RESEARCH ARTICLE

Generation Mean Analysis Studies in Safflower (*Carthamus tinctures* L.)

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Abstract

The present investigation was conducted at experimental research farm of Agriculture Botany College of Agriculture, Latur, in 2021, with a view to study the genetics of yield and yield components through generation mean analysis. The scaling test exhibited that, there was presence of epistatic gene interaction. The duplicate epistasis were observed in days to maturity and test weight in cross, JMU-1339 x NARI-6 and cross, JMU-1339 x EC-757665 for days to 50% flowering, number of branches per plant, number of seeds per capitulum and oil contents in cross-I; for plant height, number of capitulum per plant and hull contents in cross, JMU-1339 x EC-757665. This suggests the need of specific breeding procedure such as intermating of most desirable segregants followed by selfing and selecting superior genotypes coupled with progeny testing to exploit the population under study. Selection in early generation would be effective when additive effects are larger than non-additive ones. Further if the non-additive portions are larger than additive one, the improvement of the character need intensive selection through later generations.

Keywords: Additive, Complementary epistasis, Dominance, Duplicate epistasis, Epistasis, Gene action.

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Introduction

Safflower (*Carthamus tinctorius* L.) is an important oilseed crop which belongs to the family Compositae or Asteraceae. It is a drought tolerant multi-purpose crop where in it is grown not only for oil but also for petals from which orange-red dye (carthamin) is extracted. The petals have several medicinal properties and are useful in curing several chronic ailments. The oil constitutes 76% of Linoleic acid (PUFA) which helps in reducing cholesterol level in human blood. The common practice of safflower growing by the farmers in India is as an inter-crop under rainfed and as sole crop under irrigated conditions. The importance of additive and non-additive genetic effects is well established in controlling many traits in safflower. It was shown that the dominance effects of the genes played a major role in the variation of seed yield per plant in safflower (Ehdaie and Ghaderi, 1978). For genetic improvement of the crop, the breeding method to be adopted depends on the nature of gene action involved in the expression of quantitative traits. The presence or absence of epistasis can be detected by the analysis of generation means using the scaling test, which measures epistasis accurately, whether it is complimentary or duplicate at the digenic level. Two genetic models (Cavalli 1952: and Hayman, 1958) were simultaneously used for determining the nature of gene action involved in the inheritance of yield and yield contributing characters. The information regarding gene action involved in control of inheritance for yield and yield contributing characters through generation mean analysis is of immense use to the plant breeder to decide suitable breeding strategy for improvement of these characters.

Materials and Methods

The present investigation was conducted at Department of Agriculture Botany, college of Agriculture, Latur. VNMKV Parbhani (M.S.) during period of *rabi* 2019 and *rabi* 2020. By hand emasculation and pollination, two crosses involving three genetically diverse parents *viz.,* JMU-1339, NARI-6 and EC-757665 were effected in *rabi*, 2018-19. For advance the F_2's and to prepare BC_1 and BC_2 crosses, the F_1's and parents were grown in *rabi*, 2019-20. Thus, seed of six generation, P_1, P_2, F_1, F_2, BC_1 and BC_2 of two crosses were produced. In Randomized Block Design two different safflower crosses were sown during *rabi* 2020-21, from the experimental material comprised of six generations *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 and replicated twice. Five plants are selected from each generation, except F_2, from which twenty plants are selected. From all the selected plants which are chosen randomly in each genotype, ten observations of quantitative character were recorded.

Data were first evaluated for non-allelic interaction by individual scaling tests (A, B, C, D) as described by Hayman and Mather (1955) were used to check the adequacy of additive-dominance model in each cross. Further, the chi- square value for ten characters in all the crosses were calculated as per the method of Joint scaling test proposed by Cavalli (1952). If Chi-square value for character was nonsignificant, it indicated the absence of higher order interaction and linkage. In presence of non-allelic interactions various gene effects were estimated using six parameter model suggested by Hayman (1958).

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Result and Discussion

The results of generation mean analysis of six genetic populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two crosses (JMU-1339 x NARI-6 and JMU-1339 x EC-757665) for ten different traits in safflower are discussed here. Scaling tests were significant suggesting the presence of digenic interaction in the inheritance of these characters are presented in Table 1 and 2. The individual scaling tests A, B, C and D revealed the presence of epistasis for most of the traits in all the crosses. The generation means, a six-parameter model involving three digenic interaction parameters proposed by Hayman (1958) was applied.

The highly significant mean values from the generation mean analysis in two crosses showed that, the six-generation differed from each other and these all studied traits are quantitatively inherited. The additive (d) effect found significant and positive for test weight and hull content in the cross, JMU-1339 x NARI-6 and in the cross, JMU-1339 x EC-757665. These results are in agreement with those obtained by Gadekar and Jambhale (2002) and Nakhaei *et al*. (2014).For days to 50 % flowering, days to maturity, plant height, number of branches per plant, number of capitulum per plant, number of seeds per capitulum, seed yield per plant and oil content, the additive (d) effect found significant and negative in the cross, JMU-1339 x NARI-6and in the cross, JMU-1339 x EC-757665. The additive component of variation can be exploited by simple pedigree selection. Mass selection for several early generation aimed at the improvement of heterozygous population by modifying the frequencies of desirable gene followed by single plant selection in the resulting material would be cheapest and quickest procedure. However, the presence of non-fixable (h, j and *l*) component together with duplicate type of epistasis may cause delay in the improvement in this trait through selection in early generations. Under this situation the selection is delayed to later generations. These results agree with those

Table 1: Scaling test and joint scaling test for different characters in two crosses in safflower.

Crosses	*A*	*B*	*C*	*D*	X^2 *values*
Days to 50 % flowering					
JMU-1339 x NARI-6	-0.20 ± 0.42	2.90** ± 0.18	8.20** ± 1.06	2.75* ± 0.55	S
JMU-1339 x EC-757665	1.90* ± 0.26	6.50** ± 0.34	15.40** ± 1.12	3.50** ± 0.60	S
Days to maturity					
JMU-1339 x NARI-6	-3.80** ± 0.27	-1.70 ± 0.16	12.10** ± 1.89	8.80** ± 0.95	S
JMU-1339 x EC-757665	2.10 ± 0.66	3.20* ± 0.73	12.70** ± 1.35	3.70* ± 0.78	S
Plant height (cm)					
JMU-1339 x NARI-6	8.80** ± 1.27	13.30** ± 0.99	27.50** ± 2.68	2.70 ± 1.46	S
JMU-1339 x EC-757665	1.80 ± 0.33	10.20** ± 1.23	24.70** ± 2.94	6.35** ± 1.57	S
Number of branches per plant					
JMU-1339 x NARI-6	-1.20 ± 0.08	2.60* ± 0.14	-4.2 ± 1.06	-2.8* ± 0.53	S
JMU-1339 x EC-757665	-2.40* ± 0.16	-0.30 ± 0.13	-1.90 ± 0.75	0.40 ± 0.35	S
Number of capitulum per plant					
JMU-1339 x NARI-6	-5.70** ± 0.69	-0.70 ± 0.34	-10.90** ± 1.76	-2.25 ± 0.92	S
JMU-1339 x EC-757665	3.00** ± 0.24	5.30** ± 0.33	2.90 ± 1.68	-2.70 ± 0.80	S
Number of seeds per capitulum					
JMU-1339 x NARI-6	-3.50** ± 0.13	1.20 ± 0.17	-8.70* ± 1.45	-3.2 ± 0.72	S
JMU-1339 x EC-757665	-5.00** ± 0.45	0.50 ± 0.47	-6.70* ± 1.08	-1.10 ± 0.33	S
Test weight (g)					
JMU-1339 x NARI-6	1.00* ± 0.02	-0.50* ± 0.04	0.00 ± 0.13	-0.25 ± 0.06	S
JMU-1339 x EC-757665	0.70* ± 0.02	-0.20 ± 0.10	-0.60 ± 0.05	-0.55 ± 0.05	S
Hull content (%)					
JMU-1339 x NARI-6	2.60* ± 0.22	5.60** ± 0.07	6.00* ± 0.78	-1.10 ± 0.39	S
JMU-1339 x EC-757665	2.40* ± 0.06	-0.70 ± 0.22	7.10** ± 1.03	2.70* ± 0.52	S
Oil content (%)					
JMU-1339 x NARI-6	-3.22** ± 0.12	-2.15* ± 0.08	-1.42 ± 0.48	1.98** ± 0.24	S
JMU-1339 x EC-757665	-2.72* ± 0.47	-0.46 ± 0.29	-6.09** ± 0.75	-1.45 ± 0.44	S
Seed yield per plant (g)					
JMU-1339 x NARI-6	-9.40** ± 0.49	-1.20 ± 0.22	-17.50** ± 1.95	-3.45 ± 0.99	S
JMU-1339 x EC-757665	-4.46** ± 0.92	-3.90** ± 0.75	-11.20** ± 2.19	-1.35 ± 1.12	S

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

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

Crosses	*m*	*d*	*h*	*i*	*j*	*l*	*Types of Epistasis*
Days to 50 % flowering							
JMU-1339 x NARI-6	79.02** ± 0.26	-4.10** ± 0.20	-11.45** ± 1.12	-5.50* ± 1.11	-1.55* ± 0.22	2.80 ± 1.33	Duplicate
JMU-1339 x EC-757665	80.70** ± 0.28	-5.10** ± 0.21	-13.10** ± 1.20	-7.00** ± 1.19	-2.30** ± 0.22	-1.40 ± 1.41	Complementary
Days to maturity							
JMU-1339 x NARI-6	127.10** ± 0.47	-4.20** ± 0.14	-25.75** ± 1.91	-17.60** ± 1.91	-1.05 ± 0.02	23.10** ± 1.98	Duplicate
JMU-1339 x EC-757665	127.00** ± 0.32	-3.70** ± 0.44	-15.65** ± 1.58	-7.40* ± 1.56	-0.55 ± 0.49	2.10 ± 2.24	Duplicate
Plant height (cm)							
JMU-1339 x NARI-6	80.05** ± 0.64	-10.40** ± 0.71	-19.55** ± 2.96	-5.40 ± 2.93	-2.25* ± 0.80	-16.70** ± 3.91	Complementary
JMU-1339 x EC-757665	77.62** ± 0.72	-8.70** ± 0.60	-24.00** ± 3.14	-12.70** ± 3.14	-4.20** ± 0.60	0.70 ± 3.82	Duplicate
Number of branches per plant							
JMU-1339 x NARI-6	12.75** ± 0.26	-2.50** ± 0.07	10.20** ± 1.06	5.60* ± 1.06	-1.90* ±	-7.00 ± 1.10	Duplicate
JMU-1339 x EC-757665	13.35** ± 0.17	-1.70** ± 0.03	1.95 ± 0.72	-0.80 ± 0.70	-1.05 ± 0.050	3.50 ± 0.76	Complementary
Number of capitulum per plant							
JMU-1339 x NARI-6	31.25** ± 0.42	-5.20** ± 0.34	11.50** ± 1.85	4.50 ± 1.84	-2.50** ± 0.36	1.90 ± 2.23	Complementary
JMU-1339 x EC-757665	32.50** ± 0.40	-3.90** ± 0.074	7.25* ± 1.62	5.40 ± 1.60	-1.15 ±	-13.70** ± 1.70	Duplicate
Number of seeds per capitulum							
JMU-1339 x NARI-6	28.250** ± 0.36	-3.90** ± 0.07	12.55** ± 1.45	6.40 ± 1.44	-2.35** ± 0.083	-4.10 ± 1.48	Duplicate
JMU-1339 x EC-757665	27.05** ± 0.16	-3.40** ± 0.10	5.75 ± 0.80	2.20 ± 0.67	-2.75** ± 0.11	2.30 ± 1.16	Complementary
Test weight (g)							
JMU-1339 x NARI-6	4.10** ± 0.03	0.550** ± 0.01	0.40 ± 0.13	0.50 ± 0.13	0.75** ±	-1.0 ± 0.15	Duplicate
JMU-1339 x EC-757665	4.05** ± 0.008	0.35* ± 0.05	1.40* ± 0.10	1.10 ± 0.10	0.45* ± 0.05	-1.60 ± 0.20	Duplicate
Hull content (%)							
JMU-1339 x NARI-6	36.20** ± 0.19	1.10 ± 0.10	-2.60 ± 0.79	2.20 ± 079	-1.50* ± 0.11	-10.4** ± 0.87	Complementary
JMU-1339 x EC-757665	37.70** ± 0.25	3.30** ± 0.10	-9.650** ± 1.04	-5.40* ± 1.04	1.55* ± 0.11	3.70 ± 1.10	Duplicate
Oil content (%)							
JMU-1339 x NARI-6	29.73** ± 0.11	-1.73** ± 0.06	-0.20 ± 0.49	-3.96** ± 0.49	-0.53 ± 0.06	9.34** ± 0.55	Duplicate
JMU-1339 x EC-757665	29.11** ± 0.17	-2.29** ± 0.26	7.07** ± 0.88	2.91 ± 0.88	-1.13 ± 0.26	0.27 ± 1.28	Complementary
Seed yield per plant (g)							
JMU-1339 x NARI-6	38.18** ± 0.48	-10.40** ± 0.23	23.40** ± 1.99	6.90 ± 1.99	-4.10** ± 0.26	3.70 ± 2.17	Complementary
JMU-1339 x EC-757665	33.23** ± 0.51	-3.40** ± 0.52	12.65** ± 2.34	2.70 ± 2.31	-0.35 ± 0.54	5.80 ± 3.02	Complementary

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

obtained by Shivani *et al*. (2011) and Mirzahashemi *et al*. (2013).

The hybrid showing positive and significant dominance (h) effects for number of branches per plant, number of capitulum per plant, number of seeds per capitulum and seed yield per plant was observed in the cross, JMU-1339 x NARI-6. For numbers of capitulum per plant, test weight, oil content and seed yield the hybrid of the cross, JMU-1339 x EC-757665 exhibited positive and significant dominance (d) gene effect. These results agree with those obtained by Shivani and Varaprasad (2016). In the cross,JMU-1339 x NARI-6 significant and negative dominance (h) effect was observed for traits like days to 50% flowering, days to maturity and plant height. In cross, JMU-1339 x EC-757665 significant and negative dominance (d) effect was recorded for traits like days to 50% flowering, days to maturity, plant height and hull content. This indicating dominance of earliness in respective crosses for above traits. These results agree with those obtained by Gupta and Singh (1993). Greater importance of dominance effect in the expression of all the studied traits, was estimated through result by estimating magnitude of dominance (h) component, which was higher than that of additive (d) gene effect. For the exploitation of dominance effect non-conventional breeding procedure might be adopted. Epistasis gene effects are known to contribute a sizable part of variation in the genetic makeup of character which shows higher estimate of dominance effects (Gamble, 1962). In the present investigation also, high estimate of dominance (h) effect for above traits were associated with significant epistasis interaction in the respective crosses.

Considering the contribution of epistasis gene effect for any character in relation to magnitude, dominance x dominance (*l*) interaction had enhancing effect as compare to additive x additive (i) and additive x dominance (j) in the expression of days to 50% flowering, days to maturity, and oil content in the cross,JMU-1339 x NARI-6 and for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of seed per capitulum, hull content and seed yield per plant in the cross, JMU-1339 x EC-757665. These results are in harmony with those reported by; Kumar *et al.* (2012) and Mirzahashemi *et al*. (2013). Non fixable gene effect was important in the expression of these traits in these crosses could be exploited by bi-parental mating of recurrent selection or the use of population improvement concept as an alternative to conventional method. The sign of dominance x dominance (l) effect was negative for plant height, number of branches per plant, number of seed per capitulum test weight and hull content in the cross,JMU-1339 x NARI-6 and for days to 50% flowering, number of capitulum per plant and test weight in the cross, JMU-1339 x EC-757665 indicating their reducing effect in the expression of these characters. These results are in harmony with those reported by Gadekar and Jambhale (2002) and Golkar *et al* (2018). The sign of dominance x dominance (*l*) component was positive in the other character indicating their enhancing effect in the expression of that character. The additive x additive (i) interaction had greater effect as compare to additive x dominance (j) and dominance x dominance (*l*) effect in the expression of number of branches per plant, number of capitulum per plant, number of seeds per capitulum, seed yield per plant and hull content in the cross, JMU-1339 x NARI-6; number of capitulum per plant, test weight and oil content in cross, JMU-1339 x EC-757665. This indicated better response to selection pressure in population for these characters. In these crosses, improvement could be made by cyclic method of breeding*i.e.* recurrent selection, in which desirable recombinants are selected and intercrossed to pool the favorable genes for synthesizing the elite population.

According to result estimated, the significance values for additive and additive x additive epistasis was observed in cross, JMU-1339 x NARI-6for traits like days to 50% flowering, days to maturity, number of branches per plant and oil content. And in cross, JMU-1339 x EC-757665 for days to 50% flowering, days to maturity, plant height and hull content. These results are in harmony with those reported by Shivani *et al.* (2011). The sign of dominance (h) and dominance x dominance (l) parameter being opposite indicates involvement of duplicate type of epistasis in the inheritance of a trait. Such type of gene actions also observed for various traits in the present investigation. The presence of duplicate epistasis would be detrimental for rapid progress, making it difficult to fix genotypes with increased level of character manifestation because the opposite effect of one parameter would be cancelled out by the negative effect of another parameter. The duplicate epistasis was observed in days to 50% flowering, days to maturity, number of branches per plant, number of seed per capitulum, test weight and oil content in cross, JMU-1339 x NARI-6. In cross, JMU-1339 x EC-757665 duplicate epistasis was observed for traits like days to maturity, plant height, number of capitulum per plant, test weight and hull content. The present findings are akin to the results reported by Gupta and Singh (1991); Golkar *et al* (2012) and Kumar *et al.* (2012).

The involvement of complementary epistasis in the expression of a trait indicated by the similar sign of dominance (h) and dominance x dominance (l) parameter. Complementary epistasis was observed for plant height, number of capitulum per plant, hull content and seed yield per plant in cross, JMU-1339 x NARI-6; for days to 50% flowering, number of branches per plant, number of seed per capitulum, oil content and seed yield per plant in cross, JMU-1339 x EC-757665. These results are in harmony with those reported by Kumar *et al.* (2012); Mirzahashemi *et al*. (2013), Nakhaei *et al.* (2014) and Golkar *et al.* (2018).

Conclusion

In crosses for some characters duplicate epistasis were involved. This suggests the need of specific breeding procedure such as intermating of most desirable segregants followed by selfing and selecting superior genotypes coupled with progeny testing to exploit the population under study. Also, these traits might be improved through recurrent selection in bi-parental progenies that would help in exploiting the duplicate type of non-allelic interaction and allow recombination and concentration of gene having cumulative effects in population as this method is helpful in breaking up undesirable linkage. When additive effects are larger than non-additive ones, selection in early generation would be effective, while if the non-additive portions are larger than additive one, the improvement of the character need intensive selection through later generations.

Also, the characters controlled by additive gene effect can be improved by pedigree method of selection. In contrast to it other characters were controlled by or non-additive gene effects in different crosses, hence those could be successfully improved by heterosis breeding or hybridization.

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