Generation mean analysis to estimate genetic parameters of quantitative traits in Safflower (Carthamus tinctorius L.)

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ABSTRACT

Generation mean analysis was employed in a cross between GMU-2830 X GMU-7612 of safflower to partition the mean into various components viz., additive, dominance and epistasis. Five generations viz., P_1, P_2, F_1, F_2 and F_3 of this cross were evaluated. The scaling tests were applied to the data to detect the presence or absence of non-allelic interactions. The results of the scaling test showed significant values of C & D scales for majority of traits under study. In several traits positive significant additive gene effects was found viz., days to 50% flowering, number of primary branches/plant, number of capitulum/plant, 100 seed weight(g), and oil percentage. Significant negative additive gene effects was found in traits viz., number of seeds/capitulum and seed yield(g). Similarly, dominant gene effects was positively significant for seed yield(g) and oil percentage. Significant negative dominant gene effects was found for days to 50% flowering, days to maturity, plant height, number of primary branches/plant, number of capitulum/plant, number of seeds/capitulum and 100 seed weight(g). Epistasis was present in all of the characters under study. Additive × additive gene effects were found significant for days to 50% flowering, plant height, number of primary branches/plant, number of capitulum/plant, number of seeds/capitulum, seed yield(g) and oil percentage. Significant dominance × dominance gene interaction were found for days to 50% flowering, days to maturity, number of primary branches/plant, number of capitulum/plant, number of seeds/capitulum, seed yield(g) and oil percentage.

Keywords: Generation mean analysis, safflower, scaling test and five parameters.

I. INTRODUCTION

Safflower, one of humanity's oldest crops, belongs to Compositae family with chromosome number, 2n=24. was first cultivated in the New World in 1899, but it wasn't until the 1950s that it was put to commercial use. It is a winter annual plant that has many spines on both the leaves and the bracts. The crop is mostly farmed as an oilseed in dry, hot areas. Around the world, it is cultivated as a source of pigment and edible oil. The seed contains 24-36% oil thatcontain good amount of linoleic acid (78%), which is helpful for reducing blood cholesterol content..

Generation mean analysis is one such useful tool for estimation of gene effects for polygenic traits which can estimate epistatic gene effects such as additive × additive, dominance × dominance and additive × dominance effects (Kearsey and Pooni, 1996). Development of hybrids is an important phase of crop improvement; Generation mean analysis (Mather and Jinks, 1982) provides information on the relative importance of average effects of the genes (additive effects), dominance deviations and effects due to non-allelic genetic interactions such as additive x additive (aa), dominance x dominance (dd) and additive x dominance (ad) effects to determining genotypic values of the individuals and consequently, mean genotypic values of families and generations., Such analysis is very useful for rapidly obtaining the overall information on the various genetic system involving and for fixing selection indices for speedy gains in segregating generations. Therefore, in the present study gene interaction was estimated for yield attributing characters in safflower by using generation mean analysis.

II. MATERIAL AND METHODS:

To understand the genetic nature of yield and its contributing traits have been carried out by growing the parents, P_1 and P_2 along with F_1, F_2 and F_3 in Randomized Block Design (RBD) replicated four times. The experimental material for this investigation was two safflower genotypes namely, GMU-2830 and GMU-7612. Within each replicate, cross populations were first randomized and separate randomization was followed for all the replications. Generations within crosses/populations were also randomized separately. The row to row spacing was 45 cm and

the plant to plant spacing was kept at 20 cm for each replication. Generations i.e., P_1, P_2 and F_1 were grown in five rows each where as F_2 & F_3 generation in 15 rows each were grown. Irrigation at sowing was given to ensure complete seed germination. Thereafter, irrigation, weeding and other agronomical operations were adopted for normal growth of the plant. Scaling test was conducted as suggested by Mather (1949). The adequacy of simple additive-dominance model was detected by employing C and D scaling test suggested by Mather and Jinks (1971). The additive-dominance model was considered inadequate when any one of the two scales was found to deviate significantly from zero.

III. RESULTS AND DISCUSSION
Quantitative characters which are of great interest, are governed by large number of genes having their own effects. These are too modified by

several environmental factors (Johansen, 1926). Thus, analysis at the level of individual genes become impractical and whole genome analysis over the totality of the gene should be undertaken (Wright, 1956). The genetic variability, thus, should be partitioned into its broad components. The present study was planned to estimate the nature and magnitude of allelic and non-allelic interactions in black gram. The result of scaling test either both or C and D alone revealed significant values indicates the additive-dominance model was not found adequate for all traits in this cross. The failure of additive-dominance model was attributed mainly due to the epistasis. The generation mean analysis was adopted to detect non-allelic interaction component of the mean of the phenotypic distribution. The results of scaling test and genetic parameters in this cross were presented in (Table 1, 2 and 3)

Table 1: Mean performance of the five generations (P_1, P_2, F_1, F_2 and F_3) of the cross GMU-2830 x GMU-7612

Generations/Traits	P_1	P_2	F_1	F_2	F_3
Days to 50 % Flowering	93.75 ± 0.456	86.8 ± 0.762	94.3 ± 0.617	93.517 ± 0.46	102.75 ± 0.54
Days to maturity	147.65 ± 0.758	146.65 ± 0.837	141.2 ± 0.494	141.55 ± 0.69	144.31 ± 0.78
Plant Height	97.5 ± 1.56	97.95 ± 2.188	89.05 ± 2.301	95.733 ± 1.237	101.05 ± 1.561
No. of primary branches/plant	6.65 ± 0.685	5.6 ± 0.588	8.95 ± 0.672	7.933 ± 0.43	8.55 ± 0.76
No. of capitulum /plant	20.85 ± 1.431	17.4 ± 1.402	31.35 ± 1.438	24.617 ± 0.919	29.917 ± 0.091
No. of Seeds /capitulum	25 ± 1.24	44.9 ± 2.419	53.6 ± 2.399	49.083 ± 2.391	52.9 ± 1.720
100 seed weight (g)	4.2 ± 0.234	4.35 ± 0.219	5.35 ± 0.333	4.467 ± 0.254	4.333 ± 0.065
Seed yield (g/plot)	11.665 ± 0.528	17.79 ± 1.279	23.32 ± 0.753	25.345 ±0.613	22.512 ± 1.344
Oil %	36.41 ± 0.225	34.283 ± 0.352	39.205 ± 0.295	37.955 ± 0.536	36.205 ± 0.667

Table 2: Estimation of scaling test of five generations viz., P_1, P_2, F_1, F_2 and F_3 of the cross GMU-2830 x GMU-7612

Scaling Test		
Characters	C	D
Days to 50 % Flowering	-4.917 ± 1.193**	-162.083 ± 0.959**
Days to maturity	10.5 ± 1.57**	-288.767 ± 1.294**
Plant Height	-9.383 ± 3.606**	-184.817 ± 3.775**
No. of primary branches/plant	-1.583 ± 1.181	-11.017 ± 1.135**

No. of capitulum /plant	2.483 ± 2.54	-27.65 ± 2.119**
No. of Seeds /capitulum	-19.233 ± 5.52**	-62.267 ± 5.99**
100 seed weight	1.383 ± 0.628*	-8.817 ± 0.481**
Seed yield	-25.286 ± 1.596**	-35.122 ± 1.678**
Oil %	-2.717 ± 1.131*	-74.193 ± 0.743**

** significance at 1% probability level, * significance at 5% probability level

Table 3: Estimation of gene effects based on performance of five generations viz., P_1, P_2, F_1, F_2 and F_3 of the cross GMU-2830 x GMU-7612

Characters	m (Hayman)	d-j (Hayman)	H (Hayman)	i (A X A)	l (D X D)	χ^2	Type of epistasis
Days to 50 % Flowering	93.52 ± 0.23**	3.47 ± 0.22**	-24.1 ± 0.69**	-28.12 ± 0.76**	51.33 ± 2.22**	541.15**	Duplicate
Days to maturity	141.55 ± 0.34**	0.50 ± 0.28	-7.61 ± 0.94**	-1.66 ± 1.08	13.82 ± 3.10**	73.02**	Duplicate
Plant Height	95.73 ± 0.62**	-0.22 ± 0.70	-18.63 ± 2.61**	-9.98 ± 2.50**	10.53 ± 7.25	12.62**	Duplicate
No. of primary branches/plant	7.93 ± 0.21**	0.52 ± 0.22*	-0.96 ± 0.91	-3.79 ± 0.89**	6.00 ± 2.48*	6.95*	Duplicate
No. of capitulum /plant	24.61 ± 0.46**	1.72 ± 0.50**	-9.64 ± 1.50**	-21.86 ± 1.70**	46.22 ± 4.68**	42.3**	Duplicate
No. of Seeds /capitulum	49.08 ± 1.19**	-9.95 ± 0.67**	-7.16 ± 4.35	-25.82 ± 4.06**	32.4 ± 12.33*	157.06**	Duplicate
100 seed weight	4.46 ± 0.12**	-0.07 ± 0.08	0.94 ± 0.37*	-0.13 ± 0.40	1.64 ± 1.21	0.93	Complementary
Seed yield	25.34 ± 0.30**	-3.06 ± 0.34**	6.20 ± 1.14**	-2.38 ± 1.12*	-20.51 ± 3.24**	231.46**	Duplicate
Oil %	37.95 ± 0.26**	1.06 ± 0.10**	5.50 ± 0.63**	1.64 ± 0.71*	-6.00 ± 2.27**	597.03**	Duplicate

** significance at 1% probability level, * significance at 5% probability level

Days to 50% flowering

Components of gene effect m, d, h, i and l were found highly significant. The largest interaction was found for 'l' which estimates the presence of dominance × dominance epistasis more predominantly. The components of gene effect 'h' and 'l' was not with similar sign and so duplicate gene action is governing for this trait. The chi square value for joint scaling test exhibited highly significant predicting the presence of non-allelic interaction Hence accordingly more reliance should be placed on simple selection between the families or recurrent selection can be advocated for improvement of this cross. (Iqbal & Nadeem. 2003).

Days to Maturity

The components of gene effect m, d and l have positive value while the gene effect h and i have negative value. The gene effect m, h, and l were found highly significant. The highest interaction was found for 'l' (dominance × dominance) gene interaction. Since the value of gene effect 'h' and 'l' have contrasting sign, the trait is controlled by duplicate gene action. The chi square value for the joint scaling test was found highly significant. Higher value of non-fixable gene effect was present as compare to fixable gene indicating the presence of higher contribution of non-additive gene effect suggesting the possibility for improvement of the trait through recurrent selection. (Kumar et al., 2012).

Plant height (cm)

Components of gene effect m, h and i were found highly significant and the gene effects d and l were found non-significant. The components of gene effects m, l possess positive sign while d, h, and i possess negative sign. The trait is governed by duplicate gene action as the gene effect 'h' and 'l' do not have similar sign. The chi square value for joint scaling test exhibited highly significant. Similar result was also obtained by Kotecha and Zimmerman (1978), Shahbazi and Saeidi, (2007),

Mirzahashemi et al. (2013), Nakhaei et al. (2014) and Waghmode et al. (2021).

Number of Primary branches/plant

Components of gene effect m, and i were noted highly significant while the component of gene effect d and l were significant and h was non significant. Highest interaction was obtained for dominance × dominance. Since the dominance effect and dominance × dominance gene effect have contrasting sign, the trait is governed by duplicate gene action. The joint scaling test was found significant. The result is in association with earlier findings of Narkhede and Patil (1987), Kumar et al. (2012); Mirzahashemi et al. (2013); Nakhaei et al. (2014); Shivani and Varaprasad (2016); Varaprasad (2016); Waghmode et al. (2021).

Number of capitulum/plant

Components of the gene effect m, d, h, i and l were highly significant with highest gene interaction found for 'l' (dominance × dominance) and duplicate gene action is governing for this trait as the gene effect 'h' and 'l' had opposite sign. The chi square test for the joint scaling test was found highly significant. Mandal and Banerjee (1997) and Golkar et al. (2012) reported dominance inheritance for this character..

Number of seeds /capitulum

Components of gene effect m, h, i were found highly significant and l as significant while the gene effect h was found non-significant. For this trait, duplicate gene action was present as the gene effect 'h' and 'l' had opposite sign. The chi square test for joint scaling test was found highly significant. Waghmode et al. (2021) found the presence of non-allelic interaction for the inheritance of the trait.

100 seed weight (g)

Components of gene effect m and h was found significant. The component of gene effect d, i and l were not significant. Since the components of gene effect h and l have same sign, complementary gene action is governing for the inheritance of this trait. The chi square value for joint scaling test was not found significant. Mirzahashemi et al. (2013) reported similar results.

Seed yield (g)

Components of gene effects m, d, h, and l were found highly significant while the gene effect "i" was found significant. The gene effect "h" and "l" have opposite sign so duplicate gene action is governing for this trait. The chi square value was found highly significant. Similar findings also reported by Shivani et al. (2011); Kumar et al.

(2012); Mirzahashemi et al. (2013); and Waghmode et al. (2021).

Oil content (%)

The components of gene effect m, d, h, and l were found highly significant and i was found significant. The highest interaction was found for 'l' (dominance × dominance) interaction. Since the components of gene effect h and l have opposite sign, duplicate gene interaction is governing for inheritance of this trait. The chi square value for joint scaling test was found highly significant..Similar findings also observed by Kumar et al. (2012) and Waghmode et al. (2021).

The results of this study showed that as a consequence of higher magnitude of interactions, the non-fixable gene effects were higher than the fixable indicating the major role of non additive gene effects. In view of high magnitude of gene interactions the successful breeding methods will be the ones, which can mop-up the genes to form superior gene constellations interacting in a favourable manner. Some forms of recurrent selection namely, diallele selective mating or biparental mating in early segregating generations and selections followed by hybridization might prove to be effective alternative approaches.

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