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CONTENTS

Review Article

QTL mapping for rust resistance in groundnut (*Arachis hypogaea* L.)

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ABSTRACT

Among biotic stress, rust is the major fungal disease of groundnut which causes drastic yield loss globally. Cultivation of resistant genotype is better than the use of chemical fungicides for sustainable agriculture. Considering the limitations of traditional breeding method which rely on the phenotypic selection, Marker assisted breeding (MAB) is more advantageous for the development of resistant genotype. Many different types of molecular markers are being developed in the groundnut and also being used to map Quantitative trait loci (QTL) for rust resistance. Identification of molecular markers which are closely linked to the QTL and/or candidate gene for rust resistance and their utilization in the Marker assisted selection (MAS) has been noticed in this review. Breeders can implement those molecular markers for the screening and development of rust resistant genotypes in groundnut..

Keywords: Groundnut, Linkage map, Marker assisted selection, Molecular markers, QTL, Rust

Groundnut (*Arachis hypogaea* L.) is an allotetraploid (2n=4x=40), leguminous oilseed crop which is cultivated in tropical and subtropical regions of the world. Groundnut seeds contain 40-60 % oil, 20-40 % protein and 10-20 % carbohydrate. Groundnut has high nutritional value, possessing vitamin E, niacin, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and potassium. Groundnut is mainly used for direct consumption, as a vegetable oil in cooking, in the confectionary industry and also as a source of protein feed in the animal industry. These multiple uses of groundnut make it an excellent cash crop for domestic as well as international trade. Groundnut is grown in more than hundred countries globally with a production of 40.31 million metric tons from an area of 24.75 million hectares wherein a production of 4.47 million metric tons from 4.56 million hectares area was from India alone during 2015-16 (Anonymous, 2016). India ranks second in the production of groundnut after China. In India, it is mainly grown in five states namely Gujarat, Tamil Nadu, Andhra Pradesh, Karnataka and Rajasthan. Though India is a major producer of groundnut the productivity is low due to the damage caused by biotic and abiotic stresses.

Rust disease in groundnut: Major fungal disease of groundnut is rust (*Puccinia arachidis* Speg.) which causes adverse effect on the yield as well as pod quality. Temperature ranging between 20°C and 28°C, free water on the leaf surface and high relative humidity are the favourable environmental conditions for the rust disease development (Mallaiah and Rao, 1979; Savary *et al.,* 1988). Rust pustules are orange colored (uredia) and appear on all aerial parts except on flowers. In leaflets, they initially appear on the lower surface and spreads to adaxial surfaces later in susceptible varieties. Pustules may also form on shells of developing pods (Van Wyk *et al.,* 2000). Subrahmanyam and McDonald (1987) reported that rust causes 57 % yield loss. The incidence and severity of disease vary with environment, location, and cultivar (Mehan *et al.,* 1996). Rust disease damage plant by reducing the green leaf area available for photosynthesis and by stimulating leaflet abscission leading to extensive defoliation (McDonald *et al.,* 1985) which results in lower seed quality, reduced seed size and oil content besides affecting the haulm production and quality. Different approaches are available to control this foliar disease including agronomic practices, chemical and biological methods. The success of biological control of fungal plant pathogens depends on the favourable geological and environmental conditions (Gohel *et al.*, 2006). Use of high yielding, well adapted resistant/tolerant cultivars of groundnut can be the best approach to manage this disease considering the cost and hazardous effect of fungicides on environment.

Components of rust resistance: Identification of resistant genotypes, knowledge of components and mechanism of resistance are the pre-requisite for the success of disease resistance breeding programmes. Several sources of resistance to rust have been reported in *A. hypogaea* (Anderson *et al.*, 1993; Waliyar *et al.*, 1993; Mehan *et al.*, 1996; Singh *et al.*, 1997). Resistance to rust in *A. hypogaea* is attributed to longer incubation period, less number of pustules, smaller pustules, and less ruptured pustules and leaf

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area damage (Subrahmanyam and McDonald, 1983; Reddy and Khare, 1988; Mehan *et al.*, 1994). Infection frequency, pustule diameter, per cent ruptured pustules and leaf area damage are correlated with each other and with mean field rust score. The incubation period is negatively correlated with other components (Subrahmanyam and McDonald, 1983).

Genetics of rust resistance: Better understanding of the genetics of disease resistance will enable breeders to design an efficient breeding strategy. Resistance to rust in *A. hypogaea* is conferred either by a few recessive genes (Bromfield and Bailey, 1972; Kalekar *et al.,* 1984; Tiwari *et al.,* 1984; Knauft, 1987; Paramasivam *et al.,* 1990; Motagi *et al.,* 2013) or 2-3 genes acting in duplicate complementary interactions in rust resistance (Vasanthi and Raja Reddy, 1997). The resistance is predominantly controlled by additive, dominance and additive × additive and additive × dominance genetic effects (Reddy *et al.,* 1987; Varman *et al.,* 1991). Singh *et al.* (1984) concluded that rust resistance in diploid species is partially dominant as compared to the recessive resistance in *A. hypogaea.*

Resistance genes (R genes) have been studied in groundnut. Proite *et al.* (2007) identified 35 putative non-redundant resistance gene analogs (RGAs) and 26 pathogenesis-related expressed sequence tags (ESTs) from *A. stenosperma* which is resistant to rust and other foliar diseases. Nucleotide-binding-leucine-rich repeat (NB-LRR)-encoding genes are of particular interest because they confer resistance against pests and diseases. Genome sequencing has identified 345 and 397 NB-LRR genes in *A. duranensis* and *A. ipaensis,* respectively (Bertioli *et al.,* 2016). The largest clusters were on distal regions of chromosomal pseudomolecule 02, the lower arms of chromosomal pseudomolecule 04 and the upper arms of chromosomal pseudomolecule 09. The genome assemblies could associate Quantitative Trait Loci (QTL) with candidate genes.

Conventional breeding efforts including screening of cultivated and wild genotypes, interspecific hybridization and development of amphidiploid from wild species of groundnut have been attempted to enhance the resistance to rust. But the success with these traditional breeding programmes has been limited due to narrow genetic base, cross incompatibility, linkage drag with agronomically unacceptable traits from wild species and difficulty in accurate phenotyping, etc. Also, these methods are time consuming (Janila *et al.,* 2013). Biotechnological approaches have great potential in improving groundnut against different stresses. Plant breeders are turning to the molecular breeding with the advancement in the molecular marker development and trait mapping to breed variety within a short period of time. Marker assisted selection (MAS) became advantageous with the availability of genomic resources, development of mapping populations and trait mapping for disease resistance in groundnut (Janila *et al.,* 2013).

QTL mapping for rust resistance in groundnut: Development of molecular markers would hasten the construction of genetic linkage maps and QTL analysis for several traits in different crops. Large number of molecular markers like restriction fragment length polymorphism (RFLP) (Halward *et al.,* 1993), random amplified polymorphic DNA (RAPD) (Halward *et al.,* 1991), amplified fragment length polymorphism (AFLP) (Herselman, 2003), simple sequence repeat (SSR), Diversity Array Technology (DArT) markers (Hilu and Stalker, 1995; Kochert *et al.,* 1996; Subramanian *et al.,* 2000; Dwivedi *et al.,* 2001; He and Prakash, 2001; Bravo *et al.,* 2006; Kilian, 2008; Huang *et al.,* 2016; Zhou *et al.,* 2016), Single Nucleotide Polymorphism (SNP) (Alves *et al.,* 2008; Nagy *et al.,* 2012; Khera *et al.,* 2013; Chopra *et al.,* 2015; Gupta *et al.,* 2015, Janila *et al.,* 2016b, Shirasawa *et al.,* 2016) and Transposable elements (TE) based markers (Shirasawa *et al.,* 2012) have been developed and used in groundnut genetic studies. From the last decade, there has been enormous improvement in the linkage maps for groundnut along with the advancement in the molecular markers (Guo *et al.,* 2013; Mishra *et al.,* 2015; Janila *et al.,* 2016a; Singh and Nigam, 2016; Stalker *et al.,* 2016). More dense and saturated linkage maps help to identify closely linked/functional markers for gene/genes governing the important traits.

Considerable efforts have been made to map resistance to rust in groundnut using simple association studies and linkage mapping. Bulk segregant analysis and marker-trait association studies among the diverse genotypes, germplasm sets and mapping populations have been identified a few markers associated with rust disease resistance (Varma *et al.,* 2005; Mace *et al.,* 2006; Mondal and Badigannavar, 2010; Mondal *et al.,* 2013).

At very first, Varma *et al.* (2005), identified two SSR alleles (pPGPseq3A1271 and pPGPseq3A1390) and seven SSR alleles (pPGPseq5D5270, pPGPseq5D5295, pPGPseq5D5325, pPGPseq5D5315, pPGPseq5D5424, pPGPseq5D5128 and pPGPseq5D5292) associated with rust resistance from the linkage maps developed from F_2 populations of ICGV 99003 × TMV 2 and ICGV 99005 × TMV 2, respectively.

Twenty groundnut genotypes with varying response to the rust disease were screened with 26 SSR markers and detected the significant association of three SSR markers (PM 50110, PM 179120 and PM 35124) with rust resistance by using Kruskal-Wallis one way ANOVA and simple regression analysis (Mondal and Badigannavar, 2010). Linkage map was developed from the mapping population comprising 117 F2 individuals from a cross between the rust resistant parent VG 9514 and rust susceptible parent TAG 24. Two RAPD markers (J71300 and J71350) were suggested for the rust

resistance by using linkage analysis (Mondal *et al.,* 2007). Further, for the recombinant inbred line (RIL) population of 164 lines from VG 9514 × TAG 24, linkage map was developed by using SSR markers and population was phenotypically evaluated in the F8 generation. Two SSR markers (pPGPseq4a05 and gi56931710) were found to be flanked the rust resistance gene (Mondal *et al.,* 2012a). Whereas, two EST-SSR markers, SSR_GO340445 and SSR_HO115759 were found to be closely linked to the rust resistance gene when earlier developed linkage map was saturated with EST-SSR markers for the same mapping population (Mondal *et al.,* 2012b).

Two RILs populations were developed by crossing rust susceptible cultivar TAG 24 and TG 26 with rust resistant cultivar GPBD 4 and extensively studied to map QTL for rust resistance. Partial genetic linkage maps were developed by using 56 and 45 SSR loci for TAG 24 × GPBD 4 and TG 26 × GPBD 4 RIL populations with a coverage of 462.24 and 657.9 cM distance, respectively (Khedikar *et al.,* 2010; Sarvamangala *et al.,* 2011). These two maps were enriched with 188 and 181 SSR loci covering a distance of 1,922.4 cM and 1,963 cM, respectively. A consensus map of 1,152.9 cM was constructed from these two mapping populations with 225 SSR loci (Sujay *et al.,* 2012). In addition to this, Kolekar *et al.* (2016) mapped 139 markers (28 SSR and 111 AhTE) on the linkage map of TAG 24 × GPBD 4 giving a length of 1730.8 cM which already had 188 SSR markers. From these linkage maps, Khedikar *et al.* (2010) identified 12 QTL for rust [Pheotypic Variance Explained (PVE) of 1.70-55.20 %] using TAG 24 × GPBD 4 RIL population. A major QTL (IPAHM103-pPGSseq19D6) was reported for rust resistance with high PVE (R2) of 6.90-55.20%. Sarvamangala *et al.* (2011) identified five QTL for rust from the map of TG 26 × GPBD 4 including one major QTL (XIP103-PM36) governing rust resistance with PVE of 48.90 %. From the enriched maps of TAG 24 × GPBD 4 and TG 26 × GPBD 4, three QTL were identified for rust (up to 82.96 % PVE) from candidate genomic region present on the linkage group AhXV. SSR markers GM2009, GM1536, GM2301, GM2079 and IPAHM 103 were reported for rust resistance from this region on linkage group AhXV (Sujay *et al.,* 2012). Saturation of linkage map for TAG 24 × GPBD 4 with some SSR and *Arachis hypogaea* transposable element (AhTE) markers could locate five major QTL (up to 70.4 % PVE) for rust resistance from the same candidate genomic region (Kolekar *et al.,* 2016) from the phenotypic data of eleven seasons. Two transposable element based markers, AhTE0498 and AhTE0928 were also found to be closely linked to the rust resistance gene along with the SSR markers reported in the previous study (Kolekar *et al.,* 2016). SSR markers linked to the QTL for rust resistance (Sujay *et al.,* 2012; Kolekar *et al.,* 2016) were validated in different genotypes and populations (Khedikar *et al.,* 2010; Gajjar *et al.,* 2014; Yeri *et al.,* 2014; Sukruth *et al.,* 2015; Yol *et al.,* 2016). A QTL region located on linkage group AhXV, explaining up to 82.62 % of the phenotypic variation for rust resistance (Sujay *et al.,* 2012) was introgressed from cultivar 'GPBD 4' into three rust susceptible varieties (ICGV 91114, JL 24 and TAG 24) through marker assisted backcrossing (MABC) approach by employing four markers, IPAHM103, GM2079, GM1536, GM2301 (Varshney *et al.,* 2014). This has generated several promising introgression lines with enhanced rust resistance and higher yields.

An effort was made at the Department of Biotechnology, UAS, Dharwad to develop a large number of straight cross and backcross lines for introgressing rust resistance into a susceptible elite varieties, JL 24 and TMV 2 from the resistant donor GPBD 4 through Marker Assisted Backcrossing (MABC) (Yeri and Bhat, 2016; Kolekar *et al.,* 2017). Few superior lines were selected by phenotypic evaluation for productivity and disease resistance traits followed by genotyping with rust resistance-linked markers. In another breeding programme, synthetic amphidiploids (ISATGR 278-18 and ISATGR 5B) were used as a source of rust resistance. Few advanced backcrossed lines from three different crosses (ICGS 76 × ISATGR 278-18, Dh 86 × ISATGR 278-18 and Dh 86 × ISATGR 5B) were selected for rust resistance by using molecular markers and also selected for higher productivity than the susceptible checks (Dh 86 and ICGS 76) which have been proposed for large scale field evaluation (Paratwagh and Bhat, 2015). These promising lines are being developed into commercial variety and also as the parents in breeding programme.

Linkage map of total distance 678.2 cM was developed by using microsatellite and transposon markers to locate QTL for rust resistance from the RILs population of *A. ipaensis* × *A. magna* (Leal-Bertioli *et al.,* 2015). Two strong QTL (upto 59.3 % PVE) for the components of rust resistance (total number of lesions/leaf area, number of sporulated lesions/leaf area, incubation period and susceptibility index) were identified on the linkage group B08 spanning with the three closest SSR markers Ah-280, AHGS1350 and AHGS2541. Single-nucleotide polymorphism Kompetitive allele-specific polymerase chain reaction markers were designed in the vicinity of those three microsatellite markers, validated and are now being used for the Marker Assisted backcross breeding programme in the cultivated groundnut in the Instituto Agronomico de Campinas, Sao Paulo, Brazil (Leal-Bertioli *et al.,* 2015).

Precise candidate QTL mapping by using next generation sequencing approach is more advantageous than the traditional QTL mapping. Pandey *et al.* (2017) used whole genome re-sequencing approach called as 'QTL-seq' for the screening of rust resistant and susceptible bulk of TAG 24 × GPBD 4 mapping population and identified 30 nonsynonymous SNPs affecting 25 candidate genes for rust

resistance which are located on the pseudomolecule A03. Based on this, three allele specific diagnostic markers were identified for rust resistance which can be used in the breeding programme (Pandey *et al.,* 2017).

Further, Khedikar *et al*. (2018) identified 62 main effect and epistatic quantitative trait (M-QTLs) for the morphological and yield related traits in groundnut from the linkage map of TAG 24 × GPBD 4 RILs population which was evaluated for seven environments at two locations. From this study, it was revealed that major QTL for rust resistance showed pleiotropic effect for yield related traits.

Phenotypic evaluation of VG 9514 × TAG 24 RIL population at five environments for rust disease and QTL analysis identified major Rust QTL flanked by two SSR markers, FRS72 and GO340445 in A03 chromosome. The chromosome region of 1.25 cM map interval for Rust QTL contained 331.7 kb in the physical map of *A. duranensis* and had a TIR-NB-LRR category R gene (Aradu.Z87JB) and four glucan endo-1,3 β glucosidase genes (Aradu.RKA6 M, Aradu.T44NR, Aradu.IWV86 and Aradu.VG51Q). In the near vicinity of this major QTL for rust resistance, the chromosome region between two SSR markers, FRS72 and FRS49 contain LRR-PK (Aradu.JG217) R gene which is similar to soyabean RHG4. It is predicted that protein kinase domain in AhRHG4 will be playing a major role in rust resistance by providing TIR-NB-LRR R-protein which imparts in the controlled programme cell death in resistant peanut plants (Mondal *et al.,* 2018).

Genomics tools can enhance the efficiency of breeding programmes through their use in marker assisted selection (MAS) where selection of target traits can be achieved indirectly using molecular markers that are closely linked to genes or gene itself. Molecular markers identified for rust resistance from different studies are being used in the breeding programme for the precise selection of rust resistant genotype which can be developed into commercial variety like other successful studies for different traits in the groundnut (Simpson *et al.,* 2003; Chu *et al.,* 2011).

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A simple and rapid method for isolation of DNA for molecular markers and transgene analysis in safflower

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ABSTRACT

In spite of the possibility of analysing large samples and the rapidity of Polymerase Chain Reaction (PCR) technology, the usual protocols for DNA plant extraction remain time-consuming, slow and involves use of hazardous chemicals. To lessen labor, time or cost of DNA extraction, a simple and instant method for genomic DNA extraction from leaf tissue of safflower (*Carthamus tinctorius* L.) leaf is established. Small quantity of tissue material (typically 3-5 mg) was ground in a centrifuge tube using plastic pestle in extraction solution. Extracted DNA was suitable for PCR analysis, without centrifugation. The feasibility of this method was confirmed by testing molecular markers and transgene detection. This method requires less than 1 mg of plant tissue stored frozen or used fresh and is useful for molecular marker analyses as well as transgene detection.

Keywords: DNA extraction, ISSR, PCR analysis, RAPD, Safflower

Safflower (*Carthamus tinctorius* L.) is an important *rabi* oilseed crop and produces high quality oil rich in polyunsaturated fatty acids, which helps in reducing the cholesterol level in the blood (Popov and Kang, 2011). India is the largest producer of safflower (2 lakh tonnes) in the world with highest acreage of 4.3 lakh hectares. Unfortunately, the area and production of safflower in India has experienced a downward trend for the last 4-5 years. The full potential of the crop is far from being exploited and the yield levels of the country are the lowest in the world due to several reasons such as occasional adverse climatic conditions, poor agronomic methods of cultivation, biotic and abiotic stresses. Therefore, it is needed to improve the yield potential of safflower varieties/hybrids to increase safflower production of the country. Substantial effort has been directed toward molecular analysis of this crop for various purposes, such as genetic enhancement for qualitative and quantitative traits (Patel and Shrivastava, 2016; Kadirvel *et al.,* 2017).

Marker assisted selection is of increasing importance in plant breeding programs, where large numbers of genotypes are screened for numerous traits in a short time period. While the availability of DNA markers linked to traits of interest has increased, available DNA extraction procedures have limited the number of samples able to be processed (Rehman *et al.,* 2007). The genomic DNA extraction methods for PCR-quality DNA from safflower are not time efficient, since they require several steps, like the tissues be ground in liquid nitrogen, followed by precipitation of the DNA pellet in ethanol, washing and drying the pellet, etc. However, several DNA extraction procedures have been published in several plants and although some of these are undoubtedly rapid, many require the use of expensive, often environmentally hazardous chemicals, and specialized laboratory equipment (Rehman *et al.,* 2007; Kang and Yang, 2004; Amani *et al.,* 2011).

In recent years commercial manufacturers have developed kits that allow rapid and efficient isolation of high quality DNA from a wide variety of plant species. However, the disadvantage of any commercial kit is the high per-sample cost. The need for a rapid and simple procedure is urgent, especially when hundreds of samples need to be analyzed. Here, we describe an instant, cheaper and efficient genomic DNA extraction method for PCR amplification. In this method, no liquid nitrogen, no centrifugation, no DNA precipitation and washing steps were used.

MATERIALS AND METHODS

Plant materials: Leaf samples (young immature to mature leaf) of safflower were used for DNA extraction.

DNA extraction protocol: Small quantity of tissue material (typically 3-5 mg) was ground in a centrifuge tube using plastic pestles in warm extraction solution (Tris-Cl- 10 mM, pH 8.0; EDTA- 1 mM, pH 8.0; SDS- 0.1 %). The solution was mixed by vigorous vortexing followed by incubation of tubes at 50-600C for 15 min. Lysate were diluted (1:10) with nucleases free water. Approximately 2µl of diluted lysate were used in 20 µl for PCR analysis. The PCR was carried out for different molecular markers [Random Amplified Polymorphic DNA (RAPD) and Inter Simple Sequence Repeat (ISR)] and transgene detection.

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Molecular marker analysis: RAPD amplification was performed in 20 µl volume containing 10 µl of Premix Taq® Version 2.0 (Xcelris Lab Ltd. Ahmedabad, Gujarat), 0.2 µM primer and 2 µl of diluted lysate DNA in a Thermalcycler (Agilent Technologies) for cyclic amplification and the conditions for amplification was programmed as follows: a denaturation step of 5 min at 94°C, followed by 40 cycles of 1 min at 94°C, 30 s at 35°C, an extension at 72°C for 2 min and a final extension at 72°C for 10 min. Amplification products were then subjected to electrophoresis in 1.2% agarose gel using 1 X TBE and detected by ethidium bromide staining, viewed under UV light and photographed with gel documentation system.

ISSR analysis was carried out in 20 µl volume containing 10 µl of Premix Taq® Version 2.0 (Xcelris Lab Ltd. Ahmedabad, Gujarat), 0.2 µM forward primer, 0.2 µM reverse primer and 2 µl of diluted lysate DNA in a thermal cycler (Agilent Technologies). The amplification reaction involved an initial 94°C for 5 min for denaturation followed by 35 cycles of 1 min at 94°C, 30 sec at 42°C, and 1 min at 72°C and final extension at 72°C for 3 min. Agarose gel (1.2%) was prepared to separate the amplified product gel documentation system was used for visualization of amplified DNA fragments. Each experiment was repeated three times with each primer to test the reproducibility of ISSR primer.

Transgene identification: For transgene identification analysis, leaf of transgenic safflower transformed with vector having double CaMV 35S promoter (unpublished data) was used. PCR amplification of the transgene from WT and transgenic lines using CaMV35S specific primer pair (CaMV35S F: CTCGGATTCCATTGCCCAGCTAT & CaMV35S R: TTGCGAAGGATAGTGGGATTGTGC) was performed in a reaction volume of 20 µl containing the 2 µl of diluted lysate DNA, 10 µl of Premix Taq® Version 2.0 (Xcelris Lab Ltd. Ahmedabad, Gujarat) and 0.5 µM of each primer with an initial denaturation step of 94°C for 5 min, followed by 30 cycles of denaturation (30 s at 94°C), annealing (30 s at 53°C), and extension (40 s at 72°C). After the last cycle, a final extension was carried out for 5 min at 72°C. Amplification products were separated on 1% agarose gel and gels were visualized under UV using gel documentation system.

RESULTS AND DISCUSSION

The objective of this investigation was to develop a high throughput DNA isolation method suitable for the molecular analysis in safflower. While determining the final protocol for DNA isolation, different combinations of Tris-Cl; EDTA and SDS were tried without use of phenol:chloroform: isoamyl treatment. The optimized protocol works very well for different marker as well as transgene detection in safflower.

Molecular marker analysis: Different types of molecular markers like RAPD and ISSR were checked for the amplification using DNA extracted from our optimized protocol (Fig. 1). The reproducibility was checked by repeating the extraction of DNA and PCR several times. List of primers used in different marker analysis are mentioned in Table 1.

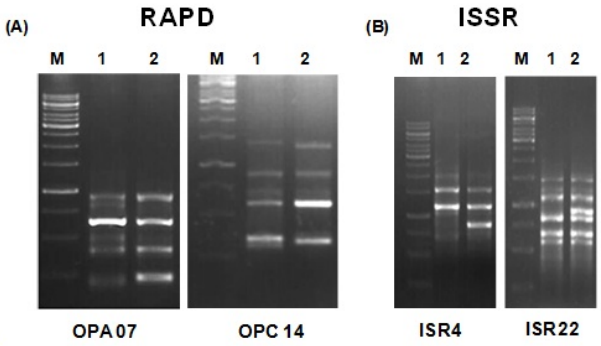

Fig. 1. Molecular marker analysis using DNA extracted from safflower plants. (A) RAPD and (B) ISSR analysis. M: molecular weight marker; 1 & 2: two different safflower genotypes

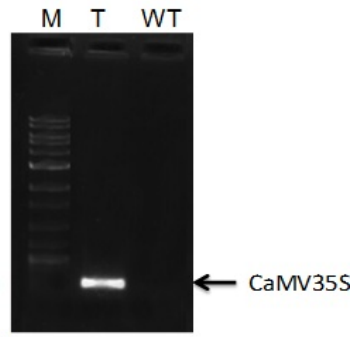

Fig. 2. Transgene detection by PCR amplification using CaMV35S F & R primer. M: molecular weight marker; T: transgenic safflower; WT: wild type

Table 1 Sequences of primer used in RAPD and ISSR analysis

Name of Primer	Sequence
OPA 07	GAAACGGGTG
OPC14	TGCGTGCTTG
ISR4	ACACACACACACACACAG
ISR22	ACACACACACACACACAA

Transgene identification: The transgenic safflower plants (unpublished data) were characterized for the presence of CaMV35S promoter by PCR. DNA from transformed and wild type (WT) were extracted using the optimized protocol. An amplification product of 400 bp was observed in transformants whereas no amplification was observed in WT

plant (Figure 2). These results showed that our one step DNA isolation protocol is suitable for transgenic plant characterization.

A plethora of literature is available regarding the DNA extraction procedure using plant tissues (Huang and Sun, 2000; Doyle and Doyle, 1987; Kasajima *et al.,* 2017). The Cetyl Trimethyl Ammonium Bromide (CTAB) method and its modifications (Huang and Sun, 2000; Doyle and Doyle, 1987) were extensively used in different laboratories, but these methods are time consuming (Cheng *et al.,* 2003). Other conventional DNA extraction protocols, which can remove some contaminants (Jobes *et al.,* 1995), require large amounts of plant tissue to be grounded. On the other hand, these methods require long periods for plant growth and are not efficient for screening and analyzing transgenic plants. Other methods use liquid nitrogen and other carcinogenic chemicals (Sharma *et al.,* 2002), which are not considered to be safe. There are also a number of protocols which require small quantities of tissues, but these methods have limitations, such as the use of specialized apparatus (e.g. the matrix mill) (Hill-Ambroz *et al.,* 2002). Today, numerous DNA isolation kits are available, but the main problem with these commercially available kits, is their high cost per sample (Kang and Yang, 2004; Ahmed *et al.,* 2009). There are several reports of rapid method of DNA extraction. But most of these methods requires treatment of either phenol:chloroform:isoamyl alcohol (Kang and Yang, 2004) or chloroform: isoamyl alcohol (Amani *et al.,* 2011). Some earlier reported methods require alkali treatment followed by DNA precipitation by cold ethanol (Rehman *et al.,* 2007). This DNA extraction procedure promises simplicity, speed, and efficiency, both in terms of time and the amount of plant sample required. In addition, this method does not require expensive facilities for plant genomic DNA extraction.

This method has the following advantages

- The quality of the extracted DNA is high enough for PCR
- The procedure is simple and rapid, because it does not require any centrifugation steps that pellet the DNA
- No dangerous organic solvents such as phenol or chloroform are used

The efficiency and the speed of this method together with the use of inexpensive facilities and the absence of toxic chemicals make the present method an attractive alternative for the extraction of genomic DNA. These results show that the DNA produced by this simple, low cost, fast and safe protocol can be used in PCR-based techniques and in laboratories lacking state-of-the-art equipments and technology.

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Generation mean analysis for seed yield and its related attributes in Pusa Gold x YST-151, Ragni x NDYS-425 and Ragni x YST-151 crosses of yellow sarson

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ABSTRACT

Three cross combinations were attempted by using Pusa Gold, YST-151, Ragni and NDYS-425 cultivars of yellow sarson as parents. Parents were selected on the basis of variability for days to maturity, seed yield, oil content and other agronomic traits. Six generations (P_1, P_2, F_1, F_2, BC_1, BC_2) in each cross (Pusa Gold x YST-151, Ragni x NDYS-425 and Ragni x YST-151) were evaluated in a compact family block design with three replications during 2011-12 cropping season. Data were recorded for several morpho-physiological traits like seed yield per plant, plant height, primary branches per plant, Days to 50% flowering, length of fruiting zone, siliqua per plant, siliqua length, days of maturity, 1000-seed weight and oil content. Analysis of variance for six generations revealed significant differences among the progenies (generations) within family (cross) for most of the evaluated traits except for siliqua length and days to maturity. The differences were highly significant ($p \leq 0.001$) for length of fruiting zone and seed yield per plant. For the traits primary branches per plant, siliqua per plant and seed yield per plant, the performance of hybrids was superior to their respective parents in all crosses studied. Six parameter model (m, d, h, i, j, l) and scaling tests revealed the presence of inter-allelic interactions (epistasis) for most of evaluated traits except days to maturity in Pusa Gold x YST-151cross and indicated the inadequacy of additive-dominance model. The prime objective of current study was to estimate gene effects controlling yield and its related attributes by generation mean analysis and scaling test.

Keywords: Generation mean analysis, Epistasis, Gene interaction, Yellow sarson, Yield

Yellow sarson (*Brassica rapa* L. var. yellow sarson) belongs to family Brassicaceae and considered to be the most drought-tolerant among the three sub-species of *Brassica rapa* L. i.e. yellow sarson, brown sarson and toria. In India, it is mainly grown in Assam, Bihar, North-eastern States, Orissa, eastern Uttar Pradesh and West Bengal (Singh and Murty, 1980; Kaur *et al.,* 2016; Kumar *et al.,* 2017). The knowledge of genetic architecture of yield components is essential because yield is a quantitative trait that is influenced by the interaction of different yield related attributes and environmental effects. Because of these complex interactions, it is difficult to improve yield through breeding if yield is the only factor considered, suggesting that component traits should also be used as selection criteria for yield improvement (Misra *et al.,* 1994). The information about the nature and magnitude of gene effects involved in the expression of important characters is essential for formulation and execution of intensive breeding programme in any crop. For genetic improvement of the crop, the breeding method to be adopted depends mainly on the nature of gene action involved in the expression of quantitative traits. The Line x Tester analysis is used to select the parents based on their combining ability but fails to detect the epistasis. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately whether it is complimentary (Additive x Additive) or duplicate (Additive x Dominance) and (Dominance x Dominance) at the digenic level (Sharmila *et al.,* 2007). According to Hallauer and Miranda (1988), generation mean analysis is a quantitative genetic method that will be able to estimate additive, dominance and epistatic effects in quantitative traits like yield and it is better than other mating designs such as diallel because of high level of sensitivity and decreased error rate in genetic analysis. In order to determine genotypic values of the individuals and consequently mean genotypic values of families and generations, researchers use generation mean analysis to estimate the relative importance of average effects of the genes (additive effects), dominance deviations, and effects due to non-allelic genic interactions (Viana, 2000). The main aim of this research was to generate information on the nature of gene action that provide a basis for an evaluation of selection methods for the improvement of yellow sarson crop.

MATERIALS AND METHODS

The six basic generations involved in current studies included two parents (P_1, P_2), first and second hybrid generations (F_1, F_2), first and second backcrosses BC_1 (P_1 F_1), BC_2 (P_2 F_1) of three cross combinations between Pusa Gold, YST-151, Ragni and NDYS-425 cultivars of yellow sarson (*Brassica rapa* L. var. yellow sarson) (Table 1). During 2009-2010 crop season, different crosses were performed and F_1 seeds harvested. In subsequent year

(2010-11), F_1s were crossed with respective parents (P_1 and P_2) for developing back cross (BC_1 and BC_2) populations and also selfed to obtain F_2 seeds. Simultaneously, fresh crosses were attempted to produce F_1 seeds during the same year.

The produced materials were experimented in Compact Family Block Design (CFBD) with three replications during *rabi,* 2011-12 under timely sown condition at Research Farm, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, India. The P_1, P_2, F_1s were grown in single row, BC_1, BC_2 in 2 rows and F_2s in 4 rows of 5m length each. The inter and intra row spacing was maintained at 30 x 10 cm.

The number of competitive plants were randomly selected from each generation per replication (5 plants from P_1, P_2, F_1; 20 from F_2 and 10 from BC_1, BC_2). The data were recorded on randomly selected plants for plant height (cm), primary branches/plant, Number of siliqua per plant, length of fruiting zone (cm), seed yield per plant, 1000-seed weight and oil content (%) on plot basis. For each family (cross), the plot means for each generation were averaged over the number of replications to get the generation means. These generation means formed the basis for calculation of various genetic parameters.

The six basic generations statistically analyzed using Compact Family Block Design analysis of variance by following procedure of Singh and Chaudhary (1985). The mean squares of treatments and replications were tested against corresponding mean square of error. The calculated 'F' value was compared with table value of 'F' at 5%, 1% and 0.1% level of significance. Obtained data were used for calculating estimative values and genic effects based on six parameter model of generation mean analysis as suggested by Jinks and Jones (1958):

$$m = \bar{F}_1 - 4\bar{F}_2 - (1/2)\,\bar{P}_1 - (1/2)\,\bar{P}_2 + 2\overline{BC}_1 + 2\,\overline{BC}_2$$

$$d = \overline{BC}_1 - \overline{BC}_2$$

$$h = \bar{F}_1 - 4\bar{F}_2 - (1/2)\,\bar{P}_1 - (1/2)\,\bar{P}_2 + 2\overline{BC}_1 + 2\,\overline{BC}_2$$

$$i = 2\,\overline{BC}_1 + 2\,\overline{BC}_2 - 4\,\bar{F}_2$$

$$j = \overline{BC}_1 - \tfrac{1}{2}\,\bar{P}_1 - \overline{BC}_2 + \tfrac{1}{2}\,\bar{P}_2$$

$$l = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\,\bar{F}_2 - 4\overline{BC}_1 - 4\overline{BC}_2$$

Where, m (mean), *d* (additive effect), *h* (dominance effect), *i* (additive x additive gene interaction), *j* (additive x dominance gene interaction), *l* (dominance x dominance gene interaction). $\bar{P}_1, \bar{P}_2, \bar{F}_1, \bar{F}_2, \overline{BC}_1$ and $\overline{BC}_2$ are the mean values for different generation. The test for significance of genic effects was accomplished by 't' test. Further the analyses of data were performed by using simple scaling test based on formulae of Hayman and Mather (1955) for testing the validity of additive dominance model or for detecting non-allelic interactions:

$$A = 2\overline{BC}_1 - \bar{P}_1 - \bar{F}_1 \qquad V_A = 4V(\overline{BC}_1) + V(\bar{P}_1) + V(\bar{F}_1)$$

$$B = 2\overline{BC}_2 - \bar{P}_2 - \bar{F}_1 \qquad V_B = 4V(\overline{BC}_2) + V(\bar{P}_2) + V(\bar{F}_1)$$

$$C = 4\,\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2 \qquad V_C = 16\,V(\bar{F}_2) + 4\,V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$$

$$D = 2\,\bar{F}_2 - \overline{BC}_1 - \overline{BC}_2 \qquad V_D = 4V(\bar{F}_2) + V(\overline{BC}_1) + V(\overline{BC}_2)$$

Where, A, B, C, and D are the simple scales and P_1, P_2, F_1, F_2, BC_1 and BC_2 are generation means for a particular character. V_A, V_B, V_C, and V_D are corresponding variances of the scales and $V(\bar{P}_1)$, $V(\bar{P}_2)$, $V(\bar{F}_1)$, $V(\bar{F}_2)$, $V(\overline{BC}_1)$, $V(\overline{BC}_2)$ are the variance of the sample means of respective generations. The joint scaling test (Cavalli, 1952) was also performed for detection and estimation of genic effects and testing the adequacy of model. All statistical analyses were carried out using Windostat software (V 8.6) from Indostat services.

RESULTS AND DISCUSSION

Compact family block design analysis of variance for six generations revealed significant differences among the progenies (generations) within Family (cross) for most of the evaluated traits except for siliqua length and days to maturity (Table 2). On the other hand, it was highly significant ($p \leq 0.001$) for length of fruiting zone and seed yield per plant. The mean values and their standard errors of six generations for ten morpho-physiological traits are presented in Tables 3. The performance of hybrids (F_1) was inferior to their parents in respect of plant height and days to maturity in each cross. For the traits primary branches per plant, siliqua per plant and seed yield per plant, mean values of F_1s were higher than their respective parents in all the crosses. For the other traits, differences were not so conspicuous. Estimates of gene effects for digenic epistasis interaction model or additive-dominance model and simple scaling test (A, B, C, D) for the evaluated traits of Pusa Gold x YST-151, Ragni x NDYS 425 and Ragni x YST-151are presented in Table 4, 5 and 6, respectively. In Pusa Gold x YST-151 cross, estimates of genetic effects for the six parameter model and scaling test (A, B, C, D) indicated that additive (*d*), dominance (*h*), gene interactions (additive x additive (*i*), additive x dominance (*j*), dominance x dominance (*l*)) were significant in regard of length of fruiting zone and oil content. For the length of fruiting zone and oil content, complementary and duplicate type epistasis were observed, respectively (Table 4). Non-additive gene effects and A, B, C, D scales were non-significant in respect of days to maturity. At least one type of non-allelic gene interactions (*i, j, l*) were significant for all the agronomic traits except days to maturity. For the traits, length of fruiting zone, primary branches per plant, siliqua per plant, siliqua length, seed yield per plant, 1000-seed weight and oil content, both additive (*d*) and dominance (*h*) genic effects were significant along with the

epistatic gene interaction. Additive (*d*) gene effects were significant for all the traits studied except plant height and days to 50% flowering. Duplicate type of epistasis was observed in regard of plant height, siliqua per plant, siliqua length and oil content, on the contrary, complementary epistasis for the traits length of fruiting zone, primary branches per plant, seed yield per plant, 1000-seed weight and days to 50 % flowering.

In Ragni x NDYS 425 cross, additive (*d*) and dominance (*h*), non-allelic gene interactions (*i, j, l* type) with duplicate epistasis and scaling test (A, B, C, D) were significant for oil content (Table 5). Additive (*d*), dominance (*h*) gene effects along with at least one non-allelic gene interactions type and scaling test were significant in regard of primary branches per plant, seed yield per plant and oil content. For seed yield per plant, additive (*d*) and dominance (*h*) gene effects as well as *i* and *l* type of gene interactions were significant. Duplicate type of epistasis was observed for the traits days to maturity, length of fruiting zone and oil content, on the other hand, for siliqua per plant, seed yield per plant and 1000-seed weight, complementary type of epistasis was pronounced. Both additive (*d*), dominance (*h*) were non-significant for days to 50% flowering and plant height indicated the presence of epistasis and inadequacy of additive-dominance model in inheritance of these traits. For siliqua length, only additive gene effect was significant.

In Ragni x YST-151 cross, additive (*d*), dominance (*h*), additive x additive (*i*), additive x dominance (*j*) and dominance x dominance (*l*) were significant for days to 50% flowering, plant height, length of fruiting zone and siliqua per plant (Table 6). Additive gene effects along with *i, j* and *l* type of gene interactions were significant for primary branches per plant. For seed yield per plant, additive and dominance and *j, l* type of gene interactions were significant. Duplicate type of epistasis was observed for days to 50% flowering, plant height, length of fruiting zone and siliqua per plant, whereas, for the traits days to maturity, seed yield per plant and 1000-seed weight, complementary type of epistasis was pronounced. For length of fruiting zone, 1000-seed weight and oil content all the four scales (A, B, C and D) were significant. A, C and D were significant for primary branches per plant, days to 50% flowering, days to maturity siliqua length and siliqua per plant. A, B and C were significant only for seed yield per plant. The significance of at least one scale indicated presence of epistasis and inadequacy of additive-dominance model in the inheritance of evaluated morpho-physiological traits.

The estimates of joint scaling test and chi-square values for the seed yield and its components in three crosses of yellow sarson are presented in Table 7. All the crosses showed significant chi-square values for all the evaluated traits except for days to maturity in Pusa gold x YST-151 cross.

Analysis of variance revealed significant variation among the progenies (generations) within sets of crosses (families) for most of agronomical traits considered except for siliqua length and days to maturity. It indicates the presence genetic variability and feasibility of opting the appropriate selection methods for exploiting the information generated in current studies in regard of genetic components of variation. Information about the genetic components of variation helps the breeder in the selection of desirable parents for crossing programs and also in deciding a suitable breeding procedure for the genetic improvement of various quantitative traits (Singh and Narayanan, 2013). The improvement in yield potential of yellow sarson can be brought by either altering the genetic makeup of existing variation through the process of recombination or employing the appropriate selection methods for exploiting the different diverse populations (Joshi and Dhawan, 1966; Joshi, 1979). The superior performance of hybrids (F_1) to their respective parents in the crosses understudy for primary branches per plant, siliqua per plant and seed yield per plant, indicating the possibility of exploitation the heterosis through hybridization. However, Tomar *et al.* (2017) observed high heritability in F_1 generation of 100 crosses of yellow sarson for 1000-seed weight and oil content. In current findings, all the morpho-physiological traits (except days to maturity in Pusa gold x YST-151) were significant for at least one of the scaling test in all the crosses. The significance of any one of the scale reveals the presence of non-allelic interaction, indicating that the estimate of genetic parameters of the trait does not fit to the additive-dominance model.

These finding were in concurrence of Singh *et al.* (2017). In our results, since, epistasis was present for most of evaluated traits in all three crosses, therefore, generation mean analysis was carried out according to Jinks and Jones (1958). Importance of epistasis in inheritance of yield and yield components in Indian mustard has also been reported by Sachan and Singh (1987) and Verma *et al.* (1992). The estimates of six parameters under generation mean analysis showed that the additive (*d*) and dominance (*h*) gene effects were significant in all the crosses though the relative contribution of the dominance gene effect was higher that of additive gene effect. Akhshi *et al.* (2014) and Singh *et al.* (2017) also reported that in comparison with the additive gene effects, dominance genes are the most important factors contributing to the genetic control of the traits.

The gene effects, dominance (*h*) and dominance x dominance (*l*), were in opposite direction for plant height, siliqua per plant, siliqua length, oil content in Pusa Gold x YST-151 cross, for the traits days to maturity, length of fruiting zone, oil content in Ragni x NDYS-425 cross and for days to 50% flowering, plant height, length of fruiting zone, siliqua per plant in Ragni x YST-151, suggesting the occurrence of duplicate epistasis. Duplicate-type epistasis

played a greater role than complementary epistasis in expression of most of agronomical traits in Ragni x YST-151 cross. On the contrary, in Pusa Gold x YST-151 cross, complementary gene interaction was more pronounced for most of the agronomical traits. According to Singh *et al.* (2014) the dominance (*h*) and dominance x dominance (*l*) non-allelic interactions were most important for water use efficiency in BPR-543-2 x BPR-2 cross of Indian mustard. The non-allelic gene action was absent for the trait days to maturity in Pusa Gold x YST-151 cross.

Generation mean analysis by using six parameters model and scaling test suggested the presence of duplicate or complementary epistasis that indicates the inadequacy of additive-dominance model in all crosses for most of the traits studied. The estimates of joint scaling test showed significant chi-square values for all the evaluated traits in three crosses except for day to maturity in Pusa Gold x YST-151 cross. It further confirmed the inadequacy of additive-dominance model.

In general, when quantitative traits are governed by additive or dominance gene action, hybrid breeding programs may easily be resorted. However, when inheritance of physiological traits influenced by the non-allelic gene interaction, it becomes very difficult to improve such quantitative traits by conventional breeding methods. Our results showed that both additive and non-additive type of gene action were significant in governing the inheritance of the evaluated traits. The significance of additive gene effects for the evaluated traits in three crosses indicated that substantial improvement in yield could be achieved by following conventional breeding methods. The dominance and additive x dominance and dominance x dominance epistatic effects indicating non-fixable, non-additive gene action, were also significant for many traits in the crosses understudy. Importance of one or more types of non-additive components of genetic variance for most of the traits suggested the exploitation of heterosis in those traits for developing hybrid varieties. The application of methods like biparental mating and diallel selective mating system may be recommended for exploitation of dominance and epistatic effects for purpose of isolating transgressive segregants in advanced generations or inter-mating among the selected segregants followed by at least one selfing, could be suggested to knockdown the undesirable linkage and allow the accumulation of favorable alleles for the improvement of desired traits.

Table 1 List of parents, pedigree and crosses produced

Generations	Parents and crosses	Parents and crosses	Parents and crosses
P_1	Pusa Gold (Selection from Mirzapur)	Ragni (Selection from material obtained from Allahabad)	Ragni (Selection from material obtained from Allahabad)
P_2	YST-151 (Selection from material obtained from Aligarh)	NDYS 425 (Selection from Mirzapur)	YST-151 (Selection from material obtained from Aligarh)
F_1	Pusa Gold ×YST-151	Ragni × NDYS 425	Ragni × YST-151
F_2	Pusa Gold × YST-151	Ragni × NDYS 425	Ragni × YST-151
BC_1	(Pusa Gold × YST-151) × Pusa Gold	(Ragni × NDYS 425) × Ragni	(Ragni × YST-151) x Ragni
BC_2	(Pusa Gold × YST-151) × YST-151	(Ragni × NDYS 425) × NDYS 425	(Ragni × YST-151) x YST-151

Table 2 Analysis of Variance (ANOVA) for six generations of different agronomical traits (Mean squares)

Crosses	S.O.V.	d.f.	PH (cm)	PBPP	DF	LFZ (cm)	SPP	SL (cm)	DM	SYPP (g)	TSW (g)	OC (%)
Ragni × YST-151	Replications	2	2.43	0.06	2.72	0.27	1.56	0.47	1.56	3.12	0.01	0.15
	Progenies	5	49.84***	1.96	27.82*	52.91***	19.26**	0.81	29.42	10.57***	0.38**	0.64***
	Error	10	2.18	1.06	5.06	2.33	1.76	0.27	9.29	0.97	0.05	0.04
Pusa Gold × YST-151	Replications	2	3.12	1.06	11.17	0.66	5.72	0.32	1.72	1.08	0.03	0.01
	Progenies	5	17.53**	2.22	19.97*	20.74***	14.62*	0.63	24.19	10.28***	0.31**	1.47***
	Error	10	1.77	0.72	3.03	1.24	3.12	0.25	8.66	0.87	0.05	0.04
Ragni × NDYS 425	Replications	2	3.75	0.39	3.72	1.60	9.56	0.13	6.72	0.29	0.01	0.05
	Progenies	5	6.41	2.59**	25.00**	33.63***	19.92**	0.15	8.09	16.86**	0.42***	0.50**
	Error	10	2.13	0.46	3.52	1.56	2.09	0.24	6.12	0.84	0.04	0.09

*, **, *** Significant at 5%, 1% and 0.1 % level of significance, respectively, S.O.V. (Sources of Variance), PH (Plant height),
PBPP (Primary branches per plant), DF (Days to 50% flowering), LFZ (Length of fruiting zone), SPP (Siliqua per plant), SL (Siliqua length),
DM (Days to maturity), SYPP (Seed yield per plant), TSW (Thousand grain weight), OC (Oil content)

Table 3 Means and their standard error of six generations for ten physiological traits of yellow sarson

Generations	Pusa Gold × YST-151									
	PH (cm)	PBPP	DF	LFZ (cm)	SPP	SL (cm)	DM	SYPP (g)	1000-SW (g)	OC (%)
P_1	120.43±0.14	4.67±0.13	42.67±0.67	51.67±0.18	44.33±0.33	4.98±0.08	120.00±0.22	15.52±0.23	4.23±0.03	44.29±0.07
P_2	118.23±0.30	6.00±0.22	47.33±0.33	54.83±0.24	40.33±0.13	5.79±0.21	118.33±0.45	16.57±0.11	3.80±0.02	43.30±0.02
F_1	113.53±0.58	7.00±0.22	40.67±0.33	52.67±0.11	45.00±0.58	6.15±0.09	112.00±0.65	20.77±0.27	4.53±0.09	44.21±0.02
F_2	115.50±0.09	5.00±0.11	46.33±0.22	48.10±0.16	43.33±0.27	5.03±0.03	115.00±0.21	16.63±0.12	3.80±0.01	44.12±0.01
BC_1	118.50±0.19	5.00±0.15	46.00±0.15	50.53±0.12	44.67±0.32	5.70±0.07	116.33±0.38	16.38±0.09	3.70±0.02	45.49±0.04
BC_2	118.20±0.08	5.67±0.09	46.00±0.40	48.17±0.20	47.00±0.15	5.38±0.01	114.67±0.68	16.74±0.14	3.90±0.03	44.18±0.01
Ragni × NDYS-425										
P_1	110.23±0.34	5.33±0.13	39.00±0.22	42.53±0.27	38.67±0.25	5.51±0.07	112.33±0.33	17.16±0.22	4.40±0.04	44.22±0.01
P_2	110.83±0.31	5.33±0.13	45.67±0.25	52.97±0.31	43.67±0.13	5.29±0.04	115.00±0.87	15.05±0.01	4.23±0.03	44.50±0.13
F_1	106.80±0.31	6.33±0.13	41.67±0.13	47.14±0.23	46.67±0.50	5.32±0.09	111.33±0.25	22.08±0.23	4.77±0.03	44.16±0.02
F_2	108.07±0.12	5.33±0.06	45.67±0.16	47.13±0.15	42.33±0.27	4.95±0.06	110.67±0.06	16.86±0.11	3.80±0.01	45.29±0.03
BC_1	109.30±0.30	4.33±0.09	45.33±0.46	48.50±0.20	42.67±0.23	5.28±0.10	113.33±0.44	16.76±0.12	3.90±0.03	44.71±0.01
BC_2	109.00±0.25	7.00±0.15	46.00±0.40	48.20±0.15	42.33±0.32	4.95±0.08	114.00±0.45	17.27±0.13	3.90±0.04	44.58±0.01
Ragni × YST-151										
P_1	117.97±0.35	5.33±0.13	39.00±0.22	42.53±0.27	40.00±0.22	6.01±0.07	112.33±0.33	17.16±0.22	4.36±0.06	44.22±0.01
P_2	115.80±0.25	5.00±0.22	46.67±0.45	54.83±0.24	40.33±0.13	4.50±0.06	118.33±0.45	16.71±0.34	3.80±0.02	43.22±0.04
F_1	110.70±0.25	7.00±0.22	40.33±0.13	46.67±0.20	45.00±0.22	5.40±0.13	109.33±0.13	20.54±0.30	4.64±0.04	44.19±0.01
F_2	112.67±0.19	5.67±0.06	43.33±0.16	50.67±0.15	46.33±0.22	4.80±0.07	116.33±0.40	15.94±0.11	3.70±0.03	44.53±0.03
BC_1	114.37±0.32	4.67±0.09	46.00±0.66	48.82±0.28	43.67±0.18	5.05±0.13	114.67±0.49	15.01±0.11	3.93±0.02	44.34±0.05
BC_2	106.43±0.11	5.67±0.23	44.00±0.15	46.80±0.26	42.33±0.23	5.16±0.6	114.33±0.61	17.11±0.15	4.01±0.03	44.24±0.05

Table 4 Estimates of components of generation means for different traits, simple scaling test and type of epistasis in Pusa Gold x YST-151 cross

Characters	Gene effects						Scales				Type of epistasis
	m	*d*	*h*	*i*	*j*	*l*	A	B	C	D	
Days to 50% flowering	46.33 ±0.22	0.00 ±0.43	-5.67** ±1.33	-1.33 ±1.23	2.33** ±0.57	-11.33** ±2.17	8.67** ± 0.81	4.00** ±0.93	14.00** ±1.34	0.67 ±0.62	CE
Days to maturity	115.00 ±0.21	1.67* ±0.78	-5.17* ±1.92	2.00 ±1.78	0.83 ±0.82	-1.67 ±3.54	0.67 ±1.03	-1.00 ±1.58	-2.33 ±1.64	-1.00 ±0.89	-
Plant height(cm)	115.50 ±0.09	0.30 ±0.21	5.70** ±0.82	11.40** ±0.55	-0.80** ±0.26	-18.87** ±1.51	2.93** ±0.71	4.53** ±0.67	-3.93** ±1.26	-5.70** ±0.28	DE
Length of fruiting zone (cm)	48.10 ±0.16	2.37** ±0.24	4.41** ±0.82	5.00** ±0.80	3.95** ±0.28	9.43** ±1.20	-3.27** ±0.32	-11.17** ±0.48	-19.43** ±0.74	-2.50** ±0.40	CE
Primary branches / plant	5.00 ±0.11	-0.67** ±0.18	3.00** ±0.61	1.33* ±0.55	0.00 ±0.22	2.00* ±0.96	-1.67** ±0.39	-1.67** ±0.36	-4.67** ±0.66	-0.67* ±0.28	CE
Siliquae/plant	43.33 ±0.27	-2.33** ±0.35	12.67** ±1.41	10.00** ±1.28	-4.33** ±0.39	-18.67** ±2.14	0.00 ±0.92	8.67** ±0.66	-1.33 ±1.61	-5.00** ±0.64	DE
Siliqua length (cm)	5.03 ±0.03	0.32** ±0.06	2.80** ±0.25	2.03** ±0.20	0.73** ±0.13	-1.11* ±0.44	0.27 ±0.19	-1.19** ±0.23	-2.95** ±0.32	-1.01** ±0.10	DE
Seed yield / plant (g)	16.63 ±0.12	-0.36* ±0.17	4.46** ±0.65	-0.27 ±0.58	0.17 ±0.21	7.65** ±1.02	-3.52** ±0.40	-3..86** ±0.41	-7.11** ±0.77	0.13 ±0.29	CE
1000-seed weight (g)	3.80 ±0.01	-0.20** ±0.03	0.52** ±0.12	0.00 ±0.08	-0.42** ±0.04	1.90** ±0.23	-1.37** ±0.10	-0.53** ±0.11	-1.90** ±0.19	0.00 ±0.04	CE
Oil content (%)	44.12 ±0.01	1.31** ±0.04	3.27** ±0.11	2.85** ±0.09	0.81** ±0.05	-6.16** ±0.20	2.46** ±0.11	0.84** ±0.05	0.45** ±0.12	-1.43** ±0.04	DE

*, ** Significant at 5% and 1% level of significance, respectively; CE= Complementary epistasis and DE = Duplicate epistasis,

m=mean, d=additive, h=dominance, i=additive x additive, j=additive x dominance, l=dominance x dominance.

Table 5 Estimates of components of generation means for different traits, simple scaling test and type of epistasis in Ragni x NDYS-425 cross

Characters	Gene effects						Scales				Type of epistasis
	m	*d*	*h*	*i*	*j*	*l*	A	B	C	D	
Days to 50% flowering	45.67 ±0.16	-0.67 ±0.61	-0.67 ±1.40	0.00 ±1.39	2.67** ±0.64	-14.67** ±2.57	10.00** ± 0.96	4.67** ±0.85	14.67** ±0.77	0.00 ±0.69	-
Days to maturity	110.67 ±0.06	-0.67 ±0.63	9.67** ±1.39	12.00** ±1.29	0.67 ±0.79	-16.67** ±2.75	3.00** ±0.97	1.67 ±1.29	-7.33** ±1.09	-6.00** ±0.64	DE
Plant height (cm)	108.07 ±0.12	0.30 ±0.39	0.60 ±1.00	4.33** ±0.92	0.60 ±0.45	-6.27** ±1.81	1.57* ±0.76	0.37 ±0.67	-2.40* ±0.92	-2.17** ±0.46	-
Length of fruiting zone (cm)	47.13 ±0.15	0.37 ±0.25	4.39** ±0.85	5.00** ±0.80	5.58** ±0.32	-8.76** ±1.32	7.46** ±0.54	-3.70** ±0.48	-1.24 ±0.87	-2.50** ±0.40	DE
Primary branches / plant	5.33 ±0.06	-2.67** ±0.18	2..33** ±0.46	1.33** ±0.43	-2.67** ±0.20	-0.67 ±0.80	-3.00** ±0.25	2.33** ±0.35	-2.00** ±0.39	-0.67** ±0.21	-
Siliquae/plant	42.33 ±0.27	0.33 ±0.39	6.17** ±1.43	0.67 ±1.33	2.83** ±0.42	5.00* ±2.17	0.00 ±0.10	-5.67** ±0.82	-6.33** ±1.50	-0.33 ±0.63	CE
Siliqua length (cm)	4.95 ±0.06	0.32* ±0.13	0.58 ±0.36	0.66 ±0.35	0.21 ±0.14	0.31 ±0.60	-0.27 ±0.23	-0.70** ±0.19	-1.63** ±0.31	-0.33 ±0.18	-
Seed yield/plant (g)	16.86 ±0.11	-0.51* ±0.17	6.58** ±10.76	0.61** ±0.56	-1.57 ±0.21	7.71** ±0.67	-5.72** ±0.40	-2.59** ±0.34	-8.92** ±0.67	-0.30 ±0.28	CE
1000-seed weight (gm	3.80 ±0.01	0.00 ±0.05	0.85** ±0.12	0.40** ±0.11	-0.09 ±0.06	2.18** ±0.22	-1.37** ±0.08	-1.20** ±0.09	-2.98** ±0.10	-0.20** ±0.06	CE
Oil content (%)	45.29 ±0.03	0.13** ±0.01	-2.80** ±0.16	-2.60** ±0.12	0.27** ±0.07	1.07** ±0.20	1.04** ±0.03	0.49** ±0.14	4.13** ±0.19	1.30** ±0.07	DE

*, ** Significant at 5% and 1% level of significance, respectively; CE= Complementary epistasis and DE = Duplicate epistasis,
m=mean, d=additive, h=dominance, i=additive x additive, j=additive x dominance, l=dominance x dominance.

Table 6 Estimates of components of generation means for different traits, simple scaling test and type of epistasis in Ragni YST-151 cross

Characters	Gene effects						Scales				Type of epistasis
	m	*d*	*h*	*i*	*j*	*l*	A	B	C	D	
Days to 50% flowering	43.33 ±0.16	2.00* ±0.68	4.17* ±1.53	6.67** ±1.50	5.83** ±0.72	-20.33** ±2.85	12.67** ± 1.35	1.00 ±0.56	7.00** ±0.86	-3.33** ±0.75	DE
Days to maturity	116.33 ±0.40	0.33 ±0.78	-13.33** ±2.27	-7.33** ±2.25	3.33** ±0.83	-1.33 ±3.58	7.67** ±1.04	1.00 ±1.31	16.00** ±1.72	3.67** ±1.12	CE
Plant height (cm)	112.47 ±0.19	7.93** ±0.34	-14.45** ±1.07	-8.27** ±1.02	6.85** ±0.40	21.83** ±1.69	0.07 ±0.77	-13.63** ±0.41	-5.30** ±1.01	4.13** ±0.51	DE
Length of fruiting zone (cm)	50.67 ±0.15	2.02** ±0.38	-13.85** ±1.02	-11.43** ±0.98	8.17** ±0.42	10.10** ±1.73	8.83** ±0.65	-7.50** ±0.61	12.77** ±0.82	5.72** ±0.49	DE
Primary branches / plant	5.67 ±0.06	-1.00** ±0.25	-0.17 ±0.61	-2.00** ±0.56	-1.17** ±0.28	5.67** ±1.14	-3.00** ±0.31	-0.67 ±0.56	-1.67** ±0.56	1.00** ±0.28	-
Siliquae/plant	46.33 0.22	1.33** ±0.29	-8.50** ±1.09	-13.33** ±1.06	1.50** ±0.32	11.67** ±1.55	2.33** ±0.47	-0.67 ±0.53	15.00** ±1.02	6.67** ±0.53	DE
Siliqua length (cm)	4.80 ±0.07	-0.11 ±0.14	1.37** ±0.42	1.22** ±0.40	-0.86** ±0.15	-0.33 ±0.69	-1.31** ±0.30	0.42 ±0.18	-2.11** ±0.38	-0.61** ±0.20	-
Seed yield/plant (g)	15.94 ±0.11	-2.10** ±0.18	4.09** ±0.68	0.49 ±0.57	-2.32** ±0.27	10.20** ±1.12	-7.67** ±0.43	-3.02** ±0.54	-11.19** ±0.85	-0.25 ±0.29	CE
1000-seed weight (g)	3.70 ±0.03	-0.07 ±0.04	1.64** ±0.15	1.07** ±0.14	-0.35** ±0.05	0.49* ±0.22	-1.13** ±0.09	-0.43** ±0.08	-2.64** ±0.16	-0.54** ±0.07	CE
Oil content (%)	44.53 ±0.03	0.09 ±0.07	-0.48* ±0.20	-0.95** ±0.20	-0.42** ±0.07	-0.42 ±0.32	0.27* ±0.10	1.10** ±0.11	2.32** ±0.14	0.47** ±0.10	-

*, ** Significant at 5% and 1% level of significance, respectively; CE= Complementary epistasis and DE = Duplicate epistasis,
m=mean, d=additive, h=dominance, i=additive x additive, j=additive x dominance, l=dominance x dominance.

Table 7 Joint scaling test for seed yield and its components in three crosses of yellow sarson

Characters	χ^2 values		
	Pusa Gold × YST-151	Ragni × NDYS 425	Ragni × YST-151
Days to 50% flowering	143.09**	439.18**	151.02**
Days to maturity	4.84	130.16**	130.65**
Plant height (cm)	589.72**	25.78**	1225.25**
Length of fruiting zone (cm)	1005.99**	318.79**	647.95**
Primary branches / plant	51.97**	228.01**	114.79**
Siliquae/plant	340.60**	67.92**	241.29**
Siliqua length (cm)	144.24**	33.82**	79.91**
Seed yield/plant (g)	121.61**	248.69**	330.62**
1000-seed weight (g)	247.88**	954.16**	310.77**
Oil content (%)	1271.98**	2026.72**	342.12**

*, ** Significant at 5% and 1% level of significance, respectively

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Diversity analysis in parental lines of winter oilseed rape (*Brassica napus* L.)

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ABSTRACT

Genetic diversity is essential for crop genetic improvement. Genetic diversity among breeding lines helps breeders in selecting parents for hybrid production with maximum heterosis and combining useful genes in a genetic background. Twenty five genotype of *Brassica napus* from different places of the country were evaluated to study the diversity pattern among the genotypes. The genotypes were grouped into six clusters. The distribution pattern indicated that maximum number of genotypes 8 was grouped into the cluster II followed by cluster IV (6), and cluster I (5). Cluster V had 3 genotypes, cluster VI contained 2 genotypes while cluster III had only one genotype. The mode of distribution of genotypes from different geographic regions into various clusters was at random, indicating no association between geographical distribution of genotypes and the genetic divergence. The inter cluster distance in most of the cases was higher than the intra-cluster distance, indicationg wider genetic diversity among the accessions of different groups. The maximum intracluster distance (7.158) was observed for cluster I, the minimum intra cluster distance (2.642) was observed for cluster VI. The genotypes of cluster III and cluster VI exhibited maximum inter cluster distance (30.102) indicating higher genetic divergence and revealed that the genotypes Neelam and Sheetal were more divergent. Thus these genotypes may be used to produce superior hybrids and transgressive segregants with heterobeltiosis effects in rapeseed.

Keywords: *Brassica napus,* Diversity, Germplasm, Parental diversity, Rapeseed

Brassicas belonging to family Brassicaceae, and commonly known as rapeseed and mustard, are mostly grown for their oilseed. Rapeseed mustard group of crops are next to soybean in terms of area and production and rank first in terms of vegetable oil supply in India (Kumar *et al.,* 2017). *B. napus* L. is a relatively young species that originated in a limited geographic region through spontaneous hybridisations between turnip rape (*B. rapa* L. s.str.; AA, 2n=20) and cabbage (*B. oleracea* L. p.p.; CC, 2n = 18) genotypes (Kimber and McGregor, 1995). Today oilseed rape (*B. napus* ssp. napus) is the most important source of vegetable oil in Europe and the second most important oilseed crop in the world after soybean. Rapeseed and mustard, groundnut, linseed, castor all put together account of 13 per cent of the annual cropped area. In money value, the oilseed are only second to food grains and contribute about 10 per cent of the total agricultural income. Different oilseed crops grown in India account for more than 30 per cent of world acreage and 18 to 32 per cent of the world's annual oilseed production (Anonymous, 2004). The average productivity of this crop in India is very low due to natural calamities. In order to meet out the oilseed requirement of the increasing population development of high yielding varieties becomes essential (Singh *et al.,* 2016). Thus, in order to improve the productivity potential, a breakthrough would be desirable by way of increasing biological efficiency through hybridization followed by the selection in which diverse parents are used. The importance of genetic diversity for selection of parents for in autogamous crops such as *B. napus* to recover transgressive segregants has also been repeatedly emphasized and therefore, characterization of genetic divergence for selection of suitable and diverse genotypes should be based on sound statistical procedure such as D^2 statistic. There is a need to identify the genetically diverse accessions with desired genes for better utilization in crop breeding programme (Stokes *et al.,* 2010; Harper *et al.,* 2012). Keeping these in view, 25 *B. napus* germplasm accessions from different places of India were evaluated with the objective of identifying the genetically diverse genotypes for their further exploitation in rapeseed improvement programme.

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MATERIALS AND METHODS

The experimental material consists of 25 rapeseed germplasm were collected from NRCRM Bharatpur, Rajastan (Table 1). These genotypes were evaluated in a randomized complete block design with three replication during *rabi* season 2012-13 and 2013-14 at Agricultural Research farm of Narain College, Shikohabad (U.P.), India. Experimental plot consisted of 3 m long rows spaced 40 cm apart and plant within row were spaced 15 cm apart. The recommended agronomic practices were followed. Five plants from the middle row of each entry in each replication were randomly taken for recording observation on following ten quantitative characters i.e. plant height (cm), length of main raceme (cm), number of primary branches, number of secondary branches, number of siliquae on main raceme,

length of siliqua (cm), harvest index (%), 1000 seed weight or test weight (g), oil content (%) and seed yield per plant (g) were recorded. Mahalanobis (1928) D^2 statistic was employed to measure the genetic distance between the genotypes. The distance were estimated from the sample on the basis of p characters by the formula

$$D^2 p = \sum_{i-1}^{p} (\Delta ij)\, \Delta i \Delta j = where, \Delta ij\ is\ the$$

reciprocal of (ij), the pooled common matrix i.e., error matrix; i is the difference in the mean value for i^{th} character and j is the difference in the mean value for j^{th} character. The genotypes were grouped into number of clusters by Tocher's method as described by Rao (1952).

Table 1 List of genotypes collected from ICAR-NRCRM, Bharatpur, Rajasthan used in the study

Genotypes	
TERRI Unnat	PRM-101
Neelam	HNS-4
Sheetal	PBN-2001
NPJ-52	NUDB-42
RN-101	HNS-99(OE)3
OCN-3	CAN-138
TKG-G-16	PBN-2002
RTM-365	RGN-20
RKN-9806	NUDB-09
GSL-441	Phaguni
BCN-14	Shyamali
NUDB-38	TERI (00) R-985
GSC-5	

RESULTS AND DISCUSSION

A clear understanding of the extent of variability that prevails for each trait in germplasm is essential for the improvement of characters through selection. Moreover in hybridization programme where, selection of genetically diverse parent is important to obtain wide array of recombinants, the knowledge of genetic diversity among the accessions is necessary. The analysis of variance indicated the existence of significant amount of variability among the genotypes for all the traits (Table 2). The 25 genotypes were grouped into six clusters by using D^2 statistic in such a way that the genotypes within a cluster had a small or low D^2 value than those of in between the clusters. The composition of clusters has been presented in Table 3 and Fig. 1.

Cluster II had the maximum number of genotypes (8) followed by cluster IV (6) and cluster I (5). The minimum number of genotype was observed in cluster III in which only one genotype was included. The clustering pattern showed that genotypes collected from the same geographic region got distributed in several clusters. It might be due to selection differential and/or genetic drift under diverse environmental conditions within the same geographical region. This pattern of clustering further indicated that there was no association between geographical distribution of genotypes and genetic divergence. The maximum intra cluster distance (7.158) was observed for cluster I, the minimum intra cluster distance (2.642) was observed for cluster VI. The genotypes of cluster III and VI exhibited maximum divergence with inter cluster distance of 30.102 and also indicated that the genotypes Neelam and Sheetal were more divergent. Thus these genotypes may be used to produce superior hybrids and transgressive segregants with heterobeltiosis effects. Conversaly the members of II and IV were less divergent (intercluster distance, 5.214) than the other clusters (Table 4). The use of D^2 statistic in estimating genetic divergence in heterogenous populations and breeding material of different Brassica species has also been reported by Rezai and Saeidi (2005) and Lefort-Buson *et al*. (1982).

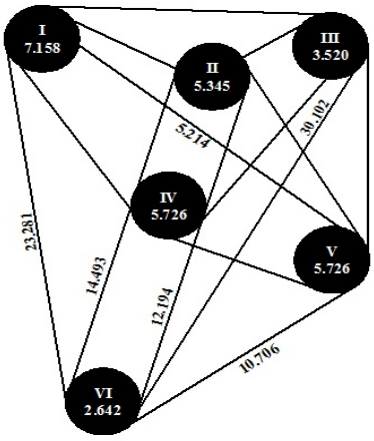

Fig. 1. Intra and inter cluster distance (D) in rapeseed germplasm

The relative importance of some yield components towards divergence may be understood by comparing the group means of these clusters. The group mean of ten characters were in accordance with the distance between the clusters (Fig.1). Means for primary branches was highest in cluster IV and lowest in the cluster II. Similarly the means for secondary branches was highest in cluster V and lowest in cluster I, but the mean for number of siliquae on main raceme was highest in cluster VI and lowest in cluster I. The genotypes grouped in cluster IV and V showed highest mean values for large number of yield contributing characters namely, length of main raceme, number of primary and secondary branches, number of siliquae on main raceme, length of siliqua, oil content per cent and seed yield. Therefore, estimates of present study concluded that the selection of parents for hybridization programmes from cluster IV and V might be beneficial as compared to parents taken from other clusters.

To summarize, a significant genetic variability existed among the 25 oilseed rape germplasm at morphological level. The information generated in the present study could be used in the future by breeders to select germplasms that can be used for rapeseed breeding programmes in order to obtain new hybrids with higher yield potential.

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Table 2 Analysis of variance for ten quantitative characters in *Brassica napus*

Source of variance	d.f.	Plant height (cm)	Main raceme length (cm)	No. of primary branches	No. of secondary branches	Siliquae on main raceme	Length of siliqua (cm)	1000-seed weight (g)	Oil content (%)	Seed yield per plant (g)	Harvest index (%)
Replications	2	30.00	0.94	0.89	4.48	0.98	0.52	0.01	0.12	0.65	0.91
Treatments	34	438.53**	97.73**	6.53**	281.57**	133.27**	0.56**	0.59**	14.03**	295.34**	4.84**
Error	68	7.66	3.32	0.11	2.48	2.97	0.03	0.03	0.48	2.40	0.09

**Significant at 1% level

Table 3 Distribution of 25 genotypes of *Brassica napus* into various clusters

Cluster	Numbers of genotypes	Name of genotypes
I	5	NPJ-52, RTM-365, RKN-9806, GSL-441, BCN-14
II	8	NUDB-38, PBN-2001, NUDB-42, HNS-99(OE)3, CAN-138, PBN-2002, TERI (00) R-985, HNS-004
III	1	OCN-3
IV	6	RN-101, TKG-G-16, GSC-5, PRM-101, RGN-20, NUDB-09
V	3	TERRI Unnat, Phaguni, Shyamali
VI	2	Neelam, Sheetal
Total	25	

Table 4 The inter and intra cluster average value of D^2 and D (given in parenthesis)

Cluster	I	II	III	IV	V	VI
I	7.158 (2.675)	11.614 (3.408)	29.246 (5.408)	14.183 (3.766)	24.079 (4.907)	23.281 (4.825)
II		5.345 (2.312)	17.573 (4.192)	5.214* (2.236)	10.804 (3.287)	14.493 (3.807)
III			3.520 (1.876)	18.293 (4.277)	16.663 (4.082)	30.102** (5.480)
IV				5.726 (2.393)	7.156 (2.675)	12.194 (3.492)
V					5.726 (2.393)	10.706 (3.272)
VI						2.642 (1.625)

* and ** denote lowest and highest intra and inter D^2 values, respectively.

Table 5 Character means in different clusters of *Brassica napus* genotypes

Cluster	Characters									
	1	2	3	4	5	6	7	8	9	10
I	182.45	65.15	6.68	18.94	44.09	4.64	7.05	6.27	41.72	36.11
II	189.15	61.73	7.62	23.88	50.28	5.73	5.73	5.97	40.45	25.30
III	180.63	67.67	8.50	36.27	46.93	4.00	5.36	6.45	38.50	31.07
IV	195.67	62.83	8.57	27.29	53.86	6.76	6.06	5.67	42.48	37.85
V	193.25	72.85	8.92	37.35	49.94	4.98	5.33	5.35	38.80	34.50
VI	196.32	60.82	8.85	30.17	54.58	5.00	7.25	5.62	39.26	28.13
G. Mean	189.57	65.17	8.19	28.98	49.94	5.18	6.13	5.88	40.20	32.16
C.V. (%)	6.27	8.09	17.28	34.36	13.16	8.58	20.13	7.40	4.95	33.31

1. Plant height (cm); 2. Main raceme length (cm); 3. Number of primary branches; 4. Number of secondary branches; 5. Siliquae on main raceme; 6. Length of siliqua (cm); 7. Harvest index (%); 8. 1000-seed weight (g); 9. Oil content (%); 10. Seed yield (g)

Table 6 Desirable genotypes for different traits in *Brassica napus*

Characters	Desirable genotypes
Plant height (cm)	TERI (00) R-985 (191.5), RGN-20 (190.1), PRM-101(186.2)
Main raceme length (cm)	NUDB-09 (76.5), RGN-20 (70.5), HNS-4 (66.8)
No. of primary branches	NUDB-09 (13.2), NUDB-42 (11.3), RTM-365 (10.3)
No. of secondary branches	PBN-2002 (31.1), RTM-365 (31.0), RKN-9806 (30.2)
Siliquae on main raceme	Shyamali (78.0), RN-101 (76.1), HNS-4 (69.2)
Length of siliqua (cm)	RN-101(7.7), NPJ-52 (7.5), Shyamali (7.3), RTM-365 (7.2)
Harvest index (%)	Neelam (11.52), RKN-9806 (11.31), GSC-5 (11.10)
1000-seed weight (g)	NUDB-09 (6.20). RGN-20 (5.20), Phaguni (5.20)
Oil content (%)	PBN-2002 (43.00), HNS-99 (OE)3 (42.85), TKG-G-16 (42.55), PBN-2001 (42.50)
Seed yield (g)	NUDB-09 (27.40), RGN-20 (22.80), NPJ-52 (22.10)

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NDSH 1012 (Prabhat) : A high yielding and high oil content sunflower hybrid suitable for Andhra Pradesh

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ABSTRACT

Sunflower is one of the most important edible oilseed crops in the world including India due to its wide range of adaptability and high oil content. The feasibility studies conducted at the time of introduction of sunflower cultivation in India indicated that Andhra Pradesh is ideally suited for growing sunflower. Though, a large number of private sector hybrids are available in the market, quality seed is always a question. Of late, AICRP on sunflower scheme at Regional Agricultural Research Station, ANGRAU, Nandyal, Andhra Pradesh has developed a sunflower hybrid 'PRABHAT' (NDSH 1012), which is a short duration and a high oil yielding and suitable for cultivation in Andhra Pradesh. It is a robust plant type, matures in 90-95 days with a yield potential of 20-25 q/ha (irrigated condition) and an oil content of 40-41%. In All India coordinated trials during *kharif* 2014 and *rabi* 2015-16, 'NDSH 1012' registered an increase of oil yield by 12.2 % and 5.3 % over national checks KBSH 44 and DRSH 1, respectively. Moreover, 'NDSH 1012' was found to be moderately resistant to downy mildew disease. Hence, it can be concluded that cultivation of 'NDSH 1012' can be a better option for improving the productivity of sunflower in Andhra Pradesh.

Keywords: High oil, High yield, Hybrid, Prabhat, Sunflower

Sunflower (*Helianthus annuus* L.; 2n=2x=34), being a day neutral crop can be grown in all seasons and is globally considered as an important edible oilseed crop next to soybean, rapeseed-mustard and groundnut (Vanitha *et al.,* 2017). In India, cultivation of sunflower crop was initiated in late 1960's with four promising introductions *viz.,* VNMIK 8931 (EC 68413), Peredovic (EC 68414), Armavirskii (EC 68415) and Armaverts (EC 69874) from USSR along with a Canadian introduction, Sunrise. Sunflower is highly cross pollinated crop and hence, ideal for heterosis exploitation. The development of commercial hybrids with high vigour was made possible with the discovery of cytoplasmic male sterility by Leclercq (1969) in the progeny of a cross between Helianthus petiolaris Nutt. and cultivated sunflower (cv. Armavirskii 9345) and identification of genes responsible for genetic restoration of fertility by Kinman (1970) in wild *Helianthus* spp. By using cytoplasmic male sterility, commercial hybrids were first developed in USA in 1972 and subsequently their cultivation extended to other parts of the world. In India, the first sunflower hybrid developed by using male sterility systems was BSH-1 (Seetharam *et al.,* 1980), that gave a fillip and renewed interest in improvement of the crop. The major sunflower growing states in India are Karnataka, Maharashtra, Andhra Pradesh, Tamil Nadu and area is picking up in North Eastern States like Odisha, Bihar and West Bengal. The feasibility studies conducted at the time of introduction of sunflower cultivation in India indicated that Andhra Pradesh (A.P.) is ideally suited for growing sunflower. In Andhra Pradesh, the crop is cultivated under an area of 0.22 lakh ha with an average production of 0.20 lakh tonnes and productivity of 909 kg/ha (Anonymous, 2018). It is grown under both rainfed and irrigated conditions. In rainfed situation, farmers are realizing poor yields owing to many abiotic factors, of which terminal stress during crop period is more prominent. Further, majority of the sunflower cultivated area is grown with hybrids with a crop duration of 105-110 days. These hybrids are prone to terminal stress, resulting in poor seed filling and thereby drastically reducing the seed and oil yields (Meena *et al.,* 2017). Under this situation, cultivation of hybrids with shorter duration can be one of the strategies to mitigate terminal stress condition. Hence, there is a need to develop high yielding hybrid with short duration. An attempt was made to develop a high seed and oil yielding short duration (90-95 days) sunflower hybrid, NDSH1012 (Prabhat) under All India Co-ordinated Research Project (AICRP) on sunflower scheme at Regional Agricultural Research Station (RARS), Nandyal of Andhra Pradesh.

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MATERIALS AND METHODS

The NDSH 1012 (Prabhat) was developed through hybridization between female parent NDCMS 30 A (high oil content) and male parent R 843 (proliferous pollen producer). The female parent was characterized with high seedling vigour, strong stem, broad leaves and with good nicking ability. The male parent was shorter, non branching, small leaves, pigmentation on stem and petiole.

Hybridization between these two parents was attempted during 2009-10 at RARS, Nandyal with the objective of development of high yielding and high oil content sunflower hybrid. The crossed product, NDSH 1012 (Prabhat) was tested in a hierarchy of initial, advanced, multilocation, AICRP trials and popularized in mini-kits and on farm trials against local popular sunflower hybrids during 2010 - 2016 (Fig.1). Further, the hybrid was subjected to DNA finger printing study with comparison to KBSH 44 and DRSH 1.

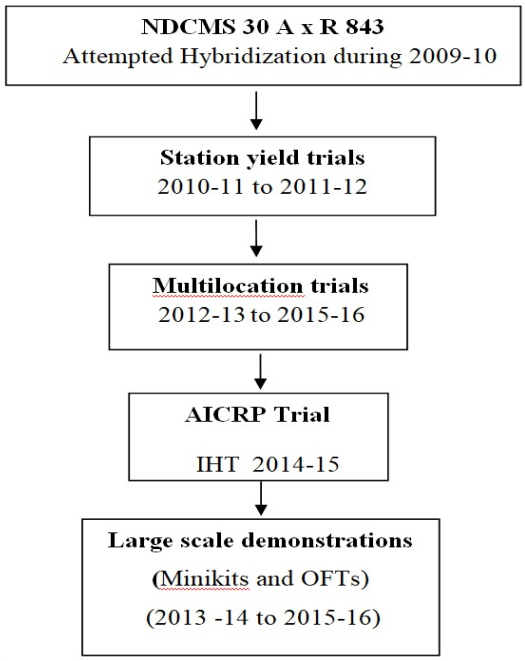


Fig. 1. Flow chart depicting details of evaluation development of NDSH 1012 in different trials

RESULTS AND DISCUSSION

The data of yield trials conducted during 2011-12 at RARS, Nandyal revealed that the highest seed yield was realized in NDSH 1012 (1910 kg/ha), which was 19.2 % and 38.2% higher than NDSH 1 (1597 kg/ha) and Kaveri (1382 kg/ha), respectively (Table 1). As a part of multilocation trials, NDSH1012 was tested for its performance in different districts of Andhra Pradesh for four consecutive years (2012-13 to 2015-16). The mean seed yield, averaged over the years, indicated that NDSH1012 resulted a maximum seed yield of 1989 kg/ha and was found to have an yield advantage of 35.2 %,49.1%, 14.2% and 3.7% over NDSH 1, Sunbred 275, DRSH 1 and KBSH 44, respectively (Table 2).

The performance of NDSH1012 in All India coordinated trials conducted during *kharif* 2014 revealed that NDSH 1012 resulted in the highest oil yield (705 kg/ha), which was 13.5 % and 3.1% higher over KBSH 44 (621 kg/ha) and DRSH1 (684 kg/ha), respectively. Moreover, the oil content noticed in NDSH 1012 (40.9%) was higher as compared to DRSH1 (40.4%) and KBSH44 (34.4%). Also, the performance of NDSH1012 in All India coordinated trials taken up during *rabi* 2015-16 in Zone V of Andhra Pradesh clearly showed that NDSH1012 out yielded compared to KBSH44 (National check for seed yield) by 2.4% for seed yield and DRSH1 (National check for oil yield) by 8.1% for oil yield.

In large scale demonstrations (Table 4), conducted at farmers fields for three consecutive years (2013-14 to 2015-16) as minikit entry NDSH 1012 registered a mean seed yield of 1563 kg/ha and was found to have an yield advantage of 12.8 % over the cultivated private hybrid checks. Whereas, in on farm trials conducted during 2015-16, NDSH1012 had an yield advantage of 15% than that of SB 275 and Kaveri hybrids grown by farmers. In addition, the results of All India coordinated trials conducted during 2014 indicated that NDSH1012 was moderately resistant to downy mildew; and low necrosis disease compared to the local popular private hybrid checks.

DNA finger printing: DNA fingerprinting studies were carried out at ICAR-IIOR, Hyderabad. The sunflower hybrid NDSH 1012 was subjected to molecular analysis using sunflower specific SSR markers as per the protocols. Molecular profiles of NDSH-1012 were compared with the check hybrids, DRSH-1 and KBSH-44.

A total of 120 SSR primers were tested on the 3 hybrids of which 30 primers showed polymorphism among the hybrids. From these 9 markers (ORS 203, OR S686, ORS 830, ORS 836, ORS 840, ORS 847, ORS 852, ORS 921, ORS 924) with good allelic variation among the hybrids were used to distinguish the three hybrids.

Seed production and distribution: The hybrid line, Prabhat (NDSH 1012) has been assigned with national identity, IC 618736 and its parental lines, NDCMS 30 A (IC 618737), NDCMS 30 B (IC 618738) and R 843 (IC 618739) by ICAR-NBPGR, New Delhi. The hybrid seed production was taken up by AICRP Sunflower Breeder and distributed to farmers for seed under front line demonstrations during 2016-17 and 2017-18.

Quality seed is the prime importance especially in sunflower. Although a number of private hybrids available in the market availability of quality seed is always a problem. The public sector short duration hybrid NDSH 1012 once released, would address the problem of terminal stress to some extent and increase productivity in rainfed situation. In public sector, till now KBSH 44 is the ruling hybrid, but has low oil content. On the other hand, DRSH 1 has high oil content but relatively lower seed yield. However, the newly developed hybrid NDSH1012 is out yielding over KBSH 44 for seed yield and DRSH1 for oil yield and hence, NDSH 1012 can be a better alternative for KBSH 44 and DRSH 1 in Andhra Pradesh.

Table 1 The growth parameters, yield attributes and seed yield of NDSH 1012, local check hybrids in advanced hybrid trial during ***rabi*** season (2011-12) at RARS, Nandyal

Character	NDSH 1012	Check 1 NDSH 1	Check 2 Kaveri	CD (P=0.05)
Days to 50% flowering	53	52	54	2.6
Days to maturity	85	82	84	2.6
Plant height (cm)	158	93	85	15.8
Head diameter (cm)	15.0	11.1	11.8	2.4
100 seed weight (g)	4.60	4.93	4.84	1.04
Volume weight (g/100 ml)	36.0	32.0	34.0	NS
Seed yield (kg/ha)	1910	1597	1382	302
		+ 19.6 % increase over NDSH 1		
		+ 38.2 % increase over Kaveri		

Table 2 Performance of NDSH 1012 in multilocation trials of Andhra Pradesh

Entry	Seed yield (kg/ha) (2012-13)				Per cent increase over check
	RARS, Nandyal	ARS, Utukur	ARS, Darsi	Mean	
NDSH 1012	1639	1849	1329	1606	
NDSH 1 ©	1306	1728	1343	1459	
SB 275 ©	1038	1784	756	1193	
Seed yield (kg/ha) (2013-14)					
	RARS, Nandyal	ARS, Utukur	RARS, Palem	Mean	35.2 % over NDSH 1
NDSH 1012	2299	1276	1666	1747	49.13 % over SB 275
NDSH 1	1044	765	1258	1022	14.15 % over DRSH 1
Seed yield (kg/ha) (2014-15)					3.65 % over KBSH 44
	RARS, Nandyal	ARS, Utukur	---	Mean	
NDSH 1012	1904	2839		2371	
KBSH 44	1404	3293		2348	
SB 275	344	2605		1474	
Seed yield (kg/ha) (2015-16)					
	RARS, Nandyal	ARS, Utukur	---	Mean	
NDSH 1012	1295	3173		2234	
KBSH 44	1059	3130		2094	
DRSH 1	1160	2753		1957	

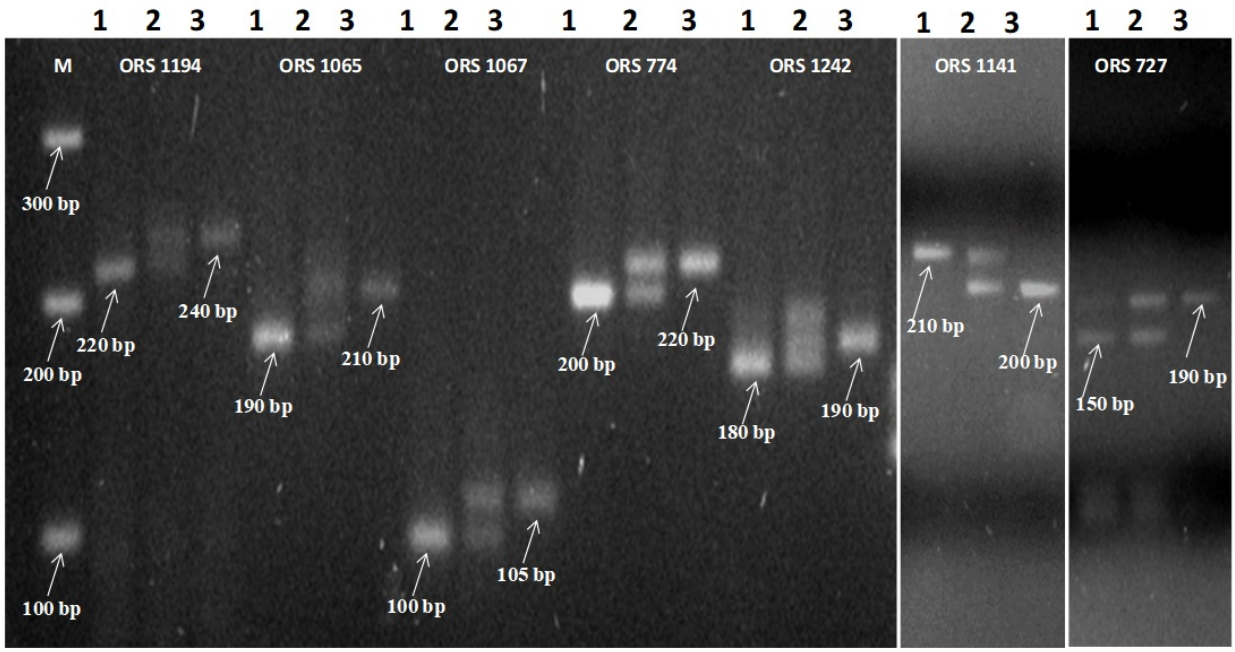
Table 3 Performance of NDSH 1012 in all India coordinated trials

Entry	Seed yield (kg/ha)		Mean	% increase over	Oil content (%)		Mean	% increase over	Oil yield (kg/ha)		Mean	% increase over
	2014 (*Kharif*)	2015-16 (*Rabi*)			2014 (*Kharif*)	2015-16 (*Rabi*)			2014 (*Kharif*)	2015-16 (*Rabi*)		
NDSH 1012	1558	2088	1823	+ 4.95 % over DRSH 1	41.1	38.9	40.0	+ 7.6 % over DRSH 1 + 19.76 % over KBSH 44	642	850	746	+ 5.37 % over DRSH 1
DRSH 1*	1532	1942	1737	- 2.0 % over KBSH 44	41.2	37.5	39.3		631	786	708	+ 12.2 % over KBSH 44
KBSH 44**	1682	2040	1861		31.7	35.0	33.4		586	744	665	

* National check for oil yield; ** National check for seed yield

Table 4 Performance of PRABHAT (NDSH 1012) in farmer's fields

	Year	Seed yield in farmer's field (kg/ha)		% increase over popular check
		NDSH 1012	SB 275/Kaveri	
Minikit	2013-14	1339	1183	13.0
	2014-15	1733	1566	10.67
	2015-16	1618	1409	14.0
	Average	1563	1386	12.8
OFTs	**2015-16**	**1621**	**1408**	**15.0**



Hybrid Purity confirmation of NDSH_1012 using sunflower specific SSR primers

1=NDSH-1012 A line, 2=NDSH-1012 Hybrid, 3=NDSH-1012 R line

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Evaluation of sunflower (*Helianthus annuus* L.) germplasm using multivariate statistical techniques

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ABSTRACT

Evaluation of sunflower hybrids using morphological data is necessary and essential in sunflower breeding programs. The aim of this paper was to evaluate the productive possibilities of some sunflower germplasm using multivariate technique. Fifty sunflower genotypes were characterized using eleven morphological traits. Among the traits studied, high coefficient of variation was observed for duration of reproductive phase (11.73%), seed yield per plant (11.49%), 100-seed weight (8.98%) and head diameter (8.33%). Agglomerative hierarchical clustering method classified the fifty genotypes into five clusters. A large number of genotypes were placed in cluster III (22) followed by cluster I (14), cluster II (6), cluster V (6) and cluster IV (2). The maximum inter-cluster distance of 47.83 was observed between clusters I and cluster IV indicating the possibility of high heterosis. The first four principal components showed 71.61% of the total variation. The genotype EC-512687 and EC-601746 had found top rank by both the methods. The results of PCA were closely in line with those of composite indices. These results can be used by breeders in sunflower breeding program.

Keywords: Morphological Variables, Composite Index, Cluster Analysis, PCA, Sunflower

Sunflower (*Helianthus annuus* L.) is one of the most important oilseed crops in the world because it is edible vegetable oil, after soybean and rapeseed (Hu *et al.,* 2010; Yadava *et al.,* 2012). Sunflower oil is widespread because of its high quality and is one of the five basic nutrients for human food (Kholghi *et al.,* 2011; Rani *et al.,* 2016; Vanitha *et al.,* 2017). Knowledge of diversity patterns allows the plant breeders to better understand the evolutionary relationships among accessions (Liu *et al.,* 2003). Future of breeding programs depends on the availability of genetic variability to increase productivity. According to Smith *et al.* (1991) the evaluation and characterization of morphological traits are the first and basic step in description of germplasm. A lots of research work have been done on evaluation and morphological characters in commercial cultivars of sunflower (Karaaslan *et al.,* 2010). Multivariate statistical techniques, which simultaneously analyze multiple measurements on each individual under investigation, are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections (Dong *et al.,* 2007). Multivariate analysis has been used frequently for genetic diversity analysis in many crops such as barley (Cross, 1992), sorghum (Ayana and Becele, 1999), wheat (Hailu *et al.,* 2006), peanut (Upadhyaya *et al.,* 2009) and vineyard peach (Nikolic *et al.,* 2010). Among the multivariate technique, cluster analysis, principal component analysis (PCA), principal coordinate analysis (PCoA) and multidimensional scaling (MDS) are most commonly employed and appear particularly useful (Grahic *et al.,* 2013). The aim of this paper was to evaluate the productive possibilities of some sunflower germplasm using multivariate technique.

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MATERIALS AND METHODS

Plant materials and experimental design: The present study comprised of 50 sunflower genotypes maintained at the Oilseed Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The experiment was laid out in a randomized complete block design (RBD) with three replications, in spring season (2015) having double row plot of 3.5 m length and maintaining row to row and plant to plant distance of 60cm and 30cm, respectively. All other cultural and agronomic practices were performed uniformly for all the experimental units. Data was collected after flowering and harvesting stage. Different morphological and agronomical traits that measured were; days to 50% flowering (days), duration of reproductive phase (days), days to maturity(days), plant height (cm), stem girth (cm), head diameter (cm), seed yield per plant (g), 100-seed weight (g), seed volume weight (g/100 ml), hull content (%) and oil content (%).

Data analysis: Descriptive statistics such as mean, Standard Deviation (SD) and Coefficient of Variation (CV) for each one of 11 studied traits were calculated. Composite Index (CI) for ranking of genotypes was calculated as method suggested by Narain *et al.* (1991). Smaller value of C.I. indicates the best genotypes while higher value indicates

poor genotypes. Cluster analysis (CA) and principal component analysis (PCA) were performed with statistical package programs XLSTAT-18.02 (2016). Clustering of genotypes into similarity groups was performed using Ward's hierarchical algorithm based on euclidean distances. In order to identify the patterns of morphological variation, principal component analysis (PCA) was conducted. Those PCs with Eigen values greater than one were selected, as proposed by Jeffers (1967). The first principal component has the largest possible variance because it accounts for much of the variability in the observed variables and each succeeding component has the highest possible variance under the constraint that it is orthogonal i.e., uncorrelated with the preceding components. The principal components are orthogonal because they are the eigenvectors of the covariance matrix, which is symmetric. A high value of the eigenvalue indicates a high variance of the data on the corresponding eigenvector.

RESULTS AND DISCUSSION

Descriptive statistics: Evaluation and characterization of morphological traits is the first and basic step in description of germplasm (Smith *et al.,* 1991). Descriptive statistics analysis such as mean, range, critical difference and coefficient of variation of the studied characters are given in Table 1. These value were in accordance as reported by Rani *et al.* (2017) and Supriya *et al.* (2016). Plant height, seed yield, and hull content had highest variation, which are in accordance as reported by Kholghi *et al.* (2011). The value for oil content was ranged from 27.35% to 45.81% and were in range as reported by Rani *et al.* (2017) but higher than reported by Supriya *et al.* (2016). In this study, the 100-seed weight ranged from 3.46 g and 6.47 g, respectively, with an average value of 4.93 g. The highest coefficient of variation correspond to duration of reproductive phase (11.73%), seed yield per plant (11.49%), 100-seed weight(8.98%) and head diameter (8.33%) while Nooryazdan *et al.* (2010) reported the highest coefficient of variation for seed weight, plant height, head diameter and sowing-flowering in oily sunflower types.

Cluster analysis indicates the extent of genetic diversity in the material that could be reflected towards the parental lines, which is of practical use in plant breeding (Sultana and Ghafoor, 2008). The association among different genotypes is presented in the form of dendrogram (Fig. 1). Hierarchical Cluster analysis in XLSTAT-18.02 programs package, classified the 50 sunflower genotypes into five groups (Table 2; Fig. 1). Most of the genotypes were included in cluster III and I (22 and 14 genotypes) followed by cluster II and cluster V (each with 6 genotypes). Two genotypes, EC-601875 and Nandyal-01, with poor mean value for seed yield, 100-seed weight and oil content constituted cluster IV as reported earlier by Kholghi *et al.* (2011). The statistical distances among the different clusters are presented in Table 3. The maximum inter-cluster distance was observed between cluster I and cluster IV (47.83), while the cluster III and cluster V were found more compact or homogeneous clusters having minimum distance (21.44). Crossing between individuals from clusters with maximum inter-cluster distance may result in high heterosis. The minimum cluster distance found between cluster III and cluster V suggested a close relationship between individuals placed in clusters. Such a narrow range of genetic variability among the lines within the clusters has been reported by earlier sunflower workers (Ramasubrhamanyam *et al.,* 2003; Srinivas *et al.,* 2006). The genotypes which are lying nearer to each other in the dendrogram are more similar to one another than those lying away from each other. The genotype CSFI-5304 found the extreme place from Nandyal-01 meaning that they had maximum genetic distance between them. Cluster I had higher values for days to maturity, plant height and head diameter. Cluster II had higher values for oil content, seed volume weight and days to flowering, whereas minimum for hull content. On other hand, cluster III had highest value for seed yield, and lowest values for stem girth. Thus, the genotypes with contrast mean performance from these clusters may be identified as potential parents and could be utilized in the development of new varieties.

Table 1 Descriptive statistics for different agro-morphological traits

Characters	Min.	Max.	Mean ± S.E.	C.D. (5%)	C.V. (%)
Seed yield per plant (g)	13.83	50.93	34.90 ± 2.32	6.50	11.49
Days to 50% flowering (days)	56.33	71.33	62.64 ± 2.38	6.67	6.57
Duration of reproductive phase (days)	10.97	19.67	15.36 ± 1.04	2.92	11.73
Days to maturity (days)	86.33	101.00	92.43 ± 2.41	6.76	4.51
Plant height (cm)	102.00	169.07	127.85 ± 2.27	6.38	3.08
Stem girth (cm)	5.67	8.73	7.42 ± 0.29	0.81	6.76
Head diameter (cm)	9.83	15.07	12.54 ± 0.60	1.69	8.33
100-seed weight (g)	3.46	6.47	4.93 ± 0.26	0.72	8.98
Seed volume weight (g/100 ml)	30.52	45.52	35.73 ± 0.86	2.42	4.18
Hull content (%)	31.13	65.70	49.34 ± 2.22	6.24	7.80
Oil content (%)	27.35	45.81	35.13 ± 0.67	1.87	3.28

Table 2 Cluster membership of 50 sunflower genotypes

Clusters	No. of genotypes	Name of genotypes
I	14	CSFi-5304, HB-15, RCR-39, HRHA-271-P3, MR-01, EC-601746, EC-512687, EC-512686, RHA-298-P3, IB-43, EC-152673, 1-OH-07-41, GPB-61, EC-601755
II	6	MSF-1-4, RHA-271, EC-601800, EC-601861, RHA-298 Early, MR-06
III	22	RHA-297-P3, HRHA-5-3, GPB-07, RHA-03, EC-601874, EC-601820, NDR-02, ACC-350-2, RHA-297-P2, EC-512681, GPB-51, RHA-856, RHA-274, LSF-902, 1-OH-07-45, NDLR-06, 1-OH-04-29, EC-512684, MSF-2-16, EC-601747, RHA-265, MSF-1-7
IV	2	EC-601875, Nandyal-01
V	6	IHT-298, AH-14, EC-601751, DRSF-160 R, IHT-201, IB-04

Table 3 Estimates of inter-cluster distances for 5 clusters in sunflower germplasm

Cluster	I	II	III	IV	V
I	0				
II	31.668	0			
III	30.822	25.439	0		
IV	47.834	34.381	29.438	0	
V	36.277	36.381	21.436	21.604	0

Principal Component Analysis (PCA): Principal component analysis was used to identify the most significant variables in the data set (Kholghi *et al.,* 2011; Tabrizi *et al.,* 2011). Arshad *et al.* (2010) reported that the principal component analysis could help in identification of best sunflower hybrids, which could contribute toward selection of genotypes. In the present study, using this analysis, four main components have been extracted with eigen value of more than one. They account for 71.61% of the total variability (Table 4; Fig. 2). The first main component (PC1) explaining 27.11% of total variation was positively correlated with plant height, days to maturity, days to 50% flowering, head diameter, stem girth and seed yield, and negatively correlated with duration of reproductive phase (Fig. 3).This implies that, genotypes with high values of PC1 have lower reproductive phase and *vice versa*. The second main component (PC2) accounted 20.10% of the total variation and was negatively associated with hull content, 100-seed weight, head diameter and seed yield, while positively associated with oil content, days to 50 % flowering and seed volume weight (Fig. 3). This means that, genotypes with high values of PC2 have lower number for hull content, higher oil content and days to 50 % flowering. In this condition selecting the genotypes for higher oil content is easy because both the main components had positive coefficients with oil content. Distribution of the fifty sunflower genotypes along with the first and second principal components based on measured morphological characters is presented in Fig. 4. Based on the principal component analysis and scatter plot, the genotypes ACC-350-02 (16), MR-01 (1), RHA-271 (3) and NDR-02 (24) had low PC1 values and high PC2 values. Out of fifty genotypes, only ten genotypes had positive values for both main components. Those genotypes were: MR-06 (12), GPB-51 (28), NDLR-06 (36), EC-152673 (37), EC-512681 (38), EC-512687 (41), EC-601746 (42), EC-601800 (46), EC-601861 (48) and EC-601847 (43). This means that these genotypes can be used in future exploitations.

Table 4 Principal component analysis of sunflower genotypes

Main components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalue	2.98	2.21	1.63	1.06	0.80	0.75	0.62	0.37	0.26	0.21	0.11
Variability (%)	27.11	20.07	14.81	9.63	7.26	6.83	5.66	3.39	2.35	1.88	1.02
Cumulative (%)	27.11	47.18	61.99	71.61	78.88	85.71	91.37	94.75	97.10	98.98	100.00

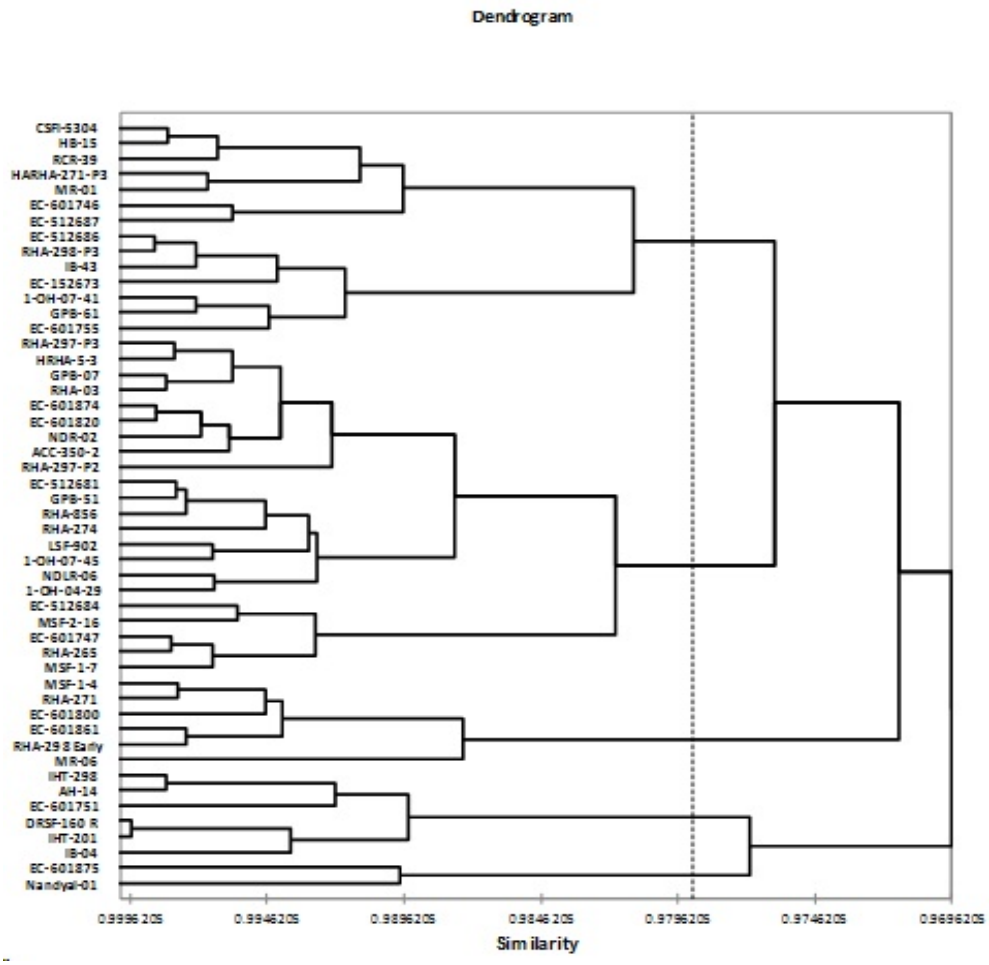

Fig. 1A. cluster diagram generated after hierarchical cluster analysis of the means for eleven morphological variables

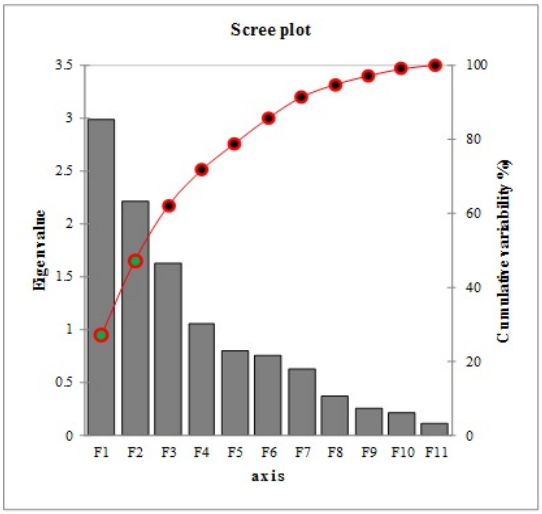

Fig. 2. Scree plot showing variation for different PC values

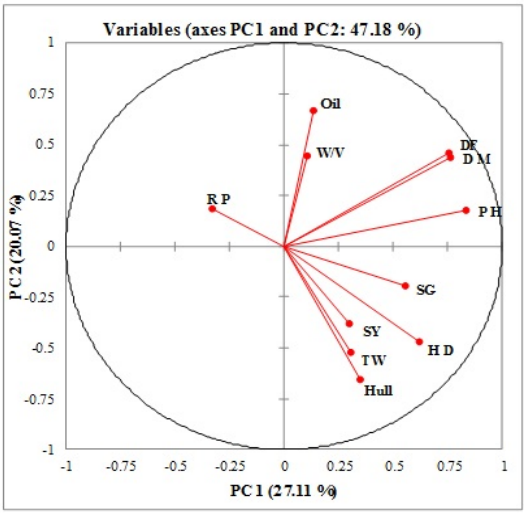

Fig. 3. Correlation between PC1 and PC2

Composite index (Genotypic index): The composite indices of sunflower germplasm have been worked out for yield and its attributing traits. The genotypes have been ranked on the basis of composite indices. The values of composite indices along with the rank of genotypes are given in Table 5, which indicates MR-06 (0.00) was the best genotype followed by 1-OH-07-41 (0.07), EC-512687 (0.07), EC-601746 (0.12) and EC-512681 (0.13), whereas genotype MR-01 (1.00) was in the last place preceded by ACC-350-2 (0.88), NDR-02 (0.83), Nandyal-01 (0.79) and RHA-297-P2 (0.78). The genotype HB-15 (0.51), EC-512684 (0.51) and RHA-274 (0.52) were found to be moderate genotypes.

In the present study, sunflower genotypes were also ranked on the basis of first PC scores. The values of first PC score along with the rank of genotypes are given in Table 6.The genotype EC-152673 was found to be the best genotype followed by EC-512687, EC-601746, EC-512686 and RCR-39, whereas genotype ACC-350-02 was in the last place followed by the MR-01, RHA-271, GPB-07 and NDR-02. Five genotypes namely, GPB-61, EC-512684, LSF-902, IB-43 and RHA-274 were found to be moderate genotype. The results of PCA were closely correlated with the results obtained from composite indices (and clustering pattern). On the basis of ranking from the both methods, the genotype EC-512687 and EC-601746 were among the top five genotypes, whereas the genotypes NDR-02, ACC-350-02 and MR-01 were found lowermost. On other hand, the genotypes EC-512684 and RHA-274 were found moderate in both the methods.

Table 5 Ranking of genotypes based on composite (genotypic) index

Genotypes	C.I.	Rank	Genotypes	C.I.	Rank	Genotypes	C.I.	Rank
MR-6	0.00	1	EC – 601820	0.46	18	IHT-298	0.65	35
1-OH-07-41	0.07	2	EC – 601800	0.47	19	RHA-265	0.65	36
EC – 512687	0.07	3	MSF-2-16	0.47	20	CSFI-5304	0.66	37
EC – 601746	0.12	4	EC – 601861	0.49	21	RHA-297-P3	0.67	38
EC – 512681	0.13	5	HRHA-5-3	0.49	22	IHT-201	0.72	39
EC – 152673	0.20	6	1-OH-07-45	0.51	23	GPB-07	0.72	40
EC – 601755	0.21	7	HB-15	0.51	24	IB-4	0.74	41
GPB-51	0.21	8	EC – 512684	0.51	25	DRSF-160 R	0.74	42
NDLR-06	0.24	9	RHA-274	0.52	26	EC – 601875	0.75	43
RCR-39	0.32	10	EC – 601751	0.55	27	HRHA-271-P3	0.76	44
EC – 601874	0.38	11	AH-14	0.55	28	RHA-271	0.77	45
GPB-61	0.38	12	MSF-1-7	0.57	29	RHA-297-P2	0.78	46
EC – 512686	0.38	13	1-OH-04-29	0.58	30	Nandyal-1	0.79	47
LSF-902	0.42	14	RHA-298 Early	0.58	31	NDR-2	0.83	48
RHA-298-P3	0.43	15	RHA-3	0.61	32	ACC-350-2	0.88	49
EC – 601747	0.44	16	RHA-856	0.62	33	MR-1	1.00	50
IB-43	0.44	17	MSF-1-4	0.63	34			

Table 6 Ranking of genotypes based on analyzed PC Scores of sunflower genotypes

Genotypes	PC Score	Rank	Genotypes	PC Score	Rank	Genotypes	PC Score	Rank
EC – 152673	4.47	1	EC – 601747	0.28	18	AH-14	-1.19	35
EC – 512687	4.25	2	EC – 601861	0.22	19	MSF-2-16	-1.24	36
EC – 601746	3.52	3	HB-15	0.18	20	RHA-856	-1.43	37
EC – 512686	2.76	4	IHT-201	0.17	21	RHA-265	-1.49	38
RCR-39	2.54	5	EC – 601874	0.17	22	IHT-298	-1.53	39
EC – 512681	2.24	6	GPB-61	0.02	23	RHA-297-P3	-1.62	40
1-OH-07-41	2.14	7	EC – 512684	-0.06	24	RHA-297-P2	-1.66	41
MR-06	2.14	8	LSF-902	-0.09	25	Nandyal-1	-1.69	42
EC – 601755	2.10	9	IB-43	-0.12	26	EC – 601875	-1.75	43
NDLR-06	1.37	10	RHA-274	-0.18	27	MSF-1-4	-1.86	44
CSFi-5304	1.26	11	IB-4	-0.37	28	HRHA-271-P3	-1.89	45
RHA-298-P3	1.22	12	EC – 601820	-0.37	29	NDR-2	-1.99	46
EC – 601800	0.95	13	RHA-3	-0.60	30	GPB-07	-2.15	47
1-OH-07-45	0.62	14	RHA-298 Early	-0.63	31	RHA-271	-2.22	48
1-OH-04-29	0.51	15	DRSF-160 R	-0.74	32	MR-01	-2.56	49
GPB-51	0.44	16	MSF-1-7	-0.87	33	ACC-350-2	-2.78	50
EC – 601751	0.38	17	HRHA-5-3	-0.89	34			

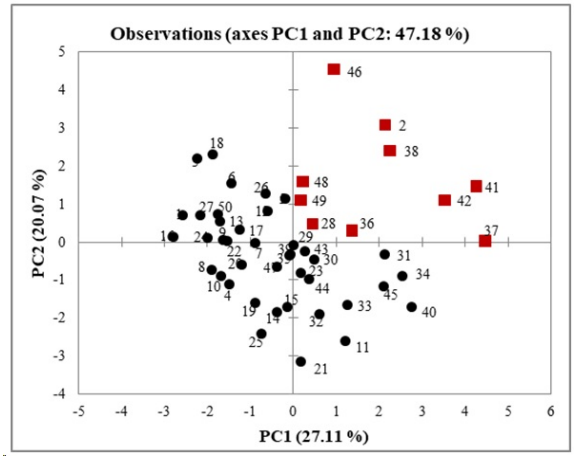

Fig. 4. Scatter plot of 50 sunflower genotypes using first and second components of PCA

A high genetic variability was observed in the fifty sunflower genotypes studied. It is suggested that, selection of parents for hybridization need to be based on genetic diversity. The maximum inter-cluster distance was observed between cluster I and cluster IV (47.83) and crossing between individuals from these clusters may result in high heterosis for yield and yield components traits. Among the fifty genotypes studied, ten had positive values for both the main components. The genotypes EC-512687 and EC-601746 were top ranked with both methods. These genotypes can be used in future breeding program.

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GNCH-1: a high yielding, wilt and leafhopper resistant castor hybrid suitable for Gujarat

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ABSTRACT

GNCH-1 a high yielding, wilt and leafhopper resistant castor hybrid was developed by Pulses and Castor Research Station, Navsari Agricultural University, Navsari, Gujarat and released by Central Sub-Committee on Crop Standards, Notification and Release (CVRC) of Variety for Agricultural Crops in 2017 for commercial cultivation under irrigated situation of Gujarat State, India. The hybrid GNCH-1 was developed by crossing a pistillate line SKP-84 with a male line DCS-94. On an average of 18 trials conducted for five years in south and middle Gujarat, the hybrid GNCH-1 recorded a seed yield of 2545 kg/ha which is 13.8, 35.9 and 31.0 per cent higher yield over the checks GCH-7, DCH-519 and DCH-177, respectively. The hybrid had long primary spike (64.8 cm), more numbers of capsules per primary spike (78.4), matures within 110-112 days and medium height (70-80 cm) which makes it suitable for easy harvesting. The oil content of the hybrid GNCH-1 (47.0 to 48.0 %) revealed that it is at par with the checks. The hybrid screened for wilt at national wilt sick plots showed resistance reactions (< 20%) to wilt. GNCH-1 screened against leafhopper using infester row method during 2014-17 showed resistant reaction to leafhopper (hopper burn grade 0 to 1 on 0-4 scale). The hybrid demonstrated in the farmers fields for two years (2016-18) showed higher seed yield than the existing cultivars. Due to plasticity for sowing time, this new hybrid is a suitable choice for the farmers of south and middle Gujarat under irrigated condition during late kharif and rabi seasons and paddy based cropping system.

Keywords: Castor, GNCH-1, Hybrid, Late *kharif,* Leafhopper, *Rabi,* Resistance, Wilt

Castor (*Ricinus communis* L.) is an industrially important non-edible oilseed crop belonging to the family Euphorbiaceae. Castor oil has diversified uses and has great value of foreign trade. In India, castor is mainly grown in Gujarat, Rajasthan, Andhra Pradesh and Telangana states, accounting for about 95 per cent of the area and production. Gujarat ranks first in area, production and productivity with 5.41 lakh hectares, 11.21 lakh tonnes and 2072 kg/ha, respectively during 2016-17 (DES, 2018). Gujarat state alone produces 80 per cent of the total castor of our country from about 67 per cent of the area with the highest productivity. Though northern and middle Gujarat region is the traditional castor growing belt, castor is also gaining popularity in south Gujarat due to high fertile soil, irrigation facility, suitable climatic condition and diversity of terrain.

Due to heavy rainfall and heavy black soil having poor drainage capacity, castor cultivation in *kharif* season is not possible in south Gujarat conditions. The other released hybrids grow very tall due to prolonged moisture retention in the soil. Therefore, farmers prefer late *kharif* or *rabi* season for castor cultivation in vacant field after *kharif* paddy. Further, the *kharif* paddy area in south Gujarat is more than 2.0 lakh hectares and castor will be the best alternative after *kharif* paddy. So, there was a need to develop suitable varieties/hybrids of castor for *rabi* season to meet the desired production levels. Wilt (*Fusarium oxysporum* f. sp. *ricini*) is the major constraint in castor cultivation in Gujarat area under irrigated conditions. Fusarium wilt occurs in castor plant at any time throughout growing period. The extent of seed yield loss ranges from 39 to 77 per cent depending upon the stage of the crop (Pushpavathi, 1995). Losses in yield were realized in all cultivated castor hybrids in Gujarat (Dange *et al.,* 1997) and as high as 85 per cent wilt incidence has been reported under North Gujarat conditions (Dange, 2003). Sucking insect pests *viz.,* leafhopper (*Empoasca flavescens*), whitefly (*Trialeurodes ricini*) and thrips (*Retithrips syriacus* and *Scirtothrips dorsalis*) are considered as serious concern to late *kharif* and *rabi* castor crops and yield losses to the tune of 12.4 to 15 per cent was reported from Gujarat (Patel *et al.,* 1999; Lakshminarayana and Duraimurugan, 2014; Patel *et al.,* 2015). Host plant resistance is an economical and environment-friendly method of insect pest and disease management. Resistance to insect pests and diseases should be given as much emphasis as yield to identify new varieties and hybrids for cultivation by the farmers (Sharma and Ortiz, 2002; Anjani *et al.,* 2014; Kavani *et al.,* 2016). Thus, castor hybrid GNCH-1 was developed which exhibited desirable features *viz*., high yielding, resistance to wilt and leafhopper and suitable for cultivation

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in south and middle-Gujarat for late-*kharif* and *rabi* season. The hybrid was released by CVRC for Agricultural Crops during 2017 for commercial cultivation under irrigated situation of Gujarat. The present paper deals with the development and evaluation of hybrid in multilocation trials.

MATERIALS AND METHODS

GNCH-1 was developed by crossing of wilt resistant pistillate line SKP-84 obtained from Castor and Mustard Research Station, SDAU, SK Nagar and male line DCS-94 from ICAR-Indian Institute of Oilseeds Research (ICAR-IIOR), Hyderabad during 2010-11 at Pulses and Castor Research Station, Navsari Agricultural University, Gujarat. The hybrid, GNCH-1 (NCH-1) was evaluated in preliminary station trial at Navsari during 2011-12 in RBD along with check hybrids to record various ancillary and yield contributing characters. Based on the best performance in the preliminary station trial, GNCH-1 was included in Initial Varietal Hybrid Trial under All India Coordinated Research Project on Castor (AICRP on Castor) during 2012-13. Due to its best performance, it was further evaluated in Advanced Varietal and Hybrid Trials during 2013-14 and 2014-15 at multi locations along with check hybrids. The hybrid was also evaluated for its yield potential along with check hybrids under State trials *viz*., Preliminary Varietal Hybrid Trial (PVHT), Small Scale Varietal Hybrid Trial (SSVHT) and Large Scale Hybrid Trial (LHT) during 2013-14 to 2015-16. Further the hybrid GNCH-1 was demonstrated in 5 adaptive trials and 10 FLDs on farmers' fields during 2016-18. The recommended packages of practices were followed while conducting the trials to raise a healthy crop. Yield potential and ancillary observations with respect to yield traits of GNCH-1 and the checks were recorded as described by AICRP (Castor) guidelines. The yield data was analyzed according to Panse and Sukhatme (1985).

Screening for wilt resistance of the hybrid was carried out during 2012-13 to 2014-15, along with wilt susceptible (JI-35) and resistant (48-1) checks and hybrid checks (DCH-177, DCH-519, GCH-7) under permanent wilt sick plots maintained at ICAR-IIOR, Hyderabad and Castor and Mustard Research Station, SK Nagar, Gujarat. The wilt incidence recorded as total plants and wilt infected plants at 30 days interval upto 150 and 180 days at ICAR-IIOR, Hyderabad and SK Nagar, respectively and per cent was calculated. Reaction of experimental material against wilt was categorized as per the scale given by Lakshminarayana and Raoof (2006). Based on the wilt incidence, the genotypes found free from wilt disease (0% wilt disease) were regarded as highly resistant. The cultivars with wilt incidence up to 20% were classified as resistant and those with more than 20% wilt incidence were considered as susceptible.

Screening of the hybrid and its parents against major insect pests was carried out using infester row method (Anjani *et al.,* 2018) along with susceptible checks (DPC-9, DCS-9 and DCS-107), resistant checks (M-574) and existing hybrid checks (DCH-519, DCH-177, GCH-7) during 2014-17 at three locations (ICAR-IIOR, Hyderabad; RARS, Palem and TCRS, Yethapur). Observations on incidence of sucking pests (leafhopper, thrips), defoliators (semilooper and spodoptera) and capsule borer on five randomly selected plants were recorded. The data on leafhopper were recorded on three leaves, representing top, middle and lower canopy of each entry and the respective hopper burn was recorded on 0-4 scale (Duraimurugan and Alivelu, 2017). Population of thrips was observed on the top most tender but not fully opened leaf and also on immature spikes. The absolute population of adult whitefly was recorded from fully developed top leaf. Absolute larval population of defoliators from each plant was recorded. Number of capsules damaged by the capsule borer was recorded from five randomly selected plants and then per cent capsule damage was worked out (Lakshminarayana, 2005; Duraimurugan and Lakshminarayana, 2016). The data was subjected to statistical analysis using AGRES statistical software. Following ANOVA, differences between datasets were determined using least significant difference at P = 0.05.

RESULTS AND DISCUSSION

The yield performance of castor hybrid GNCH-1(NCH-1) along with three check hybrids (GCH-7, DCH-519 and DCH-177) in the Initial Varietal Hybrid Trial (IVHT) and Advanced Varietal and Hybrid Trials (AVHT) under AICRP on Castor at multi locations during 2012-13 to 2014-15 is presented in Table 1. The hybrid GNCH-1 exhibited higher mean seed yield of 2848 kg/ha from 26 trials as compared with state and national check hybrids *viz*., GCH-7 (2679 kg/ha), DCH-519 (2564 kg/ha) and DCH-177 (2621 kg/ha) with an economic heterosis 6.3 per cent, 11.1 per cent and 8.6 per cent, respectively (Table 1). The hybrid was found promising in Preliminary Evaluation Trial (PET) conducted at Pulses and Castor Research Station, Navsari during 2011-12, where the hybrid out yielded the check GCH-7 by 40.5 per cent (Table 2). Hence, it was nominated in AICRP and state trials, simultaneously. During 2012-13, two trials conducted at Navsari centre *viz.,* IVHT and Pre Release Hybrid trial-I, the hybrid GNCH-1 produced 20.0 and 10.1 per cent more seed yield as compared to the check GCH-7.

In Pre Release Hybrid Trial-II and AVHT-I trials conducted during late *kharif*/*rabi* 2013-14, the hybrid surpassed the check GCH-7 by 5.8 and 20.3 per cent, respectively at Navsari centre (Table 2). In 2014-15, the hybrid was tested under various trials in South Gujarat i.e. Navsari (3), Vyara (1) and Achhalia (1). In AVHT-II,

SSVHT (state) and LHT (station) conducted at Navsari, GNCH-1 showed 24.5, 24.1 and 18.0 per cent increase over the state check GCH-7. In rest of the two locations i.e. Vyara and Achhalia in LHT trial the hybrid out yielded the check by 17.1 and 25.2 per cent, respectively (Table 2). In multiplications trial (LHT) 2015-16 at three locations, GNCH-1 surpassed the state and national checks viz., GCH-7, DCH-519 and DCH-177 by 11.8, 16.9 and 13.5 per cent, respectively. Thus, on an average of 18 trials conducted for five years in south and middle Gujarat, the hybrid showed 13.8, 35.9 and 31.0 per cent higher yield over the state check, GCH-7 and national checks DCH-519 and DCH-177, respectively. The hybrid had long primary spike (64.8 cm), more numbers of capsules per primary spike (78.4), matures within 110-112 days and medium height (70-80 cm) which makes it suitable for easy harvesting. A representative picture of the plants of the parents and the hybrid is given in Fig. 1. The data of oil content of the hybrid GNCH-1 (47.0-48.0 %) revealed that it is at par with the checks. GNCH-1 was tested in Adaptive trials and Tribal Sub-plan during 2016-17 and 2017-18 at Navsari, Surat, Bharuch, Vadodara and Narmada districts in farmers fields where it recorded overall 13.0 and 7.43 per cent increased yield over local check, respectively (Table 3). Castor is found more suitable and economical under south Gujarat due to its yield potential, low cost of cultivation and more economic returns (Patel, 2011). Local variety of castor grown in rice fallows on residual moisture is a common practice in south Gujarat. The crop survives without any additional inputs like nutrients, water and adoption of other cultural practices. Consequently, the average yield realized by the farmers is as low as 4 to 5 q/ha and most of the hybrids commonly grown by the farmers were developed for *kharif* season planting. Therefore, to over come these problems, GNCH-1 was developed suitable for late *kharif* and *rabi* seasons under irrigated areas of south and middle Gujarat. This hybrid gave significant higher yield than existing cultivars and has the potential to be replaced with the local cultivars for irrigated castor areas of south and middle Gujarat especially in *rabi* season.

Table 1 Yield (kg/ha) performance of NCH-1 (GNCH-1) at all AICRP (Castor) centers under irrigated condition (2012-2015)

Year	Trials	Centres	All India Irrigated (AICRP on Castor)					% Increase over		
			NCH-1	GCH-7	DCH-519	DCH-177	(P=0.05)	GCH-7	DCH-519	DCH-177
First 2012-13	PRE-Rel-I	Navsari	2471 (1)	2244(8)	1634(18)	1906(13)	612	10.1	51.2*	29.6
	IVHT	Navsari	2321(1)	1934(3)	1586(5)	1323(12)	417	20.0	46.3*	75.4*
		Derol	2924(1)	2329(5)	2053(10)	2320(6)	514	25.5*	42.4*	26.0*
		Anand	3764(3)	3807(2)	2234(14)	2572(11)	308	-1.1	68.5*	46.3*
		Bawal	2734(3)	897(16)	1425(10)	2901(2)	204	204.8*	91.9*	-5.8
		Junagadh	2645(6)	2922(2)	2848(3)	2270(15)	576	-9.5	-7.1	16.5
		Mandor	3061(13)	4859(1)	2999(14)	3214(12)	840	-37	2.1	-4.8
		Talod	2824(2)	2748(3)	1924(8)	1681(11)	397	2.8	46.8*	68*
		Mean	**2843**	**2718**	**2088**	**2273**	**-**	**4.6**	**36.2**	**25.1**
Second 2013-14	PRE-Rel-II	Navsari	1815(1)	1715(6)	1144 (13)	1357 (8)	415	5.8	58.7*	33.8*
	AVHT-I	Navsari	2426(1)	2016(7)	1795 (12)	1926 (10)	227	20.3*	35.2*	26*
		Bawal	2946(3)	2020(9)	2783 (4)	3105 (2)	309	45.8*	5.9	-5.1
		Junagadh	2409(5)	2707(2)	2698 (3)	2005 8)	478	-11.0	-10.7	20.1
		Mandor	4028(3)	3910(5)	4193 (1)	4001 (4)	273	3.0	-3.9	0.7
		SK nagar	3641(4)	3444(7)	3084 (7)	2897 (8)	NS	5.7	18.1	25.7
		Talod	3754(12)	3944(10)	4478 (8)	4753 (5)	880	-4.8	-16.2	-21.0
		Anand	2501(5)	2125(8)	2994 (1)	2833 (3)	364	17.7*	-16.5	-11.7
		Kanpur	890(4)	738(9)	700 (10)	906 (2)	100	20.6*	27.1*	-1.8
		Mean	**2712**	**2513**	**2652**	**2643**	**-**	**7.9**	**2.3**	**2.6**
Third 2014-15	AVHT-II	Navsari	2651(1)	2129(3)	2137(1)	2007(4)	325	24.5*	24.1*	32.1*
		Anand	3941(2)	3460(3)	2654(8)	3039(5)	488	13.9	48.5*	29.7*
		Bawal	2936(3)	2518(5)	3118(2)	3639(1)	356	16.6*	-5.8	-19.3
		Bhatapara	1647(4)	1586(7)	1695(2)	1611(6)	NS	3.8	-2.8	2.2
		Junagadh	3599(7)	4349(2)	4228(3)	3791(4)	397	-17.2	-14.9	-5.1
		Kanpur	1405(2)	1123(5)	1055(9)	1516(1)	256	25.1*	33.2*	-7.3
		Mandor	3216(4)	2970(6)	3245(3)	3347(2)	293	8.3	-0.9	-3.9
		SK nagar	4830(3)	4061(7)	4734(4)	4886(2)	622	18.9*	2.0	-1.1
		Talod	2669(7)	3092(5)	3234(3)	2550(8)	527	-13.7	-17.5	4.7
		Mean	**2988**	**2810**	**2900**	**2932**	**-**	**6.4**	**3.0**	**1.9**
		Over all mean (26)	**2848**	**2679**	**2564**	**2621**	**-**	**6.3**	**11.1**	**8.6**
		Frequency in top three groups	15/26	10/26	10/26	8/26	-	-	-	-

*Significant at 5%; Figures in parenthesis indicate ranking

The male parent DCS-94 was tested under sick plot conditions at IIOR, Hyderabad during 2013-14 and it showed resistant reaction of 10.1 per cent. The hybrid GNCH-1 was screened for wilt at national wilt sick plots where, it showed resistance reaction in IVHT, AVHT-I and II trials conducted at Castor and Mustard Research Station, SK Nagar and IIOR, Hyderabad from 2012-2015 (Table 4). The wilt incidence ranges from 9.3 to 19.6 per cent in GNCH-1 with an average of 14.2 per cent under sick plot of S.K. Nagar, Gujarat. The wilt incidence was 0.0 to 17.6 per cent in GCH-7 with an average of 10.8 per cent and disease incidence varied from 11.5 to 44 per cent with an average of 32.9 per cent in DCH-519. In resistant check 48-1 and susceptible check JI-35 recorded an average of 2.3 and 100 per cent wilt incidence, respectively. At sick plot of IIOR, Hyderabad the wilt incidence in GNCH-1 varied from 14 to 30.9 per cent with an average of 19.9 per cent, while disease ranged from 23.8 to 31.9 per cent in GCH-7 with an average wilt of 27.2 per cent. Wilt disease was 1.2 per cent in 48-1, resistant check however 100 per cent wilt recorded in susceptible check, JI-35 (Table 4). Wilt caused by *Fusarium oxysporum* f. sp. *ricini* is a devastating disease of castor. Chemical control of castor wilt is not effective and economical as the pathogen is soil and seed-borne in nature and difficult to eradicate. The use of wilt resistant cultivars is the best and cost effective method (Anjani *et al.,* 2014). GNCH-1 found resistant to wilt (wilt incidence up to 20%) under sick plots at SK Nagar and IIOR, Hyderabad. This hybrid has the potential to be replaced with the previously approved cultivars with resistance to wilt disease and higher yield parameters.

Table 2 Yield (kg/ha) performance of GNCH-1 in South and Middle Gujarat (2012-2016)

Year	Trial	Centre	Middle & South Gujarat					% Increase over		
			GNCH-1	GCH-7	DCH-519	DCH-177	(P=0.05)	GCH-7	DCH-519	DCH-177
2011-12	PET	Navsari	4549	3237	-	-	926	40.5*	-	-
2012-13	IVHT (AICRP)	Navsari	2321	1934	1586	1323	417	20.0	46.3*	75.4*
		Derol	2924	2329	2053	2320	514	25.5*	42.4*	26.0*
		Anand	3764	3807	2234	2572	308	-1.1	68.5*	46.3*
	Pre-Rel-I (ACIRP)	Navsari	2471	2244	1634	1906	612	10.1	51.2*	29.6*
		Mean	**3206**	**2710**	**1877**	**2030**	**-**	**11.3**	**52.9**	**41.4**
	Pre-Rel-II (ACIRP)	Navsari	1815	1715	1144	1357	415	5.8	58.7*	33.8*
2013-14	AVHT-I (AICRP)	Navsari	2426	2016	1795	1926	227	20.3*	35.2*	26.0*
		Anand	2501	2125	2994	2833	364	17.7*	-16.5	-11.7
	PVHT (State)	Anand	2331	3188	-	-	534	-26.9	-	-
		Mean	**2268**	**2261**	**1978**	**2039**	**-**	**0.3**	**13.6**	**10.2**
	AVHT-II	Navsari	2651	2129	2136	2007	325	24.5*	24.1*	32.1*
		Anand	3941	3460	2654	3039	488	13.9	48.5*	29.7*
	SSVHT (State)	Navsari	2789	2247	-	-	404	24.1*	-	-
2014-15	LHT(MLT)	Navsari	2271	1924	1490	1693	372	18.0*	52.4*	34.1*
		Vyara	1783	1523	949	792	280	17.1	87.9*	125.1*
		Achhalia	1477	1180	971	707	268	25.2*	52.1*	108.9*
		Mean	**2485**	**2077**	**1640**	**1648**	**-**	**19.7**	**47.8**	**47.2**
2015-16	LHT(MLT)	Navsari	2350	2095	1889	2050	304	12.2	24.4*	14.6
		Vyara	1825	1615	1624	1553	262	13.0	12.4	17.5*
		Achhalia	1626	1481	1451	1507	148	9.8	12.1*	7.9
		Mean	**1934**	**1730**	**1655**	**1703**	**-**	**11.8**	**16.9**	**13.5**
		Overall mean (18)	**2545**	**2236**	**-**	**-**	**-**	**13.8**	**-**	**-**
		Over all mean (15)	**2410**	**-**	**1774**	**1839**	**-**	**-**	**35.9**	**31.0**

*Significant at 5% level

The hybrid GNCH-1 (NCH-1) and its parental lines were screened against major insect pests of castor for three years (2014-15 to 2016-17) and the reaction of the hybrid and checks to major insect pests is presented in Table 4 and 5. GNCH-1 found resistant to leafhopper consistently for three years with hopper burn grade of 0 to 1 (on 0-4 scale) with lower leafhopper populations in the range of 0.5 to 14.0/3 leaves/plant, while the susceptible check (DPC-9) recorded hopper burn grade of 2 to 4 with higher leafhopper populations of 14.3 to 129.1/3 leaves/plant (Table 4). The

parental lines of GNCH-1 *viz.,* SKP-84 and DCS-94 were also exhibited resistance reaction to leafhopper with hopper burn grade of 0 to 2. The hybrid GNCH-1 was found promising against thrips and harboured low infestation of thrips (3.6 to 66.0 thrips/spike) as compared to susceptible checks *viz*., DCS-9 and DPC-9 (0.7 to 116.0 thrips/spike). No significant difference was observed in the population of whitefly among the hybrid and susceptible check (M-574). The reaction of GNCH-1 to defoliators *viz*., semilooper and spodoptera (0.0 to 14.5 larvae/plat) was found similar to the hybrid checks *viz*., DCH-519, DCH-177 and GCH-7 (0.0 to 13.0 larvae/plant). GNCH-1 recorded lower capsule borer damage (upto 24.3%) as compared to susceptible check, DCS-9 (upto 43.4%) (Table 5). One of the most limiting factors in the production of castor is the high incidence of insect-pests (Duraimurugan and Lakshminarayana, 2016). The problem of sucking pests *viz*., leafhopper, whitefly and thrips was reported to be high in Gujarat and Rajasthan (Patel *et al.,* 1999; Patel *et al.*, 2015). Resistant cultivars can be the simplest, practical, effective and economical method of insect pest control. The hybrid GNCH-1 found resistant to leafhopper provide an inherent control of the pest without any expenses or environmental pollution problems.

Table 3 Yield (kg/ha) performance of GNCH-1 in farmers fields at Gujarat (2016-2018)

Name of the village	Tahasil/Block	District	No. of demonstrations	Area in ha	Mean Yield kg/ha		
					GNCH-1	Farmers hybrid	Yield increase (%) over farmers hybrid
Year 2016-17 (Adaptive trial on GNCH-1)							
Arthan	Olpad	Surat	1	0.36	3380	2960	14.19
Bhatgam	Olpad	Surat	1	0.4	3860	3350	15.22
Navanagar	valiya	Bharuch	1	0.5	3580	3250	10.15
Satisana	Sinor	Vadodara	1	0.5	4120	3690	11.65
Kolasana	Maroli	Navsari	3	1	3120	2740	13.87
Mean					**3612**	**3198**	**13.0**
Year 2017-18 (FLD under TSP castor scheme)							
Almavadi	Dediapada	Narmada	10	4	2760	2370	16.46
Nivalda	Dediapada	Narmada	3	1.2	2640	2420	9.09
Khabji	Dediapada	Narmada	2	0.8	3000	2730	9.89
Ghankhetar	Dediapada	Narmada	3	1.2	2750	2470	11.34
Navagam	Dediapada	Narmada	1	0.4	2660	2400	10.83
Khurdi	Dediapada	Narmada	1	0.4	2260	2100	7.62
Gopaliya	Dediapada	Narmada	1	0.4	2100	1960	7.14
Khokaraumar	Dediapada	Narmada	1	0.4	2450	2280	7.46
Songam	Garudeshwar	Narmada	4	1.6	2390	2200	8.64
Sajanpura	Garudeshwar	Narmada	4	1.6	2500	2350	6.38
Mean					**2340**	**2178**	**7.43**

Table 4 Reaction of NCH-1 (GNCH-1) to wilt disease

Inoculation	Year of testing	Centre	Proposed hybrid	Check 1	Check 2	Check 3	Resistant check	Susceptible check
		IIOR, Hyderabad	NCH-1 (GNCH-1)	GCH-7	DCH-519	DCH-177	48-1	JI-35
Artificial (sick plot)	1st year (2012-13)		14.0	31.9	27.4	22.2	0.0	100
	2nd year (2013-14)		30.9	23.8	19.3	32.2	0.0	100
	3rd year (2014-15)		14.9	25.9	18.8	43.2	3.8	100
Fusarium wilt incidence (%)		Mean	19.9	27.2	21.8	32.5	1.2	100
		SK Nagar						
	1st year (2012-13)		13.7	17.6	44.0	34.6	6.8	100
	2nd year (2013-14)		9.3	0.0	43.3	57.7	0.0	100
	3rd year (2014-15)		19.6	14.8	11.5	36.4	0.0	100
		Mean	14.2	10.8	32.9	42.9	2.3	100

Scale: 0-20 % resistant, >20% susceptible

Table 5 Reaction of GNCH-1 (NCH-1) and its parents to sucking pests of castor (2014-15 to 2016-17)

Genotype	2014-15					2015-16						2016-17				
	Leafhopper				Thrips (No./ spike)	Leafhopper				Thrips (No./ spike)	Whitefly (No. of adults/leaf)	Leafhopper				Thrips (No./ spike)
	Yethapur		IIOR, Hyderabad			Yethapur		IIOR, Hyderabad				Yethapur		IIOR, Hyderabad		
	No./ 3 leaves /plant	Hopper burn (0-4 grade)#	No./ 3 leaves /plant	Hopper burn (0-4 grade)	Yethapur	No./ 3 leaves /plant	Hopper burn (0-4 grade)	No./ 3 leaves /plant	Hopper burn (0-4 grade)	Yethapur	Yethapur	No./ 3 leaves /plant	Hopper burn (0-4 grade)	No./ 3 leaves /plant	Hopper burn (0-4 grade)	Yethapur
NCH-1	5.2	0	8.5	1	3.6	15.3	1	14.0	1	65.0	4.0	0.5	0	3.9	1	13.8
SKP-84	5.0	0	16.6	2	7.1	5.6	0	12.0	1	107.0	2.0	5.5	0	5.5	1	1.5
DCS-94	5.3	0	9.8	1	6.9	14.3	1	13.1	1	38.0	2.0	7.7	0	6.3	1	2.2
DPC-9©	14.3	3	129.1	4	1.8	18.3	2	88.7	4	106.0	7.0	55.0	4	68.7	4	0.7
DCS-9©	5.7	1	19.7	3	5.9	2.3	0	43.4	3	66.0	5.0	0.0	0	24.1	3	6.7
DCS-107©	5.7	1	16.0	4	4.6	13.0	1	47.5	4	112.0	9.0	21.2	2	35.6	4	1.8
M-574©	-	-	-	-	-	12.3	0	11.2	1	66.0	4.0	0.0	0	8.2	0	4.2
GCH-7©	-	-	-	-	-	12.6	1	16.3	1	72.0	2.0	8.8	0	5.8	1	5.7
DCH-519©	4.7	0	8.3	1	2.4	9.3	0	17.0	1	70.0	2.0	0.0	0	8.9	1	0.7
DCH-177©	20.0	3	68.3	4	3.3	11.0	1	70.1	4	115.0	5.0	15.2	1	46.4	4	3.0
CD (P=0.05)	1.52	-	21.7	0.9	1.21	1.9	-			17.1	0.7	5.10	-	4.72	-	2.09

© Checks (Susceptible checks - DPC-9, DCS-9, DCS-107; Resistant checks - M-574; Hybrid checks - GCH-7, DCH-519; DCH-177)
#Hopper burn grade: 0 - No injury (Highly Resistant), 1- up to 10% (Resistant), 2 - 11 to 25% (Moderately Resistant), 3 - 26 to 50% (Susceptible), 4 - above 50% (Highly Susceptible)

Table 6 Reaction of GNCH-1 (NCH-1) and its parents to defoliators and capsule borer (2014-15 to 2016-17)

Genotype	2014-15						2015-16						2016-17	
	Defoliators (Larvae/plant)				Capsule damage (%)		Defoliators (Larvae/plant)				Capsule damage (%)		Defoliators (Larvae/plant)	
	Palem		Yethapur		Yethapur	IIOR, Hyderabad	Palem		Yethapur		Yethapur	IIOR, Hyderabad	Palem	
	Semi-looper	*Spodoptera litura*	Semi-looper	*Spodoptera litura*			Semi-looper	*Spodoptera litura*	Semi-looper	*Spodoptera litura*			Semi-looper	*Spodoptera litura*
NCH-1	0.9	0.7	1.6	1.4	6.4(14.6)	14.7(22.5)	0.9	0.9	0.0	0.0	5.4	24.3 (29.5)	14.5	0.9
SKP-84	1.3	0.3	1.6	1.0	7.4(15.7)	17.5(24.6)	0.9	0.4	0.0	0.2	0.0	42.1 (40.4)	10.1	0.5
DCS-94	0.8	0.3	1.3	0.6	7.5(15.9)	12.2(20.5)	1.2	0.4	0.0	0.2	3.2	40.6 (39.5)	15.2	1.0
DPC-9©	2.5	1.6	0.6	0.0	5.6(13.7)	10.5(18.9)	2.1	5.0	0.2	10.3	1.1	18.6 (25.6)	7.8	0.2
DCS-9©	1.4	0.9	1.0	0.1	5.4(13.5)	40.6(39.5)	1.1	1.0	0.0	0.0	1.3	43.4 (41.2)	8.3	0.4
DCS-107©	1.3	0.7	2.1	0.6	6.8(15.1)	11.5(19.8)	5.4	0.8	0.0	0.0	3.5	28.4 (32.1)	12.3	0.3
M-574©	-	-	-	-	-	-	3.4	0.8	0.0	0.0	10.7	29.8 (33.0)	9.2	1.1
GCH-7©	-	-	-	-	-	-	1.1	0.5	0.0	0.0	5.8	22.2 (27.9)	10.1	0.4
DCH-519©	0.9	0.4	1.1	0.6	9.3(17.7)	9.4 (17.9)	6.5	0.9	0.3	0.0	0.0	27.9 (31.7)	13.0	0.5
DCH-177©	2.6	1.6	1.1	0.1	8.0(16.5)	7.6 (16.1)	2.8	4.3	0.2	0.0	0.0	13.6 (21.6)	11.3	1.2
CD (P=0.05)	0.20	0.21	0.57	0.03	0.97	6.06	0.49	0.36	0.52	13.85	2.68	9.74	4.8	-

©- Check; #Figures in parentheses are arc sine values

Fig. 1. Representative plants of the hybrid, GNCH-1 and its parents, SKP-84 and DCS-94, at physiological maturity stage

In nutshell, the hybrid GNCH-1 (Gujarat Navsari Castor Hybrid-1) has high yield potential coupled with wilt and leafhopper resistance, plasticity for sowing time makes this hybrid a suitable choice for the farmers of south and middle Gujarat under irrigated condition during late *kharif* and *rabi* seasons. Thus, hybrid GNCH-1 was released by CVRC for Agricultural Crops, and notified vide S.O 2805 (E) dated 25/08/2017 for commercial cultivation under irrigated situation of Gujarat.

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Evaluation of sunflower hybrids for their suitability in North Eastern Hill Regions of India

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ABSTRACT

Five sunflower hybrids and a variety were evaluated in four different centres of North Eastern Hill (NEH) regions to study their suitability in terms of growth, yield and oil content to tap the potential rice fallow areas in NEH regions (Jharnapani, Medziphema, Tadong, and Lembucherra). Uniform layout was adopted at four locations to conduct field trials with RBD design. The soils of the region except Lembucherra were found to be acidic (ranged between 4.6 and 5.7 pH) and therefore requires regular lime application for obtaining high seed yields of sunflower. The location Tadong was on high altitude (1300 m MSL) and recorded less number of average sunshine hours (2.5 hours/day) during the sunflower crop period was responsible for lanky growth of sunflower with low oil content. However, Lembucherra was highly suitable for growing sunflower as weather conditions were highly favourable. Further, assessment of various growth and yield parameters it was found that average yield of sunflower in Tadong location was the highest (1814 kg/ha) but had low average oil content (28.6%) and attained average maturity in 135 days. While Lembucherra centre recorded seed yield of 1532 kg/ha with average oil content of 37.1 per cent and found to complete crop cycle at the earliest over other centres by attaining maturity on an average in 113 days. Among all the hybrids, DRSH-1 showed highest oil content in all the locations and mean value across the centres was 39.6 per cent.

Keywords: Hybrids, North Eastern Hill Regions of India, Suitability, Sunflower

Environmental variables, especially temperature is the key factor which affect plant growth, development and productivity (Kaleem *et al*., 2009). Differences in yield attributes to varying seasons might be due to the different climatic conditions that are based on temperature prevailing during the crop life cycle (KII and Altunbay, 2005). Most crop species are adapted to a particular set of temperature, as temperature is a major environmental factor that not only modifies plant phenology, but also causes many physiological and qualitative changes. Environmental variations affect crop growth, development, yield, oil and fatty acid accumulation through agronomic, physiological and qualitative functions of crop plant (Kaleem *et al.,* 2010). A number of plant's developmental and physiomorphic adaptations to the environment, influence sunflower yields and oil quality (Hassan *et al.,* 2005). Although, sunflower is temperate zone crop, it can perform well under various climatic and soil conditions. Sunflower is a C_4 plant having higher physiological activity but it is sensitive to cold temperatures, prevailing during autumn planting and is called a warm season plant when compared to C_3 plants (Bruder *et al.,* 2008). Sunflower growth and productivity is affected in relation to prevailing growing environment and crop will be influenced with the environmental variables like temperature, photoperiod, rainfall and relative humidity (Paramasivan and Selvarani, 2016). This study was thus, planned to investigate performance of sunflower hybrids with the objectives of assessing the growth parameters of sunflower hybrids in NEH region during rabi season, understanding location effect on yield parameters and oil content of sunflower and relating weather parameters for suitability of sunflower in NEH region.

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MATERIALS AND METHODS

The field trials aimed to evaluate five ruling hybrids (DRSH-1, KBSH-41, KBSH-44, KBSH-53 and LSFH-171) and a variety (DRSF-113) of sunflower hybrids for their suitability were conducted during November to April 2016-17 at 4 centres in NEH region after the harvest of the rice crop. Experiment was laid out in randomized block design with genotypes of sunflower as treatments and with three replications. The gross treatment plot measured 5.8 m x 4.8 m, with 9 rows and a spacing of 60 cm x 30 cm was adopted uniformly in all the locations. The site details are mentioned in Table 1. The soils of the region was either sandy loam or loamy sand type mainly dependent on land topography with steep slopes. The detailed initial soil fertility status of the four locations is shown in Table 1. The soils of all the centres were acidic in reaction (pH1:2.5) and low in

soluble salt content (EC1:2). The organic carbon content of all the soils was in the higher range i.e., > 0.75%, and highest value of 2.3% was recorded in the soils of Lembucherra, Tripura state followed by Medziphema (1.54%) Nagaland state. The available nitrogen content in the soils varied from a low value (188 kg/ha) in Jarnapani, Nagaland state to medium value (402 kg/ha) in Lembucherra, Tripura state and Tadong, Sikkim state. Soil in Jarnapani and Medzipherma had medium level of available phosphorus except in Tadong (48 kg/ha) and Lembucherra (59 kg/ha) which were high. Available potassium content was high in the soils of Tadong and Medziphema (i.e. > 260 kg/ha), medium in Lembucherra (between 110-260 kg/ha) and low in the soils of Jarnapani (i.e., <110 kg/ha). Sunflower was sown between last week of November 2016 and first week of December 2016 at all the four centres. The date of sowing and harvesting for each location has been depicted in Fig. 1. On the basis of initial soil test, fertilizers were applied to meet the nutrition requirement of sunflower @ 60:60:30 kg/ha NPK at all centres except in Tadong where nutrient requirement was met through only organics. The soils were acidic in nature and therefore uniform lime application was recommended @ 500 kg/ha. Hand weeding was carried out at 30 and 45 days after sowing followed by top dressing and earthing up. Irrigation and pest management was practiced based on their requirement. At maturity stage, growth and yield parameters were recorded. After harvest, in each treatment the test weight, plot yield and total yield were recorded. Oil content in the seed was analyzed by NMR equipment at Biochemistry laboratory at IIOR, Hyderabad. The data were tabulated and statistically analyzed adopting MSTAT programme to derive ANOVA for important variables (Freed and Eisensmith, 1986).

Table 1 Site details of experimental locations in NEH regions for evaluation of sunflower during 2016-17

Centre/Parameter	Jarnapani, Nagaland	Lambuchera, Tripura	Tadong, Sikkim	Medziphema, Nagaland
pH	5.40	5.95	5.74	4.60
EC (dS/m)	0.21	0.07	0.25	0.18
OC (%)	0.80	2.29	1.00	1.54
Av N (kg/ha)	188	433.5	402	288
Av. P (kg/ha)	20.0	58.8	48.0	19.2
Av. K (kg/ha)	48.0	132.2	324	257
Soil type	Sandy loam	Loamy sand	Loamy sand	Sandy loam
Latitude	25°45'24"N	23°54'46.34" N	27°32’ N	25° 45'43"N
Longitude	93°50'26"E	91°19'02.13" E	88°60’ E	95° 53'04"E
Altitude	295m	38 m	1300 m	310 m

RESULTS AND DISCUSSION

Meteorological data of trial centres in NEH Region: The standard meteorological data during the crop duration depicted in Figure 1(a-d) was obtained from all the four centres after the harvest of sunflower trials. The crop season at Jarnapani centre in Nagaland was between 49 and 14 standard meteorological weeks (SMW) during 2016-17. The average maximum and minimum temperature of this centre was 26.9° and 11.5° C and average maximum and minimum relative humidity was 93.6 and 49.2 percentage, respectively. The total rainfall during the crop period was 298 mm and most the rain was received between 10 and 14 SMW when the crop was in seed filling and maturity stages (Fig 1a). At Tadong centre in Sikkim, the crop period was between 49 and 22 SMW indicating the longest duration in NEH region. The mean maximum and minimum temperature of this centre was 22.7° and 12.3°C (Fig 1b). The maximum temperature throughout the crop period was below 30°C indicating the coolest weather among all the centres and prolonged growth period. The total rainfall of this location during crop period was 100.6 mm majorly distributed between 18 and 22 SMW. At Lambuchera centre in Tripura, the sunflower was grown between 49 and 19 SMW (Fig. 1c). The average maximum and minimum temperature of this location was 30° and 15.1°C and average maximum relative humidity was 75.5%. At initial stages, the crop was almost without rainfall. The actual rainfall was received between 13 and 18 SMW. The total rainfall received during sunflower crop period was 409 mm. The average sunshine hours at this centre was 6.0 hours, the maximum amongst all centres. At Medziphema in Nagaland, the sunflower crop was grown between mid of November 2016 and mid of April 2017. The mean maximum and minimum temperature of this location was 27.5° and 13.1°C, the maximum and minimum relative humidity was 93 and 52.3 percentages, respectively (Fig. 1c). The total rainfall received in the crop period was 492mm and the maximum amount was rain was received in March and April months during 2017.

Plant height: The data for plant height of sunflower hybrids grown at different locations in NEH region has been presented in Table 2. The trend in plant height of sunflower hybrids at 4 locations was in the following order

Lembucherra > Tadong > Medziphema > Jarnapani. At Jarnapani, non significant effect among the hybrids was noticed for plant height. At remaining three locations of NEH region, significant variation in growth of sunflower hybrids with respect to plant height was noticed. At Lembucherra, DRSH-1 was found to grow tallest (193cm) which was on par with KBSH-53 (187cm). At Tadong centre, hybrids KBSH-41 (175cm) and KBSH-53 (165cm) had grown tallest and were on par to each other. At Mezdiphema, though hybrid KBSH-53 had recorded 101cm plant height but the variation within the hybrids was found non-significant. Across the centres, KBSH-41 was tallest (126cm) and hybrid LSFH-171 (109cm) was shortest. The performance of sunflower crop as a whole in terms of plant height was compared across the NEH region and the tallest sunflower crop was noticed at Lembucherra location. This might be due to the fact that this location recorded about 6.0 hours of sunshine during the crop period.

Head diameter: The effect of locations on the growth and development of head diameter among sunflower hybrids was found significant in all centres except Medziphema (Table 2). At Jarnapani, though there was significance difference among the hybrids, the maximum diameter was recorded in DRSH-1 (11 cm) and minimum head diameter was recorded in LSFH-171 (6 cm). At Lembucherra centre the highest diameter was found in the hybrid KBSH-1 (17 cm) which was significant over KBSH-53 and LSFH-171 however it was found to be on par with DRSH-1 and KBSH-44. And this might be due to the fact that Lembucherra is located at an altitude of 86 m above MSL and received about 6 hours average sunshine during crop growth period. In Tadong centre the head diameter among different hybrids was above 11 cm. The highest head diameter of 19cm was recorded in KBHS-44 and LSFH-171 and was significantly higher over observed in DRSH-1 and KBSH-53. However, they were on par with KBSH-41 (18.6). Interestingly it was noticed that the head diameter of all the hybrids grown at Medziphema were above 15cm but there was no significant difference among them. Amongst all the hybrids, the top 3 hybrids in terms of head diameter across the centres were KBSH-44 (15.2 cm) followed by KBSH-41 (15.0 cm) and DRSH-1 (14.7 cm). The performance of sunflower crop as a whole in terms of head diameter was compared across the NEH region and the sunflower crop with largest head diameter was noticed at Medziphema > Tadong > Lembucherra > Jarnapani locations.

Maturity: It was essential to study the length of growing period to know the suitability of sunflower in NEH regions. Except in Medziphema centre, the sunflower hybrids showed variation in number of days to maturity at different locations (Table 3). Among all the hybrids, DRSH-1 recorded minimum number of days to mature across all the centres. All the hybrids showed more than 140 days to mature and for this character showed non significant variation at Medziphema, while, at Lembucherra most of the hybrid matured in 111 days (DRSH-1, KBHS-53 and LSFH-171). This may be due to the prevailing high temperature and sunshine hours during growth period (Fig. 1). The shortest duration for sunflower was noticed in Lembucherra centre with a mean maturity of less than 120 days for sunflower hybrids.

Seed yield and oil content: The performance of different sunflower hybrids in terms of seed yield was found significant and recorded variation in their oil content at different NEHR locations (Table 3). All the hybrids except KBSH-44 produced more than 15 quintals of seed yield per hectare at Tadong centre and the highest yield was recorded in KBSH-41 (2250 kg/ha). At Lembucherra centre, the seed yield ranged from lowest in KBSH-53 (1014 kg/ha) to highest in KBSH-41 (1932 kg/ha). This location also recorded highest oil content for different hybrids ranging between 33 % (in KBSH-44) and 41% (in DRSH-1). This may be due the fact that mean average weather conditions *viz*., minimum-maximum temperature, relative humidity and average sunshine hours (>5.5 hours) were more favourable compared to Tadong centre which had cold conditions and the maximum temperature during crop period was below 30°C (Fig. 1) and also had received low sunshine hours (2.5 hrs per day) during crop period. Similarly it was reported by Hassan et al. (2005), Kaleem et al. (2009) and Kumar et al. (2008). Though Jarnapani centre recorded low seed yield for hybrids, highest oil content of 41.8% (in DRSH-1) at this centre which might be due to high temperature prevailing in crop period. Such findings were also corroborated by Qadir et al. (2006). The performance of sunflower crop in terms of seed yield across NEH locations was in the following order: Tadong > Lembucherra > Medziphema > Jarnapani (Fig. 2d). Among all the hybrids, DRSH-1 showed highest oil content in all the locations and it might be due to the expression of its genetic trait as this hybrid has been reported to record highest oil content.

This study was conducted to evaluate sunflower hybrids in North Eastern Hill Regions to find the suitability for growing in the rice fallow areas. The potential of sunflower hybrids depends upon their performance in terms of growth, days to mature, seed yield and oil content as influenced by different locations. It was found that average yield of sunflower in Tadong location was highest (1814 kg/ha) but had low average oil content (28.6%) and it took on an average 135 days to mature. While Lembucherra centre recorded seed yield of 1532 kg/ha with average oil content of 37.1 per cent and completed maturity on an average in 113 days. Hence, in the present study, Lembucherra could be best suitable for tapping the potential of sunflower in rice fallow areas.

Meteorological data in standard meteorological week (SMW) and month wise of the trial centres at NEH Region

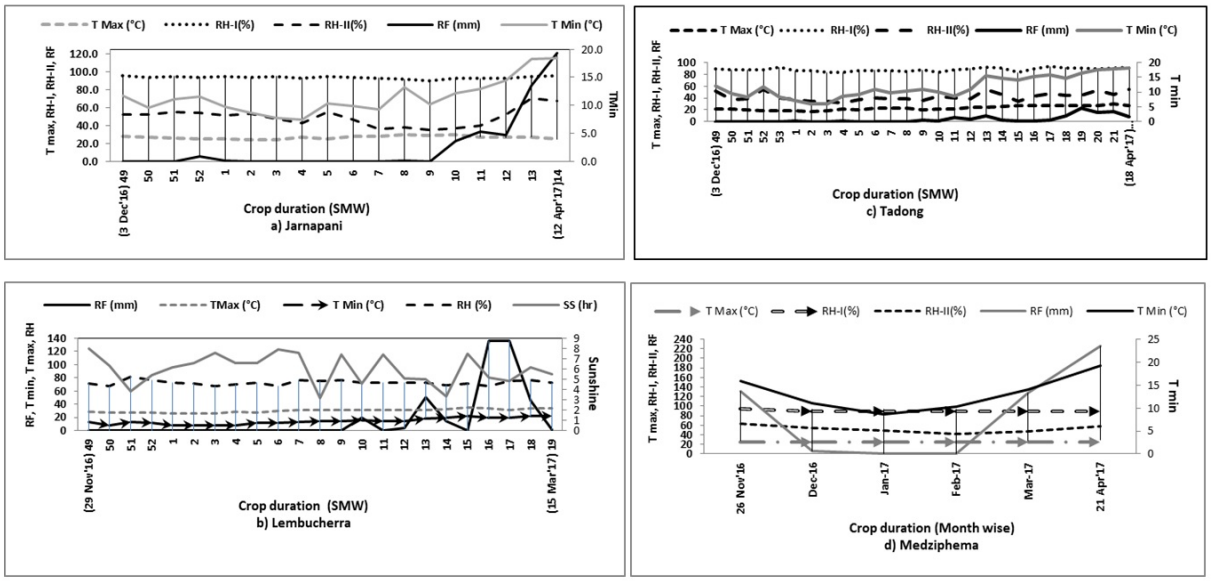

Fig. 1(a-d). Indicating the meteorological data at 4 locations in NEH regions during growth period of sunflower during 2016-17

Table 2 Plant height, head diameter and days to maturity of sunflower hybrids in different NEH Regions (locations)

Hybrid	Jarnapani			Lembucherra			Tadong			Medziphema		
	PH (cm)	HD (cm)	DM (days)	PH (cm)	HD (cm)	DM (days)	PH (cm)	HD (cm)	DM (days)	PH (cm)	HD (cm)	DM (days)
DRSH-1	53	11	127	193	15	111	135	15	134	92	18	151
KBSH-41	52	9	134	179	17	117	175	18.6	138	99	17	147
KBSH-44	55	10	130	167	15	117	165	19	137	90	17	144
KBSH-53	55	10	140	187	14	111	132	12	137	101	17	144
LSFH-141	53	6	130	154	14	111	146	19	135	86	16	148
Mean	53.6	9.2	132.2	176	15.0	113.4	150.6	12.9	136.2	93.6	17.0	146.8
CD (0.05)	NS	0.67	1.7	17.7	2.1	4.3	8.5	2.0	3.7	NS	NS	NS
CV (%)	6.35	4.1	0.72	9.4	8.8	3.2	2.7	6.1	2.1	10.5	16.4	11.4

PH = plant height; HD = head diameter; DM = No. days to maturity

Table 3 Effect of location on the seed yield of sunflower hybrids in NEH region

Sunflower (Hybrid/ Variety)	Medziphema (Nagaland)	Lembucherra (Tripura)	Tadong (Sikkim)	Jarnapani (Nagaland)	Pooled analysis for yield (across locations)
DRSH-1	1001.3 (39.6)*	1854.0 (41.0)	1970.0 (36.0)	848.0 (41.8)	1418.3
KBSH41	1142.6 (37.6)	1932.0 (39.0)	2250.0 (34.8)	1026.0 (40.0)	1587.6
KBSH44	1083.3 (31.1)	1633.0 (33.0)	1490.0 (28.4)	1426.0 (30.4)	1416.6
KBSH53	1219.6 (34.6)	1017.3 (38.9)	1520.0 (23.2)	1026.0 (39.6)	1195.7
DRSF113	972.3 (38.1)	921.0 (36.9)	1780.0 35.5)	833.0 (37.6)	1126.5
LSFH171	1019.3 (32.0)	1228.0 (33.4)	1840.0 (30.8)	709.0 (31.4)	1199.0
Mean	1073.0	1430.8	1808.3	983.7	--
SE m±	51.3	115.3	34.9	4.1	1.95
CD(P=0.05)	154	346	100	11.5	5.58
CV (%)	7.9	30.4	30	0.64	0.51

*Values in parentheses indicate percentage of oil content of pooled replication without statistical analysis

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Bio-efficacy and economics of newer insecticides against whitefly (*Trialeurodes ricini*) infesting castor

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ABSTRACT

A field experiment was conducted to evaluate the efficacy of newer insecticides against whitefly in castor during *kharif* season 2016 and 2017 at Tapioca and Castor Research Station, Tamil Nadu Agricultural University, Yethapur, Tamil Nadu. Based on whiteflies number/3 leaves/plant and per cent reduction over control recorded after two sprays concluded that all the treatments showed significant difference in reducing whiteflies over control. Among the insecticides, buprofezin 25 SC @ 0.8ml/l was found significantly most effective followed by profenophos 50 EC @ 2ml/l, imidacloprid 17.8 SL @ 0.5ml/l, dimethoate 30 EC @ 1.7ml/l and flonicamid 50 WG @ 0.2g/l for reducing the whiteflies population. Highest seed yield was obtained with buprofezin 25 SC @ 0.8 ml/l (2034 kg/ha) followed by flonicamid 50 WG @ 0.2g/l (1723 kg/ha) as against 694 kg/ha in untreated control. The maximum incremental cost-benefit ratio of 1: 16.74 was obtained with application of buprofezin 25 SC @ 0.8 ml/l.

Keywords: Bio-efficacy, Castor, Insecticides, Management, Whitefly

Castor (*Ricinus communis* L.) belonging to Euphorbiaceae family is an important industrially valued non-edible oilseed crop. Globally castor is cultivated in more than 30 different countries over an area of 14.48 lakhs hectare during 2014-15 with a production of 19.48 lakh tonnes and productivity of 1346 kg/ha. India is one of the world principal producers of castor, covering 9.16 lakh hectares area with an annual seed production of 11.20 lakh tonnes and an average seed yield of 1223 kg/ha representing 73 per cent of world castor production, followed by China (12 %) and Brazil (6.4 %) (Anonymous, 2016; Kathirvelan *et al.,* 2017). The average productivity is low in *rabi* season (309 kg/ha) in Tamil Nadu and other states in Southern and Central India due to castor whitefly with severe infestation is high during March - June (Rai, 1976). Both nymphs and adults suck sap mostly from under surface of the leaves and cause yellowing of leaves and stunting of plants in case of infestation. Sooty mould is developed on the honey secreted by the pest. The yield losses to the tune of 12.4 to 15 per cent due to whitefly were reported from Gujarat (Khanpara and Patel, 2002). Seed yield may be reduced in castor due to sooty moulds (Patel *et al.,* 1986). To overcome the problems of resistance and ensuring safety to natural enemy, identification of new chemical molecules with better insecticidal properties is a continuous process for integration in IPM (Venkataiah *et al.,* 2016). The present investigation was carried out to evaluate the efficacy of certain newer insecticides against the castor whitefly, *Trialeurodes ricini* (Homoptera: Aleyrodidae) with the capability of controlling the whitefly population throughout the cropping season and to bring out new insecticides with no harmful residual toxicity and lower environmental threat with newer compounds having novel modes of action to check infestation by this pest.

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MATERIALS AND METHODS

Field experiment was conducted at Tapioca and Castor Research Station, Tamil Nadu Agricultural University, Yethapur, Tamil Nadu during *kharif* 2016 and 2017 on the castor hybrid DCH-519 sown in plots of 5.4 m x 6.0 m with the spacing of 90 cm x 90 cm. The experiment was conducted in a randomized block design with ten treatments and three replications. Ten treatments included clothianidin 50 WDG @ 0.1 g/l, flonicamide 50 WG @ 0.2 g/l, acetamiprid 20 SP @ 0.2 g/l, thiamethoxam 25 WDG @ 0.4 g/l, imidacloprid 17.8 SL @ 0.5 ml/l, buprofezin 25 SC @ 0.8 ml/l, diafenthiuron 50 WP@ 0.8 g/l, profenophos 50 EC @ 2ml/l, dimethoate 30 EC @ 1.7 ml/l along with an untreated control. The treatments were imposed by using knapsack sprayer with 500 liters of spray solution per hectare. The crop received two sprays at 15 days intervals. Soil type in the experimental plot was red soil. Straight fertilizers of NPK were applied @ 60 kg N, 30 kg $P_2 0_5$ and 30 kg K_2O in the form of urea, single superphosphate and muriate of potash respectively. The entire dose of phosphate and potash and half the dose of nitrogen were applied before sowing by broadcasting and the remaining half of nitrogen at 30 days after sowing and proper plant stand was maintained. Observation for whitefly population at 1, 3, 7 and 14 days before and after the application of insecticides in randomly selected ten plants was observed and the average was worked out. The per cent reduction of pests over untreated control

was worked out by using the formula given by Henderson and Tilton (1955). The monetary returns and incremental cost-benefit ratios of treatment were also worked out for selecting economical treatment against the pests. All the above data were subjected to RBD analysis using AGRES package (Gomez and Gomez, 1984).

RESULTS AND DISCUSSION

Efficacy of newer insecticides against whitefly (*kharif*, 2016-17): Observation recorded before spraying of insecticides showed that the population of whitefly varied between 5.20/3 leaves/plant to 26.0/3 leaves/plant (Table 1). After first spray data revealed that buprofezin 25 SC @ 0.8 ml/l was most effective in reducing the whitefly population. It was reduced from 26.0 to 11.45 whiteflies/3 leaves/plant followed by profenophos 50 EC@2 ml/l which was found to reduce whitefly population from 24.20 to 11.65 whiteflies/3 leaves/plant in their population observed at 1, 3, 7 and 14 days after spraying as compared to conventional insecticide dimethoate 30 EC @ 1.7 ml/l in which reduction observed was from 14.0 to 6.20 whiteflies/3 leaves/plant.

Data of second spray revealed that buprofezin 25SC @ 0.8ml/l was found most effective in reducing mean population of whitefly from 14.0 to 7.35 whiteflies/3 leaves/plant at 1, 3, 7 and 14 days after spraying followed by profenophos 50 EC @ 2ml/l from 9.80 to 4.43 whiteflies/3 leaves/plant as compared to conventional insecticide dimethoate 30 EC @ 1.7 ml/l in which reduction was observed from 4.80 to 3.50 whiteflies/3 leaves/plant in mean reduction of whitefly population. Per cent reduction over control indicated that buprofezin 25 SC @ 0.8 ml/l reduced the whiteflies population upto 62.70 per cent closely followed by profenophos 50 EC @ 2 ml/l registered 62.40 per cent. Where as in clothianidin 50 WDG @ 0.1g/l, dimethoate 30 EC @ 1.7 ml/l, imidacloprid 17.8 SL @ 0.5 ml/l, thiamethoxam 25 WDG @ 0.4 g/l, acetamiprid 20 SP@ 0.2g/l, flonicamid 50WG @ 0.2g/l and diafenthiuron 50 WP @ 0.8 g/l recorded 61.80, 59.0, 58.90, 56.40, 56.30, 55.80, 51.50 per cent reduction of whiteflies over untreated control, respectively.

Efficacy of newer insecticides against whitefly (*kharif*, 2017-18): Observation recorded before spraying of chemicals showed that the population of whitefly was almost homogenously distributed throughout the experimental field and varied between 26.0 whiteflies/3 leaves/plant to 36.0 whiteflies/3 leaves/plant (Table 2). After first spray the trend was almost similar as that of the previous year. The data revealed that buprofezin 25 SC @0.8ml/l was most effective in reducing the whitefly population. It was reduced from 14.30 to 5.38 whiteflies/3 leaves/plant followed by profenophos 50 EC @ 2 ml/l which was found to reduce whitefly population from 25.50 to 10.15 whiteflies/3 leaves/plant in their mean population observed at 1, 3, 7 and 14 days after spraying as compared to conventional insecticide dimethoate 30 EC @ 1.7 ml/l in which reduction observed from 26.70 to 15.05 whiteflies/3 leaves/plant.

Data of second spray revealed that buprofezin 25 SC @ 0.8 ml/l was found most effective in reducing mean population of whitefly from 29.10 to 3.55 whiteflies/3 leaves/plant at 1, 3, 7 and 14 days after spraying followed by profenophos 50 EC @ 2 ml/l from 34.0 to 7.35 whiteflies/3 leaves/plant as compared to conventional insecticide dimethoate 30 EC @ 1.7 ml/l in which reduction was observed from 29.50 to 15.23 whiteflies/3 leaves/plant in mean reduction of whitefly population. Per cent reduction over control indicated that buprofezin 25 SC @ 0.8 ml/l reduced the whiteflies population upto 89 per cent followed by profenophos 50 EC @ 2 ml/l registered 84 per cent. Whereas in imidacloprid 17.8 SL@ 0.5ml/l, dimethoate 30 EC@ 1.7ml/l, flonicamid 50 WG@ 0.2g/l, acetamiprid 20 SP @ 0.2g/l, thiamethoxam 25 WDG @ 0.4g/l, clothianidin 50 WDG @ 0.1 g/l and diafenthiuron 50 WP @ 0.8 g/l recorded 82, 71, 67, 66, 62, 62 and 44 per cent reduction of whiteflies over untreated control, respectively.

Earlier, monocrotophos and dimethoate effective against whitefly (Patel *et al*., 1986). Buprofezin 25 SC was proved to be effective against nymphs and acetamiprid 20 SP, diafenthiuron 50 SC and imidacloprid 17.8 SL were effective against the whitefly adults on cotton (Amjad *et al.,* 2005).

Effect on yield and economics: The data on seed yield conclude that buprofezin 25SC @ 0.8 ml/l recorded significantly highest (2034 kg/ha) seed yield followed by flonicamid 50 WG @ 0.2 g/l (1723 kg/ha), imidacloprid 17.8 SL @ 0.5 ml/l (1618 kg/ha), thiamethoxam 25 WG @ 0.4 g/l (1592 kg/ha), profenophos 50 EC @ 2 ml/l (1512 kg/ha), dimethoate 30 EC @ 1.7ml/l (1472 kg/ha), clothianidin 50 WDG @ 0.1 g/l (1307 kg/ha), acetamiprid 20 SP @ 0.2g/l (1243 kg/ha) and diafenthiuron 50 WP @ 0.8 g/l (1110 kg/ha) (Table 3). The economics of the treatment presented in Table 5 conclude that the maximum net profit was obtained with buprofezin 25 SC @ 0.8 ml/l followed by flonicamid 50 WDG @ 0.2g/l, imidacloprid 17.8 SL @ 0.5 ml/l, thiamethoxam 25 WDG @ 0.4g/l, profenophos 50 EC @ 2 ml/l and dimethoate 30 EC @ 1.7 ml/l. Moreover, the highest Incremental Cost Benefit Ratio (ICBR) was obtained with buprofezin 25 SC @ 0.8 ml/l (1:16.74) followed by imidacloprid 17.8 SL @ 0.5ml/l (1:12.34), dimethoate 30 EC @ 1.7ml/l (1:9.11), profenophos 50 EC @ 2 ml/l (1:7.82), flonicamid 50 WG @ 0.2 g/l (1: 7.66), clothianidin 50 WDG @ 0.1g/l (1: 6.90), thiamethoxam 25 WDG @ 0.4g/l (1: 2.46), diafenthiuron 50 WP @ 0.8 g/l (1:4.14) and acetamiprid 20 SP @ 0.2g/l (1:2.46).

Table 1 Bioefficacy of newer insecticides against whitefly in castor (*kharif,* 2016-17)

Treatments	Dose	Mean population of whiteflies (Number per 3 leaves/plant)* 1st spray					Mean population of whiteflies (Number per 3 leaves/plant)* 2nd spray					Mean population of whiteflies (Number per 3 leaves/plant)* Pooled mean				
		PTC	1 DAT	3 DAT	7 DAT	14 DAT	PTC	1 DAT	3 DAT	7 DAT	14 DAT	PTC	1st spray	2nd spray	Pooled	PRC
T1-Clothianidin 50 WDG	0.1 g/l	14.50 (3.80)	10.50 (3.23)d	5.10 (2.26)	1.10 (1.05)	6.40 (2.53)	11.70 (3.41)	12.10 (3.47)	8.10 (2.84)	5.40 (2.32)	2.00 (1.41)	13.10 (1.41)	5.78 (2.27)	6.90 (3.01)	6.34 (2.64)	61.80
T2-Flonicamid 50 WG	0.2 g/l	26.00 (5.08)	23.40 (4.82)bcd	17.80 (4.22)	5.40 (2.32)	7.00 (2.64)	11.20 (3.34)	10.00 (3.15)	9.40 (3.06)	6.00 (2.45)	3.80 (1.95)	18.60 (1.95)	13.40 (3.50)	7.30 (3.00)	10.35 (3.25)	55.80
T3-Acetamiprid 20 SP	0.2 g/l	19.40 (4.39)	6.80 (2.60)cd	9.80 (3.13)	4.40 (2.10)	18.00 (4.24)	22.40 (4.72)	19.80 (4.44)	13.80 (3.71)	11.20 (3.34)	8.20 (2.86)	20.90 (2.86)	9.75 (3.02)	13.25 (4.05)	11.50 (3.53)	56.30
T4-Thiamethoxam 25 WDG	0.4 g/l	5.20 (2.27)	3.80 (1.94)d	2.00 (1.41)	0.40 (0.63)	7.60 (2.75)	9.20 (3.02)	7.60 (2.75)	5.60 (2.36)	2.80 (1.67)	1.80 (1.34)	7.20 (1.34)	3.45 (1.69)	4.45 (2.45)	3.95 (2.07)	56.40
T5-Imidacloprid 17.8 SL	0.5 ml/l	14.20 (3.76)	11.00 (3.31)ab	6.80 (2.61)	1.80 (1.34)	8.80 (2.96)	12.00 (3.45)	10.60 (3.25)	7.80 (2.79)	4.80 (2.19)	2.60 (1.61)	13.10 (1.61)	7.10 (2.55)	6.45 (2.92)	6.78 (2.74)	58.90
T6-Buprofezin 25 SC	0.8 ml/l	26.00 (5.08)	22.80 (4.76)a	9.40 (3.06)	4.20 (2.05)	9.40 (3.06)	14.00 (3.73)	12.20 (3.48)	10.20 (3.19)	4.80 (2.19)	2.20 (1.48)	20.00 (1.48)	11.45 (3.23)	7.35 (3.15)	9.40 (3.19)	62.70
T7-Diafenthiuron 50 WP	0.8 g/l	6.00 (2.44)	5.00 (2.23)d	3.00 (1.73)	0.40 (0.63)	8.00 (2.83)	13.80 (3.70)	12.80 (3.57)	8.80 (2.96)	6.00 (2.45)	4.40 (2.10)	9.90 (2.10)	4.10 (1.85)	8.00 (3.17)	6.05 (2.51)	51.50
T8 - Profenophos 50 EC	2ml/l	24.20 (4.91)	20.00 (4.46)ab	13.40 (3.66)	4.40 (2.10)	8.80 (2.96)	9.80 (3.12)	8.80 (2.96)	4.80 (2.19)	2.80 (1.67)	1.30 (1.14)	17.00 (1.14)	11.65 (3.29)	4.43 (2.49)	8.04 (2.89)	62.40
T9 - Dimethoate 30 EC	1.7 ml/l	14.00 (3.73)	12.20 (3.48)abc	8.80 (2.96)	3.60 (1.90)	0.20 (0.45)	4.80 (2.18)	4.60 (2.14)	4.60 (2.14)	3.80 (1.95)	1.00 (1.00)	9.40 (1.00)	6.20 (2.20)	3.50 (2.10)	4.85 (2.15)	59.00
T10 - Control	-	20.40 (4.50)	22.60 (4.74)d	25.20 (5.02)	36.60 (6.04)	53.00 (7.27)	57.80 (7.58)	64.00 (7.98)	66.00 (8.12)	66.00 (8.12)	60.00 (7.74)	39.10 (7.74)	34.35 (5.77)	64.00 (7.95)	49.18 (6.86)	-
SEd		0.31	0.27	0.12	0.09	0.14	0.32	0.31	0.15	0.14	0.12	0.32	0.16	0.18	0.17	
CD(P=0.05)		0.65	0.57	0.26	0.20	0.31	0.67	0.66	0.33	0.30	0.26	0.66	0.34	0.39	0.36	
CV%		9.53	9.47	5.18	5.97	5.76	10.32	10.46	5.85	6.19	6.75	9.93	6.60	7.31	6.95	

DAT= Days after treatment; PTC = Pre Treatment Count; PRC = Percent Reduction Over Control;
Figures in parentheses are square root transformed values; * Mean of three replications

Table 2 Bioefficacy of newer insecticides against whitefly in castor (*kharif,* 2017-18)

Treatments	Dose	Mean population of whiteflies (Number per 3 leaves/plant)* 1st spray					Mean population of whiteflies (Number per 3 leaves/plant)* 2nd spray					Mean population of whiteflies (Number per 3 leaves/plant)* Pooled mean				
		PTC	1 DAT	3 DAT	7 DAT	14 DAT	PTC	1 DAT	3 DAT	7 DAT	14 DAT	PTC	1st spray	2nd spray	Pooled	PRC
T1-Clothianidin 50 WDG	0.1 g/l	41.20 (6.40)	34.30 (5.84)	24.50 (4.95)	14.00 (3.74)	22.30 (4.72)	30.00 (5.46)	31.30 (5.58)	19.90 (4.46)	13.30 (3.64)	19.10 (4.37)	35.60 (5.93)	23.78 (4.81)	20.90 (4.51)	22.34 (4.66)	66
T2-Flonicamide 50 WG	0.2 g/l	27.10 (5.19)	25.90 (5.08)	21.80 (4.67)	9.90 (3.14)	13.90 (3.73)	26.00 (5.08)	22.90 (4.77)	17.20 (4.14)	9.30 (3.05)	10.70 (3.27)	26.55 (5.14)	17.88 (4.15)	15.03 (3.81)	16.45 (3.98)	67
T3-Acetamiprid 20 SP	0.2 g/l	33.50 (5.77)	33.30 (5.75)	28.90 (5.37)	16.80 (4.10)	19.90 (4.46)	32.00 (5.64)	30.30 (5.49)	24.30 (4.93)	16.20 (4.02)	16.70 (4.08)	32.75 (5.71)	24.73 (4.92)	21.88 (4.63)	23.30 (4.77)	62
T4-Thiomethaxam 25 WDG	0.4 g/l	32.60 (5.69)	34.30 (5.84)	26.30 (5.12)	20.90 (4.57)	20.40 (4.51)	36.00 (5.98)	31.30 (5.58)	21.70 (4.65)	20.20 (4.49)	17.20 (4.14)	34.30 (5.84)	25.48 (5.01)	22.60 (4.72)	24.04 (4.86)	62
T5-Imidacloprid 17.8 SL	0.5 ml/l	27.00 (5.18)	15.40 (3.91)	11.30 (3.36)	3.90 (1.97)	16.50 (4.06)	32.90 (5.72)	12.40 (3.51)	6.70 (2.59)	3.30 (1.82)	13.30 (3.64)	29.95 (5.45)	11.78 (3.33)	8.93 (2.89)	10.35 (3.11)	82
T6-Buprofezin 25 SC	0.8 ml/l	14.30 (3.77)	6.90 (2.62)	4.90 (2.21)	1.90 (1.38)	7.80 (2.79)	29.10 (5.38)	3.90 (1.97)	0.30 (0.55)	1.30 (1.14)	8.70 (2.95)	21.70 (4.58)	5.38 (2.25)	3.55 (1.65)	4.46 (1.95)	89
T7-Diafenthiuron 50 WP	0.8 g/l	26.50 (5.13)	37.60 (6.11)	35.60 (5.96)	29.70 (5.45)	24.20 (4.92)	32.70 (5.70)	34.60 (5.87)	31.00 (5.56)	29.00 (5.38)	20.80 (4.56)	29.60 (5.42)	31.78 (5.61)	28.85 (5.34)	30.31 (5.48)	44
T8-Profenophos 50 EC	2ml/l	25.50 (5.04)	11.70 (3.41)	13.50 (3.67)	5.60 (2.36)	9.80 (3.13)	34.00 (5.81)	8.70 (2.94)	8.90 (2.98)	5.20 (2.28)	6.60 (2.57)	29.75 (5.43)	10.15 (3.14)	7.35 (2.69)	8.75 (2.92)	84
T9-Dimethoate 30 EC	1.7 ml/l	26.70 (5.15)	17.90 (4.22)	4.30 (2.07)	22.80 (4.77)	15.20 (3.90)	29.50 (5.42)	14.90 (3.85)	11.70 (3.42)	22.20 (4.71)	12.10 (3.48)	28.10 (5.28)	15.05 (3.74)	15.23 (3.86)	15.14 (3.80)	71
T10-Control	-	31.00 (5.55)	39.60 (6.28)	61.90 (7.86)	62.60 (7.91)	71.10 (8.43)	31.90 (5.63)	36.60 (6.03)	57.30 (7.56)	62.10 (7.87)	68.20 (8.25)	31.45 (5.59)	58.80 (7.62)	56.05 (7.43)	57.43 (7.52)	-
SEd		0.54	0.49	0.42	0.34	0.33	0.44	0.37	0.19	0.18	0.18	0.49	0.40	0.23	0.31	
CD(P=0.05)		1.13	1.04	0.89	0.72	0.70	0.92	0.79	0.40	0.38	0.39	1.03	0.84	0.49	0.66	
CV%		8.19	8.20	8.50	8.98	8.97	9.71	10.12	5.71	5.84	5.57	8.95	8.66	6.81	7.74	

DAT= Days after treatment; PTC = Pre Treatment Count; PRC = Percent Reduction Over Control;
Figures in parentheses are square root transformed values; * Mean of three replications

Table 3 Effect of different insecticides on yield in castor

Treatments	Dose	Yield (kg/ha)		
		2016	2017	Pooled
T1-Clothianidin 50 WDG	0.1 g/l	1150	1463	1306.5
T2-Flonicamide 50 WG	0.2 g/l	1165	2281	1723.0
T3-Acetamiprid 20 SP	0.2 g/l	1270	1215	1242.5
T4-Thiomethaxam 25 WDG	0.4 g/l	1290	1893	1591.5
T5-Imidacloprid 17.8 SL	0.5 ml/l	1330	1905	1617.5
T6-Buprofezin 25 SC	0.8 ml/l	1480	2587	2033.5
T7-Diafenthiuron 50 WP	0.8 g/l	1105	1115	1110.0
T8-Profenophos 50 EC	2ml/l	1427	1597	1512.0
T9-Dimethoate 30 EC	1.7 ml/l	1390	1554	1472.0
T10-Control	-	670	717	693.5
SEd		188.2	259.5	219
CD(P=0.05)		395.3	545.3	460
CV%		18.8	19.5	18.8

Table 4 Effect of different insecticides on economics in castor

Treatments	Yield (kg/ha)	Increase in yield over control (kg)	Increase in yield over control (%)	Cost of increased (₹) (A)	Plant protection cost * (₹) (B)	Net profit (₹) A-B	ICBR
T1-Clothianidin 50 WDG @ 0.1 g/l	1306.5	613.0	46.9	24520	3100	21420	6.90
T2-Flonicamide 50 WG @ 0.2 g/l	1723.0	1029.5	59.7	41180	4754	36426	7.66
T3-Acetamiprid 20 SP @ 0.2 g/l	1242.5	549.0	44.1	21960	6340	15620	2.46
T4-Thiomethaxam 25 WDG @ 0.4 g/l	1591.5	898.0	56.4	35920	4800	31120	6.48
T5-Imidacloprid 17.8 SL @ 0.5 ml/l	1617.5	924.0	57.1	36960	2770	34190	12.34
T6-Buprofezin 25 SC @ 0.8 ml/l	2033.5	1340.0	65.8	53600	3020	50580	16.74
T7-Diafenthiuron 50 WP @ 0.8 g/l	1110.0	416.5	37.5	16660	3240	13420	4.14
T8-Profenophos 50 EC @ 2ml/l	1512.0	818.5	54.1	32740	3710	29030	7.82
T9-Dimethoate 30 EC @ 1.7 ml/l	1472.0	778.5	52.8	31140	3080	28060	9.11
T10-Control	693.5	-	-	-	-	-	-
SEd	259.57	-	-	-	-	-	-
CD (P=0.05)	545.35	-	-	-	-	-	-
CV %	19.47	-	-	-	-	-	-

Market price of castor: ₹40/kg; Standard spray volume: 500 lit/ha; * Labour charges included ; ICBR = Net profit/Plant protection cost

The results conclude that buprofezin 25 SC @ 0.8ml/l was significantly most effective followed by profenophos 50 EC @ 2ml/l, imidacloprid 17.8 SL @ 0.5ml/l, dimethoate 30 EC @ 1.7ml/l and flonicamid 50 WG @ 0.2g/l for reducing the whitefly population. However the highest Incremental Cost Benefit Ratio (ICBR) was recorded with buprofezin 25 SC @ 0.8 ml/l followed by imidacloprid 17.8 SL @ 0.5ml/l

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Character association and path coefficient studies on capsule shattering related traits and yield attributing character in sesame

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ABSTRACT

Thirty five sesame genotypes were evaluated for the estimation of heritability, correlation, path analysis and genetic divergence for twenty traits. High estimates of heritability were recorded for all characters. High heritability coupled with high genetic advance was recorded for characters capsule split before drying, retained seed weight, unattached and retained seed number. Seed yield showed a highly significant and positive correlation with branch number per plant, capsule number per plant, 1000-seed weight, unattached and retained seed number. The character potential seed weight contributed maximum towards genetic divergence. From the combined results of correlation coefficient and path analysis, it was observed that branch per plant; capsules per plant, 1000-seed weight, unattached and retained seed number are the major yield contributing characters to be given selection pressure for improving yield. Also the genotypes possessing combination of above characters should be used in a breeding program for obtaining desirable high yielding segregants.

Keywords: Capsule shattering characters, Genetic divergence, Path analysis, Sesame

In India most of the commercial sesame (*Sesamum indicum* L.) varieties are of indeterminate growth habit with continuous flowering. The plant continues to flower even when the earliest set capsules at the lower portion of the plant are mature which leads to non-synchronous maturity of the capsules and shattering of seeds in the field (Weiss, 1971; Ashri, 1989; Parameshwarappa, 2017). Sesame genotypes having higher seed retention capacity will delay opening of mature capsules in the field but release seeds easily on threshing (Langham, 1998). Such genotypes will reduce seed loss due to shattering in the field. Hence information on the association of capsule shattering characters with seed yield will be of great importance to breeders in selecting and developing desirable semi shattering genotypes.

Path coefficient analysis is an effective mean to find out the direct and indirect effects of various components on a dependent variable like seed yield (Sumathi *et al.,* 2007). Although a large number of studies have been carried out dealing with correlation and component analysis for agronomic characters in sesame no studies on aspect of capsule characters related to shattering are available in literature. Further, information on cause and effect analysis involving capsule shattering characters which determine the seed yield is scanty. Also, among the several methods of multivariate analysis available to study the genetic divergence in biological population, the D^2-analysis (Mahalanobis, 1936) has been a perfect test in the quantitative estimation of genetic diversity. In view of the aforesaid, the present investigation was undertaken with the objective to have information on direct and indirect effects of agronomic and capsule characters related to shattering on seed yield. Also studies were done to estimate the available genetic variability in the sesame genotypes.

The material for the present investigation comprised thirty five sesame genotypes of diverse genetic background grown in a Randomized Complete Block Design with three replications under rainfed conditions during *kharif,* 2016-17. There were 4 rows of 2 meter length for each entry in a replication. The row spacing was 30 cm and plant spacing within a row was maintained at 10 cm by thinning. Normal agronomic practices including fertilizer application and necessary plant protection measures recommended for sesame were followed. Observations were recorded on ten quantitative traits, *viz.* days to maturity (DM), plant height in cm (PL), branch number per plant (B/P), capsule number per plant (C/P), capsule length in mm (CL), capsule width in mm (CW), seed number per capsule (SN/C), seed weight per capsule in mg (SW/C), 1000-seed weight in grams (TSW) and seed yield per plant in grams (SY/P). Capsule width was measured with the aid of a dial thickness gauge. Days to maturity were recorded on plot basis and observations on other quantitative characters were taken from a sample of five random competitive plants from each replication from the two central rows and averaged for per plant values.

To study capsule characters related to shattering, five to ten mature closed capsules were selected randomly from the mid portion of plants in a replication and were packed in brown paper bags following which the ten capsule shattering related traits, viz. capsule split before drying of capsules in cm (CS-1), capsule split after drying of capsules in cm (CS-2), capsule open before drying of capsules in cm (CO-1), capsule open after drying of capsules in cm (CO-2), unattached seed weight in mg (USW), retained seed weight

in mg (RSW), potential seed weight in mg (PSW), unattached seed number (USN), retained seed number (RSN) and potential seed number (PSN) were recorded. The data for capsule split (CS) was obtained as extent of split between the carpel exposing the capsule membrane but not exposing the seed. This was measured from base to top of the seed chamber along the suture (Fig.1 A-D). CS-1 and CS-2 was recorded before sun drying and after sun drying the capsules for 10 days respectively. Capsule Open (CO) was measured as extent of opening between carpel with membranes opening enough to expose the seed and/or seed chamber. This was measured from base to top of seed chamber along the placenta for capsules sampled for CS. Thus CO-1 and CO-2 were measured for capsules sampled for CS-1 and CS-2 respectively. The RSN and USN was recorded as the total number of seeds retained in the capsule and released from the capsule respectively after the capsule has been inverted and twirled. RSW and USW was recorded as the total weight of seeds retained in the capsule and released from the capsule respectively from the capsules sampled for RSN and USN. Potential Seed Number (PSN) was recorded as the total number of seeds for five randomly selected capsules from the mid portion of plant per observation. For this the capsules were collected between physiological maturity (the time when 3/4th of the seed present in the capsule still attached to the plant is mature) and harvest maturity (first dry capsules). PSW was recorded as the total weight of seeds sampled for PSN.

The character means for each replication were subjected to analysis of variance according to the procedure outlined by Panse and Sukhatme (1985). Phenotypic and genotypic correlation coefficients of seed yield (effect) with various yield related and capsule characters (causes) were partitioned into direct and indirect effects by path coefficient analysis as per Al -Jibouri *et al.* (1958) and Dewey and Lu (1959). The generalized Mahalanobis (1936) distances (D^2) was used for grouping the genotypes and assessing the cause of genetic variability.

The analysis of variance revealed significant difference for all the characters studied suggesting presence of genetic variability in the experimental materials. High values of phenotypic (PCV) and genotypic (GCV) coefficients of variation for most of the characters indicate relatively higher contribution of these characters towards genetic variability (Table 1). The narrow difference between PCV and GCV indicated that these characters were less affected by environment. High GCV for RSW, RSN, CS-1, CO-1, USW, SW/C, PSW, USN & RSN indicates presence of better scope of genetic improvement in these traits which could be achieved using simple selection procedures. Higher value of both PCV and GCV for number of primary branches was reported by Gadisa *et al.* (2015), capsules per plant by Shabana *et al.* (2015) and seeds per capsule by Gadisa *et al.* (2015). PCV was higher than GCV for all characters as also reported by Ahadu (2012), Narayanan and Murugan (2013). This implies that the characters had interacted with the environment to some extent for their expression.

Capsule shattering in field is a major cause of yield loss in sesame due to which the characters determining capsule shattering need to be studied for their degree of association with yield. The magnitude and nature of association of characters at genotypic and phenotypic levels are presented in Table 2. In case of genotypic correlation, highest positive significant association (1.111) was found between PH and SY/P whereas lowest positive significant association (0.334) was found between CS-1 & CO-2. Similarly in case of phenotypic correlation highest positive significant association (0.978) was found between PH and SY/P.

At phenotypic level SY/P showed a highly significant and positive correlation with B/P, C/P, USN, RSN & TSW. Similar results of highly significant and positive correlation of seed yield with component traits were reported by many researchers including Ismaila and Usman (2012), Gadisa *et al.* (2015), Mahmoud and Zeinab (2015) and Mohamad and Firew (2015).

At both genotypic and phenotypic levels, the association of days to maturity with different traits was positive and negative. The character B/P had significantly positive phenotypic correlation with C/P, PH, RSN & TSW. The most important yield component, C/P, showed significant positive correlation with PH, USW, RSW, RSN & TSW. It showed negative correlation for CS-1, CS-2, CO-1, SW/C & PSW. Plant height showed significant positive correlation with USN, RSN &TSW. Capsule length and width showed both positive and negative association with all the characters.

The important capsule shattering characters in sesame are CS and CO before and after drying, seed retention in the capsule, and weight of retained and detached seeds. At phenotypic level CS-1 exhibited significant positive correlation with CS-2 and CO-1. It showed negative association with B/P, C/P, PH, CL and TSW. Capsule split after drying showed significant positive association with CS-1 and CO-2. CS-1 showed significant positive association only with CS-2 at both phenotypic and genotypic level. CO-2 exhibited significant positive association with CS-2 and RSW. The USW showed significant positive correlation with C/P, RSW, SW/C, PSW, USN, RSN and PSN. Retained seed weight per capsule exhibited significant positive phenotypic correlation with C/P, USW and RSN. SW/C showed significant positive association with USW, USN, PSW, SN/C and PSN at both genotypic and phenotypic level. Similarly PSW exhibited significant positive correlation with USW, USN, SN/C and PSN at both phenotypic and genotypic level. USN exhibited significant positive association with C/P, PH, USW, SN/C,SW/C, PSW, RSN and TSW at both genotypic and phenotypic level. At phenotypic levels SN/C exhibited

significant positive association with USW, SW/C, PSW, PSN, USN and RSN. At genotypic level it showed significant positive association with RSW and PSN. The character PSN exhibited significant positive correlation with USW, USN, SW/C, RSN, SN/C and PSW at both genotypic and phenotypic levels. It showed negative correlation with DM and CO-1. At both genotypic and phenotypic levels TSW showed positive significant association with B/P, C/P, PH and USN.

Among the characters the magnitude of association between two sets (i.e. between PH and CL and between SN/C and CO-1) was not same at phenotypic and genotypic level. This indicates that environment factors played a significant role in changing the magnitude of correlation coefficients both at genotypic and phenotypic level. Though the directions of both genotypic and phenotypic correlations were same, the genotypic correlation coefficients were of higher magnitude as compared to phenotypic correlation coefficient in most of the cases. Similar results were reported by Sumathi *et al.* (2007) and Shekhawat *et al.* (2013).

The effect of correlation coefficients may not be always fruitful or could give misleading results because the correlation between two variables may be due to third factor. When more variables are considered in correlation matrix, path coefficient analysis becomes more useful in specifying the cause and also measures the relative importance of each character. Hence path coefficient analysis utilized by Dewey and Lu (1959) helps in identifying the importance of each character included in study. In the present investigation, cause and relationship between seed yield and other 19 characters were investigated both at phenotypic and genotypic level (Table 3).

At the phenotypic level maximum positive direct effect on SY was exerted by PSW (0.899), followed by PH (0.826), TSW (0.176) and SN/C (0.159) whereas SW/C had the highest direct negative effect (- 0.910). The highest direct positive effect on SY/P at phenotypic level was exhibited by PSW whereas the correlation between these two characters was negative (rp= -0.121). Next to PSW, a higher positive direct effect of PH on SY/P was observed, whereas its correlation with SY/P was found to be highest (rp= 0.978) and positive. The higher magnitude of correlation coefficient was due to the positive indirect effect via C/P, B/P, CS-2, CO-1, USW, SN/C, RSN and TSW.

The lower magnitude of correlation coefficient of SN/C with SY/P was low (rp= 0.180) was due to partial nullification of positive direct effects by negative indirect effects via characters like CL, CW, CS-2, RSW, SW/C, USN, PSN and TSW. The value of residual effect of undefined factors was 0.153. Path coefficient analysis at phenotypic level indicated that selection for seed yield would be more effective through the choice of characters like PH, C/P, B/P, TSW, USW, RSN and RSW. Selection for these characters should be done along with indirect causal factor. Plant height was found to be the most contributing character for seed yield in sesame which may be due to its indeterminate growth habit (Engin *et al*., 2010).

Table 1 Estimation of different parameters of variability for 20 characters in sesame

Characters	Range	Mean±S.E	GCV %	PCV %	Heritability %	GA% over Mean
DM	76.33-97.33	83.71±2.12	6.73	7.21	87.27	11.07
B/P	1.89-4.89	3.54±0.25	18.99	20.37	86.95	31.17
C/P	18.57-45.30	28.56±1.89	29.32	30.07	95.11	50.33
PH	71.63-114.37	89.37±4.68	10.88	12.12	80.70	17.21
CL	18.67-29.33	24.48±0.42	8.84	9.01	96.21	15.26
CW	5.20-8.46	6.78±0.13	9.99	10.19	96.21	17.25
CS-1	0.60-26.80	15.66±0.70	48.89	49.11	99.14	85.68
CS-2	6.60-29.40	20.62±0.75	26.71	26.96	98.10	46.55
CO-1	1.07-9.40	5.23±0.44	46.90	47.67	96.77	81.20
CO-2	4.60-19.67	9.47±0.68	34.08	34.86	95.57	58.63
UW	22.33-861.20	463.78±26.42	49.17	49.51	98.64	85.95
RW	14.60-495.57	192.96±16.46	56.32	56.98	97.69	97.98
SW/C	59.67-369.60	203.81±11.85	48.68	49.04	98.55	85.05
PSW	321.43-1832.33	1026.32±18.14	49.09	49.13	99.87	86.35
UN	10.00-278.00	142.96±9.12	50.71	51.12	98.39	88.53
RN	3.47-101.00	33.90±2.87	80.25	80.71	98.86	140.43
SN/C	13.40-67.00	40.02±4.91	33.22	35.49	87.65	54.75
PSN	67.00-339.00	201.05±20.28	34.63	36.11	91.97	58.45
TSW	1.63-3.55	2.72±0.18	15.76	17.16	84.27	25.46
SY/P	1.81-6.79	3.62±0.17	30.00	30.41	97.31	52.09

DM (Days to maturity), B/P(Branches per plant), C/P(Capsules per plant), PH(Plant height), CL(Capsule length), CW(Capsule Width), CS-1(Capsule split before drying), CS-2(Capsule split after drying), CO-1(Capsule Open Before drying), CO-2(Capsule split after drying), UW(Unattached seed weight), RW(Retained seed weight), SW/C (seed weight per capsule), PSW(Potential seed weight), UN (Unattached seed number), RN (Retained seed number), SN/C (Seed number per capsule), PSN (Potential seed number), TSW(Thousand seed weight), SY/P(Seed yield per plant)

Table 2 Phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among yield and capsule shattering characters in sesame genotypes

Character	DM	B/P	C/P	PH	CL	CW	CS-1	CS-2	CO-1	CO-2	UW	RW	SW/C	PSW	UN	RN	SN/C	PSN	TSW	SY/P
DM		-0.082	-0.106	-0.178	-0.450**	-0.302	0.125	0.032	0.033	0.33	0.205	0.201	-0.031	-0.005	0.091	0.011	-0.084	-0.179	-0.193	-0.155
B/P	-0.101		0.489**	0.496**	0.219	0.07	-0.296	-0.073	-0.157	0.153	0.211	0.238	-0.102	-0.106	0.31	0.384*	-0.009	0.032	0.514**	0.518**
C/P	-0.108	0.561**		0.833**	0.028	0.185	-0.133	-0.207	-0.068	0.046	0.387*	0.366*	-0.05	-0.067	0.449**	0.412*	0.051	0.102	0.653**	0.832**
PH	-0.235	0.559**	0.964**		0.001	0.063	-0.142	-0.232	-0.095	-0.05	0.312	0.159	-0.114	-0.133	0.474**	0.381*	0.178	0.251	0.772**	0.978**
CL	-0.055	0.238	0.039	-0.014		-0.186	-0.095	0.305	-0.332	0.124	0.157	0.126	0.267	0.271	0.115	0.03	0.123	0.153	0.125	-0.007
CW	-0.347*	0.057	0.204	0.069	-0.201		0.211	0.104	0.177	0.193	0.183	0.055	0.151	0.156	0.282	0.206	0.047	0.045	-0.083	0.051
CS-1	0.137	-0.317	-0.134	-0.162	-0.099	0.221		0.636**	0.726**	0.328	0.075	0.025	0.167	0.161	0.064	-0.051	0.005	0.012	-0.314	-0.151
CS-2	0.028	-0.075	-0.214	-0.271	0.311	0.106	0.646**		0.247	0.479**	0.172	0.142	0.266	0.261	0.158	0.202	0.26	0.26	-0.207	-0.232
CO-1	0.032	-0.154	-0.076	-0.096	-0.339	0.187	0.737**	0.253		0.227	-0.146	-0.076	-0.001	-0.015	-0.098	-0.21	0.007	-0.031	-0.332	-0.11
CO-2	0.367	0.187	0.053	-0.048	0.12	0.2	0.334*	0.495**	0.24		0.305	0.373*	0.146	0.137	0.329	0.207	0.148	0.107	-0.031	-0.02
UW	0.219	0.218	0.401*	0.342*	0.163	0.187	0.078	0.175	-0.144	0.317		0.496**	0.596**	0.591**	0.891**	0.435**	0.375*	0.366*	0.291	0.312
RW	0.217	0.257	0.388*	0.178	0.125	0.055	0.027	0.146	-0.075	0.382*	0.505**		0.321	0.322	0.313	0.509**	0.315	0.289	0.156	0.213
SW/C	-0.038	-0.107	-0.057	-0.127	0.279	0.156	0.171	0.272	-0.009	0.154	0.603**	0.327		0.997**	0.449**	0.164	0.397*	0.38*	0.006	-0.105
PSW	-0.005	-0.11	-0.069	-0.145	0.277	0.159	0.162	0.263	-0.016	0.139	0.597**	0.326	1.005**		0.447**	0.182	0.407*	0.391*	-0.017	-0.121
UN	0.105	0.332	0.461**	0.522**	0.125	0.294	0.065	0.162	-0.099	0.341*	0.897**	0.325	0.455**	0.452**		0.429**	0.428**	0.448**	0.358*	0.447**
RN	0.012	0.414*	0.427**	0.427**	0.028	0.216	-0.053	0.206	-0.214	0.214	0.443**	0.515**	0.166	0.183	0.436**		0.582**	0.585**	0.261	0.435**
SN/C	-0.095	-0.008	0.072	0.199	0.141	0.065	0.005	0.284	-0.001	0.164	0.403*	0.342**	0.419*	0.435**	0.463**	0.618**		0.961**	-0.028	0.18
PSN	-0.198	0.031	0.118	0.289	0.17	0.053	0.014	0.28	-0.039	0.118	0.378*	0.307	0.393*	0.408*	0.469**	0.61**	1.001**		0.041	0.245
TSW	-0.239	0.594**	0.749**	0.906**	0.115	-0.091	-0.35	-0.237	-0.378	-0.052	0.329	0.161	0.006	-0.019	0.396*	0.284	-0.02	0.069		0.807**
SY/P	-0.161	0.579**	0.863**	1.111**	-0.006	0.053	-0.151	-0.235	-0.114	-0.018	0.317	0.219	-0.107	-0.123	0.456**	0.443**	0.195	0.26	0.911**	

* , ** significant at 5% and 1% of probability, respectively.

Table 3 Phenotypic (P_p) and genotypic (P_g) path-coefficient analysis showing direct and indirect effects of different traits on seed yield in sesame

Charac-ter	Path Coeff.	DM	B/P	C/P	PH	CL	CB	CS-1	CS-2	CO-1	CO-2	UW	RW	SWC	PSW	UN	RN	SNC	PSN	TSW	Correlation with yield (r)
DM	Pp	-0.038	-0.003	-0.005	-0.147	0.001	0.007	0.012	-0.002	-0.001	0.019	0.0.17	-0.001	0.028	-0.004	-0.013	0.000	-0.013	0.020	-0.034	-0.155
	Pg	0.372	0.015	0.001	0.090	-0.013	-0.127	0.017	-0.007	0.015	-0.082	-0.038	0.019	0.038	-0.003	0.012	0.001	0.012	-0.155	-0.368	-0.161
B/P	Pp	0.003	0.032	0.022	0.410	-0.006	-0.002	-0.028	0.005	0.003	0.009	0.017	-0.001	0.093	-0.095	-0.043	0.014	-0.001	-0.004	0.090	0.518
	Pg	-0.038	-0.149	-0.004	-0.215	0.058	0.021	-0.040	0.018	-0.073	-0.042	-0.037	0.022	0.106	-0.067	0.039	0.044	0.001	0.018	0.916	0.579
C/P	Pp	0.004	0.016	0.044	0.688	-0.001	-0.004	-0.013	0.014	0.001	0.003	0.032	-0.001	0.046	-0.060	-0.062	0.015	0.008	-0.012	0.115	0.832
	Pg	-0.040	-0.083	-0.007	-0.371	0.009	0.075	-0.017	0.052	-0.036	-0.012	-0.069	0.034	0.057	-0.042	0.054	0.045	-0.009	0.069	1.155	0.863
PH	Pp	0.007	0.016	0.037	0.826	0.000	-0.001	-0.013	0.015	0.002	-0.003	0.026	-0.001	0.104	-0.120	-0.066	0.014	0.028	-0.029	0.136	0.978
	Pg	-0.088	-0.083	-0.007	-0.385	0.003	0.025	-0.020	0.065	-0.045	0.011	-0.059	0.015	0.126	-0.088	0.061	0.045	-0.025	0.017	1.397	1.111
CL	Pp	0.002	0.007	0.001	0.001	-0.029	0.004	-0.009	-0.020	0.007	0.007	0.013	0.000	-0.243	0.244	-0.016	0.001	0.020	-0.017	0.022	-0.007
	Pg	-0.020	-0.035	0.000	0.005	0.242	-0.074	-0.012	-0.075	-0.160	-0.027	-0.028	0.011	-0.277	0.168	0.015	0.003	-0.018	0.099	0.177	-0.006
CB	Pp	0.011	0.002	0.008	0.052	0.005	-0.023	0.020	-0.007	-0.004	0.011	0.015	0.000	-0.137	0.140	-0.039	0.008	0.007	-0.005	0.011	0.015
	Pg	-0.129	-0.008	-0.001	-0.027	-0.049	0.367	0.028	-0.026	0.088	-0.045	-0.032	0.005	-0.155	0.097	0.035	0.023	-0.008	0.031	-0.140	0.053
CS-1	Pp	-0.005	-0.009	-0.006	-0.117	0.003	-0.005	0.095	-0.042	-0.016	0.019	0.006	0.000	-0.152	0.145	-0.009	-0.002	0.001	-0.001	-0.055	-0.151
	Pg	0.051	0.047	0.001	0.062	-0.024	0.081	0.126	-0.156	0.348	-0.075	-0.013	0.002	-0.170	0.098	0.008	-0.006	-0.001	0.008	-0.540	-0.151
CS-2	Pp	-0.001	-0.002	-0.009	-0.192	-0.009	-0.002	0.060	-0.066	-0.005	0.028	0.014	-0.001	-0.242	0.235	-0.022	0.008	0.041	-0.030	-0.036	-0.232
	Pg	0.010	0.011	0.002	0.104	0.075	0.039	0.081	-0.241	0.119	-0.111	-0.030	0.013	-0.270	0.160	0.019	0.022	-0.036	0.163	-0.365	-0.235
CO-1	Pp	-0.001	-0.005	-0.003	-0.078	0.010	-0.004	0.069	-0.016	-0.022	0.013	-0.012	0.000	0.001	-0.013	0.014	-0.008	0.001	0.004	-0.058	-0.110
	Pg	0.012	0.023	0.001	0.037	-0.082	0.069	0.093	-0.061	0.472	-0.054	0.025	-0.006	0.009	-0.010	-0.012	-0.023	0.000	-0.023	-0.583	-0.114
CO-2	Pp	-0.013	0.005	0.002	-0.041	-0.004	-0.004	0.031	-0.032	-0.005	0.059	0.025	-0.001	-0.133	0.123	-0.046	0.008	0.023	-0.012	-0.005	-0.020
	Pg	0.137	-0.028	0.000	0.018	0.029	0.073	0.042	-0.119	0.113	-0.224	-0.054	0.033	-0.153	0.084	0.040	0.023	-0.021	0.069	-0.080	-0.018
UW	Pp	-0.008	0.007	0.017	0.258	-0.005	-0.004	0.007	-0.011	0.003	0.018	0.082	-0.002	-0.543	0.531	-0.124	0.016	0.060	-0.042	0.051	0.312
	Pg	0.082	-0.032	-0.003	-0.132	0.039	0.069	0.010	-0.042	-0.068	-0.071	-0.172	0.044	-0.598	0.363	0.106	0.047	-0.051	0.220	0.507	0.317
RW	Pp	-0.008	0.008	0.016	0.131	-0.004	-0.001	0.002	-0.009	0.002	0.022	0.041	-0.004	-0.292	0.289	-0.043	0.019	0.050	-0.033	0.027	0.213
	Pg	0.081	-0.038	-0.003	-0.068	0.030	0.020	0.003	-0.035	-0.035	-0.086	-0.087	0.087	-0.324	0.198	0.038	0.055	-0.043	0.178	0.248	0.219
SWC	Pp	0.001	-0.003	-0.002	-0.094	-0.008	-0.003	0.016	-0.018	0.000	0.009	0.049	-0.001	-0.910	0.896	-0.062	0.006	0.063	-0.043	0.001	-0.105
	Pg	-0.014	0.016	0.000	0.049	0.068	0.057	0.021	-0.066	-0.004	-0.035	-0.104	0.028	-0.991	0.611	0.054	0.018	-0.053	0.228	0.009	-0.107
PSW	Pp	0.000	-0.003	-0.003	-0.110	-0.008	-0.004	0.015	-0.017	0.000	0.008	0.048	-0.001	-0.908	0.899	-0.062	0.007	0.065	-0.044	-0.003	-0.121
	Pg	-0.002	0.016	0.000	0.056	0.067	0.058	0.020	-0.063	-0.008	-0.031	-0.103	0.028	-0.996	0.608	0.053	0.019	-0.055	0.237	-0.029	-0.123
UN	Pp	-0.003	0.010	0.020	0.392	-0.003	-0.006	0.006	-0.010	0.002	0.019	0.073	-0.001	-0.409	0.402	-0.139	0.016	0.068	-0.051	0.063	0.447
	Pg	0.039	-0.049	-0.003	-0.201	0.030	0.108	0.008	-0.039	-0.047	-0.076	-0.154	0.028	-0.451	0.275	0.118	0.046	-0.059	0.272	0.611	0.456
RN	Pp	0.000	0.012	0.018	0.315	-0.001	-0.005	-0.005	-0.013	0.005	0.012	0.036	-0.002	-0.149	0.164	-0.060	0.037	0.092	-0.066	0.046	0.435
	Pg	0.004	-0.061	-0.003	-0.164	0.007	0.079	-0.007	-0.050	-0.101	-0.048	-0.760	0.045	-0.165	0.111	0.051	0.106	-0.078	0.354	0.438	0.443
SNC	Pp	0.003	0.000	0.002	0.147	-0.004	-0.001	0.000	-0.017	0.000	0.009	0.031	-0.001	-0.361	0.366	-0.059	0.022	0.159	-0.109	-0.005	0.180
	Pg	-0.035	0.001	-0.001	-0.077	0.034	0.024	0.001	-0.068	0.000	-0.037	0.069	0.030	-0.415	0.264	0.055	0.066	-0.127	0.582	-0.031	0.195
PSN	Pp	0.007	0.001	0.004	0.207	-0.004	-0.001	0.001	-0.017	0.001	0.006	0.030	-0.001	-0.346	0.351	-0.062	0.022	0.153	-0.114	0.007	0.245
	Pg	-0.074	-0.005	-0.001	-0.111	0.041	0.019	0.002	-0.068	-0.018	-0.026	0.065	0.027	-0.390	0.248	0.055	0.065	-0.127	0.581	0.106	0.260
TSW	Pp	0.007	0.016	0.029	0.638	-0.004	0.002	-0.030	0.014	0.007	-0.002	0.024	-0.001	-0.005	-0.015	-0.050	0.010	-0.004	-0.005	0.176	0.807
	Pg	-0.089	-0.088	-0.005	-0.348	0.028	-0.033	-0.044	0.057	-0.178	0.012	-0.057	0.014	-0.006	-0.012	0.047	0.030	0.003	0.040	1.542	0.911

Underlined figures denote direct effect, Residual phenotypic effect = 0.153, Residual genotypic effect = 0.232

Table 4 Average Intra-(Diagonal bold) and Inter-Cluster (D^2) values among sesame genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I (5)	261.41	661.40	1880.79	2645.03	884.92	808.25	1053.06	1508.64	1458.66	2203.19	2804.21
II (6)		281.55	1884.88	2958.60	623.77	1141.13	1039.47	1498.31	2020.29	2638.85	2600.35
III (5)			337.67	476.15	1573.45	1047.38	678.51	583.80	658.38	704.67	650.29
IV (6)				332.09	2494.97	1587.50	1078.35	982.91	710.50	671.20	754.38
V (3)					245.34	653.29	1313.62	813.80	2189.70	2675.21	2030.14
VI (3)						328.53	1019.90	750.83	1346.56	1572.63	1741.42
VII (2)							333.96	995.78	585.57	671.45	1327.11
VIII (2)								340.11	1186.49	1460.09	859.08
IX (1)									0	582.01	1605.83
X (1)										0	1340.70
XI (1)											0

The number in parenthesis indicate the number of genotypes grouped

Table 5 Cluster means of 20 characters in sesame genotypes

Characters	Clusters										
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
DM	83.47	83.72	83.80	85.78	84.33	**58.22**	80.17	76.83	78.67	81.00	94.33
B/P	4.04	3.22	3.13	3.65	3.69	**4.04**	3.28	3.66	**1.89**	4.00	4.00
C/P	30.85	21.17	23.39	**303.03**	38.48	36.11	21.60	44.22	**19.67**	21.23	35.57
PH	92.92	80.50	85.49	87.77	105.42	92.54	**80.21**	**106.87**	82.43	84.40	91.37
CL	23.87	24.00	25.48	24.33	23.43	23.71	26.83	23.33	**22.33**	**29.33**	26.33
CW	6.61	6.41	7.20	6.78	6.97	6.75	6.49	7.72	6.93	**6.10**	6.40
CS-1	4.57	20.77	20.59	17.48	20.65	6.15	14.50	21.30	10.00	**3.93**	**26.80**
CS-2	**10.15**	23.63	23.13	20.63	21.78	19.96	25.06	22.97	11.60	**29.40**	27.40
CO-1	3.32	7.07	5.85	5.38	6.60	2.89	3.76	5.30	**5.50**	**1.07**	**9.40**
CO-2	6.35	8.58	11.47	8.80	10.93	11.73	9.40	8.30	5.80	9.40	**19.67**
UW	318.88	198.18	618.71	657.84	363.33	618.22	**146.16**	712.60	345.00	540.00	**861.20**
RW	155.85	109.37	184.79	277.00	213.67	282.89	182.40	168.37	**16.20**	75.00	**449.97**
SW/C	109.43	**93.13**	275.38	**335.33**	106.95	155.98	243.26	222.33	300.07	326.87	291.40
PSW	545.63	**468.48**	1386.84	**1705.30**	540.64	794.37	1227.07	1084.95	1525.87	1630.23	1432.33
UN	100.96	55.71	197.29	168.18	156.29	193.33	**50.00**	237.54	115.00	180.00	**250.00**
RN	12.65	12.90	40.81	47.10	58.53	**80.67**	16.10	36.70	**5.40**	25.00	5.60
SN/C	**22.47**	33.71	45.84	45.37	47.87	51.71	31.83	33.74	54.00	**60.60**	40.20
PSN	**112.33**	165.78	229.20	226.83	256.00	258.56	159.17	168.67	270.00	**303.00**	**201.00**
TSW	2.91	**2.40**	2.46	2.65	2.87	3.04	2.51	3.37	2.67	2.77	3.08
SY	3.96	2.72	3.08	3.57	5.32	4.04	**2.60**	5.31	2.95	3.14	3.87

The bold figures indicate minimum and maximum values for each character

Path coefficients of genotypic level revealed that the pattern of direct and indirect effects was of different magnitude and direction in many cases. At genotypic level TSW had the highest positive direct effect (1.542) on SY/P whereas, the highest negative direct effect was recorded for SW/C (-0.991).

1000-seed weight had the highest positive direct effect (1.542) on SY/P, whereas the correlation between these two characters was also high (rg= 0.911). This higher magnitude of correlation coefficient was due to the positive indirect effect via other characters such as CL, CS-2, CO-2, RSW, USN, RSN, SN/C and PSN. The correlation coefficient was almost equal to its direct effect. This explains the true relationship between these two characters and a direct selection through this trait will be effective.

A low to moderate level of direct positive effect on SY/P was observed for RSW (0.087), whereas the correlation coefficients for this character with SY/P was found to be high (rg = 0.219). The genotypic correlation between DM and SY/P was negative (rg= -0.161), but the direct effect was found to be positive (0.372) due to the nullifying indirect effects of other characters such as B/P, PH, RSW and SW/C. The association of PH with SY/P was significantly high and positive (rg= 1.111), but its direct effect on seed yield was found to be negative (-0.385). This direct negative effect was nullified by positive indirect effects via CL, CW, CS-2, CO-2, RSW, SW/C, USN, RSN, PSN and TSW. In this situation the indirect causal factors are to be considered simultaneously for selection.

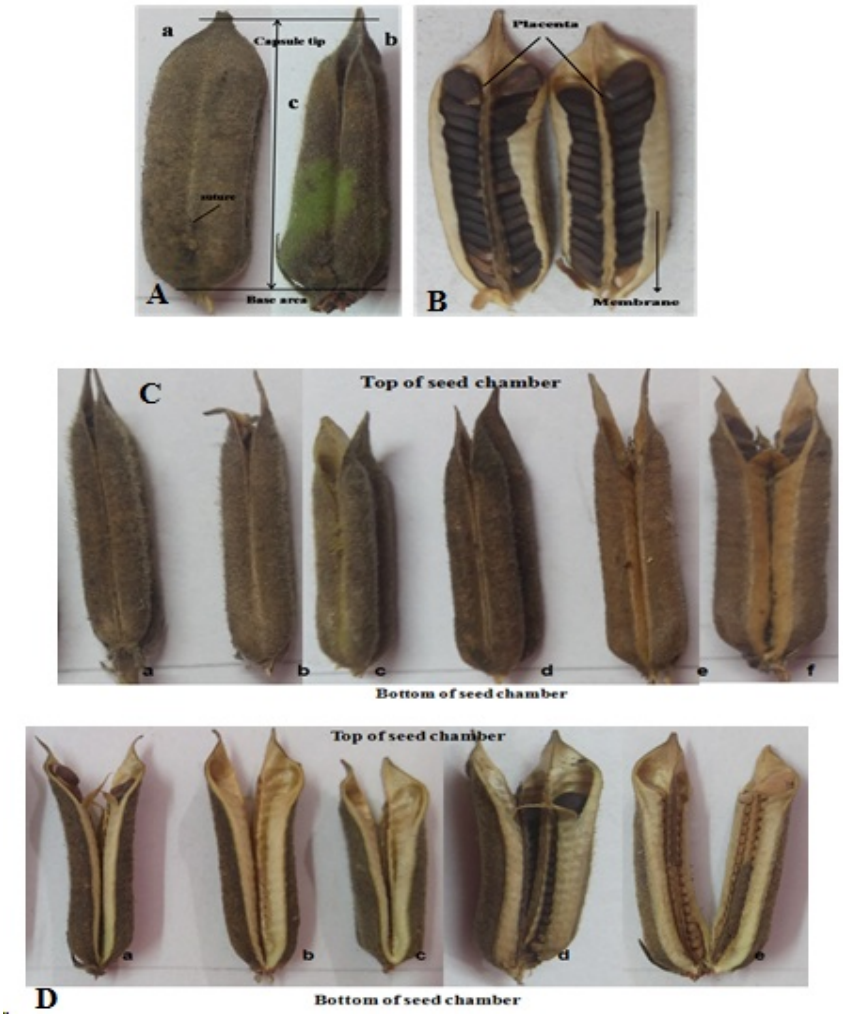

Fig. 1. A. Front and side view of sesame capsule; B. Seed chamber containing seeds still attached to placenta; C. Extent of capsule split along suture from (a) near top of seed chamber up to (f) bottom of seed chamber; D. Extent of capsule open along suture exposing the membrane and seeds from (a) near top of seed chamber up to (f) bottom of seed chamber

The genotypic correlation with seed yield of other characters was found to be high, but their direct effect on seed yield was found to be low and also negative in some cases which were accelerated by positive indirect effect via other characters. The value of residual effect of undefined factors was 0.232. The positive direct effect of one or more of these characters on seed yield was earlier reported by Engin *et al.* (2010), Renuka *et al.* (2011), Mohan (2011), Shekhawat *et al.* (2013) and Abhijitha *et al.* (2017).

At genotypic level TSW, PSN, USN, RSN and RSW could be of more value while selecting for high seed yield in sesame. A direct selection for SY/P through TSW will be more effective. It is evident from both direct and indirect effects of the component characters at phenotypic and genotypic levels that selection would be more effective when based on characters like C/P, PH, TSW, B/P, USN, RSN, USW, CO-2 and SN/C.

The generalized Mahalanobis distances (D^2) divided the thirty five genotypes into eleven clusters (Table 4). Genotypes of cluster III and IV were the most genetically related (D^2= 476.15) while the most genetically divergent genotypes were from cluster II and IV (D^2= 2958.60). The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 5). The maximum cluster means were revealed by cluster IV for the characters C/P, SW/C, and PSW while cluster II showed minimum cluster means for SW/C, PSW and TSW. High cluster means for various characters have also been reported by Parameshwarappa *et al.* (2012) and Tripathi *et al.* (2013).

Table 6 Relative contribution of yield and its components toward total genetic divergence in 35 sesame genotypes

Character	Average D^2	% Contribution
DM	5.24	0.40
B/P	5.17	0.39
C/P	17.49	1.32
PH	4.06	0.31
CL	20.08	1.52
CW	25.52	1.93
CS-1	94.47	7.14
CS-2	46.45	3.51
CO-1	11.77	0.89
CO-2	19.09	1.44
UW	62.32	4.71
RW	40.31	3.05
SW/C	61.59	4.6
PSW	646.82	48.91
UN	50.40	3.81
RN	92.56	7.00
SN/C	10.78	0.81
PSN	37.77	2.86
TSW	23.85	1.80
SY/P	46.74	3.53

Amongst the characters PSW had the highest (48.91%) contribution to total divergence while B/P contributed least to genetic divergence (Table 6). Contribution of characters to divergence depends on the number of characters studied and the influence of the environment on the expression of characters as reported by Baraki et al. (2015) and Kiranmayi *et al.* (2016).

In the present study three different analyses were used to assess the relationship among the characters in sesame. The study clearly indicated the differential association of capsule characters related to shattering in sesame genotypes. In correlation analysis PH exhibited the highest positive correlation with SY/P. In path analysis PSW followed by PH indicated very high direct effect on SY/P. Genetic divergence analysis also indicated that PSW contributed maximum to genetic variability. So from the combined results it may be concluded that PH and PSW along with B/P, C/P, TSW, USN & RSN are the major yield contributing characters to be given selection pressure for improving yield. It is also suggested that donors possessing combination of above characters should be used in a breeding program for obtaining desirable high yielding segregants.

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Identification of superior high yielding sunflower (*Helianthus annuus* L.) hybrids for *rabi*-summer season in West Bengal

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ABSTRACT

An experiment was carried out during 2012-13 to 2014-15 at Nimpith Centre of Ramkrishna Ashram Krishi Vigyan Kendra Research Farm, West Bengal to identify suitable sunflower hybrids for *rabi*-summer season. A total of 150 sunflower hybrids were tested including two National check hybrids (KBSH-44 and DRSH-1). The field observation revealed that the hybrid PSCHT-12-38 (2260 kg/ha, 36.0% oil content), PSCHT-12-42 (2250 kg/ha, 37.5% oil), PSCHT-12-26 (2217 kg/ha, 37.7%) and PSCHT-12-36 (2151 kg/ha, 37.9% oil content) recorded higher seed yield as well as high oil content in comparison to the national check hybrids. The new experimental hybrids *viz.,* PSCHT-12-42, SAHT-12-09, PSCHT-12-26, PSCHT-12-36, PSCHT-12-38, PSCHT-12-66, PSCHT-12-76 and PSCHT-12-29 were tolerant to sunflower wilt (PDI score 10-12.5%) in comparison to the checks (PDI score 20-25%). Considering the other yield attributing parameters like plant height, days to 50% flowering or days to maturity, hull content and volume weight, hybrids like PSCHT-12-38, PSCHT-12-42 , PSCHT-12-26 and PSCHT-12-36 were promising due to their 7-10 days earliness and 30-50 cm shorter plant height at harvest coupled with good seed yield and oil yield as well as high degree of tolerance to sunflower wilt.

Keywords: Hybrids, *Rabi*-summer, Seed Yield, Sunflower, West Bengal

Among the oilseed crops, sunflower gains much popularity because of its photo insensitivity and wider adoptability to different agro-climatic regions and soil types. Development of hybrids is the primary objective of most sunflower breeding programs in the world (Rani *et al.,* 2016). First sunflower hybrids were produced in US in 1972 and occupied 80% of the area in five years (Fick and Miller, 1997) and soon single-cross hybrids quickly became predominant cultivars in the world. Use of hybrids reached over 95 per cent in India sunflower area in the last 10 years. In India, sunflower is mostly grown in the states of Karnataka, Maharashtra, Andhra Pradesh and Tamil Nadu with potential scope of growing in the non-traditional areas like West Bengal (Dutta, 2011). In West Bengal, sunflower is the second important oilseed crop after rapeseed-mustard during *rabi*-summer season and it was grown on about 21,000 ha during 2014-15 *rabi* season. Sunflower being a photoperiod neutral crop has wide scope to replace the rapeseed-mustard cultivation with high yield potentiality. The present study was aimed at evaluating the performance of sunflower hybrids with respect to yield and yield components and to identify the superior sunflower hybrids suitable for *rabi*-summer season in West Bengal.

The experiment was carried out during December 2012-13 to 2014-15 under AICRP Sunflower, Nimpith Centre of RAKVK Research Farm, South 24 Parganas, West Bengal to identify the suitable sunflower hybrids for cultivation in *rabi*-summer season in West Bengal. A total of 150 sunflower hybrids developed at AICRP (Sunflower), Nimpith centre and collected from AICRP (Sunflower), UAS, GKVK, Bangalore, Karnataka; AICRP (Sunflower), UAS, Raichur, Karnataka and AICRP (Sunflower), Latore, Maharashtra were tested including the two national check hybrids, KBSH-44 and DRSH-1 in randomized complete block design with three replications. The plot size was 4.5m x 3.0 m. In the first year (2012-13). Out of the 150 sunflower hybrids, thirteen superior hybrids were selected as per their better yield and yield attributing components. In the next two years (2013-14 and 2014-15), the same hybrids were tested including two national checks (KBSH-44 and DRSH-1) in "on-station" trial at Nimpith centre and another three locations at Research Farm, Institute of Agriculture Sciences, Calcutta University, Baruipur; Radhakantapur (KVK-adopted Village of Mathurapur-II block of South 24 Parganas district) and Kultali as multilocation trials. The soil texture was clay loam in "on station" and "MLT" plots. Three irrigations were provided during the cropping period. One foliar spray was given with Boron @ 2g/l of water in ray floret stage. The row per plot were five in number with a row spacing of 60 cm and plant to plant spacing was 30 cm. Uniform dose of fertilizer @80 kg N, 40 kg P_2O_5 and 40 kg K_2O per ha was applied. The germinated seed of sunflower was used as the planting material and one per hill was maintained throughout the cropping period. The data was recorded on ten randomly selected plants from each plot of all replications on the following characters *viz.,* days to 50% flowering, days to maturity, plant height at harvest (cm), head diameter per plant (cm), seed weight per head (g), 100-seed weight (g), husk content (%), volume weight (g/cc) and percentage of infected plants by sunflower wilt (on plot basis). The seed yield (kg/ha), oil percentage and oil yield (kg/ha) were estimated on plot basis. The mean values were subjected to statistical analysis.

Evaluation of resistant sunflower hybrids is considered to be the most feasible and durable solution of controlling the wilt disease. Per cent disease incidence was worked out and it varied from 5.0 to 35.0 per cent in sunflower under natural field conditions when sunflower seed was treated with *T. viride* and *Pseudomonas fluorescens.* The study revealed that the maximum number of entries were grouped under moderately resistant category with respect to wilt. The field observation also revealed that experimental hybrids like PSCHT-12-42, SAHT-12-09, PSCHT-12-26, PSCHT-12-36, PSCHT-12-38,PSCHT-12-66, PSCHT-12-76 and PSCHT-12-29 were highly tolerant to wilt (PDI score 10-12.5%) in comparison to the checks, KBSH-44 and DRSH-1 (PDI score 20-25%) (Table 1 and 2).

Maximum 100-seed weight of 6.1 g was observed in hybrid P-KH-12-26 and P-KH-12-42 which was closely followed by P-KH-12-35 (5.9 g) (Table 2). Dutta (2015) reported significant variation for 100-seed weight and other agronomic variation among sunflower hybrids. This study also revealed that the volume weight (g/100cc), hull content (%) and oil content (%) significantly varied among the tested hybrids. The highest value for the volume weight (g/100cc) was noticed in P-KH-12-42 (43.5g) and P-KH-12-29 (42.6g). The lowest hull content (%) was recorded in P-KH-12-36 (29%) followed by SAHT-KH-12-21 (29.5%) and P-KH-12-42(30.5%) respectively. The similar type of findings has been reported by Chandra *et al.* (2013).

Table 1 Evaluation of superior sunflower hybrids in "On Station Trial" at Nimpith (2012-2015)

Hybrid	Seed yield (kg/ha)			Seed yield (kg/ha)	PDI of *S. rolfsii* (%)	PDI of *S. rolfsii* (%)	PDI of *S. rolfsii* (%)	Average PDI of *S. rolfsii* (%)
	2014-15	2013-14	2012-13		2014-15	2013-14	2012-13	
PSCHT- KH-12-38	2480	2256	2044	2260.0	11.5	12.0	11.0	11.5
PSCHT-KH-12-42	2130	2233	2389	2250.7	9.0	11.0	10.0	10.0
PSCHT-12-26	2153	2156	2330	2216.7	9.5	11.0	9.5	9.5
PSCHT-12-29	1740	2111	2044	1964.0	9.0	11.0	10.0	10.0
SAHT-12-21	2222	2028	2333	2194.3	12.0	13.0	12.5	12.5
PSCHT-12-76	1898	1967	1911	1925.3	12.0	13.5	12.0	12.5
PSCHT-12-36	2222	1900	2333	2151.7	9.0	10.0	11.0	10.0
SAHT-12-18	2025	1889	2367	2093.7	12.0	13.5	12.5	12.5
PSCHT-12-35	1820	1760	2200	1926.7	12.5	14.0	13.0	12.5
SAHT-KH-12-09	1866	1975	1940	1927.0	9.0	11.0	10.0	10.0
PSCHT-KH-12-66	2016	1740	1890	1898.7	8.0	12.0	10.0	10.0
PSCHT-KH-12-68	2373	2040	2300	2237.7	10.0	14.5	13.0	12.5
SAHT-12-15	1898	1980	2044	1974.0	14.0	17.0	14.0	15.0
KBSH-44	2407	2190	2070	2222.3	22.0	25.0	21.0	22.5
DRSH-1	2030	1856	1860	1915.3	19.0	21.5	18.5	20.0
Mean	2096.1	2002.9	2150.5	2083.2	11.9	14.0	12.5	12.7
SEm (±)	41.5	32.5	37.8	37.6	0.68	0.82	0.73	0.74
CD (P=0.05)	129.2	87.5	114.7	-	2.12	2.55	2.36	2.5
CV (%)	9.7	9.3	9.8	-	7.4	8.6	8.1	7.7

Statistical analysis of the data on seed yield in multilocation trials over the years revealed that highest seed yield of 2226 kg/ha was recorded with P-KH-12-38 which was closely followed by hybrid P-KH-12-42 and hybrid P-KH-12-26 with 2154 kg/ha and 2105 kg/ha, respectively (Table 3). The best national check, KBSH-44 recorded at par yield (2035 kg/ha) while DRSH-1 yielded 1805 kg/ha. Statistical analysis of the data on seed yield in MLT and in "on station" hybrid trial (Table 2) revealed that highest seed yield of 2296 kg/ha was recorded in the hybrid P-KH-12-38 which was closely followed by hybrid P-KH-12-42 and hybrid P-KH-12-68 with 2167 kg/ha and 2146 kg/ha, respectively. The seed yield of the check hybrids, KBSH-44 and DRSH-1, recorded were 2167 kg/ha and 1872 kg/ha, respectively. P-KH-12-42 was the highest oil (839 kg/ha) yielding which was closely followed by hybrid P-KH-12-26, P-KH-12-68,P-KH-12-38 and SAHT-KH- 12-18 with oil yield of 834 kg/ha (37.7% oil), 828 kg/ha (37.6%), 815 kg/ha (36% oil) and 805 kg/ha (38.4 % oil), respectively. The oil yield of the check hybrids, KBSH-44 and DRSH-1, were 629 kg/ha (28.3% oil) and 748 kg/ha (39.1% oil), respectively. The oil yield (kg/ha) of the sunflower hybrid P-KH-12-42 was 12.3% higher over DRSH-1 followed by P-KKH-12-26, P-KH-12-68, P-KH-12-38 and SAHT-KH-12-18 with 11.5%, 9.0%, 10.1% and 7.6%, respectively. Evaluation of the hybrids for resistance to wilt is considered to be the most feasible and durable solution of controlling the wilt disease. Per cent

disease incidence (PDI) was worked out and it varied from 5.0-35.0 in sunflower in last three years in natural field condition when sunflower seed was treated with *T. viride* and *P. fluorescens*. The study revealed that the maximum number of entries was grouped under moderately resistant category for wilt. The field observation also indicated that among the hybrids tested, PSCHT-12-42, PSCHT-12-26, PSCHT-12-38 and SAHT-KH-12-18 were superior for high degree of tolerance to wilt (PDI score10-12.5%) in comparison to KBSH-44 and DRSH-1 which had PDI score of 20-25% (Table 5 and 6).

Table 2 Evaluation of selected sunflower hybrids (out of 150 hybrids) in "on station trial" at Nimpith, in respect to yield and yield component

Hybrid	Seed Yield (kg/ha) over the MLT and SHT over the years	Oil Yield (kg/ha)	Oil%	Days to 50% flowering	Days to maturity	Pl. ht. (cm)	Head Dia. (cm)	100 seed Wt. (g)	Vol. Wt.(g/cc)	Hull cont. (%)	PDI (%) of *S. rolfsii*
P-KH-12-38	2296.5	815.0	36.0	74.5	104.5	166.2	14.3	5.4	40.1	34.5	11.5
P-KH-12-42	2167.5	839.8)	37.3	71.0	101.0	149.3	14.4	6.0	43.5	30.5	10
P-KH-12-26	2129.5	834.1	37.7	70.5	100.5	156.8	14.3	6.1	42.3	34.4	9.5
P-KH-12-29	1872.0	749.1	38.1	65.0	95.0	148.3	14.4	5.3	42.6	32.5	10.0
SAHT-12-21	2029.5	754.0	35.7	65.0	95.0	147.7	14.2	5.1	41.2	29.5	12.5
P-KH-12-76	1908.5	695.7	37.9	67.0	97.0	150.3	14.6	5.1	39.4	32.8	12.5
P-KH-12-36	2041.5	796.5	37.8	68.0	98.0	159.3	14.7	5.6	42.5	29.0	10.0
SAHT-KH-12-18	1955.0	805.0	38.4	69.5	99.5	152.7	14.8	5.5	39.5	32.5	12.5
P-KH-12-35	1727.5	670.7	38.2	64.0	94.0	154.8	14.4	5.9	39.1	37.1	12.5
SAHT-K-12-09	1838.5	708.0	38.1	66.8	96.8	144.3	14.6	4.7	41.6	34.0	10.0
P-KH-12-66	1888.0	764.2	38.5	70.0	100.0	142.3	14.1	5.4	41.9	32.7	10.0
P-KH-12-68	2146.5	828.6	37.0	74.0	104.0	154.3	14.5	5.5	40.3	34.4	12.5
SAHT-KH-12-15	1901.5	696.6	37.7	63.7	93.7	148.4	14.7	5.3	38.7	35.5	15.0
KBSH-44	2167.0	628.9	28.3	79.0	109.0	181.7	15.3	5.7	42.5	37.2	22.5
DRSH-1	1872.5	748.0	39.1	74.0	104.0	166.3	14.5	5.7	41.3	33.0	20.0
G. Mean	1996.1	769.4	37.0	69.5	99.5	154.9	14.5	5.5	40.6	33.3	12.7
S. Em(±)	41.5	14.6	0.14	0.9	0.8	2.3	0.38	0.17	0.26	0.81	0.74
CD (at 5%)	130.6	41.2	0.4	2.7	2. 3	6.8	1.2	0.5	0.8	2.6	2.5
CV%	9.5	9.4	9.1	8.9	8.1	9.2	8.6	7.8	7.2	8.8	7.7

Table 3 Performance of sunflower hybrid entries in multilocation trial and station hybrid trials in West Bengal (2013-14 to 2014-15)

Hybrid	2014-15			2013-14			Seed Yield (kg/ha) over the MLT and SHT over the Years (2014-15 and 2013-14)
	Seed yield (kg/ha) over the MLT (3 Location)	Seed yield (kg/ha) in SHT, Nimpith	Seed yield (kg/ha) over the MLT and SHT	Seed yield (Kg/ha)in MLT(3 location)	Seed yield (kg/ha in SHT, Nimpith	Seed Yield (kg/ha) over the MLT and SHT	
PSCHT -KH-12-38	2387	2480	2433	2065	2256	2160	2296.5
PSCHT -KH-12-42	2348	2130	2239	1960	2233	2096	2167.5
PSCHT -KH-12-26	2242	2153	2198	1967	2156	2061	2129.5
PSCHT -KH-12-29	1853	1740	1797	1783	2111	1947	1872.0
SAHT-12-21	2165	2222	2194	1703	2028	1865	2029.5
PSCHT -KH-12-76	1841	1898	1870	1927	1967	1947	1908.5
PSCHT -KH-12-36	2138	2222	2180	1907	1900	1903	2041.5
SAHT-K-12-18	1938	2025	1982	1967	1889	1928	1955.0
PSCHT -KH-12-35	1667	1820	1744	1663	1760	1711	1727.5
SAHT-K-12-09*	1906	1866	1886	1607	1975	1791	1838.5
PSCHT -KH-12-66	1894	2016	1955	1903	1740	1821	1888.0
PSCHT -KH-12-68	2223	2373	2298	1950	2040	1995	2146.5
SAHT-KH-12-15	1967	1898	1933	1760	1980	1870	1901.5
KBSH-44	2230	2407	2319	1840	2190	2015	2167.0
DRSH-1	1912	2030	1971	1693	1856	1774	1872.5
SEm(±)	49.5	41.5	45.4	32.5	41.5	38.1	41.5
G. Mean	2047.5	2085.3	2066.4	1846.3	2005.4	1925.9	1996.1
C.D.(P=0.05)	151.8	129.2	139.5	87.5	116.4	122.8	130.6
C.V%	9.6	9.2	9.4	9.1	9.6	9.5	9.5

Table 4: Evaluation of superior sunflower hybrids in "On Station Trial" at Nimpith (2012-13 to 2014-2015)

Name of the Hybrid	Oil %			Avg. oil %	Oil yield (kg/ha)			Avg. seed yield (kg/ha)	Avg. oil yield (kg/ha)	Oil yield improvement over DRSH-1	PDI (%) of *S. rolfsii*
	2014-15	2013-14	2012-13		2014-15	2013-14	2012-13				
PSCHT-KH- 12-38	35.6	36.4	36.2	36.0	852.9	812.5	776.4	2260.0	815.0 (3rd)	9.0	11.5%
PSCHT-KH-12-42	36.3	36.8	38.7	37.3	773.2	821.7	924.5	2250.7	839.8	12.3	10.0
PSCHT-KH-12-26	36.5	37.9	38.6	37.7	785.8	817.1	899.4	2216.7	834.1	11.5	9.5
PSCHT-KH-12-29	38.4	38.2	37.8	38.1	708.2	760.4	772.6	1964.0	749.1	0.1	10.0
SAHT-KH-12-21	35.4	35.2	36.5	35.7	786.6	713.9	751.5	2194.3	754.0	0.8	12.5
PSCHT-KH-12-76	37.3	37.8	38.6	37.9	708.0	693.5	680.6	1925.3	695.7	-7.0	12.5
PSCHT-KH-12-36	37.7	36.8	37.6	37.8	825.5	725.9	837.2	2151.7	796.5	6.5	10.0
SAHT-KH 12-18	38.4	37.6	39.2	38.4	832.9	812.5	776.4	2093.7	805.0	7.6	12.5
PSCHT-KH 12-35	37.6	38.2	38.8	38.2	684.3	672.3	653.6	1926.7	670.7	-10.3	12.5
SAHT-KH-12-09	37.5	38.2	38.5	38.1	732.9	712.5	676.4	1927.0	708.0	-5.3	10.0
PSCHT-KH-12-66	38.9	38.1	38.6	38.5	812.0	752.9	729.5	1898.7	764.2	2.2	10.0
PSCHT-KH-12-68	36.6	37.0	37.5	37.0	858.5	804.8	832.5	2237.7	828.6	10.5	12.5
SAHT-KH-12-15	37.6	37.4	38.0	37.7	723.6	690.5	676.7	1974.0	696.6	-6.9	15.0
KBSH-44	27.9	27.5	29.6	28.3	671.6	602.3	612.7	2222.3	628.9	-	22.5
DRSH-1	38.5	39.2	39.5	39.1	781.6	727.6	734.7	1915.3	748.0	-	20.0
S Em (±)	0.09	0.12	0.13	0.12	13.7	11.6	18.1	41.5	14.6	-	12.7
Mean	36.6	36.8	37.6	37.0	767.2	736.4	804.5	2083.2	769.4	-	0.74
C.D	0.28	0.36	0.41	0.35	41.6	34.7	54.2	130.6	44.2	-	2.5
C.V%	8.9	9.4	9.1	9.2	9.3	9.1	9.7	9.5	9.4	-	7.7

Table 5 Ranking of sunflower hybrids as per their performance in on station and multilocation trials

Hybrid	Oil %			Avg. oil %	Oil yield (kg/ha)			Avg. Seed yield (kg/ha)	Avg. Oil yield (kg/ha)	PDI (%) of *S. rolfsii*
	2014-15	2013-14	2012-13		2014-15	2013-14	2012-13			
PSCHT-KH- 12-42	36.3	36.8	38.7	37.3	773.2	821.7	924.5	2250.7	839.8	10.0
PSCHT-KH-12-26	36.5	37.9	38.6	37.7	785.8	817.1	899.4	2216.7	834.1)	9.5
PSCHT-KH-12-68	36.6	37.0	37.5	37.0	858.5	804.8	832.5	2237.7	828.6	12.5
PSCHT-KH-12-38	35.6	36.4	36.2	36.0	852.9	812.5	776.4	2260.0	815.0	11.5
SAHT-KH-12-18	38.4	37.6	39.2	38.4	832.9	812.5	776.4	2093.7	805.0	12.5
DRSH-1 (Ch-1)	38.5	39.2	39.5	39.1	781.6	727.6	734.7	1915.3	-	20.0
KBSH-44(Ch-2)	27.9	27.5	29.6	28.3	671.6	602.3	612.7	2222.3	-	22.5

Based on the overall performance in various locations across years, PSCHT- KH-12-26, PSCHT-KH-12-42 and PSCHT-KH-12-38 were identified as promising hybrids for cultivation in *rabi*-summer season in West Bengal agro-climatic condition.

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Screening of genotypes against castor wilt (*Fusarium oxysporum* f.sp. *ricini*)

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ABSTRACT

Assessment of genotypes by artificial wilt screening was done on a set of forty genotypes of castor grown during *rabi* 2015-16 at Pulses and Castor Research Station, Navsari Agricultural University, Navsari, Gujarat. Among the genotypes studied, 16 (JI-422, JI-384, JI-416, JI-402, JI-258, SKP-84, GEETA, JP-86, JI-368, JI-403, JI-423, JI-424, SKP-72, SKP-106, RG-43 and 48-1) showed resistant reaction for wilt disease. Thus the resistant genotypes can be used in breeding programme to develop wilt resistant varieties/hybrids in castor.

Keywords: Artificial screening, Castor, *Fusarium* wilt, Genotypes, Resistance

Castor (*Ricinus communis* L.) is an economically important oilseed crop grown historically in India and various countries. Castor is one of the few oilseeds having very high genetic variability for oil content ranging between 25 and 58 per cent (Anjani, 2012). In most of the cultivars, the oil content is about 48 per cent. Oil is unique among vegetable oils in terms of the presence of a hydroxyl fatty acid known as ricinoleic acid (12-hydroxyl-cis-9-octadecenoic acid), which constitute approximately 85 per cent of the total fatty acids of the oil. Castor oil is also distinguished from other vegetable oils by its high specific gravity, thickness and hydroxyl value. Castor oil is used either in its crude form, or in the refined hydrogenated form. Because of its unique chemical and physical properties, castor oil and its products are used in manufacturing of several industrial products including lubricants, paints and coatings, plastics, anti-fungal compounds, cosmetics etc (Kavani *et al.,* 2016). The importance of castor crop has gained further momentum in the recent time due to its biodiesel potential.

Castor crop is affected by several serious pests and diseases. Among the diseases the castor wilt is an important soil-borne disease of castor. Wilt in castor is primarily caused by *Fusarium oxysporum* f.sp. *ricini.* Castor wilt is a major problem in all castor growing areas of India leading to heavy yield losses, up to 80 per cent depending on the stage at which the plants are attacked by wilt (Pushpavati, 1995; Anjani *et al.,* 2004). The disease occurs frequently in severe form and results in heavy losses. Being a soil-borne disease, chemical control is difficult and non-economical. Hence, development of castor cultivars with inherent resistance to wilt is the only viable option to sustain the castor cultivation. However, breeding for wilt resistance has been challenging due to complex inheritance and pathogen variability.

A large number of segregating populations is to be screened for wilt resistance to identify the rare recombinants possessing agronomically superior traits coupled with wilt resistance. Although the pathogen is host-specific, different isolates show great deal of variation in pathogenicity (Nanda and Prasad, 1974). Screening several breeding lines for different isolates is a complex and cumbersome process. A breeding programme for disease resistance requires simple, rapid and reliable procedure for routine screening of progenies.

The experimental material for the present study comprised of forty genotypes obtained from SDAU Dantiwada; JAU Junagadh; IIOR, Hyderabad and AAU Anand. These genotypes were grown at Pulses and Castor Research Station, Navsari Agricultural University, Navsari during *rabi* 2015-16. Castor genotypes used in the study included VP-1, ANDCP-8-1, GEETA, JP -86, SKP-72, SKP -106, JP-65, RB-1, JI-96, JI-244, JI-258, JI-263, JI-346, JI-357, JI-368, JI-378, JI-380, JI-384, JI-390, JI-398, JI-397,JI-401, JI-402, JI-403, JI-406, JI-409, JI-412, JI-415, JI-416, JI-422, JI-423, JI-424, JI-430, SKI-271, SKI-332, SKI-343, RG-43, 48-1 and JI-35.

Root dip inoculation method given by Raoof and Nageshwar Rao (1996) was utilized for screening of experimental material against wilt under protected condition. The number of plants affected by wilt was counted per pot and per cent of wilt incidence was calculated by using the following formula:

$$\text{Wilt incidence (\%)} = \frac{\text{Number of wilt infected plants}}{\text{Total number of plants}} \times 100$$

The selected set of 40 genotypes were screened for reaction to *F. oxysporum* f.sp. *ricini* using under protected condition at Castor and Pulses Research Station. The genotypes, 48-1 and JI-35 were used as resistant and susceptible checks, respectively. The initial inoculum of *F. oxysporium* f.sp. *ricini* was prepared by isolating the pathogen from the infected roots of a susceptible castor genotypes and culturing it on Potato Dextrose Agar (PDA) medium.

A. Pure culture of *Fusarium oxysporium* f.sp. *ricini* was isolated from infected roots of castor and grown on PDA and was purified by single spore isolation technique.

B. Castor seedlings were grown using cocopit media in a tray (30 seedlings were grown for each genotypes).

C. Fifteen day old castor seedlings were uprooted, roots were washed using tap water then root tips were trimmed and dipped in spore suspension (1×10^6 spores/ml) for about 60-90 seconds.

D. Two seedlings were transplanted in a bag filled with pottery mixture (garden soil : vermiculite 3 : 1) after making holes in the soil. Plants were observed for the development of wilt periodically and final wilt incidence was recorded at the end of the month.

Fig. 1. Artificial screening procedure followed for identifying wilt resistant genotypes (Raoof and Rao, 1996)

The culture was purified by single spore isolation technique and maintained on PDA slants. The mass multiplication of the pathogen was done on sorghum (*Sorghum bicolour* L.) grains as substrate. The semi-cooked sorghum grains (100gm in 250 ml conical flask) were sterilized in autoclave at 15 psi for 20 min at 121°C. Then, the petri plates were inoculated with the pure fungus culture from the PDA slants and incubated at 27°C in a BOD incubator.

The observations on the disease reaction were continued till one week after the susceptible check died. Genotypes were grouped into two categories as resistant (>20% wilt incidence) and susceptible (>20% wilt incidence). Out of 40 genotypes screened for wilt disease artificially, 16 castor accessions showed resistant reaction for wilt disease while, remaining 24 genotypes showed susceptible reaction. Wilt disease incidence and reactions is mentioned in Table 1. The genotypes JI-422 (6.7 %) followed by JI-384, JI-416 (10 %); JI-402, JI-258, SKP-84 (13.3 %); GEETA, JP-86, JI-368, JI-403, JI-423, JI-424 (16.7 %); SKP-72, SKP-106 and RG-43 (20 %) showed resistance reaction while, remaining genotypes showed susceptibility for wilt disease. The genotypes showing resistant reaction with high yield and other desirable characters can be used to develop high yielding lines in castor. Thus, results of our study are in line with the results reported by various workers viz., Anjani *et al*. (2014), Desai and Dange (2003) and Raoof and Nageshwar (1996). The present findings are more or less in agreement with the findings of the above workers.

Table 1 Per cent wilt incidence and reaction of castor genotypes

Genotypes	Wilt incidence (%)	Reaction by genotype
SKP-84	13.3	R
VP-1	56.7	S
ANDCP-8-1	40.0	S
GEETA	16.7	R
JP -86	16.7	R
SKP-72	20.0	R
SKP-106	20.0	R
JP-65	46.7	S
RB-1	23.3	S
JI-96	23.3	S
JI-244	26.7	S
JI-258	13.3	R
JI-263	36.7	S
JI-346	46.7	S
JI-357	50.0	S
JI-368	16.7	R
JI-378	26.7	S
JI-380	30.0	S
JI-384	10.0	R
JI-390	26.7	S
JI-398	30.0	S
JI-397	40.0	S
JI-401	50.0	S
JI-402	13.3	R
JI-403	16.7	R
JI-406	43.3	S
JI-409	46.7	S
JI-412	50.0	S
JI-415	56.7	S
JI-416	10.0	R
JI-422	6.7	R
JI-423	16.7	R
JI-424	16.7	R
JI-430	66.7	S
SKI-271	60.0	S
SKI-332	50.0	S
SKI-343	53.3	S
RG-43	20.0	R
48-1	6.7	R
JI-35	96.7	S

R=Resistant; S=Susceptible

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AICRP on Soybean 1992. *Proceedings of 23rd Annual Workshop of All-India Co-ordinated Research Project on Soybean*, held during 7-9 May 1992 at University of Agricultural Sciences, Bangalore, Karnataka, National Research Centre for Soybean, Indore, pp.48.

Devakumar C. 1986. Identification of nitrification retarding principles in neem (*Azadirachta indic*a A.Juss.) seeds. Ph D Thesis, Indian Agricultural Research Institute, New Delhi.

Reference to unpublished work should normally be avoided and if unavoidable it may be mentioned only in the text.

Short Communication

Conceptually short communication is a first report on new concept, ideas and methodology which the author(s) would wish to share with the scientific community and that the detailed paper would follow. Short Communication is akin to an advance booking for the report on the findings. Short communications may include short but trend-setting reports of field or laboratory observation(s), preliminary results of long-term projects, or new techniques or those matters on which enough information to warrant its publication as a full length article has still not been generated but the results need to be shared immediately with the scientific community. The style is less formal as compared with the "full-length" article. In the short communications, the sections on abstract, materials and methods, results and discussion, and conclusion are omitted; but the material is put concisely in the same sequence but without formal sections. The other instructions are the same as in the case of the full-length articles.

Tables

Tables should not form more than 20% of the text. Each table should be typed on separate sheet and should have on the top a table number (in Arabic numerals *viz*. 1, 2, 3 etc.) and a caption or title which should be short, but sufficiently explanatory of the data included in the table. Information in the table should never duplicate that in the text and vice versa. Symbols (asterisks, daggers, etc. or small letters, *viz*., a, b, etc.) should be used to indicate footnotes to tables. Maximum size of table acceptable is what can be conveniently composed within one full printed page of the journal. Over-sized tables will be rejected out-right. Such tables may be suitably split into two or more small tables.

The data in tables should be corrected to minimum place of decimal so as to make it more meaningful. Do not use full stop with CD, SEm $\pm$, NS (not C.D., S.E.m $\pm$, N.S.). Do not put cross-rules inside the table. Tables should be numbered consecutively and their approximate positions indicated in the margin of the manuscript. Tables should not be inserted in the body of the text. Type each table on a separate sheet. Do not use capital letters for the tabular headings, do not underline the words and do not use a full-stop at the end of the heading. All the tables should be tagged with the main body of the text i.e. after references.

Figures

Figures include diagrams and photographs. Laser print outs of line diagrams are acceptable while dot-matrix print outs will be rejected. Alternatively, each illustration can be drawn on white art card or tracing cloth/ paper, using proper stencil. The lines should be bold and of uniform thickness. The numbers and letterings must be stenciled; free-hand drawing will not be accepted. Size of the illustrations as well as numbers, and letterings should be sufficiently large to stand suitable reduction in size. Overall size of the illustrations should be such that on reduction, the size will be the width of single or double column of the printed page of the Journal. Legends, if any, should be included within the illustration. Each illustration should have a number followed by a caption typed/ typeset well below the illustration.

Title of the article and name(s) of the author(s) should be written sufficiently below the caption. The photographs (black and white) should have a glossy finish with sharp contrast between the light and the dark areas. Colour photographs/ figures are not normally accepted. One set of the original figures must be submitted along with the manuscript, while the second set can be photocopy. The illustrations should be numbered consecutively in the order in which they are mentioned in the text. The position of each figure should be indicated in the margin of the text. The photographs should be securely enclosed with the manuscript after placing them in hard board pouches so that there may not be any crack or fold. Photographs should preferably be 8.5 cm or 17 cm wide or double the size. The captions for all the illustrations (including photographs) should be typed on a separate sheet of paper and placed after the tables.

Expression of Plant Nutrients on Elemental Basis

The amounts and proportions of nutrient elements must be expressed in elemental forms e.g. for ion uptake or in other ways as needed for theoretical purposes. In expressing doses of nitrogen, phosphatic, and potassic fertilizers also these should be in the form of N, P and K, respectively. While these should be expressed in terms of kg/ha for field experiments, for pot culture studies the unit should be in mg/kg soil.

SI Units and Symbols

SI Units (System International d 'Unities or International System of Units) should be used. The SI contains three classes of units: (i) base units, (ii) derived units, and (iii) supplementary units. To denote multiples and sub-multiples of units, standard abbreviations are to be used. Clark's Tables: Science Data Book by Orient Longman, New Delhi (1982) may be consulted.

Some of these units along with the corresponding symbols are reproduced for the sake of convenience.

Names and Symbols of SI Units

Physical Symbol for SI Unit Symbol Remarks quantity physical quantity for SI Unit

Primary Units					
length	l		time	t	
metre	m		second	s	
mass	m		electric current	I	
kilogram	kg		ampere	A	
Secondary Units					
plane angle	radian	rad	Solid angle	steradian	sr
Unit Symbols					
centimetre	cm		microgram	µg	
cubic centimetre	cm^3		micron	µm	
cubic metre	m^3		micronmol	µmol	
day	d		milligram	mg	
decisiemens	dS		millilitre	mL	
degree-Celsium	°C [=(F-32)x0.556]		minute	min	
gram	g		nanometre	nm	
hectare	ha		newton	N	
hour	h		pascal	Pa	
joule J	(=10^7 erg or 4.19 cal.)		second	s	
kelvin	K (=°C+273)		square centimetre	cm^2	
kilogram	kg		square kilometre	km^2	
kilometre	km		tonne	t	
litre	L		watt	W	
megagram	Mg				

Some applications along with symbols

adsorption energy	J/mol (=cal/molx4.19)	leaf area	m^2/kg
cation exchange capacity	cmol (p+)/kg (=m.e./100 g)	nutrient content in plants (drymatter basis)	µg/g, mg/g or g/kg
Electrolytic conductivity	dS/m (=mmhos/cm)	root density or root length density	m/m^3
evapotranspiration rate	$m^3/m^2/s$ or m/s	soil bulk density	Mg/m^3 (=g/cm^3)
heat flux	W/m^2	specific heat	J/kg/K
gas diffusion	$g/m^2/s$ or $m^3/m^2/s$ or m/s	specific surface area of soil	m^2/kg
water flow	$kg/m^2/s$ (or) m^3m^2s (or) m/s	thermal conductivity	W/m/K
gas diffusivity	m^2/s	transpiration rate	$mg/m^2/s$
hydraulic conductivity ion uptake	m/s	water content of soil	kg/kg or m^3/m^3
(Per kg of dry plant material)	mol/kg	water tension	kPa (or) MPa

While giving the SI units the first letter should not be in capital i.e cm, not Cm; kg not Kg. There should not be a full stop at the end of the abbreviation: cm, not cm. kg, not kg.; ha, not ha.

In reporting the data, dimensional units, viz., M (mass), L (length), and T (time) should be used as shown under some applications above. Some examples are: 120 kg N/ha; 5 t/ha; 4 dS/m etc.

Special Instructions

I. In a series or range of measurements, mention the unit only at the end, e.g. 2 to 6 cm2, 3, 6, and 9 cm, etc. Similarly use cm2, cm3 instead of sq cm and cu m.

II. Any unfamiliar abbreviation must be identified fully (in parenthesis).

III. A sentence should not begin with an abbreviation.

IV. Numeral should be used whenever it is followed by a unit measure or its abbreviations, e.g., 1 g, 3 m, 5 h, 6 months, etc. Otherwise, words should be used for numbers one to nine and numerals for larger ones except in a series of numbers when numerals should be used for all in the series.

V. Do not abbreviate litre to` l' or tonne to `t'. Instead, spell out.

VI. Before the paper is sent, check carefully all data and text for factual, grammatical and typographical errors.

VII. Do not forget to attach the original signed copy of `Article Certificate' (without any alteration, overwriting or pasting) signed by all authors.

VIII. On revision, please answer all the referees' comments point-wise, indicating the modifications made by you on a separate sheet in duplicate.

IX. If you do not agree with some comments of the referee, modify the article to the extent possible. Give reasons (2 copies on a separate sheet) for your disagreement, with full justification (the article would be examined again).

X. Rupees should be given as per the new symbol approved by Govt. of India.

Important Instructions

- Data on field experiments have to be at least for a period of 2-3 years
- Papers on pot experiments will be considered for publication only as short communications
- Giving coefficient of variation in the case of field experiments Standard error in the case of laboratory determination is mandatory. For rigorous statistical treatment, journals like Journal of Agricultural Science Cambridge, Experimental Agriculture and Soil Use and Management should serve as eye openers.

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