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Research Article

Character association and identification of trait specific introgression in restorer lines of sunflower (*Helianthus annuus* L.)

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Abstract
The study was carried out involving 40 MAGIC crosses of sunflower restorer lines along with 10 parental checks during *rabi,* 2020 grown in augmented block design with four blocks at MARS, UAS Raichur with an objective of assessing variation and character association for yield attributing traits. The highest estimates of GCV, PCV, heritability and genetic advance as per cent of mean were recorded for seed yield per plant followed by 100-seed weight. Seed yield per plant recorded a highly significant positive association with plant height and head diameter. Path analysis studies indicated plant height had the highest positive direct effect on seed yield per plant followed by oil content. Trait specific introgression studies revealed that R-127-1 × RⅡ, CSFI-99 × RⅢ and No-30 × RⅣ showed the highest percentage (87.5%) of introgression with the expression of seven out of eight traits.

Keywords: MAGIC population, Sunflower, GCV, PCV, Heritability, Correlation co-efficient and path coefficients

INTRODUCTION

Sunflower (*Helianthus annuus* L.) is the second most important oilseed crop after soybean for its good quality oil and health benefits. In India, sunflower cultivation and development of CMS and R-lines for the exploitation of the heterosis phenomenon started over a year's however, the hybrids yield levels also plateaued because of a narrow genetic base. Hybrid performance mainly depends on the diversity in a genetic base of male sterile female parent and its restorer R line. Generally in a breeding programme introgression of character will be carried out from wild genotypes or land races, but here cultivated R lines are considered for introgression because all the 16 cultivated parental R lines have superiority in one or other character, so the final introgressed has line have all the superior character from diverse parental R lines which will increase the chances of getting heterotic hybrids. Hence, it is very much necessary to study the introgression of characters in progenies in the current study. To create high diversity, variability and broadening genetic base of the current R lines, the population developed from bi-parental crossing *viz*., F_2, backcross or recombinant inbred population are not enough because of having fewer recombinant events. So, presently multifounder equivalents of advance intercross called as Multiparent Advanced Generation Intercross population (MAGIC) was introduced by several generations of intercrossing among multiple founder lines leading to greater accumulation of recombination events (Scott *et al.,* 2020). The ultimate aim of every

breeding programme is to obtain a higher yield and it is a quantitative trait governed by poly genes and depends on other characters also. Hence, it is necessary to study the association of component traits on seed yield and its direct and indirect effects. In this direction, the present investigation was carried out to analyze correlation and path analysis co-efficient among yield and component traits. In the current study, 16 founder R lines were used to develop MAGIC population to broaden the genetic base of restorer lines.

MATERIALS AND METHODS
The experimental material consisted of 40 sunflower MAGIC crosses developed and evaluated at Main Agricultural Research Station, University of Agricultural Sciences, Raichur by using 16 Restorer lines along with ten parental checks *viz*., R-127-1, R-630, PM-81, RGM-49, RHA-97, RHA-93, No-30, No-15, CSFI-99 and CSFI-8002 grown in augmented block design with four blocks. The experiment was conducted during *rabi*, 2020 by following standard recommended agronomic practices and plant protection measures to raise a good crop.

The data was recorded on eight quantitative traits *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), head diameter (cm), 100 seed weight (g), volume weight (g/100 ml), seed yield per plant (g) and oil content (%) from five randomly selected plants in each entry. The averages were computed to represent cross/ lines mean. The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in a broad sense and genetic advance as a percentage of the population mean (GAM %) were estimated using standard procedure as described by Burton (1952) by using R statistical software. The PCV and GCV values were classified into three categories, *viz*., high (>20 %), moderate (10-20 %) and low (<10 %) values (Robinson *et al.,* 1949). Broad sense heritability was classified as low (<30 %), medium (30-60 %) and high

(>60 %). The genetic advance was also classified as low (0-10 %), moderate (10-20 %) and high (>20 %) (Johnson *et al*., 1955). Correlation co-efficient and standard path coefficients which are the standardized partial regression coefficients were analysed using a statistical INDOSTAT software package.

RESULTS AND DISCUSSION
In the case of MAGIC population, multiple parents were intercrossed in a definite pattern to get progenies which have transferred character from all the parents which have genetic variability for desired character. The significant variability for all the eight characters revealed the variability present in MAGIC crosses. However, trait specific variability was evaluated by estimating phenotypic and genotypic co-efficients of variation (GCV and PCV).

The yield component traits are quantitative in nature and the variability present in them is both heritable and non-heritable (Stuber and Edwards, 1987). Estimation of *per se* performance of phenotypic and genotypic co-efficients of variation, heritability in a broad sense and genetic advance as per cent of mean for yield and yield contributing characters is essential for variability study. Thus the calculated variability components of this study are presented in **Table 1**.

In the current study, high estimates of GCV and PCV were observed for seed yield per plant (55.28 and 55.92 %), 100-seed weight (31.96 and 34.14%) and head diameter (22.03 and 22.87%). Moderate estimates of GCV and PCV were observed for plant height (11.82 and 13.45%) suggesting that these traits can be improved through direct selection for restorer line development. Low estimates of GCV and PCV were observed for days to maturity (3.07 and PCV 3.39%) followed by volume weight (6.45 and 7.51%), days to 50 per cent flowering (6.7 and 7.03%) and oil content (7.02% and 7.26%) indicating to search for variation for these traits from other

Table 1. Estimation of mean, range and genetic parameters for yield and yield attributing traits in sunflower MAGIC crosses

Characters	Mean ± SE	Range		PCV%	GCV%	h² (BS) (%)	GAM (%)
		Minimum	Maximum				
Days to 50 per cent flowering	63.65 ± 0.62	57.15	71.85	07.03	06.70	90.97	13.19
Days to maturity	98.46 ± 0.48	91.48	104.98	03.39	03.07	82.26	05.75
Plant height (cm)	157.16 ± 3.82	100.50	199.9	13.45	11.82	77.16	21.41
Head diameter (cm)	17.20 ± 0.66	08.70	24.32	22.87	22.03	92.84	43.79
100-seed weight (g)	04.61 ± 0.23	01.60	07.91	34.14	31.96	87.63	61.72
Volume weight (g/100 ml)	39.12 ± 0.46	30.59	47.70	07.51	06.45	73.77	11.43
Seed yield per plant (g)	35.85 ± 3.13	03.78	96.90	55.92	55.28	97.74	112.75
Oil content (%)	35.72 ± 0.38	30.37	41.10	07.26	07.02	93.57	14.02

SE = Standard Error, GCV (%) = Genotypic Co-efficient of Variation, PCV (%)= Phenotypic Co-efficient of Variation,
h ²(bs) %= Broad Sense Heritability, GAM (%) = Genetic Advance Mean

breeding material. Similar results have been reported by Safavi *et al*. (2015), Supriya *et al*. (2017),Vikas (2015) and Supriya *et al*. (2016) with different levels of variability for different traits in Sunflower.

High heritability values with high genetic advance as per cent of mean were recorded for seed yield per plant (97.74 and 112.75%) followed by 100-seed weight (87.63 and 61.72%), head diameter (92.84 and 43.79%) and plant height (77.16 and21.41%) indicating additive genetic effect where, direct selection can be practised for improvement using these set of material. High heritability and moderate genetic advance as per cent mean were recorded for oil content (93.57 and 14.02%), days to 50 per cent flowering (90.97 and 13.19%) and volume weight (73.77 and 11.43%) suggesting these traits are governed by both additive and non-additive gene action and hence can be improved through population improvement breeding programmes for developing restorer lines in sunflower. High heritability and low genetic advance as per cent of mean were observed for days to maturity (82.26

and 5.75%) indicating the importance of environmental influence in the expression of these characters. The same sets of findings were reported by Supriya *et al*. (2016), Dudhe *et al*. (2017) and Basha (2020).

Correlation studies provide a better understanding of yield components which directly or indirectly contribute for yield, while selection for yield improvement (Robinson *et al*., 1949). The phenotypic correlation co-efficient of the eight component traits with seed yield and among themselves were calculated and represented in **Table 2**. Correlation studies on seed yield and component characters indicated a highly significant positive association of seed yield with plant height (0.442) followed by head diameter (0.411) indicating the importance of these two traits in improving seed yield and suggesting the selection of crosses based on these two traits for improvement in sunflower yield. The results are similar with findings of Sowmya *et al*. (2010), Sincik and Goksoy (2014), Abu (2019) and Lakshman *et al*. (2021).

Table 2. Phenotypic correlation co-efficients for yield and yield attributing traits in sunflower MAGIC crosses

CHARACTER	DFF	DM	PH	HD	100-SW	VW	OC	SYPP
DFF	1	0.5926 **	-0.2199 *	-0.3265 **	-0.5259 **	0.2493 *	-0.0855	-0.0631
DM		1	0.1126	-0.0014	-0.2496 *	0.2243 *	0.1372	0.1438
PH			1	0.6145 **	0.4228 **	0.2634 *	0.0766	0.4420**
HD				1	0.6501 **	0.2570 *	0.1988	0.4110**
100-SW					1	-0.1247	-0.0269	0.2602
VW						1	0.3492 **	0.2242
OC							1	0.2200
SYPP								1

* = Significant at 5 per cent, ** = Significant at 1 per cent
DFF = Days to 50 per cent flowering,   DM = Days to maturity, PH = Plant height, HD = Head diameter, 100-SW = 100-seed weight, VW = Volume weight,   SYPP = Seed yield per plant,   OC = Oil content

Table 3. Path of different yield components on seed yield per plant in sunflower MAGIC lines

Character	Days to 50 per cent flowering	Days to maturity	Plant height	Head diameter	100-seed weight	Volume weight	Oil content	Correlation coefficient on Seed yield per plant
Days to 50 per cent flowering	**0.0678**	0.0402	-0.0149	-0.0221	-0.0356	0.0169	-0.0058	-0.0631
Days to maturity	0.0395	**0.0666**	0.0075	-0.0001	-0.0166	0.0149	0.0091	0.1438
Plant height	-0.0651	0.0333	**0.2961**	0.1819	0.1252	0.0780	0.0227	0.4420**
Head diameter	-0.0474	-0.0002	0.0891	**0.1451**	0.0943	0.0373	0.0288	0.4110**
100-seed weight	-0.0534	-0.0254	0.0430	0.0661	**0.1016**	-0.0127	-0.0027	0.2602
Volume weight	0.0089	0.0080	0.0094	0.0091	-0.0044	**0.0355**	0.0124	0.2242
Oil content	-0.0133	0.0213	0.0119	0.0309	-0.0042	0.0543	**0.1554**	0.2200

Residual effect = 0.358
* = Significant at 5 per cent, ** = Significant at 1 per cent

Table 4. Comparison of different yield related traits with their mean value to identify the best introgression lines

S. No.	Genotype	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Head diameter (cm)	100-Seed weight (g)	Volume weight (g/100 ml)	Seed yield per plant (g)	Oil content (%)	Number of traits with more than mean value	Percentage of introgression of character
1	R-127-1 × R I	67.00 -	97.00 +	143.00 -	12.70 -	02.62 -	42.96 +	28.86 -	39.09+	3	37.50
2	R-630 × R I	64.00 -	98.00 +	172.00 +	17.10 -	03.94 -	36.96 -	32.72 -	35.64-	2	25.00
3	PM-81 × R I	71.00 -	104.00 -	163.00 +	18.30 +	03.50 -	41.36 +	39.02 +	39.14+	5	62.50
4	RGM-49 × R I	70.00 -	103.00 -	161.00 +	16.10 -	03.70 -	35.84 -	40.34 +	38.29+	3	37.50
5	RHA-97 × R I	65.00 -	97.00 +	152.00 -	21.00 +	05.30 +	38.80 -	45.08 +	36.60+	5	62.50
6	RHA-93 × R I	66.00 -	102.00 -	180.00 +	22.80 +	07.12 +	38.88 -	73.56 +	35.86+	5	62.50
7	No-30 × R I	59.00 +	99.00 -	167.00 +	24.50 +	07.66 +	37.96 -	22.00 -	35.47-	4	50.00
8	No-15 × R I	61.00 +	100.00 -	170.00 +	22.40 +	06.92 +	39.30 +	28.42 -	36.66+	6	75.00
9	CSFI-99 × R I	60.00 +	100.00 -	150.00 -	23.60 +	05.76 +	39.28 +	51.56 +	35.83+	6	75.00
10	CSFI-8002 × R I	58.00 +	93.00 -	142.00 -	22.60 +	05.64 +	40.16 +	42.28 +	35.61+	6	75.00
11	R-127-1 × R II	58.00 +	98.00 +	173.00 +	18.20 +	03.68 -	42.08 +	42.62 +	38.57+	7	87.50
12	R-630 × R II	65.00 -	98.00 +	154.00 -	11.30 -	02.78 -	41.76 +	35.06 -	40.32+	3	37.50
13	PM-81 × R II	65.00 -	104.00 -	170.00 +	16.10 -	04.42 -	38.48 -	44.08 +	35.36-	2	25.00
14	RGM-49 × R II	70.00 -	103.00 -	147.00 -	09.00 -	03.20 -	36.16 -	14.40 -	34.52-	0	00.00
15	RHA-97 × R II	70.00 -	99.00 -	188.00 +	23.60 +	07.64 +	40.72 +	81.56 +	34.89-	5	62.50
16	RHA-93 × R II	61.00 +	100.00 -	188.00 +	20.80 +	06.60 +	40.48 +	76.04 +	35.46-	6	75.00
17	No-30 × R II	61.00 +	99.00 -	188.00 +	23.90 +	06.68 +	38.00 -	25.56 -	36.27+	5	62.50
18	No-15 × R II	57.00 +	99.00 -	182.00 +	23.80 +	06.38 +	39.92 +	27.62 -	36.20+	6	75.00
19	CSFI-99 × R II	57.00 +	93.00 +	162.00 +	23.00 +	04.22 +	41.52 +	34.56 -	34.37-	5	62.50
20	CSFI-8002 × R II	60.00 +	93.00 +	128.00 -	16.40 -	03.70 -	40.08 +	18.38 -	33.17-	3	37.50
21	R-127-1 × R III	62.00 +	97.00 +	189.00 +	20.20 +	02.96 -	46.96 +	33.70 -	39.89+	6	75.00
22	R-630 × R III	64.00 -	95.00 +	120.00 -	09.90 -	02.74 -	35.90 -	09.44 -	37.75+	2	25.00
23	PM-81 × R III	71.00 -	104.00 -	188.00 +	18.90 +	03.92 -	47.16 +	51.96 +	37.86+	5	62.50
24	RGM-49 × R III	70.00 -	103.00 -	189.00 +	17.00 -	04.36 -	42.24 +	47.96 +	38.00+	4	50.00
25	RHA-97 × R III	64.00 -	96.00 +	189.00 +	19.50 +	06.66 +	36.48 -	78.16 +	31.62-	5	62.50
26	RHA-93 × R III	65.00 -	100.00 -	188.00 +	19.50 +	06.92 +	38.80 -	54.50 +	32.71-	4	50.00
27	No-30 × R III	59.00 +	100.00 -	179.00 +	19.00 +	06.16 +	39.44 +	65.90 +	35.50-	6	75.00
28	No-15 × R III	60.00 +	99.00 -	168.00 +	16.70 -	03.74 -	37.76 -	49.10 +	36.93+	4	50.00
29	CSFI-99 × R III	60.00 +	96.00 -	159.00 +	21.80 +	04.94 +	41.60 +	52.98 +	34.84-	7	87.50
30	CSFI-8002 × R III	58.00 +	93.00 +	121.00 -	16.60 -	03.70 -	38.96 -	12.08 -	31.02-	2	25.00
31	R-127-1 × R IV	62.00 +	100.00 -	172.00 +	21.70 +	03.42 -	40.80 +	37.20 +	39.49+	6	75.00
32	R-630 × R IV	63.00 +	100.00 -	181.00 +	15.30 -	02.96 -	44.96 +	31.64 -	41.16+	4	50.00
33	PM-81 × R IV	71.00 -	101.00 -	151.00 -	14.20 -	04.78 +	42.24 +	23.92 -	37.38+	3	37.50
34	RGM-49 × R IV	71.00 -	103.00 -	202.00 +	16.90 -	04.50 -	43.20 +	58.56 +	37.83+	4	50.00
35	RHA-97 × R IV	64.00 -	99.00 -	195.00 +	16.10 -	05.02 +	37.20 -	50.34 +	32.35-	3	37.50
36	RHA-93 × R IV	65.00 -	99.00 -	182.00 +	23.30 +	07.74 +	39.04 -	97.34 +	32.21-	4	50.00
37	No-30 × R IV	61.00 +	96.00 -	163.00 +	18.10 +	05.42 +	36.82 -	49.60 +	36.40+	7	87.50
38	No-15 × R IV	60.00 +	96.00 -	169.00 +	20.70 +	06.92 +	32.92 -	18.46 -	31.31-	5	62.50
39	CSFI-99 × R IV	59.00 +	93.00 +	129.00 -	16.60 -	03.3 -	40.42 +	26.62 -	32.13-	3	37.50
40	CSFI-8002 × R IV	58.00 +	93.00 +	140.00 -	16.40 -	05 +	42.48 +	37.78 +	33.88-	5	62.50
Parents											
1	R-127-1	67.75 -	99.00 -	136.50 -	10.13 -	02.12 -	35.23 -	10.91 -	35.58-	0	
2	R-630	68.25 -	100.00 -	111.25 -	09.20 -	01.60 -	36.85 -	06.78 -	35.82+	1	
3	PM-81	66.75 -	101.75 -	114.75 -	11.60 -	03.49 -	36.64 -	11.97 -	39.47+	1	
4	RGM-49	66.50 -	95.75 +	100.50 -	09.05 -	01.87 -	38.98 -	06.19 -	35.08-	1	
5	RHA-97	68.50 -	100.50 -	123.50 -	07.93 -	02.94 -	35.44 -	03.78 -	30.37-	0	
6	RHA-93	65.00 -	100.25 -	109.75 -	13.15 -	03.53 -	36.81 -	10.58 -	37.37+	1	
7	No-30	57.75 +	93.50 +	147.75 -	15.90 -	06.06 -	36.30 -	12.08 -	36.35+	4	
8	No-15	61.00 +	95.25 +	114.50 -	10.45 -	04.50 -	30.60 -	12.00 -	34.63-	2	
9	CSFI-99	61.75 +	95.25 +	123.00 -	11.60 -	03.92 -	36.51 -	12.44 -	33.33-	2	
10	CSFI-8002	67.25 -	99.50 -	122.50 -	14.10 -	04.00 -	31.60 -	14.84 -	30.54-	0	

Note: (+) = Character having observed value more than mean value;(-) = Character having observed value less than mean value

The path co-efficient analysis is the statistical tool which is used to determine the direct or indirect effects of one variable (cause) through another on seed yield and bisecting the correlation association into direct and indirect effects (Wright, 1921). Selections based only on correlation co-efficient without considering the direct and indirect effects of different yield components may mislead the plant breeders to reach their main bree ding goals. Path co-efficient analysis makes it possible to measure the interrelationship among yield components for their direct and indirect effects on seed yield *via* correlation (Singh and Chaudhary, 1985).

In the present investigation, the estimated phenotypic correlations were analyzed bisecting association into direct and indirect effects of component traits on seed yield (**Table 3**). Path co-efficient analysis of different yield component traits contributing toward seed yield per plant showed that plant height (0.2961) had the highest positive direct effect followed by oil content (0.1554), head diameter (0.1451), 100-seed weight (0.1016), days to 50 per cent flowering (0.0678), days to maturity (0.0666) and volume weight (0.0355). These findings are in confirmation with the earlier findings of Sowmya *et al*. (2010), Basha (2020) and Lakshman *et al*. (2021). The phenotypic path co-efficient analysis using eight quantitative characters resulted in a residual effect of 0.358. In other way the residual effect of 35.80 per cent in the present study may be reduced by including more number of traits.

Development of MAGIC population not only offers great potential for the introgression of novel variation, it also widens the genetic base of elite lines. Introgression of genes can be identified with the help of markers to identify the QTLs for different traits. However, in conventional methods only those characters expressed in the progeny will be considered as introgressed characters based on a parental combination. In the present study, 40 MAGIC crosses along with 10 parental checks were evaluated for the introgression of different characters. The values were recorded for all eight characters and compared with the mean value. Those lines having observed values more than the mean value were considered for selection and those lines having more characters introgressed is considered as the best introgressed line among MAGIC crosses. Similar method was followed by Sankar *et al*. (2001) in sunflower and Sowmyashree (2016) in chickpea for the identification the of best introgression line. The comparison of observed traits with mean value is represented in **Table 4**.

Out of 40 MAGIC crosses none of the cross showed introgression of all eight characters observed, whereas MAGIC crosses R-127-1 × RⅡ, CSFI-99 × RⅢ and No-30 × RⅣ showed the highest percentage (87.5%) of introgression with the expression of seven out of eight traits, followed by No-15× RⅠ, CSFI-99 × RⅠ, CSFI-

8002 × RⅠ, RHA-93× RⅡ, No-15 × RⅡ, R-127-1 × RⅢ, No-30 × RⅢ and R-127-1 × RⅣ revealed 75 per cent of introgression with the expression of six out of eight traits. Sowmyashree (2016) conducted an experiment on 140 chickpea MAGIC lines, out of which 40 lines were identified based on variation, correlation and path analysis studies.

Hybrid efficiency is not only depends on male sterile A line, it is also depends on the performance and diversity in restorer lines, which cannot be attained only by bi-parental crosses. So, introgression from multiple parents is necessary in a population to increase recombination events and variability. It can be done by the development of MAGIC population in sunflower restorer lines. Selection is effective for the characters *viz.,* seed yield, 100-seed weight, head diameter and plant height with high heritability estimate and high genetic advance. Correlation and path analysis studies on seed yield and component characters indicated a highly significant positive association and the direct effect of plant height and head diameter on seed yield indicates the importance of these two traits in improving seed yield in sunflower. The efficacy of MAGIC crosses to create variability involving multiple parents can be estimated through analysing trait specific introgression over bi-parental crosses. Identification of trait specific introgressed lines revealed the maximum introgression of characters in R-127-1 × RⅡ, CSFI-99 × RⅢ and No-30 × RⅣ indicating the use of these MAGIC crosses in a future breeding programme.

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