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Review

A critical review on role of biofertilizers in enhancing the productivity of oilseed crops

M JAYAKUMAR[1*], A SOLAIMALAI AND K BASKAR

Agricultural Research Station, Tamil Nadu Agricultural University, Kovilpatti-628 501, Tamil Nadu

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ABSTRACT

Oilseeds are mainly cultivated as rainfed crop with poor input resources. This will have impact on plant health particularly plant nutrition, pests, diseases and weeds. Further, this problem is region specific and depends on the soil condition and climate. Biofertilizers are the products containing different types of beneficial microorganisms. Applications of biofertilizers have definite advantage over chemical fertilizers in oilseed crops. Chemical fertilizers supply nitrogen in higher concentrations whereas bio-fertilizers provide nutrients in small amounts in a sustained way. In addition to nutrients, certain growth promoting substances like hormones, vitamins, amino acids, etc are made available to plants. Bio-fertilizers application will have impact on organic agriculture, reduction of environmental pollution, soil health improvement and reduction in input use for oilseed crops. Current soil management strategies are mainly dependent on chemical based fertilizers, which caused a serious threat to human health and environment. The exploitation of beneficial microbes as a biofertilizer has become important in agriculture sector for their potential role in food safety and sustainable crop production. The eco-friendly approaches inspire a wide range of application of plant growth promoting rhizobacteria (PGPRs), endo and ectomycorrhizal fungi and many other useful microscopic organisms led to improved nutrient uptake, plant growth and plant tolerance to abiotic and biotic stress. The knowledge gained from the literatures appraised herein helped us to understand the physiological bases of biofertlizers towards sustainable agriculture in reducing problems associated with the use of chemicals fertilizers in oilseeds production.

Keywords: *Azospirillum, Azotobacter*, Biofertilizers, PGPR, Phosphobacteria, VAM, Oilseed crops

Application of high input technologies such as chemical fertilizers, pesticides, herbicides have improved the production of oilseed crops but there is a growing concern over the adverse effects of the use of chemicals on soil productivity and environment quality. Thus, integrated nutrient management has become an accepted strategy to bring about improvement in soil fertility and protecting the environment. This strategy utilizes a judicious combination of fertilizers, organic manures and bio-fertilizers. Bio fertilizer is a natural product carrying living micro-organisms derived from the root or cultivated soil. So they are not expected to have any ill effect on soil health and environment. Besides, their role in atmospheric nitrogen fixation and phosphorous solubilisation also help in stimulating the plant growth hormones providing better nutrient uptake and increased tolerance towards drought and moisture stress (Sheraz Mahdi *et al.,* 2010). A small dose of bio-fertilizer is sufficient to produce desirable results because each gram of quality carrier of biofertilizers contains at least 10 million viable cells of a specific strain (Alori and Babalola, 2018).

[1]Central Coffee Research Institute, Coffee Research Station, Chikmagaluru-577 117, Karnataka;
[*]Corresponding author's E-mail: agrokumar2013@gmail.com

Biofertilizers, a cost effective renewable energy source helps in reducing the inorganic fertilizer level and at the same time enhances the crop yield besides maintaining the soil fertility. The replenishment of nutrients lost by crop removal through the use of chemical fertilizers alone is not advisable in the long run, since their continuous use, impaired the soil health and productivity. Biofertilizers such as bacteria, fungi and actinomyces can help in reducing the input of inorganic fertilizers to an extent of 25% for obtaining the same or higher yield (O'Callaghan, 2016). Biofertilizers are microbial preparations containing live cells of specific microorganisms to be applied to the seed or soil, which multiply and bring out several activities such as nitrogen fixation or phosphate solubilization /mobilization in the root region of crop plants.

The aim of using N-biofertilizers is to increase soil content of free living bacteria such as *Azotobacter* sp., *Azospirillum* sp., *Klebsiella* sp. and others which are expected to increase N-fixation in the soil. Of course symbiotic bacteria of genus *Rhizobium* is also considered as a good way of N-fixation in legume crops. Bio-fertilizers add about 20-200 kg N/ha (by fixation) under optimum conditions and solubilize/mobilize 30-50 kg P_2O_5/ha (Senthilkumar and Kanjana, 2009). They release growth

promoting substances and vitamins and thus help to maintain soil fertility. They increase crop yield by 10-15 %, N-fixers reduce depletion of soil nutrients and provide sustainability to the farming system. They improve soil physical properties, tilth and soil health in general. The nitrogen-fixing microorganisms like *Rhizobium*, *Azospirillum, Azotobacter, Azolla*, Cyanobacteria, etc fix nearly 175 x 10^6 tonnes of N on the earth surface and it may be possible to meet a large part of nitrogen demand through proper manipulation of these organisms in crop production system (Kumar, 2013).

Azotobacter

Azotobacter represents the main group of heterotrophic free living nitrogen-fixing bacteria. They are gram negative, large ovoid pleomorphic cells of 1.5-2.0 µm or more in diameter ranging from rods to coccoid cells. They occur singly or in paired or irregular clumps and sometime in chains of varying length. They do not produce endospores but form cysts. They are motile by peritrichous flagella or non-motile. *Azotobacter* sp. is most specifically noted for their nitrogen fixing ability. But they have also been noted for their ability to produce different growth hormones (IAA, gibberellins and cytokinins), vitamins. *Azotobacter* is capable of converting nitrogen to ammonia, which in turn is taken up by the plants. *Azotobacter* sp. can also produce antifungal compounds to fight against many plant pathogens (Jacob *et al*., 2016).

Azospirillum

They are called associative endosymbiont on roots of grasses and similar types of plants. They are also known to fix atmospheric nitrogen and benefit host plants by supplying growth hormones indole acetic acid and vitamins. *Azospirillum* is considered to be more efficient. *Azospirillum* inoculation is reported to have increased the growth, nitrogen uptake and yield in a number of crops (Ram *et al*., 1992).

Phosphobacteria

Microorganisms also involves in enhancing the availability of phosphorus which is second most important nutrient required by crop plants. The phosphate solubilizing bacteria (PSB) solubilize the insoluble phosphates and make them available for crop plants. Several soil bacteria and fungi notably species of *Pseudomonas, Bacillus, Penicillium* and *Aspergillus* etc. secrete organic acids and lower the pH in their vicinity to bring about solubilization of bound phosphates in soil. Increase in the yield of various crops has been demonstrated due to inoculation of peat based cultures of phosphobacteria which saves up to 50% of recommended level of P_2O_5 (Daravath Raja and Takankhar, 2018).

Vesicular Arbuscular Mycorrhiza (VAM)

Mycorrhiza is the mutualistic association between plant roots and fungal mycelia. Many graminaceous plants, legumes and horticultural crops are colonized by VAM fungi. The transfer of nutrients mainly phosphorus from the soil to the cells of the root cortex is mediated by intracellular obligate fungal endosymbiont of the genera *Glomus, Gigaspora, Acaulospora, Scleroscystis* and *Endogone* which possess vesicles for storage of nutrients and arbuscular for funneling these nutrients into the root system. The mycorrhizal fungi mobilize phosphates and other micronutrients like zinc, boron and molybdenum from adjacent soil to the root system through hyphal network (Selim and Zayed, 2018).

Effect of biofertilizers on growth, yield and quality of groundnut

In groundnut, higher dry matter production in application of both *Rhizobium* and phosphobacteria was due to the fact that it produced maximum shoot length, higher number of branches per plant and leaf area index (LAI) (Chetti *et al.,* 1995). Phosphate solubilizing bacteria had indirect effect on nodulation which contribute to increase in yield of groundnut crop (Ghosh and Poi, 1998). Inoculation of *Rhizobium* sp. seed treatment recorded superiority over PSB inoculation (More *et al.,* 2002; Zalate and Padmani, 2009).Seed inoculation with *Rhizobium* has increased the number of nodules, pods/plant, 100-seed weight and gave kernel yield of 1.27 t/ha in groundnut as compared to 1.11 t/ha without seed inoculation (Joshi *et al.,* 1989). Asha *et al.* (1996) observed that seed inoculation with *Pseudomonas striata* or *Paecilomyces fussisporus* resulted in higher number and dry weight of nodules/plant, protein content in kernels and haulm yield of groundnut over control. Patel and Thakur (1997) found that recorded the 8.23% increase in groundnut yield due to Rhizobium inoculation compared to uninoculated control.

Baig *et al.* (2002) revealed that significant increase in the growth and yield of groundnut plants treated with *Rhizobium* + PGPR followed by PGPR alone both in field and pot trials. Panwar and Singh (2003) reported that seed inoculation with *Rhizobium* or PSM marginally improved yield, but their combined use increased pod yield significantly. Both the organics, i.e. FYM and neem cake, significantly increased pod and haulm yields, but when half quantity of these organics was integrated with *Rhizobium*

and PSM, the highest pod yield of 31.80 q/ha with FYM 5 t/ha + *Rhizobium* + PSM was obtained. Debasree Gupta (2007) reported that nodule number and weight/plant improved marginally with VAM and mossori rock phophate (MRP) treatment, but was much better in cases where FYM was applied. Growth parameters such as plant height, leaflet number and shoot dry weight showed a trend similar to each other. The improvement in all the parameters took place in the following order of the treatments: VAM + FYM (almost 30% over the control) > FYM > VAM+MRP (almost 14% over the control) > VAM > MRP > control. Pod number and pod weight per plant improved significantly over the control in FYM, VAM + MRP and VAM + FYM (45, 35 and 50% over the control, respectively).

Patra *et al*. (2008) observed that application of recommended dose of fertilizer (25:50:75 N, P and K kg/ha) along with inoculation of groundnut seeds with *Rhizobium* strain 1GR-6 or NRCG-9 significantly increased nodules/ plant and nodule dry weight/plant at 40 and 80 days after sowing (DAS) over control. There was significant influence of nitrogen and *Rhizobium* inoculation on enhanced vegetative growth in terms of number of branches (Edna Antomy *et al.,* 2000). Farmers' practice supplemented with Rhizobium inoculation significantly increased dry pod yield under medium deep black soils of Maharashtra (Karmakar *et al.,* 2005). In sandy loam soils of mid hill zone of Meghalaya, inoculation with *Rhizobium* culture resulted in improvement of pod yield of groundnut but higher benefit were obtained with dual inoculation of Rhizobium and phosphate solubilizing bacteria (Panwar *et al.,* 2002). At Umiam (Meghalaya), Patel *et al.* (2002) reported a significant increase in pod yield, 100-pod weight and shelling percentage due to *Rhizobium* inoculation but as of pods/plant and pod weight/plant were at par with uninoculated treatment. Datta *et al.* (2014) found that inoculation of *Rhizobium* culture along with 50 kg P_2O_5 + 50 kg K_2O/ha showed 45 % increment in pod yield (from 1.37 to 1.95 t/ha) over control during *kharif* season.

Mohapatra and Dixit (2010) observed that inoculation with Rhizobium improved the nodulation that enhanced N fixation, activation of amino acids for synthesis of carbohydrate and consequently expressed in increase in number of pods/plant, 100 kernel weight and pod yield. Bandyopadhyay *et al.* (2011) reported that local strain of West Bengal of *Rhizobium* inoculation performed better (*Rabi* 2.22 tonnes/ha and pre-*kharif* 2.50 tonnes/ha) than BR 3267 and control during both the seasons. Sharma *et al.* (2013) observed that application of Rhizobium, being at par with PSB and VAM, significantly increased number of pods/plant, kernels/pod, seed index, pod, haulm and biological yield and shelling percent over control.

Singh *et al.* (2013) reported that higher pod and haulm yield were recorded in groundnut which was 35.5 and 26.1% higher over untreated control. Singh *et al.* (2013) observed that maximum seed yield of 1713 kg/ha was recorded with combined inoculation with *Rhizobium* + PSM which was 5.67, 16.60 and 28.60% higher over Rhizobium, PSM (Porous surface model) and inoculated control respectively. Application of *Rhizobium* + PSM increased uptake of N, P, and Ca significantly over the control. Patra *et al.* (2008) found that recommended dose of fertilizer (RDF) + *Rhizobium* inoculation with IGR-6 strain increased pod yield by 62% over control and 14.2% over RDF. Sharma *et al.* (2014) observed that the inoculation of *Rhizobium* recorded higher uptake of N, P and K to the tune of 25.5, 23.0 and 18.5 % over no inoculation but remained at par with PSB and VAM inoculation during *kharif* season.

Ola *et al*. (2013) reported that seed inoculation with Rhizobium recorded the higher N content and uptake than PSB and found significantly superior to control. Singh *et al.* (2011) reported that application of *Rhizobium* + PSM (Porous surface model) recorded higher net returns of ₹.22755/ha with benefit cost ratio of 1.49 followed by *Rhizobium*. Biofertilizers enriched vermicompost recorded increased growth attributes, yield, protein and oil content. The organic fractions of flower waste vermicompost and biofertilizers could be an alternative to chemical fertilizers to improving the growth and yield of groundnut (Senthil Kumar *et al.,* 2014). Application of 50% RDF + 5 t FYM/ha + *Rhizobium* @ 25 gram/kg of seeds + PSB @ 30 gram/kg of seeds to groundnut provided an effective option of nutrient management in groundnut-pigeonpea relay intercropping system (Poonia *et al.,* 2014). Seed inoculation with biofertilizers (Rhizobium+PSM) significantly increased the plant height, nodules/plant, yield attributing characters and yield of groundnut. Manuring the crop with FYM 6 t/ha + *Rhizobium* + PSM gave significantly 40.19 and 35.96% higher pod and haulm yields of groundnut, respectively over no manuring.

Groundnut (variety JL-1085) (Phule Dhani) inoculated with *Rhizobium* + phosphate-solubilizing bacteria recorded significantly higher pod (1.74 t/ha) and haulm yields (3.64 t/ha) of groundnut and grain (5.34 t/ha) and straw yields (5.52 t/ha) of succeeding rice over the control. Inoculation of groundnut with biofertilizers significantly increased N, P, K uptake by groundnut and succeeding rice as well as total N, P and K uptake (393.1 kg/ha), rice grain equivalent yield (9.92 t/ha), net returns (66.8×10^3/ha) and benefit: cost ratio (2.01) in groundnut - rice cropping system over no inoculation (Chavan *et al.,* 2014). At Latur (Maharashtra), seed inoculation of *Rhizobium* + PSB recorded higher growth and yield attributes, dry pod yield (2381 kg/ha) and haulm yield (3630 kg/ha) individual inoculation of *Rhizobium* (2159 kg/ha) or PSB (1831 kg/ha) alone in summer groundnut crop (Patil *et al*., 2014).

At Bhubaneswar (Odisha), integrated application of RDF (20:40:40 kg NPK/ha) + *Rhizobium* (20 gram/kg of kernel) + FYM (10 t/ha) + lime (0.2 LR) and gypsum (250 kg/ha) produced higher pod yield, haulm yield, harvest index, oil content % and oil yield of 2292, 4067, 39.30, 49.8 and 850 kg/ha. Supplementation of RDF + *Rhizobium* + FYM, RDF + gypsum, RDF + *Rhizobium* + FYM + Lime, RDF + *Rhizobium* + FYM + Lime + gypsum produced 16.82, 17.73, 26.26 and 39.16% higher pod yield respectively over RDF alone (Baruna Kumar 2015).

At Junagadh (Gujarat), application of 100% RDF for Gujarat Groundnut 20 for groundnut and Gujarat Tur 101 for pigeonpea recorded higher pigeonpea equivalent (PE) seed yield (2546 kg/ha) which was on par with 50% RDF + FYM 5 t /ha + *Rhizobium* @ 25 g/kg seed + PSB @ 30 g/kg seed by producing 2350 kg/ha PE seed yield). However, the reduction in chemical fertilizers up to 50% of RDF gave 7.7% less yield over 100% RDF application. Similarly, higher net returns was recorded in 100% RDF recommended doses of fertilizers for groundnut and pigeon pea are 12.5:25:00 and 25:50:00 kg NPK/ha to both the crops (₹ 64400/ha) than 50% RDF + FYM 5 t/ha + *Rhizobium* + PSB (₹59300/ha). Application of 50 % RDF + FYM 5 t/ha + *Rhizobium* + PSB to groundnut provided an effective option of nutrient management in groundnut - pigeonpea relay intercropping system (Poonia *et al*., 2014).

At Jhansi (Uttar Pradesh), maximum plot yield was recorded in arbuscular mycorrhizal fungi + *Rhizobium* + PSB (260.8 g/plot) which was significantly higher than control. Combined application of bio-inoculants gave better results than single inoculation (Naresh Kumar *et al.,* 2018). At Gwalior (Madhya Pradesh), application of bioformulation as liquid NPK with Zn solublizing bacteria (B2) resulted in better physiological growth and highest kernel (2114 kg/ha) and haulm yield (6676 kg/ha) of groundnut crop. Same treatment also resulted in highest protein and oil yield. Application of 100% RDF with bioformulation as NPK liquid formulation + Zn solubilizing bacteria produced highest LAI, CGR, RGR values as well as protein and oil yield of groundnut followed by 100% RDF with biogrow application of groundnut crop (Neelam Singh *et al*., 2018).

It could be concluded that application of both *Rhizobium* and phosphobacterium culture along with 50 kg P_2O_5 + 50 kg K_2O/ha produced maximum growth and yield attributes and 8.25-45% increment in pod yield and highest benefit cost ratio over control.

Effect of biofertilizers on growth, yield and quality of sesame

Imayavaramban *et al.* (2002) reported that integrated nutrient supply with FYM 12.5 t/ha + recommended NPK of 35:23:23 kg/ha + *Azospirillum* seed inoculum favourably improved the yield attributes and yield of sesame. In red loam soils of Tirupati (Andhra Pradesh), Sarala and Jagannatham (2002) reported that application of 60 kg N/ha to sesame produced seed yield which was comparable to that of application of 45 kg N/ha + *Azospirillum*. Jaishankar and Wahab (2005) reported that application of recommended dose of NPK + vermicompost at 5.0 t/ha + *Azospirillum* recorded higher yield components of sesame *viz.,* number of capsules/plant and number of seeds/capsule. Duhoon *et al.* (2002) reported that higher yield of sesame was recorded under 50 % N through urea + 50 % N through FYM + 50 % P with soil application of PSB (Phosphate Solubilizing Bacteria) at 500 g/ha + 100 % potash. Further Munji *et al.* (2010) reported that combined application of RDF + FYM + *Azospirillum* showed higher yield and yield components of sesame. At Rahuri (Maharashtra), seed weight/plant, seed and stalk yields and grain to stalk ratio were favourably influenced the application of 100% RDF+FYM 5 t/ha + vermicompost 5 t/ha+seed treatment of *Azospirillum* and PSB followed by the application of 75 % RDF + FYM 5 t/ha + vermicompost 5 t/ha + seed treatment of *Azospirillum* and PSB in summer sesame on clayey soil (Deshmukh *et al.,* 2010a).

Palaniappan *et al.* (1999) reported that integrated application of FYM at 10 t/ha and 100% recommended dose of N and P and biofertilizers (*Azospirillum* and Phosphobacteria) significantly increased the number of capsules/plant and seed yield. Ghosh and Mohiuddin (2002) reported that combined application of biofertilizers and growth regulators improved all the yield and yield attributes and thus markedly increased grain and stalk yields. Azospirillum increases dry matter production and yields in sesame (Senthilkumar *et al.,* 2000). Application of *Azospirillum* increased protein yield of sesame (Thiruppathi *et al.,* 2001). Significant yield increase was due to inorganic and biofertilizers in Tamil Nadu (Kalaiselvan *et al.,* 2002). Integrated application of chemical fertilizer and biofertilizer supplied plant nutrients for a longer period and higher uptake of nutrients by sesame (Duhoon *et al.,* 2004). Seed inoculation with Azospirillum showed higher yield and yield component of sesame (Shaikh *et al.* 2010; Munji *et al.* 2010). At Latur (Maharashtra), combined application of *Azotobacter* + PSB registered higher number of seeds/plant, capsules/plant, test weight, seed yield, straw yield, biological yield and harvest index (Wayase *et al.,* 2014).

The oil yield increased by 33.3%, while protein yield increased by 47.5% with treatment of half dose of fertilizer along with LES 4 (*Pseudomonas aeruginosa*) bacterized seeds, as compared to full dose of fertilizers (Kumar *et al.,* 2009). Seed inoculation of *Azotobacter* was able to produce seeds with either significantly higher compared with control

or similar 1000 seed weight (Debnath *et al.,* 2007). Soil inoculation with micro-symbiont inocula (particularly *Azospirilium* sp.) may be suitable for improving sesame performance where soils are mostly very low in nitrogen (Babajide and Fagbola, 2014). At Jhansi (Uttar Pradesh), significantly higher plot yield (246.2 g/plot) was recorded with application of arbuscular mycorrhizal fungi+ *Azosprillium* + PSB over control (Naresh Kumar *et al.,* 2018).

It could be concluded that 75% RDF + 5 t/ha each of FYM and vermicompost + seed treatment with *Azospirillum* and PSB seed inoculum favorably improved the growth, yield attributes and oil yield increased by 33.3%, while protein yield increased by 47.5% compared to control.

Effect of biofertilizers on growth, yield and quality of sunflower

Application of PSB (*Bacillus* M-13) was able to mobilize P efficiently in the sunflower and enhanced the head diameter, 1000 seed weight, kernel ratio and oil content and led to seed and oil yield increase to 15 and 24.7% respectively over untreated control. However, higher seed yield of sunflower possible with 100 kg P_2O_5/ha fertilizer was achieved with about 50 kg P_2O_5/ha when used in conjunction with PSB (Zehra Ekin, 2010). Inoculation of biofertilizers such as PSB + VAM + *Azotobacter* and application of sulphur @ 40 kg/ha was considered as the best treatment for sunflower, with respect to height, total chlorophyll content, thalamus diameter, weight of thalamus, filled seeds/capitulum and 100 seed weight, grain yield, stalk yield, biological yield, harvest index and oil content (Patra *et al.,* 2013). Biofertilization of *Azospirillum* + *Bacillus* plus 100% chemical fertilizers produced higher values in all growth and yield parameters compared with the control (Mostafa and AboBaker, 2010; Dhanasekar and Dhandapani, 2012).

Higher stem girth was recorded with the 100% N+ *Azospirillum* + *Azotobacter* which was significantly superior over all other treatments, except 75 % N + *Azospirillum* + *Azotobacter* (Keshta *et al.,* 2006; Javahery and Rokhzadi, 2011; Farnia and Moayedi, 2014; Farnia and Moayedi, 2015). Patra *et al.* (2013) also reported that bio fertilizers helped in increasing plant height and leaf chlorophyll content of sunflower. At Tehran (Iran), biofertilizer improved plant productivity and quality in sunflower seed. Application of bio fertilizer decreased the saturated fatty acids (palmitic and stearic) and increased unsaturated fatty acids (linoleic acid and oleic acid) and oil content compared with untreated plants (Akbari *et al.,* 2011). At Birbhum (West Bengal), inoculation of biofertilizers significantly increased aerial biomass production, crop growth rate (CGR), test weight, weight of thalamus, number of filled seeds/capitulum, seed yield, biological yield and oil content. The combined inoculation of PSB + VAM + *Azotobacter* recorded higher seed yield (3225 kg/ha) over control (Pramanik and Bera, 2013). At Parbhani (Maharashtra), combined application of the microbes enhanced the content and uptake of NPK better than individual application. NPK content and uptake by sunflower was significantly higher in dual inoculated plots with liquid form of *Azotobacter* and PSB compared with control (Dahiphale *et al.,* 2017).

At Parbhani (Maharashtra), application of 100% N + *Azospirillum* + *Azotobacter* recorded significantly higher seed yield, Filled seeds/plant and Unfilled seeds/plant (1848 kg/ha, 802 and 99) of sunflower with higher net monetary returns (₹ 34313) and B:C ratio (1.96) (Khandekar *et al*., 2018).

Effect of biofertilizers on growth, yield and quality of soybean

Seed inoculation with *Rhizobium* has increased the number of nodules, pods per plant, 100-seed weight and gave yields of 0.97 t/ha as compared to without seed inoculation (0.88 t/ha) (Joshi *et al.,* 1989). Inoculation of *Rhizobium* increased the seed yield from 21 to 41% in soybean and there was no significant difference between seed treatment and soil application (Pandzou *et al.,* 1990; Singh *et al.,* 2007). *Rhizobium* RS-1 significantly increased the N and K availability by 19.57 and 5.47% over control (Dubey, 1998; 2000; Meshram *et al.,* 2005). Interaction effect of liquid Brady-rhizobium and PSB increased the seed yield of soybean (Deshmukh, 2005).

Inoculation of soybean seeds with proper bacterial strains increased seed production by 70-75% (Simanungkalit *et al.,* 1996). Application of phosphate-solubilizing bacteria i.e., *Bacillus aryabhattai* in soybean crop was better than chemical fertilizer (Singh *et al.,* 2009; Zarei *et al.,* 2012). Soybean plants, as inoculated *Bradyrhizobium japonicum* with plots appeared much greener (Thelen and Schulz, 2010). Variety JS-335 showed significantly better response to *Bradyrhizobium japonicum* biofertiizer treatment compared to other varieties (Naveen kumar *et al.,* 2010).

Sawarkar and Thakur (2001) found that nodule number and nodule weight/plant, plant height, number of branches, number of pods and seed index had significantly improved with seed/soil inoculation of PSB in combination with chemical fertilizers. Meshram *et al.* (2004) found that there was significant improvement in soil fertility status by co inoculation of *Rhizobium* + PSB along with chemical fertilizers in soybean. There was significant improvement in

the amounts of available N, P_2O_5 and K_2O in all the bio fertilizer treated plots. Menaria and Pushpendra Singh (2004) observed that application of 40:40:20:40 kg N, P, K, S/ha significantly increased the yield attributing characters in soybean. Seed inoculation with various inoculants *viz., Rhizobium japonicum,* phosphate solubilizing bacteria and *Bradyrhizobium japonicum* + phosphate solubilizing bacteria has significantly improved the seed and stover yield over control. Jain and Trivedi (2005) found that the combined application of *Rhizobium* and PSB (phosphate solublizing bacteria) resulted in higher seed and oil yield and protein content.

At Latur (Maharashtra), soyabean variety MAUS-81 as a test crop, the availability of nitrogen in soil was increased by seed inoculation with liquid 10 ml of *Bradyrhizobium* (A2). Phosphorus availability in soil was improved by seed inoculation with liquid 10 ml of PSB (B2) (21.65 kg/ha), compared with control (15.77 kg/ha). However, in later stages N uptake was increased significantly due to seed inoculation with 10 ml of PSB. Organic carbon content in experimental soil was improved due to residual effect of soybean crop grown under liquid biofertilizers treatment (Raja and Takankhar, 2017).

The seed yield increases with the progressive increase in nutrient input and integration of organic and inorganic sources including zinc and magnesium and biofertilzers. The seed inoculation of biofertilizers increased the yield of soybean (Kumrawat *et al.,* 1997; Sharma and Namdeo, 1999; Thanki *et al.,* 2005). At Raipur (Chhattisgarh), maximum seed yield was observed in the application of 100% RDF + FYM 10 t/ha + zinc 5 kg/ha + magnesium 10 kg/ha + Rhizobium (25 gram/kg of seeds) + PSB (30 gram/kg of seeds) (65% increased yield compared over control), which was on par with 100% RDF or 50% RDF + FYM 10 t/ha + zinc 5 kg/ha + magnesium 10 kg/ha (Joshi, 2003; Sonkar *et al.,* 2008).

At Hyderabad (Telangana), 75% RDF + liquid based biofertilizers (LBF) (*Bradyrhizobium* and Phosphate Solubilizing Bacteria) soil application had more, seeds per pod, test weight and seed yield. LBF were considered as best alternative for the conventional carrier based biofertilizers (Hima Bindu *et al.,* 2016). At Latur (Maharashtra), number of pods and number of grains/plant, grain yield and straw yield were significantly affected due to integrated nutrient management (INM) treatments (Table 5). Application of 100% RDF+ 10 t FYM/ ha + 45 kg S/ha + biofertilizer) recorded significantly higher number of flowers, number of pods/plant, grain yield and straw yield/ha followed by 50% RDF + 10 t FYM+ 45 kg S/ha + biofertilizer under rainfed condition during *kharif* season (Ghodke *et al.,* 2018).

At Akola (Maharashtra), application of 50% N through glyricidia green manure + 50 % N through inorganic + biofertilizers (*Rhizobium* and PSB) used as seed treatment (@25 g/kg seed) + 25 kg k/ha resulted in higher grain and straw yield and nutrient uptake by soybean over other INM practices in Vertisols during *kharif* season (Satpute *et al.,* 2018). At Latur (Maharashtra), nitrogen content in plant was significantly increased, at maturity 7.93% and at harvest 3.62%, by seed inoculation with 10ml of *Bradyrhizobium* (A2) over control. Phosphorus content was significantly improved (at maturity 28.57% and at harvest 31.25%) by seed inoculation with 10 ml of liquid PSB over control (Daravath Raja and Takankhar, 2018).

It could be concluded that application of 100% RDF + FYM (10 t/ha) + zinc (5 kg/ha) + magnesium (10 kg/ha) + *Rhizobium* + PSB increased the seed yield between 21 to 65% in soybean and there was no significant difference between seed treatment and soil application compared over control. *Rhizobium*, both as seed treatment and soil application significantly increased the N and K availability by 19.57 and 5.47% over control.

Effect of biofertilizers on growth, yield and quality of safflower

Seed inoculation with *Azospirillum* alone resulted in enhanced growth in terms of plant height and other yield attributing characters and was on par with 50 % recommended inorganic N application. Seed inoculation with *Azospirillum* could result in absolute saving of 50 % of inorganic nitrogen (Sudhakar and Sudha Rani, 2010). Increasing uptake of NPK was observed with the increase in RDF level along with seed treatment with *Azospirillum* + PSB (Naseri Rahim *et al.,* 2010).

At Parbhani (Maharashtra), Kadu and Ismail (2008) reported improvement in dry matter (3154 kg/ha) and seed yield (1230 kg/ha) of safflower with application of full RDF (60:40:0 kg NPK/ha) + vermicompost 5 t/ha + vermiwash spray + biofertilizer (Azotobacter was used as a source of biofertilizer) + cow dung urine slurry as compared to RDF alone or organics alone in Vertisol. Hedge (1998) observed that there was an increase seed yield up to (6.71 q/ha) due to the 100% of recommended NPK through inorganic fertilizers and 100% N or P by the use of *Azotobacter* and phosphorus solubilising bacteria (PSB) in safflower based cropping systems. At Solapur (Maharashtra), significantly higher seed yield (1189 kg/ha) of safflower was recorded under RDF (50:25:0 NPK kg/ha + chemical pest control). Application of FYM @ 5 t/ha + biofertilizer (*Azotobacter* was used as a source of biofertilizer) + bio pesticide (Neem cake @ 200 kg/ha, *Trichoderma* seed treatment @ 5 g/kg seed + spray of NSKE 5 %) and FYM alone @ 6.5 t/ha were at par with RDF (50:25:0 NPK kg/ha + chemical pest control). Numerically higher values of test weight (5.87 g)

were recorded under FYM @ 2.5 t/ha + biofertilizer and FYM (equal to 50 kg N = 6.5 t/ha). Significantly higher uptake of nitrogen was recorded under RDF (50:25:0 NPK kg/ha) + chemical pest control and it was at par with FYM @ 5 t/ha + biofertilizer + biopesticide in respect of P_2O_5 and K_2O (Naik *et al.,* 2007; Khadtare *et al.,* 2016).

At Nagpur (Maharashtra), higher organic carbon (6.5 g/kg), available NPK (112.02, 16.99 and 173.88 kg/ha) and available Fe, Mn, Zn and Cu (7.26, 15.72 1.12 and 1.80 mg/kg respectively) were recorded in the treatment of 100% RDF + *Azospirillum* + PSB. Application of 100 % RDF + *Azospirillum* + PSB improved the grain and straw yields and significantly increased the uptake of NPK by safflower (Shillode *et al.,* 2016).

It could be concluded that seed inoculation with *Azospirillum* and in combination with 50% recommended inorganic N resulted in significantly higher seed yield followed by seed inoculation with *Azospirillum* could result in saving of 50% of inorganic nitrogen and 20-30% increased yield. Similarly increase in nutrient use efficiency and benefit cost ratio.

Effect of biofertilizers on growth, yield and quality of castor

At Tindivanam (Tamil Nadu), application of FYM 5 t/ha + 100% RDF + seed treatment with *Azospirillum* @ 50 g/kg seed resulted in significant increase in castor yield (1068 kg/ha) over 50% RDF + *Azospirillum* @ 50 g/kg seed and 50% RDF + phosphorus solubilizing bacteria (PSB) @ 50 g/kg seed (646 kg/ha) (DOR, 1994). Likewise, Baby and Reddy (1998) reported that conjunctive use of 0.25 t/ha neem cake + 100% RDF + seed inoculation with PSB @ 50 g/kg seed resulted in significantly higher seed yield over 0.25 t/ha neem cake + 100% RDF and 5/t ha FYM + 100% RDF rainfed castor. Similarly in Andhra Pradesh, application of 50% RDF + *Azospirillum* seed treatment @ 2 kg/ha + 25% N through FYM gave increased castor yields under rainfed conditions (DOR, 1999). Whereas, for Saurashtra region of Gujarat integrated use of 75% RDF + 25% N through FYM + seed treatment with *Azospirillum* @ 50 g/kg seed resulted in significantly higher yields of castor over 100% RDF, while for North Gujarat 75% RDF + 25% N through FYM + seed treatment with *Azospirillum* @ 50 g/kg seed + PSB @ 50 g/kg seed gave significantly higher yields over 100% RDF (DOR, 2000). Similarly, at Palem (Telangana), Pooran Chand *et al.* (2004) observed that application of 50% RDF in conjugation with seed treatment of *Azospirillum* @ 50 g/kg, 25% N through FYM and phosphate solubilising bacteria @ 2 kg/ha gave significantly higher seed yield of castor over 100% RDF and on par with 50% RDF + seed treatment of *Azospirillum* @ 50 g/kg seed + 25% N through FYM. Likewise, Reddy and Reddy (2008) opined that integrated nutrient management in castor with 75% RDF + 25% N through FYM + *Azospirillum* @ 2 kg/ha recorded significantly higher seed yield over other treatments like 75% RDF, 100% RDF (80:40:30 kg NPK/ha), 75% RDF + *Azospirillum* @ 2 kg/ha, 75% RDF + 25 % N through FYM, 100% RDF + *Azospirillum* @ 2 kg/ha and 100% RDF + 25% through FYM.

At Madurai (Tamil Nadu), application of FYM @ 12.5 t/ha + biofertilizers like *Azospirillum* + Phosphobacteria each 2 kg /ha was mixed with 50 kg fine sand recorded significantly maximum length of primary spike, more number of spikes per plant, capsules per spike, seed yield (1457 kg/ha), oil yield (734 kg/ha) and nutrient uptake as compared to press mud @ 2 t /ha + *Azospirillum* + Phosphobacteria and sugarcane biocompost @ 1 t/ha (Senthil kumar and Kanjana, 2009). At Hisar (Haryana), conjunctive use of organic (FYM 4 t/ha) and seed inoculation of biofertilizers (*Azotobacter* and PSB) with inorganic fertilizer application (20 kg N/ha) gave promising results when compared with 40 kg N/ha alone (Sangwan *et al.,* 2015). At Dibrugarh (Assam), isolate MAJ PSB12 produced higher soluble P concentration (322.20 µmol/litre) phosphate medium after 96 hour of incubation with a maximum drop in pH to 5.4 from 7.0. Among the isolates, maximum content of IAA (24.6 mg/litre) and GA_3 (3.921 mg/litre) was also found to be produced by the same strain. The most potential isolate was identified as *Bacillus firmus* MAJ PSB12 by 16S rRNA gene homology analysis. Although many species belonging to the genus *Bacillus* are efficient P solubilizer, application of native *Rhizobacteria* is easier for adaptation and succession during biofertilization process. *B. firmus* MAJ PSB12 can be utilized as potential biofertilizer to promote sustainable castor cultivation (Sandilya *et al.,* 2018).

It could be concluded that application of FYM 5 t/ha + 100% RDF + seed treatment with *Azospirillum* @ 50 g/kg seed resulted in 40-65% increment in castor yield and 50% fertilizer saving over 50% RDF + *Azospirillum* @ 50 g/kg seed and 50% RDF + phosphorus solubilising bacteria (PSB) @ 50 g/kg seed.

Effect of biofertilizers on growth, yield and quality of linseed

Treatment receiving dual inoculation of *Azotobacter* and PSB recorded higher values of plant height and primary per branches/plant compared to *Azotobacter* and PSB alone (Hussein, 2007). Samie *et al.* (2002) also reported higher yield attributes with 100% mineral nitrogen alone or two third mineral nitrogen + biofertilizer in linseed. Protein content in linseed increased significantly with the

application of 75 kg N/ha + biofertilizer (*Azotobacter*) as compared to all other treatments except 50 kg N/ha + biofertilizer and 75 kg N/ha (Mangatram *et al.,* 2003). Application of biofertilizer (*Azotobacter*) alone resulted in 18.49 % higher seed yield of linseed over absolute control. Seed yield (1322 kg/ha) increased significantly with the application of 50 kg N/ha + biofertilizer as compared to all other treatments. However, it was at par with 75 kg N/ha and 75 N/ha + biofertilizer (Sarangthem *et al.,* 2008). Application of 100% RDF combined with biofertlizers (*Azotobacter* + PSB) significantly increased seed and stover yield of linseed and it was at par with 75 % RDF + biofertilizers (*Azotobacter* + PSB). In terms of percentage, the seed and stover yield increased by 27.27 and 21.69% over 50% RDF with no seed inoculation. Combined application of fertilizers and biofertilizers improved the nutrient content in soil and so better utilized by crop (El-Nagdy *et al.,* 2010). Lawania *et al.* (2011) reported that application of nitrogen fertilizers in combination with biofertilizers (*Azotobacter*) reduced the iodine value of linseed oil.

Regarding economics, combined application of 100% RDF + biofertilizers (*Azotobacter* + PSB) recorded higher values of gross return (₹ 35595/ha), net return (₹ 20809/ha) and B:C ratio (1.41) followed by 100 % RDF + PSB (Meena *et al*., 2011). Higher seed yield (209.7 g/m^2) had been related to usage of 1000 kg/ha sulphur with 100 g/ha phosphate solublizing bacteria (PSB) and 2 % *Thibacillus* and least seed yield (92.86 g/m^2) was related to the usage of 2000 kg/ha sulphur with 100 g/ha PSB and 2% *Thibacillus* (Khoshkhooi *et al*., 2013). At Nagpur, growth characters, yield contributing characters, seed yield, gross and net return, oil content and oil yield were significantly higher in treatment receiving 100% RDF+ *Azotobactor* + PSB, but remained at par with treatments 100% RDF + *Azotobactor,* 100% RDF and 75% RDF + *Azotobactor* + PSB during *rabi* season in clayey soil (Rafeek Mahammad *et al.,* 2013). At Patna (Bihar), higher number of seeds/capsule (8.1) and seed yield (898 kg/ha) were recorded under 100% RDN + PSB + *Azotobacter* during *rabi* season in vertisol under irrigated condition (Acharya and Nirala, 2015). At Kanpur (Uttar Pradesh), application of nutrients @ 75% NPK+ 3t/ha FYM + *Azotobacter* + PSB to maize and 75% NPK + *Azotobacter* + PSB to linseed would be more beneficial and sustainable to the farmers adopting maize - linseed crop system in central plain zone of Uttar Pradesh and keeping each inputs constant, the quantity of 5t/ha FYM may be replaced by 3 t/ha FYM (Karam Husain *et al.,* 2017).

It could be concluded that application of 100% RDF combined with biofertilizers (*Azotobacter* + PSB) significantly increased seed and stover yield of linseed and it was at par with 75% RDF + biofertilizers (*Azotobacter* + PSB). In terms of percentage, the seed and stover yield increased by 27.27 and 21.69% over 50% RDF.

Effect of biofertilizers on growth, yield and quality of Indian mustard

Azotobacter inoculation decreases the nitrogen requirement of crop (Chauhan *et al.,* 1996; Gudadhe *et al.,* 2005; Singh and Dutta, 2006). Indian mustard crop also responds favorably to biofertilizers *viz., Azotobacter* and phosphorus solubilizing bacteria (Vyas, 2003; Khan *et al.,* 2012). At Kukma (Gujarat), interaction between biofertilizers and N was found to be significant. On an average *Azosprillum* increased seed yield by 27.1% over control, but this increase was 22.7% only in case of PSB. The crop receiving 30 kg N/ha and inoculated with biofertilizer (*Azosprillum*) produced seed equivalent to the crop receiving 60 kg N/ha (Vyas, 2005). Phosphate solubilizing bacteria inoculants when applied to mustard promote seed germination and initial vigour of plants by producing growth promoting substances. Application of biofertilizers resulted in increased mineral and water uptake, root development, vegetative growth and nitrogen fixation (Gangwal *et al*., 2011).

At Chittorgarh (Rajasthan), seed yield of 1814 and straw yield 4704 q/ha with biofertilizer seed inoculation was significantly greater than seed yield of 1728 and straw yield 4252 kg/ha in plants from control during *rabi* season (Solanki *et al.,* 2015; Kumar and Kumar, 1994). The maximum increase in yield was obtained with applied sulphur @ 40 kg/ha and 200 g *Azotobacter*/10 kg seed inoculate. The slight decrease in pH and EC and increase in organic carbon, available nitrogen, phosphorus, potassium and sulphur were recorded by the application of sulphur and biofertilizer applied alone or in conjunction with each other (Yadav *et al*., 2010).

At Kolkata (West Bengal), leaf area index (1.75 at 40 days after sowing DAS), dry matter accumulation (1367 g/m^2 at 80 DAS) and higher number of siliquae/plant (118.3), number of seeds/siliquae (21.8), seed yield (1.90 t/ha), stover yield (3.86 t/ha) were significantly higher due to the application of poultry manure (PM) @ 2.5 t/ha + 50% RDF (100% RDF i.e. 80:40:40 kg NPK/ha) + PSB (phosphate solubilizing bacteria) + AZ (*Azotobacter*). An average of 30.5% and 233% increase in seed yield by this treatment was recorded over sole application of RDF and control respectively. Integrated application of PM (2.5 t/ha) + 50% RDF + PSB + AZ recorded higher and positive effect on soil fertility status during winter season (Amrit Raj and Mallick, 2017). Application of sulphur @ 40 kg/ha and biofertilizer @ 200 g *Azotobacter* per 10 kg seed inoculated treatment combination was the best treatment as compared

to other treatments (Yadav *et al.,* 2010). Integrated use of biofertilizers, FYM with 40 kg of nitrogen gave seed yield equivalent to the 80 kg N/ha alone. Maximum seed yield was obtained with the application of higher doses of N fertilizer in conjunctions with biofertilizers and FYM (Singh *et al.,* 2014).

At Allahabad (Uttar Pradesh), seed inoculation of *Azotobacter* + PSB + 30 kg/ha N through inorganic fertilizer + 30 kg/ha N through poultry manure produced significantly higher growth parameters, yield attributes, seed yield (1500 kg/ha), stover yield (3790 kg/ha), harvest index (28.36%), oil content (42.03%), gross returns (₹ 67740/ha), net returns (₹ 33265/ha) and benefit cost ratio (1.96) (Saini *et al.,* 2017). At Allahabad (Uttar Pradesh), growth parameters such as plant height (167.50 cm), dry weight (44.40 g), number of branches (6.80/plant), yield attributes *viz.,* number of siliqua (291.20/plant) and test weight (4.51 g) were significantly higher with application of *Azotobacter* + Phosphate Solubilizing bacteria + 40 kg S/ha as compared to control (no seed inoculation of biofertilizers) (Jitendra Meena *et al.,* 2018). At Karbi Anglong (Assam), seed inoculation with *Azotobacter* and PSB (phosphorus solubilizing bacteria) @ 40 g/kg seed + 75% recommended NPK recorded maximum grain yield (11.15 q/ha) due to the higher plant height (88.52 cm), branches/plant (4.96), siliqua/plant (164.76), root growth (2.30 g /plant), seeds/siliqua (10.97) and 1000-seed weight (4.82 g) in toria (Nilim *et al.,* 2019).

It could be concluded that biofertilizer *viz., Azotobacter* and phosphorus solubilizing bacteria inoculation significantly decreases the nitrogen requirement. On an average *Azosprillum* increased seed yield by 27.1% over control, but this increase was 22.7% only in case of PSB. Similarly it resulted in increased nutrient use efficiency and benefit cost ratio.

Effect of biofertilizers on growth, yield and quality of niger

Niger a tropical and subtropical cropis mainly grown in Odisha, Maharashtra, Madhya Pradesh, Karnataka and also in other states which is mostly confined to degraded lands with resource poor farming. At Sarkanda (Madhya Pradesh), *Azosprillum* and farm yard manure increased seed yield by 34 and 65% over control respectively. When *Azosprillum* combined with 40:30:20 kg NPK/ha gave 63% yield increase over control (Ram *et al.,* 1992). At Jabalpur (Madhya Pradesh), integrated nutrient management consisting of 75% RDF + *Azotobacter* + PSB, 50% RDF + Vermicompost 2 t /ha and 50% RDF + FYM 5 t/ha recorded significantly higher growth and yield attributes and seed yields as compared to control (100 % RDF) during autumn season in clay loam soil under irrigated production system (Badole *et al.,* 2015).

Haldar *et al.* (1997) reported that seed inoculation with Azotobactor significantly gave higher seed yield than the uninoculated treatment during rainy season at Semiliguda (Odisha). Likewise, Sawarkar (1997) found that soil inoculation of *Azospirillum* 2 kg/ha + 10 kg N/ha was appropriate for achieving higher seed yield of niger under rainfed conditions of Chhindwara (Madhya Pradesh). Application of 40 kg N/ha along with seed inoculation through *Azotobactor* at Semiliguda (Odisha) and 10 kg N/ha with seed inoculation with *Azospirillum* at Chhindwara (Odisha) were appropriate for low-cost nutrient management for most remunerative seed yield (DOR, 2002). Patil *et al.* (2010) found that niger crop responded to application of 20 to 60 kg N, 30 to 67.5 kg P_2O_5, 10 to 30 kg K_2O, 15 to 40 kg S, 15 kg $ZnSO_4$/ha, 5 t FYM/ha and inoculation of *Azospirillum* or *Azotobacter* in seeds or soil depending upon the crop varieties and agro climatic conditions.

At Jorhat (Assam), the application of biofertilizer based INM package (3 t FYM/ha + *Azospirillum* for rice/*Azotobacter* for niger and phosphate solubilising bacteria dual culture at 3 kg/ha + rock phosphate at 50% P_2O_5 of RDF + MOP at100% K_2O of RDF) significantly higher yield (310 kg/ha) and maximum benefit:cost ratio for the sequence was recorded as 1.95 as compared with RDF (60:20:40 kg N, P_2O_5 and K_2O/ha for rice and 20:10:10 kg N, P_2O_5 and K_2O/ha for niger) (Singh *et al.,* 2009).

Dalei *et al.* (2014) revealed that application of 75% recommended dose of fertilizer integrated with *Azotobacter* and phosphorus solubilizing bacteria (PSB) recorded higher growth parameters and seed yield (405 kg/ha) with net monetary return (₹ 4083/ha) and B: C ratio (1.50) followed by recommended dose of fertilizer alone (386 kg/ha) with net monetary return of ₹ 3650/ha and B:C ratio of 1.45. Application of 50 % recommended dose of fertilizer + *Azotobacter* + PSB recorded seed yield of 370 kg/ha with net monetary return of ₹ 3313/ha and B:C ratio of 1.42.

The results revealed that integrated nutrient management consisting of 75 % RDF + *Azotobacter* + PSB or 50% RDF + 5t FYM/ha significantly increased higher growth, yield attributes, increased yield (63%) and also increased in net return and benefit cost ratio as compared to control (100% RDF).

Conclusions

The nitrogen fixing bioagents like *Azospirillum, Rhizobium*, phosphorus-solubilizing bacteria such as *Bacillus* and *Pseudomonas* and the vesicular arbuscular mycorrhizae play a triggering role in nitrogen and

phosphorus nutrition of oilseed crops under irrigated and rainfed cultivation. Locally available organic manures, green manures and biofertilizers in different combinations can improve growth and yield of oilseed crops and can improve the monetary returns from the cultivation of oilseed crops. These potential biological fertilizers would play a key role in increased productivity and sustainability of soil and also protect the environment as eco-friendly and cost effective inputs for the farmers. With the use of the biological and organic fertilizers, a low input system can be carried out and it can help in achieving sustainability of agricultural farms.

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Genetic variability studies for yield and yield attributes in breeding lines of sesame (*Sesamum indicum* L.)

P VAMSHI*, K T RAMYA, M SANTHALAKSHMI PRASAD, J V RAMANA[1] AND S R KUMHAR[2]

ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500 030, Telangana

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ABSTRACT

Twenty seven breeding lines along with three checks were evaluated for twelve different traits *viz*., days to 50% flowering, days to maturity, number of primary branches/plant, number of capsules/plant, capsule length, capsule width, plant height, harvest index, test weight, seed weight/capsule, oil content and seed yield/plot at ICAR-Indian Institute of Oilseeds Research, Hyderabad during late *kharif*, 2020. Analysis of variance (ANOVA) indicated significant variation among the genotypes for all the characters except for capsule width indicating the presence of substantial amount of variability for selection. High variation was observed for plant height, number of primary branches/plant, number of capsules/plant and seed yield/plot. The GCV for all the characters studied were lesser than the PCV indicating the influence of environment on expression of these traits. High heritability with high genetic advance was observed for plant height, number of primary branches/plant, number of capsules/plant, harvest index, oil content and seed yield/plot indicating additive gene action in the expression of these traits. Simple phenotypic selection may be effective for improving these characters. High heritability coupled with low genetic advance was observed for oil content suggesting involvement of non-additive gene action in the expression of this trait indicating limited scope for further improvement through simple selection.

Keywords: Genetic advance, GCV, Heritability, PCV, Sesame

India holds a premier position in the global oilseeds scenario accounting for 29 per cent of the total area and 26 per cent of production. Sesame is cultivated in an area of 12.82 million hectares with a production of 6.549 million tones globally (FAOSTAT, 2019). In India, it is grown in an area of 15.8 lakh hectares with an overall production of 7.92 lakh tonnes (DAC&FW, 2021). Six states, Rajasthan, Gujarat, Madhya Pradesh, Andhra Pradesh, West Bengal and Tamil Nadu account for about 72 per cent of total area and 58 per cent of sesame production in the country indicating that there is a dire need to enhance the productivity potential of this crop by producing high yielding varieties suitable for different agro-climatic regions. Despite its prominence among oilseeds, sesame has a low average productivity (of ~500 kg/ha) when compared to other oilseed crops due to its narrow adaptability, non-synchronous maturity, seed shattering, yield instability and lack of high yielding cultivars resistant to major insect pests and diseases. Thus, there is a need to enhance the productivity of this crop by developing high yielding genotypes which depends on the availability of variability for seed yield and its component traits in the population. The requirement of high yield and quality edible oil is raising day by day, and there is a need to increase the area, production and productivity of oilseed crops which, is possible through crop improvement strategies. The efficiency of selection depends on identification of genetic variability by the phenotypic expression of characters (Umate, 2020). Sometimes phenotypic selection based on their performance may not be sufficient because these genotypes may perform poor in further segregating generations, so it is essential to select the genotypes based on their genetic worth i.e., based on heritability and genetic advance (Hamouda *et al.*, 2016). Genetic variability along with heritability estimates would provide the amount of genetic gain expected out of selection (Burton, 1952; Swarup and Chaugale, 1962). Information on variability and heritability is useful to formulate selection criteria for improvement of seed yield and its component traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Paul *et al.*, 2006). The present study was conducted keeping in view the importance and need to evaluate the extent of genetic variability, heritability and genetic advance over mean for seed yield and its component traits in sesame.

[1]Agricultural College, Bapatla-522 101, Andhra Pradesh; [2]Agriculture Research Station, Agriculture University, Jodhpur, Rajasthan;
*Corresponding author's E-mail ID: vamshipoloju10@gmail.com

MATERIALS AND METHODS

The present investigation was carried out during *kharif*, 2020 at ICAR-Indian Institute of Oilseeds Research,

Rajendranagar, Hyderabad. The experimental material consisted of 30 genotypes (Table 1). Each genotype was sown in two rows of 3.0 m length following a spacing of 45 cm between the rows and 15 cm between the plants in a randomised block design (RBD) with three replications. Standard agronomic practices were performed uniformly for all the experimental units. Mean performance of the genotypes were calculated and the genotypic coefficient (GCV) and phenotypic coefficient of variation (PCV) coefficients of variation was estimated by using the formula given by Burton (1952).The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) as per Sivasubramanian and Madhavamenon (1973). Heritability in broad sense (h^2b) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956). Estimation of genetic advance was carried out following the formula given by Johnson *et al.* (1955).

Table 1 Mean performance of 30 sesame (*Sesamum indicum* L.) genotypes for all the characters under study

Genotype	Days to 50% flowering	Days to maturity	Primary branches/ plant	Capsules/ plant	Capsule length (cm)	Capsule width (cm)	Plant height (cm)	Harvest index (%)	Oil content (%)	Test weight (g)	Seed weight/ capsule (mg)	Seed yield/ plot (g)
SES-K-19-2104	38.0cdef	85.3cdef	4.3bcdef	88.7bcdefghi	2.7abcd	0.6	124.1hijklmn	32.1abcd	43.1ghi	3.0ijklm	135.8cdef	372.8bc
SES-S-20-1037	41.6b	88.6abc	6.0a	92.2bcdefg	2.8ab	0.6	144.0cdefgh	22.9def	46.5bcde	3.4cdef	151.3bc	286.3cdefgh
SES-S-19-3104	40.6bc	83.0fg	5.6ab	88.2bcdefghi	2.8abc	0.6	130.7fghijk	32.4abcd	35.5nop	3.0ijklm	135.1cdef	339.4bcd
GT-10	38.6bcdef	87.6bcde	5.0abcd	116.2b	2.7 abcd	0.6	125.0hijklm	31.1abcd	45.6efg	3.1fghij	132.6def	230.2efghij
SES-S-20-2005	40.0bcde	83.6defg	4.6abcde	87.1bcdefghi	2.6bcd	0.6	133.1defghij	35.1abc	48.5abcd	2.8lm	129.2efg	311.2bcdef
SES-S-20-1038	40.7bc	84.6cdefg	4.3bcdef	103.0bcde	2.8ab	0.6	149.4bcdef	39.9a	49.8a	2.8lm	129.1efg	367.1bc
RT-311	31.0ij	81.6fg	3.0gf	58.5ijh	2.7abcd	0.6	111.1klmno	28.8abcd	48.0abcde	3.2efghi	134.3def	182.6ijkl
SES-S-19-1036	35.7fgh	83.3efg	3.6defg	90.9bcdefgh	2.7abcd	0.6	121.9ijklmno	23.2cdef	47.3abcde	3.6bc	160.2ab	227.0efghij
Swetha til	39.7bcde	81.6fg	5.0abcd	76.3defghij	2.9a	0.6	124.6hilklmn	15.0ef	50.1a	3.5cd	123.2fg	182.3ijkl
SES-S-20-2001	40.6bc	80.3g	4.6abcde	72.5efghij	2.7abcd	0.6	148.4bcdef	28.8abcd	34.5o	2.9jklm	132.9def	239.5efghij
SES-S-20-1039	41.6b	91.0ab	4.0cdefg	99.6bcdef	2.7abcd	0.6	145.4cdefg	25.4bcdef	43.8fgh	3.8ab	170.0a	317.1bcde
RT-340	33.3hi	84.6cdefg	2.6g	63.7ghij	2.8abcd	0.6	121.3ijklmno	24.6cdef	47.4abcde	3.3defgh	148.3bcd	128.7kl
SES-K-19-3005	40.3bcd	84.6cdefg	4.0cdefg	115.7bc	2.6abcd	0.6	167.0ab	37.0ab	35.1po	2.6n	114.8g	375.3bc
SES-S-19-3103	34.7gh	82.3fg	3.3efg	95.2bcdefg	2.7abcd	0.6	130.4fghijk	29.9abcd	46.2def	3.3defg	141.3cde	296.7bcdefg
SES-S-20-2003	41.0bc	91.0ab	3.6defg	87.3bcdefghi	2.9ab	0.6	150.5bcde	26.1bcdef	40.4ijk	3.9a	173.9a	280.7cdefgh
ISWG-20-05	31.3ij	83.0fg	3.gf	66.1fghi	2.8abcd	0.6	104.0o	30.8abcd	49.1abc	3.4cde	142.1cde	191.2hijkl
SES-R-18-3002	46.0a	93.0a	5.6ab	158.3a	2.6bcd	0.6	186.4a	31.4abcd	46.4cde	2.9klm	132.1def	508.1a
SES-S-19-2102	38.0cdef	85.3cdef	4.6abcde	97.7bcdef	2.4d	0.6	114.1jklmno	29.1abcd	37.6mnlo	3.1fghij	128.6efg	230.2efghij
SES-S-1043	30.7ij	81.6fg	2.6g	66.9fghi	2.9a	0.6	107.9mno	24.4cdef	48.7abcd	3.4cde	132.4def	110.7l
RT-323	32.7hij	83.0fg	3.0gf	47.7j	2.5bcd	0.6	109.2lmno	21.5def	47.5abcde	2.9jklm	124.8fg	110.3l
RT-289	33.0hij	83.6defg	3.0gf	56.3ij	2.5bcd	0.6	117.3ijklmno	32.1abcd	48.6abcd	3.1fghij	143.2cde	217.5fghijk
SES-S-20-3003	41.6b	88.0bcd	4.3bcdef	95.3bcdefg	2.5bcd	0.6	136.1defghi	33.5abcd	42.8hij	2.9jklm	133.1def	267.1efghi
SES-S-19-1042	40.6bc	85.6cdef	4.0cdefg	98.7bcdef	2.7abcd	0.6	119.4ijklmno	15.0f	45.3efgh	3.0hijkl	120.2fg	108.4l
SES-S-20-2002	41.3b	88.3bc	4.3bcdef	93.0bcdefg	2.7abcd	0.6	153.7bcd	32.7abcd	36.5mnop	3.1fghij	127.7efg	383.6b
CUMS-17	37.3defg	83.0fg	3.6defg	70.8efghij	2.5dc	0.6	106.5mno	30.3abcd	40.1jkl	2.7mn	129.5efg	181.9ijkl
SES-S-19-2006	37.0efg	82.3fg	4.0cdefg	92.6bcdefg	2.7abcd	0.6	114.8jklmno	25.4bcdef	49.1abc	2.9klm	123.3fg	196.8hijkl
RT-215	30.0j	83.0fg	2.6g	45.1j	2.7abcd	0.6	104.8no	27.6bcde	49.2ab	3.2efghi	143.3cde	152.7jkl
SES-S-20-2007	40.0bcde	87.6bcde	4.3bcdef	82.3cdefghi	2.9a	0.6	125.7ghilklm	40.3a	38.3klmn	3.3defgh	148.2bcd	303.5bcdefg
S-20-2004	40.0bcde	84.6cdefg	5.3abc	107.3bcd	2.7abcd	0.6	128.1ghijkl	25.2bcdef	36.5nop	2.9jklm	133.2def	210.9hijk
SES-S-20-2008	40.6bc	81.6fg	4.0cdefg	113.5bc	2.7abcd	0.6	156.6bc	16.4ef	39.3klm	3.0ijklm	122.3fg	265.2efghi
Mean	37.9	84.9	4.1	87.6	2.7	0.6	130.4	28.3	43.9	3.16	136.5	252.5
SEM	1.08	1.64	0.48	11.86	0.13	0.03	7.06	4.30	0.98	0.09	5.76	34.32
F-value	14.17	3.71	3.70	3.88	1.18	0.88	8.01	2.17	27.60	10.64	5.75	7.62
C.V. %	4.96	3.36	20.50	23.46	8.10		9.38	26.30	3.86	4.80	7.30	23.54
C.D at 0.05%	3.07	4.66	1.36	33.60	0.36		20.00	12.15	2.80	0.25	16.30	97.16
P value	<0.01	<0.01	<0.01	<0.01	<0.01	p=0.63	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01

Significant differences among the genotypes were represented with the alphabets in the superscript of each trait mean value

RESULTS AND DISCUSSION

The analysis of variance (Table 2) exhibited a significant difference for all the traits except for capsule width, indicating sufficient variation present in the material. The results of mean, variability, heritability and genetic advance of each trait are presented in Table 3. Maximum variation was observed for seed yield per plot (108.4 - 508.4 g) followed by plant height (104.0 - 186.4 cm) and lowest for capsule length (2.4 -2.9 cm) followed by test weight (2.6 - 3.9 g). Highest variation for plant height was also reported by Mohanty *et al.* (2020), Saravanan *et al.* (2020) and Kadvani *et al.* (2020).

The PCV ranged from 4.6 (days to maturity) to 42.2 (seed yield/plot); whereas, GCV ranged from 2.0 (capsule length) to 35.0 (seed yield/plot). High PCV and GCV were recorded for seed yield per plot (42.2, 35.0) and number of capsules/plant (32.8, 23.0). High PCV and moderate GCV was observed for harvest index (30.9, 16.4) and number of primary branches/plant (28.2, 19.4). Further, moderate PCV and GCV were recorded for plant height (17.1, 14.3), oil content (12.1, 11.5) and days to 50% flowering (11.5, 10.4). The character seed weight/capsule recorded moderate PCV (11.8) coupled with low GCV (9.2). Low PCV and GCV were recorded for the traits days to maturity (4.6, 3.2); capsule length (8.3, 2.0); and test weight (10.0, 8.7). In the present study, values of PCV were higher for all characters than corresponding GCV and the difference between PCV and GCV was high indicating the influence of environment over the expression of these characters. Similar results of high PCV and GCV for number of capsules/plant, seed yield/plant were reported by Abhijatha *et al.* (2017), Padmaja *et al.* (2020) and Pavani *et al.* (2020); high PCV and moderate GCV for the traits harvest index by Mohanty *et al.* (2020), number of primary branches/plant by Saravanan *et al.* (2020); moderate PCV and GCV was recorded for plant height, oil content and days to 50% flowering by Mohanty *et al.* (2020).

The estimates of heritability ranged from 5.6 (capsule length) to 89.9% (oil content) whereas, genetic advance as per cent of mean ranged as low as 1.0 (capsule length) to 59.8% (seed yield/plot). Heritability estimates are more useful when combined with the genetic advance of a trait of interest. Hence, high heritability estimates along with high genetic advance is more useful in predicting genetic gain under selection than heritability estimates alone. High heritability coupled with high genetic advance as percent of mean was observed for three characters *viz.,* oil content, plant height and seed yield/plot, indicating that these characters are governed by additive gene action. Hence, response to selection would be more for these traits. Similar results of high heritability along with high genetic advance for plant height and seed yield/plot have been reported earlier (Sumathi and Muralidharan, 2010) and oil content (Mohanty *et al.,* 2020). High heritability estimates coupled with moderate genetic advance was manifested in three other traits *viz.,* days to 50 per cent flowering, test weight and seed weight/capsule indicating involvement of both additive and non-additive gene action in the inheritance of these traits. The results are in accordance with the findings of Abhijatha *et al.* (2017) for days to 50 per cent flowering, Sumathi and Muralidharan (2010) and Selvamani *et al.* (2020) for test weight and Ismaila and Usman (2014) for seed weight/capsule. Further, number of primary branches/plant and number of capsules/plant exhibited moderate heritability coupled with high genetic advance suggesting non-additive gene action in inheritance of this trait. Hence, simple selection may not be rewarding in improving this trait.

From the present study, it could be concluded that oil content, plant height and seed yield/plot are controlled by additive gene action suggesting that these traits can be improved by simple selection. Days to 50% flowering, test weight and seed weight/capsule were under the influence of non-additive gene action and appropriate breeding and selection strategy should be employed in selection of these traits.

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Table 2 Analysis of variance for different characters in sesame

Source of variation	d.f.	Days to 50% Flowering	Days to maturity	Primary branches/ plant	Capsules/ plant	Capsule length (cm)	Capsule width (cm)	Plant height (cm)	Harvest index (%)	Oil content (%)	Test weight (g)	Seed weight/ capsule (mg)	Seed yield/ plot (mg)
		Mean sum of squares											
Replications	2	0.63	0.14	1.64	1983.65*	0.08	0.001	2488.00**	10.61	3.37	0.01	403.86*	23114.41**
Treatments	29	50.17**	30.15**	2.60**	1637.54**	0.06*	0.001	1198.49**	119.68**	79.26**	0.25**	573.47**	26919.96**
Error	58	3.54	8.13	0.70	422.44	0.05	0.001	149.65	55.26	2.87	0.03	99.76	3533.95

** - Significant at 1% level *- Significant at 5% level

Table 3 Mean, range, coefficient of variation, heritability and genetic advance as per cent of mean for different traits in sesame

Character	Mean	Standard error	Range		Coefficient of Variation		Heritability (%)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
Days to 50% flowering	37.9	1.08	30.0	46.0	11.5	10.4	81.4	19.4
Days to maturity	84.9	1.64	80.3	93.0	4.6	3.2	47.4	4.5
Primary branches/plant	4.1	0.48	2.6	6.0	28.2	19.4	47.5	27.6
Capsules/plant	87.6	11.86	47.7	158.3	32.8	23.0	48.9	33.1
Capsule length (cm)	2.7	0.13	2.4	2.9	8.3	2.0	5.6	1.0
Plant height (cm)	130.4	7.06	104.0	186.4	17.1	14.3	70.0	24.7
Harvest index (%)	28.3	4.30	15.0	39.9	30.9	16.4	28.0	17.8
Oil content (%)	43.9	0.98	34.5	50.1	12.1	11.5	89.9	22.4
Test weight (g)	3.2	0.09	2.6	3.9	10.0	8.7	74.5	15.4
Seed weight/capsule (mg)	136.6	5.76	114.8	173.8	11.8	9.2	61.3	14.8
Seed yield/plot (g)	252.5	34.32	108.4	508.1	42.2	35.0	68.8	59.8

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Genetic diversity analysis in sunflower (*Helianthus annuus* L.) restorer lines using SSR markers

C RAMANAIAH AND P KADIRVEL*

ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad-500 030, Telangana

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ABSTRACT

Sunflower is a staple oilseed crop of the world. Genetic diversity in the parental lines is key for hybrid breeding programmes in sunflower. In this study, genetic diversity in a set of 102 parental lines (100 restorer and two CMS) of sunflower was assessed using 69 polymorphic SSR markers. The genetic diversity parameters: average number of alleles (3.07) per locus, gene diversity (0.356) and polymorphism information content (0.296) revealed low to moderate genetic diversity in the restorer lines. The SSR marker ORS447 located on linkage group 2 was more informative with high number of alleles (10) and high *PIC* value (0.89). Cluster analysis (neighbour-joining tree) revealed three major genotypic groups. Model based STRUCTURE analysis showed recognizable population structure; based on membership coefficients (>80%), 82 genotypes were classified into two populations (K=2) and the remaining 20 genotypes were classified into admixture group. The *Fst* value (0.278) suggested that the populations were differentiated. Analysis of molecular variance results showed that maximum of genetic variation (72%) was observed between the individuals within the population suggesting that the population was weakly structured. These results would be useful for selecting SSR markers for genotype characterization as well as choosing diverse parents for hybrid development programme in sunflower.

Keywords: Genetic diversity, Parental lines, Restorers, SSR markers, Sunflower

Sunflower is the fourth largest oil crop worldwide after the oil palm, soybean and rapeseed. Total sunflower oil production was 56 million tons (MT) during 2019 (FAOSTAT, 2019). Ukraine had the highest production volume (15.25 MT) of sunflower in the world followed by the Russian Federation (15.37 MT) and European Union (10.28 MT) during 2019, which together accounted for more than 75% of the total harvested area (FAOSTAT, 2019). The world average achene yield was 2364.68 kg/ha in 2020 (Carvalho, 2020). Sunflower was grown over an area of 0.26 million hectare with a production of 0.21 MT in India during 2019 (FAOSTAT, 2019). India needs about 24 MT of vegetable oil supply to meet the domestic consumption demand; therefore, imports are expected to be about 16 MT to fill the supply gap annually. The demand for high-quality edible oil is increasing enormously due to the rise in per capita income and health consciousness of Indian families. The sunflower oil is of a high quality type due to its high polyunsaturated fatty acid (PUFA) content (~60%); thus, it is preferred by the Indian consumers and becomes a significant part of the edible oil imports in India.

Hybrid technology has been a great commercial success in sunflower. Genetic diversity in the parental lines is a prerequisite for hybrid superiority due to manifestation of heterosis. Positive relationship between genetic distance and the best parent heterosis has been observed in sunflower (Hladni *et al.*, 2018). Single cross hybrids are developed in sunflower using cytoplasmic genetic male sterility (CGMS) system involving CMS (A), maintainer (B) and fertility restorer (R) lines. Maintenance of the 'R' lines and 'A/B' lines as distinct breeding pools helps in maximizing the heterosis. Furthermore, identification and utilization of diverse parental lines are quite essential to increase the hybrid vigour and adaptation to various stresses.

In sunflower, the CMS system, PET1, has so far been exploited in hybrid breeding (Serieys, 2005) and several restorer lines are available for use in the PET1 system. Molecular markers play a prominent role in evaluating the genetic diversity in the parental lines. Among them, SSR markers are the most preferred as they are highly polymorphic, co-dominant, abundant, analytically simple and readily transferable (Zeinalzadeh *et al.*, 2018). Several authors performed genetic diversity analyses in sunflower germplasm using molecular markers (Lawson *et al.*, 1994; Liu *et al.*, 2003; Yue *et al.*, 2009; Tang and Knapp, 2003; Liu and Burke, 2006; Kolkman *et al.*, 2007). With this background, the present study was taken up to assess genetic diversity in a set of restorer lines of sunflower using SSR markers.

MATERIALS AND METHODS

Plant material: A set of 100 restorer lines and two CMS lines were used in the study. The materials were sourced from Ganga Kaveri Seeds Pvt. Ltd, Hyderabad, which is one

Corresponding author's E-mail: kadirvel.palchamy@icar.gov.in

of the leading companies involved in sunflower hybrid seed production in India.

Extraction of genomic DNA: Genomic DNA was isolated according to the procedure of Doyle and Doyle (1990) with some modifications. The quality and quantity of the genomic DNA were assessed using 0.8% agarose gel and then normalized to 25 ng/µl for use in genotyping.

SSR analysis: A total of 108 SSR markers distributed across 17 linkage groups of sunflower were used for genotyping work. The following PCR procedure was followed. A 20 µl reaction volume was prepared using 2 µl of 10X reaction buffer, 2 mM dNTP mix, 1 µl forward and reverse primers of 5 pM concentration each, 0.1 µl of 5U Taq DNA polymerase (Thermo Fisher Scientific, USA), 12.9 µl of double distilled water and 1 µl of genomic DNA (50 ng). The PCR was set in Eppendorf thermo cycler using 96-wells plate type with an initial denaturation at 95°C for 5 minutes. The next step included denaturation at 94°C for 30 seconds, annealing at 55°C for 30 seconds, extension at 72°C for 1 min and these steps were repeated for 35 cycles. The final extension was carried out at 72°C for 5 mins and the storage temperature was set to 4°C. The PCR products along with the DNA ladder (50 bp) were resolved on 3.5% agarose gel electrophoresis stained with EZ vision (a non-mutagenic and non-toxic fluorescent DNA dye) containing 1X TBE buffer (CBS Scientific, USA) for 3 hours at 100V and documented under UV light using gel documentation system. The amplified DNA bands were scored as '1' for its presence and '0' for absence in the respective allele position.

Data analysis: Genetic diversity parameters such as allele number (*NA*), allele frequency expected, heterozygosity (*He*), and polymorphism information content (*PIC*) values were obtained using PowerMarker Version 3.25 software (Liu and Muse, 2005). Clustering of genotypes was performed based on an unweighted neighbour-joining tree method using pair wise distance matrix as implemented in DARwin Version 6 software (Perrier and Jacquemoud-Collet, 2006).

Population structure was determined based on a Bayesian-based approach using the Structure Version 2.3.4 software (Pritchard *et al.,* 2000). Based on the true 'K' value, the population was classified into subpopulations by following admixture model. The true 'K' value was obtained by running the model with the 'K' values ranging from 1 to 25 with a burning period length set to 200,000 with Markov Chain Monte Carlo (MCMC) method. A clear peak at ΔK was recognized by loading the output in the structure harvester (http://taylor0.biology.ucla.edu/structure Harvester/).

Analysis of molecular variance (AMOVA) [based on Nei's distance matrix (Nei, 1973)], estimation of fixation index (*Fst*) and principal coordinate analysis (*PCoA*) was performed using GenAlEx 6.5 software (Peakall and Smouse, 2012).

RESULTS AND DISCUSSION

Genetic diversity in sunflower restorer lines: A total of 69 SSR primer pairs were polymorphic (out of 108), which produced a total of 212 alleles across 102 sunflower parental lines. The *NA* ranged from 2 to 10 (ORS-447) with an average of 3.07 alleles per locus. Majority of the primer pairs (28) produced only two alleles. Major allele frequency ranged from 0.38 to 0.99 with an average of 0.75. About 12 rare alleles (frequency of < 0.005) were found. The *He* values ranged from 0.062 to 0.687 with an average of 0.356. The *PIC* value of SSR primer-pairs ranged from 0.013 to 0.895 with an average of 0.296. The locus wise details are provided in the Table 1.

The SSR markers showed that diversity in sunflower restorer lines was low to moderate (*NA* = 3.07, *He* = 0.356 and *PIC* = 0.296). Only five primer pairs (ORS447, ORS1114, ORS1065, ORS838 and ORS1209) showed high *PIC* values (>0.6). The *PIC* values observed in this study were comparable with other studies in sunflower, which ranged from 0.20 to 0.56 (Darvishzadeh *et al.,* 2010; Erasmus *et al.,* 2010; Zhang *et al.,* 2005; Lochner *et al.,* 2011). The *PIC* values are a good indication of informative markers, which can be used for genotyping of plant populations and studying the genetic diversity (Salem and Sallam, 2016). The number of alleles per locus was also comparable with other studies in sunflower, which ranged from 2.32 to 3.5 (Paniego *et al.,* 2002; Solodenko and Sivalop *et al.,* 2005; Darvishzadeh *et al.,* 2010; Zeinalzadeh *et al.,* 2018).

Genetic relationships among sunflower restorer lines: NJ tree showed three major genotypic clusters within the set of 102 parental lines (Fig.1). The cluster 1 (named as G1) included 30 genotypes and was clearly distinct from the cluster 2 and 3 genotypes with high bootstrap support (62%) and the cluster 2 (G2) was a major group consisting of 60 genotypes with four subgroups. The cluster 3 (G3) consisted of 12 genotypes. The pairwise dissimilarity coefficients ranged from 0.012 (genotypes 57, 58) to 0.725 (genotypes 21, 50) with an average of 0.471.

Table 1 Mean and range values of genetic diversity measures in a set of 102 sunflower genotypes based on SSR markers

SSR locus	Linkage group	*NA*	*He*	*PIC*
ORS598A	1	2	0.062	0.057
ORS610	1	3	0.581	0.467
ORS474	1	3	0.383	0.463
ORS728	1	2	0.062	0.019
ORS509	1	4	0.373	0.291
ORS662	1	4	0.362	0.417
ORS959	1	4	0.579	0.532
ORS371	1	5	0.589	0.023
ORS423	2	3	0.499	0.490
ORS925	2	5	0.289	0.218
ORS1065	2	4	0.687	0.638
ORS447	2	10	0.666	0.895
ORS342	2	6	0.237	0.184
ORS1040B	3	4	0.487	0.025
ORS1112	3	2	0.225	0.013
ORS1021	3	3	0.323	0.245
ORS752	3	2	0.062	0.082
ORS1222	3	3	0.231	0.177
ORS477	3	2	0.062	0.019
ORS924	3	4	0.416	0.100
ORS949	3	5	0.341	0.173
ORS488	3	3	0.370	0.368
ORS1114	3	5	0.618	0.723
ORS822A	3	5	0.279	0.044
ORS665	3	5	0.570	0.522
ORS644	4	2	0.350	0.162
ORS785	4	3	0.497	0.510
ORS1217	4	2	0.237	0.198
ORS337	4	3	0.622	0.384
ORS1068	4	2	0.062	0.019
ORS309	4	2	0.062	0.034
ORS1024	5	2	0.062	0.029
ORS484	5	3	0.549	0.594
ORS840	5	3	0.285	0.094
ORS1193	6	3	0.231	0.146
ORS650	6	2	0.062	0.057
ORS331	7	2	0.225	0.190
ORS762	8	2	0.495	0.493
ORS1013	8	3	0.416	0.290
ORS826	8	2	0.062	0.430
ORS1001	9	3	0.271	0.256
ORS1265	9	2	0.062	0.021
ORS333A	9	3	0.429	0.437
ORS887	9	3	0.179	0.093
ORS838	9	3	0.620	0.629
ORS844	9	2	0.475	0.423
ORS617	9	3	0.562	0.427
ORS541	10	2	0.096	0.088
ORS1209	10	4	0.562	0.627
ORS878	10	4	0.562	0.572
ORS1088	10	4	0.631	0.526
ORS78	10	2	0.271	0.190
ORS537	10	4	0.508	0.517
ORS684	10	4	0.547	0.407
ORS1095	10	2	0.062	0.035
ORS613	10	3	0.604	0.410
ORS818	10	3	0.331	0.334
ORS1146	11	2	0.271	0.220
ORS607	11	2	0.437	0.364
ORS934	11	2	0.225	0.086
ORS799	13	2	0.312	0.190
ORS1079	14	2	0.412	0.418
ORS307	14	2	0.487	0.425
ORS857	15	2	0.271	0.145
ORS899	16	3	0.591	0.584
ORS788	16	2	0.271	0.177
ORS297	17	2	0.271	0.360
ORS988	17	3	0.283	0.147
ORS561	17	3	0.441	0.528
Mean	-	3.07	0.356	0.296
Range	-	02-10	0.062-0.687	0.013-0.895

(*NA*: number of alleles for the locus; *He*: Expected heterozygosity; *PIC*: Polymorphism information content)

The pairwise dissimilarity coefficients of G1 ranged from 0.073 (genotypes 32, 34) to 0.704 (genotypes 21, CMS 1), G2 ranged from 0.012 (genotypes 57, 58) to 0.725 (genotypes 21, 50) and G3 ranged from 0.119 (genotypes 38, 41) to 0.691 (genotypes 21, 40). Lines from G1, G2 and G3 groups were further clustered into three, six and two subgroups, respectively.

The wide range of simple matching coefficients within the G1 and G2 suggested that substantial diversity existed with the restorer parental lines. Cluster analysis has been routinely used in genotypic grouping of sunflower inbred lines. Cheres and Knapp (1998) separated 156 inbred lines into broad market (oilseed versus confection) and fertility restorer (restorer versus maintainer) classes. Yue *et al.* (2009) reported 177 inbred lines grouped into two classes, i.e. oilseed and confection. Similarly, Zeinalzadeh-Tabrizi *et al.* (2018) used the distance-based clustering method to group the 68 genotypes into two clusters.

Population structure in the restorer lines of sunflower: The mean posterior probability [LnP(D)] value for each given K increased with the increase of K. A delta-K (ΔK) analysis of LnP(D) (Evanno *et al.,* 2005), showed a sharp peak of ΔK at K = 2, suggesting two populations within the 102 genotypes (Fig. 2). The genotypes were assigned to specific population group based on the threshold value (≥0.8) of membership coefficients; 82 genotypes into two populations referred as SG1 and SG2 and remaining 20 genotypes to the admixture group. The classification of genotypes falling under respective population and admixture group is depicted in the bar diagram (Fig. 2). The SG1, composed of 32 genotypes, had the membership coefficients more than threshold value, which ranged from 0.800 to 0.997. The SG2 composed of 50 genotypes with membership coefficients ranging from 0.926 to 0.998. The average gene diversity between individuals in the same cluster was 0.370 and 0.269 for SG1 and SG2, respectively. The mean *Fst* values within SG1 and SG2 were 0.199 and 0.458, respectively. Several researchers have analyzed the population structure using the model-based approach in sunflower (Scott *et al.,* 2013; Filippi *et al.,* 2015; Filippi *et al.,* 2020).

AMOVA partitioned the total genetic variance into two components among and within populations. Maximum genetic variation was explained by individuals within the populations (72%). It was observed that the genotypes showed moderate genetic differentiation (F_{ST} - 0.278) and inbreeding (F_{IS} - 0.468) across and within the population (Table 3). The pair-wise F_{ST} estimate among subgroups indicated that the two groups were different from each other. The *PCoA* showed that 20.67% and 10.75% of genetic variation were accounted by the populations (Fig. 3). Similar results were reported in previous works in sunflower (Jannatdoust *et al.,* 2016; Sahranavard Azartamar *et al.,* 2015; Kholghi *et al.,* 2012 and Basirnia *et al.,* 2014). Using TRAP marker system, Zeinalzadeh-Tabrizi *et al.* (2015) reported that the genetic variation in sunflower genotypes was higher within the groups (87%) than among the groups (13%). Overall, the genotyping results pointed out that the genetic diversity is moderate in the restorer lines used in this study. This observation is in accordance with the results of Filippi *et al.* (2020), who reported that the international collection of sunflower breeding lines is genetically narrowed.

In summary, the present study assessed the genetic diversity in a genotype panel comprised of 100 restorer parental lines and two CMS lines using 69 polymorphic SSR markers. The parameters namely allele number, gene diversity and PIC revealed that the genetic diversity within the panel of sunflower restorers was low to moderate. Cluster analysis grouped the total 102 genotypes into three major groups with different subgroups and the structure analysis indicated two major populations, which are weakly differentiated. The results of the study would be useful for selecting SSR markers for genotyping applications and choosing diverse parental lines for hybrid development in sunflower.

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Table 2 AMOVA between structured genotypes and pair-wise comparison using FST values

Source	Degrees of freedom	Sum of squares	Variance Components	Est. Var.	% of variation
Among Populations	2	545.085	272.542	4.047	28
Among Individuals	99	1530.866	15.463	4.933	34
Within Individual	102	571	5.598	5.598	38
Total	203	2646.951	-	14.577	100

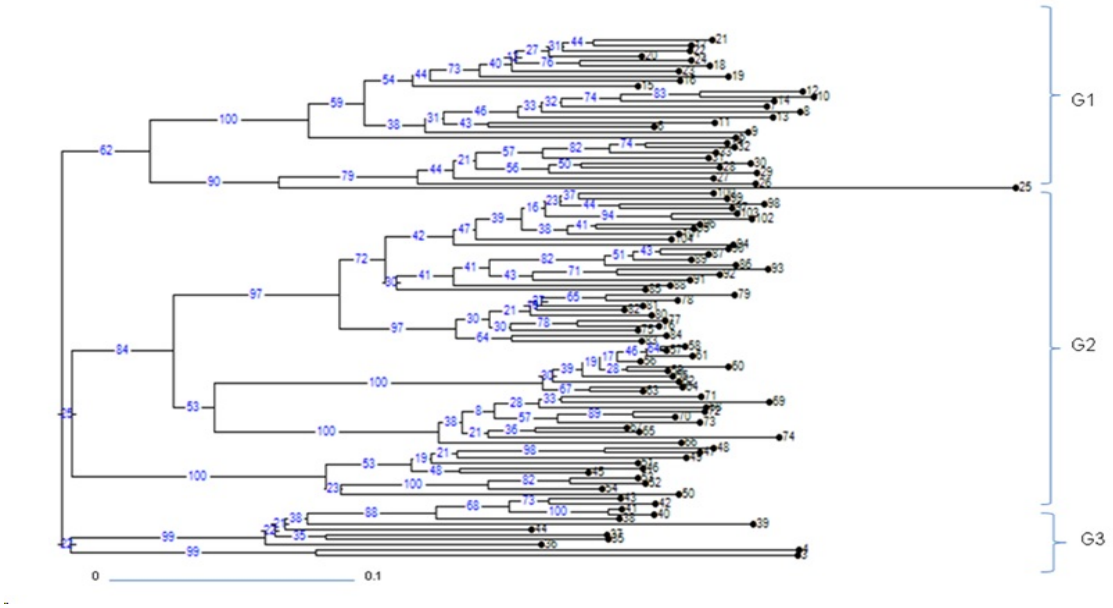

Fig. 1. Unweighted NJ tree based dendrogram depicting genetic relationships among 102 genotypes of sunflower

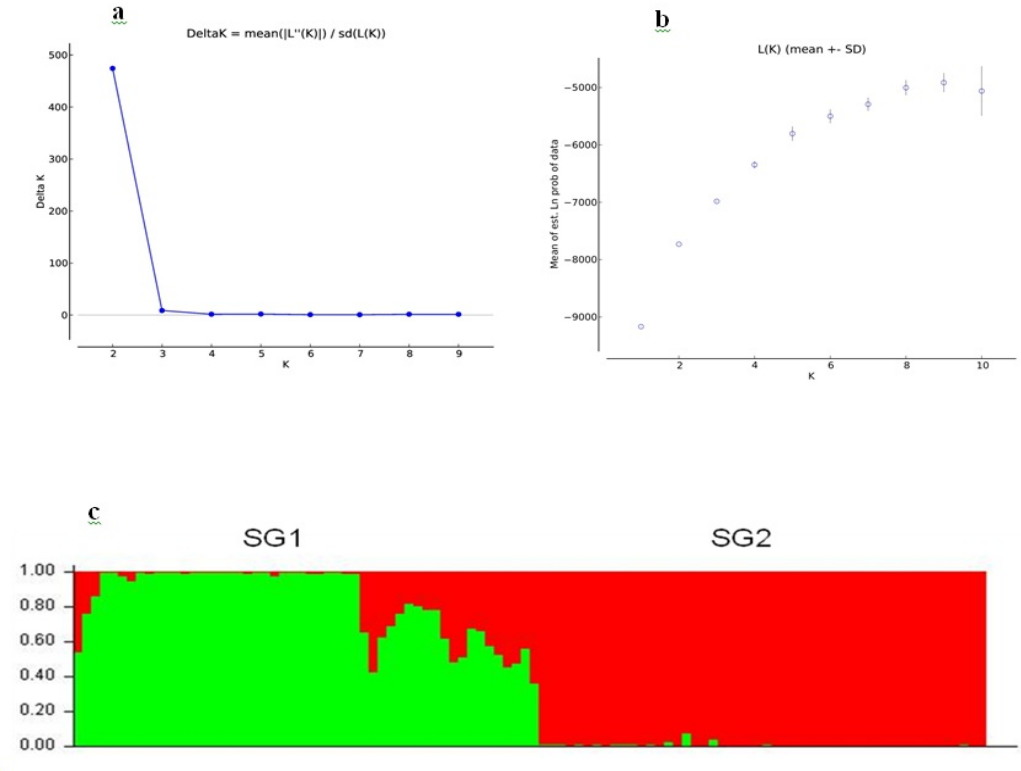

Fig. 2. a) Representation of population structure dividing the genotypes into two subgroups based on K value. Predicted value of K based on Evanno *et al.* (2005). b) Determination of optimum value of K in the 102 sunflower genotypes based on procedure described by Pritchard *et al.* (2000). C) Representation of population structure dividing the genotypes into two subgroups based on K value model based clustering of the sunflower core subset into two main populations. SG1 and SG2 indicate the number of populations (K) along with admixture

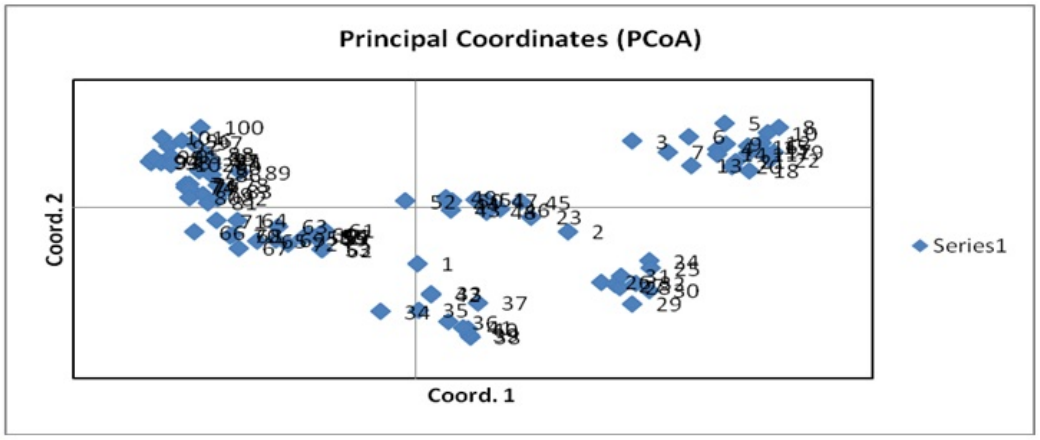

Fig. 3. Principal Coordinates of 102 genotypes based on 69 SSR loci. Coord.1 and Coordi.2 represent first and second coordinates, respectively. The *PCoA* axes accounted for 20.67 and 10.75% of the genetic variation among the populations

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Combining ability analysis of newly developed monoecious lines of castor (*Ricinus communis* L.) in Rajasthan

RAMESH*, RAKESH CHOUDHARY, MAMTA NEHRA AND MANISH KUMAR

Agricultural Research Station, Mandor, Agriculture University, Jodhpur-342 304, Rajasthan

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ABSTRACT

Genetic parameters of 50 castor hybrids developed from 10 newly developed monoecious lines and 5 stable pistillate lines were estimated in line x tester design. Analysis of combining ability depicted significant mean sum of squares for both general combining ability (GCA) and specific combining ability (SCA) for all the characters which indicated the presence of both additive and non-additive gene actions. The high amount of σ^2 SCA and ratio of GCA to SCA variances near to zero indicated that the dominance gene effect was predominant in newly developed lines for all the characters under study. The highest positive gca effect was exhibited by MCP-1-1, for seed yield and number of capsules on primary raceme, effective length of primary raceme and height up to primary raceme. SKP-84 was also a good general combiner for 100 seed weight, number of capsules on primary raceme, nodes to primary raceme and height up to primary raceme. Among the male parents, MP-11-17 was found the best general combiner for cumulative seed yield, raceme length and numbers of capsules. Cross M-574 x MP-17-17 was the best cross for cumulative seed yield followed by MCP-3 x MP-7-17 and SKP-84 x MP-11-17. These combinations would be useful in breeding programme for improvement in seed yield of castor.

Keywords: Castor, Combining ability, Gene action, Line x tester

Castor (*Ricinus communis* L., 2n = 2x = 20, Family: Euphorbiaceae) is an industrially important non-edible oilseed crop widely cultivated in the arid and semi-arid regions of the world. The genus *Ricinus* is monotypic and *R. communis* is the only species with the most polymorphic forms known (Weiss, 2000). It is cultivated in about 30 countries on commercial scale, among those, India, Brazil, China, Russia, Thailand and Philippines are the principal castor growing countries. Being the largest producer, India is also largest exporter of castor seed oil. Total area under castor crop in India for the year 2019-20 was 9.38 lakh hectares, which was 7.07% increased as compared to previous year. While total production of castor seeds in India for the year 2019-20 was 17.37 lakh tones, which was an increase 42.96% over previous year. Average yield for the year 2019-20 was 1852 kg/ha as against 1387 kg/ha during the year 2018-19 (Anonymous, 2019).

Castor is a crop where varieties/populations and hybrids are available for commercial cultivation. However, hybrids are more popular in India due to significantly higher yields than pure lines or open pollinated varieties (Gopani *et al.,* 1968; Punewar *et al.,* 2017). Higher magnitude of heterosis and genetically superior hybrids can be obtained by combining diverse parents in hybrid development. Even though many mating designs are being used by various research workers, line x tester design is widely used in cross pollinated crops including castor to estimate general and specific combining ability effects and it also provides information on fixable genetic variance. At the same time, it provides the nature and magnitude of components of genetic variance on which success of plant breeding programme depends. Line x tester analysis technique becomes more manageable with a large number of parents besides being more comprehensive for understanding the genetic basis at population level (Kempthorne, 1957). Keeping this in view combining ability analysis was carried out at ARS, Mandor to estimate gca and sca of the newly developed male lines of castor.

*Corresponding author's email agrico.ramesh@gmail.com

MATERIALS AND METHODS

The material for present investigation was generated by crossing 10 newly developed pollen parents (tester), *viz.,* MP-1-17, MP-4-17, MP-7-17, MP-9-17, MP-10-17, MP-11-17, MP-14-17, MP-17-17, MP-18-17 and MP-20-17 with 5 already stabilised pistillate parents (line) *viz.,* MCP 1-1, VP-1, MCP-3, M-574 and SKP-84 during *kharif*, 2017-18. A total of 50 F_1 were grown during *kharif*, 2018-19 at Agriculture Research Station, Mandor (Agriculture University, Jodhpur) in three replications in a randomized block design (RBD). Each genotype was grown in in two rows of 9 m length with a spacing of 120 cm between rows and 90 cm between plants.. Recommended agronomic practices with drip irrigation and protection technologies were followed for growing a healthy crop.

Observations were recorded on cumulative seed yield (q/ha) at 120, 150, 180 and 210 days after sowing (DAS), days to 50% flowering, number of nodes up to primary raceme, height up to primary raceme (HPR, cm), effective length of primary raceme (ELPR, cm), number of capsules on primary raceme (NCPR), number of effective spikes (NES), 100 seed weight (g), volume weight (g/100 ml) and oil content (%). The data were subjected to analysis of variance as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

The results of the analysis of variance for the newly developed castor hybrids are presented in Table 1. All the hybrids, testers and lines showed significant differences with respect to the traits tested, indicating that there was a significant variation among lines, testers and hybrids. Therefore, it was possible to compute the general and specific combining abilities. Likewise, interactions between lines and testers also significantly varied for all the characters, giving sufficient evidence for the availability of variability and diversity among new male lines developed at ARS, Mandor.

The variance due to general combining ability (σ^2 GCA) and specific combining ability (σ^2 SCA), ratio of GCA to SCA variances, additive variance (σ^2D), non-additive variance (σ^2H) and degree of dominance [σ^2D/σ^2H]1/2 for the traits under study are presented in Table 1. SCA variance was greater than GCA variance for all the characters under study revealing that non-additive gene effects were dominant and controlled the characters genetically. The high amount of σ^2 SCA and ratio of GCA to SCA variances near to zero indicated that the dominance gene effect was predominant in newly developed lines for all the traits studied. The proportion of additive effect was very low among all the characters in gene action. It indicated the predominance of non-additive gene action for all the characters, thus, exploitation of hybrid vigour could be the best method for improvement of all the characters. Similar observations were also made by Patel *et. al.* (2015); Punewar *et al.* (2017) and Bindu Priya *et al.* (2018) with minor deviations.

Table 1 Analysis of variance for various characters in castor

Source	DF	Cumulative seed yield (q/ha)				Days to 50% flowering	Nodes up to primary raceme	Height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of Effective Spikes	100 seed weight (g)	Volume weight (g/100 ml)	Oil content (%)
		120 DAS	150 DAS	180 DAS	210 DAS									
Replication	2	0.18	58.23	50.83	62.41	5.95	0.55	41.61	34.16	804.08	5.45	2.24	19.83	0.27
Treatment	49	36**	243.39**	261.67**	370.58**	53.39**	7.56**	579.15**	332.47**	4171.01**	57.79**	24.48**	35.04**	6.31**
Lines	4	61.81**	471.73**	761.03**	1151.22**	169.38**	39.78**	2112.19**	771.93**	13441.6**	71.29**	92.27**	55.83**	2.37*
Tester	9	99.28**	761.02**	571.22**	620.53**	102.15**	13.32**	1049.62**	632.13**	10294.32**	55.37**	57.3**	65.97**	12.94**
L x T	36	17.31**	88.61**	128.8**	221.35**	28.32**	2.54**	291.20**	208.73**	1610.12**	56.89**	8.75**	24.99**	5.09**
Error	98	1.73	2.13	12.37	17.94	3.71	0.85	31.24	20.17	104.78	10.67	1.92	4.32	0.77
σ^2GCA	-	0.28	2.29	1.96	2.21	0.37	0.07	4.26	1.83	37.85	0.01	0.23	0.15	0.02
σ^2SCA	-	5.19	28.83	38.81	67.80	8.20	0.56	86.65	62.85	501.78	15.41	2.28	6.89	1.44
σ^2GCA/ σ^2 SCA		0.053	0.079	0.051	0.033	0.045	0.131	0.049	0.029	0.075	0.001	0.102	0.022	0.013
σ^2D	-	0.55	4.58	3.93	4.41	0.74	0.15	8.51	3.66	75.71	0.03	0.47	0.30	0.04
σ^2H	-	5.19	28.83	38.81	67.80	8.20	0.56	86.65	62.85	501.78	15.41	2.28	6.89	1.44
Degree of Dominance	-	0.33	0.40	0.32	0.26	0.30	0.51	0.31	0.24	0.39	0.04	0.45	0.21	0.16
G. Mean	-	10.3	20.0	33.3	40.6	46.4	13.3	70.7	55.5	113.3	33.8	27.7	62.6	45.5
SEm ±	-	0.8	0.8	2.0	2.4	1.1	0.5	3.2	2.6	5.9	1.9	0.8	1.2	0.5
C.D. (P=0.05)	-	2.1	2.4	5.7	6.9	3.1	1.5	9.1	7.3	16.6	5.3	2.2	3.4	1.4
C.V. (%)	-	12.8	7.3	10.6	10.4	4.2	6.9	7.9	8.1	9.0	9.7	5.0	3.3	1.9

*, ** Significant at 5% & 1%, respectively

Among the female parents, the highest positive *gca* effect was exhibited by MCP-1-1, for seed yield and number of capsules on primary raceme, effective length of primary raceme and height up to primary raceme. SKP-84 was a good general combiner for traits such as 100 seed weight, number of capsules on primary raceme, nodes to primary raceme and height up to primary raceme (Table 2). Among the male parents, MP-11-17 was found the best general combiner for cumulative seed yield, raceme length and number of capsules. For cumulative seed yield, MP-11-17 followed by MP-17-17, MP-18-17 and MP-9-17 were good general combiners. The parent, MP-4-17 was good combiner for traits such as, HPR, ELPR, NCPR, NES, Volume weight and oil per cent. This male was also average combiner for seed yield, could be exploited for development of new hybrids and as a good source for a new combiner development. The MP-9-17 was the best combiner for earliness in flowering, volume weight and oil content. MP-17-17 was also good combiner for days to flowering, 100 seed weight and nodes to primary raceme. These parents can be effectively used in breeding programmes in various cross combinations for improvement in seed yield and other agronomic characters because of their ability to transmit characters to off springs.

The *sca* effects of all 50 crosses are presented in Table 3. Cross M-574 x MP-17-17 was the best cross among all the crosses for cumulative seed yield followed by MCP-3 x MP-7-17 and SKP-84 x MP-11-17. The cross VP-1 x MP-20-17 had significant and positive *sca* effect for 100 seed weight, M-574 x MP-20-17 for volume weight and M-574 x MP-18-17 for oil content. Similar reports were also made earlier by Lavanya and Chandramohan (2003); Solanki *et al*. (2004); Patel *et al*. (2015) and Bindu Priya *et al*. (2018).

In this study, a set of hybrids developed from newly developed male lines along with existing female lines was evaluated and ANOVA indicated significant mean squares for genotypes indicating the sufficient amount of diversity that existed among parents as well as hybrids. Variance due to GCA and SCA and ratio of GCA/SCA indicated predominance of non-additive gene action for all the characters. Thus, exploitation of hybrid vigour could be the best method for improvement of all the characters. Based on combining ability, good general combiner parents were involved in generation of good SCA hybrids, although, some of the hybrids deviated. Therefore, improvement of such character can be done through recurrent selection or bi-parental mating.

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Table 2 General combining ability of various pistillate and pollen parents

Source	Cumulative seed yield (q/ha)				Days to 50% flowering	Nodes up to primary raceme	Height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of Effective Spikes	100 seed weight (g)	Volume weight (g/100 ml)	Oil content (%)
	120 DAS	150 DAS	180 DAS	210 DAS									
Lines													
MCP-1-1	1.44**	6.28**	7.37**	9.00**	0.11	0.14	7.39**	8.21**	28.02**	-0.69	0.19	-0.49	0.1
VP-1	1.01**	-0.30	1.03	1.00	-1.95**	-1.24**	-9.48**	-5.30**	-8.25**	1.09	-1.46**	1.30**	0.02
MCP-3	-0.19	-2.38**	-2.89**	-3.32**	-2.65**	-1.00**	-8.80**	-2.71**	-29.14**	0.61	0.29	1.39**	0.41*
M-574	-2.26**	-4.17**	-6.11**	-7.71**	3.15**	0.52**	5.93**	-0.24	-0.09	1.37*	-1.70**	-0.34	-0.27
SKP-84	0.01	0.57*	0.60	1.02	1.35**	1.58**	4.96**	0.04	9.46**	-2.37**	2.68**	-1.86**	-0.26
Testers													
MP-1-17	-2.84**	-7.32**	-6.51**	-6.36**	-0.05	1.29**	-2.43	-1.08	-3.10	0.59	0.46	-1.41*	0.26
MP-4-17	-1.45**	-3.08**	-0.88	0.66	2.88**	1.22**	14.63**	10.59**	40.66**	2.12*	-0.86*	1.97**	0.46*
MP-7-17	-3.27**	-8.07**	-7.69**	-7.97**	1.88**	-0.14	-10.06**	-2.26	-18.21**	-0.48	3.52**	-0.17	-0.38
MP-9-17	0.06	-3.42**	0.29	3.33**	-4.85**	-0.47	-4.66**	2.97*	3.50	0.88	-2.6**	3.05**	1.1**
MP-10-17	-3.39**	-7.23**	-6.96**	-7.36**	1.75**	0.93**	9.72**	-5.83**	-18.56**	1.85*	1.93**	1.45**	0.46*
MP-11-17	2.1**	14.04**	12.33**	13.05**	3.48**	0.42	2.34	8.86**	47.08**	-1.92*	-2.96**	-1.27*	0.16
MP-14-17	1.88**	1.57**	-0.16	-1.95	-1.79**	-1.27**	-7.68**	0.10	-6.88*	-1.44	-0.41	1.38*	0.82**
MP-17-17	3.27**	5.24**	4.16**	3.44**	-2.45**	-1.11**	0.41	-6.23**	-33.56**	-3.88**	1.24**	0.88	0.25
MP-18-17	2.82**	5.35**	4.69**	4.00**	-1.19*	-0.02	6.77**	-9.70**	-19.16**	0.63	-0.24	-2.37**	-1.25**
MP-20-17	0.82*	2.92**	0.72	-0.84	0.35	-0.85**	-9.06**	2.59*	8.24**	1.65	-0.08	-3.51**	-1.89**

*, ** Significant at 5% & 1%, respectively.

Table 3 Specific combining ability for seed yield and its related traits

Source	Cumulative seed yield (q/ha)				100 Seed weight (g)	Volume weight (g/100 ml)
	120 DAS	150 DAS	180 DAS	210 DAS		
MCP-1-1 x MP-1-17	-0.20	-2.92**	-2.77	-3.16	0.18	-1.80
MCP-1-1 x MP-4-17	1.82*	1.24	3.41	5.04*	0.56	-0.18
MCP-1-1 x MP-7-17	1.84*	0.58	2.77	4.42	-0.09	1.03
MCP-1-1 x MP-9-17	-0.44	-4.01**	-4.10*	-4.73	0.76	-0.59
MCP-1-1 x MP-10-17	2.06**	0.81	3.23	5.10*	0.37	1.01
MCP-1-1 x MP-11-17	-0.86	2.29**	1.12	1.29	-1.43	-0.39
MCP-1-1 x MP-14-17	1.75*	3.45**	4.88*	7.66**	-0.64	-2.84*
MCP-1-1 x MP-17-17	-5.17**	-7.16**	-12.65**	-16.8**	0.14	0.74
MCP-1-1 x MP-18-17	1.20	2.46**	3.34	5.58*	0.71	-0.35
MCP-1-1 x MP-20-17	-1.79*	-1.47	-3.58	-4.34	-1.03	2.82*
VP-1 x MP-1-17	0.22	0.8	1.33	1.78	-0.86	-0.58
VP-1 x MP-4-17	-3.10**	-5.24**	-8.03**	-10.9**	-0.12	-1.69
VP-1 x MP-7-17	0.12	1.77*	2.21	2.56	1.47	-3.15*
VP-1 x MP-9-17	-1.66*	-2.45**	-3.79	-5.22*	0.12	-0.34
VP-1 x MP-10-17	-5.04**	-5.4**	-10.12**	-14.93**	-4.26**	-2.14
VP-1 x MP-11-17	0.73	1.15	1.56	1.62	2.58**	1.88
VP-1 x MP-14-17	-1.65*	2.62**	0.65	-1.67	-0.39	1.24
VP-1 x MP-17-17	-0.68	1.37	0.37	-0.97	0.66	1.08
VP-1 x MP-18-17	2.69**	4.76**	7.13**	9.16**	-1.14	-0.84
VP-1 x MP-20-17	3.27**	4.65**	7.59**	10.19**	3.86**	0.26
MCP-3 x MP-1-17	0.11	-1.32	-1.23	-1.53	-0.47	0.87
MCP-3 x MP-4-17	1.19	-2.08*	-0.91	-0.13	0.58	3.46**
MCP-3 x MP-7-17	3.89**	3.43**	7.30**	10.78**	-2.18**	0.30
MCP-3 x MP-9-17	-1.80*	-0.77	-2.59	-4.79	-0.46	2.11
MCP-3 x MP-10-17	1.49	1.41	2.88	3.97	1.05	-1.95
MCP-3 x MP-11-17	-2.71**	0.90	-0.67	-1.34	-0.02	4.90**
MCP-3 x MP-14-17	0.03	2.69**	0.34	1.41	0.77	0.18
MCP-3 x MP-17-17	-1.25	0.29	-2.62	-4.87*	-0.11	-0.38
MCP-3 x MP-18-17	-0.50	0.77	1.08	-1.06	0.60	0.23
MCP-3 x MP-20-17	-0.66	-0.35	-0.67	-0.82	-3.03**	-4.42**
M-574 x MP-1-17	1.72*	-8.61**	-6.41**	-8.11**	0.00	1.94
M-574 x MP-4-17	-0.21	4.05**	4.12*	4.97*	-1.08	-0.91
M-574 x MP-7-17	2.27**	-2.05*	1.23	0.40	0.30	0.02
M-574 x MP-9-17	1.01	0.67	1.83	1.69	1.22	3.40**
M-574 x MP-10-17	0.08	6.36**	6.12**	7.66**	1.82*	-4.45**
M-574 x MP-11-17	1.54*	-8.58**	-5.92**	-7.73**	0.32	0.76
M-574 x MP-14-17	5.13**	3.19**	9.57**	10.08**	-0.60	-0.66
M-574 x MP-17-17	2.54**	10.20**	11.05**	16.50**	-0.68	-1.20
M-574 x MP-18-17	0.52	-0.12	-2.16	0.71	1.80*	3.18**
M-574 x MP-20-17	-0.26	5.83**	5.87**	7.16**	2.80**	5.80**
SKP-84 x MP-1-17	-0.80	5.08**	4.76*	7.08**	0.48	-2.58*
SKP-84 x MP-4-17	-2.35**	-4.06**	-6.13**	-6.71**	-0.94	4.23**
SKP-84 x MP-7-17	-1.10	-5.58**	-5.67**	-6.78**	-1.55	0.86
SKP-84 x MP-9-17	-1.58*	-8.02**	-9.46**	-11.18**	-2.40**	-5.29**
SKP-84 x MP-10-17	1.47	-1.96*	-0.82	-0.76	-1.17	-0.84
SKP-84 x MP-11-17	0.25	11.21**	8.24**	10.10**	-0.77	-5.03**
SKP-84 x MP-14-17	-2.61**	-5.87**	-7.90**	-9.75**	1.85*	-2.85*
SKP-84 x MP-17-17	-2.45**	-2.86**	-3.99	-5.24*	2.04*	0.69
SKP-84 x MP-18-17	0.55	6.71**	8.70**	9.84**	-1.22	-1.53
SKP-84 x MP-20-17	-0.62	-9.87**	-10.51**	-13.24**	-0.42	3.91**

Table 3 contd...

Table 3 contd...

Source	Days to 50% flowering	Nodes up to primary raceme	Height up to primary raceme (cm)	Effective length of primary raceme (cm)	Number of capsules on primary raceme	Number of effective spikes	Oil content (%)
MCP-1-1 x MP-1-17	-1.45	0.95	10.79**	-1.06	12.93*	-1.51	0.59
MCP-1-1 x MP-4-17	1.29	0.01	9.50**	4.61	-10.38	1.74	-0.92
MCP-1-1 x MP-7-17	-3.71**	-0.08	1.19	-2.43	1.38	1.00	-0.53
MCP-1-1 x MP-9-17	0.02	-0.41	3.79	-5.77*	-1.22	-1.46	0.03
MCP-1-1 x MP-10-17	-3.91**	0.52	-6.70*	6.70*	-3.60	2.00	0.52
MCP-1-1 x MP-11-17	0.95	-0.23	-7.79*	0.68	-19.68**	-1.84	-0.43
MCP-1-1 x MP-14-17	-1.65	-1.28*	-17.08**	0.68	3.45	-1.15	-0.85
MCP-1-1 x MP-17-17	8.35**	-0.48	-5.39	8.97**	1.76	-1.78	-0.26
MCP-1-1 x MP-18-17	-4.58**	-1.03	-4.90	8.41**	3.05	7.65**	-0.39
MCP-1-1 x MP-20-17	-1.85	-0.43	1.83	-11.12**	2.01	11.22**	0.62
VP-1 x MP-1-17	0.32	-1.02	0.53	-0.80	-1.57	8.19**	0.20
VP-1 x MP-4-17	-1.61	0.27	-1.20	2.42	14.45*	-2.45	-0.20
VP-1 x MP-7-17	-1.95	0.29	4.49	-6.29*	-5.79	0.26	-0.60
VP-1 x MP-9-17	3.12**	1.18*	5.42	2.60	14.61*	-3.21	-0.03
VP-1 x MP-10-17	-1.15	-1.66**	-10.29**	-6.82**	-39.77**	-7.96**	-1.47**
VP-1 x MP-11-17	-0.15	-0.88	-7.42*	-1.93	-1.74	-2.79	-0.45
VP-1 x MP-14-17	1.59	0.52	3.73	-3.04	22.62**	3.35	-0.17
VP-1 x MP-17-17	1.92	0.10	-2.58	1.24	7.60	1.72	1.96**
VP-1 x MP-18-17	-0.68	-0.34	-9.31**	-1.20	-4.56	1.92	-0.67
VP-1 x MP-20-17	3.39**	0.48	3.09	0.49	9.51	-1.61	0.26
MCP-3 x MP-1-17	0.32	1.18*	3.89	3.11	10.05	-2.05	0.09
MCP-3 x MP-4-17	0.39	0.47	5.04	-4.67	-30.15**	-1.48	2.13**
MCP-3 x MP-7-17	-4.61**	0.16	2.29	-1.49	-4.95	-1.21	-0.56
MCP-3 x MP-9-17	2.12	0.60	5.00	-4.04	-11.88*	-4.90*	1.06*
MCP-3 x MP-10-17	3.52**	1.09*	12.07**	10.76**	31.85**	-3.65	0.08
MCP-3 x MP-11-17	1.02	0.48	2.46	7.01**	48.64**	5.67**	0.41
MCP-3 x MP-14-17	-1.05	-0.50	-6.30	-1.01	3.04	-1.15	-0.74
MCP-3 x MP-17-17	0.62	-0.43	6.94*	-1.01	-15.71**	-6.15**	0.63
MCP-3 x MP-18-17	2.35*	-0.19	-12.74**	2.90	-20.78**	0.78	0.68
MCP-3 x MP-20-17	4.82**	-0.36	-8.92**	-9.94**	-14.29*	-0.91	-0.65
M-574 x MP-1-17	-2.58*	-0.70	-1.57	7.52**	-2.3	-4.89*	-0.2
M-574 x MP-4-17	3.02**	1.55**	15.9**	2.83	15.21*	-3.38	0.13
M-574 x MP-7-17	-1.65	-0.16	-15.08**	-3.17	6.23	-1.04	0.88
M-574 x MP-9-17	-1.25	1.30*	25.9**	-11.03**	-13.95*	-3.78*	1.49**
M-574 x MP-10-17	1.22	1.46**	8.17*	-3.77	4.21	-1.02	-1.00
M-574 x MP-11-17	-3.55**	0.29	-6.80*	-16.07**	-21.08**	-1.30	-1.66**
M-574 x MP-14-17	0.05	0.87	5.78	-5.87*	-22.12**	-1.79	-0.41
M-574 x MP-17-17	3.05**	-0.18	4.58	-0.76	11.45	0.88	-0.63
M-574 x MP-18-17	0.79	-0.49	-7.44*	3.82	23.28**	5.92**	2.49**
M-574 x MP-20-17	0.92	0.45	4.93	27.76**	26.54**	1.46	2.31**
SKP-84 x MP-1-17	-0.01	-0.45	2.69	-6.87**	-63.58**	-1.83	1.67**
SKP-84 x MP-4-17	-1.08	-0.54	-0.07	2.00	1.93	1.90	0.67
SKP-84 x MP-7-17	-1.75	1.19*	11.4**	10.67**	-7.05	1.12	0.97
SKP-84 x MP-9-17	-0.35	-0.23	2.60	3.36	34.89**	-4.93*	-2.33**
SKP-84 x MP-10-17	-2.88*	0.15	-4.13	-4.71	0.38	1.15	-1.90**
SKP-84 x MP-11-17	5.12**	0.38	3.22	8.40**	38.32**	2.35	-0.23
SKP-84 x MP-14-17	-0.95	-1.38*	-15.31**	2.04	1.94	4.41*	0.35
SKP-84 x MP-17-17	-0.28	-0.42	-7.84*	-5.73*	5.08	5.19**	-1.85**
SKP-84 x MP-18-17	-1.55	-0.40	-8.31*	0.96	-23.44**	2.01	-2.32**
SKP-84 x MP-20-17	-4.08**	-1.69**	-0.04	-9.33**	-16.84**	-0.68	1.25*

*, ** Significant at 5% & 1%, respectively

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Standardization of GR_{50} dose of gamma rays in safflower (*Carthamus tinctorius* L.) to develop beneficial mutants

RAJEEV SHRIVASTAVA, NIRMALA B PATEL, SHAMPA PURKAYASTHA, YENGKHOM LINTHOINGAMBI DEVI AND BHASKAR SAHOO

College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur-492 012, Chhattisgarh

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ABSTRACT

Practicing an optimal dose for mutation induction is the first key step in any mutation breeding programme. The study optimized the GR_{50} dose of gamma rays in four different genotypes of safflower. During early seedling stage an *in vitro* experiment detected very high GR_{50} value of 579.2 Gy based on reduction of root length. Field experiments revealed significant difference in GR_{50} values among four safflower genotypes in two phenophases. Based on the seedling height data at 42 days after sowing, the GR_{50} values varied in between 248.7 to 374.3 Gy. While, GR_{50} values of 301.2 to 447.6 Gy were noticed at 72 days after sowing. Based on this finding a consensus optimal dose of 300 Gy was used for large scale mutation breeding programme that fetched beneficial mutants in safflower crop with an overall mutation frequency of 7.3×10^{-4}.

Keywords: Gamma rays, GR_{50} dose, Mutation breeding, Mutation frequency, Safflower

To create genetic variability in any crop species induced mutagenesis is considered as an important breeding technique. The success of study depends on the use of suitable mutagens and handling of mutant generations towards the isolation of superior mutants in plant. Safflower (*Carthamus tinctorius* L.) is an ancient oilseed crop valued for its quality oil from seed and dye from its petals. Since this crop has very narrow genetic variability for various morphological, agronomical and biochemical traits (Rampure *et al.*, 2014), mutation breeding may be a good tool to create variability. Moreover, negative correlations exist between 'seeds/capitulum and capitula/plant' and 'test weight and capitulum size' that limit its further genetic improvement towards high yielding varieties development (Ranga Rao *et al.*, 1977; Roopa and Ravikumar, 2008; Rampure *et al.*, 2014). Such limitations can be surmounted by induced mutagenesis. Only a few studies are available with respect to the use of mutation technique, mostly chemical mediated, for improvement of safflower (Mallikarjunradhaya, 1978; Ramchandram and Goud, 1983; Velasco *et al.*, 2000; Kotcha *et al.*, 2007). Usage of gamma rays and other physical mutagens (like electron beam, proton beam and charge particles/ion beam) are limited in the literature.

Comparative genotoxic potential of laser and gamma rays on somatic and gametic cells of safflower was studied by Kumar and Srivastava (2010). Mutagenic parameters like mitotic and meiotic consequences were accessed from the plants that showed a dose dependent decrement in mitotic index and revealed chromosomal anomalies. In the subsequent analysis, Verma and Shrivastava (2014) reported gamma rays induced reciprocal translocation in safflower and revealed unequal chromosome distribution at anaphase-I, reduced vigour, delayed flowering, low flower number, low pollen fertility, and low seed sets in induced variants from 10 and 25 kR (100 and 250 Gy) gamma rays as compared to control plants. Their observation further corroborated by the findings from Srivastava and Kumar (2011). Rampure *et al*. (2017) reported the use of EMS, sodium azide and gamma rays for the induction of useful mutants in safflower and detected varietal difference in terms of mutation efficiency and effectiveness.

The median lethal dose (LD_{50}) and the median growth reduction (GR_{50}) are the major parameters utilized to establish the adequate gamma irradiation dose to induce mutations in crop plants. Notably, both LD_{50} and GR_{50} parameters are based on the assumption that low doses of irradiation produce minimum impacts on the genome, which rarely generate phenotypic changes; whereas, high doses may produce multiple impacts on the genome which consistently produce aberrations or negative changes (Álvarez-Holguín *et al.,* 2019). Therefore, the first step in a mutagenesis-based breeding process is to determine the LD_{50} and the GR_{50}. But reports on GR_{50} dose (gamma rays) for safflower are not mentioned correctly in any literature. According to the FAO/IAEA 2018, manual of mutation breeding, high GR_{50} dose is prescribed for safflower crop. Such high GR_{50} dose limits the stand of M_1 plant in field and also brings down the size of M_2 population. For successful mutation induction in plants the applied dose

Corresponding author's E-mail: rajeevigkv@gmail.com

should be below GR_{50} so that the size of M_2 population in field and higher mutation efficiency can easily be obtained. Present research effort intended to standardize GR_{50} dose of gamma rays towards isolation of beneficial mutants in safflower. Further, the study also depicted the varietal difference in radiation sensitivity among safflower genotypes.

MATERIALS AND METHODS

***In vitro* experiments for determination of GR_{50} dose**: Genetically pure seeds of RSS 7 genotype was obtained from IGKV, Raipur in 2016. In each lot 50 seeds were irradiated with 100 to 800 Gy of gamma rays in a ^{60}CO Gamma Cell 5000 irradiator (BRIT, Mumbai, India) at the dose rate of 40.9 Gy/min. Irradiated and non-irradiated samples were immediately used for further experiments. Dosimetry was carried out by cerric-cerrous dosimeters calibrated with Fricke's dosimeter. The irradiated seeds along with control were germinated in different sterile petri plates for different doses at room temperature (25°C) in dark for 3 days. The germinated healthy seedlings were then transferred to Gibson tube containing 0.5 X Steinbergs solution. For healthy root establishment, the tubes were kept again at dark for next two days and then transferred to growth chamber maintained at 24°C, 65% RH, 12 h light and 12 h dark. After 15 days of growth at growth chamber, the seedlings were used for measurement of seedling height and root length. For each dose, data were obtained from 10 seedlings and then data were transformed into 'percentage length over control' and probit analyses were performed. Based on the probit analysis, GR_{50} values were obtained.

***In vivo* experiments for determination of GR_{50} dose**: For *in vivo* experiments, pure seeds from four different genotypes, RVS 2012-13, RSS 3, RSS 7, and Annigeri 1 were exposed to gamma radiation at doses of 100 to1200 Gy in a ^{60}CO Gamma Cell 5000 irradiator as mentioned above during October 2016. All these four genotypes were then sown in field in different blocks (for genotypes) and in different rows for each treatment along with control in *rabi*-summer 2016-17. Since safflower has rosette growth habit for 21- 30 days, the seedling height was taken during 42 and 72 days after sowing in the field. The seedling height/plant heights were taken from base of the plant to the shoot tip portion. The seedling height data from 10 plants for each dose were then used for probit analysis as mentioned above.

Mutation breeding experiments: For the actual mutation breeding experiments, two lots (each containing 1000 seeds) of seeds from each genotype were taken and irradiated with 300 Gy and 500 Gy gamma rays in a gamma cell 5000 at Bhabha Atomic Research Centre, Mumbai, India. Both the lots were grown separately in different blocks during *rabi*-summer 2016-17 (November 2016 to April 2017). In M_1 generation, only the germination percentage and final plant stand at harvest were counted. From each plant the seeds of the main capitulum were harvested and kept in a single packet. The M_2 seeds were grown as plant to row progenies during *rabi*-summer 2017-18 (November 2017 to April 2018) at experimental field facility, Indira Gandhi Krishi Viswavidyalaya, Raipur, India. Mutants were identified and tagged and tested for their true breeding behaviour by growing plant to row progenies in the M_3.

Data analysis: Seedling height data were analyzed using probit analysis and 50% growth reduction (GR50) values were calculated at 95% confidence limit (SPSS 12.0 for Windows). The GR_{50} data of four genotypes from in vivo experiments were used to reveal significant genotypic difference based on analysis of variance using IRRISTAT 2.0 software (IRRI, 2003).

RESULTS AND DISCUSSION

Effect of gamma rays on safflower in *in vitro* growth experiment: In an *in vitro* experiment of effect of gamma rays (100-1000 Gy) on growth of safflower, dose dependent gradual shoot and root length reduction was observed (Fig 1). No germination and growth were obtained in above 800 Gy. Since safflower crop undergoes rosette growth for 3-4 weeks in field, we could observe less growth reduction in shoot as compared to root. The calculated GR_{50} based on root length reduction was 579.2 Gy. Whereas in terms of shoot growth the calculate GR_{50} was 764 Gy. One of the drawbacks of this in vitro experiment in safflower is the rosette growth of safflower during initial seedling growth stage that hinders in taking actual seedling height. Thus it is prescribed to use root length as a parameter to measure radiation injury in hydroponically grown seedlings of safflower in *in vitro* condition.

Effect of gamma rays on safflower in *in vivo* (field) growth experiment: In order to study the effect of gamma rays on mutation induction in this crop, the irradiated seeds of the above dose range were also grown in field condition. No emergence of seedling was obtained in the dose of 700 Gy and above for all the four tested genotypes. Further the seedlings showed very diminutive growth in 600 Gy. Due to the rosette growth habit of the crop in seedling stage, no seedling height data were taken up to 30 DAS. The seedling

height data were collected on 42 DAS and 72 DAS. Gradual seedling height reduction was also observed for all the tested genotypes in response to increment of dose of gamma rays (Fig 2). When the data from 10 seedlings each of the genotypes were used in probit analysis, variations were noted in GR_{50} dose among the genotypes. A significant difference in GR_{50} dose among the tested genotypes in both the pheno-phases of the crop (42 DAS & 72 DAS) were revealed in ANOVA analysis (Table 1). At both 42 and 72 DAS, RVS 2012-13 had the least GR_{50} dose compared to other three genotypes (Fig 3 a & b). Since the crop start to recover well from the radiation damage in their mature stage, the damage in terms of GR_{50} dose was almost same in case of RSS 3, RSS 7 and Annigeri 1 at 72 DAS (Fig 3b). But, at 42 DAS, both RVS 2012-13 and RSS 7 had significant lower GR_{50} values compared to other two tested genotypes (Fig 3a). The analysis revealed the least GR50 values for RVS 2012-13: 248.7 Gy (42 DAS) and 301.2 Gy (72 DAS). Annigeri 1 had the highest GR50 value: 374.3 Gy (42 DAS) and 447.6Gy (72 DAS). The second least sensitive genotype was RSS 7: 257.9 (42 DAS) and 477.3 Gy (72 DAS). The other moderate sensitive genotype was RSS 3: 294.8 Gy (42 DAS) and 427 Gy (72 DAS). The GR50 values of three genotypes (RSS 3, RSS 7 and Annigeri 1) did not differ significantly at 42 DAS and thus consider same in terms of their radio sensitivity.

Table 1 Analysis of variance of GR_{50} dose on four genotypes tested in present study

Source of Variation	Degree of freedom	Mean sum of squares of GR_{50} dose		F. table		F. calc. (P = 0.05)
		DAS72	DAS 42	DAS72	DAS 42	
Replication	9	55.17	1518.4	0.27	5.35	4.60
Genotype	3	37339.51**	9964.8**	183.67	35.10	2.96
Error	27	203.29	283.86			

Table 2 Details of M_1 and M_2 data and number of true breeding mutants obtained in this study

Parameters/type of mutants	RVS 2012-13	RSS 3	RSS 7	Annigeri 1	Total
GR_{50} (42 DAS)	248.7 Gy	294.8 Gy	257.9 Gy	374.3 Gy	-
GR_{50} (72 DAS)	301.2 Gy	427.0 Gy	477.3 Gy	447.6 Gy	-
M_1 plants (@ 500 Gy)	45	61	72	122	200
M_1 plants (@ 300 Gy)	700	735	745	820	3000
M_2 population size	18700	22300	24000	27000	92000
Number of true breeding mutants and frequency (mentioned in parenthesis)					
Early rosette	3	2	6	-	11 (1.2 x 10^{-4})
Early flowering	2	1	2	1	6 (6.5 x 10^{-5})
Fused capitulum	-	-	-	1	1 (1.1 x 10^{-5})
Dwarf plant	1	1	2	2	6 (6.5 x 10^{-5})
Tall plant	1	1	2	-	4 (4.3 x 10^{-5})
Large bud/capitulum	1	-	2	1	4 (4.3 x 10^{-5})
More branches	6	5	5	-	16 (1.7 x 10^{-4})
Appressed stem	1	-	2	2	5 (5.4 x 10^{-5})
Spineless	4	2	2	6	14 (1.5 x 10^{-4})
Total	19	12	23	13	67 (7.3 x 10^{-4})

Survival of M_1 plants in bulk irradiation for mutation breeding: Based on the derived GR_{50} values *in vitro* experiment, a sub-lethal dose of 500 Gy was applied to 1000 seeds of each genotype (RVS2012-13, RSS 3, RSS 7 and Annigeri 1). The germination of the irradiated seeds were very low (far below 50%) which did not produce enough population to generate M_2 population. From this initial experiment, we come to know about the lethality of 500 Gy gamma rays in *in vivo* field condition. So, we applied 300 Gy dose to 1000 seeds of each genotype to raise M_1 population. In case of each genotype 700 to 820 plants survived and seeds were harvested. Shortening of

internodes, chlorosis, mosaic, and other leaf deformation were noticed in M_1 plants. The least plant population was obtained in case of RVS 2012-13 and the highest in Annigeri 1. The seeds from main capitulum from each survived plants were kept separately to raise M_2 population.

Mutants obtained in large scale mutation breeding experiments: From the above M_1 progenies large numbers of M_2 population were grown in field. For each genotype 20000 to 25000 plants got established in the field. In total, 92000 plants were obtained in whole M_2 population of four genotypes (Table 2). Variants like early rosetting, early flowering, capitulum size, plant height, leaf shape, bud shape, appressed branches and fused capitulum etc. were tagged in the field. In average, 55 to 65 progenies from each genotype were grown at M_3 generation to test true breeding behavior of each putative mutant in the M_2. In total, 250 plant progenies were grown in field to test true breeding behavior of each variant identified in M_2. In total, 67 true breeding mutants were obtained from this mutation breeding experiment (Table 3). Of the several true breeding mutants, a fused capitulum (Fig 4a), early flowering (Fig 4b), more number of branches, dwarf plant and early rosette plants are of economic importance and may be useful in improvement of yield parameters of safflower (Table 3). The frequency of early rosette breaking mutants was 1.2 x 10-. The mutation frequency of fused capitulum was 1.1 x 10^{-5}. The highest number of mutants was obtained in RSS 7, followed by RVS 2012-13 and RSS 3. The lowest number of mutants was isolated in Annigeri 1 genetic background.

Absorbed dose of ionizing radiation plays a trade-off between radiation-induced damage/lethality and effective number of mutants in an induced mutation breeding programme. Furthermore population size is an important criterion for induction of a number of beneficial mutants. Thus dose optimization in case of physical mutagenesis is the prime step in mutation breeding. In order to exploit radiation-induced mutagenesis for crop improvement, the radio-sensitivity test and/or GR_{50} estimation in a crop species is necessary to recover high frequency of desirable mutations (Ahloowalia *et al.,* 2004). Doses of mutagen that lead to 50% lethality or 50% growth reduction are considered as LD_{50} or GR_{50}, respectively (Viana *et al.,* 2019).Whereas, the dose of a mutagen that achieves the optimum mutation frequency with the least possible unintended damage is considered as the optimal dose (Mba *et al*., 2010). Normally, this optimal dose lies in between GR_{30} and GR_{50} values (Roy *et al.,* 2019). Based on in vitro experiment, a GR_{50} value of 579.2 Gy was obtained based on root length parameters in hydroponic experiment. This calculated GR_{50} dose is well matched with the published report where the dose varied from 600 -700 Gy (FAO/IAEA 2018). Thus we initially selected an optimal dose of 500 Gy for mutation induction. But more lethality (95%) was noticed in actual field condition and only a few plants survived in that dose (Table 2). Such observation forced us to conduct field based radiation sensitivity experiments for safflower crop. In most of the radiation sensitivity experiments, seedling height was considered a prime criterion to assess GR_{50} dose (Kodym *et al.,* 2011). The ancient oilseed crop, safflower has unique rosette behaviour in seedling stage that varies from 20 to 35 days (Singh and Nimbkar, 2006). So, it is difficult to measure seedling height in this stage. Besides measurement of seedling height can be erroneous and dose dependent height reduction can be misinterpreted. We therefore measured height of seedling at 42 DAS and 72 DAS and compared the observed data and analyzed for determining the GR_{50} dose. Significant variation for GR_{50} dose observed that signified the genotypic difference among the genotypes for radiation sensitivity. RVS 2012-13 were found most radiation sensitive while Annigeri 1 was the most radiation tolerant. Such a significant difference in radiation sensitivity was noted in case of electron beam implanted rice genotypes (Shu *et al.,* 1996), rice landraces irradiated with various physical mutagen (Sao *et al.,* 2020) and groundnut genotypes exposed to gamma rays and electron beam (Mondal *et al.,* 2017).The GR_{50} dose at 42 DAS was varied from 248.7 to 374.3 Gy (Table 3). We then chose 300 Gy as optimal dose for large scale mutation breeding experiments in four genotypes, RVS 2012-13, RSS 3, RSS 7 and Annigeri 1. The field emergence of M_1 plant at this dose was almost 75% and found to be sub-lethal. The M_2 population of each genotypes exhibited variation for different morphological traits which enhanced genetic variability in the crop (Rampure *et al.,* 2017). Furthermore, the whole mutageneized population showed variation for rosette breaking period and 11 true breeding mutants were generated for this early rosette trait. Safflower crop is usually sown in second fortnight of November in Chhattisgarh after harvesting of rice. Development of early rosette mutant lines will allow farmers to choose a stretchable window for sowing and harvest the crop much before onset of monsoon in Chhattisgarh. Besides early flowering mutants were also obtained in this study. Ranga Rao *et al.* (1977) analyzed inter-relationship of various component characters with yield and oil content using 215 entries of safflower from India and USA. The correlation of capsule number per plant and capsule weight with yield per plant was positive and pronounced. The isolation of large capitulum in RSS 7 background will help to recombine thus induced mutant character with high oil content in future. The mutants selected for higher branches in RSS3, RVS 2012-13 and RSS 7 also showed stability in M_4 generation.

This will give more seed yield since number of primary branches has positive correlation with number of capitulum/plant (Ghorpade *et al*., 1993; Kurhade *et al*., 2015).

The present experiment has demonstrated the usage of proper calibrated dose for induction of beneficial mutation in safflower. The study reiterated the importance of proper calibration of GR_{50} dose before conducting of large scale mutation breeding experiment and generation of large M_2 population size towards isolation of economical mutants in this crop.

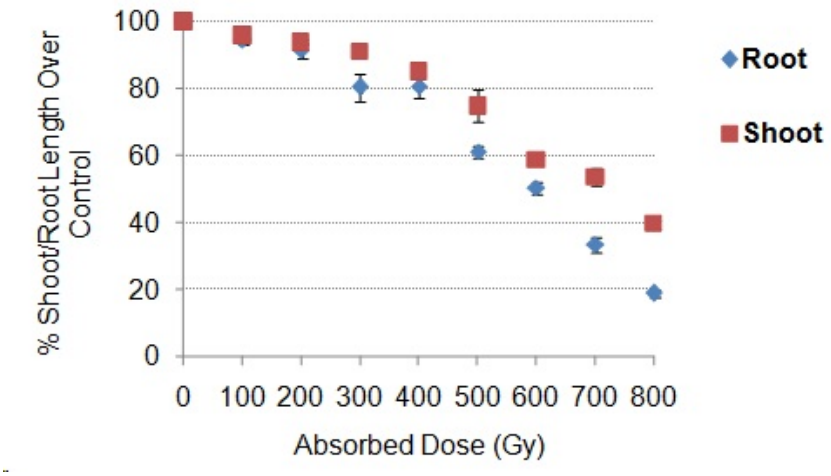

Fig. 1. Dose dependent shoot and root length reduction in response to gamma rays

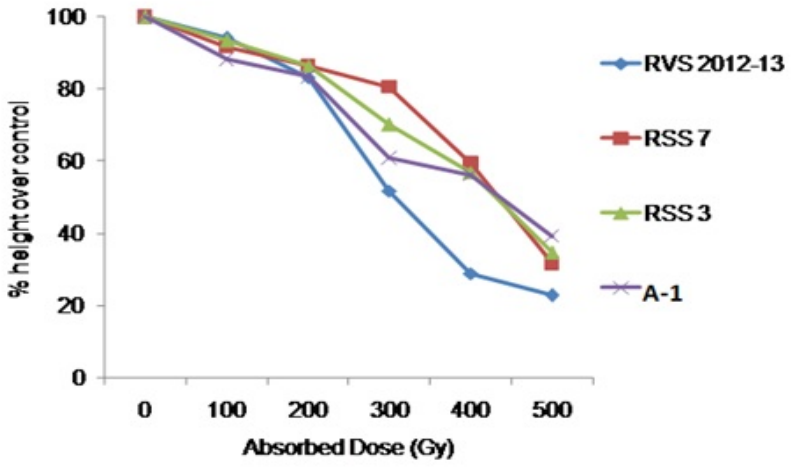

Fig. 2. Differential behavior of radiation-sensitivity of four safflower genotypes

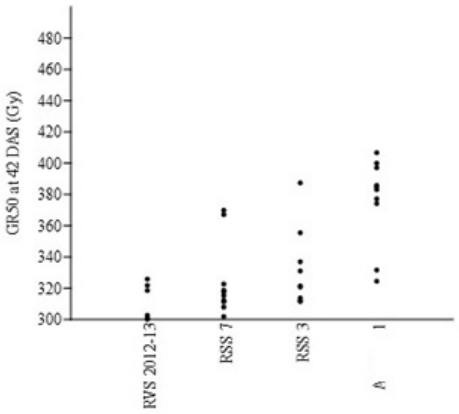

Fig. 3a. Jitter plot analysis of GR_{50} doses of four safflower genotypes at 42 DAS

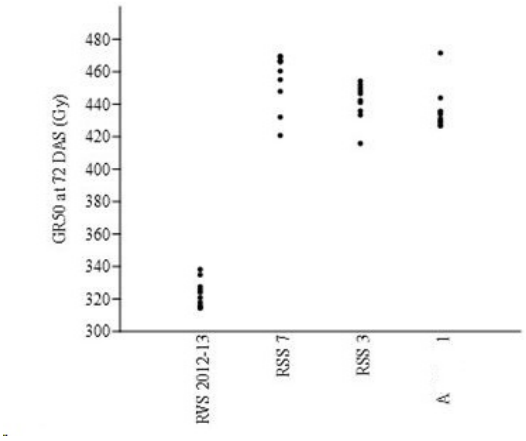

Fig. 3b. Jitter plot of GR_{50} doses of four safflower genotypes at 72 DAS

Fig. 4a. A unique fused capitulum mutant in safflower isolated in this study

Fig. 4b. Early flowering mutant of safflower isolated in this study

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Genetic variability, heritability, association and divergence studies in safflower (*Carthamus tinctorius* L.) genotypes

S NEELIMA*, K PRABHAKAR AND K V RAMANAMMA

Regional Agricultural Research Station, Nandyal, Kurnool-518 501, Andhra Pradesh

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ABSTRACT

Genetic variability, heritability, genetic advance, divergence, association and path analysis studies were carried out in 13 safflower genotypes for nine yield and its contributing traits. Results of ANOVA showed highly significant mean sum of squares for all the traits indicating presence of high variability in the experimental material. Wide range of variation was noticed in seed yield followed by plant height, number of capitula/plant and number of seeds/capitulum. High phenotypic and genotypic coefficient of variation were recorded for number of seeds/capsule, 100 seed weight and seed yield. Low heritability coupled with high genetic advance as percent of mean was exhibited for seed yield indicated that yield is governed by additive gene effects and is highly influenced by environment. Hull content recorded strong correlation with seed yield followed by volume weight and 100 seed weight and in turn these traits were also strongly inter-correlated. Volume weight had high direct effect on seed yield and its indirect effect *via* hull content and 100 seed weight was also of high magnitude. In the experimental material, genetic divergence was mainly contributed by oil content, days to 50% flowering and number of seeds/capitulum.

Keywords: Safflower, Genetic variability, Heritability, Divergence, Association path analysis

Safflower (kusum, kusumbha, kardi) has been under cultivation in India for its brilliantly coloured florets and the orange red dye (carthamin) extracted from them and seed oil. The seed contains 24-36% oil and is largely used for cooking purpose. The oil is as good as sunflower oil having high amount of linoleic acid (78%) which is very useful for reducing blood cholesterol content. Safflower oil has good drying properties and is used in the manufacture of paints, varnishes and linoleum. The unsaturated fatty acids of safflower lower the serum cholesterol. The oil cake particularly from decorticated seeds is used as cattle feed. Safflower cake contains about 40-45% protein. In India it is cultivated in an area of 45,890 ha with a production of 24,640 t and with a productivity of 537 kg/ha. Karnataka and Maharashtra are the major safflower growing states, which contribute > 90% of India's production of safflower. In Andhra Pradesh, at present only 1000 ha is under safflower cultivation and it is the best alternate *rabi* oilseed crop in low yield potential chickpea areas. The present investigation has been carried out to assess the magnitude of phenotypic and genotypic variability, phenotypic and genotypic coefficient of variation, heritability in broad sense, correlation coefficient and path analysis and genetic divergence among safflower genotypes.

*Corresponding author's E-mail: Siddareddyneelima@gmail.com

MATERIALS AND METHODS

Thirteen safflower genotypes (ISF-849-sel-16, SSF-17-01, ISF-87-15, PBNS-12, ANG-18-02, RVS-18-3, ISF-116, SSF-17-04, PBNS-184, RVS-18-1, A-1, SSF-17-05 and PBNS-183) were evaluated in Randomized Block Design (RBD) during *rabi,* 2019-20 using two checks at Regional Agricultural Research Station, Nandyal with a spacing of 45 cm between the rows and 20 cm between the plants. Recommended agronomic practices were followed to raise a good crop. Data were recorded for nine characters *viz.,* days to 50% flowering, plant height, number of capitula/plant, number of seeds/capitulum, 100 seed weight (g), volume weight (g/100 ml), oil content (%), hull content (%) and seed yield (kg/ha) in each genotype across all the three replications. Analysis of variance was computed based on RBD for each of the character separately as per standard statistical procedure given by Panse and Sukhatme (1978). Heritability (h^2) in the broad sense was calculated according to the formula given by Allard, 1960. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Genotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955a). The path coefficient analysis was performed as per the formula given by Wright (1921) and adopted by Dewey and Lu (1959). Mahalonobis D^2 statistic was used to analyze genetic divergence among safflower

genotypes. For statistical analysis, TNAUSTAT software (Manivannan, 2014) package was used.

RESULTS AND DISCUSSION

The results of ANOVA (Table 1) carried out in the present study showed highly significant mean sum of squares for all the traits indicating presence of high variability in the experimental material.

The estimates of range and genetic variability parameters were assessed for nine characters and these are presented in Table 2. Wide range of variation was observed for seed yield (482 - 1688 kg/ha) followed by plant height (68 - 98 cm), number of capitula/plant (21- 48) and number of seeds/capitulum (10 - 29) which indicates better scope for selection of these traits. These results are in agreement with Mukta *et al.* (2020). Narrow range of variation was noticed for oil content (26.2 - 40.5%), hull content (40 - 52%) and days to 50% flowering (60 - 71) while the variation was high for 100 seed weight (2.30 - 6.70 g).

The PCV values were higher than GCV for number of capitula/plant, number of seeds/capitulum, hull content and seed yield, which implied the effect of environment on variability in these traits. However, PCV and GCV values did not differ greatly for traits like days to 50% flowering, plant height, test weight, volume weight and oil content indicating stable expression of these traits and least influence of environment. High PCV and GCV were recorded for number of seeds/capitulum, 100 seed weight and seed yield. These results are in agreement with Minnie *et al.* (2018) and Pushpavalli and Kumar (2017). Moderate PCV and GCV were noticed in oil content. Number of capitula/plant exhibited moderate PCV and low GCV. Low PCV and GCV values were recorded for days to 50 % flowering, plant height, volume weight and hull content. Low coefficients of variation for these traits indicated that the variation in the material was low, therefore, search for variation in other material may be required.

The coefficients of variation indicate only the extent of variability that exists for different characters and do not indicate heritable portion of a character. Hence, heritability is estimated, which is a good index of transmission of characters to off spring (Falconer, 1981). In this study, heritability estimates were high for oil content (88.07%) followed by days to 50% flowering (86.83%), 100 seed weight (73.08%) and volume weight (71.38%) indicating that these traits were less influenced by the environment and selection based on phenotypic observations would be effective. Moderate heritability was noticed for plant height (61.14%) and number of seeds/capitulum (56.46%). Low heritability was noticed for seed yield (37.58%) followed by number of capitula/plant (19.58 %) and hull content (18.79%). These results are in contrary to Minnie *et al.* (2020) and Pushpavalli and Kumar (2017).

Johnson *et al.* (1955b) suggested that heritability considered together with genetic advance is more reliable in predicting the effect of selection than heritability alone. High heritability coupled with high genetic advance as percent of mean (GAM) was noticed for 100 seed weight and oil content, which indicated that these traits are governed by additive gene action and directional selection could be more effective. High heritability coupled with low GAM was observed for volume weight suggesting the role of favourable environment rather than genotype and therefore, selection may not be not rewarding. High heritability coupled with moderate GAM was noticed for days to 50% flowering indicating the role of both additive and non-additive gene actions; therefore, population improvement by reciprocal recurrent selection could be useful. Low heritability coupled with high GAM was observed for seed yield indicating that yield is governed by additive gene effects and is highly influenced by environments and therefore, selection would be effective. Whereas, high heritability coupled with high GAM was reported for yield by Minnie *et al.* (2020) and Pushpavalli (2016). Hull content and number of capitula/plant showed low heritability as well as low genetic advance as these traits may be governed by non-additive gene action.

In association analysis (Table 3), hull content (1.083**) recorded strong correlation with seed yield followed by volume weight (0.848**) and 100 seed weight (0.880**). In turn, these traits were also strongly inter-correlated. This clearly implied that improvement for seed yield can be achieved if directional selection is practiced for these traits. Among yield contributing characters, 100 seed weight showed strong association with hull content (1.488**) followed by volume weight with hull content (1.284**), 100 seed weight with volume weight (0.897**), number of capitula/plant with hull content (0.668**) and plant height with number of seeds/capitulum (0.428**). Similar results were reported by Vinod Kumar and Rajesh (2020), Pavithra *et al*. (2016) and Dambal and Patil (2016). However, oil content (-0.791**) exhibited strong negative association with seed yield which indicates selection for these traits should be made in opposite direction. Among yield component traits, plant height showed strong negative association with number of capitula/plant (-1.073**); number of capitula/plant with number of seeds/capitulum (-1.161**); number of seeds/capitulum with hull content (-0.493**); 100 seed weight with oil content (-0.997**); volume weight with oil content (-0.834**) and oil content with hull content (-1.403**).

Correlation simply measures the mutual association without any regard to causation, while path coefficient

analysis provides direct and indirect causes of association. The path analysis (Table 4) showed that volume weight has higher magnitude of direct effect on seed yield (0.5701). The indirect effect of volume weight is even more than its direct effect via hull content (0.7321) and 100 seed weight (0.5114). Even hull content exhibited high indirect effect through seed weight (0.1268), volume weight (0.1094) and number of capitula/plant (0.0570). This was clearly evident from strong inter-correlations. Oil content (-0.1960), number of seeds/capitulum (-0.1579), days to 50% flowering (-0.1591) and number of capitula/plant (-0.0837) exhibited negative direct effect on seed yield. Vinod Kumar and Rajesh (2020), Lucy Kumari and Ravikumar (2010), Ahmadzadeh *et al*. (2012) also reported similar results. The direct effect of seed weight on seed yield was found to be low in magnitude (0.0196) but its indirect effect via volume weight (0.0176) and hull content (0.0291) may be the chief cause of strong positive correlation with seed yield.

The genetic divergence analysis implied grouping of 13 genotypes of safflower into 4 clusters which indicated presence of considerable variability in the material. Cluster II had more number of genotypes (6) followed by clusters I (4), III (2) and IV (1). Cluster I (42.74) had maximum intra cluster distance followed by cluster II (29.61) and cluster III (14.63). The maximum intercluster distance was recorded between cluster III and IV (355.92) followed by cluster II and IV (213.55). Hence, it is suggested that if genotypes from diverse groups are used in the breeding programme, it is expected to produce a wide range of genetic variability in the population. Cluster I exhibited higher mean values (Table 5) for plant height and number of seeds/capitulum; Cluster II for number of capitula/plant, hull content and seed yield; Cluster III for 100 seed weight and volume weight. Oil content, days to 50% flowering and number of seeds/capitulum were the major traits contributing for genetic divergence among the genotypes (Table 6). However, earlier studies by Pushpavalli and Kumar (2017), Shivani and Sreelaxmi (2013) concluded seed yield as the major trait contributed for divergence.

Table 1 General ANOVA for yield and yield components in safflower

Character	Mean sum of squares		
	Replications (2 df)	Genotypes (12 df)	Error (24 df)
Days to 50 % flowering	5.1026	45.4359**	2.1859
Plant height (cm)	51.769	94.175**	16.464
Number of capitula/plant	19.410	32.342**	18.69
Number of seeds/capitulum	49.000	44.970**	9.194
100 Seed weight (g)	0.070	2.712*	0.297
Volume weight (g/100 ml)	1.615	22.658**	2.671
Hull content (%)	7.487	20.731**	12.237
Oil content (%)	0.390	43.613**	1.885
Seed yield (kg/ha)	11077	198904**	70875

** Significant at 1% level

Table 2 Mean, range and genetic variability parameters for different traits in safflower

Character	Mean	Range		PCV (%)	GCV (%)	Heritability (%)	GAM
		Min.	Max.				
Days to 50% flowering	67	60.0	71	6.09	5.67	86.83	10.89
Plant height (cm)	86	68.0	98	7.56	5.91	61.14	9.52
Number of capitula/plant	29	21.0	48	16.86	7.46	19.58	6.80
Number of seeds/capitulum	18	10.0	29	25.97	19.52	56.46	30.21
100 Seed weight (g)	5	2.30	6.70	20.84	17.82	73.08	31.38
Volume weight (g/100 ml)	52	46.0	57	5.83	4.93	71.38	8.58
Oil content (%)	30	26.2	40.45	13.05	12.25	88.07	23.67
Hull content (%)	46	40.0	52	8.39	3.64	18.79	3.25
Seed yield (kg/ha)	1240	482.0	1688	27.18	16.67	37.58	21.04

PCV: Phenotypic co-efficient of variation, GCV : Genotypic co-efficient of variation, GAM : Genetic advance as per cent of mean

Table 3 Genotypic correlations among seed yield and its attributes in safflower

Character	Days to 50% flowering	Plant height (cm)	Number of capitula/ plant	Number of seeds/ capitulum	100 seed weight (g)	Volume weight (g/100 ml)	Oil content (%)	Hull content (%)
Days to 50% flowering	1.000							
Plant height (cm)	0.170	1.000						
Number of capitula/plant	0.173	-1.073**	1.000					
Number of seeds/capitulum	-0.528**	0.428**	-1.161**	1.000				
100 Seed weight (g)	-0.140	-0.020	0.153	-0.143	1.000			
Volume weight (g/100 ml)	-0.152	-0.215	0.234	-0.222	0.897**	1.000		
Oil content (%)	0.041	0.142	-0.468**	0.302	-0.997**	-0.834**	1.000	
Hull content (%)	0.001	-0.252	0.668**	-0.493**	1.488**	1.284**	-1.403**	1.000
Seed yield (kg/ha)	-0.147	0.063	0.099	-0.104	0.880**	0.848**	-0.791**	1.083**

*,** Significant at 5% and 1% levels, respectively

Table 4 Genotypic path coefficients for seed yield and its attributes in safflower

	DF	PH	NCP	NSC	SW	VW	OC	HC	SY
DF	-0.1591	0.0409	-0.0144	0.0833	-0.0027	-0.0865	-0.0081	0.0001	-0.1467
PH	-0.0271	0.2403	0.0897	-0.0675	-0.0004	-0.1227	-0.0278	-0.0215	0.0632
NCP	-0.0275	-0.2578	-0.0837	0.1832	0.0030	0.1335	0.0916	0.0570	0.0994
NSC	0.0840	0.1028	0.0971	-0.1579	-0.0028	-0.1263	-0.0591	-0.0420	-0.1043
SW	0.0223	-0.0048	-0.0128	0.0225	0.0196	0.5114	0.1955	0.1268	0.8805**
VW	0.0242	-0.0517	-0.0196	0.0350	0.0176	0.5701	0.1634	0.1094	0.8483**
OC	-0.0066	0.0340	0.0391	-0.0476	-0.0195	-0.4752	-0.1960	-0.1196	-0.7914**
HC	-0.0001	-0.0606	-0.0559	0.0779	0.0291	0.7321	0.2751	0.0852	1.0827**

Residual effect (Genotypic) = 0.205; Diagonal values = Direct effects; Off-Diagonal values = Indirect effects; *, ** Significant at 0.05 and 0.01 levels, respectivelyDF : Days to 50 % flowering ; PH : Plant height (cm) ; NCP : Number of capitula/plant ; NSC : Number of seeds/capitulum ; SW : 100 Seed weight (g) ; VW : Volume weight (g/100 ml); OC : Oil content (%);HC : Hull content (%); SY : Seed yield (kg/ha)

Table 5 Cluster means for nine characters in safflower genotypes

Cluster	Days to 50 % flowering	Plant height (cm)	Number of capitula/ plant	Number of seeds/ capitulum	100 Seed weight (g)	Volume weight (g/100 ml)	Oil content (%)	Hull content (%)	See yield (kg/ha)
I	65.08	91.42	26.58	21.42	4.64	50.5	32.82	44.42	1268.92
II	69.34	85.34	30.84	14.73	5.50	53.6	28.06	47.83	1342.73
III	61.17	79.50	27.34	19.50	5.70	55.17	28.65	47.67	1238.17
IV	71.70	82.34	25.67	17.00	2.57	46.67	38.96	41.34	512.0

Table 6 Percent contribution of characters towards genetic divergence in safflower

Character	Contribution	Times Ranked First
Days to 50% flowering	19.24	15
Plant height (cm)	6.42	5
Number of capitula/plant	2.53	2
Number of seeds/capitulum	16.67	13
100 Seed weight (g)	0	0
Volume weight (g/100 ml)	12.83	10
Oil content (%)	42.31	33
Hull content (%)	0	0
Seed yield (kg/ha)	0	0

In conclusion, the present study has shown (1) wider range of variability, high PCV and GCV, low heritability and high GAM for seed yield in safflower indicating variability, high influence of environment, additive gene action and effectiveness of selection procedure, (2) directed selection for seed yield in safflower can be achieved if selection is practiced for hull content, volume weight and 100 seed weight. These traits were also strongly inter-correlated and had either direct effect or indirect effect via other traits on seed yield and (3) genetic divergence in safflower was mainly contributed by oil content, days to 50% flowering and number of seeds/capitulum.

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Genetic studies of oil content in safflower (*Carthamus tinctorius* L.)

MANJUNATH HUGAR, MANJULA MARALAPPANAVAR AND LAKSHMI GANGAVATI*

Agriculture Research Station, University of Agricultural Sciences (Dharwad), Annigeri-582 201, Karnataka

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ABSTRACT

Safflower is an ancient oilseed crop and has been acknowledged as a healthy vegetable oil. Though India is the largest producer, the area under safflower has been declining mainly due to low productivity and less profitability. Safflower genotypes with higher oil content would help to make the crop commercially viable and regain its area owing to its high oil quality compared to its competitive counter parts. The genetic improvement of safflower for higher oil content is an urgent need and involves an understanding of genetics of the trait. A-1, a popular highly resilient variety in India since 1969 with good yield has low oil content of 28% and needs to be improved for oil content. Baccum-92, a Mexican line with high oil of 37% was used in a cross with A-1 to develop 6 generations to study the inheritance of oil content and to simultaneously identify the segregants with high yield and oil content. The six generation mean analysis revealed that additive, dominance components and epistatic interactions of additive × additive and dominance × dominance with duplicate gene interaction determined the inheritance of oil content. One (43.52%) and 3 (ranging from 39.06 to 39.98%) segregants having 5% superiority over the better parent Bacum-92 were observed in F_2 and BC_1P_1, respectively. 5 segregants with higher yield than A-1 coupled with high oil content of more than 31% were identified across the populations which can be stabilized and used in safflower improvement.

Keywords: Duplicate gene interaction, Generation mean analysis, Inheritance, Oil content, Safflower

Safflower (*Carthamus tinctorious* L.) is an ancient oilseed crop which is widely grown under the hot and dry climate of the Middle East, the centre of its origin and diversity. Around the world, it is cultivated mainly for edible seed oil and flower, more specifically for petals used for food coloring and preparing dyes in the textile industry. Safflower has recently been acknowledged as a healthy vegetable oil due to its various health benefits. The safflower seeds contain 25-50 per cent oil, 15-20 per cent protein and 35-45 per cent hull fraction. The standard safflower oil shows the variability for fatty acid composition in seed oil, and contains about 6-8 per cent palmitic acid, 2-3 per cent stearic acid, 16-20 per cent oleic acid and 71-75 per cent linoleic acid. Hence the safflower oil is of two types: one high in monounsaturated fatty acid (oleic acid) and the other high in polyunsaturated fatty acid (linoleic acid). The high oleic type is comprised of low saturated fats than olive oil and hence is very suitable for hypo-cholesterol diet, for frying and for the preparation of frozen food. The high content of linoleic acid ranks first in all kind of vegetable oils and it is the best edible oil in the world (Knowles, 1958). The high linoleic type also has a large industrial potential to be used in manufacturing of varnishes, alcohols, surfactants. In addition, safflower oil contains predominantly α-tochopherols, which exhibits highest vitamin-E activities (Johnson *et al*., 1999). The safflower oil is very stable at high temperatures and does not produce any smoke or bad smell during frying. Its consistency does not change at low temperatures also, making it particularly suitable for use in chilled foods. It is better suited to hydrogenation for margarine than soy or canola oil, which are unstable in this process.

India is the largest producer of safflower in the world; it ranks first in area and production. The area under safflower in India has declined from 10 lakh ha in 1988 to 4.3 lakh ha in 2020 (FAOSTAT, 2020) which is mainly due to low productivity and less profitability. Though there are reports of yield improvements in the present cultivars, the oil content has remained quite constant at 28-30 per cent, with only an occasional cultivar reaching to 35 per cent oil, which is a serious concern for safflower cultivation in India (Mukta *et al*., 2012).

Safflower genotypes with higher oil content would help to make the crop commercially viable and regain its area owing to its high oil quality compared to its competitive counter parts. Hence, the genetic improvement of safflower for higher oil content involves an understanding of genetics of the trait. Breeding procedures for improving oil content is mainly dependent on the type of gene action and relative amount of the genetic variance components in the population. Genetic models have been deployed for estimation of different genetic effects (Kearsey and Pooni,

*Corresponding author's E-mail: lakshmirg8@gmail.com

2004). Among them, Generation Mean Analysis is a simple but useful technique used to estimate gene effects for a polygenic trait (Kearsey and Pooni, 2004; Nakhaei *et al*., 2014). Its greatest merit lies in the ability to estimate epistatic gene effects, such as additive × additive, dominance × dominance and additive × dominance (Kearsey and Pooni, 2004). The presence or absence of epistasis can be detected by the analysis of generation means using the joint scaling test, which measures epistasis accurately, no matter if it is complementary (additive × additive: i) or duplicate (additive × dominance: j) and (dominance × dominance: l) at the digenic level (Kearsey and Pooni, 2004).

A-1 (Annigeri-1), a resilient variety having oil content of 28% was crossed with Baccum-92, a Mexican line with high oil of 37 to develop six generations for investigating the gene action operating in the inheritance of oil content in safflower.

MATERIALS AND METHODS

The experimental material comprised of P_1, P_2, F_1, BC_1P_1, BC_1P_2, and F_2 population of the cross Baccum-92 (High oil) × A-1 (Low oil) developed at Agricultural Research Station, Annigeri, University of Agricultural Sciences, Dharwad during *rabi* 2017-18 under rainfed condition by following the recommended agronomic practices. The parents used in the development of six populations included Baccum-92, a Mexican line having high oil content of 37% and A-1, a popular high yielding variety with potential yield of 1500 kg/ha since 1969 developed at AICRP Safflower centre, Annigeri. Initial crossing between A-1 and Baccum-92 was carried out in 2015-16 to generate F_1 population. During 2016-17, the F_1 was selfed to get F_2 and BC_1P_1 and BC_1P_2 was attempted. In 2017-18, P_1, P_2 and F_1 generated were sown following replicated blocks and BC_1P_1, BC_1P_2, and F_2 populations were sown in unreplicated trials. The six populations were subjected to generation mean analysis to study the mode of inheritance of oil content. The row spacing was 45 cm and between plants spacing was 20 cm. The seeds were collected from 5 random plants tagged to record the observations in non segregating generation and from all the individual plants of the segregating populations. The oil content was estimated with the help of Nuclear Magnetic Resonance (NMR) spectrometer installed at the AICRP (Groundnut), MARS, Dharwad.

Genstat software was used to carry out the generation mean analysis. Mather's scaling tests A, B, C and D were applied, to test the adequacy of simple additive-dominance model for oil content in the study. Significant estimates of the scaling test insist six parameter model to know information on the nature of gene action governing the trait under study. All the six components of generation means were calculated by joint scaling test given by Jinks and Jones (1958). The significance of the scales and gene effects were tested using the t-test (Singh and Chaudhary, 1985). To provide information on the nature of gene action governing the trait under study, all the six components of generation means were calculated following six parameter model outlined by Jinks and Jones (1958). Six parameters viz., mean (m), additive gene effects (d), dominance gene effects (h), and three types of non-allelic gene interactions, *viz*., additive × additive (i), additive × dominance (j) and dominance × dominance (l) were estimated. The oil content was analyzed statistically and tested for significance. The significance of the joint scaling test was determined by the using 't' test and expected 't' values were compared with observed at 5 and 1% level of significance. To identify transgressive segregants for oil and yield, the plants in F_2, BC_1P_1 and BC_1P_2 with above 5% superiority over the best parent were identified as transgressive segregants.

RESULTS AND DISCUSSION

Generation mean analysis for oil content: Oil content in safflower is a complex trait as it is negatively associated with many yield related traits making the breeding efforts less responsive. The trait involves genotypic and environmental interactions. Understanding the mode of inheritance of such a complex quantitative character is a basic element for formulating breeding strategy to improve such character. Generation mean analysis is proven to be a powerful technique for understanding inheritance of a trait along with epistatic interactions involved in governing a particular trait. The significance of any one of the scales 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. The estimates of gene effects help in understanding the genetic potential of the population under study while the relative magnitude of additive and non additive genetic variance decides the breeding procedure to be followed for improving a particular character of a population. There is also possibility of identifying the superior segregants for high yield coupled with high oil content in segregating generations.

Mean performances of the six populations of the cross Baccum-92 (High oil) × A-1 with respect to oil content are given in Table 1. The highest mean performance for this trait was recorded in the female parent i.e. Baccum-92 (High oil) with 37.10 per cent oil content. The male parent A-1 was found to have lower oil content with 27.35 per

cent. The F_1 and F_2 had intermediate values of oil content i.e. 29.22 and 29.58 per cent, respectively. The backcross generations BC_1P_1 and BC_1P_2 had still lower performance having 25.97 and 22.68 percent oil content respectively. Back cross means were lower when compared to the F_1 and F_2 means and were related with their corresponding recurrent parental means. Similar findings were obtained by Jotothu *et al*. (2013), Nakhaei *et al.* (2014) and Shivani and varaprasad (2016).

Estimation of gene effects: The significance of B and D scaling tests revealed the inadequacy of simple additive - dominance model to explain the total genetic variability indicating the presence of epistasis (Table 2). The results of joint scaling test revealed that both additive as well as dominant component were significant for this trait, however the values of dominant component was higher than additive indicating the predominance of dominance in determining this trait. Among epistasis, additive × additive and dominance × dominance were found to be significant and the opposite signs of dominance (h) and dominance × dominance (l) indicated the presence of duplicate epistasis.

Gadekar and Jambhale (2011) also have reported the involvement of epistasis in inheritance of oil content in safflower using scaling tests. Six parameter model was used and dominance gene effect and involvement of additive x dominance (G) gene interactions in the inheritance of per cent oil content was confirmed in their study. Golkar *et al.* (2011) reported quantitative inheritance and involvement of non-additive gene effects in controlling genetics of oil content. Some studies also have reported the involvement of dominant gene effects and the preponderance of dominant alleles than recessive alleles in controlling oil content in safflower (Gupta and Singh, 1988: Ramachandram and Goud, 1981). Ratnaparkhi *et al.* (2012) identified the influence of both additive and non additive gene action in inheritance of oil content and suggested to go for population improvement to accommodate favorable alleles for oil content in safflower.

Eventhough only a few studies have been conducted in safflower with respect to genetic studies of oil content, the inheritance studies in other edible vegetable oils reported similar findings. Wilson *et al.* (2013) revealed significant additive, dominance, and epistatic effects for oil concentration in groundnut. Their study using generation mean analysis also found duplicate gene interaction to be involved in inheritance of oil concentration in peanut. Non additive gene action in controlling oil content was observed in sunflower by Lakshman *et al.* (2019).

Table 1 Mean and standard error of oil content measured by nuclear magnetic resonance spectroscopy (NMR) in parents (P_1 and P_2), and their F_1, F_2, BC_1 ($F_1 \times P_1$), and BC_2 ($F_1 \times P_2$) generations in Baccum-92 (High oil) × A-1 at Agricultural Research Station, Annigeri

Generations	Population size	Oil content (%)	Variance
P_1	42	37.00±0.55	1.56
P_2	42	27.35±0.77	3.02
F_1	42	29.22±1.57	12.43
F_2	333	29.58±0.17	10.24
BC_1	140	25.97±1.18	13.49
BC_2	41	22.68±2.18	7.9

Table 2 Scaling tests and estimates of components of genetic variation for oil content in Baccum-92 (High oil) × A-1 cross of safflower at Agricultural Research Station, Annigeri

Cross	Scaling tests				Variance components					
Baccum-92 × A-1	A	B	C	D	m	d	h	i	j	l
Oil content (%)	-2.80	8.55**	-4.59	-5.17**	21.88**	4.87**	23.45**	10.35**	-16.10**	-5.68

** Significant at 1% level

Table 3 List of segregants with higher oil content than Baccum-92

Segregating generation	Segregant. No	Oil content (%)
F_2	73	43.52
	63	39.98
BC_1P_1	39	39.80
	44	39.06
Baccum-92 (P_1)	-	37.00
A-1 (P_2)	-	27.35

Table 4 Superior segregants with high yield and oil content across segregating generations

Segregant No.	Segregating population	Oil content (%)	Seed yield/plant (g)
252	F_2	31.43	123.50
328	F_2	34.81	98.04
290	F_2	31.35	97.08
116	BC_1P_1	34.05	70.65
34	BC_1P_1	31.48	62.87
Baccum-92 (High oil) (P_1)		37.00	14.86
A-1 (P_2)		27.35	43.62

Identification of desirable segregants for oil and seed yield: The identification of safflower genotypes with high oil content and with both high yield and improved oil content is critical. The segregating generations in the present study were used to identify such segregants. Four segregants showing 5% superiority over the Baccum-92 (37%) for oil content across the generations are presented in Table 3. Segregant No. 73 (F_2) had the highest oil content of 43.52 per cent. Three segregants with oil content 39.98%, 39.80% and 39.06% were observed in BC_1P_1 generation. The individual plants with high oil content upon stabilization can serve as important germplasm in crossing programs.

The top five segregants with both high yield and oil were identified from the segregating generations and are listed in Table 4. Segregant No. 252 recorded high yield of 123.50g per plant and oil content of 31.43 % followed by segregant No. 328 (Yield-98.04 g/plant and oil content-34.81%), segregant No. 290 (Yield-97.08 g/plant and oil content-31.35%), segregant No. 116 (Yield-70.65 g/plant and oil content-34.05%) and segregant No. 34 (Yield-62.87 g/plant and oil content-31.48%).

Naik *et al.* (2009) identified safflower segregants with oil content ranging from 27.6 to 31.8% in back cross generations of cross (AS 98-29 X PBNS-40) X PBNS-40. Similarly, Biradar *et al.* (2012) identified segregants with oil content ranging from 29.5 to 29.8% with only 1% improvement and seed yield per plant ranging from 19.72 to 21.54 g in F_3 generation derived from crossing, 98-29 (Yield-35.6g and oil content 29.5%) with Annigeri-1 (Yield-36.8g and oil content-28.6%).

The present study revealed that the oil content in safflower is governed by both additive and dominant components and also involved the epistatic interactions of additive × additive and dominance × dominance with duplicate gene interactions. This knowledge of genetics on oil content in safflower would help in adopting suitable breeding programs such as recurrent selection in which all favorable alleles for oil content can be accumulated to increase the trait expression. The superior segregants with higher oil content identified in various segregating generations need to be confirmed in the next generations for stable expression and can be used as parents in the breeding programmes and upon stabilization the lines can be used to develop genotypes superior to A-1 Such stabilized lines can also be used as parents in the hybridization programs.

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Effect of biosynthesized ZnO nanoparticles on the seed germination and seedling vigour index of sesame (*Sesamum indicum* L.)

P SARAVANANE*, M DJANAGUIRAMAN[1], T RAMANADANE, K RAJA[1] AND S NADARADJAN

Pandit Jawaharlal Nehru College of Agriculture & Research Institute, Karaikal-609 603, Puducherry UT

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ABSTRACT

Sesame is an important oilseed crop, and the establishment of sesame in the field is critical because of its poor seed quality. One of the opportunities to improve seed germination and seedling establishment is the use of nanoparticles. Therefore, the study was conducted to evaluate the effects of biosynthesized zinc oxide nanoparticles (ZnO NPs) from a medicinal weed, *Tridex daisy* (*Tridex procumbens* L.) on seed germination, and seedling vigour of sesame (*Sesamum indicum* L.). Zinc oxide nanoparticles were synthesized through the green synthesis method by using zinc acetate as precursor and *Tridax procumbens* leaf extract as reductant. The synthesized product has been characterized by Particle Size Analyzer (PSA), UV-visible spectroscopy, scanning electron microscope (SEM), and transmission electron microscope (TEM). Then, the sesame seeds were treated with ZnO NPs, and seed germination and seedling vigour were quantified. The result indicated that the size of the ZnO NPs was 94 nm, assessed through a particle size analyzer. The UV-visible spectrum of synthesized colloidal ZnO NPs had the maximum absorbance peak at 298 nm. The SEM and TEM analysis indicates that ZnO NPs are spherical in shape. EDX confirms the purest form of Zn in ZnO NPs. The ZnO improved the seed germination and root growth of sesame compared to untreated control. Thus, it is evident that seed treatment with ZnO NPs can be a potential approach to improve the seedling establishment of sesame.

Keywords: Medicinal weed, Seedling vigour, Sesame, *Tridex daisy,* ZnO nanoparticles

Sesame (*Sesamum indicum* L.) is a member of the Pedaliaceae family and is considered the most conservative oilseed crop cultivated for edible oil (Pathak *et al.*, 2014). It is also known as the king of oilseeds due to its seeds' high oil content (50-60%). In India, it is cultivated over an area of 1.78 million hectares, with a production of 0.72 million tonnes and productivity of 426 kg/ha. In Tamil Nadu, sesame is cultivated over an area of 0.57 lakh hectares with a production of 0.34 lakh tonnes and a productivity of 596 kg/ha. Sesame crop is generally grown as a sequence crop after rice in rice fallow regions of Tamil Nadu because of its short duration nature. However, a major problem associated with sesame is seed germination and seedling establishment, because of the unfavourable conditions prevails during seedling establishment. *Tridax procumbens* L. (Family Asteraceae), a weed of medicinal importance, native to the tropical America, which is a perennial creeper herb but it is growing worldwide. The phytochemical characterization of *Tridax procumbens* L. indicated the presence of alkaloids, flavonoids, carotenoids, fumaric acid, β-sitisterol, luteolin, glucoluteolin, n-hexane, tannin, quercitin, oxoester, lauric acid, myristic, palmitic, arachidic, linoleic acid and minerals such as sodium, potassium and calcium (Manokari and Shekhawat, 2017), which is suitable for green synthesis of nanoparticles. Therefore, the study was conducted to evaluate the effects of zinc oxide nanoparticles (ZnO NPs) synthesized from *Tridax procumbens* on seed germination, and seedling vigour of sesame.

[1]Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu; *Corresponding author's Email: psaravanane@rediffmail.com

MATERIALS AND METHODS

Synthesis of ZnO NPs: Biosynthesis of ZnO NPs was done as per the procedure of Gnanasangeetha and Thambavani (2013). Zinc acetate dehydrate (Sigma Aldrich, 99%), and sodium hydroxide (Sigma Aldrich, Pellet 99%) was used as the precursor material. A 100 grams of fresh leaves of *Tridax procumbens* was taken and grounded using a pestle and mortal without any liquid. Before that 0.02 M zinc acetate dihydrate solution was prepared and heated at 50-60°C for 30 min in a magnetic stirrer cum heater. Leaf extract of *T. procumbens* was slowly added drop by drop to zinc acetate solution under stirring for 2 h, followed by that, 2.0 M NaOH was added and the pH was adjusted to 12. The above reaction has resulted in the formation of white suspension, which was covered with an aluminium foil and kept undisturbed for 2 h. After expiry of the time, a white precipitate was obtained, which was washed three times with distilled water and finally washed with absolute alcohol.

Characterization of nanoparticles: The synthesized ZnO NPs were characterized at Department of Nano Science & Technology, TNAU, Coimbatore during 2017. Particle size and the distribution pattern of synthesized sample suspensions were determined using Horiba Scientific Nanopartica SZ-100 (Nanoparticle analyzer), Japan. Accurately, 0.5 mg sample was dispersed in 20 ml distilled water, sonicated for 15 min and the suspension was analyzed under dynamic light scattering method. UV-Vis optical spectra of ZnO nanoparticles was recorded in UV-Visible spectroscopy (Model SPECORD plus 210 BU, Analytik Jena AG, German) for wave length of 200 -800nm. About 0.5mg of ZnO NPs was dissolved in 10 ml of double distilled water and used for scanning UV-Vis spectroscopy. UV-Vis spectra was obtained between 200-500 nm by keeping the suspension of nanoparticles and deionised water in the sample and reference cuvette, respectively. Scanning electron microscope (SEM Model: FEI QUANTA 250) was used to characterize the size and morphology of the synthesized ZnO nanoparticles. Sample of test nanoparticles (0.5 to 1.0 mg) was dusted on one side of the double sided adhesive carbon conducting tape mounted on the 12 mm dia. aluminum stub. Sample surface was observed at different magnifications and the images were recorded. Transmission electron microscope (TEM Model: FEI TECHNAI SPRIT) was used to analyze the sample. Diluted suspensions of synthesized ZnO nanoparticles (0.5 mg) in pure ethanol (15 ml) were prepared by ultrasonication. A drop of the suspension was placed on 300-mesh lacy carbon coated copper grid, dried and the images were captured at different magnifications.

Germination study: Sesame variety VRI 2 was used for the vigour study during 2017. The seeds were soaked in ZnO NPs suspension prepared with different concentrations *viz*., 0, 0.125, 0.250, 0.750, 1.00, 1.25, 1.50, 1.75, and 2.0 mg/L. MilliQ water was used in the soaking process. A filter paper (Whatman No.42, Maidstone, England) was kept in each Petri dish (90 mm x 15 mm). Exactly 5 ml of ZnO NPs suspensions at various concentrations was added for all the treatments except the untreated control in the Petri plate, which contained 25 numbers of sesame seeds. A 5 ml of milliQ water was added to the untreated control.

Petri plates were covered by parafilm and placed in an incubator. Experiments were carried out in quadruplicate and repeated twice, and mean values were recorded. Speed of germination was calculated by recording seed germination from 3rd day onwards to until 6 days after sowing (DAS) as per the procedure of ISTA (2014). The length of root, shoot, seedling length was recorded at 6 DAS, and vigour index was computed from the above seedling traits (Abdul Baki and Anderson, 1973).

Statistical analysis: The data were statistically analysed under CRD plot design as suggested by Gomez (1984). Wherever the treatment differences were found significant ('F' test), the critical differences were worked out at five per cent (0.05) probability level, and the treatment differences that were not significant were denoted as NS in the respective tables.

RESULTS AND DISCUSSION

Characterization of zinc oxide (ZnO) nanoparticles: The optical absorption spectra of zinc oxide nanoparticle in the wavelength range between 200 and 800nm were recorded using UV-vis spectrophotometer (Model SPECORD plus 210 BU, Analytik Jena AG, German). The UV-visible spectrum of synthesized colloidal ZnO NPs using *Tridax procumbens* leaves extract had the maximum absorbance peak at 298 nm. The particle size of synthesized ZnO NPs was in the range from 50 to 300 nm, and the highest particle distribution was observed at 270 nm. The average zinc oxide nanoparticle size is 94 nm (Fig 1). The morphology of the prepared nanoparticles was examined using SEM, and the result indicated that almost all the ZnO NPs are spherical in shape. The average nanoparticle size was 95 nm (Fig. 2). The elemental composition, particle morphology, and size analyzed using TEM, showed that the ZnO NPs are 60-75 nm (Fig. 3). The Energy Dispersive X -ray Diffractive (EDX) study confirms the presence of zinc and oxygen atoms in the synthesized ZnO NPs, indicating it is pure (Fig. 4). This analysis also shows a peak for copper and carbon because the ZnO NPs were coated in a carbon-coated copper grid. The elemental analysis of the synthesized ZnO NPs indicates that the particle synthesized has 30% zinc and 38% oxygen, which confirms the purity of synthesized nanoparticles. Pandey *et al.* (2010) observed that ZnO nanoparticles are spherical in shape with diameter around 30 nm.

Influence of biosynthesized nanoparticles on seed germination and vigour index: The seed germination percentage, root length, shoot length, and vigour index were significantly ($P \leq 0.05$) influenced by seed treatment with biogenic ZnO nanoparticles (Table 1). Seed treatment with ZnO nanoparticles at a concentration of 1.0 g/L had caused increased seed germination (68.2%) and vigour index (727.0). It is because germination is normally known as a physiological process beginning with water imbibition by seeds and culminating in the emergence of rootlet (Pandey *et al*., 2010). ZnO NP's is a metallic co-factor of an enzyme

tryptophan that influences IAA synthesis and results in a positive response in seed germination. Earlier studies showed that ZnO NP's at 1000 ppm concentration can promote seed germination, seedling vigor in peanuts (Prasad *et al*., 2012).

Significant differences in root length and shoot length was observed when treated with ZnO NP compared to control. Zn is a metallic cofactor of an enzyme Tryptophan monooxygenase, which is a rate limiting enzyme in auxin biosynthesis which is an important plant hormone in growth of seedling. However, decreased root length was observed at a higher concentration (4.22 to 2.77 cm) at 6 DAS. More pronouncing effect in reduction of root length at 6 DAS was noticed at 2.0 g/L concentration, which was 23.9% reduction compared to untreated control. It is because of the toxicity effect of ZnO at higher concentrations. Roots are in direct contact with nanoparticles and accumulation in the root tissue or on the root surface is cause for shorter root length (Zafar *et al*., 2016). Therefore, the concentration of nanoparticles and plant species had a significant role in defining toxicity. Sosan *et al*. (2016) have reported that nanoparticles trigger Ca^{2+} and reactive oxygen species (ROS) signaling at the cellular level, causing complex physiological modifications at the organism level. The growth regulation through ROS is through the regulation of calcium channel by the production of superoxide, which affects root growth and root hair development (Foreman *et al*., 2003).

From the above study, it is concluded that ZnO NPs can be synthesised through biological method is more economical, efficient and environmentally safe. Zinc nanoparticles synthesised using *Tridax procumbens* extract-treated at the rate of 1.0 g/L had improved the germination and vigour index of sesame.

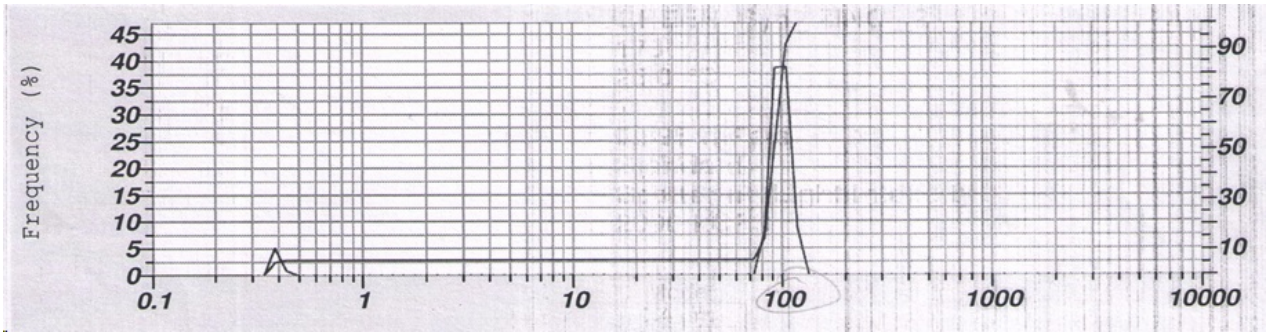

Fig. 1. Particle size distribution of synthesized zinc nanoparticles

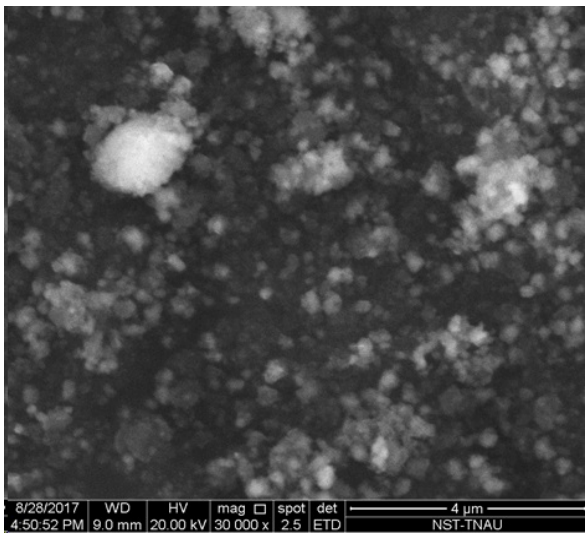

Fig. 2. The SEM image of ZnO NPs synthesized through biological method. The size of the ZnO NPs was 95 nm

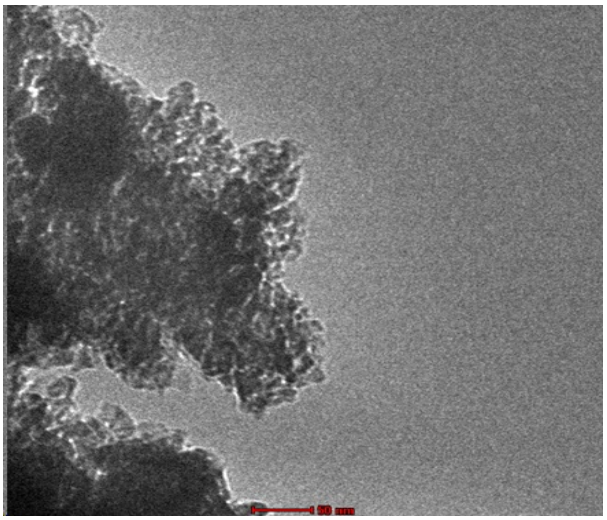

Fig. 3. Characterization of ZnO NPs using TEM. The size of the ZnO NPs was 60-75 nm

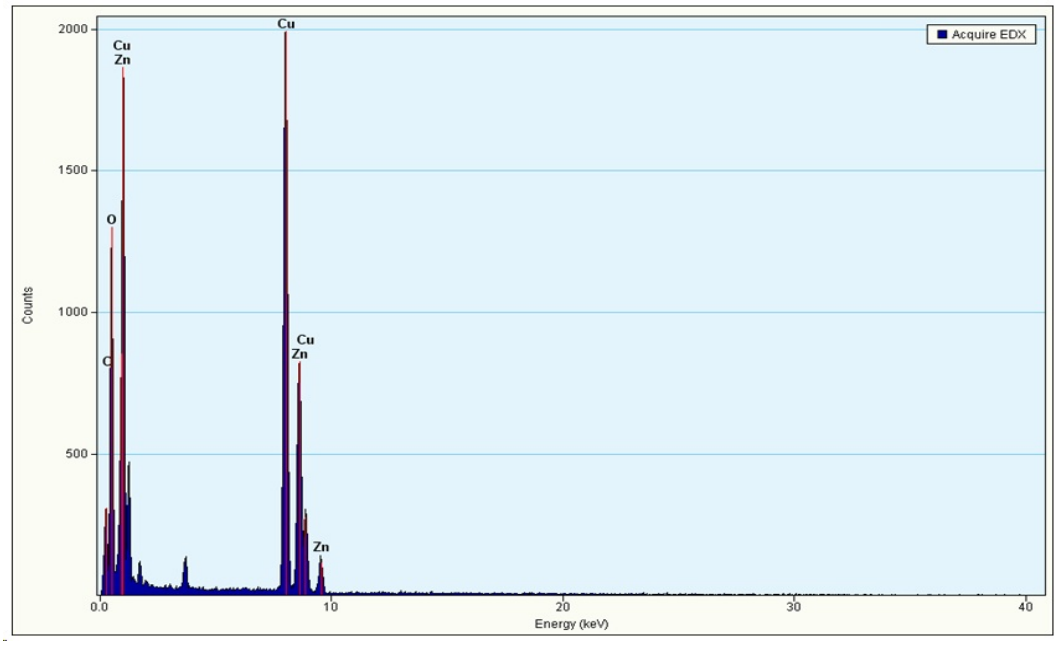

Fig. 4. EDX of ZnO NPs, showing the purest form

Table 1 Effect of biogenic zinc nanoparticles (g/L) on seed germination and vigour index

Treatments (g/L)	Germination (%)	Speed of germination (days)	Root length (cm)	Shoot length (cm)	Seedling length (cm)	Vigour index
T1: 0.125 ZnO	62.2	30.7	3.52	5.51	9.03	563.1
T2: 0.250 ZnO	63.4	31.5	3.53	5.66	9.19	583.0
T3: 0.750 ZnO	66.2	32.7	4.12	5.30	9.42	623.0
T4: 1.000 ZnO	68.2	33.5	4.57	6.09	10.66	730.02
T5:1.250 ZnO	67.8	33.4	4.22	5.44	9.66	653.9
T6:1.500 ZnO	62.6	31.1	3.69	5.04	8.73	546.2
T7:1.750 ZnO	60.0	30.0	3.33	4.72	8.05	482.3
T8: 2.000 ZnO	53.8	26.6	2.77	4.67	7.44	400.1
T9:Untreated control	59.6	29.4	3.64	4.65	8.29	489.4
SEd (±)	4.10	2.09	0.37	0.31	0.51	48.75
CD (P= 0.05)	8.43	4.29	0.76	0.63	1.03	100.04

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Screening of elite lines of sesame (*Sesamum indicum* L.) against major diseases

A SANGEETHA*, K SUBRAHMANIYAN, B MEENA[1] AND KAILASHNARAYAN GUPTA[2]

Regional Research Station, Tamil Nadu Agricultural University, Vridhachalam-606 001, Tamil Nadu

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ABSTRACT

Powdery mildew, *Alternaria* 1eaf spot, root rot and phyllody are the major diseases affecting the cultivation of sesame. Twenty entries under Initial Varietal Trial (IVT) and seven entries under Advanced Varietal Trial (AVT) were screened against important diseases of sesame under field (sick plot) conditions. In IVT entries, the diseases severity of root rot ranged between 21.13% (IVT-20-14) to 62.03% (IVT-20-13) and the susceptible check VRI-1 recorded the disease severity of 66.13%. Incidence of phyllody ranged between 13.0% to 20.9%. The check variety VRI-1 recorded 24.3% disease incidence. Powdery mildew incidence ranged between 0 to 2 grade and *Alternaria* leaf spot incidence ranged from 1 to 3 grade. Among the seven AVT entries screened under sick plot conditions, root rot incidence ranged between 12.1% (AVT-20-4) to 35.2% (AVT-20-7). The susceptible check variety VRI-1 recorded 67.0 % root rot incidence. Phyllody disease incidence in these entries ranged between 9.7% to 15.8% whereas the susceptible check variety VRI-1 recorded 22.4% incidence.

Keywords: AVT entries, IVT entries, Leaf spot, Phyllody, Root rot, Screening, Sesame

Sesame (*Sesamum indicum* L.) is considered as 'Queen of oilseeds' as the quality of its oil is nutritional, with unique taste, aroma and has therapeutic value. Temperature stability of its oil with distinct sweet flavor have made it as an obvious choice for culinary uses. Sesame is inherently low yielding plant (450 kg/ha). Its yield is further limited by various biotic and abiotic stresses. Among the diseases, four major diseases namely root rot, leaf spot, powdery mildew and phyllody further limit its yield potential. The root rot/stem rot/charcoal rot disease is caused by *Macrophomina phaseolina* (Tassi.) Goid, is the major disease of sesame which affect the crop from seedling to maturity stage. The disease is wide spread in all sesame growing areas and causes huge yield loss (>25%). The most common symptom of the disease is the sudden wilting of growing plants, mainly after the flowering stage, and the stem and roots turn black as disease progress. The pathogen survives as sclerotia in the soil and crop residues. It is also been reported to be seed-borne, and hence makes it difficult to control (Maiti *et al.,* 1988). Foliar diseases like leaf spot, powdery mildew and phyllody are equally devastating is sesame cultivation. In *Alternaria* leaf spot attacked all parts of the plant at all stages. Small, dark brown water soaked, round to irregular lesions, with concentric rings, 1-8 mm diameter appeared on the leaves. The pathogen is greatly influenced by weather, with the highest disease incidence reported in wet seasons, under excessive atmospheric and soil humidity, the spot increased in size and number (Meena *et al.*, 2010; Hubballi *et al.*, 2010). Powdery mildew appears as small, cottony spots on the upper surface of the leaves starting from 45 days old plants to crop maturity stage. Phyllody, an important disease of sesame is caused by a pleomorphic mycoplasma-like organism (phytoplasma) and transmitted by leafhopper (Tan, 2010). The phyllody disease occurs from the flowering stage. The affected plants become stunted and the floral parts get modified in to leafy structures bearing no fruits and yield loss up to 33.9% has been reported (Madhupriya *et al.*, 2015)

Other than agronomic practices, host resistance is one of the important components of integrated disease management and hence it is a pre-requisite to get higher productivity. Resistance against any of the diseases of sesame has not been reported so far. However, research on evaluating and identifying resistance sources against major disease through hybridization techniques, continuous breeding efforts and identification of elite lines are essential to ward off the complex diseases. Breeding for disease resistance requires efficient, low-cost and rapid screening techniques (Foolad *et al.*, 2000). Therefore, field resistance among available germplasm need to be assessed for further strengthening disease resistance breeding programmes. In spite of many varieties released for cultivation against many sesame diseases, screening elite pre-breeding material of IVT and AVT are routinely carried out in AICRP (Sesame) project since its inception in 1968. Therefore, the present study was carried out with the objective of screening germplasm and elite lines against cocktail of sesame diseases under IVT and AVT trials.

[1]Coconut Research Station, Tamil Nadu Agricultural University, Aliyarnagar-642 101, Tamil Nadu; 2Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur-482 004, Madhya Pradesh; Corresponding author's E-mail: sangeepat@gmail.com

MATERIALS AND METHODS

In uniform disease nursery, 20 entries of initial varietal trial and seven entries of advanced varietal trial were screened against important diseases of sesame under field (sick plot) conditions during July to November 2020. The IVT and AVT entries were sown along with local check VRI-1 in a randomized block design in two rows of 3 m length and replicated thrice. A spacing of 15x20 cm was followed for all the entries. Seeds were sown during 28 July 2020 and all the entries were harvested by 11 November 2020. Standard scientific cultivation practices were followed uniformly for all the entries starting from field preparation, sowing, intercultural operations and plant protection measures. A total rainfall of 700 mm has been received during the study period. Maximum and minimum temperature and relative humidity was also recorded (Table 1 and Fig. 1). The root rot and phyllody disease incidences were recorded at 90 days after sowing and calculated as percentage of plants infected.

$$\text{Disease incidence} = \frac{\text{Number of infected plants}}{\text{Total number of plants}} \times 100$$

Leaf spot and powdery mildew diseases intensity were recorded at 75 days after sowing, using 0-5 disease rating scale as described by Pawelec *et al.* (2006) [0 : No visible disease damage; 1 : <5% leaf area damaged; 2 : 5-20% leaf area damaged; 3 : 20-40% leaf area damaged; 4 : 40-60% leaf area damaged; 5 : severe defoliation].

Analysis of variance (ANOVA) was carried out on the data to test for differences using SPSS software. The significant difference between the isolates means were compared with the least significant differences (LSD) at a 5% level of probability ($P \leq 0.05$).

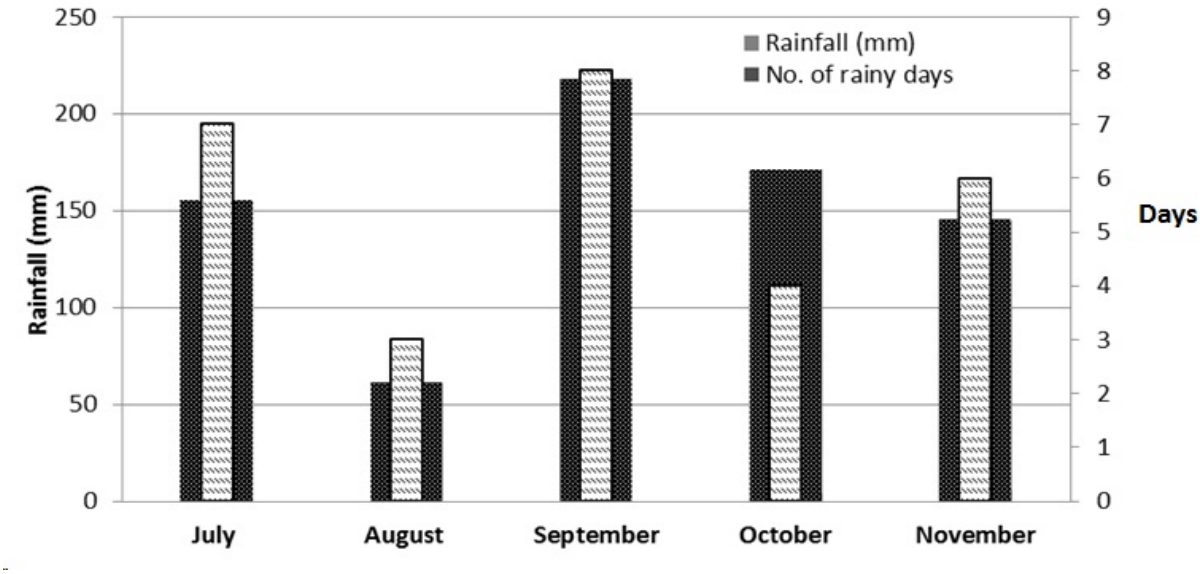

Fig. 1. Rainfall (mm) pattern and rainy days during the crop growth period (July- November 2020)

Table 1 Weather data recorded during the crop growing season (July-Nov 2020)

Weather Parameters		July	August	September	October	November
Maximum temperature °C		35.9	36.2	34.3	34.9	30.5
Minimum temperature °C		25.6	25.5	24.7	24.8	20.8
Relative humidity (%)	Morning	77.0	83.0	88.0	85.0	81.0
	Evening	59.0	62.0	70.0	71.0	76.0
Sunshine hours (hrs/day)		5.24	6.2	7.89	5.09	3.38

RESULTS AND DISCUSSION

In general, the pathogenic microorganisms reduce seed germination, plant growth and yield. Pre-disposing factors like micro-climate plays a major role in the disease spread. From the Fig. 1, it is observed that all through the crop season, with a total of 28 rainy days, a good spread of rainfall was observed in all the months. The maximum average temperature of 36.2°C was observed during August whereas November month recorded the maximum temperature of 30.5°C. Similarly minimum temperature of 20.8°C and 24.7°C was observed during November and September months respectively. As relative humidity (RH) plays a major role in the disease spread, the morning and evening relative humidity were also recorded (Table 1). It ranged from 77-88% with the average of 82.8% during morning hours whereas in the evening, RH was in the range of 59-76% with an average of 67.6%. As expected, minimum sunshine hours were recorded during the month of November. In the present study, the meteorological observations were correlated with the disease spread (Table 2). There was a positive correlation between maximum and minimum temperature, relative humidity and sunshine hours per day with the severities of *Alternaria* leaf spot and powdery mildew diseases. A negative correlation was observed between morning relative humidity and rainy days with the severities of *Alternaria* leaf spot and powdery mildew diseases. Phyllody was negatively correlated with temperature and relative humidity with its severity, while sunshine hours per day and rainy days showed positive correlation.

In the present study, under the Initial varietal trial, among the twenty IVT entries screened under sick plot condition, root rot, phyllody, powdery mildew and *Alternaria* leaf spot diseases were observed in all the entries (Table 3). In IVT entries, the diseases severity of root rot ranged between21.1 % (IVT -20-14) to 62.0 % (IVT-20-13) and the susceptible check VRI-1 recorded disease severity of 66.1%. None of the entries scored less than 10% disease severity to designate it as a resistant line. With the wider host range, complete resistance is not available against root rot disease of sesame (Avila, 2003; Anwar *et al.,* 2006; Rao, 2007; Deepthi *et al.,* 2014; Shabana *et al.,* 2014; Farooq *et al.,* 2019; Bedawy and Moharm, 2019). However, many lines have been identified as moderately resistant against the root rot disease. Among the other entries, IVT-20-16 (25.7%), IVT-20-19 (26.8%), IVT-20-2 (29.6%) and IVT-20-17 (29.7%) showed moderate tolerance to root rot compared to the check variety. It is difficult to breed a resistant variety with good yield in the absence of reliable and stable source. Therefore, the germplasm lines showing moderate resistance will be effective in improving the yields in sesame.

Table 2 Correlation co-efficient (r) for diseases of sesame with weather variables

Weather parameters	Correlation Co-efficient (r)		
	Alternaria leaf spot	Powdery mildew	Phyllody
Maximum temperature (°C)	0.58	0.83*	-0.61
Minimum temperature (°C)	0.25	0.21	-0.44
Morning relative humidity (%)	-0.37	-0.73	-0.21
Evening relative humidity (%)	0.64	0.42	-0.27
Sunshine hours (hrs/day)	0.32	0.63	0.33
Rainy days (No.)	-0.6	-0.57	0.85

Phyllody disease incidence ranged between 13.0 to 20.8%. The check variety VRI-1 recorded 24.3% disease incidence. The entries, IVT-20-6(13.13%), IVT-20-18(13.80%), IVT-20-7(14.53%) and IVT-20-17(14.63%) have recorded lesser percentage of disease infection than the check variety. Several workers had previously reported about the resistance sources against phyllody of sesame. Anwar *et al.* (2006) reported GT-1 and DS-9 as resistant to phyllody. Singh *et al.* (2007) documented that a single recessive gene governs phyllody resistance. Therefore compared to other diseases, resistant varieties could be developed with good resistance against phyllody. *Alternaria* leaf spot incidence ranged from 1 to 3 grade and powdery mildew incidence ranged between 0 to 2 grade (Table 3). In the present study, none of the sesame entry was found immune or resistant to the disease. The check variety VRI-1 recorded the PDI of 3 whereas the entries, IVT-20-1, IVT-20-5, IVT-20-8, IVT-20-11, IVT-20-17, IVT-20-19 and IVT-20-20 recorded the PDI of 1, thus could be the efficient material for developing resistant/tolerant lines in the future breeding programmes. These results are in conformity with the findings of those reported earlier by several workers against, *Alternaria sesami* of sesame (Gupta *et al.,* 2001; Marri *et al.,* 2012).

Rani and Kiranbabu (2017) reported that sesame entries JCS 2846, JCS 2892, JCS 3102 and JCS 3258 showed maximum seed development and survival when the material was exposed to thermo-stress (>40°C) during flowering, capsule formation and seed development for two weeks. For powdery mildew, IVT-20-1, IVT-20-4, IVT-20-8, IVT-20-10, IVT-20-13, IVT-20-16 and IVT-20-19 recorded the 0 PDI and thus proved to be the potential lines to develop varieties against powdery mildew. In the IVT trials, the line IVT-20-17 has shown multiple tolerances to root rot, phyllody and *Alternaria* leaf spot diseases where as IVT-20-1, IVT-20-8 and IVT-20-10 recorded moderate tolerance against *Alternaria* leaf spot and powdery mildew.

Therefore, these elite lines showing moderate resistance need to be assessed for their yield and other yield contributing characters, so that they can be further applied in horizontal resistance breeding programmes. In Advanced varietal trial, seven entries were sown along with local check VRI-1 (Table 4). In AVT entries, root rot incidence ranged between 12.07% (AVT-20-4) to 35.23% (AVT-20-7).The susceptible check variety VRI-1 recorded 67.0% root rot incidence. Phyllody disease incidence ranged from 9.73% to 15.77% whereas the check variety VRI 1 recorded 22.43% incidence. The entries, AVT-20-5 (10.30%), AVT-20-2 (11.87%), AVT-20-7 (12.50%) and AVT-20-1 (14.40%) have recorded moderate tolerance against phyllody. The entries, AVT-20-1, AVT-20-5, AVT-20-6 and AVT-20-7 (2 PDI) has recorded lower PDI than the check variety. Deepthi *et al.* (2014) indicated the effect of additive genes or polygene or cluster gene on mechanism of tolerance to *Alternaria* blight. Interestingly, none of the entries was found to be immune, suggesting lack of stable sources of resistance to the disease and these findings broadly agree with earlier report that no reliable source of resistance/immunity could be identified (Singh *et al.,* 2007).

Similarly, the entries, AVT-20-4 and AVT-20-6 (0 PDI) has shown the better results against powdery mildew. However a few have reported existence of resistant sources. The contradictory observations may be due to differences in the disease scaling, screening techniques adopted, species/and race spectrum. The difference in disease rating may be attributed to stringent screening method (spreader row + dusting of spore inoculum artificially) in the present case as against natural infection adopted. In nutshell, two entries, AVT-20-5, AVT-20-1 have shown triple tolerance against root rot, Alternaria leaf spot and phyllody whereas the entries. AVT-20-6 has shown tolerance against leaf spot and powdery mildew. Therefore, these entries could be the best sources for the breeder to develop tolerant varieties in sesame. Marri *et al.* (2012) has also showed multiple tolerance of some tested lines against some notable diseases.

Table 3 Screening of IVT entries against major sesame diseases (n=3)

Entries	Root rot (%)	Phyllody (%)	Alternaria leaf spot (0-5 scale)	Powdery mildew (0-5 scale)
IVT-20-1	49.43	20.00	2	0
IVT-20-2	29.57	20.87	1	1
IVT-20-3	44.00	16.53	2	1
IVT-20-4	42.23	13.00	3	0
IVT-20-5	44.67	16.87	1	2
IVT-20-6	46.17	13.13	2	1
IVT-20-7	44.40	14.53	3	1
IVT-20-8	37.47	18.53	1	0
IVT-20-9	53.90	16.80	2	1
IVT-20-10	57.17	16.00	2	0
IVT-20-11	58.53	18.63	1	2
IVT-20-12	35.13	18.07	3	1
IVT-20-13	62.03	14.83	3	0
IVT-20-14	21.13	17.00	2	1
IVT-20-15	36.87	16.17	3	1
IVT-20-16	25.70	15.03	2	0
IVT-20-17	29.73	14.63	1	1
IVT-20-18	34.47	13.80	2	1
IVT-20-19	26.83	15.83	1	0
IVT-20-20	42.30	16.57	1	2
Check VRI-1	66.13	24.33	3	2

Table 4 Screening of AVT entries against major sesame diseases (n=3)

Entries	Root Rot (%)	Phyllody (%)	Alternaria leaf spot (0-5 scale)	Powdery Mildew (0-5 scale)
AVT-20-1	31.40	14.40	2	1
AVT-20-2	27.04	11.87	1	2
AVT-20-3	31.83	15.77	3	1
AVT-20-4	12.07	15.20	3	0
AVT-20-5	20.70	10.30	2	1
AVT-20-6	34.00	9.73	2	0
AVT-20-7	35.23	12.50	2	2
Check VRI-1	67.03	22.43	3	0

The identification of disease resistant varieties is a major goal for agricultural scientists and plant breeders. The results of present study described the presence of sufficient genetic variation with respect to fungal diseases within the screened germplasm with a wide range of infection per cent. In nutshell, two entries, AVT-20-5, AVT-20-1 and in IVT trials IVT-20-17 have shown triple tolerance against root rot, Alternaria leaf spot and phyllody whereas the entries AVT-20-6, IVT-20-1, IVT-20-8 and IVT-20-10 have shown tolerance against leaf spot and powdery mildew. These findings provide a major incentive for breeders to plan a significant breeding program for resistance to diseases.

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Determinants of adaptation practices to climate change: insights from soybean growers in Central India

B U DUPARE, PURUSHOTTAM SHARMA AND S D BILLORE

ICAR-Indian Institute of Soybean Research, Khandwa Road, Indore-452 001, Madhya Pradesh

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ABSTRACT

The study analyzed the determinants of adaptation practices of soybean growers toward climate change in Central India using primary data collected through household survey from 280 soybean growers. The influence of a set of explanatory variables on each of the different adaptation strategies was simultaneously modeled using multivariate probit analysis. The most widely practiced adaptation measure was change in the variety (71% farmers) followed by the change in time of farm operations and crop change or crop diversification. To cope with the insect-pest and disease attack on the crops, farmers adopted resistant varieties to minimize the cost of chemical spray. More than one-third of the sampled farmers practiced change in input application, while soil and water management practices were practiced by nearly 28% of the farmers. Analysis of results indicated that the change in varieties of crops is significantly more likely to be adopted by households with larger family size, higher involvement in extension activities, having a tractor, higher educated head of household. Households with higher family income, possessing mobile phones and other infrastructure are more likely to adopt the change in varieties, whereas farmers having higher social participation, extension contact, larger land holding, and belonging to ethnic origin other than scheduled caste or scheduled tribe do not necessarily do so. The government should frame out policies towards the promotion of technological and institutional measures suitable to various categories of farmers so that the adaptation strategies could be helpful in maintaining and/or increasing the sustainability of the production systems.

Keywords: Adaptation practices, Climate change, Determinants, Multivariate probit analysis

Climate change is one of the major environmental concerns and will have serious implications on all the stakeholders *viz*., farmers, industries, and policymakers alike in the 21st century. Climate change is likely to impact more on the rainfed agricultural economies (McCarthy *et al.*, 2018), and consequently the food security, access, and utilization of food as well as price stability (Porter et al., 2014). Therefore, climate change is expected to further complicate the millennium goal of meeting the demand for food and nutrition considering the global population and rising consumer incomes (UN, 2015). To minimize the negative impact as well as realize the positive impact of climate changes, it is pertinent to make suitable adjustments and changes in the agricultural production system. Since the local actors are worst affected by the severity of climate change, farm-level adaptation measures deserve significance for sustaining the productivity and profitability of agricultural production systems (UNFCCC, 2009; Singh *et al.,* 2015). According to UNFCCC, "Adaptation refers to adjustments in ecological, social, or economic systems in response to actual or expected climatic stimuli and their effects or impacts. It refers to changes in processes, practices, and structures to moderate potential damages or to benefit from opportunities associated with climate change. In simple terms, countries and communities need to develop adaptation solution and implement action to respond to the impacts of climate change that are already happening, as well as prepare for future impacts" (UNFCCC, 2020).

The adaptation involves correctly perceiving the consequences of climate change and applying measures to minimize the impact. Perception is a cognitive process involving exposure to sensory information and its interpretation for choosing available appropriate solutions. But due lack of information or resources or capacity to use the alternatives, some people do not respond to the effect of climate changes despite perceiving correctly. The earlier studies have indicated that farmers rely on farm level strategies like change in crop and/or variety, changing the agronomic practices, adoption of resource conservation technologies as well as soil and water management practices, and some risk management strategies for minimizing the losses due to climate change (Sharma, 2013; Pathak *et al.*, 2014; Tripathi and Mishra, 2017).

The major challenge is adapting agriculture to climate change, especially in a developing country like India, where a vast majority of farmers are marginal and small holders having small and fragmented land holdings, less educated,

and have a significantly lower adaptive capacity. Autonomous adoption of farm-level adaptation strategies is the order of the day but maybe insufficient to offset the losses caused by climate change (McCarthy, 2001). In this situation, adaptation strategies with incentives and policy-driven support can help the farming community to sustain the productivity and profitability of their farming enterprise. The major challenge in study of adaptation by small holders identifying the actual adaptation (Lobell, 2014), as the adaptation strategies varies with the variation in climatic, economic, social and institutional factors (Below *et al.*, 2012).

The climate change impact on Indian agriculture is well researched and documented by various studies including in major soybean producing region, i.e. Central India (accounting for more than 90 per cent share, also major producer of wheat, pulses and other oilseed crops) having policy implications considering the country's economic situation. Studies available on the adaptation to climate change in India as well as elsewhere, mainly focus on adaptation strategies at the regional or national level, crucial for macro level planning (Singh *et al.,* 2015; Singh *et al.,* 2019). Nevertheless, the studies focusing on the micro level adaptation strategies, at farm or household level, are inevitable to identify and design effective measures for adaptation at the local level. The study aims to understand strategies followed by growers of soybean based cropping system in Central India along with the factors determining the decision of adopting the adaptation strategy. In this study, we assessed the actual adaptation measures adopted by soybean growing farmers and the determining factors. In order to minimize the impact of climate change on the soybean-based cropping system, it is high time to devise appropriate local level adaptation strategies and prioritize them for the benefit of the farming community.

MATERIALS AND METHODS

Data and collection method: Three states in central India *viz.,* Madhya Pradesh, Maharashtra, and Rajasthan together account for more than 90 percent of area and production of soybean in India. Looking into the importance of the area, the study was conducted in Malwa and adjoining regions of Central India with farmers practicing mainly soybean based cropping system. The study was mainly based on the primary data collected through a household survey conducted during the period 2016-17. The data were collected with the help of a pre-structured interview schedule developed specifically for the purpose which was divided into two parts. The first part of the survey schedule focused on demographics, livelihood activities, assets, and income, etc. The second part focused on seeking information on farmers' perceptions of climate change; the resultant impacts of climate change including the extreme climate events on the crop; and the households' adaptation or coping strategies in response to these events. The focused group discussions were conducted in selected villages in order to assess the gradual changes witnessed by the farmers in local climate involving a time line of climate-related extreme events.

Survey instrument was also pre-tested in two villages. Based on the pre-testing, the schedule was revised before conducting a household survey with a provision of seeking the information on farmers' perception of changes in the local climate as well as open ended questions related to the agronomic practices/adaptation strategies being followed by them consequent to their perception of change in climate. The interview schedule was numbered, coded, and scored using standard procedures. The present study was conducted in three major soybean growing districts covering Malwa (Dewas and Indore districts) and Nimar Plateau (Dhar district) of Madhya Pradesh state in Central India, popular for soybean revolution in the country. The sample for the study consisted of 280 soybean growers drawn randomly from selected six villages (50 farmers from each of four villages from Indore and Dewas districts under Malwa Plateau and 40 from each of two villages of Dhar district in Nimar Plateau). Open-ended questions were also included in the interview schedule relating to long-term changes in rainfall and temperature, farmers adaptations in response to climate changes they experienced.

Empirical model: Since the adaptation measures practiced by sample farmers are not mutually exclusive, the present study used a multivariate probit (MVP) model to analyze the determinants of adaptation measures. The influence of a set of explanatory variables on each of the different adaptation strategies was simultaneously modeled using multivariate probit analysis. MVP allows the unobserved and unmeasured factors (error term) to be freely correlated. Substitutability (negative correlation) and complementarities (positive correlation) among different adaptation measures may be the source of the correlation between error terms, which are taken into account in the MVP model. The MVP econometric model used in this study is characterized by a set of n binary dependent variables *yi*, such that;

$$y_i = 1 \; if \; x'\beta_i + \varepsilon_i > 0,$$
$$= 0 \; if \; x'\beta_i + \varepsilon_i \leq 0, i = 1,2,\ldots,n. \quad \ldots(1)$$

Where x is a vector of explanatory variables, βi are the vector of parameters to be estimated, and the random error terms εi are distributed as a multivariate normal distribution

with zero means, unitary variance, and an n x n contemporaneous correlation matrix R=[ ], with density ?(ε1, ε2, ….., εn; R). The likelihood contribution for an observation is the *n*-variate standard normal probability

$$\Pr(y_1, \ldots, y_n \mid x) = \int_{-\infty}^{(2y_1-1)x'\beta_1} \int_{-\infty}^{(2y_2-1)x'\beta_2} \ldots \times \int_{-\infty}^{(2y_n-1)x'\beta_n} \phi(\varepsilon_1, \varepsilon_2, \ldots, \varepsilon_n; Z'RZ)d\varepsilon_n \ldots \varepsilon_2\varepsilon_1 \quad \ldots\ldots (2)$$

Where, Z= diag [2y1 -1, …, 2yn -1]. The maximum-likelihood estimation maximizes the sample likelihood function, which is the product of probabilities (eq. 2) across sample observations. The present study used the estimation process developed by Cappellari and Jenkins (2003) to estimate the MVP model in STATA using the simulated maximum likelihood using Geweke-Hajivassiliou-Keane (GHK) simulator approach. The simulated maximum likelihood is consistent as the number of observations and number of draws tends to infinity. In this study, the number of draws (R) was set to 100 (default R = 5) in order to ensure consistent estimates.

The multicollinearity in explanatory variables and heteroscedasticity in the model are major problems in econometric analysis of survey data, which can lead to imprecise estimates. The multicollinearity was diagnosed by estimating individual ordinary least squares (OLS) regression for each individual choice variable against the same set of explanatory variables and running the variation inflation factor (VIF) test, and results found VIF values less than 5.0 for all explanatory variables, below threshold level, with an average of 2.05. The heteroscedasticity in the model was addressed through model estimation using robust standard errors that compute a robust variance estimator based on a variable list of equation level scores and covariance matrix. The use of robust standard errors is an effective way of dealing with heteroscedasticity (Wooldridge 2006) and does not change the significance of the model and the coefficients but gives relatively accurate P values.

Model variables: Based on the literature review and location-specific characteristics, thirteen independent variables were selected for analysis in the study and presented in Table 1. Both positive, as well as the negative influence of the age of household head on adaptation choices, was reported in the literature (Seo and Mendelsohn, 2008a; Hassan and Nhemachena, 2008; Deressa *et al.,* 2009). It is hypothesized in this study that older farmers, in the productive age group, have more farming experience and are better able to perceive climate change and assess the characteristics of technology, positively influence climate change adaptation. The access to improved production technology and information on crop management aspects under changing climatic situations which helps farmers to utilize the suitable adaptation strategies is facilitated by the education of the household head (Maddison, 2007; Deressa *et al.,* 2009), mobile phone connectivity, and households with higher extension participation index. A positive relationship between years of education of household head, having mobile connectivity and higher extension participation, and various farm-level adaptation mechanism was hypothesized in this study.

The size of household influences farmers' adoption behavior and the required amount of labor for adopting labor-intensive adaptation measures could be met through the availability of family labor (Deressa, 2010) and thus, a positive relation is anticipated between the household size and adaptation measures which are labor-intensive in nature (Bryan *et al.,* 2009; Gbetibouo, 2009; Di Falco *et al.,* 2011; Bahinipati, 2015). It is evident that the adoption of various adaptation strategies involves cost and thus, requires financial resources and availability of farm machines and equipment. Hence, the rich households and farmers having farm machines and equipment are expected to undertake a greater number of different adaptation measures (Hassan and Nhemachena, 2008; Panda *et al.,* 2013; Bahinipati, 2015). The size of landholding is reported to influence the adaptation positively (Maddison, 2007; Seo and Mendelsohn, 2008b; Hassan and Nhemachena, 2008; Gbetibouo, 2009; Below *et al.,* 2012). It was hypothesized, in this study, that larger farms are more likely to adopt all the adaptation practices except traditional strategies. Since, majority of the sample farmers, more than 90 per cent, responded positively for the variables such as the change in pattern and spread of rainfall, increasing incidences of weather abnormalities, and temperature changes, hence not included as explanatory variables.

The institutional representation factors, formal or informal, included in the study are social participation, extension contact, and extension participation. Agricultural extension is anticipated to be a reliable and better source of agricultural technology information for farmers. Some of the studies stated that farmers getting climate change information through contacting extension agents or participation in extension activities govern the decision on adaptation choices (Patt *et al.,* 2005; Deressa *et al.,* 2009; De Falco *et al.,* 2011 and 2012; Arimi, 2013). In the present study, it was hypothesized that farmers having higher social participation, contact with extension agencies, and/or participation in extension activities, are positively related to the adoption of farm-level adaptation measures.

The descriptive statistics for the independent variables used in the study are presented in Table 1. The average age of the head of households was nearly 45 years, and the mean years of the schooling of farmers were about 8 years indicating that farmers in the study area were middle-aged

and fairly educated. The mean family size was about 4 having on an average 8.53 hectares of cultivable land. About 85 per cent of the farmers were connected through mobile phones and majority of them belonged to other backward castes. The mean family income of the sample households from all sources reported was the ₹2.06 lakhs/annum/family. Nearly three-fourths of the respondents were actively involved in social activities. About 42 per cent possessed tractor, nearly half of the respondents had farm machines and implements, and about half possessed irrigation infrastructure. More than 80 per cent of the sample farmers participated in one or the other extension activities such as farmers' fairs, field days, institute visits, training, etc. About 57 per cent of the respondents had regular contact with the extension agents.

RESULTS AND DISCUSSION

Farm-level adaptation strategies followed by farmers in the study area: The analyses presented in this study identified the important determinants of adoption of various adaptation measures to provide policy information on which factors to target and how so as to encourage farmers to increase their use of different adaptation measures. Farmers in the study area had adopted one or a combination of adaptation measures to cope with the effect of climate change in the crop sector. The sample farmers were specifically probed to state the farm-level adaptation measures which the farmers have been undertaking to mitigate the impact from previous climate extreme events. The farmers of the study area reported various adaption measures practiced and the widely practiced farm-level adaptation measures were included for empirical analysis in the present study as presented in Table 2. The most widely practiced adaptation measure was the change in the variety (by nearly 71 % of the sample farmers) followed by the change in time of farm operations and crop change or crop diversification (about half of the respondent farmers). As has been observed in the study area, majority of the farmers in Central India changed their cropping pattern from soybean-wheat cropping system to soybean in the rainy season followed by potato/onion/garlic followed by wheat in the late *rabi* season in irrigated conditions. In the case of rainfed conditions, farmers have changed to soybean-gram. Therefore, short-duration crops and varieties of crops are more prevalent in the area. To cope with the insect-pest and disease attack on the crops, farmers prefer to go for resistant varieties to minimize the cost of chemical spray. In Central India, more than one-third of the sample farmers practiced change in input application, while soil and water management practices were adopted by nearly 28% of the farmers. Aggarwal (2008) reported that most common adaptation measures like change in varieties and altering sowing time could help in reducing the impact of climate change to some extent.

Farmer group discussions revealed that majority of farmers perceive the increase in incidence of climatic disturbances such as increase in maximum temperature, disturbances in quantum and duration of rainfall - increase in frequency of high rainfall in short span of time, long dry spells, etc. leading to increased incidences of insect and diseases and in turn decline/ high variability in yield of soybean and other rainfed crops. The discussions further revealed that the area under short duration crops like soybean and pulses, has increased and along with increase in demand of short duration varieties of crops to minimize the effect of harvest period weather disturbances.

Determinants of adaptation to climate change results from the MVP model: The factors determining the adaptation strategies to climate change were analyzed using a multivariate probit (MVP) model and the results are presented in Table 3. The results indicated a number of location-specific insights into the determinants of adaptation choices for the crop sector. The results of the MVP model indicated that the direction of influence for most of the explanatory variables was as expected with some exceptions. The Wald χ^2 (likelihood ratio statistics) was highly significant (P=0.0000), showing that the variables included adequately explained the model. Further, the estimation of all equations simultaneously by the MVP model instead of individual equation is validated as the likelihood ratio test for the null hypothesis of the absence of correlation between the individual equations is strongly rejected (P=0.0005). The complementarities (positive correlation) and substitutability (negative correlation) among different adaptation measures was indicated by the significant correlation coefficients (t-test statistics) of the error terms for any pair of equations. Also, substantial differences are there in estimated coefficients across equations which further support the aptness of multivariate analysis of adaption options.

Results of the multivariate probit analysis indicated that the change in varieties of crops was significantly more likely to be adopted by farmers with the higher educated head of household and larger family size, having a tractor and higher involvement in extension activities. Surprisingly, the direction of influence of extension contact and the age of household head were significantly negative, contrary to our hypothesis, on the farmers' option to choose for change in varieties as an adaptation strategy. Households with higher family income, having mobile phones, and possessing other infrastructure are more likely to adopt the change in varieties, whereas farmers having higher social

participation, extension contact, larger land holding, and belonging to ethnic origin other than scheduled caste or scheduled tribe do not necessarily do so.

Households with larger land holding, having mobile phone, belong to other backward caste or general caste, possessed tractor and farm machines & implements, and with higher extension participation are significantly more likely to adopt change in crops or crop diversification option of adaptation to climate change. Whereas, households with higher social participation and possessed other infrastructures are significantly less likely to go for crop diversification of change in crop selection. The direction of influence of age was positive, but contrary to hypotheses the household family income, family size, and extension contact are negatively influencing the option of crop diversification.

The change in the use of inputs as an adaption option was significantly more likely to be adopted by the farmers with larger land holding, higher family income, higher educated head, and in possession of farm machines and implements. Contrary to the hypothesis, the relationship between the age of the head of household, mobile phone connectivity, and change in inputs use was found to be negative and significant. The direction of influence of number of family members and social participation was as expected, whereas the influence of ethnic origin, households in possession of tractor and other infrastructure, extension participation, and contact on change in input use were not as per our hypothesis. Soil and water conservation measure as an adaptation measure to mitigate the effect of climate change in the crops sector significantly increases with the age and education of the head, land holding, and family income. Mobile phone connectivity does not have any influence on the adoption of this adaptation choice, whereas the influence of extension contact and ethnic origin with SC/ST as reference class was not as hypothesized. Social participation, possession of tractor, farm machines and implements and other infrastructure, and higher extension participation increases the propensity to adopt the soil and water conservation measure.

Change in timing of farm operations is significantly and positively influenced by larger land holdings, education of head, family size, extension participation, ethnic origin other than SC and ST category, and possession of tractor. Contrary to our hypothesis, this adaptation option was significantly less likely to be adopted by households with higher income, higher social participation, and in possession of other infrastructure. The direction of influence of extension contact, possession of farm machines and implements was as expected, while the influence of mobile connectivity on change in timing of farm operationswas not as hypothesized. The age of the head of household does not have any influence on the adoption of the change in timing of farm operations.

Table 1 Explanatory variables selected for the model

Variables	Unit	Mean (%)	Standard deviation	Expected sign
Age of head of household	Years	45.21	14.16	±
Education of household head	Years of schooling	7.65	4.66	+
No. of family members	Number	3.88	1.27	±
Land holding	Hectares	5.83	6.90	±
Mobile phone	Dummy; 1=Yes, 0= No	0.85	0.36	+
Family Income	₹ 2.06 lakhs/HH	2.92	2.64	±
Ethnic origin	1= Scheduled caste/tribe 2= Other backward caste 3= General	18.57 70.71 10.71	0.54	±
Social participation	0= No participation 1= member of any coop. society/ institution 2= office bearer of any coop. society/ institution 3= Active involvement in social activities	17.14 5.00 5.00 72.86	1.16	+
Have tractor	Dummy; 1=Yes, 0= No	0.42	0.49	+
Have farm machines and implements	Dummy; 1=Yes, 0= No	0.49	0.50	+
Have irrigation infrastructure	Dummy; 1=Yes, 0= No	0.27	0.44	+
Extension participation index	Index ranging 0 to 1	0.84	0.18	+
Extension contact index	Index ranging 0 to 1	0.57	0.24	+

Table 2. Adaptation strategies practiced by soybean growers in Central India

Adaptation measures	Details of adaptation practice	Percentage of household adopting the practice (n=280)
Change in variety	Use of short duration/ drought/ pest/ disease resistant variety	70.71
Change in time of farm operations	Change in sowing/ harvesting/ weeding/ pesticide application time	48.57
Crop diversification/ change	Shifted to short duration crop/ crop rotation/ intercropping	47.86
Change in input application	Increased use of organic manure/ fertilizers/ plant protection chemicals/ use of herbicides	35.71
Soil and water management	Creation of irrigation facility/ use of BBF/ FIRBS for sowing/ rain water harvesting/ drainage of excess water	28.57
No adaptation		10.71

Table 3 Parameter estimates of the multivariate probit model

Explanatory variable	Change in variety		Change in crop		Change in inputs		Soil & water conservation		Change in sowing time	
	Coeff.	Prob	Coeff.	Prob	Coeff.	Prob	Coeff.	Prob	Coeff.	Prob
Age	-0.022	0.002***	0.010	0.182	-0.030	0.007***	0.018	0.056*	-0.004	0.575
Land	-0.022	0.145	0.067	0.006***	0.134	0.000***	0.066	0.003***	0.056	0.002***
Income	0.223	0.146	-0.056	0.765	0.852	0.000***	1.008	0.002***	-0.434	0.008***
Education	0.069	0.004***	0.138	0.000***	0.056	0.040**	0.136	0.000***	0.056	0.017**
Family members	0.192	0.005***	-0.063	0.380	0.027	0.751	0.121	0.152	0.157	0.027**
Mobile	0.130	0.597	0.544	0.023**	-1.086	0.001***	0.007	0.982	-0.138	0.639
Tractor	0.575	0.058*	1.025	0.002***	-0.274	0.473	0.132	0.719	1.779	0.000***
Machine & implements	-0.376	0.209	0.998	0.003***	1.193	0.001***	0.350	0.353	0.383	0.312
Other infrastructure	0.175	0.493	-0.761	0.006***	-0.231	0.381	0.210	0.416	-1.137	0.000***
Caste	-0.124	0.472	0.392	0.062*	-0.208	0.318	-0.569	0.127	0.306	0.080*
Social participation	-0.172	0.122	-0.783	0.000***	0.116	0.364	0.214	0.129	-0.596	0.000***
EPI	2.208	0.001***	2.422	0.001***	-0.741	0.263	0.206	0.798	2.609	0.001***
ECI	-0.827	0.057*	-0.464	0.294	-0.368	0.412	-0.596	0.199	0.509	0.202
Constant	-3.092	0.088*	-2.986	0.148	-9.100	0.000***	-15.356	0.000***	1.703	0.350
Correlation			Coeff.		Prob.					
$\hat{\rho}_{21}$			-0.380		0.001***					
$\hat{\rho}_{31}$			0.067		0.615					
$\hat{\rho}_{41}$			-0.066		0.680					
$\hat{\rho}_{51}$			-0.080		0.505					
$\hat{\rho}_{32}$			-0.206		0.094*					
$\hat{\rho}_{42}$			0.091		0.497					
$\hat{\rho}_{52}$			0.399		0.000***					
$\hat{\rho}_{43}$			0.342		0.028**					
$\hat{\rho}_{53}$			-0.070		0.684					
$\hat{\rho}_{54}$			0.460		0.001***					
Draws			100							
Observations			280							
Wald $\chi 2$ (65)			1065.63							
P value			0.000***							
Log Likelihood			-536.82							

Likelihood ratio test of rho21 = rho31 = rho41 = rho51 = rho32 = rho42 = rho52 = rho43 = rho53 = rho54 = 0:
χ^2 (10) = 30.2053 Prob > χ^2 = 0.0008***; *; **; *** Significant at 10%, 5%, and 1%, respectively

The educated younger farmers are more likely to adopt these adaptation measures as compared to their older counterparts, possibly for being innovative, having the higher risk-taking capacity and keen to try new methods and technologies to improve farming (Sharma *et al*., 2018). The size of landholding has significantly increased the propensity to adopt the adaptation strategies, as farmers with larger landholdings can afford to make the necessary investments (Maddison, 2007; Gbetibouo, 2009; Below *et al.,* 2012; Sharma *et al.,* 2018). Households with higher income also have money to invest in improved technologies and thus, are more likely to adapt to change in the input application and soil and water conservation measures. It was also possible to reduce the further reduction in grain yield by adopting new management practices or through replacement of new varieties which could sustain the growth under increased temperature (Mohanty *et al.,* 2015).

The size of the household, on the other hand, influences the choice of the crop as well as the application of required inputs and decision of planting the crop at right time. The larger the size of the household, there are better the chances of adopting various measures (Bahinipati and Venkatachalan, 2015). The possession of mobile phone connection helps the farmers to access the relevant and updated information on various farming enterprises and helps the farmers in the decision-making process (Mittal and Hariharan, 2018) about which variety to be grown under the prevailing circumstances along with specific practices to be followed for aversion of risk. Similarly, it was seen that the possession of tractors, machines, and improved farming implements helped the farmers to adopt suitable crop, soil and moisture conservation practices, and time of planting to cope up with the climatic adversities. It was also observed that the factors like farmers' participation in social activities, possession of tractor/agricultural machines and implements as well as other infrastructure, and higher extension participation increased the propensity to adopt the soil and water conservation measure.

The estimated correlation coefficients ($Þ_{kj}$) among the various adaptation strategies were found to be significant for five out of ten combinations. Change in variety was negatively correlated with crop diversification/ change in crops, soil and water conservation, and change in timing of farm operations, while it was positively correlated with change in inputs. This implies that the change in a variety of the crop minimizes the vulnerability to climate change for the crop sector and thus, reduces the dependence on other adaptation options but complements with the change in input application. Crop diversification or change in the crop was complemented with soil and water conservation and change in sowing time of the crops, while negatively correlated with change in input application. Change in input application was positively correlated with soil and water conservation, whereas negatively with the change in sowing time. A complementary relation was found between soil and water conservation and change in the sowing time of the crops.

Results from the study indicated that the change in varieties of crops was significantly more likely to be adopted by households with more number of family members, having higher involvement in extension activities, having a tractor, higher educated head of household. Households with higher family income, having mobile phones, and possessing other infrastructure are more likely to adopt the change in varieties, whereas farmers having higher social participation, extension contact, larger land holding, and belonging to ethnic origin other than scheduled caste or scheduled tribe do not necessarily do so.

As a follow up, the work on the development and dissemination of climate-smart technologies and practices including varieties resistant to various biotic and abiotic factors may be strengthened. Efforts are also needed for studying the vulnerability as well as validation and assessment of technologies and practices in the prevailing climatic situations. The officers belonging to extension services should be sensitized to create awareness among the farming community about the climate changes and its overall impact on agricultural production and processes. Organization of skill-oriented programs may be planned for the field level extension personnel for promoting the access, utilization, and dissemination of weather-specific advisories as well as adaptation strategies in order to achieve the yields in the changed climatic situations. To do this, the extension services need to be upgraded through the provision of additional manpower and climate-smart policies like crop insurance schemes considering the increased risk of adverse climate particularly successive drought situations as well as crop damage due to biotic factors.

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Unlocking the genetic variations in sesame (*Sesamum indicum* L.) germplasm for waterlogging tolerance

NEMI CHAND JATAV, RAKESH CHOUDHARY, ARTIKA SINGH KUSHWAHA AND S K CHATURVEDI*

College of Agriculture, Rani Lakshmi Bai Central Agricultural University, Jhansi-284 003, Uttar Pradesh

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ABSTRACT

Undulating topography and higher precipitation intensity leading to waterlogging during rainy season adversely affects productivity of the *kharif* crops including sesame (*Sesamum indicum* L.) in Bundelkhand region. Limited information is available on existence of genetic variations for waterlogging tolerance in oilseed crops including sesame. In the present study, 609 germplasm accessions of sesame were phenotyped under field conditions during *kharif* 2019 to identify accessions having waterlogging tolerance. Out of these 609 sesame accessions seven accessions *viz.,* EC334449, EC334965, EC 334970, EC 334981, EC346727, IC204414 and IC96095 exhibited tolerance against waterlogging at three different growth stages (seedling stage, flower and capsule initiation stage) when natural waterlogging was allowed for 48 hours during experimentation. Identification of donors and development of waterlogging tolerant varieties is the most feasible and economically viable approach to bring desired stability in sesame production at the fields of resource poor farmers.

Keywords: Genetic variations, Sesame, Tolerance, Waterlogging

Sesame (*Sesamum indicum* L., 2n =2x=26) is one of the ancient oilseed crops in the world known to mankind, with archeological evidences dating back 2250 and 1750 BC at Harappa in the Indus valley, both for seeds and its oil (Najeeb *et al.,* 2012). Interspecific hybridization, molecular analysis and presence of eight species out of 23 known sesame species confirm India as one of the centres of origin for sesame (Bedigian, 2004; Bhat *et al.,* 1999). Sesame oil is known for its quality (high cooking quality, ethnic uses and medicinal importance - anti-aging and antifungal properties) and therefore, is also popular as 'Queen of oilseeds'. Sesame seeds are used to prepare wide array of edible products (confectionary, sweets and bakery product) for human consumption and animal feed (Bedigian, 2011). The seeds are used in industries for making soaps, perfumes, lubricants, cosmetics and antioxidants (Myint *et al*., 2020).

India, China, Myanmar, Sudan, Tanzania, Nigeria, Ethiopia and Uganda are the major sesame growing countries in the world. In 2018, India ranked second in the area (1.73 million ha) and third in the production (0.75 million tonnes) globally (FAOSTAT, 2020). The productivity of sesame in India is very low (431 kg/ha) as compared to neighboring country China (1393 kg/ha). In India sesame is mainly grown in Uttar Pradesh (30%), Madhya Pradesh (23%), Rajasthan (20%) and Gujarat (8%) but its productivity in Uttar Pradesh (239 kg/ha) far less than the national average yield (IOPEPC, 2019) mainly due to sensitivity of the crop towards waterlogging. The sesame crop is highly sensitive to waterlogging (Wang *et al.,* 2012; Wang *et al.,* 2016a). As per empirical estimates in previous years nearly 60-70% of the sesame crop in Bundelkhand region was affected due to waterlogging and during *kharif* 2018 sesame crop almost failed due to heavy rains (938.8 mm rainfall during 27-40 standard meteorological weeks). At Jhansi, normally 615 mm rain is recorded in 27-40 standard meteorological weeks with 37 rainy days which affected the sesame crop in this region. The genetic variation for the waterlogging tolerance have been reported earlier in case of wheat (Huang *et al.,* 1994), maize (Fausey *et al.,* 1985), cotton (Conaty *et al.,* 2008), soybean (Valliyodan *et al.,* 2017) and *Brassica napus* (Mustroph, 2018). However, waterlogging lines have not been reported in sesame. Therefore, efforts towards identifying genetic variations for waterlogging tolerance among various sesame accessions was planned so that varieties having waterlogging tolerance can be developed in future.

In order to identify waterlogging tolerant accessions, an experiment was conducted during *kharif* 2019 at the Research Farm of Rani Lakshmi Bai Central Agricultural University, Jhansi, Uttar Pradesh, India. A total of 609 germplasm accessions (indigenous and exotic) of sesame were procured from ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi (India) for the purpose of characterization and phenotyping against waterlogging. In addition to germplasm accessions, five released sesame varieties *viz.,* TKG306, TKG308, JT14, PT1 and RT346 were also included for phenotyping against waterlogging. All 614 accessions were planted in a single row of one meter length and spaced 30 cm apart in 14 blocks following

*Corresponding author's E-mail: sushilk.chaturvedi@gmail.com

augmented block design on a flat field located in a low lying area of the RLBCAU research farm where water stores from whole field due to slope. The same set of 614 accessions was also grown in an upland area of the same field. All the recommended package of practices was followed to maintain a good crop stand. The preliminary screening for waterlogging was done in field with natural rainfall as there was continuous heavy rain during the month of August and September (Table 1). The drainage of water from field was controlled along with field practices to assure equal water stagnation up to 48 hours in the each block of the experiment. A series of waterlogging treatments up to 48 hours were naturally applied on different intervals like seedling stage, flower initiation stage and pod filling duration. The meteorological data were collected from ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi (Uttar Pradesh) and presented (Table 1). Waterlogging stress symptoms like drooping, chlorosis and recovery after stress were visually observed and based on survival of the accessions under severe and frequent stress the accessions were identified as tolerant accessions (Fig. 1). These waterlogging tolerant accessions were compared with accessions grown under normal conditions for the nine agro-morphological traits like days to 50% flowering, days to maturity, plant height (cm), number of capsules on main axis, number of capsules/plant, capsule length (cm), number of seeds/capsule and seed yield/plant (g).The data on days to 50 % flowering and days to maturity was taken on plot basis and rest other parameters were recorded by averaging of five plants or capsules. Yield and yield attributing parameters were compared to estimate the yield reduction due to waterlogging.

Table 1 Weekly average values for weather parameters during crop season (*kharif*, 2019)

Months	Date	Temperature (°C)		Rainfall (mm)	Rainy days
		Max.	Min.		
July	15-21	37.0	26.6	4.2	1
July	22-28	34.2	26.1	67	4
July-Aug.	29-4	32.8	26.4	56.6	2
August	5-11	32.7	25.7	29.6	3
August	12-18	31.5	24.0	92.8	3
August	19-25	32.0	24.7	33	1
Aug –Sept	26-1	33.0	25.9	7.2	1
Sept.	2-8	34.6	26.5	5.6	1
Sept.	9-15	32.5	25.4	87	3
Sept.	16-22	31.4	21.1	56.2	4
Sept.	23-29	30.6	23.5	10	2
Sept.-Oct.	30-6	32.0	22.4	23.4	1
Oct.	7-13	33.0	19.3	0	0
Oct.	14-20	32.4	18.7	0	0
Oct.	21-27	30.7	16.2	0	0
Oct-Nov	28-3	31.6	16.1	0	0
Total				472.6	26

Excess water conditions affect plant growth and biomass production at all the physiological stages resulting in plant mortality. Waterlogging at seedling stage caused a significant effect on plant growth and symptoms like severe chlorosis, rotting and drooping of plants were observed in the present study. Significant genotypic variations were noticed for tolerance against waterlogging though majority of the accessions showed sensitivity and showed seedling mortality. Thirty two accessions exhibited tolerance at seedling stage and were again subjected to waterlogging for 48 hours at 30 days after sowing further showed chlorosis, stunting and necrosis and adversely affected the plant growth. Only 13 germplasm accessions survived after 30 days of sowing and again heavy rains (87 mm rains in 3 rainy days) created excess waterlogging during 50-55 DAS and crop was allowed to stand under waterlogging condition for 48 hours which affected the capsule formation in these accessions. Waterlogging during capsule initiation considerably reduced seed filling, yield and straw quality. Finally, out of 614 accessions including check varieties only 7 accessions *viz.,* EC334449, EC334965, EC334970, EC334981, EC346727, IC204414 and IC96095 were

selected as promising ones against waterlogging which includes indigenous as well as exotic accessions. These seven waterlogging tolerant lines were compared for eight agro-morphological traits with crop grown under normal condition (Table 2 and Fig. 2). It was observed that 5-8 days delayed maturity (IC204414 and IC96095), 13-15 cm reduction in plant height (EC346727, IC96095 and IC204414), reduced number of capsules on main axis (4-5 capsules), reduced capsule length (1 cm) and fewer seeds/capsule (3-4 seeds) were the main effects of waterlogging. Reduction in yield attributes due to waterlogging stress has been reported by many workers (Mai Nhat Linh *et al.,* 2021; Athul, 2016; Ameri *et al.,* 2014; Saha *et al.,* 2016; Sarkar *et al.,* 2016). Two accessions (EC334965 and IC204414) exhibited minimum reduction in number of capsule/plant whereas IC204414 and EC334981 showed minimum effect of waterlogging on capsule length. Based on the minimum reduction in number of capsules/plant, capsule length, and yield, accession IC204414 could be identified as tolerant to waterlogging. The reason for reduction in yield can be due to loss of chlorophyll content led reduced photosynthetic rate (Olgun *et al.,* 2008; Marashi and Chinchanikar, 2014; Athul, 2016; Sarkar *et al.,* 2016).

It has been predicted that abiotic stress alone limits the global crop production by almost 70% (Boyer, 1982) due to extreme events that alter water availability, like droughts and floods (FAO, 2017). In low lying areas, heavy rainfall over a period creates two types of situations depending on depth of the water table either in one form of waterlogging in which water is superficial and covers only root and some portion of the stem or submergence, and in the other when whole plants go under water and covers all aerial tissues (Sasidharan *et al.,* 2017). Under both the conditions, disruption in movement of oxygen from air to plant tissues, especially the roots, was observed and this produces hypoxic or anoxic situation (Lee *et al.,* 2011). In most of the plant species, the capacity of root system to transfer plant nutrients and water which is necessary for plant growth and development is restricted under water logged condition (Musgrave and Ding 1998; de Simone *et al.,* 2002) which limits the shoot and root growth under the water logged situation (Kozlowski, 1984; Smethurst and Shabala, 2003). Excessive waterlogging also enhances the vulnerability of the plants to pathogens, limits the flow of light to the plant and during recovery from waterlogging plants generally faces the oxidative stress (Yeung *et al.,* 2018).

Among the total 609 accessions included in this study, seven genotypes *viz.,* EC334449, EC334965, EC334970, EC334981, EC346727, IC204414 and IC96095 exhibited tolerance to waterlogging condition and these lines can be used as potential donors for the development of waterlogging tolerant cultivars.

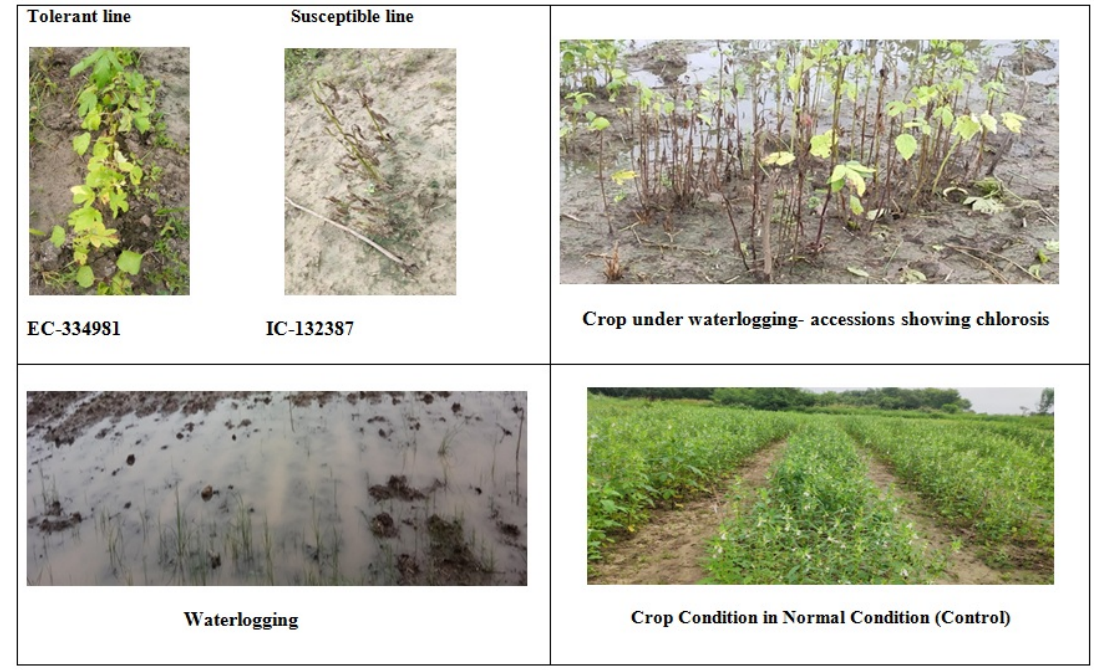

Fig. 1. Field view of waterlogging and normal condition

Table 2 Yield attributes traits of sesame accessions under waterlogging and normal condition

Accessions name	Days to 50% flowering		Days to maturity		Plant height (cm)		Capsules on main axis		Capsules/ plant		Capsule length (cm)		Seeds/ capsule		Seed Yield/ plant (g)	
	W*	C*	W	C	W	C	W	C	W	C	W	C	W	C	W	C
EC334449	42	36	92	79	80.25	105.74	4.23	12.98	11.35	43.14	2.2	2.72	28.43	34.2	2.46	7.19
EC334965	55	46	97	88	85.3	105.14	5.54	10.18	13.66	18.34	2.35	2.5	26.54	34.61	2.52	4.59
EC334970	55	47	95	81	74.6	90.14	4.32	10.58	12.28	29.14	2.14	2.52	24.54	37.4	2.64	7.12
EC334981	56	42	90	77	85.8	119.74	6.67	10.38	10.89	20.14	2.24	2.33	29.42	33.39	2.23	4.61
IC204414	52	50	98	92	64.6	79.7	3.27	6.79	7.54	12.77	2.3	2.28	26.87	35.74	2.28	2.93
IC96095	55	49	94	88	82	96.09	3.5	6.71	8.33	19.21	2.1	2.43	24.26	37.33	2.5	4.95
EC346727	49	40	95	83	78	91.09	7.37	15.71	7.54	35.81	2.45	2.77	29.33	36.53	3.32	6.93

*W- Waterlogging for 48 hours and C- Control (Normal condition)

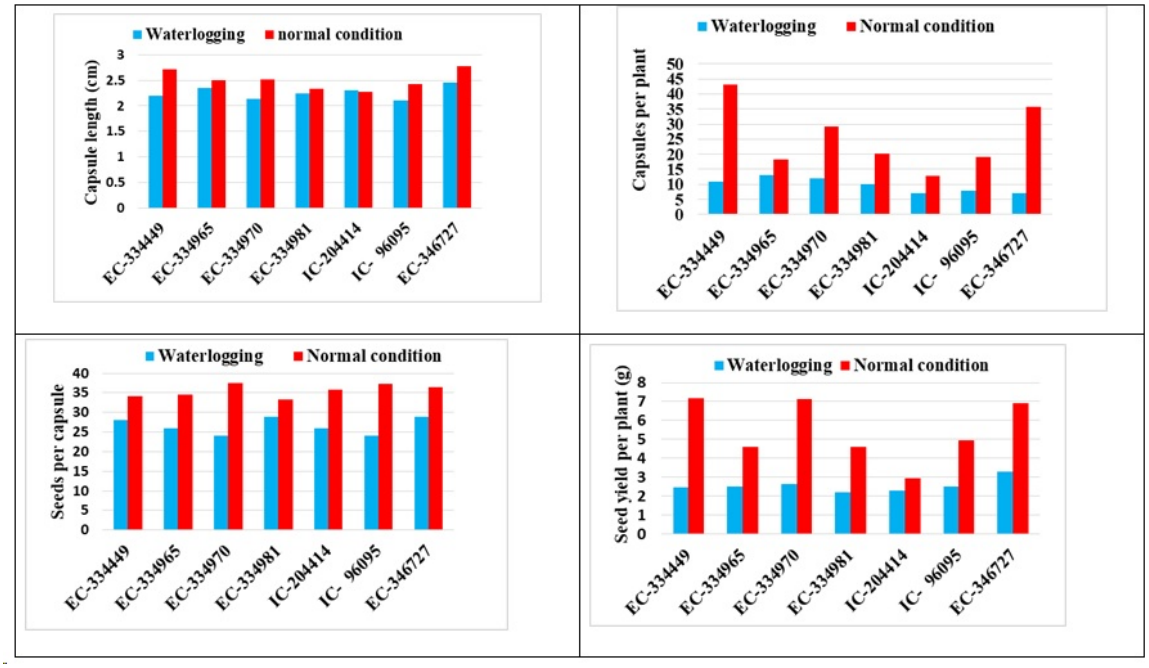

Fig. 2. Graphical representation of yield components of sesame genotypes under waterlogging and normal condition

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Studies on host range of *Alternaria* spp. causing blight disease in linseed

H H ASMA, K AJITHKUMAR[1*], A S SAVITHA, S T YENJERAPPA,
M R GOVINDAPPA[2] AND D KRISHNAMURTHY[3]

College of Agriculture, University of Agricultural Sciences, Raichur-584 104, Karnataka

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ABSTRACT

Alternaria blight is one of the most serious diseases of linseed caused by different *Alternaria* spp. The genus *Alternaria* Nees ex Fr. is widely distributed all over the world and is represented by a number of species. The genus occupies a prime position and is significantly important as its members are well known in causing wide spread diseases of economic plants such as cereals, oilseed crops, spices, vegetables and ornamentals. The studies on host range of *Alternaria* spp. revealed that the pathogen was unable to infect any of the crop plants taken for study under the pot conditions but showed mycelial growth on all the crops tested through detached leaf technique under laboratory condition. The maximum mycelial growth of *Alternaria* spp. was noticed on carrot grass (9.56 mm) followed by groundnut (8.82 mm), whereas, minimum mycelial growth was observed on sesame (2.52 mm). Therefore, based on this host range test, it can be concluded that *Alternaria* spp., infecting linseed may also be pathogenic to other hosts only under controlled and favourable conditions.

Keywords: *Alternaria* spp., Host range, Linseed

Linseed (*Linum usitatissimum* L.) is an oldest oilseed crop, popularly called as poor man's crop of India. Linseed is also referred as 'flax', an important *rabi* oilseed crop next to rapeseed and mustard in India. The crop is grown for seed as well as for fibre purpose in South West Asia including Turkistan, Afghanistan and India, whereas, in Asia and South Russia the crop is primarily grown for its oil. The crop is traditionally cultivated for oil, which is used for industrial purposes. Almost every part of the plant is commercially utilized either directly or after processing. On small scale, the seed and its oil are directly used for human consumption as flaxseed breads, bagels and other baked and fried food stuffs. The major portion (80 %) of the oil is used for paints, varnishes, a wide range of coating oils, linoleum, pad, printing inks, leather and soap industries.

Linseed is adversely affected by different diseases, the most important pathogens that cause diseases in linseed are *Alternaria linicola* (blight), *Fusarium* spp. (wilt), *Botrytis cinerea* (gray mould), *Oidium lini* (powdery mildew), *Ascochyta linicola* (foot rot), *Melampsora lini* (rust), *Rhizoctona solani* (Rhizoctonia seedling blight), *Pythium megalacanthum* (scorch), *Septoria linicola* (pasmo), *Polyspora lini* (browning or stem break) and *Colletotrichum linicolum* (anthracnose).

Alternaria blight is a major disease which causes heavy loss in terms of quality and quantity of the fiber and seed of linseed. Three species of *Alternaria, A. linicola* (Groves and Skolko, 1944), *A. alternata* (Fr.) (Tokumasu and Aoiki, 2002) and *A. lini* (India) (Dey, 1933), commonly occur on linseed. Alternaria blight caused by *A. lini* (Dey) and *A. linicola* (Groves and Skolko) is known to inflict 40-60 per cent of yield losses in linseed (Singh *et al.,* 2003; Singh and Singh, 2005).

The genus *Alternaria* spp. is widely distributed all over the world and is represented by a number of species. The genus occupies a prime position and is significantly important as its members are well known in causing wide spread diseases of economic plants such as cereals, oilseeds, spices, vegetables and ornamentals. The pathogen may be host specific or may cause diseases on other crops too. The host range of any pathogen has one criteria which shows its virulence and host preference. Hence studies were carried out to record the host range of Alternaria species that causes blight in linseed.

The host range of the pathogen was studied through two methods detached leaf method and pot culture method. Briefly, in the detached leaf assy, the wet blotter paper was kept in the sterilized Petri plates and fresh sterilized young leaves (30 DAS) of different oilseed crops such as castor, groundnut, safflower, sesamum, sunflower and weed host carrot grass were placed on it and inoculated with *Alternaria* spp. spore disc of 5 mm size. The plates were incubated at 25 ± 2°C for four days and observed for typical symptoms on the leaf (Das and Raj, 1996). In pot culture method, other than linseed, some of the cultivated oilseed crops such as castor, groundnut, safflower, sesame, sunflower, as well as carrot grass, a common weed were

[1]AICRP on Linseed, Main Agricultural Research Station, University of Agricultural Sciences, Raichur-584 104, Karnataka; [2]Krishi Vigyana Kendra, Hagari, Ballari-583 111, Karnataka; [3]Agricultural Research Station, Hagari, Ballari-583 111, Karnataka; *Corresponding author's E-mail: ajithk.path@gmail.com

raised in earthen pots in polyhouse. The surface sterilized seeds of selected crops were sown in the pot mixture containing sand: soil: FYM (3:1:1) with three replications. In each pot two to three seedlings were retained after germination and suitable un-inoculated control pots were also maintained and 30 days old seedlings were inoculated with spore suspension of pathogen culture @ 1×10^3 conidia/ml. Observations for disease symptoms were recorded at five days interval for up to 27 days of post inoculation and blight severity was measured by using 0-5 scale (Wheeler, 1969).

The present investigation was conducted in laboratory under controlled condition (temperature at 25°C and relative humidity 95%) to know the sporulation of *Alternaria* spp., on other hosts through detached leaves of test plants. Laboratory conditions in our study were optimal for the infection of the *Alternaria* blight pathogen under pot condition. The results showed that, the mycelial growth of the pathogen was significantly maximum on carrot grass (9.56 mm) followed by groundnut (8.82 mm), which were on par with each other and statistically superior over other hosts (Table 1 and Fig. 1). Whereas, the mycelial growth on castor, safflower, sesame and sunflower were on par with each other and differed statistically with carrot grass and groundnut. Significantly least mycelial growth was observed on sesame (2.52 mm). Therefore, based on this host range test, *Alternaria* spp., infecting linseed is host specific and but may also infect other hosts only under controlled and favourable conditions.

The pot culture experiments showed differential reaction of the Alternaria when tested on many host plants (Table 1).The observations revealed that, the blight pathogen was unable to infect different host plants other than linseed. Out of the six host plants inoculated, none of them were infected by *Alternaria* spp. and did not show any sign of infection to this pathogen and this indicated that Alternaria species tested is host specific and causes blight symptoms only on linseed not on other hosts.

The results are in confirmation with what is reported by Gupta (2008). He had assessed the host range of *A. lini* and *A. linicola* on 72 different crop plants and weeds belonging to different families such as Solanaceae, Chenopodiaceae, Euphorbiaceae, Fabaceae, Rubiaceae, Convolvulaceae, Linaceae, Poaceae, Papaveraceae, Canabinaceae, Asteraceae, Rosaceae, Primulaceae, Umbellifereae, Brassicaceae, Amaranthaceae, Acanthaceae, Nyctaginaceae, Malvaceae, Lamiaceae, Verbenaceae, Rutaceae, Apocynaceae, Caesalpinaceae, Asclepiadaceae, Cucurbitaceae and Aizoaceae. Among the 72 host plants tested, *A. lini* was able to infect groundnut and was highly pathogenic as it infected a wide variety of hosts belonging to different families including the member of Linaceae, *Linum grandiflorum.* The observations also revealed that this blight fungus i.e. *A. linicola* was unable to infect Indian diversified species of various families except *L. grandiflorum* belonging to Linaceae.

Mangala *et al.* (2006) made an investigation regarding pathogenicity of *A. alternata* on chilli cultivars and other host plants. The fungus isolated from diseased chilli leaves produced typical leaf blight symptoms upon inoculation of healthy chilli plants that were similar to those recorded on naturally infected plants. Upon artificial inoculation, small necrotic spots appeared on other hosts such as tomato, redgram, blackgram, greengram, groundnut, cabbage and mustard, while blight symptoms were observed on aubergine, tobacco, soybean, clusterbean, potato and cauliflower. The leaf spot symptoms were also observed on the weeds such as *Solanum nigrum, Physalis minima, Datura metel, Amaranthus viridis* and *Digera arvensis,* while no symptoms were observed on *Parthenium hysterophorus.*

Virulence of *A. solani* and *A. alternata* on tomato and potato crops was analyzed by Stammler *et al.* (2014). The pathogens were isolated from potato at different regions worldwide and the same isolates were inoculated on tomato in the greenhouse and potato in the greenhouse and in the field. Conditions and host cultivars varied to increase chances infections. However, in all trials *A. solani* isolates were highly virulent while *A. alternata* isolates showed low or no symptoms after inoculation.

Table 1 The reaction of the different host plants to Alternaria spp. under pot culture and in detached leaf technique

Host plant leaves	Botanical Name	Growth of *Alternaria* spp. under pot condition (mm)	Growth of *Alternaria* spp., under laboratory condition (mm)
Carrot grass	*Parthenium hysterophorus*	No symptom	9.56*
Castor	*Ricinus communis*	No symptom	3.79
Groundnut	*Arachis hypogaea*	No symptom	8.82
Safflower	*Carthamus tinctorius*	No symptom	3.27
Sesame	*Sesamum indicum*	No symptom	2.52
Sunflower	*Helianthus annuus*	No symptom	3.02
	SEm(±)		1.02
	CD (1%)		3.07

*Mean of four replications

Fig. 1. Growth of *Alternaria* spp. on different plant species under detached leaf technique

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Book Review

OILSEED CROPS

Author: **M.V.R. Prasad**
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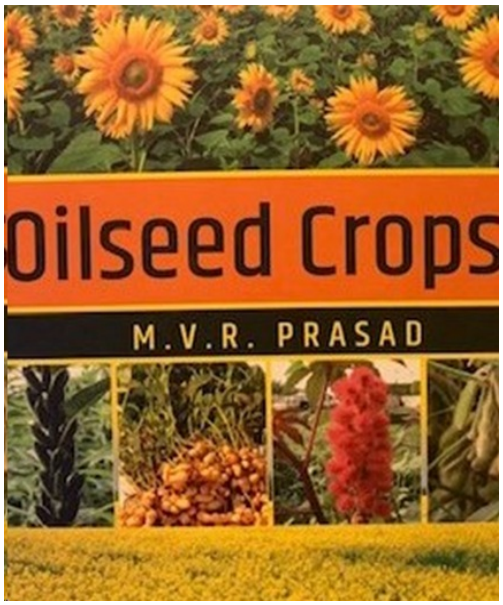

Despite its ranking third in acreage on the global oil crops map, cultivation of enviably large basket of diverse oil crops suited to varying agro-ecological and growing situations spread over more than 25 million hectares and massive research network, the country's vegetable oil sector continues to pose grave concern to policy makers, and administrators on account of burgeoning demand-supply gap as well as ever growing dependency on external vegetable oil imports at a huge cost to the exchequer. Nevertheless, on-farm researches undertaken across country with already available improved crop cultivars highlight existence of huge untapped yield reservoir in all the annual oil crops even at current levels of their realisable productivity potentials.

There is still on date no single source of comprehensive and up-to date information is available on this highly heterogeneous and diversified group of oil crops, be it annuals or oil bearing trees. The book on "Oilseed Crops" brought out by Dr. M.V.R. Prasad, a reputed plant breeder with rich experience in oilseed crops' improvement, both annuals and oil bearing trees, as well as management of national oilseeds research system as its former Director is expected to bridge the above critical gap and ably meet the growing needs of researchers, students, extension workers alike.

The book not only gives an authoritative and up-to date account of oilseed crops in the country namely groundnut, rapeseed mustard, soybean, sesame, sunflower, safflower, niger, linseed and castor, their current status, performance to date, ecology, origin, botany of the plant, cytogenetics and species relationships, genetic resources, conventional breeding as well as state of art biotechnological tools such as genomics, genetic transformation, gene editing, marker assisted selection, agronomy, available agro production and protection technologies tailored to different growing situations, key constraints holding-up breakthroughs on productivity front, their management and a host of other aspects.

The book is well organised into 12 highly structured individual chapters: chapter1 gives a panoramic view of oilseed sector, chapters 2 to10 deal with individual 9 annual oilseed crops in all their totality while chapter 11 covers individual oil bearing tree species of immense potential to the country namely *Jatropha* species, *Pongamia pinnata, Melia azedarach* (China berry tree), neem, mahua, sal, drumstick tree, Jojoba, Simarouba and kokum. What is more important, the book also includes a special chapter on designer oilseed crops which are attracting increased attention from the point of view of varied industrial applications, be it in pharmaceuticals, surfactants, plasticisers, emulsifiers, detergents, lubricants, adhesives, cosmetics, oleo-chemicals, biofuels, nutrition, or animal feeds etc.

The testimonial for the book comes in the form of Foreword from none other than world renowned agricultural scientist and father of India's Green Revolution, Prof. Dr. M.S. Swaminathan. No doubt, the book would be of great value to all oil crop researchers as well as teachers and those engaged in extension. Nevertheless, it's current cover price (₹5995) is too expensive to be within the reach of most of the book's potential clientele. Let us earnestly hope the publishers of the book will have a re-look at its cover price and make it accessible to many students, young and upcoming oil crop research scientists.

Dr. Ranga Rao Veerapaneni
Former Director, ICAR-Indian Institute of Oilseeds Research
(erstwhile integrated Directorate of Oilseeds Research)
Rajendranagar, Hyderabad-500 030, India

INDIAN SOCIETY OF OILSEEDS RESEARCH
Instructions to Authors for Preparation of Manuscript for Journal of Oilseeds Research

Prospective author(s) are advised to consult **Issue No. 27(1) June, 2010 of the Journal of Oilseeds Research** and get acquainted with the minor details of the format and style of the Journal. Meticulous compliance with the instructions given below will help quick handling of the manuscript by the reviewers, editor and printers. **Manuscripts are considered for publication in the Journal only from members of the ISOR.**

General

Full-length articles, short communications, book reviews and review articles are published in the Journal. Review articles and book reviews are published usually by invitation. Full length articles and short communications should report results of original investigations in oilseeds, oil bearing plants and relevant fields of science. Choice of submitting the paper(s) either as full length paper or short communication rests with the authors. The Editor(s) or Reviewer(s) will examine their suitability or otherwise only in that specific category. Each article should be written in English correctly, clearly, objectively and concisely. All the statements made in the manuscript should be clear, unambiguous, and to the point. Plagiarism is a crime and therefore, no part of the previously published material can be reproduced exactly without prior permission from the original publisher or author(s) as deemed essential and the responsibility of this solely rests on the authors. Also, authors shall be solely responsible for the authenticity of the results published as well as the inferences drawn thereof. Telegraphic languages should be avoided. The data should be reported in a coherent sequence. Use active voice. Active voice is clear, unambiguous and takes less space. Use past tense while reporting results. Do not repeat ideas in different forms of sentences. Avoid superfluous sentences such as `it is interesting to note that', `it is evident from the table that' or `it may be concluded that' etc. Use % for percent, %age for percentage, / for per, @ for at the rate of hr for hours, sec for seconds. Indicate date as 21 January 2010 (no commas anywhere). Spell out the standard abbreviations when first mentioned eg. Net assimilation rate (NAR), general combining ability (GCA), genetic advance (GA), total bright leaf equivalents (TBLE), mean sum of squares (MSS).

Manuscript

Language of the Journal is English. Generally, the length of an article should not exceed 3,000 words in the case of full-length article and 750 words in the case of short communication. However completeness of information is more important. Each half-page table or illustration should be taken as equivalent to 200 words. It is desirable to submit manuscript in the form of soft copy either as an e-mail attachment to editorisor@gmail.com (preferred because of ease in handling during review process) or in a **compact disk (CD) (in MS Word document; double line space; Times New Roman; font size 12).** In exceptional cases, where the typed manuscript is being submitted as hard copy, typing must be done only on one side of the paper, leaving sufficient margin, at least 4 cm on the left hand side and 3 cm on the other three sides. Faded typewriter ribbon should not be used. Double space typing is essential throughout the manuscript, right from the **Title** through **References** (except tables), foot note etc. Typed manuscript complete in all respects, is to be submitted to the Editor, Journal of Oilseeds Research, Directorate of Oilseeds Research, Rajendranagar, Hyderabad-500 030. Every page of the manuscript, including the title page, references, tables, etc. should be numbered. Punctuation marks help to show the meanings of words by grouping them into sentences, clauses, and phrases and in other ways. These marks should be used in proper manner if the reader of a paper is to understand exactly the intended meaning. Receipt of the manuscript (in the form of either soft or hard copy) will be acknowledged by the editorial office of the Society, giving a manuscript number which should be quoted in all subsequent correspondence regarding that particular article.

Full-length Articles

Organization of the Manuscript

Before reading the instructions given below, the author(s) would better have a close look at the latest issue of the Journal.

Full-length article comprises the following sections.

(a) Short title
(b) Title
(c) Author/Authors
(d) Institution and Address with PIN (postal) code
(e) Abstract (along with key words)
(f) Introduction
(g) Materials and Methods
(h) Results and Discussion
(i) Acknowledgments (if any)
(j) References
(k) Tables and figures (if any)

Guidelines for each section are as follows:

All these headings or matter thereof should start from left hand side of the margin, without any indent.

Short Title

A shortened title (approximately of 30 characters) set in capital letters should convey the main theme of the paper.

Title

Except for prepositions, conjunctions, pronouns and articles, the first letter of each word should be in capital letter. The title should be short and should contain key words and phrases to indicate the contents of the paper and be attractive. Jargons and telegraphic words should be avoided. In many cases, actual reading of the paper may depend on the attractiveness of the title.

Author/Authors

The name(s) of author(s) should be typed in capital letters a little below the title, starting from the left margin. Put an asterisk on the name of the corresponding author. **Give the Email ID of the corresponding author** as a footnote.

Institution and Address

This matter will come below the name(s) of the author(s). Name of the Laboratory/Department, followed by the name of the Institution/Organization/University where the work reported in the paper was carried out shall come below the name(s) of author(s). Complete postal address, which should include city/town, district, and state, followed by PIN (postal) code is to be furnished. In case any author has left the above address, this should be indicated as a footnote.

Abstract

The paragraph should start with the word Abstract (in bold font). The abstract should comprise brief and factual summary or salient points of the contents and the conclusions of the investigation reported in the paper and should refer to any new information therein. As the abstract is an independent entity, it should be able to convey the gist of the paper in a concise manner. It will be seen by many more people than will read the paper. The abstract, as concise as possible, should not exceed 250 words in length. Everything that is important in the paper must be reflected in the abstract. It should provide to the reader very briefly the rationale, objectives or hypothesis, methods, results and conclusions of the study described in the paper. In the abstract, do not deflect the reader with promises such as 'will be discussed' or 'will be explained'. Also do not include reference, figure or table citation. At first mention in the abstract, give complete scientific name for plants and other organisms, the full names of chemicals and the description of soil order/series. Any such names or descriptions from the abstract need not be repeated in the text. It must be remembered that the abstracting journals place a great emphasis on the abstract in the selection of papers for abstracting. If properly prepared, they may reproduce it verbatim.

"Key words" should, follow separately after the last sentence of the abstract. "Key words" indicate the most important materials, operations, or ideas covered in the paper. Key words are used in indexing the articles.

Introduction (To be typed as side-heading, starting from the left-hand margin, a few spaces below the key words)

This section is meant to introduce the subject of the paper. Introduction should be short, concise and indicate the objectives and scope of the investigation. To orient readers, give a brief reference to previous concepts and research. Limit literature references to essential information. When new references are available, do not use old references unless it is of historical importance or a landmark in that field. Emphasis should be given among other things on citing the literature on work done under Indian conditions. Introduction must include: (a) a brief statement of the problem, justifying the need for doing the work or the hypothesis on which the work is based, (b) the findings of others that will be further developed or challenged, and (c) an explanation of the approach to be followed and the objectives of the research described in the paper. If the methods employed in the paper are new, it must be indicated in the introduction section.

Materials and methods (To be typed as side-heading, starting from the left-hand margin, a few spaces below the introduction)

This part of the text should comprise the materials used in the investigation, methods of experiment and analysis adopted. This portion should be self-explanatory and have the requisite information needed for understanding and assessing the results reported subsequently. Enough details should be provided in this section to allow a competent scientist to repeat the experiments, mentally or in fact. The geographical position of soil site or soils used in the experiment or site of field trial should be identified clearly with the help of coordinates (latitude & longitude) and invariably proper classification according to Soil Taxonomy (USDA), must be indicated to the level of Great-group, Suborder or Order as far as possible. Specify the period during which the experiment(s) was conducted. Send the article after completion of the experiment(s) not after a gap of 5 years. Instead of kharif and rabi use rainy and winter season respectively. Please give invariably the botanical names for local crop names like raya, bajra moong, cholam etc. Botanical and zoological names should confirm to the international rules. Give authorities. Go through some of our recent issues and find out the correct names. Give latest correct names from authentic source. For materials, give the appropriate technical specifications and quantities and source or method of preparation. Should a product be identified by trade name, add the name and location of the manufacturer or a major distributor in parenthesis after the first mention of the product. For the name of plant protection chemicals, give popular scientific names (first letter small), not trade names (When trade name is given in addition, capitalize the first letter of the name). Known methods of analysis should be indicated by referring to the original source, avoiding detailed description. Any new technique developed and followed should be described in fair detail. When some specially procured or proprietary materials are used, give their pertinent chemical and physical properties. References for the methods used in the study should be cited. If the techniques are widely familiar, use only their names in that case.

Results and Discussion (To be typed as a side-heading, a few spaces below the matter on "Materials and Methods")

This section should discuss the salient points of observation and critical interpretation thereof in past tense. This should not be descriptive and mere recital of the data presented in the tables and diagrams. Unnecessary details must be avoided but at the same time significant findings and special features should be highlighted. For systematic discussion, this section may be divided into sub-sections under side-heading and/or paragraph side heading. Relate the results to your objectives. While discussing the results, give particular attention to the problem, question or hypothesis presented in the introduction. Explain the principles, relationships, and generalizations that can be supported by the results. Point out any exceptions. Explain how the results relate to previous findings, support, contradict or simply add as data. Use the Discussion section to focus on the meaning of your findings rather than recapitulating them. Scientific speculation is encouraged but it should be reasonable and firmly founded in observations. When results differ from previous results, possible explanations should be given. Controversial issues should be discussed clearly. References to published work should be cited in the text by the name(s) of author(s) as follows: Mukherjee and Mitra (1942) have shown or It has been shown (Mukherjee and Mitra, 1942)..... If there are more than two authors, this should be indicated by et al. after the surname of the first author, e.g., Mukherjee et al. (1938).

Always conclude the article by clearly crystallizing the summary of the results obtained along with their implications in solution of the practical problems or contribution to the advancement of the scientific knowledge.

Acknowledgments (To be typed as given above, as a side-heading, well below the concluding portion of Conclusions)

The author(s) may place on record the help, and cooperation, or financial help received from any source, person or organization. This should be very brief, and omitted, if not necessary.

References (To be typed as above, as side heading below Acknowledgement)

The list of references must include all published work referred to in the text. Type with double line spacing. Do not cite anonymous as author; instead cite the name of the institute, publisher, or editor. References should be arranged alphabetically according to the surnames of the individual authors or first authors. Two or more references by the same author are to be cited chronologically; two or more in the same year by the letters a, b, c, etc. All individually authored articles precede those in which the individual is the first or joint author. Every reference cited in the article should be included in the list of References. This needs rigorous checking of each reference. Names of authors should not be capitalized.

The reference citation should follow the order: author(s), year of publication, title of the paper, periodical (title in full, no abbreviations, italics or underlined), volume (bold or double underlining), starting and ending pages of the paper. Reference to a book includes authors(s), year, title (first letter of each word except preposition, conjunction, and pronouns in capitals and underlined), the edition (if other than first), the publisher, city of publication. If necessary, particular page numbers should be mentioned in the last. Year of publication cited in the text should be checked with that given under References. Year, volume number and page number of each periodical cited under "References" must be checked with the original source. The list of references should be typed as follows:

Rao C R 1968. *Advances in Statistical Methods in Biometrical Research*, pp.40-45, John Wiley & Sons, New York.

Kanwar J S and Raychaudhuri S P 1971. *Review of Soil Research in India*, pp 30-36. Indian Society of Soil Science, New Delhi.

Mukherjee J N 1953. The need for delineating the basic soil and climatic regions of importance to the plant industry. *Journal of the Indian Society of Soil Science*, **1** : 1-6.

Khan S K, Mohanty S K and Chalam A B, 1986. Integrated management of organic manure and fertilizer nitrogen for rice. *Journal of the Indian Society of Soil Science*, **34** : 505-509.

Bijay-Singh and Yadvinder-Singh 1997. Green manuring and biological N fixation: North Indian perspective. In: Kanwar J S and Katyal J C (Ed.) *Plant Nutrient Needs, Supply, Efficiency and Policy Issues 2000-2025*. National Academy of Agricultural Sciences, New Delhi, India, pp.29-44.

Singh S, Pahuja S S and Malik R K 1992. Herbicidal control of water hyacinth and its effect on chemical composition of water *(in) Proceedings of Annual Weed Science Conference*, held during 3-4 March 1992 by the Indian Society of Weed Science, at Chaurdhary Charan Singh Haryana Agricultural University, Hisar, 127p.

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.

Details of the peer review process

Manuscripts are received mainly through e-mails and in rare cases, where the authors do not have internet access, hard copies of the manuscripts may be received and processed. Only after the peer review the manuscripts are accepted for publication. So there is no assured publication on submission. The major steps followed during the peer review process are provided below.

Step 1. ***Receipt of manuscript and acknowledgement***: Once the manuscript is received, the contents will be reviewed by the editor/associate editors to assess the scope of the article for publishing in JOR. If found within the scope of the journal, a Manuscript (MS) number is assigned and the same will be intimated to the authors. If the MS is not within the scope and mandate of JOR, then the article will be rejected and the same is communicated to the authors.

Step 2. ***Assigning and sending MS to referees***: Suitable referees will be selected from the panel of experts and the MS (soft copy) will be sent to them for their comments - a standard format of evaluation is provided to the referees for evaluation along with the standard format of the journal articles and the referees will be given 4-5 week time to give their comments. If the comments are not received, reminders will be sent to the referees for expediting the reviewing process and in case there is still no response, the MS will be sent to alternate referees.

Step 3. ***Communication of referee comments to authors for revision***: Once the referee comments and MS (with suggestions/ corrections) are received from the referees, depending on the suggestions, the same will be communicated to the authors with a request to attend to the comments. Authors will be given stipulated time to respond and based on their request, additional time will be given for attending to all the changes as suggested by referees. If the referees suggest no changes and recommend the MS for publication, then the same will be communicated to the authors and the MS will be taken up for editing purpose for publishing. In case the referees suggest that the article cannot be accepted for JOR, then the same will be communicated to the authors with proper rationale and logic as opined by the referees as well as by the editors.

Step 4. ***Sending the revised MS to referees***: Once the authors send the revised version of the articles, depending on the case (like if major revisions were suggested by referees) the corrected MS will be sent to the referees (who had reviewed the article in the first instance) for their comments and further suggestions regarding the acceptability of publication. If only minor revisions had been suggested by referees, then the editors would look into the issues and decide take a call.

Step 5. ***Sending the MS to authors for further revision***: In case referees suggest further modifications, then the same will be communicated to the authors with a request to incorporate the suggested changes. If the referees suggest acceptance of the MS for publication, then the MS will be accepted for publication in the journal and the same will be communicated to the authors. Rarely, at this stage also MS would be rejected if the referees are not satisfied with the modifications and the reasoning provided by the authors.

Step 6. ***Second time revised articles received from authors and decision taken***: In case the second time revised article satisfies all the queries raised by referees, then the MS will be accepted and if not satisfied the article will be rejected. The accepted MS will be taken for editing process where emphasis will be given to the language, content flow and format of the article.

Then the journal issue will be slated for printing and also the pdf version of the journal issue will be hosted on journal webpage.

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.

SPECIAL ANNOUNCEMENT

In a recently conducted Executive Committee meeting of the Indian Society of Oilseeds Research, it was decided to increase the scope of the Journal of Oilseeds Research by accommodating vibrant aspects of scientific communication. It has been felt that, the horizon of scientific reporting could be expanded by including the following types of articles in addition to the Research Articles, Shor Communications and Review Articles that are being published in the journal as of now.

Research accounts (not exceeding 4000 words, with cited references preferably limited to about 40-50 in number): These are the articles that provide an overview of the research work carried out in the author(s)' laboratory, and be based on a body of their published work. The articles must provide appropriate background to the area in a brief introduction so that it could place the author(s)' work in a proper perspective. This could be published from persons who have pursued a research area for a substantial period dotted with publications and thus research account will provide an overall idea of the progress that has been witnessed in the chosen area of research. In this account, author(s) could also narrate the work of others if that had influenced the course of work in authors' lab.

Correspondence (not exceeding 600 words): This includes letters and technical comments that are of general interest to scientists, on the articles or communications published in Journal of Oilseeds Research within the previous four issues. These letters may be reviewed and edited by the editorial committee before publishing.

Technical notes (less than 1500 words and one or two display items): This type of communication may include technical advances such as new methods, protocols or modifications of the existing methods that help in better output or advances in instrumentation.

News (not exceeding 750 words): This type of communication can cover important scientific events or any other news of interest to scientists in general and vegetable oil research in particular.

Meeting reports (less than 1500 words): It can deal with highlights/technical contents of a conference/ symposium/discussion-meeting, etc. conveying to readers the significance of important advances. Reports must

Meeting reports should avoid merely listing brief accounts of topics discussed, and must convey to readers the significance of an important advance. It could also include the major recommendations or strategic plans worked out.

Research News (not exceeding 2000 words and 3 display items): These should provide a semi-technical account of recently published advances or important findings that could be adopted in vegetable oil research.

Opinion (less than 1200 words): These articles may present views on issues related to science and scientific activity.

Commentary (less than 2000 words): This type of articles are expected to be expository essays on issues related directly or indirectly to research and other stake holders involved in vegetable oil sector.

Book reviews (not exceeding 1500 words): Books that provide a clear in depth knowledge on oilseeds or oil yielding plants, production, processing, marketing, etc. may be reviewed critically and the utility of such books could be highlighted.

Historical commentary/notes (limited to about 3000 words): These articles may inform readers about interesting aspects of personalities or institutions of science or about watershed events in the history/development of science. Illustrations and photographs are welcome. Brief items will also be considered.

Education point (limited to about 2000 words): Such articles could highlight the material(s) available in oilseeds to explain different concepts of genetics, plant breeding and modern agriculture practices.

Note that the references and all other formats of reporting shall remain same as it is for the regular articles and as given in Instructions to Authors

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Ph: (040) 24598110 / 24598113; Fax: (040) 24017969
Web site: http://www.isor.in; E-mail: oilseedsociety@gmail.com