STUDY OF GENETIC VARIABILITY FOR YIELD AND QUALITY PARAMETERS IN NEWLY DEVELOPED SUNFLOWER (*Helianthus annuus* L.) INTERSPECIFIC DERIVATIVES OVER TWO SEASONS

ABSTRACT

The present investigation was carried out to study genetic parameters for sixteen characters *viz.*, days to 50% flowering, days to maturity, plant height, head diameter, leaf length, leaf width, number of leaves per plant, 100 seed weight, volume weight, seed yield/plant, seed length, seed width, stem girth, leaf area index, chlorophyll content and oil content at ICAR-Indian Institute of Oilseeds Research during *kharif*-2022 and *rabi*-2022-23, respectively. The study included a total of 50 advanced (BC_2F_6) interspecific derivatives derived using five diploid annual compatible *Helianthus* species along with three checks (ARM-243B, DRSF-108 and DRSF-113). Analysis of variance revealed significant differences for all the traits. High variation was observed for plant height and seed yield/plant and lowest was observed for 100 seed weight, oil content and head diameter. The difference between GCV and PCV was low for all the characters indicating less influence of environmental factors on the expression of these traits. High heritability coupled with high genetic advance in percent of mean was observed for plant height, leaf width, number of leaves/plant, volume weight, 100 seed weight, stem girth, leaf area index and chlorophyll content 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 days to maturity and oil content suggesting involvement of non-additive gene action in the expression of these traits indicating little scope for further improvement through individual plant selection. The results indicated that experimental material taken into consideration had sufficient amount of genetic variability which can be utilized further in crop improvement programme.

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Keywords: Genetic advance, GCV, *Helianthus annuus*, Heritability, PCV

1. Introduction

Sunflower (*Helianthus annuus* L.; 2n = 34) is the fourth most important oilseed crop in the world following soyabean, peanut and rapeseed [23,31]. It belongs to the genus *Helianthus*, family Asteraceae, tribe Heliantheae, sub tribe Helianthae, which includes 20 genera with 400 sub-species and originated in

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the USA [7]. It has recorded a production of 2.28 lakh tonnes from 2.25 lakh ha with the productivity of 1011 kg/ha according to the Directorate of Economics & Statistics [3]. It is a rich source of edible oil (40–45%) and because of the high concentration of polyunsaturated fatty acids with 55 to 60% of linoleic acid and 25 to 30% of oleic acid, which reduces the risk of coronary diseases by reducing blood cholesterol levels [9]. The requirement of high yield and quality edible oil is raising day by day and therefore, there is a need to increase the area, production and productivity of the crop which is possible through crop improvement strategies [21]. Developing genotypes with higher yield and oil content has become the ultimate objective of current sunflower breeding programmes. The seed yield of sunflower is a complex trait, which is highly influenced by the environmental variations due to narrow genetic base, while the production of superior hybrids which yield more for seed yield and oil content would become a great lacuna in the present scenario. These traits can be improved by finding a suitable source for higher yield among the vast germplasm of sunflower and making efforts to incorporate the variability into the cultivated sunflower. The success of a crop improvement programme depends on the extent and nature of available genetic variability, heritable variation and genetic advance present within the breeding population [29]. Greater the variability, more is the possibility of getting the desired plant genotypes. However, plant breeding efforts to develop varieties/hybrids with the desired economic characteristics are constrained by the narrow genetic base of the cultivated sunflower. Utilizing these crop wild relatives, numerous breeding efforts are made to create and characterize prebred lines, which are developed by crossing cultivated sunflower with various wild relatives followed by backcrossing for several generations, that can serve as a source of desirable compositions of different agro-morphological characters that have positive influence on the seed and oil yield. For effective germplasm utilization, prior knowledge of genetic variation and genetic interactions among newly developed interspecific derivatives is essential. 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 genetic worth of the genotypes i.e., based on heritability and genetic advance [8]. Information on variability and heritability is useful to formulate selection criteria for improvement of seed yield and its component traits. So, taking all these aspects into consideration, the present study was conducted to evaluate the extent of genetic variability, heritability and genetic advance over mean for seed yield and its component traits in advanced sunflower interspecific derivatives for sixteen traits.

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2. Materials and Methods

2.1 Materials used for study: The present investigation was carried out during *kharif*-2022 and *rabi*-2021-22 at ICAR-Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad located at a latitude of 17^{o}22’31’’N and longitude 78^{o}28’27’’E. Study material consisted of 50 advanced (BC_2F_6) interspecific derivatives derived using *Helianthus annuus* (wild), *H. debilis, H. praecox, H, petiolaris* and *H. argophyllus* as male parent and cultivated sunflower inbred ARM-243B as recurrent parent. The details of material are presented in Table 1.

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2.2 Experimental design: Each genotype along with three checks *viz.,* ARM-243B, DRSF-108 and DRSF-113 was sown in two rows each of 3.0 m length following a spacing of 60 cm between the rows and 30 cm between the plants in augmented block design (ABD) in five blocks. All the recommended crop production and protection practices were followed to raise the healthy crop successfully. At physiological maturity five plants from each accession were selected randomly for recording data on days to 50% flowering, days to maturity, plant height (cm), number of leaves per plant, leaf length (cm), leaf width (cm), leaf area index, chlorophyll content, head diameter (cm), stem girth (cm), 100 seed weight (g), volume weight (g/100 ml), seed yield/plant (g), seed length (cm), seed with (cm) and oil content (%). The traits days to 50% flowering and days to maturity were recorded on a plot basis. SPAD chlorophyll meter reading was recorded at the time of anthesis with SPAD 502 plus meter for upper, middle and lower leaves and average of them was noted. Leaf area index was calculated by taking fully opened five leaves from each plant at anthesis and the area was measured by leaf area meter (LI-3000, Lincoln Nebraska, USA) and was calculated as per the method suggested by Watson [30]. Mean performance of the genotypes were calculated and the genotypic coefficient (GCV) and phenotypic coefficient of variation (PCV) was estimated by using the formula given by Burton [2]. The estimates of PCV and GCV were classified as low (0-10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Madhavamenon [24]. Heritability in broad sense (h^2b) was estimated according to the formula suggested by Johnson *et al.,* [8] and Hanson *et al.,* [6]. Estimation of genetic advance was done following the formula given by Johnson *et al.,* [8] and Allard [1].

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Table 1. List of the genotypes selected for the present investigation

S. No.	Derived from	Generation	Interspecific derivatives
1	*H. annuus* (wild)	BC_2F_6	PB-950, PB-954, PB-1007, PB-1010, PB-1015, PB-1027, PB-1054, PB-1203, PB-1209, PB-1213
2	*H. debilis*	BC_2F_6	PB-884, PB-893, PB-895, PB-896, PB-910, PB-1136, PB-1139, PB-1148, PB-1162, PB-1170
3	*H. praecox*	BC_2F_6	PB-1090, PB-1093, PB-1104, PB-1113, PB-1116, PB-1117, PB-1120, PB-1122, PB-1126, PB-1215
4	*H. argophyllus*	BC_2F_6	PB-1338, PB-1340, PB-1359, PB-1369, PB-1371, PB-1372, PB-1392, PB-1398, PB-1400, PB-1401
5	*H. petiolaris*	BC_2F_6	PB-1575, PB-1576, PB-1577, PB-1579, PB-1580, PB-1581, PB-1582, PB-1583, PB-1588, PB-1589
6	Cultivated sunflower	-	ARM-243B, DRSF-108, DRSF-113

3. Results and Discussion

3.1 Analysis of variance: Selection is a prime requisite for the crop improvement programme and it is dependent on the extent of genetic variability present in the breeding material. The analysis of variance revealed significant difference among the genotypes which validated further on the basis of genetic and statistical analysis of the data. The analysis of variance (p value at 1 and 5%) of 16 characters included in the present study revealed that the mean sum of squares due to treatments were found to be highly significant (P=0.01) for all the characters except for the trait number of leaves in *kharif* and seed length and seed width in *rabi* indicating sufficient amount of variation present in the material utilised. Whereas, variation was significant (P=0.05) for rest of the characters. The results pertaining to analysis of variance are presented in Table 2. These finding thus indicate that there is a remarkable amount of variability present in the advanced interspecific derivatives of sunflower. Which denotes that there is large scope for selecting superior breeding material among the accessions under the current study. Similar significance for all the traits under study was reported by Reena *et al.* [18].

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3.2 Variability and heritability: Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop [19]. The assessment of heritability and variation through phenotypic coefficient of variation (PCV), Genotypic coefficient of variation (GCV) and genetic advance as percent of mean (GAM) is important to understand the heritable and non-heritable components of the total variability, which in turn aids to identify the suitable breeding method for improving a particular trait of interest. Wide range of variation was observed for plant height (75.0-162.0 cm and 99.7-161.7 cm, respectively) followed by stem girth (10.4-32.8 cm and 11.5-22.3 cm, respectively) and lowest for seed length (0.67-1.2 cm and 0.75-1.25 cm, respectively) followed by seed width (0.22-0.62 cm). Sandhya Sree *et al.* [21], Sutur *et al.* [28] and Reena *et al.* [19] were reported highest variation for plant height, Supriya *et al.* [26] and Latha *et al.* [12] for seed yield. It can be observed from the results that all the characters showed closer values of PCV and GCV (Table 3). PCV is higher than GCV for all the traits in both the seasons, which revealed that the role of the environmental factors on all the characters, but the magnitude can be stated to be low, as the difference between PCV and GCV is very low, except for plant height in *rabi*, which showed equal estimates of PCV and GCV which indicates that there is least influence of environment on the expression of this trait. This was found to be similar to the findings of the study undertaken by Sandhya Sree *et al.* [21], except for plant height in *rabi*. Sivasubramanian and Madhavamenon [24] classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (>20%) values. According to this classification, high PCV and GCV values were observed for volume weight, 100 seed weight and leaf area index in both the seasons. High PCV and GCV value for 100 seed weight was also reported by Seneviratne *et al.* [22]. The traits plant height, leaf width, number of leaves, head diameter and chlorophyll content exhibited moderate PCV and GCV values in both the seasons whereas characters like days to 50% flowering, days to maturity and oil content exhibited low PCV and GCV values in both the seasons. The expression of low coefficients of variation for these traits indicates that there was low amount variation in the material evaluated, which requires search for variation in other material [12] or also due to presence of both positive and negative alleles for those in the population [16]. Seed yield showed medium PCV and GCV in *kharif* (15.26% and 15.20%), where it was observed to be high PCV and GCV in *rabi* (25.21% and 25.16%). Stem girth showed high PCV and GCV in *kharif* (22.91% and 22.89%) but medium PCV and GCV in *rabi* (10.52% and 10.24%). Moderate PCV for head diameter by Reena *et al.* [19] and moderate GCV for plant height, head diameter and 100 seed weight by Kumar *et al.* [11] and Neelima *et al.* [16]. Further, low PCV for the characters volume weight, days to 50% flowering, days to maturity and oil content was also reported by Kalukhe *et al.* [10] and Makane *et al.* [14].

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Robinson *et al.* [20] classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Falconer and Mackay [4] classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (>20%). The estimates of heritability ranged from 25.0% for days to maturity to 94.0% for leaf are index during *kharif*-2022 and 32.0% for days to maturity to 92.0% for leaf

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area index during *rabi*-2022-23 whereas, genetic advance as percentage of mean ranged from 8.1% for days to maturity to 57.0% for leaf area index during *kharif*-2022 and 5.9% for days to maturity to 57.6% for leaf area index during *rabi*-2022-23. Estimates of heritability and genetic advance as percent of mean (GAM) are essential selection parameters. The estimate of genetic advance is more useful as a selection tool when coupled with heritability estimates [8]. Heritability coupled with genetic advance will help to predict the genetic gain under selection there by also gives information on the suitable breeding method for improving a trait. High heritability coupled with high genetic advance as percent of mean was noticed for plant height, leaf width, number of leaves, volume weight, seed width, stem girth, leaf area index and chlorophyll content in both the seasons indicating that these characters are governed by additive gene action. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. Sonu Kumar *et al.,* [25] recorded high heritability coupled with high genetic advance for days to 50% flowering, days to maturity, plant height etc. High heritability and genetic advance noted for leaf area index, plant height, specific leaf area, the number of leaves per plant, oil yield, seed set per cent, seed yield, 100 seed weight, the number of seeds per head, head diameter and autogamy per cent by Varalakshmi *et al.,* [28]. High values of phenotypic and genotypic coefficient of variability, and high heritability with high genetic advance were observed for seed yield/plant, oil yield/plant. plant height, head diameter, oil content and test weight by Mohan and Seetharam [15]. High heritability coupled with medium genetic advance as percent of mean was observed for days to 50% flowering in both the seasons indicating involvement of both additive and non-additive gene action in the inheritance of these traits and population improvement by reciprocal recurrent selection can be useful. On the contrary high heritability with low GAM was found for days to maturity and oil content in both *kharif* and *rabi* seasons indicating that the role of favourable environment rather than the genotype and the selection is not rewarding. Madhavi Latha *et al.* [13] for days to 50% flowering, days to maturity and plant height and Supriya *et al.* [26] for days to 50% flowering. Medium heritability with high GAM was found for the trait seed length and seed yield/plant in both the seasons. For the trait leaf length medium heritability and GAM was observed in *kharif* whereas medium heritability with high GAM was found in *rabi* indicating that leaf length cannot be improved through selection. Head diameter showed low heritability with high GAM in *kharif* but medium heritability and GAM in *rabi.* 100 seed weight showed high heritability with medium GAM in *kharif* but medium heritability and GAM in *rabi*. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various quantitative characters.

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Table 2. Analysis of variance for different characters in sunflower interspecific derivatives over two seasons

S. No.	Characters	Mean squares					
		Blocks (df: 4)		Genotypes (df: 52)		Error (df: 8)	
		***Kharif*-2022**	***Rabi*-2022-23**	***Kharif*-2022**	***Rabi*-2022-23**	***Kharif*-2022**	***Rabi*-2022-23**
1	Days to 50% flowering	90.25**	68.13**	17.93**	12.14**	2.28	0.40
2	Days to maturity	58.21**	66.23**	21.57**	19.88*	0.53	3.97
3	Plant height	746.96**	257.35**	353.95**	215.77**	3.11	0.12
4	Leaf length	14.5**	20.72**	3.47**	4.77**	0.68	0.48
5	Leaf width	22.51**	18.24**	4.34**	4.83**	0.17	0.15
6	Number of leaves	206.44**	115.56**	28.27*	21.17**	6.18	0.73
7	Head diameter	1.27**	0.54**	5.64**	3.07**	0.08	0.06
8	Volume weight	90.16**	715.81**	87.55**	44.14**	0.57	0.05
9	Hundred seed weight	1.12**	1.08**	0.74**	1.28**	0.04	0.03
10	Seed length	0.01*	0.01	0.02**	0.01*	0.00	0.0
11	Seed width	0.01**	0.01*	0.01**	0.01*	0.00	0.00
12	Seed yield	2.74**	29.41**	7.54**	44.75**	0.07	0.18
13	Stem girth	46.47**	1.36**	184.2**	3.57**	0.03	0.16
14	Leaf area index	5.25**	3.34**	0.87**	0.97**	0.06	0.07
15	Chlorophyll content	37.73**	11.85**	11.20**	17.19**	1.43	0.13
16	Oil content (%)	4.88**	18.87**	2.95**	2.00**	0.04	0.03

* P <= 0.05; ** P <= 0.01

Table 3. Mean, range, coefficient of variation, heritability (broad sense) and genetic advance as per cent of mean for different characters in advanced interspecific derivatives of sunflower over two seasons

Character	Mean		Range		Coefficient of variation				Heritability (%)		Genetic advance as percent of mean	
					PCV (%)		GCV ((%)					
	Kharif	*Rabi*	*Kharif*	*Rabi*	*Kharif*	*Rabi*	*Kharif*	*Rabi*	*Kharif*	*Rabi*	*Kharif*	*Rabi*
DFF	63.35	63.33	51.13-71.80	56.13-71.8	7.02	6.29	6.60	6.21	86.0	92.0	11.4	11.4
DM	96.63	98.70	84.40-107.07	90.00-106.33	4.52	4.23	4.46	3.72	76.0	74.0	8.1	5.9
PH	128.63	132.12	75.02-162.08	99.78-161.71	15.89	11.60	15.83	11.60	69.0	76.0	29.3	21.5
LL	19.81	19.85	14.77-26.02	13.45-24.88	10.57	12.72	9.72	12.23	51.0	59.0	16.4	21.8
LW	17.18	17.41	11.64-22.14	10.36-22.14	13.95	14.12	13.74	13.95	66.0	82.0	25.2	25.7
NL	34.46	33.62	26.87-56.53	26.53-53.87	19.51	16.64	18.13	16.44	81.0	72.0	30.8	30.1
HD	13.13	12.72	9.98-16.77	10.35-18.41	17.11	11.84	16.97	11.69	25.0	32.0	43.3	18.5
VW	36.98	40.44	24.31-51.05	19.64-58.55	22.87	24.55	22.78	24.54	83.0	77.0	31.4	21.6
HW	3.77	4.42	2.40-5.59	2.36-7.26	22.52	23.23	21.87	22.87	69.0	57.0	18.1	11.7
SL	0.96	1.01	0.67-1.24	0.75-1.25	11.99	10.54	10.87	8.28	52.0	59.0	31.6	27.9
SW	0.43	0.43	0.22-0.62	0.22-0.62	19.85	21.03	18.44	17.99	69.0	71.0	42.8	45.7
SY	18.47	26.10	14.95-24.71	12.80-49.49	15.26	25.21	15.20	25.16	49.0	51.0	39.7	42.3
SG	17.38	16.65	10.04-32.88	11.55-22.35	22.91	10.52	22.89	10.24	88.0	76.0	28.2	46.3
LAI	3.52	3.40	1.63-6.25	1.68-6.39	32.25	32.76	31.52	31.87	94.0	89.0	57.0	57.6
CC	31.87	36.18	27.45-44.28	29.56-46.76	10.79	11.18	10.14	11.13	67.0	76.0	29.8	20.7
O	34.97	36.70	31.90-38.06	31.21-39.87	4.90	5.17	4.87	5.15	75.0	79.0	8.9	9.5

DFF: Days to 50% flowering, DM: Days to maturity, PH: Plant height, LL: Leaf length, LW: Leaf width, NL: No. of leaves, HD: Head diameter, VW: Volume weight, HW: 100 seed weight, SL: Seed length, SW: Seed width, SY: Seed yield, SG: Stem girth, LAI: Leaf area index, CC: Chlorophyll content, O: Oil content (%)

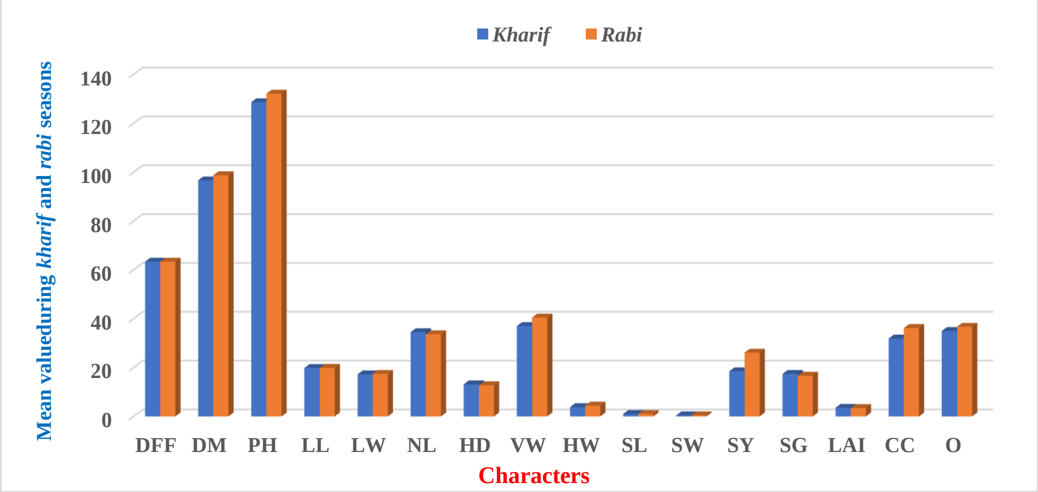

Figure 1. Mean value of different traits during *kharif*-2022 and *rabi*-2022-23 seasons

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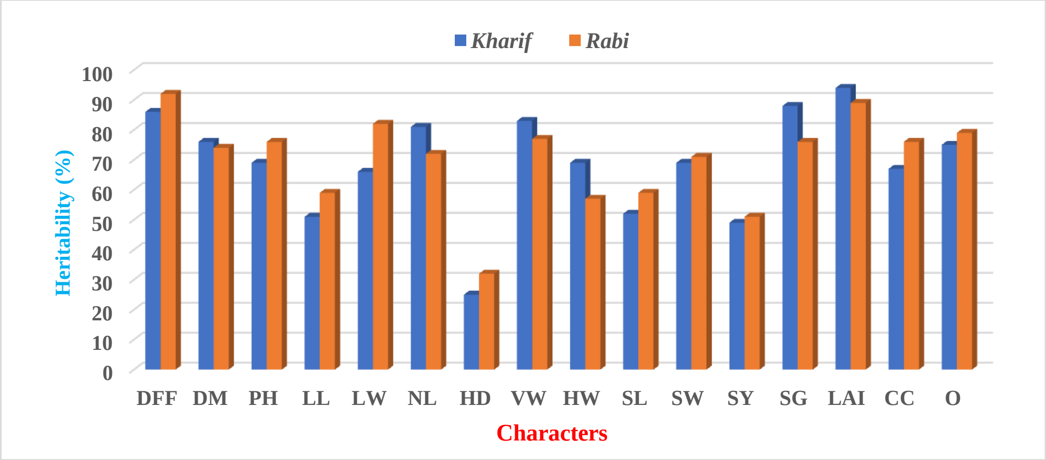

Figure 2. Heritability (%) of different traits during *kharif*-2022 and *rabi*-2022-23 seasons

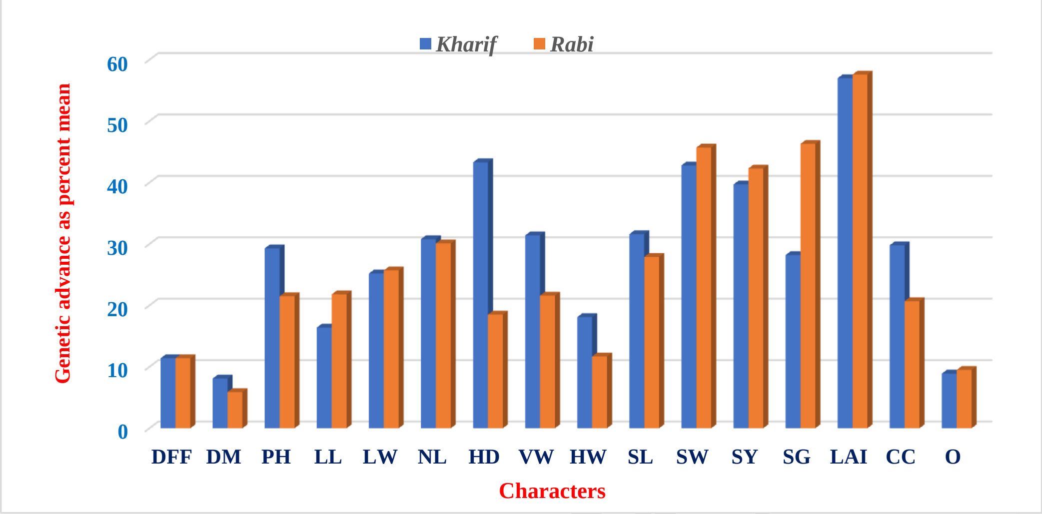

Figure 3. Genetic advance as percent of mean of different traits during *kharif*-2022 and *rabi*-2022-23 seasons

4. Conclusion

The analysis of various genetic parameters in the present investigation reveals higher values of GCV, PCV, heritability and genetic advance as per cent of mean for the traits *viz.*, leaf area index and volume weight. Hence the seed yield in segregating generations can be taken as a criteria for selection of a single plant and for promoting to next generation. Moderate values of PCV, GCV coupled with high heritability and genetic advance was recorded for plant height, leaf width, number of leaves per plant, 100 seed weight and chlorophyll content. Low values of GCV, PCV coupled with high heritability and low genetic advance for days to maturity and oil content.

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Comment [I27]: Please follow the journal's style in writing references and citations in the text.

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