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Screening of RIL population for charcoal rot resistance

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Evaluation of groundnut germplasm for pod yield and its attributes in summer

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ABSTRACT

Forty eight germplasm collections were evaluated for pod yield and its attributes during summer 2018 and 2019. High heritability coupled with high GAM were observed for pod yield per plant, HPW, HKW and kernel length indicating that selection for these characters could be more effective due to additive gene action. Pod yield per plant correlated significantly and positively with SP, SMK, and kernel length to width ratio. Both DFI and DFF correlated significantly and negatively with pod yield per plant. SLA had low heritability and GAM. Genotypes NRCG 14507, NRCG CS 254, NRCG CS 313 and Girnar 1 showed early flowering initiation (35 DAS). The surrogate trait of water use efficiency (SLA) was lowest (150<) in genotypes viz., NRCG 17284, SG 99, Gangapuri, ICGS 9114 and VRI 3. Genotypes viz., JGN3, NRCG CS 62, TMV9, ICGS 76, NRCG 8763 showed higher shelling percentage (>70%). Genotypes NRCG 10620 and TG 39 exhibited higher yields over two summer seasons.

Keywords: Genetic advance as percent of mean, Groundnut, Heritability, Pod yield, Summer

The area under irrigated summer groundnut accounts for about 16% of the total area and contributes 28% of the production. There is a greater scope to expand groundnut area under summer season, wherever irrigation facilities are available. Low temperature at germination and high temperature at flowering are major constraints in summer groundnut cultivation. Hence identification of efficient flowering and high yielding genotypes with high water use efficiency is an important breeding strategy to develop groundnut varieties suitable for summer season. Present investigation was an attempt to evaluate the 48 germplasm for pod yield and its attributes in summer season.

A total of 48 germplasm collections consisting of 17 NRCG accessions and 31 released varieties were planted in augmented design with five checks in four blocks at the experimental plots of ICAR-Directorate of Groundnut Research (ICAR-DGR), Junagadh during summer season for two years (2018 and 2019). Standard agronomic practices were followed to raise healthy crop and data collected on days to first initiation (DFI) of flowering, days to 50 per cent flowering (DFF), SLA and SCMR at

60 days, shelling per cent, hundred kernel weight and pod yield/plant. The mean values of the data recorded were subjected to statistical analysis using SPSS (version 16.0) software for descriptive statistical analysis, analysis of variance (ANOVA) and correlation among traits.

The analysis of variance revealed significant differences for all the traits. Large variation was observed for DFI (34 to 49 days); SMK (25 to 83%); SP (26 to 72%) and pod yield (1 to 13 g per plant). The PCV and GCV estimates were low for SLA, SCMR and DFI and DFF, whereas pod yield and HKW had higher estimates. SLA had low heritability and genetic advance as per cent of mean (GAM), whereas SCMR had moderate heritability and low GAM, suggesting the presence of non-additive gene action and simple selection may not be effective. SMK showed moderate estimates of heritability and GAM. High heritability coupled with high GAM were observed for pod yield per plant, HPW, HKW and kernel length indicating that selection for these characters could be more effective due to additive gene action. Pod yield per plant correlated significant positively with SP, SMK,

and kernel length to width ratio. Both DFI and DFF are correlated significant negatively with pod yield per plant (Zongo *et al.*, 2017).

Identification of trait specific germplasm and successful introgression of trait is the key activity for summer groundnut crop improvement. Genotypes NRCG 14507, NRCG CS 254, NRCG CS 313 and Girnar 1 showed early flowering initiation (35 DAS). SLA was lowest (<150) in genotypes *viz.*, NRCG 17284, SG 99, Gangapuri, ICGS 9114, VRI3 and ICGS 76. Genotypes

viz., JGN3, NRCG CS 62, TMV9, ICGS 76, NRCG 8763 showed higher shelling per centage (>70%).

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Evaluation, characterization and confirmation of hybrids derived from diverse CMS sources in sunflower (*Helianthus annuus* L.)

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ABSTRACT

The research was conducted at University of Agricultural Sciences, Dharwad, during 2016-2018 to evaluate hybrids derived from diverse CMS sources (CMS PET 1, CMS PEF and CMS-I). Among the hybrids evaluated, FMS852A× RHA6D1 recorded 98% fertility restoration with on par performance of seed yield per plant (63.17 g/plant), oil content (38.48 %) and linoleic acid (65.69 %) with the check KBSH53. The parental lines and hybrids were characterized according to PPV&FRA guidelines. The hybrids were confirmed by ORS312, ORS484, ORS460, ORS3640, ORS934, HA4011, ORS1065, ORS349, ORS309 and ORS316 SSR markers.

Keywords: *Helianthus petiolaris*, *Helianthus annuus* sp. *lenticularis*, *heterosis*, CMS

Commercial exploitation of heterosis for seed yield and oil content in sunflower during the last two decades has narrowed down the genetic variability of CMS (Petiolaris base) and restorer lines resulting in yield plateau of hybrids, besides making them vulnerable to pest and diseases. Hence, diversification is needed and the hybrids resulting from new diverse CMS sources pose problem of fertility restoration which needs to be examined and evaluated.

The experimental material comprised of eight CMS lines derived from three diverse CMS sources i.e. CMS PET 1 (*Helianthus petiolaris*) - CMS335A, CMS711A, CMS851A, CMS234A, CMS607A; CMS PEF (*Helianthus petiolaris* sp. *fallax*) - FMS852A, FMS407A and CMS-I (*Helianthus annuus* sp. *lenticularis*) - IMS850A; eight restorer lines - NS8, NS15, NS19, RHA95C1, RHA6D1, RHAIV77, R-59, DSR-35; and eleven hybrids *viz.*, FMS407A × RHA6D1, FMS407A × RHA95C1, FMS407A × NS19, FMS407A × NS8, FMS852A × RHA6D1, IMS850A × NS8, CMS711A × DSR35, CMS851A × NS15, CMS607A × R59 including checks *viz.*, DSFH 3 and KBSH 53. These were characterized according to PPV&FRA descriptors. For molecular hybridity confirmation, DNA was isolated according to Solodenko and Sivolap (2005) procedure by CTAB method. Oil content was estimated using NMR and fatty acid composition by gas chromatography.

Among the 11 hybrids evaluated, FMS852A× RHA6D1 recorded 98% fertility restoration with on a par performance of seed yield/plant (63.17 g/plant), oil content (38.48%), linoleic acid (65.69%) and less number of days (66 days) to 50 % flowering compared to check KBSH53 (100%, 62.15 g/plant, 39.03%, 25.02% and 68 days, respectively). Morphological characterization showed that all the genotypes exhibited cordate leaf shape, rounded bract shape and convex type of head. Pollen colour was yellow in all the genotypes but white in NS8. The hybrids from fallax CMS source were confirmed by SSR markers ORS312, ORS484, ORS460, ORS3640 and ORS934 while hybrids from lenticularis CMS source were identified by ORS312. The petiolaris source hybrids were confirmed by HA4011, ORS1065, ORS349, ORS309 and ORS316 SSR markers.

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