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RESEARCH ARTICLE

Generation Mean Analysis for Yield and its Contributing Traits in Safflower (*Carthamus tinctorius* L.)

Waghmode S L*, Wadikar P B , Talape A R and Patil S H

Department of Agricultural Botany, College of Agriculture, Latur, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani 431 402 (M.S), India

ABSTRACT

To study the nature and magnitude of gene effects in the present investigation for yield and its components in Safflower (Carthamus tinctorius L.), Generation mean analysis with three-parameter model with χ2 test indicated that additive-dominance model was inadequate for all the traits in all the crosses used to estimate the gene effects. Duplicate type epistasis played greater role than complementary epistasis. On the basis of six parameter model, main effect viz., m, d and h and all three digenic interactions viz., (i), (j) and (l) were significant for DF, DM, PH, NBPP, NCPP and SYPP in cross GMU-2720 x GMU-3423; for DM, PH, NSPC, SYPP and HC in cross in cross JMU-1339 x GMU-3423 indicated that involvement of d, h and epistasis interaction for controlling this trait. For DF, DM, PH, NBPP, NCPP, TW and HC in cross-1; for DF, DM, PH, NBPP, NSPC, TW, SYPP and OC in cross-2 for these characters indicating the duplicate type of interactions. For NSPC and SYPP in cross-1; for NCPP and HC in cross-2;for these characters indicating the complementary type of interactions. This suggested that duplicated type of gene action was present confirming the importance of dominance effects. The study revealed the importance of both additive and non-dominance types of gene action for all the traits studied. Thus, considerable non-additive genetic effects observed in this study suggest that selection in an advanced generation will be appropriate,

Keywords: Safflower; Quantitative trait; Joint scaling test; Gene effects; Generation mean analysis.

INTRODUCTION

Safflower is one of the most important oilseed crops. Safflower is basically self-pollinated crop but insects particularly bees are necessary for optimum pollination and maximization of yield. Cross-pollination mainly through bees to the extent of 10-28% depending on genotype and insect activity has been reported in safflower (Weiss, 2000). Safflower has been gaining increasing popularity in recent years in several parts of the country because of its adaptability under drought conditions. Yield is the complex quantitative character and it depends on contributing yield components. For crop improvement, the genetics of the yield and its components need to be thoroughly understood. Various biometrical techniques are extensively used for the estimation of the relative magnitude of the different components of genetic variation. Safflower (*Carthamus tinctorious* L.) is an oilseed crop that improvement of yield is being emphasized for this crop. Thus, breeding efforts in safflower should emphasize the improvement of seed yield and oil content (Cosge *et al.* 2007). In India, safflower cultivation is dominated by high-yielding varieties. Due to ever-increasing demand for oilseeds and particularly for oils with high level of polyunsaturated fatty acids (PUFA). Though several high-yielding varieties were released, still low productivity of safflower crop is the main challenge to the researchers because the immense potential of the crop yet to be exploited.

Out of which, techniques developed by Mather (1949); Hayman and Mather (1955); Jinks and Jones (1958); Hayman (1958) and Gamble (1962) require less number of families and are comprehensive, easy and equally informative. These models help to study the nature of gene action governing the inheritance of quantitative characters. Reliable information on this aspect which accounts for the non-allelic interactions would also facilitates the breeder to decide appropriate breeding procedures in the improvement of various continuously varying characters.

*Corresponding author's e-mail: shankarw690@gmail.com

MATERIAL AND METHODS

Three accessions of (*Carthamus tinctorious* L), namely: GMU-2720, GMU-3423 and JMU -1339 obtained from AICRP, Parbhani were used in the present study. The experiments involved the six basic generations (The P_1 and P_2 parent ,the F_1 and F_2 generations, and BC_1 and BC_2) of two cross combinations. The combinations used were GMU-2720 x GMU-3423 and JMU-1339 x GMU-3423. The experiment was conducted at the research farm of the Department of Genetics and Plant Breeding, College of Agriculture, Latur during 2019. All the six basic generations, i.e. P_1, P_2, F_1, F_2, B_1 and B_2 were planted in a randomized block design with two replications and a plot size of 15 x 8 m. The data on quantitative traits like, days to 50% flowering, days to maturity, plant height, number of branches per plant (cm), number of capitulum per plant, number of seeds per capitulum, test weight (g), seed yield per plant (g), hull content (%) and oil content (%) were recorded on 5 randomly selected plants in each of P_1, P_2 and F_1 generations, 5 plants each of B_1 and B_2 and 20 plants of F_2 generations. The estimates of generation mean analysis with three-parameter models as suggested by Jinks and Jones (1958) and Joint Scaling test (Cavalli, 1952) were carried out to estimate the presence or absence of non-allelic interaction. Six parameter model suggested by Hayman (1958) was used to estimate variance components to fit the models. The essential oil was extracted from the air-dried herb by hydro-distillation using Clevenger's apparatus for 2.30 hrs.

RESULTS AND DISCUSSION

The analysis of variance for the experimental design for all the ten characters studied in two crosses of safflower (*Carthamus tinctorius* L.) is presented in (Table 1) The general analysis of variance for randomized block design was done for each character to find out amount of variations between generation means for various characters. It was observed that there were highly significant differences for all the characters except days to 50 % flowering, days to maturity and number of branches per plant. Significant differences for days to 50 % flowering, days to maturity and number of branches per plant revealed that the mean sum of square for treatment in both crosses sufficient variation for effective selection for all the characters in the material under study. The mean of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each trait and their corresponding weights were used to estimates various gene effects for seed yield and its contributing traits. Joint scaling test was applied to test the adequacy of the additive-dominance model and estimates three parameters m (mean) d (additive effect) and h (dominance effect). In case the additive-dominance model was not found adequate, the data were analyzed for estimation of six parameters m (mean), d (additive effect), h (dominance effect) and digenic interaction effects i.e. i (additive x additive). j (additive x dominance) and l (dominance x dominance). Significant joint scaling test indicated the presence of non-allelic interaction and non-significance indicated the absence of non-allelic interaction. In such cases 6-parameter model has used to estimates the additive, dominance and epistasis effects. The estimates of gene effects obtained using 6-parameter model for the 10 traits in two crosses are presented in (Table 2). The additive, dominance and epistatic types of gene interaction in each cross for different trait were found to be different from each other. The dominance x dominance [l] interaction was larger than the additive x additive [i] and additive x dominance [j] effects put together, while for the main effects the dominance component (h) was greater than the additive [d] components. The dominance [h] and dominance x dominance [l] effects were in the opposite direction, suggesting that duplicate-type epistasis occurred in most cases and indicating predominantly dispersed alleles at the interacting loci (Jinks, and Jones, 1958). Dominance gene effects were found to be relatively more important, as indicated by the fact that in all cases the dominance [h] values were higher than additive [d] values.

For days to 50 % flowering, days to maturity and plant height, 6-parameter model was used in two crosses. All the gene effects were significant for this trait in two crosses namely, GMU-2720 x GMU-3423 and JMU-1339 x GMU-3423. The additive gene effects were significant in all crosses, whereas the dominance gene effect were significant in all crosses. All three types of non-allelic gene interactions were significant and negative in all crosses. It is clear that [i] indicates additive x additive, [j] indicate the additive x dominance and [l] indicate that dominance x dominance non- allelic interactions. For these traits, all the significant values were found negative d, h, j and i whereas 'l' was positive in all crosses. The dominance gene effects were negative and non-significant for these traits. However, significant and non-significant positive and negative estimates were recorded for these traits. A comparison of the generation mean analysis data in Table 2 indicates that estimates of the additive gene effect [d] were greater in magnitude than their corresponding dominance effects [h] for these traits in crosses. Therefore additive genes are the most important factor contributing to the genetic control of these traits. Further, in situations where additive gene effects moderately indicated fixable gene effect and therefore early selection among the segregating population could be rewarding.

Since, significant estimates of 'h' and l had opposite signs, duplicate type of epistasis was indicated in two crosses. The breeding implication is that difficulties might be encountered in the process of evolving varieties with improved days to 50 % flowering, days to maturity and plant height.

Non-fixable gene effects were higher than the fixable gene effects on environment indicating a greater role of non-additive gene effects in the inheritance of these traits, which suggested that this trait can be improved through recurrent selection. These results are in agreement with those obtained by Kumar *et al*. (2012) Shivani and Varaprasad (2016). Moreover, epistasis in these traits was of duplicate type which further confirms the complex nature of this trait, thereby suggested that difficulty would be encountered in selecting for this trait. The number of branches per plant trait for crosses, showed a significant and pronounced additive, dominance and non-allelic interactions except cross JMU-1339 x GMU-3423 for dominance type of gene effects. The opposite sign of (h) and (l) parameter in two crosses, GMU-2720 x GMU-3423 and JMU-1339 x GMU-3423 indicated the duplicate type of interaction. Both additive and dominance gene effects as well as non-allelic interaction were found significant in cross, GMU-2720 x GMU-3423. However, the dominance gene effect was non-significant in cross, JMU-1339 x GMU-3423. These results are in agreement with those obtained by Kumar *et al.* (2012) Shivani and Varaprasad (2016); Nakhaei *et al*. (2014); these traits indicating dominance gene effects and suggested that this trait can be improved through recurrent selection.

Table 1. Analysis of variance (Mean sum squares) of generation means for 10 characters in Safflower.

Sources	d.f	DF	DM	PH	NBPP	NCPP	NSPC	TW	SYPP	HC	OC
					GMU-2720 x GMU-3423						
Replication	1	5.13	11.50	1.23	1.65	0.42	2.66	0.003	0.12	0.04	0.17
Treatment	5	16.90*	49.59*	209.09**	3.88*	46.71**	144.04**	0.16**	59.00**	62.38**	7.74**
Error	5	2.68	5.33	4.61	0.35	0.71	2.14	0.003	1.18	0.06	0.13
					JMU-1339 x GMU-3423						
Replication	1	0.13	4.38	0.96	0.96	1.68	1.14	0.002	0.82	0.03	0.124
Treatment	5	13.42*	24.47*	287.26**	5.17*	42.04**	127.71**	0.25**	258.73**	71.92**	3.67**
Error	5	1.30	2.66	2.53	0.84	3.79	1.48	0.003	1.47	0.28	0.132

*Significant at 5 % level, ** Significant at 1 % level

Whereas,

DF = Days to 50 % flowering

DM = Days to maturity

NBPP = Number of branches per plant

NCPP = Number of capitulum per plant

TW = Test weight (g)

SYPP = Seed yield per plant (g)

OC = Oil content (%)

HC = Hull content (%)

NSPC = Number of seeds per capitulum

PH = Plant height (cm)

The number of capitulum per plant trait for crosses, GMU-2720 x GMU-3423 and JMU-1339 x GMU-3423 showed a significant pronounced additive, dominance and non-allelic interaction excepts cross, JMU-1339 x GMU-3423 for (i) and (l) type of gene effects. The opposite sign of (h) and (l) parameter in two cross, GMU-2720 x GMU-3423 indicated the duplicate type of interaction. The same sign of (h) and (l) parameter in two crosses, JMU-1339 x GMU-3423 indicated the complementary type of interaction. Both additive and dominance gene effects as well as non-allelic interaction, were found significant in the cross, GMU-2720 x GMU-3423. However, (h) and (j) gene effect was non-significant in the cross, JMU-1339 x GMU-3423. These results are in agreement with those obtained by Kumar *et al.* (2012) Shivani and Varaprasad (2016); Nakhaei *et al*. (2014); both additive and dominant gene effects as well as non-allelic interaction were founded by these research.

In the case of the number of seeds per capitulum, all the gene effects were significant in the cross, JMU-1339 x GMU-3423. However, (i) and (l) gene effect was non-significant in cross, JMU-1339 x GMU-3423. The magnitudes of the non-additive

effect were higher than that of an additive gene effect. The cross GMU-2720 x GMU-3423 exhibited the complimentary type of epistasis for this trait. The cross JMU-1339 x GMU-3423 which showed duplicate type of epistasis. The non-fixable gene effect were higher than fixable gene effects indicating a greater role of non-additive gene effects for this trait, which suggested that this trait can be improved through recurrent selection. Discuss their results are in agreement with those obtained by Shivani *et al.* (2011); For the trait test weight, additive gene effects were found significant in only one cross, GMU-2720 x GMU-3423 showed positive significance. Dominance gene effects significant in cross JMU-1339 x GMU-3423 showed negative significance. Among non-allelic interaction additive x additive with negative sign and additive x dominance with positive sign in cross JMU-1339 x GMU-3423. For this trait, both additive and non-additive gene effects were predominant. Duplicate type of epistasis was observed in two crosses. These results are in agreement with those obtained by Shivani *et al*. (2011); Gupta and Singh (1993); Kumar *et al.* (2012); for this trait showed duplicate type of epistasis

Table 2. Estimates of gene effects in two crosses of Safflower for 10 characters in safflower.

Crosses	m		d		h		i		j		l		Epistasis
Days to 50 % Flowering													
GMU-2720 x GMU-3423	82.62**	0.42	-5.65**	0.10	-15.95**	1.74	-14.80**	1.72	-3.20**	0.25	12.20**	1.83	Duplicat-e
JMU-1339 x GMU-3423	83.07**	0.14	-3.65**	0.40	-14.40**	1.01	-15.40**	0.98	-0.85	0.43	18.50**	1.77	Duplica-te
Days to Maturity													
GMU-2720 x GMU-3423	127.92**	0.66	-6.80**	0.30	-30.50**	2.74	-27.30**	2.74	-1.80*	0.33	22.50**	2.95	Duplica-te
JMU-1339 x GMU-3423	126.57**	0.38	-3.70**	0.30	-16.50**	1.70	-16.90**	1.67	0.90	0.36	23.10**	2.10	Duplica-te
Plant Height													
GMU-2720 x GMU-3423	84.17**	0.51	-15.20**	0.38	-23.20**	2.20	-25.90**	2.20	-2.00**	0.39	19.70**	2.58	Duplica-te
JMU-1339 x GMU-3423	79.45**	0.36	-6.90**	0.30	-12.90**	1.61	-14.80**	1.59	11.40**	0.3	9.20*	1.98	Duplica-te
Number of Branches Per Plant													
GMU-2720 x GMU-3423	14.02**	0.06	-1.80**	0.38	10.30**	0.81	8.7**	0.80	-2.60**	0.38	-15.10**	1.55	Duplica-te
JMU-1339 x GMU-3423	14.25**	0.22	1.50**	0.16	-2.75	0.96	-6.00*	0.95	2.75**	0.18	8.90**	1.14	Duplica-te
Number of Capitulums Per Plant													
GMU-2720 x GMU-3423	29.77**	0.13	-4.20**	0.09	20.35**	0.61	23.70**	0.56	-7.45**	0.18	-9.40*	0.82	Duplica-te
JMU-1339 x GMU-3423	34.90**	0.45	1.40*	0.26	9.55**	1.94	0.80	1.89	6.55**	0.26	5.30	2.25	Comple-mentary
Number of Seeds Per Capitulum													
GMU-2720 x GMU-3423	43.47**	0.38	-8.70**	0.03	4.30	1.56	-12.10**	1.55	-1.00	0.14	13.10**	1.59	Comple-mentary
JMU-1339 x GMU-3423	35.20**	0.23	-2.50**	0.34	19.15**	1.19	9.80**	1.16	8.65**	0.36	-14.30**	1.77	Duplica-te
Test Weight (g)													
GMU-2720 x GMU-3423	4.15**	0.00	0.60*	0.00	1.55	0.01	1.40	0.00	0.55	0.01	-2.90	0.03	Duplica-te
JMU-1339 x GMU-3423	4.115*	0.00	0.40	0.00	-2.16**	0.03	-2.06**	0.01	0.80**	0.00	1.86	0.06	Duplica-te
Seed Yield Per Plant (g)													
GMU-2720 x GMU-3423	53.65**	0.15	-8.80**	0.33	21.72**	0.94	13.00**	0.89	-6.82**	0.35	9.95*	1.56	Comple-mentary
JMU-1339 x GMU-3423	47.82**	0.31	-7.10**	0.10	-31.50**	1.28	-34.70**	1.28	9.70**	0.11	49.70**	1.33	Duplica-te
Hull Content (%)													
GMU-2720 x GMU-3423	49.29**	0.00	0.90	0.07	-44.85**	0.16	-39.38**	0.14	5.76**	0.09	32.95**	0.32	Duplica-te
JMU-1339 x GMU-3423	47.92**	0.07	10.20**	0.14	-20.75**	0.43	-12.10**	0.42	12.63**	0.15	-14.91**	0.68	Comple-mentary
Oil Content (%)													
GMU-2720 x GMU-3423	28.85**	0.10	-3.10**	0.00	0.13	0.41	-0.20	0.41	-0.41	0.01	0.50	0.41	—
JMU-1339 x GMU-3423	30.61**	0.09	-1.26*	0.04	-1.20	0.39	-2.92	0.39	0.42	0.04	7.16*	0.42	Duplica-te

*Significant at 5% level, ** Significant at 1% level.

In the case of the seed yield per plant, all the gene effects were significant in all crosses. The magnitudes of non-additive effect were higher than that of an additive gene effect. The cross GMU-2720 x GMU-3423 exhibited the complimentary type of epistasis for this trait. The cross JMU-1339 x GMU-3423 which showed duplicate type of epistasis. The non-fixable gene effect was higher than fixable gene effects indicating a greater role of non-additive gene effects for this trait, which suggested that this trait can be improved through recurrent selection. These results confirm the findings of Shivani and Varaprasad (2016); Kumar *et al.* (2012); Gupta and Singh (1991) Shivani *et al*. (2011); who also reported the involvement of additive type of gene action for this trait.

In the case of the hull content, all the gene effects were significant in all crosses for this trait except cross GMU-2720 x GMU-3423 for the additive type of gene effects. The magnitudes of the non-additive effect were higher than that of an additive gene effect. The cross JMU-1339 x GMU-3423 exhibited the complimentary type of epistasis for this trait the cross GMU-2720 x GMU-3423 which showed the duplicate type of epistasis. The non-fixable gene effect was higher than fixable gene effects indicating a greater role of non-additive gene effects for this trait, which suggested that this trait can be improved through recurrent selection. Discuss their results confirm the findings of Shivani *et al*. (2011); Mirzahashemi *et al.* (2014); Gupta and Singh (1991); Kumar *et al*. (2012); Gupta and Singh (1993); Shivani and Varaprasad (2016) who also reported the involvement of additive type of gene action for this trait. For the trait oil content, additive with negative sign and dominance with positive sign gene effects were found significant in cross JMU-1339 x GMU-3423. Duplicate type of epistasis was observed in cross JMU-1339 x GMU-3423. These results are in agreement with those obtained by Gadekar and Jambhale (2002); Gupta and Singh (1993); Kumar *et al.* (2012); for this trait showed the duplicate type of epistasis.

On the basis of six parameter models, the main effect viz., m, additive (d) and dominance (h) and all three digenic interactions viz., additive x additive (i), additive x dominance (j) and dominance x dominance (l) were significant for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capitulum per plant and seed yield per plant in cross-1 (GMU-2720 x GMU-3423); for days to maturity, plant height, number of seeds per capitulum, seed yield per plant and hull content in the cross in cross-2 (JMU-1339 x GMU-3423) indicated that involvement of additive, dominance as well as epistasis interaction for controlling this trait.

CONCLUSION

The different types of gene effects estimated provided a test for gene action and are useful for analyzing the genetic architecture of a crop so as to improve desirable traits further. The estimates obtained from each cross may be unique to that cross and may not be applicable to the parental population. Additive genetic variance formed the major part of the genetic variance for the important yield components and oil content. Therefore genetic improvement in the number of capitulum per plant, number of seeds per capitulum, test weight and seed yield per plant trait would be easier through indirect selection for a component trait such as the oil content trait than through direct selection for number of capitulum per plant, number of seeds per capitulum, test weight and seed yield per plant trait itself. Synthetic breeding would be beneficial if there is high additive genetic variance. If the dominance variance is predominant, the breeding objective should be towards the development of hybrids. Selection between families and lines would be rewardable if there is high epistatic variance. If all the genetic components are of equal magnitude, either composite or population improvement programme should be taken up for the development of superior lines with several desirable genes.

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