	6.70	5.63	5.95	6.09
12	GMU-242	3.78	3.85	3.49	3.71	10.59	12.54	8.10	10.41
13	GMU-244	5.23	4.67	5.10	5.00	10.28	9.88	4.16	8.10
14	GMU-248	4.16	3.84	3.56	3.85	12.57	14.75	11.96	13.09
15	GMU-252	3.10	4.44	4.44	3.99	12.75	20.41	19.75	17.64
16	GMU-254	3.75	3.90	3.43	3.69	12.58	11.03	10.90	11.50
17	GMU-257	3.56	4.44	4.11	4.03	8.26	7.34	7.50	7.70
18	GMU-258	4.97	5.00	4.55	4.84	9.94	19.57	9.21	12.91
19	GMU-260	3.94	3.87	3.69	3.83	7.19	6.54	6.38	6.70
20	GMU-261	3.76	3.93	3.61	3.76	10.58	9.12	6.68	8.79
21	GMU-262	4.22	4.13	4.29	4.21	18.43	11.73	15.32	15.16
22	GMU-265	3.46	4.16	3.84	3.82	7.31	9.29	7.12	7.90
23	GMU-267	4.04	3.83	3.54	3.80	8.99	9.66	6.88	8.51
24	GMU-268	5.12	5.23	5.17	5.17	22.32	22.95	21.90	22.39
25	GMU-270	3.56	4.36	3.70	3.87	9.72	12.98	10.56	11.09
26	GMU-273	4.93	5.10	4.78	4.93	24.12	26.82	26.93	25.96
27	GMU-274	4.03	4.44	3.56	4.01	17.31	20.91	17.66	18.63
28	GMU-275	3.72	3.76	3.90	3.79	7.28	8.12	7.09	7.50
29	GMU-276	5.37	5.22	5.14	5.24	10.28	10.98	11.55	10.94
30	GMU-277	3.89	3.82	3.31	3.67	10.16	12.34	6.52	9.67
31	GMU-278	3.99	3.68	4.27	3.98	4.81	5.06	6.86	5.58
32	GMU-279	4.83	5.13	5.14	5.03	10.23	12.67	10.77	11.22
33	GMU-280	3.67	4.08	4.21	3.99	5.55	7.30	6.29	6.38
34	GMU-281	4.01	4.22	4.05	4.09	17.66	19.34	15.14	17.38
35	GMU-282	4.18	4.18	3.42	3.92	14.14	12.23	10.22	12.19
36	GMU-284	3.43	4.13	4.07	3.87	14.60	17.10	14.30	15.33
37	GMU-285	3.71	4.23	3.35	3.76	13.14	10.68	8.54	10.79
38	GMU-286	4.07	4.23	4.14	4.15	11.34	7.71	8.14	9.06
39	GMU-287	3.84	4.07	3.32	3.74	9.33	9.56	7.95	8.94
40	GMU-288	3.82	3.79	3.60	3.74	10.17	7.09	6.78	8.01
41	GMU-289	3.93	4.05	3.36	3.78	6.39	7.32	6.38	6.69
42	GMU-290	4.15	4.42	3.72	4.09	8.04	11.45	6.92	8.80
43	GMU-291	5.42	5.50	5.52	5.48	24.92	29.94	25.18	26.68
44	GMU-292	5.08	4.79	5.14	5.00	21.23	21.23	18.74	20.40
45	GMU-293	4.31	4.08	3.20	3.86	8.13	7.75	6.70	7.52
46	GMU-294	4.33	4.59	3.99	4.30	7.12	8.06	6.59	7.26
47	GMU-296	3.72	4.15	3.50	3.79	12.11	14.63	5.26	10.66
48	GMU-297	4.15	4.46	4.38	4.33	9.74	8.58	7.59	8.63
49	GMU-298	4.19	4.00	3.43	3.87	6.23	6.33	4.35	5.64
50	GMU-300	4.14	4.05	3.86	4.01	10.82	13.76	12.78	12.45

	Genotypes	100 seed weight (g)				Seed yield per plant (g)			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
	CHECKS								
1	Morden	3.95	4.10	4.27	4.11	18.32	19.21	20.15	19.36
2	DRSF-108	3.99	4.39	4.48	4.28	20.61	21.32	22.16	21.36
	Mean	4.12	4.28	4.07	4.16	11.84	12.81	11.04	11.90
	C. V.	11.02	9.76	10.91	10.23	15.83	13.38	15.96	18.05
	SE of Difference	0.45	0.42	0.44	0.17	1.87	1.71	1.76	0.88
	CD 95%	0.91	0.84	0.89	0.48	3.76	3.44	3.54	2.44
	CD 99%	1.22	1.12	1.19	0.64	5.02	4.59	4.71	3.22

Table 6f : Mean performance of 52 genotypes over 3 seasons

	Genotypes	Oil content (%)				Hull content (%)			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
1	GMU-208	28.545	27.96	29.105	28.537	26.5	27.12	24.335	25.985
2	GMU-212	27.34	26.76	24.75	26.283	19.34	26.38	27.755	24.492
3	GMU-214	24.67	27.985	21.77	24.808	16.67	25.5	22.53	21.567
4	GMU-218	25.825	23.75	22.42	23.998	17.825	21.545	19.945	19.772
5	GMU-223	24.01	27.18	24.225	25.138	16.01	26.77	25.95	22.91
6	GMU-224	26.715	26.075	22.07	24.953	18.715	26.385	28	24.367
7	GMU-225	24.03	28.27	24.43	25.577	16.03	14.505	22.075	17.537
8	GMU-226	29.895	34.32	26.175	30.13	21.895	28.745	24.655	25.098
9	GMU-228	26.945	24.315	28.725	26.662	18.945	12.405	26.36	19.237
10	GMU-238	28.9	24.925	25.92	26.582	20.9	19.37	25.11	21.793
11	GMU-239	23.825	34.78	20.52	26.375	15.825	20.065	23.69	19.86
12	GMU-242	21.875	25.18	27.295	24.783	13.875	19.92	36.045	23.28
13	GMU-244	25.79	22.715	24.135	24.213	17.79	26.995	16.305	20.363
14	GMU-248	28.18	23.765	20.98	24.308	20.18	17.13	25.33	20.88
15	GMU-252	23.415	28.07	23.94	25.142	15.415	28.105	31.315	24.945
16	GMU-254	25.805	28.895	23.805	26.168	17.805	25.545	29.66	24.337
17	GMU-257	31.875	35.835	30.635	32.782	23.875	25.05	25.755	24.893
18	GMU-258	22.68	26.62	23.495	24.265	14.68	19.275	26.07	20.008
19	GMU-260	23.67	23.135	28.01	24.938	15.67	21.65	29.305	22.208
20	GMU-261	28.895	33.955	25.035	29.295	20.895	25.235	24.135	23.422
21	GMU-262	23.795	25.755	22.105	23.885	15.795	23.72	22.42	20.645
22	GMU-265	23.865	30.44	22.295	25.533	15.865	34.5	30.34	26.902
23	GMU-267	28.01	33.93	24	28.647	20.01	32.785	27.085	26.627
24	GMU-268	22.16	28.24	23.56	24.653	14.16	23.08	29.21	22.15
25	GMU-270	27.23	35.77	21.345	28.115	19.23	28.835	17.355	21.807
26	GMU-273	23.085	29.97	24.435	25.83	15.085	16.28	33.935	21.767
27	GMU-274	30.205	28.17	35.225	31.2	22.205	20.52	33.97	25.565
28	GMU-275	25.855	23.87	23.195	24.307	17.855	26.01	32.14	25.335
29	GMU-276	25.31	29.77	25.305	26.795	17.31	13.675	17.195	16.06
30	GMU-277	25.89	28.47	20.535	24.965	17.89	33.945	28.75	26.862
31	GMU-278	25.19	27.175	24.53	25.632	17.19	30.65	23.495	23.778
32	GMU-279	25.99	28.13	33.62	29.247	17.99	20.62	13.965	17.525
33	GMU-280	27	24.65	21.985	24.545	19	24.46	26	23.153
34	GMU-281	27	28	24.225	26.408	19	26	25.275	23.425
35	GMU-282	21.745	21.15	24.835	22.577	13.745	39.875	26.615	26.745
36	GMU-284	22.005	23.91	21.975	22.63	14.005	34.965	24.01	24.327
37	GMU-285	24.315	29.285	24.19	25.93	16.315	27.25	27.935	23.833
38	GMU-286	23.785	27.5	21.92	24.402	15.785	33.895	34.21	27.963
39	GMU-287	25.38	30.69	25.025	27.032	17.38	30.765	29.37	25.838
40	GMU-288	23.135	26.26	27.28	25.558	15.135	26.47	30.645	24.083
41	GMU-289	25.25	27.65	24.275	25.725	17.25	34.075	34.22	28.515
42	GMU-290	26.81	29.83	29.83	28.823	18.81	27.48	37.29	27.86
43	GMU-291	25.615	29.46	30.84	28.638	17.615	30.265	23.225	23.702
44	GMU-292	35.615	30.66	20.5	28.925	27.615	29.535	17.265	24.805
45	GMU-293	31.19	34.45	35.01	33.55	23.19	27.92	26.615	25.908
46	GMU-294	22.91	28.59	22.63	24.71	14.91	24.86	19.815	19.862
47	GMU-296	27.04	23.415	20.98	23.812	19.04	41.155	28.595	29.597
48	GMU-297	23.84	22.03	22.055	22.642	15.84	27.755	29.295	24.297
49	GMU-298	24.82	24.985	25.625	25.143	16.82	32.97	30.225	26.672
50	GMU-300	23.21	24.44	22.19	23.28	15.21	28.025	18.905	20.713

	Genotypes	Oil content (%)				Hull content (%)			
		Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean	Late <i>kharif</i>	Early <i>rabi</i>	<i>Rabi</i>	Pooled Mean
	CHECKS								
1	Morden	33.5	34.5	30	32.667	25.5	20.625	23.255	23.127
2	DRSF-108	35.5	36.5	34	35.333	27.5	20.165	16.415	21.36
	Mean	26.137	28.118	25.134	26.46	18.252	25.977	26.026	23.42
	C. V.	7.575	6.835	7.305	10.99	10.799	10.47	6.096	20.86
	SE of Difference	1.98	1.922	1.836	1.19	1.971	2.72	1.587	1.99
	CD 95%	3.975	3.858	3.686	3.31	3.957	5.46	3.185	5.55
	CD 99%	5.298	5.143	4.912	4.36	5.274	7.277	4.245	7.32

Table 7: Distribution of 52 genotypes of sunflower in different clusters

Cluster No.	Number of genotypes	Genotypes
Cluster I	9	GMU-208, 267, 254, 285, 224, 277, 282, 300, 238
Cluster II	3	GMU-252, 274, 284
Cluster III	5	GMU-268, 291, 273, 281, 292
Cluster IV	2	Morden, DRSF-108
Cluster V	1	GMU-214
Cluster VI	6	GMU-212, 242, 270, 248, 262, 296
Cluster VII	19	GMU-226, 257, 278, 280, 223, 298, 239, 294, 265, 275, 290, 260, 288, 261, 287, 286, 297, 289, 293
Cluster VIII	7	GMU-218, 225, 276, 279, 228, 258, 244

Table 8 : Average intra and inter cluster distances (D^2)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	14.55	39.49	59.16	150.46	396.51	24.53	35.52	40.07
Cluster II		30.52	55.26	119.58	402.87	67.67	95.30	95.59
Cluster III			26.49	87.45	432.89	61.82	98.88	80.41
Cluster IV				36.40	538.98	138.77	200.72	188.24
Cluster V					0.00	438.42	448.24	446.70
Cluster VI						8.36	22.76	24.13
Cluster VII							17.67	23.36
Cluster VIII								11.49

Table 9 : Mean of clusters for 52 genotypes of sunflower for twelve traits

Cluster Number	Days to 50 % flowering	Days to maturity	Plant height (cm)	Stem diameter (cm)	Unfilled seeds / head	Filled seeds per head	Total seeds / head	Filling seed per cent	100 seed weight (g)	Seed yield (g)	Oil content (%)	Hull content (%)
Cluster I	59.00	92.56	155.20	2.71	185.69	352.42	538.11	66.17	3.85	11.78	25.77	24.59
Cluster II	59.17	94.89	162.48	3.84	211.64	475.79	687.43	69.47	3.96	17.20	26.32	24.95
Cluster III	60.27	94.93	157.57	2.18	187.87	512.16	700.03	73.47	4.94	22.56	26.89	23.17
Cluster IV	51.42	87.83	132.00	2.35	209.33	659.82	679.15	75.98	4.19	24.18	34.00	22.24
Cluster V	59.83	93.00	171.54	4.13	186.94	344.42	631.72	70.99	4.03	12.44	24.81	21.57
Cluster VI	57.61	92.44	125.65	1.86	184.93	353.09	538.01	65.90	3.85	11.64	25.20	23.45
Cluster VII	57.58	92.70	131.87	2.01	154.17	235.80	389.96	60.99	3.91	7.53	26.65	24.66
Cluster VIII	58.83	92.38	128.18	1.94	167.52	254.76	422.28	60.47	5.04	10.63	25.82	18.64

Table 10 : Contribution of different characters towards genetic divergence (D^2) in 52 genotypes of sunflower

S.No	Character	Times ranked first	% contribution towards divergence
1	Days to 50% Flowering	122	9.2
2	Days to Maturity	23	1.73
3	Plant Height (cm)	181	13.65
4	Stem Diameter(cm)	133	10.03
5	Unfilled Seeds/Head	28	2.11
6	Filled Seeds/Head	557	42.01
7	Total Seeds/Head	51	3.85
8	Filled Seed %	11	0.83
9	100 seed weight (g)	154	11.61
10	Seed yield/plant(g)	3	0.23
11	Oil Content %	55	4.15
12	Hull Content %	8	0.6

Table 11 : Canonical root analysis per cent variation values

Canonical root	Value of canonical root	Percentage of variation observed	Cumulative per cent variation
Z1	111.4288	40.077	40.0773
Z2	67.900	24.421	64.499
Z3	28.092	10.104	74.602
Z4	23.312	8.384	82.9877
Z5	11.874	4.2707	87.2584

Table 12 : Canonical vectors for twelve characters in 52 sunflower genotypes

S.No	Characters	Z1	Z2	Z3	Z4	Z5
1	Days to 50% Flowering	-0.08236	-0.12994	0.01401	-0.80063	0.35655
2	Days to Maturity	-0.07774	-0.02283	0.12754	-0.32126	-0.12324
3	Plant Height (cm)	0.32416	-0.26885	0.44753	-0.2505	-0.22055
4	Stem Diameter(cm)	0.21224	-0.21224	0.62909	0.2175	-0.19094
5	Unfilled Seeds/Head	0.103	0.03283	0.03006	0.00522	0.15241
6	Filled Seeds/Head	0.80191	0.30491	-0.05593	-0.04006	0.34184
7	Total Seeds/Head	0.2298	-0.85152	-0.41901	0.1329	0.10624
8	Filled Seed %	-0.19314	-0.17344	0.29068	-0.10826	0.18068
9	Test Weight (g)	0.16366	0.06674	-0.32901	-0.30534	-0.70727
10	Seed yield/plant(g)	0.24066	0.07065	-0.0799	-0.1305	-0.20134
11	Oil Content %	0.05834	0.07124	-0.08259	0.01282	0.20057
12	Hull Content %	0.06598	0.03918	0.04423	0.06543	0.08704

Table 13 : Phenotypic and genotypic correlation of twelve characters

Character		Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Stem diameter	Number of unfilled seeds per head	Number of filled seeds per head	Total number of seeds per head	Filling seed per cent	100 seed weight	Oil content	Hull content	Seed yield per plant (g)
Days to 50 per cent flowering	P	1.00	0.36**	0.20**	0.03	-0.00	-0.04	-0.04	-0.00	0.06	-0.01	-0.03	-0.02
	G	1.00	0.55**	0.25**	-0.03	0.01	-0.07	-0.05	-0.02	0.13**	-0.07	-0.08	-0.03
Days to maturity	P		1.00	0.28**	0.12*	0.07	0.05	0.07	0.01	0.08	-0.03	-0.02	0.10
	G		1.00	0.36**	0.15**	0.13**	0.03	0.07	0.00	0.19**	-0.04	0.17**	0.14**
Plant height (cm)	P			1.00	0.47**	0.05	0.35**	0.33**	0.31**	0.05	0.06	0.05	0.34**
	G			1.00	0.66**	0.12*	0.43**	0.42**	0.53	0.07	0.09	0.16**	0.45**
Stem diameter	P				1.00	0.14**	0.30**	0.34**	0.20**	-0.10	0.02	0.09	0.24**
	G				1.00	0.37**	0.37**	0.45**	0.30**	-0.45**	-0.03	0.24**	0.31**
Number of unfilled seeds per head	P					1.00	0.29**	0.61**	-0.54**	-0.05	0.13*	0.07	-0.24**
	G					1.00	0.51**	0.68**	-0.06	0.03	0.41**	0.14**	-0.47**
Number of filled seeds per head	P						1.00	0.93**	0.61**	0.13*	0.22**	-0.02	0.91**
	G						1.00	0.97**	0.79**	0.20**	0.34**	-0.02	0.96**
Total number of seeds per head	P							1.00	0.30**	0.08	0.22**	0.00	0.83**
	G							1.00	0.67**	0.17**	0.38**	0.00	0.93**
Filling seed per cent	P								1.00	0.12*	0.02	-0.14	0.56**
	G								1.00	0.12*	0.04	-0.05	0.76**
100 seed weight	P									1.00	0.02	-0.029**	0.41**
	G									1.00	0.00	-0.82**	0.45**
Oil content	P										1.00	0.29**	0.09
	G										1.00	0.02	0.29**
Hull content	P											1.00	-0.08
	G											1.00	-0.20**

** Significant at 1 per cent level

P – Phenotypic; G - Genotypic

* Significant at 5 per cent level

Table 14 : Phenotypic and genotypic path analysis in twelve characters

Character		Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Stem diameter	Number of unfilled seeds per head	Number of filled seeds per head	Total number of seeds per head	Filling seed per cent	100 seed weight	Oil content	Hull content	Seed yield per plant (g)
Days to 50 per cent flowering	P	-0.01	0.00	-0.00	-0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.02
	G	0.07	0.04	-0.02	0.00	-0.00	0.01	0.01	0.00	0.02	0.00	0.01	-0.12*
Days to maturity	P	0.01	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-0.00	-0.00	0.10
	G	0.06	0.11	0.04	0.02	0.01	0.00	0.01	0.00	0.02	0.00	0.02	0.14**
Plant height (cm)	P	0.05	0.01	0.02	0.01	0.00	0.01	0.01	0.00	0.00	0.00	0.00	0.34**
	G	0.04	0.05	0.14**	0.09	0.01	0.05	0.05	0.07	0.01	0.01	0.02	0.44
Stem diameter	P	-0.00	-0.00	-0.01	-0.02	-0.00	-0.01	-0.01	-0.00	0.00	-0.00	-0.00	0.24**
	G	0.00	-0.01	-0.06	-0.09	-0.03	-0.03	-0.04	-0.03	0.01	-0.00	-0.02	0.31**
Number of unfilled seeds per head	P	0.00	-0.00	-0.00	-0.00	-0.03	-0.01	-0.02	0.01	0.00	-0.00	-0.00	-0.24**
	G	-0.00	-0.02	-0.02	-0.07	-0.18**	-0.09	-0.12*	0.01	-0.00	-0.07	-0.02	-0.47**
Number of filled seeds per head	P	-0.04	0.04	0.27**	0.24**	0.22**	0.77**	0.72**	0.47**	0.09	0.17**	-0.02	0.91**
	G	-0.07	0.04	0.40**	0.35**	0.48**	0.94**	0.91**	0.74**	0.18**	0.32**	-0.02	0.96**
Total number of seeds per head	P	0.00	0.01	0.03	0.03	0.07	0.10	0.11	0.03	0.01	0.02	0.02	0.83**
	G	-0.02	0.02	0.13*	0.14**	0.20**	0.29**	0.30**	0.20**	0.05	0.12*	0.00	0.93**
Filling seed per cent	P	0.00	0.00	0.00	0.00	-0.00	0.00	0.00	0.00	0.00	0.00	-0.00	0.56**
	G	0.00	-0.00	-0.15**	-0.08	0.02	0.22**	-0.18**	-0.27**	-0.03	-0.01	0.04	0.76**
100 seed weight	P	0.02	0.02	0.02	-0.03	-0.02	0.03	0.02	0.03	0.30**	0.01	-0.01	0.40**
	G	0.02	0.02	0.01	-0.02	0.00	0.03	0.02	0.02	0.14**	0.00	-0.12	0.45**
Oil content	P	0.00	0.00	-0.01	-0.00	-0.00	-0.00	-0.01	-0.00	-0.00	-0.01	-0.00	0.19**
	G	0.01	-0.00	-0.01	0.00	-0.04	-0.03	-0.03	-0.00	-0.00	-0.09	0.00	0.29**
Hull content	P	-0.00	-0.00	0.00	0.00	0.00	-0.01	0.00	-0.00	-0.01	0.01	-0.03	-0.08
	G	0.01	-0.02	-0.02	-0.03	-0.01	0.00	-0.00	0.02	0.09	0.00	-0.11	-0.20**

** Significant at 1 per cent level; * Significant at 5 per cent level

P – Phenotypic; G – Genotypic;

Table 15 : Analysis of variance for stability analysis

Source of variation	d.f.	Days to 50 % flowering	Days to maturity	Plant height (cm)	Stem diameter (cm)	Unfilled seeds / head	Filled seeds per head	Total seeds / head	Filling seed per cent	100 seed weight (g)	Seed yield (g)	Oil content (%)	Hull content (%)
Varieties	51	30.911 **	13.828 **	937.007 **	1.122 **	4401.271 *	42261.050 **	59644.330 **	133.600 **	0.797 **	87.559 **	24.561 **	26.063
Environments	2	162.120 **	129.929 **	3905.326 **	4.623 **	4351.944	29929.680 **	21701.390 **	322.789 **	0.594 **	40.960 **	119.908 **	1041.135 **
Var.* Env.	102	4.697*	3.222*	57.55	0.146	2358.619	1389.511 **	3605.759	47.809	0.082	3.374 **	7.817	26.372
Env.+ (Var.* Env.)	104	7.724*	5.659 *	131.546 **	0.232 **	2396.953	1938.360 *	3953.752	53.097	0.092	4.097*	9.973 *	45.887 *
Environments (Lin.)	1	324.240 **	259.859 **	7810.652 **	9.246 **	8703.888	59859.370 **	43402.780 **	645.579 **	1.188 **	81.920 **	239.816 **	2082.271 **
Var. Env.(Lin.)	51	3.62	2.983	67.849	0.197 **	2189.272	1515.628	3994.184	51.228	0.072	3.393	9.767 *	26.123
Pooled Deviation	52	5.663 **	3.394 **	46.342	0.093 **	2479.353 **	1239.098 **	3155.463 **	43.535 **	0.089	3.291 **	5.755 **	26.109 **
Pooled Error	153	0.986	1.375	50.758	0.023	155.345	321.357	581.443	3.888	0.096	1.592	1.831	2.3
Total	155	15.354	8.347	396.569	0.525	3056.438	15205.83	22277.75	79.585	0.324	31.559	14.773	39.364

* & ** Indicate significance at 5 % and 1 % level respectively

Table 16 : Environmental indices for four characters (G x E significant)

Characters	Environmental index	Late <i>kharif</i>	Early <i>rabi</i>	Rabi
Days to 50% flowering	ij.	1.923	-0.375	-1.548
Days to maturity	ij.	0.237	1.449	-1.686
Filled seeds / Head	ij.	1.487	23.213	-24.699
Seed yield per plant	ij.	-0.053	0.913	-0.86

Table 17a : Estimation of Mean and Stability Parameters

	Genotypes	Number of Filled Seeds/Head			Seed yield / plant (g)		
		Mean	bi	s ² di	Mean	bi	s ² di
1	GMU-208	344.42	0.54	-279.00	11.65	-0.26	-0.03
2	GMU-212	325.82	0.45*	-322.50	9.45	0.15	2.33
3	GMU-214	344.42	0.54	-279.00	12.44	0.93	-1.49
4	GMU-218	256.78	1.07	-176.20	11.03	1.19	0.20
5	GMU-223	268.17	-0.60	-50.40	7.87	0.42	-1.29
6	GMU-224	375.17	0.67	54.90	13.87	1.27	2.57
7	GMU-225	253.73	0.86*	791.10	10.49	-1.89	7.7904 *
8	GMU-226	245.43	1.33	-286.20	8.02	2.11	-1.42
9	GMU-228	232.72	-0.18	-231.40	9.72	-0.36	-1.44
10	GMU-238	436.99	3.32	1302.8 *	15.40	1.34*	-0.91
11	GMU-239	200.40	1.23	-7.70	6.09	-0.21	-1.07
12	GMU-242	343.99	1.79	-187.30	10.41	2.49	-1.45
13	GMU-244	195.11	2.19	3162.4 **	8.10	3.11	6.6120 *
14	GMU-248	367.34	2.95	559.10	13.09	1.59*	-1.31
15	GMU-252	500.57	0.50	-248.00	17.64	0.61	33.8176 **
16	GMU-254	352.42	0.02	-145.20	11.50	0.02	0.15
17	GMU-257	240.12	0.53	1659.3 *	7.70	-0.12	-1.14
18	GMU-258	313.88	4.24	6983.0 **	12.91	5.98	8.9550 *
19	GMU-260	216.48	0.49	-289.10	6.70	0.07	-1.24
20	GMU-261	286.54	1.38	2600.0 **	8.79	1.29	3.57
21	GMU-262	394.13	-0.52	-21.60	15.16	-2.18	13.3689 **
22	GMU-265	261.15	0.40	-77.80	7.90	1.25	-1.18
23	GMU-267	280.65	1.29	-321.40	8.51	1.54	-1.12
24	GMU-268	465.66	1.20	-129.80	22.39	0.59*	-1.59
25	GMU-270	348.89	0.22*	-320.40	11.09	1.43	0.90
26	GMU-273	599.42	1.68	3679.5 **	25.96	0.03*	3.47
27	GMU-274	498.22	0.28	2391.7 **	18.63	1.89	0.64
28	GMU-275	254.01	0.64	-272.10	7.50	0.59	-1.55
29	GMU-276	254.00	-0.38	60.00	10.94	0.29*	-0.91
30	GMU-277	323.28	2.86*	-318.50	9.67	3.25	-0.94
31	GMU-278	216.38	0.78	4069.5 **	5.58	-0.97	-0.59
32	GMU-279	277.11	0.71	-322.60	11.22	1.12	-0.28
33	GMU-280	195.61	0.64	177.70	6.38	0.61	-0.65
34	GMU-281	480.27	2.09*	227.10	17.38	2.35*	-1.35
35	GMU-282	365.67	0.03	639.70	12.19	1.03	4.41
36	GMU-284	428.58	1.31	-141.70	15.33	1.61	-0.97
37	GMU-285	327.58	0.77	-232.70	10.79	1.09	7.1571 *
38	GMU-286	247.35	0.26	5323.5 **	9.06	-0.36	6.0927 *
39	GMU-287	266.10	0.27	-312.30	8.94	0.89	-1.31
40	GMU-288	237.47	0.28	2692.2 **	8.01	0.07	5.4428 *
41	GMU-289	238.14	-0.23	120.20	6.69	0.54	-1.48

	Genotypes	Number of Filled Seeds/Head			Seed yield / plant (g)		
		Mean	bi	s ² di	Mean	bi	s ² di
42	GMU-290	243.22	1.93*	538.80	8.80	2.59	-1.01
43	GMU-291	536.85	2.51	1249.5 *	26.68	2.77	2.31
44	GMU-292	478.60	3.03*	422.50	20.40	1.36*	-0.38
45	GMU-293	232.90	-0.54	2114.8 **	7.52	0.56	-0.99
46	GMU-294	206.59	0.55*	-322.50	7.26	0.83	-1.58
47	GMU-296	338.36	3.85	3248.1 **	10.66	5.20	2.84
48	GMU-297	233.19	0.83	1734.9 *	8.63	0.50	0.32
49	GMU-298	190.89	1.38	-309.70	5.64	1.08	-0.96
50	GMU-300	365.63	-0.17	3586.8 **	12.45	0.64*	2.24
CHECKS							
1	Morden	474.66	1.03	4187.1 **	23.04	-1.30	3.87
2	DRSF-108	532.29	1.42	-310.40	25.33	1.94	0.68
	Population Mean	330.88			11.90		
	Mean of bi	1.00			1.00		
	SE (Mean)	24.90			1.28		
	SE (bi)	1.00			1.44		

*&** indicates significance at 5% & 1% level

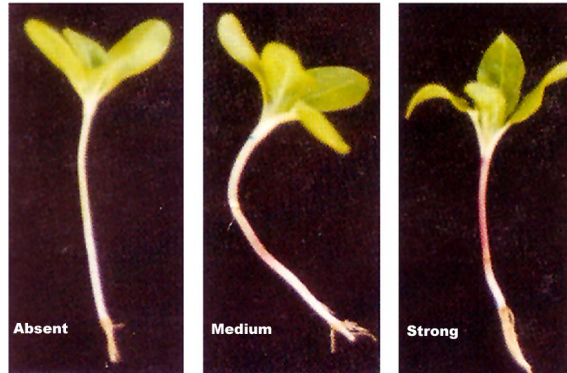
Table 17b : Estimation of Mean and Stability Parameters

	Genotypes	Days to 50 % flowering			Days to maturity		
		Mean	bi	s ² di	Mean	bi	s ² di
1	GMU-208	60.83	0.13	3.5805 *	95.50	0.38	-0.18
2	GMU-212	57.17	0.24	9.3218 **	92.33	0.07	13.7040 **
3	GMU-214	59.83	0.49	6.1927 **	93.00	0.26	1.71
4	GMU-218	56.33	3.73	12.3825 **	92.83	1.54	-0.69
5	GMU-223	63.00	0.65	-0.09	92.33	1.30	-1.24
6	GMU-224	60.67	0.43*	-0.98	95.33	0.60	-1.09
7	GMU-225	56.33	1.88*	-0.96	93.50	0.82	-1.30
8	GMU-226	59.17	1.45	-0.96	93.83	0.55	0.20
9	GMU-228	60.67	1.63	5.5696 *	91.17	2.03	-0.80
10	GMU-238	57.67	0.71	2.9973 *	89.83	2.36	-1.20
11	GMU-239	57.17	-0.30	33.6332 **	91.83	1.98	1.15
12	GMU-242	57.00	0.66	41.7808 **	90.00	2.2*	-1.03
13	GMU-244	58.00	0.93	-0.32	90.67	0.77	-1.25
14	GMU-248	57.83	1.78	40.4537 **	91.17	0.96	-1.42
15	GMU-252	62.00	2.13	-0.84	95.83	0.87	-0.03
16	GMU-254	60.33	1.70	-0.84	91.33	1.04	0.34
17	GMU-257	63.17	1.45	-0.96	94.33	1.23	-0.84
18	GMU-258	62.00	1.02	-0.96	91.67	2.39	6.1730 *
19	GMU-260	56.00	0.56	3.5568 *	93.17	1.45	4.7280 *
20	GMU-261	57.17	0.61	4.8398 *	94.33	0.41	-0.12
21	GMU-262	58.17	1.44	14.1784 **	95.00	0.51*	-1.22
22	GMU-265	57.50	1.11	0.84	90.17	1.71	-0.94
23	GMU-267	58.50	1.67	6.0446 **	91.67	1.16	-0.96
24	GMU-268	58.50	0.93	0.13	93.33	-1.16	-0.96
25	GMU-270	57.83	1.88	14.2218 **	92.67	0.48	6.0774 *
26	GMU-273	55.33	0.30	3.6043 *	96.33	-0.02	-1.28
27	GMU-274	62.33	0.96	-0.55	96.00	0.63	-1.41
28	GMU-275	57.33	1.24	-0.37	90.50	0.87	0.78
29	GMU-276	58.50	1.3*	-0.98	93.33	0.97	5.0528 *
30	GMU-277	59.00	-0.09	0.47	92.83	1.98	1.15
31	GMU-278	63.83	-0.06	6.1629 **	95.50	1.25	-1.30
32	GMU-279	60.00	1.02	-0.96	93.50	1.95	-1.00
33	GMU-280	59.33	1.79	0.11	93.00	1.81	1.68
34	GMU-281	62.33	2.35	0.72	94.17	1.59*	-1.44
35	GMU-282	57.17	0.71	-0.97	92.67	2.15	0.67
36	GMU-284	53.17	1.27	-0.84	92.83	1.11	-1.42
37	GMU-285	59.33	0.40	-0.83	93.33	2.05	-1.28
38	GMU-286	53.83	0.96*	-0.55	91.33	0.41*	-0.12
39	GMU-287	55.67	2.19	-0.80	93.00	1.43	6.9023 *

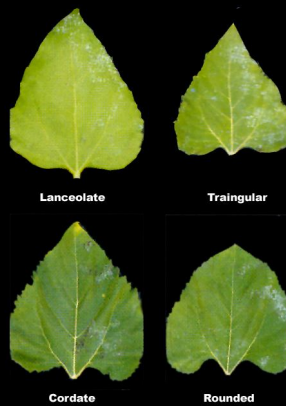
	Genotypes	Days to 50 % flowering			Days to maturity		
		Mean	bi	s ² di	Mean	bi	s ² di
40	GMU-288	55.50	0.56	-0.92	93.50	0.33	7.5008 *
41	GMU-289	53.17	1.73*	-0.98	92.50	1.88*	-1.14
42	GMU-290	55.83	-0.07	7.6540 **	92.83	0.62	4.7774 *
43	GMU-291	61.00	00.1*	-0.98	96.17	0.34	-1.34
44	GMU-292	64.17	0.15*	-0.97	94.67	0.07	0.70
45	GMU-293	52.17	1.08	-0.13	93.00	0.33	7.5008 *
46	GMU-294	57.33	1.06	9.2151 **	91.00	0.14	4.4596 *
47	GMU-296	57.67	1.09	6.8130 **	93.50	-0.73	13.9174 **
48	GMU-297	53.83	0.68*	0.83	92.50	0.89	1.09
49	GMU-298	63.00	1.38	8.5723 **	92.67	0.81	31.4120 **
50	GMU-300	57.50	0.46	4.2037 *	90.50	1.50	1.36
CHECKS							
1	Morden	48.50	0.38	6.1333 **	83.00	0.80	5.8745 *
2	DRSF-108	54.33	0.22	6.8752 **	92.67	0.89	-0.26
	Population Mean	58.15			92.76		
	Mean of bi	1.00			1.00		
	SE (Mean)	1.68			1.30		
	SE (bi)	0.95			0.82		

*&** indicates significance at 5% & 1% level

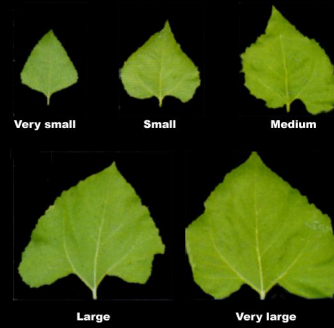
Hypocotyl: anthocyanin coloration



Leaf: Shape



Leaf: Size

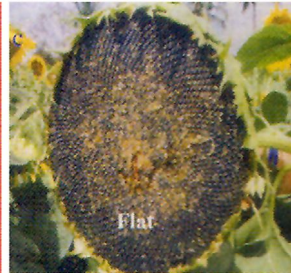


Leaf: Colour



Plate1a: Morphological characterisaton of sunflower genotypes

Head Shape of grain side



Head attitude



Plate1c

Plant branching



Absent



Present

Seed shape



Elongate



Ovoid elongate



Ovoid wide



Round

Seed base colour



White



Grey



Brown



Black

Plate1d

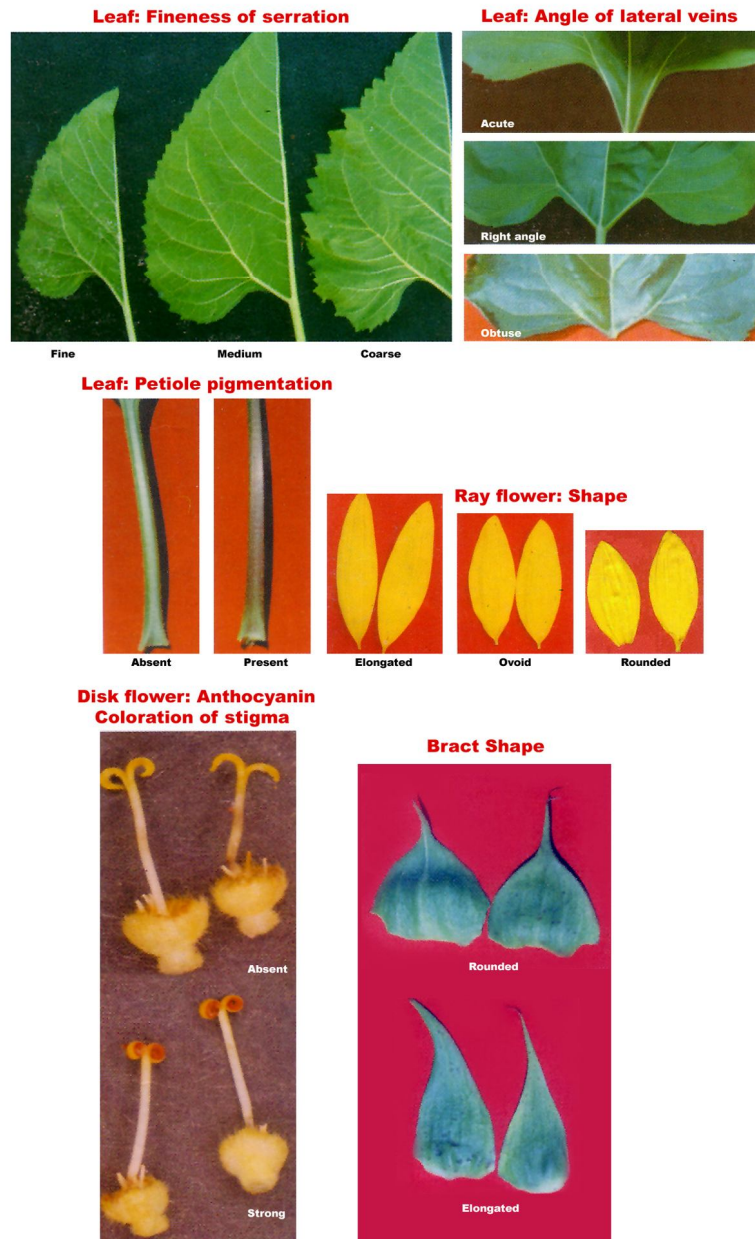


Plate1b

CHAPTER V

DISCUSSION

In the present investigations, fifty genotypes along with two checks, Morden and DRSF-108 were studied and the biometrical data were collected for the twelve characters along with morphological characters, genetic divergence, correlation analysis, variability studies, path analysis and discussed with the following headings.

1. Morphological characterisation
2. Variability, heritability, genetic advance as per cent of mean and *per se* performance.
3. Genetic diversity
4. Correlation coefficient.
5. Path analysis.
6. Stability analysis.

5.1 MORPHOLOGICAL CHARACTERISATION

Among fifty two genotypes studied, much variation was found for the characters, hypocotyl anthocyanin colouration, serration of leaf margin, angle of lateral of leaf, petiole pigmentation, anthocyanin colouration of disc flower, head attitude, head shape at grain side, seed shape and seed colour. Hypocotyl anthocyanin colour was medium for 10 genotypes, high for 6 genotypes, angle of veins acute in 15 genotypes, obtuse in 4 genotypes, leaf margin was coarse in 29 genotypes, fine in one genotype and very coarse in 21 genotypes, number of

leaves on main stem low in four genotypes and medium in 15 genotypes. Anthocyanin colouration of stigma was present in 22 genotypes and absent in 30 genotypes, head attitude was turned down in 47 genotypes, head shape of grain side was flat in 24 genotypes, convex in 20 genotypes, and concave in 8 genotypes.

Seed shape and seed colour exhibited lot of variations. Four genotypes were with elongated black, one genotype elongated brown, 3 genotypes were with elongated grey colour and two genotypes elongated slender black seed. One genotype was with round grey, two genotypes with round brown, 14 genotypes with round black seed. Eleven genotypes were with ovoid black, two genotypes with ovoid brown, five genotypes with ovoid grey, one genotype with ovoid long black and 5 genotypes with ovoid elongate black seed. These characters are consistent and are highly useful in distinguishing the genotypes from one another.

The present findings are in agreement with earlier investigations of Jagdish *et al.* (1994), Anitha (1995), Rajendraprasad *et al.* (2003) and Rajeswari (2004) which showed that morphological characterisation helps in identification of genotypes easily.

5.2 VARIABILITY, HERITABILITY, GENETIC ADVANCE AS PER CENT OF MEAN

5.2.1 Days to 50 per cent flowering

This trait showed low genotypic and phenotypic co-efficient of variation and it exhibited high heritability and low genetic advance as per cent of mean. The high heritability estimates of this trait indicated that by selection, the mean of this trait can be shifted in the desirable direction. High heritability and low genetic advance as per cent of mean indicates non additive gene action. Similar results were obtained by Chaudhary and Anand (1987), Patil *et al.* (1996) and Anuradha (2003).

5.2.2 Days to maturity

This character displayed low genotypic and phenotypic co-efficients of variation. These results are in accordance with the findings of Perumal and Rajasekharan (1994), Narsaiah (1995), Ravi (2001) and Anuradha (2003).

Moderate heritability and low genetic advance as per cent of mean were observed and it indicates that the improvement of this trait may be difficult due to environmental influence as it is controlled by non-additive gene action. Similar results were reported by Narsaiah (1995), Khan (2001) and Anuradha (2003).

5.2.3 Plant height (cm)

Plant height exhibited moderate genotypic and phenotypic coefficient of variation. It exhibited high heritability per cent and high genetic advance as per cent of mean. These indicates, that the character was controlled by additive gene action and can be modified by selection. Similar results were also reported by Kloczowski (1975), Satisha (1995), Rukminidevi *et al.* (1999), Ashok *et al.* (2000), Rajeswari (2004).

5.2.4 Stem diameter (cm)

Stem diameter recorded high phenotypic and genotypic coefficient of variation. Stem diameter recorded high heritability and high genetic advance as per cent of mean. It indicates that the character was controlled by additive gene action.

5.2.5 Number of unfilled seeds per head

Number of unfilled seeds per head recorded moderate genotypic coefficient of variation and high phenotypic coefficient of variation. It recorded moderate heritability and high genetic advance as per cent of mean and hence can be selected against during breeding programmes.

5.2.6 Number of filled seeds per head

Number of filled seeds per head recorded high genotypic and phenotypic coefficient of variation with high heritability and high genetic advance as per cent of mean indicates that the character was controlled by additive gene

action and hence improvement in this trait is possible and also relatively easy to achieve. These results were in consonance with the findings of Teklewold *et al.* (1999), Ravi (2001), Anuradha (2003) and Rajeswari (2004).

5.2.7 Total number of seeds per head

Total number of seeds per head recorded high genotypic and phenotypic coefficient of variation. It exhibited high heritability and genetic advance as per cent of mean. It indicates that the character was controlled by additive gene action.

5.2.8 Seed filling per cent

GCV and PCV for the character seed filling per cent were low with moderate heritability and genetic advance as per cent of mean. It shows that the character was controlled by non additive gene action.

5.2.9 100-seed weight (g)

Test weight possessed moderate GCV and PCV and exhibited moderate heritability and moderate genetic advance as per cent of mean. It was in agreement with the findings of Perumal and Rajesekharan (1994), Anuradha (2003) and Rajeswari (2004).

5.2.10 Seed yield per plant (g)

Seed yield per plant possessed high GCV, PCV, heritability and genetic advance as per cent of mean which indicate much variation among the germplasm for this character and the role of additive gene action controlling this

trait. So, this character can be improved by adopting suitable breeding methods. Such results were observed by Perumal and Rajasekharan (1994), Madrap *et al.* (1998), Teklewold *et al.* (1999), Ravi (2001) and Anuradha (2003).

5.2.11 Oil content (%)

Oil content along with more yield is important for sunflower crop. It was desirable to evolve a hybrid with high seed yield coupled with oil content. In the present investigation, oil content exhibited low genotypic and moderate phenotypic coefficient of variation. Both heritability and genetic advance as per cent of mean were moderate for this character. These results were similar to results reported by Chaudhary and Anand (1987), Patil *et al.* (1996), Teklewold *et al.* (1999), Ravi (2001) and Anuradha (2003).

5.2.12 Hull content (%)

Hull content exhibited low GCV and high PCV. Both heritability and genetic advance as per cent of mean were low.

5.2.13 *Per se* performance

Genotype GMU-252 marked its superiority for the following characters, days to 50 per cent flowering, stem diameter, number of filled seeds per plant and seed filling per cent. GMU-268 was superior over checks for characters filling seed percentage, test weight and seed yield per plant. GMU-273 contributed its superior performance in positive direction for the characters,

number of filled seeds per head, total number of seeds per head, filling seed percentage, test weight, yield per plant, oil content and hull content.

GMU-286 was superior over other checks for the following characters, days to 50 per cent flowering, days to maturity and test weight. GMU-291 and GMU-292 showed superior performance over the checks in characters, filled seeds per head, total number of seeds per head, filling seed percentage, test weight and yield, GMU-291 was also superior in filling seed percentage while GMU-292 is superior in oil content.

No genotype was superior over the checks, Morden and DRSF-108 for all the characters collectively. GMU-273, 291 and 292 genotypes were performing better for the majority of characters. The similar results were observed from the reports of Manjula and Seetharam (2000) and Durgaprasad (2005)

5.3 GENETIC DIVERGENCE

Genetic divergence among parents is essential since the crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability would be expected in the segregating generations. Genetic diversity between populations and genotypes indicates the differences in gene frequencies. Several measures of genetic distance have been proposed so far, of which Mahalanobis generalized distance is most widely used in plant breeding.

The multivariate analysis using Mahalanobis D^2 statistic provides a useful statistical method for measuring the amount of genetic diversity present in a population in respect of characteristics considered together. The characters responsible for discriminating between populations can narrow down the problem of selecting divergent parents for breeding programme. This statistical tool has been employed widely to resolve genetic divergence at inter-varietal and sub-species level in classifying the crop plants (FAO, 1997). This is possible by clustering the entries based on D^2 values as it represents the index of genetic diversity among genotypes and clusters. The success and usefulness of Mahalanobis's analysis in quantifying genetic divergence has been used by several workers in oilseed crops; linseed (Jeswani *et al.*, 1970), sunflower (Yadav *et al.* 1988), groundnut (Golakai and Makne 1992) etc.

The 52 genotypes of sunflower used in the present study were grouped into 8 clusters based on D^2 values (Table 4). The magnitude of D^2 values revealed considerable amount of diversity in the material used. The pattern of distribution of genotypes into various clusters was at random indicating that geographical diversity and genetic diversity were not related. This suggested that forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the diversity of genotypes. Variation in environment could also be responsible for this diversity. Similar conclusions have been drawn by several workers viz., Singh and Gupta (1968), Jeswani *et al.* (1970), in linseed,

Yadav *et al.* (1988), Haile (1994), Muppidathi *et al.* (1995) and Venkateswara Rao (1999) in sunflower.

Statistical distances represent the index of genetic diversity among clusters. The intra cluster distances were minimum between cluster V and IV indicating close relationship and similarity for most of the characters of the genotypes. On the other hand, maximum inter cluster distance was observed between cluster IV and V indicating wider genetic diversity between genotypes in these groups. In the present study though the maximum intercluster distance was obtained between cluster IV and V, but they are of no use since the cluster V had only one genotype and the cluster IV had two genotypes (Morden and DRSF-108). So the cluster distance between V and VII (448.24) consider maximum distance where cluster VII had 19 genotypes. Selection of the parents from these diverse clusters for hybridization programme would help in novel recombinants.

The genotype present in cluster V (GMU-214) and genotypes in cluster VII (GMU-226, 257, 278, 280, 223, 298, 239, 244, 265, 275, 290, 260, 288, 261, 287, 286, 297, 289 and 239) could be exploited in hybridization programme for obtaining desirable segregants with high yield potential. Cluster V displayed the least intra cluster divergence, as it comprising only one genotype. This may be explained on the basis that yield being a complex character of polygenic inheritance. Similar genotypes could be produced by different combinations of genes. Such combinations may have selective

advantage when constant selection is practiced in the segregating population. Similar plant types are expected to be established on the passing generations. The maximum intra cluster distance was recorded in cluster IV and this might be due to limited gene exchange or selection practices among the genotypes for diverse characters.

The characters contributing maximum to the D^2 values are to be given greater emphasis for deciding on the clusters for the purpose of further selections and choice of parents for hybridization in number of filled seeds/head with 42.01 and plant height (13.65) were found to have highest contribution towards genetic divergence (Narsaiah, 1995 and Sridhar, 1999).

Canonical root analysis was used to confirm the clustering pattern obtained by D^2 statistic and to help in plotting the genotypes on two or three dimensional graphs. The canonical root analysis in the present study accounted for the total variance of 87.25 per cent. The contribution of Z1, Z2, Z3, Z4 and Z5 was 40.07, 24.42, 10.10, 8.38 and 4.27 per cent respectively. The first canonical root was accounted for 40.07 per cent of total variance of uncorrelated variables indicating the differentiation of these traits in the genotypes was complete in three phases. The relative contribution of genotypes reflected in the existence of broad parallelism between groups obtained by D^2 analysis and vector analysis. For getting clear association of two dimensional representation of variation, the first 4 canonical roots should be more than 95 per cent (Patel *et al.*, 1989). On contrary the 3 vectors as a whole contributed

only 74.60 per cent towards genetic divergence because of which discernable overlapping was observed in group constellations of canonical vectors.

The characters, number of filled seeds per head and plant height contributed maximum towards genetic divergence in the first vector (Table 9). In the second vector number of filled seeds/head contributed maximum towards genetic diversity, stem diameter, plant height and filling seed per cent contributed more towards genetic divergence in third vector. In the fourth vector, stem diameter, total number of seeds per head. Days to 50 per cent flowering, number of filled seeds/head and oil content in the fifth vector contributed maximum towards genetic divergence. This was also in uniformity with the relative contribution of characters through D^2 statistic.

From the forgoing discussion, it could be concluded that days to 50 per cent flowering and stem diameter, plant height, number of filled seeds per head and oil content are the important traits contributing towards genetic divergence and for discriminating the genotypes.

5.4 CORRELATION COEFFICIENTS

Seed yield is a complex character and it is the end product of action and interaction among number of traits, hence it is important to understand the association of different characters with seed yield. Plant breeder has to find simple correlations and the extent of direct and indirect effects of attributes with seed yield that could be useful to predict the superior cross combinations and to identify traits for ideal plant type and aid in indirect selection. The present study

revealed the existence of phenotypic and genotypic correlations between several quantitative characters and seed yield.

The genotypic correlations were higher than corresponding phenotypic correlations, which indicate that the traits were inherently associated among themselves. The results of positive association of number of filled seeds with seed yield is in conformity with Suma and Virupakshappa (1994), Rao (1998), Satyanarayana (2000), Teklewold *et al.* (2000) and Ayub Khan (2001).

Positive association of stem diameter and 100 seed weight with seed yield is in accordance with earlier findings of Chandra and Anand (1977), Lakshmanaiah (1980), Sheriff *et al.* (1985), Punia and Gill (1994), Doddamani *et al.* (1997), Rao (1998) and Ayub Khan (2001).

Number of filled seeds per head and seed filling per cent were positively associated with seed yield which is in agreement with earlier reports of Lakshmanaiah (1980), Pathak *et al.* (1983a) and Punia and Gill (1994). The positive correlation of plant height with seed yield is in agreement with earlier reports of Varshney and Singh (1977), Giriraj *et al.* (1979), Sheriff *et al.* (1985), Singh and Labana (1990), Lawrence and Mohammad (1993), Patil *et al.* (1996), Doddamani *et al.* (1997), Rao (1998), Teklewold (2000) and Dagustu (2002).

Significant negative association of unfilled seeds with seed yield was recorded. It is in conformity with earlier findings of Chandra and Anand (1977) and Rao (1998). Positive association of oil content with seed yield was observed which is in consonance with Suma and Virupakshappa (1994). In

contrary to this, negative association of oil content with seed yield was reported by Rao (1998). The possible reason for the deviation could be, the difference in material used in the investigation and very low direct and indirect effects.

5.5 PATH ANALYSIS

The correlation values denote only the nature and degree of association present between the pairs of characters. A dependent character like seed yield is controlled by several mutually associated characters. If correlation between dependent and independent characters arise due to direct effect of a character, it reflects a true association relationship between them. Selection can be practiced for such character to improve the dependent character.

Path analysis is a biometrical technique developed by Wright (1921) and subsequently by Dewey and Lu (1959) and has been widely used by different workers for partitioning the correlation into direct and indirect effects of one variable on dependent variable. Thus, correlations in combination with path analysis would give a better insight into the cause and effect relationships between different pairs of characters.

Days to maturity showed direct positive effect on seed yield. It is indirectly contributed through plant height, number of filled seeds, test weight. These results are similar to the earlier report of Mishra *et al.* (1985).

The character number of unfilled seeds per head recorded negative direct effect on seed yield. These findings are in conformity with Suma and

Virupakshappa (1994). In contrast, days to 50 per cent flowering showed negative effect. It is similar with results of Sudha Rani (1992) and Ayub Khan (2001). Oil content showed negative direct effect on seed yield. Such trends are also observed by earlier workers, Pathak *et al.* (1983), Sheriff *et al.* (1985), Vanishree *et al.* (1988) and Niranjana Murthy and Shambulingappa (1989).

Days to maturity had positive association with seed yield. These results were corroborative with the earlier findings of Rukmini Devi (1994), Narasaiah (1995), Venkateswara Rao (1999) and Ayub Khan (2001).

Number of filled seeds per head was positively associated with seed yield which is in agreement with earlier reports of Anand and Chandra (1980), Lakshmana Rao (1983), Pathak *et al.* (1983) and Punia and Gill (1994). The positive correlation of plant height with seed yield is in agreement with earlier reports of Varshney and Singh (1977), Giriraj *et al.* (1979), Singh and Labana (1990), Lawrence and Mohammed (1993), Patil *et al.* (1996), Doddamani *et al.* (1997), Venkateswara Rao (1999), Teklewold (2000) and Dagustu (2002).

Maximum direct effect of days to maturity, number of filled seeds, plant height, total number of seeds and 100 seed weight were observed on seed yield. Hence, it may be concluded that these traits contributed maximum to higher seed yield compared to other characters, thus simultaneous selection for these characters is expected to improve seed yield in sunflower.

5.6 STABILITY PARAMETERS

Highly significant differences among the environments suggested that the genotypes under study were evaluated under diverse seasons, thus, justifying the seasons chosen for stability analysis. Significant mean squares due to genotype x environment suggested differential behaviour of the genotypes across the three seasons for the characters days to 50 per cent flowering, days to maturity, number of filled seeds/head and seed yield.

Genotype environment interaction being significant for most of the traits, the immediate task was to identify stable genotype which interact moderately with the environments giving a near consistent performance across environments. Eberhart and Russel (1966) suggested that both linear (b_i) and non-linear (S^2_{di}) components of genotype, environment interaction should be considered in judging the phenotypic stability of genotype. They considered three stability parameters viz., (i) mean performance (μ), (ii) regression coefficient (b_i), the mean of the cultivars regressed upon environmental index i.e., a predictable response of a genotype to either favourable or unfavourable environments, and (iii) Deviation from regression (S^2_{di}), a measure of genotype x environment interaction of unpredictable type.

To consider a genotype to be ideal and stable, it should possess high or low mean (depending on the character) performance with regression coefficient around unity ($b_i=1$) and with least deviation from regression coefficient i.e., as close to zero as possible.

S^2_{di} considered as the measure of stability in the interpretation of the results of the present investigation. Once the genotype is found to be stable based on non-significant S^2_{di} , then the type of response is determined based on the regression co-efficient and the mean values. If b_i is equal to unity and accompanied by high mean value, the genotype is considered to have below average response and adapted to only favourable environments. If regression co-efficient (b_i) is less than unity with lower mean value, it is considered to have above average response and poorly adapted to all environments. If b_i is less than unity and accompanied by higher mean value, then the genotype is considered to be specifically adapted to unfavourable environments (Finely and Wilkinson, 1963). The results pertaining to the stability parameters are discussed characterwise.

Days to 50 per cent flowering, days to maturity, number of filled seeds per head, seed yield per plant exhibited significant genotypic x environment interaction and remaining characters were non-significant G x E interaction. Stability parameters are discussed for the characters which were having significant genotypic x environment interaction. Plant height, stem diameter, number of unfilled seeds per head, total number of seeds per head, seed filling per cent, oil content and hull content were discussed based on their average mean performance only.

By partitioning the sum of squares into varieties, environments + (Genotype + Environment) and pooled error revealed that mean squares due to

environments + (Genotype x environment) were significant for all the four characters viz., days to 50 per cent flowering, days to maturity, number of filled seeds per head and seed yield per plant reemphasizing the existence of GE interactions for these traits. These findings are in accordance with Virupakshappa (1991), Muppidathi *et al.* (1996) and Laishram and Singh (1997), sum of squares due to E + (G x E) was further partitioned into that of environment (Linear), Genotype x Environment (linear) and pooled deviation. Significant variation due to environment (linear) was observed for the four characters revealing that linear contribution of environmental effects and additive variance on these characters. Similar results were reported by Muppidathi *et al.* (1996), Kallennawar *et al.* (2003) and Mohan Rao *et al.* (2004).

The linear component of GE was non significant for the four characters suggesting that the genotypes did not differ for their linear response to environments as also reported by Uma *et al.* (1995), Prusti *et al.* (1999) and Murali *et al.* (2004). The mean sum of squares for pooled deviation was significant for all the genotypes by significantly differing for stability. Significant non-linear responses were also observed by Laishram and Singh (1997), Mohan Rao *et al.* (2004) and Satyanarayana (2005).

Environmental indices of the four characters, late *kharif* was considered to be the best seasons for the trait days to 50 per cent flowering, while early

rabi was the best season for the traits days to maturity, filled seeds per head and seed yield per plant.

The trait, days to 50 per cent flowering recorded non-linear and linear component of G x E interaction was significant. Similar results were reported by Uma *et al.* (1995), Prusti *et al.* (1999), Satyanarayana (2005).

Twenty nine genotypes recorded non-significant deviation from regression values. Among them genotypes GMU-284, 286, 289, 293 and 297 were early in flowering than check, DRSF-108 and these are stable over seasons. Genotypes, GMU-224, 284, 291 and 292 recorded long duration and adaptable to poor environments. Genotypes GMU-225, 276 and 297 recorded long duration and GMU-289 recorded short duration and adaptable to favourable environments. These results were in consonance with the findings of Kallennawar *et al.* (2003), Murali *et al.* (2004) and Satyarnarayana (2005).

Days to maturity

For the traits, maturity linear and non – linear component of GE interactions was found to be significant in the present study. Similar results were reported by Pawan Kumar *et al.* (2003), Mohanrao *et al.* (2004), Murali *et al.* (2004).

Thirty nine genotypes recorded non-significant deviations from regression, among them sixteen genotypes exhibited stable performance across the seasons. Genotype GMU-286 adopted to poor environments with more than

average stability. Genotypes, GMU-242 and 289 were early in maturity than the check, DRSF-108 and genotypes, GMU-262 and 281 were late in maturity and adaptable to favourable environments with less average stability across the seasons. Similar results were reported by Uma (1995), Prusti *et al.* (1999), Murali *et al.* (2004) and Satyanarayana (2005).

Number of filled seeds per head

Trait, number of filled seeds per head recorded non-linear component significant and significant linear component of G x E interaction was reported by Muppidathi *et al.* (1996), Laishram and Singh (1997), Murali *et al.* (2004).

Thirty six genotypes recorded non significant deviation from regression and they are stable over environments. Among them, genotype GMU-252 recorded high number of filled seeds than check, Morden and stable across the seasons.

Genotypes, GMU-212, 225, 270 and 294 were adoptable to poor environments with less number of filled seeds. Genotypes, GMU 281 and 292 recorded high number of filled seeds and adaptable to favourable environments, while genotypes, GMU-277 and 290 recorded less number of filled seeds and adaptable to favourable environments. Similar results were reported by Uma *et al.* (1995), Laishram and Singh (1997), Prusti *et al.* (1999) and Satyanarayana (2005).

Seed yield per plant (g)

Seed yield per plant recorded significant non linear component and linear component of G x E interaction. Similar results were reported by Kallennwar *et al.* (2003), Murali *et al.* (2004).

Fourty four genotypes recorded non significant deviation from regression. Among them genotypes GMU-268 and 300 recorded low yield and adopted to poor environments genotypes, GMU-238, 248, 281 and 291 recorded low yield and they are adoptable to favourable environments. GMU-291 was recorded highest seed yield and stable in all seasons. Muppidathi *et al.* (1996), Prusti *et al.* (1999), Murali *et al.* (2004) and Satyanarayana (2005).

Genotypes GMU-284, 286, 289, 293 and 297 were early in flowering and are stable in all seasons. GMU-289 with short duration was adaptable to poor environments. Genotypes GMU-242 and 289 were early in maturity and adaptable to poor environments. Genotype, GMU-252 recorded high number of filled seeds and stable across the seasons. While genotypes, GMU-281 and 292 were adoptable to favorable environments. Genotypes, GMU-268, 276 and 300 low seed yield and GMU-273 recorded high seed yield and adaptable to poor environments.

CHAPTER VI

SUMMARY

The present study entitled “Studies on characterisation and evaluation of sunflower (*Helianthus annuus* L.) genotypes” was conducted to characterise and evaluate the sunflower genotypes along with two checks, Morden and DRSF-108 over environments. Experiment was done in three seasons in the field of Directorate of Oilseeds Research, Rajendranagar, Hyderabad.

Fifty genotypes along with two checks, Morden and DRSF-108 were characterised based on their morphological descriptors. Characters that had been used for characterization of sunflower genotypes were hypocotyl anthocyanin colouration, leaf size, leaf shape, leaf colour, leaf fineness of serration, angle of veins, leaf hainyness, leaf base shape, number of leaves on main stem, anthocyanin colouration of disc flower, pollen color, shape of bracts, branching habit, head attitude. Petiole pigmentation, stem pigmentation, stem pubescence, ray flower colour, ray flower shape, disc flower colour, head shape at grain side, seed shape and seed base colour and the genotypes were evaluated in three seasons for their variability, heritability, genetic advance as percent of mean, *per se* performance, genetic diversity, correlation studies, path analysis and stability analysis for the pooled data.

Characters which had been used in the evaluation were viz., days to 50 per cent flowering, days to maturity, plant height (cm), stem diameter (cm), number of unfilled seeds per head, number of filled seeds per head, total

number of seeds per plant, seed filling percent, test weight (g), seed yield per plant (g), oil content per cent and hull content .

In the characterization experiment, much variation was observed for hypocotyl anthocyanin colouration, fineness of serration, angle of lateral veins, petiole pigmentation, anthocyanin colouration of disc flower stigma, number of leaves on main stem, head attitude at maturity, head shape at grain side, seed shape and seed colour. Hypocotyl anthocyanin colour was medium in 10 genotypes, high for 6 genotypes. Angle of lateral veins acute in 15 genotypes. Leaf margin was coarse in 29 genotypes, number of leaves on main stem low in four genotypes and medium in 15 genotypes, anthocyanin colour of stigma was present in 22 genotypes. Turned down head attitude was observed in 47 genotypes, head shape at grain side convex in 20 genotypes, seed shape and seed base colour shown lot of variation.

Variability, heritability (broad sense) and genetic advance as per cent of mean calculated for the twelve characters using pooled data of three seasons. The genotypic co-efficient of variation was high in stem diameter, number of filled seeds per head, total number of seeds per head, seed yield per plant and low in days to 50 per cent flowering, days to maturity, filling seed per cent, hull content, oil content, and moderate in unfilled seeds per head, test weight and plant height. Phenotypic coefficient of variation was high in stem diameter, unfilled seeds per head, filled seeds per head, total seed per head, seed yield per plant, hull content and low in , days to 50 per cent flowering, days to maturity and moderate in plant height, test weight and oil content, high heritability and

genetic advance as per cent of mean was observed in characters viz., plant height, stem diameter, number of filled seeds per head, seed yield per plant, and total number of seeds per head. Moderate heritability and genetic advance as per cent of mean was observed in characters viz., filling seed per cent, test weight and oil content. Moderate heritability and high genetic advance as per cent of mean was observed in unfilled seeds per head. High heritability and low genetic advance as per cent of mean was observed in days to 50 per cent flowering. Moderate heritability and low genetic advance as per cent of mean was observed in days to maturity and low heritability and low genetic advance as per cent of mean was observed in hull content *per se* performance was calculated based on their respective checks Morden and DRSF-108 for the pooled data. Genotypes GMU-252, 268, 273, 286, 291, 292 performed well over the checks. GMU-273 superior in days to 50 per cent flowering, stem diameter, number of filled seeds per head, seed filling per cent, test weight and seed yield, genotypes 268 superior for the characters, filled seeds per head, total number of seeds, filling seed per cent, test weight, seed yield per plant, oil content and hull content. GMU-280 was superior for the characters, days to 50 per cent flowering, days to maturity and test weight. GMU-291 and 292 were superior for the characters filled seeds per head, total number of seeds per head, test weight and GMU-292 in addition to the above characters it also superior in oil content and filling seed per cent.

Genetic diversity was estimated by using Mahalanobis generalized distance D^2 for the pooled data. Fifty two genotypes were developed into eight

clusters. Cluster I and VII were the largest groups comprising of 9 and 19 genotypes respectively each followed by cluster VIII with 7 genotypes, cluster VI with 6 genotypes, cluster III with 5 genotypes, cluster II with 3 genotypes, cluster IV with 2 genotypes, cluster V with one genotype. Average intra cluster distance was ranged from zero (cluster V) to 36.51 (Cluster IV). Average inter cluster distance was maximum between cluster IV and V (538.977).

Canonical root analysis used to confirm the clustering pattern obtained by D^2 statistics. The contribution of roots 1, 2, 3, 4 and 5 was 40.07, 24.42, 10.10, 8.38 and 4.27 per cent respectively. Relative contribution of different characters towards diversity as following, number of filled seeds per head and plant height contributed maximum diversity in the first vector, number of filled seeds per head in the second vector. Stem diameter, plant height and filling seed per cent in third vector, stem diameter, total number of seeds in the fourth vector, days to 50 per cent flowering, number of filled seeds per head and oil content in the fifth vector.

Genotypic correlations were higher than the corresponding phenotypic correlations. Characters, days to maturity, plant height, stem diameter, filled seeds per head, total number of seeds per head, filling seed per cent and oil content contributed significant phenotypic and genotypic positive correlation with seed yield per plant and days to 50 per cent flowering, number of unfilled seeds per head, and hull content correlated negatively with seed yield per plant. Highest correlation was contributed by number of filled seeds per head with seed yield per plant.

Direct and indirect effects of eleven characters on seed yield were estimated and days to maturity, number of filled seeds per head, plant height, total number of seeds per head and test weight, exhibited positive significant direct effect on seed yield. Number days to 50 per cent flowering, stem diameter, unfilled seeds, and oil content, exhibited direct significant negative effect on seed yield.

Fifty genotypes along with two checks, Morden and DRSF-108 grown in three season and the stability analysis was done based on the procedure given by Eberhart and Russel (1966). Days to 50 per cent flowering, days to maturity, number of filled seeds per head and seed yield per plant exhibited significant genotype x environment interaction, hence the stability parameters were discussed for these characters and remaining characters were discussed based on their mean performance.

Genotypes GMU-284, 286, 289, 293 and 297 were early in flowering and are stable in all seasons. GMU-289 with short duration was adaptable to poor environments. Genotypes GMU-242 and 289 were early in maturity and adaptable to poor environments. Genotype, GMU-252 recorded high number of filled seeds and stable across the seasons. While genotypes, GMU-281 and 292 were adoptable to favorable environments. Genotypes, GMU-268, 276 and 300 recorded low seed yield and GMU-273 recorded high seed yield and adaptable to poor environments.

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