

and 5.65 g. grain yield/plant, produced by their respective increasing parents. They yielded 46.6 and 40.2 (Cross 1), 30.3 and 28.3 (Cross 2) and 28.1 and 38.0 (Cross 3) per cent more grain yield than their respective increasing parents, in B_1F_2 and B_2F_2 generations, respectively. Simultaneous transgressive segregants were also observed in B_1F_2 and B_2F_2 generations of three crosses for grain yield along with other 2 to 3 characters, more frequent with clusters/plant, pod length, 100-seed weight and seeds /pod. Out of the total transgressive segregants in B_1F_2 generation of C_2 , 2.50% were simultaneously transgressives for grain yield with other three characters, followed by 1.66% in both B_1F_2 and B_2F_2 generations of cross 1 and 3. There were nine characters combination in which 2.50% transgressive segregants transgressed grain yield simultaneously with clusters/plant, pod length and seeds/pod in B_1F_2 of C_2 and 1.66 % in both B_1F_2 and B_2F_2 generations of cross 2 and 3. This simultaneous transgressive segregation indicated that, clusters /plant, pods/plant, 100-seeds weight and seeds/pod were the important yield contributing characters. The transgressive segregants for grain yield were also found to be simultaneously transgressives for above traits, indicating their dependency on each other or there may be linkage drag among the genes of these traits. This kind of dependency or desirable linkage drag has great importance in plant breeding for simultaneous improvement. These transgressive segregants are under testing and they are in F_4 generation.

1.4 Genetics of resistance to aphid (*Uroleucon compositae*) in safflower

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Aphid is an important insect pest of safflower in India. An average of 37% yield loss has been reported throughout India by aphid infestation on safflower. Resistant cultivars are the best option for management of aphid problem in safflower cultivation. Excellent sources of resistance to aphid (A-1 and EC-523368-2) have been identified in safflower germplasm collection at ICAR-IIOR, Hyderabad. Genetic characterization of these germplasm sources would help to identify resistance genes and further breeding this resistance into improved high yielding cultivar backgrounds to realize higher productivity. Two F_3 populations of the crosses: CO-1 (susceptible) x A-1 (102 families) and CO-1 x EC-523368-2 (117 families) were screened (20 plants/family) against aphid during *rabiseason* 2014-15. A modified field screening method was used, wherein aphids were cultured on a susceptible variety (CO-1) and artificially released onto test plants at stem elongation stage (~45 days after sowing) to ensure adequate and uniform pest build up under field conditions. Scoring of resistance or susceptibility was done based on plant survival. Observed segregation of plant's reaction to aphid in CO-1 x A-1 F_3 population was 42 (Susceptible): 51 (Segregating): 9 (Resistant) (Mendelian ratio of F_3 population: 7:8:1,



$\chi^2=1.7$, significance value=5.991 at $P=0.05$ at 2 df) and in CO-1 x EC-523368-2 F_3 population was 48 (Susceptible):60 (Segregating):9 (Resistant) (7:8:1, $\chi^2=0.765$). The inheritance results suggested the possibility of two genes in recessive condition [Mendelian ratio of F_3 population 15(Susceptible):1(Resistant)] ($\chi^2=2.4$; significance value=3.841 at $P=0.05$ at 1 df) are involved in resistance against aphid in A-1 and EC-523368-2. Recombinant inbred line (RIL) populations have been developed from these crosses to map the genetic loci conferring aphid resistance. Currently, a subset of 153 F_5 -RILs of CO-1 x A-1 cross and 235 F_5 -RILs of CO-1 x EC-523368-2 cross are under aphid screening trial. Efforts are underway to establish molecular breeding programme for aphid resistance in safflower.

1.5. Study of genetic divergence in linseed (*Linum usitatissimum* L.)

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Fifty three genotypes were evaluated for genetic divergence to identify potential parents for linseed breeding programme in *rabi*2014 at College of Agriculture, Nagpur. Mahalanobis D^2 statistics for eight characters viz., days to 50% flowering, days to maturity, plant height, number of branches plant⁻¹, number of capsules plant⁻¹, harvest index, seed yield plant⁻¹ and 1000 seed weight were used in this study for computing genetic divergence. The analysis of dispersion for eight correlated variables using Wilk's criterion, revealed highly significant difference between genotypes for all the eight characters. The fifty three genotypes were grouped into eight clusters by Tocher's method. The maximum inter cluster distance was recorded between cluster III and VIII (133.95) where as minimum inter cluster distance was found between cluster IV and VI (15.24). The canonical analysis revealed that differentiation for eight characters among fifty three genotypes was completed in five phases indicating the importance of days to 50% flowering, number of branches plant⁻¹, number of capsules plant⁻¹ and seed yield plant⁻¹ for selecting parents. The canonical analysis and cluster means study revealed the importance of number of branches plant⁻¹, number of capsules plant⁻¹ and seed yield plant⁻¹ as contributors to the total divergence. The genotypes belonging to distant clusters, exhibiting high number of branches plant⁻¹, high number of capsules plant⁻¹ and seed yield plant⁻¹ were considered as criteria for selecting potential parents for hybridization programme. According to this criteria 33 parents were identified for their exploitation in linseed breeding programme by executing crossing in three sets i.e. (i) Flax-16, EC-41628, Gewargi-1-2 and T-397 to be crossed with EI-5613, ES-1456, Ex-79-59, JLS-9 and ES-1531, (ii) EC-1066, EC-1386 and EC-98994 to be crossed with ES-1462, EI-5613, Ex-79-59, JLS-9 and ES-1531 and (iii) ES-1456, ES-15888, GLC-1-1, GS-111, GS-51, NL-97, EX-3, GIF-White, Ezox-Natural, EX-28-6, EC-411539, Eita, GS-61, FRW-12, FR-11, GS-85, CI-2260, FR-15, EX-2339-6, PKVNL-260, GS-129 to be crossed with EI-5613 and Ex-79-5.

