

the smaller ear size. The highest number of days (145 days) were taken by the BL-914 to mature where as lowest (135) by BL-937. Similarly the genotypes differed significantly with respect to days taken to reach at heading stage. It was observed that the BL-937 took least number of days (92 days) to reach at heading stage as compared to BL-953 which took the maximum number of days (102 days) to reach the same stage (Table1).

Relationship of different weather parameters with yield and LAI of Barley:

The response functions developed between leaf area index, yield with agrometeorological indices such as heat use efficiency (HUE, kg/day °C), IPAR (imole/cm²/s) and has been presented in Table 3. The heat use efficiency explained the variability in LAI upto 77 percent where as a linear function of LAI with intercepted PAR explained the variability to the extent of 70 percent. A linear response between the yield and HUE, IPAR explained the variability in yield upto 88 and 84 per cent respectively indicating a direct relationship between the heat unit and light interception with yield. There was strong relationship between yield and LAI also which has been reflected by R² value of 0.87. Kumar *et al.* [2] also studied the relationship between yield, LAI and various agrometeorological indices. Mani *et al* studied [3] the effect of sowing dates on physiological parameters of barley. They observed highest values of net photosynthesis and intercellular CO₂ concentration the crop sown on 10th November as compared to 30th October and 20th November sown crops.

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Magnitude of combining ability for seed yield and oil content in sunflower (*Helianthus annuus* L.)

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Abstract

The additive components of genetic variance played the main role in the inheritance of oil content, which was confirmed by below one GCA/SCA ratio. The main role in the inheritance of seed yield was played by the non additive gene effects. The lines CMS 67A, CMS234A and P145R having highly significant gca effects for both seed yield and oil content should be used in future hybrid breeding programme to develop productive hybrids w.r.t. oil and seed yield.

Key words: Sunflower, combining ability, heterosis, gene effects and oil content

The sunflower (*Helianthus annuus* L.) is the fourth important oilseed crop after soybean, oil palm and rapeseed mustard. Hybrids are preferred by sunflower growers in many countries in the world due to high yield performance, uniformity, quality, etc. In systematic breeding program, it is essential to identify superior parents for hybridization and crosses to expand the genetic variability for selection of superior genotypes [1]. One crucial step in hybrid development is testing of inbred lines for their GCA. The line × tester analysis is one of the efficient methods of evaluating a larger number of inbreds as well as providing information on the relative importance of general

combining ability and specific combining ability effects for interpreting the genetic basis of important plant traits. Based on the combining ability analysis of different characters, higher SCA values refer to dominant gene effects and higher GCA effects indicate a greater role of additive gene effects controlling these characters. The present study was undertaken with the objective to find good combining parental lines for seed yield and oil content and identifying promising F_1 hybrid combinations for these traits.

A set of forty hybrids was developed by crossing 5 cytoplasmic male sterile (*cms*) lines (11-A, 47-A, 67-A, 68-A and 234-A) with eight restorer lines (95-C-1, P 93-R, P103-R P124-R, P134-R, P145-R, P-147-R and RCR8297) in a line \times tester fashion. During spring 2014 these synthesized hybrids along with parents were sown in the fields of the experimental area of Oilseed section, Department of Plant Breeding and Genetics, PAU, Ludhiana. These genotypes were planted in randomized complete block design with three replications in a plot size of 0.6 \times 3.0 m². Seed yield was measured from ten random plants separately for each replication. Their representative seed sample of all the genotypes was used for oil content estimation using NMR. The mean values of the inbred lines and F_1 hybrids were used for the combining ability studies for achene yield and oil content [2].

The significant mean sum of squares for female and male lines on one side and their F_1 hybrids on the other indicated presence of genetic differences among the parents and hybrids for seed yield and oil content. GCA of inbred lines, SCA of hybrids and their interactions were significant for seed yield and oil content. Magnitude of GCA of parents was higher than SCA of hybrids for oil content while for seed yield the SCA variances were more than the GCA variances. This indicated importance of additive gene effects for oil content and non-additive gene effects for seed yield. Further supporting this conclusion was the fact that the *gca/sca* ratio for oil content found in F_1 generation was more than one (1.97), while for seed yield this ratio was less than one (0.16) (Table 2). Highly significant positive GCA effects were recorded for seed yield and oil content with respect to CMS 67A, CMS 234A and P145R which were considered as good combiners for these traits (Table 1). However the lines CMS11A and 95C-1 were recorded as poor combiners for both seed yield and oil content.

Hybrid combinations *viz.*, CMS-11A \times P93R(1.46**), CMS-11A \times P103R(2.44**), CMS-11A \times P167R(1.24*) and CMS-68A \times P134R(1.75*) recorded highly significant positive SCA values for oil content. CMS-234A \times P145R(15.43**), CMS-68 \times P145R(11.01**), CMS-11A \times P93R(11.27**), were identified as having significant *sca* effects for seed yield.

Table 1. GCA values of parental lines

S.No.	Lines	Seed yield (g/plant)	OC(%)
1	CMS-11A	-6.21**	-3.79**
2	CMS-47A	-0.48	0.29
3	CMS-67A	6.98**	1.25**
4	CMS-68A	-4.6**	0.94**
5	CMS-234A	4.31**	1.31**
6	95-C-1	-2.97*	-2.97*
7	P 93 R	0.25	0.25
8	P 103 R	0.09	0.09
9	P 124 R	-1.01	-1.01
10	P 134 R	-0.58	-0.58
11	P 145 R	3.31**	3.31**
12	P 167 R	0.65	0.65
13	RCR 8297	0.26	0.26
SE GCA/lines		0.933	0.212
SE (GCA _i - GCA _j)/lines		1.469	0.335
SE GCA/testers		1.234	0.280
SE (GCA _i - GCA _j)/testers		1.866	0.424

Table 2. Components of genetic variance for seed yield and oil content

Component	Seed yield	Oil content
GCA	9.99	2.68
F = 0 V _A	39.96	10.72
F = 1 V _A	19.98	5.36
F = 0 V _D /V _A	0.61	1.98
F = 1 V _D /V _A	0.33	3.94
SCA	61.33	1.36
F = 0 V _D	245.32	5.44
F = 1 V _D	61.32	1.36
GCA/SCA	0.16	1.97

The main role in the inheritance was played by the additive component of genetic variance as shown by analysis of variance for combining ability and analysis of genetic variance components. Parameswari *et al.* [3] and Dhillon *et al.* [4] have also reported the importance of additive gene effects in the inheritance of oil content.

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Genetic variability in chickpea (*Cicer arietinum* L.)

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Abstract

Present study revealed significant genetic variability for all the morphological, maturity, yield, yield components and quality traits. Positive correlation of seed yield with number of primary branches, pods plant⁻¹, seeds pod⁻¹ reveals selection in these traits to be effective in increasing yield proportionately. Also direct effect of pods plant⁻¹ and seeds pod⁻¹ on seed yield suggest that an increase in these traits will increase yield significantly. The promising lines may be involved in hybridization programmes using exotic germplasm to widen their genetic base for further improvement and identification of superior varieties of chickpea suitable for Kashmir region.

Key words: Genetic variability, correlation coefficient, harvest index, yield

Pulses are an important crop for food security worldwide and for the livelihood of millions of people, especially in the developing countries. The newly emerging health consciousness among the people is creating a genuine need for adopting nutritionally complete vegetarian diet involving legumes as a component. Chickpea (*Cicer arietinum* L.) or Bengal gram belonging to the genus *Cicer* of the family *Leguminaceae* with chromosome number (2n=16). It is an important *rabi* pulse crop in India. India grows chickpea on about 8.75 million hectare and production of about 8.25 million tonnes with an average productivity of 9.43 kg ha⁻¹ [1]. Presence of genetic variability is of utmost importance for any breeding programme and for that reason plant breeders have emphasised the evaluation and characterization of germplasm for the improvement of crop yield. Interrelationship among direct and indirect effect of component characters of yield is important in predicting the correlated response to direct selection and in the detection of traits with much effect as markers. The present study was undertaken to elucidate the association between yield and its attributes in chickpea.

The experimental material for the present study comprised of 70 genotypes of chickpea. Out of seventy accessions, 50 were received from ICARDA and 20 genotypes were from ICRISAT. The experimental trail was laid out in randomised block design with three replications during *rabi* 2010-11 at Pulses Research Station, Habak, Shalimar (34°15' N latitude and 74°84' E longitude) at 1524 m above mean sea level. Each experimental