Inheritance pattern of important qualitative traits in Safflower

(*Carthamus tinctorious* L.)

Abstract

Safflower is an important oilseed crop with poorly studied genetic inheritance of the characters. In this study genetically diverse parents were selected which had many contrasting qualitative traits. The parents used in the study were GMU-1217, GMU- 6854, GMU-6891, GMU-2830, EC 755673 and EC755664. Crosses were made between the parents. Observations of parental traits, traits appearing in F_1 and F_2 were studied and the data were analysed for goodness of fit by χ^2 test for appropriate ratio. A total of seven qualitative characters were studied, they were, branching type, mode of branching, mode of spininess, length of bract, leaf dentation, form of leaf shape, flower colour change at maturity, segregation in F_2 generation for different traits showed the presence of either complementary or inhibitory gene action for all the characters studied while other crosses were found to have a combination of both monogenic and digenic gene action.A proper knowledge of inheritance of Agronomic traits helps in planning of efficient strategy for further crop improvement.

Keywords: Safflower, complementary gene action, inhibitory gene action, monogenic, digenic

1. Introduction

Safflower (*Carthamus tinctorious L.*) is one of the oldest major oilseed crops in the world. Its seed contains 24-36% oil. The oil of safflower contain good amount of linoleic acid (78%), which is helpful for reducing blood cholesterol content. Safflower cakes contain about 40-45% protein. Safflower oil can also be used in the manufacture of paints, varnishes and linoleum. The leaves of this crop are rich in carotene, riboflavin and vitamin C, hence young seedlings are preferred by people as a green leafy vegetables in many parts of India. In the world scenario, the largest production of safflower comes from Kazakhstan (227K tonnes), which even comprise the 37% of total world production followed by U.S (88K tonnes) and Russia (67K tonnes) (INDEXBOX World - Safflower Seed - Market Analysis, Forecast, Size, Trends and Insights). In value terms, Russia, Kazakhstan and the Netherlands account for maximum export of 70% of global export in 2020 while largest importer country is China followed by Turkey and Belgium with 50% share of global import (INDEXBOX World - Safflower Seed - Market Analysis, Forecast, Size, Trends and Insights).

Knowledge of understanding the genetics of traits is desirable in deciding breeding approaches and strategies. Understanding the mode of gene action and inheritance detection and its component is contributing to safflower breeding (Mirsa *et al.,* 1994). Study on genetic components both additive and dominance helps in understanding trait gene action in environment is necessary for exploiting required breeding method. Besides additive and dominance effect, epistatic or non-allelic interaction also played an important role in genetic trait control (Singh & Pawar, 2005). In some cases, epistatic effects contribute in the expression of hybrid (Kearsey & Pooni, 1996). Several biometrical techniques are available which can be used for estimation of the magnitude of different components of genetic variation. A proper knowledge of inheritance of Agronomic traits helps in planning of efficient strategy for further crop improvement. Diversity for different trait in a crop plays an important role for sustainability of crop (Saisanthosh *et al.,* 2018). Thus, knowing the genetics of a character helps the breeder in deciding strategies and approaches to follow. In safflower less work is done in the inheritance study of qualitative characters like branching type, mode of branching, mode of spininess, length of bract, leaf dentations, form of leaf shape, flower colour change at maturity. So, in the present study, efforts are made to understand the inheritance of these qualitative traits and also to know whether there is presence of any interaction in the gene or among the genes

2. **Materials and Methods**

The Research work was conducted in the experimental field of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur, Chhattisgarh. The statistical field layout used was Randomized Block Design (RBD).

The research material consists of six parents, six F_{1s} and six F_{2s}. The parents used in the study were GMU-1217, GMU- 6854, GMU-6891, GMU-2830, EC 755673 and EC755664. The crosses were made among the parents in the *rabi* 2019-2020. Some seeds of F_{1s} were then grown to get F_2 generation. The crosses made were EC 755673 X GMU 6891, EC 755664 X GMU 2830, GMU 6854 X GMU 1217, EC 755673 X GMU 2830, EC 755673 X GMU 1217, EC 755664 X GMU 1217. The characters of parents, and the characters appeared in F_1 generation were recorded. Seeds of F_1 were harvested and sown in bulk in year 2020-21 to get the F_2 generation. In each cross observations of qualitative traits were recorded for each and every individual plant for the traits under study. The recorded data for each trait were analysed for goodness of fit by χ^2 test by comparing the observed and expected segregating ratio.

3. Results and Discussion

Mendel's experiments established that genes exist in its alternate forms called alleles. This discovery suggested a simple functional dichotomy between alleles, as if one allele did nothing and the other did everything to determine the phenotype. Genes can exist in more than two allelic states, and each allele can have a different effect on the phenotype. The interaction within alleles of gene controlling a single character may be dominant, incomplete dominance and co-dominance and are called intra-allele interaction. When there is an interaction occurs between different pairs of alleles influencing a character of an individual is said to be inter-allelic interaction or epistatic.When two or more genes influence a trait, an allele of one of them may have an overriding effect on the phenotype. When an allele has such an overriding effect, it is said to be epistatic to the other genes that are involved.The parents and the F_1 plants show dominant nature and the dominant character of the parents and the F_1 plants are given in table no-1. A total of seven qualitative traits were used for the study.

3.1 Inheritance pattern of the character Branching type:

In the cross GMU 6854 × GMU 1217, parent GMU-6854 had appressed type of branching whereas, GMU-1217 was spreading types. In F_1 all spreading types of plants were recorded, indicated dominant nature of spreading branching over appressed type. In F_2 generation, the observed values for spreading type and appressed types were fitted well in the ratio of 13:3 (Inhibitory gene action) (Table-1).This type of gene action occurs due to inhibition of the expression of active allele by another allele present at another loci. So the inheritance of this trait was governed by two genes or digenic. The calculated *chi square* value of the cross was 2.26 which was less than the table chi square value. So, the observed and expected values of the cross were in agreement and thus the ratio obtained is valid.

EC-755673 were spreading branching habit whereas GMU-6891 had appressed type branching. In F_1 (EC-755673 × GMU-6891), all the plants exhibited spreading type of branching. In F_2, plants were segregated in the ratio of 13:3 which was due to inhibitory gene action. The calculated *chi square* value was 0.49 which was lower than the table value, hence the ratio 13:3 considered fitted well with segregated values of spreading and appressed branching types in this cross. And the modes of gene interaction for the character were illustrated in table-2 and figure no 1.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al.*, (2018); Pratibha *et al.*, (2018) and Pratibha (2019).

3.2 Degree of spininess

EC-755664 had strong spines whereas GMU-1217 had medium spiny nature. In F_1 all the plants were recorded strong spines. The segregating population of the cross EC-755664 × GMU-1217 segregate the character spininess into strong spiny and medium spiny in the ratio of 3:1 (Table: 3).The calculated *chi square* value of the cross was 0.37 which was lower than the table value. The lower value of chi square indicates the agreement between the observed and expected value of the cross. Thus the null hypothesis is accepted and the ratio obtained is thus valid.

EC-755673 had strong spines whereas GMU-1217 had medium spiny nature. In F_1 all the plants were recorded strong spines. The segregating population of the cross EC 755673 × GMU-1217 segregate the capitulum with strong spines and capitulum with medium spines in ratio of 3:1 which shows the true dominance of more spiny to medium spiny and the absence of inter-allelic gene interaction which is the presence of inhibitory gene action. The calculated value of the *chi square* was found to be 0.80. Since the calculated *chi square* value was lower than the table chi square value, the hypothesis is accepted which shows agreement between the observed and the expected value. The checker board for 3:1 inheritance pattern is illustrated in table- 3.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al*., (2018); Pratibha *et al.,* (2018) and Pratibha (2019).

3.3 Mode of Branching

Parent EC-755673 had complete branching whereas GMU-1217 had top branching habit. In F_1 all the plants were recorded complete branching. In F_2 all the population segregated for the character in the ratio of 9 complete branching : 7 top branching which indicated its digenic inheritance with complementary gene action (table-5). The calculated value of the *chi square* was 1.22 which is lower than the table *chi square* value hence expected ratio accepted. The checker board explanation for inheritance of the character is given in table-4. The different mode of branching is shown in figure-2.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al.*, (2018); Pratibha *et al.*, (2018) and Pratibha (2019).

3.4 Leaf dentations

Parent EC-755664 had very strong dentations whereas GMU-1217 had medium dentations on leaves. In F_1 all the plants were recorded very strong dentations. F_2 population segregated for leaf dentation in the ratio of 15 very strong: 1 medium which indicated its digenic nature of inheritance and duplicate gene action. The calculated *chi square* value of the cross was obtained as 5.18 which were found less than the table value when check at 1% probability level.

Parent GMU-6854 had very strong leaf dentations whereas GMU-1217 had medium dentations on leaves. In F_1 all the plants were recorded very strong dentations on leaves. The segregating population of the cross GMU 6854 × GMU 1217 segregated in very strong dentations and medium dentations in the ratio of 13:3, respectively (table-5). It indicated that this trait was governed by two genes with inhibitory gene action. The calculated *chi square* value of the cross was 1.38 which is lower than the table value. The lower chi square value indicates good agreement of the observed and expected values of the cross for the inheritance of the trait and thus the observed ratio is valid.

Parent EC 755673 had very strong leaf dentations whereas GMU-6891 had medium dentations on leaves. In F_1 all the plants were recorded very strong dentations on leaves. The cross EC 755673 × GMU 6891 segregated the trait very strong dentations and medium dentations in the ratio of 15:1, respectively which explains the duplicated gene action. The calculated *chi square* value of the cross was 0.84 which was found to be lower than the table *chi square* value. The lower calculated *chi square* value indicates the acceptance of the hypothesis and good agreement between the observed and expected value. So the observed ratio is valid and it explains the inheritance of the trait for this cross.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al*., (2018); Pratibha *et al.*, (2018) and Pratibha (2019).

3.5 Form of leaf shape

Parent EC-755664 had fusiform leaves whereas GMU-1217 had ovate leaves. In F_1 all the plants were recorded fusiform leaves. The F_2 population segregated in the ratio of 15 fusiform: 1 ovate, which indicated presence of two genes to control this trait with duplicate gene action (table-6). The calculated *chi square* value of the test is 2.89 which were lower than the table *chi square* value. The lower value of *chi square* indicates the good agreement of observed and expected value and thus the hypothesis is accepted and for the inheritance of the trait the trait being governed by two genes with duplicate gene action is valid.

Parent GMU 6854 had fusiform leaves whereas GMU-1217 had ovate leaves. In F_1 all the plants were recorded fusiform leaves, indicating its dominant nature. In F_2 the population of the cross GMU 6854 × GMU 1217 were segregated a ratio of 13:3 which indicated digenic gene with inhibitory gene action. The *chi square* calculated value of the cross was 0.11 which were lower than the table *chi square* value, indicates the good agreement of observed and expected values of the cross.

Parent EC-755673 had fusiform leaves whereas GMU-6891 had ovate leaves. In F_1 all the plants were recorded fusiform leaves, indicating its dominant nature. The segregating generation of the cross EC 755673 × GMU 6891 segregate the fusiform and ovate leaf form in the ratio of 15:1 which is the presence of epistasis in the form of duplicate gene action. The calculated *chi square* value of the cross is 0.07 which was lower than the table *chi square* value. So the lower value of calculated *chi square* value indicates the acceptance of the hypothesis and the obtained ratio is valid to explain the inheritance of the trait. The checker board calculation for inheritance of the character is illustrated in table- 6.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al*., (2018); Pratibha *et al.*, (2018) and Pratibha (2019).

3.6 Floret colour change at maturity

Parent EC-755664 had yellow to yellow floret colour at faded stage whereas GMU-2830 had yellow to red florets after faded. In all the plants of F_1 yellow to yellow floret colour were recorded at its faded indicating its dominant nature. In F_2 of the cross EC-755664 × GMU- 2830, the floret colour at faded were segregated in the ratio of 13:3 which indicate the presence of two genes interacting to give the inhibitory type of gene action (table-7). The calculated *chi square* value of the cross was 0.89 which was found to be lower than the table *chi square* value. So there is presence of good agreement of the observed and expected values. Thus the ratio obtained is valid to explain the inheritance of the character for this trait.

Parent EC-755664 had yellow to yellow floret colour at faded stage whereas GMU-1217 had yellow to red florets after faded. In all the plants of F_1 yellow to yellow floret colour were recorded at its faded indicating its dominant nature. In the cross EC-755664 × GMU-1217, the F_2 population had segregated into yellow to yellow floret colour and yellow to red floret colour in the ratio of 15:1. The presence of duplicate gene action indicates the trait was governed by two genes. The calculated *chi square* value of the cross is 0.04 which is found to be lower than the table *chi square* value. So the obtained ratio is valid to explain the inheritance of the trait.

The present findings are confirming the findings of Purkayastha (2017), Purkayastha *et al*., (2017), Das and Shrivastava, (2018), Bhat *et al*., (2018), Pratibha *et al.*, (2018) and Pratibha (2019).

3.7 Bract Length

Parent EC-755664 had medium length bracts whereas GMU-1217 had short length bracts in capitulums. In all the plants of F_1 medium bract length were recorded indicating its dominance over short bract length. The F_2 population of cross EC-755664 × GMU-1217 segregated in a ratio of 9 medium bract length : 7 short bract length, indicating its digenic inheritance, with complementary gene action (table-8). The calculated value of *chi square* was 0.69, which is lower than the table value. Hence the ratio 9:7 was found good for segregation of bracts length in capitulums.

Parent EC-755673 had medium length bracts whereas GMU-2830 had short length bracts in capitulums. In all the plants of F_1 medium bract length were recorded indicating its dominance over short bract length. The F_2 population of cross EC-755673 × GMU 2830 segregated in a ratio of 9 medium bract length : 7 short bract length, indicating its digenic inheritance, with complementary gene action. The calculated value of *chi square* was 2.24 , which is lower than the table value. Hence the ratio 9:7 was found good for segregation of bracts length in capitulums. Different bract length is shown in figure 7.

The present findings are confirming the findings of Purkayastha (2017); Purkayastha *et al*., (2017); Das and Shrivastava, (2018); Bhat *et al*., (2018); Pratibha *et al.*, (2018) and Pratibha (2019).

Table 1 : List of dominant traits observed in parents, and F_1s

Genotypes	Number of plants observed	Dominant Qualitative Characters expressed						
		Branching Type	Mode of branching	Mode of spineness	Leaf dentation	Form of leaf shape	Flower colour change at maturity	Capitulum Outer Bract Length
GMU-1217	20	Appresh	Medium and basal branching	Medium spiny	Strong	Fusiform	Yellow to Red	Medium Bract Length
GMU- 6854	20	Appresh	Medium branching	Medium spiny	Strong	Fusiform	Yellow to yellow	Medium Bract Length
GMU-6891	20	Appresh type	Medium and basal branching	Medium spiny	Strong	Fusiform	Yellow to Yellow	Medium Bract Length
GMU-2830	20	Sparsh/ spreading type	Medium and basal branching	More spiny	Very strong	Ovate	Yellow to Red	Short Bract Length
EC 755673	20	Sparsh/ Spreading type	Medium branching	Medium spiny	Strong	Fusiform	Yellow to Red	Medium Bract Length
EC755664	20	Sparsh/ Spreading type	Medium branching	Medium spiny	Strong	Fusiform	Yellow to Red	Medium Bract Length
EC 755673 X GMU 6891	20	Sparsh/ Spreading type	Medium branching	Medium to strong Spiny	Strong	Fusiform	Yellow to Yellow	Medium Bract Length
EC 755664 X GMU 2830	20	Spreading type	Medium and Basal branching	More spiny	Very strong	Ovate	Yellow to yellow	Medium Bract Length
GMU 6854 X GMU 1217	20	Appresh	Medium and basal branching	Medium to strong spiny	Strong	Fusiform	Yellow to yellow	Medium Bract Length
EC 755673 X GMU 2830	20	Spreading/ Sparsh type	Medium and basal branching	More spiny	Very strong	Ovate	Yellow to yellow	Medium Bract Length
EC 755673 X GMU 1217	20	Spreading/Sparsh type	Medium to basal branching	Medium to strong spiny	Strong	Fusiform	Yellow to yellow	Medium Bract Length
EC 755664 X GMU 1217	20	Spreading / Sparsh type	Medium to basal branching	Medium to strong spiny	Strong	Fusiform	Yellow to yellow	Medium Bract Length

Table-2: Inheritance pattern of branching type in different crosses of Safflower

S.No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Spreading type	Appreshed type	Spreading type	Appreshed type			
1.	GMU 6854 × GMU 1217	Spreading type of branching	739	149	721.5	166.5	13:3	2.26	0.10-0.20
2.	EC-755673 × GMU-6891	Spreading type of branching	711	189	731	169	13:3	2.91	< 0.10

Table-3: Inheritance pattern of degree of spininess in different crosses of Safflower

S.No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			More Spiny	Medium Spiny	More Spiny	Medium Spiny			
1.	EC-755664 × GMU-1217	Strong Spines	689	219	681	227	3:1	0.37	0.50- 0.70
2.	EC-755673 × GMU 1217	Strong Spines	647	231	658.5	219.5	3:1	0.80	0.30- 0.50

Table-4: Inheritance pattern of degree of mode of branching in different crosses of Safflower

S.No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Complete Branching	Top Branching	Complete Branching	Top Branching			
1.	EC-755673 × GMU-1217	Complete Branching	299	236	234	300.9	9:7	0.03	0.80-0.90

Table-5: Inheritance pattern of leaf dentation in different crosses of Safflower

S.No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Strong Dentation	Medium Dentation	Strong Dentation	Medium Dentation			
1.	EC-755664 × GMU-1217	Strong Dentation	794	36	778.12	51.87	15:1	5.18	> 0.1
2.	GMU-6854 × GMU-1217	Strong Dentation	754	157	740	170.8	13:3	1.38	0.20-0.30
3.	EC-755673 × GMU-6891	Strong Dentation	729	42	722.8	48.18	15:1	0.84	0.30-0.50

Table-6: Inheritance pattern of form of leaf shape in different crosses of Safflower

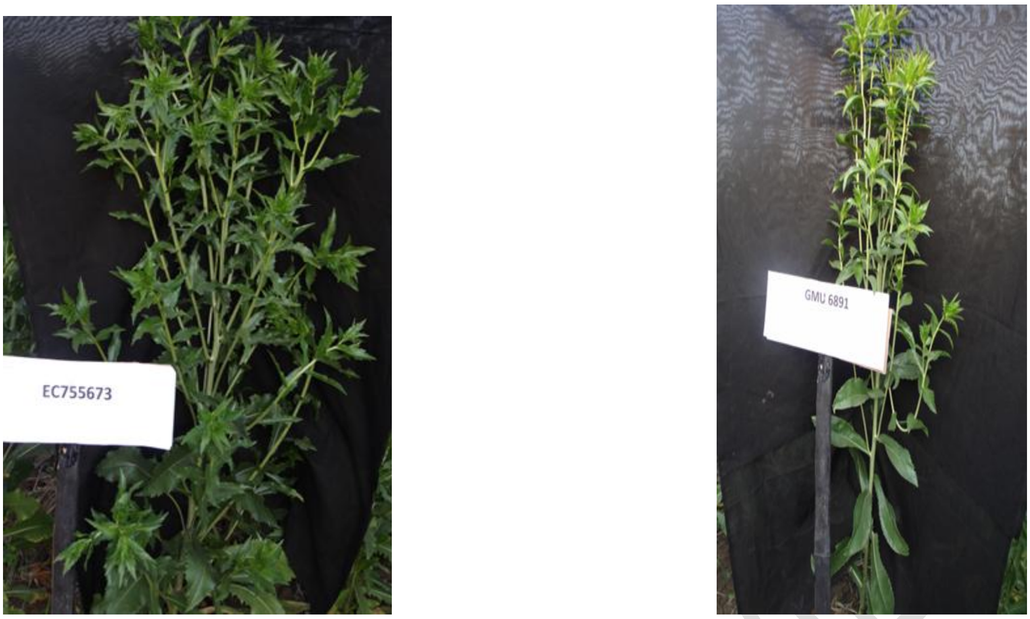
S.No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Fusiform Leaf	Ovate Leaf	Fusiform Leaf	Ovate Leaf			
1.	EC-755664 × GMU-1217	Fusiform Leaf	790	40	778.125	51.87	15:1	2.89	>0.10
2.	GMU-6854 × GMU-1217	Fusiform	745	167	741	171	13:3	0.11	0.70-0.80
3.	EC-755673 × GMU-6891	Fusiform	720	50	721.87	48.125	15:1	0.07	0.70-0.80

Table-7: Inheritance pattern of form of floret colour change at maturity in different crosses of Safflower

S. No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Yellow to Yellow	Yellow to Red	Yellow to Yellow	Yellow to Red			
1.	EC-755664 × GMU-1217	Yellow to Yellow floret Colour	850	55	848.4	56.5	15:1	0.04	0.80-0.90
3.	EC-755664 × GMU-2830	Yellow to Yellow floret colour	696	174	706.8	163.12	13:3	0.89	0.30-0.50

Table-8: Inheritance pattern of form of bract length in different crosses of Safflower

S. No.	Crosses	Character recorded in F_1	Observed frequencies in F_2		Expected Frequencies in F_2		Expected Ratio	Chi Square Value	Probability Value
			Medium Bract Length	Short Bract Length	Medium Bract Length	Short Bract Length			
1.	EC-755664 × GMU-1217	Medium Bract Length	371	450	359.18	461.81	9:7	0.69	0.30-0.50
3.	EC-755673 × GMU-2830	Medium Bract Length	388	268	369	287	9:7	2.24	0.10-0.20



Spreading type Appreshed type

Fig. 1 Branching type for the cross EC-755673 × GMU-6891

Fig 2: Mode of branching for the cross EC-755673 × GMU-1217

4. Conclusion:

Inheritance of the trait branching type was found to segregate in the ratio of 15 spreading type :1 appreshed type (Duplicate gene action) and 13 spreading type :3 appreshed type The trait degree of spininess was found to segregate in 3:1 ratio in F_2 populations depicting the true dominance nature of more spininess to less spininess and absence of epistasis. Inheritance pattern of mode of branching was segregated in 9 complete branching: 7 top branching. The trait leaf dentation segregate in the ratio of 15 very strong: 1 medium Inheritance pattern of character leaf shape was found segregated in ratio of 15 fusiform: 1 ovate and 13:3 indicating digenic gene with inhibitory gene action. Inheritance of bract length was found segregated in 9 medium bract length : 7 short bract length. The inheritance study found that except for character degree of spininess, the other characters were found governed by two genes showing presence of different types of epistasis for the inheritance of the trait in F_2 population of the crosses.

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References:

Ashri A, and Efron Y. Inheritance studies with fertile interspecific hybrids of three *Carthamus* species. Crop Sci. 1964;4: 510-514.

Bhat S, Pratibha, Shrivastava R, and Singh MK. Molecular characterization of safflower (*Carthamus tinctorious* L.) germplasm using SSR markers. J. Agril. Issues 2018; 23 (1) : 18-21.

DAS A, and SHRIVASTAVA R. Inheritance study of some qualitative traits in safflower (*Carthamus tinctorious* L.). J. Oilseeds Res. 2018; 35(4) : 260-263.

Golkar P, Arzani A, and Rezaei AM. Inheritance of flower colour and spinelessness in safflower (*Carthamus tinctorius* L.), J. Genet. 2010; 89(2) : 259– 262

Griffiths A J F, Wessler S R, Lewontin R C, Gelbart W M, Suzuki D T and Miller J H. 2004 An introduction to genetic analysis, 8th edition. W. H. Freeman, New York, USA.

Joglekar R G. and Deshmukh N. Y. Inheritance of some characters in safflower (*Carthamus tinctorious* L.). Nagpur Agricultural College Magazine 1958; 32(1): 11-19.

Kearsey M. J. and Pooni H. S. 2004 The genetical analysis of quantitative trials, 2nd edition. Chapman and Hall, London.

Mirsa SC, Rao VS, Dixit RN, Surve VD, Patil VP. Genetic control of yield and its components in bread wheat. Indian J. Genet. Plant Breed. 1994; 54:77-82

Narkhede B N. and Deokar A B. Inheritance of spininess and pericarp types in safflower. J. Maharashtra Agric. Univ. 1990; 15, 279–281.

Pratibha Bhat S and Shrivastava R. Inheritance of flower related traits in safflower (*Carthamus tinctorious* L.) J. Agril. Issues 2018; 23(1) : 70-74.

Pratibha 2019. Genetics of qualitative traits in safflower (*Carthamus tinctorius* L.) M. Sc. Thesis, Department of Genetics and Plant Breeding, IGKV, Raipur.

Purkayastha S. 2017. Inheritance and QTL study in Safflower (*Carthamus tinctorius* L.) M. Sc. Thesis, Department of Genetics and Plant Breeding, IGKV, Raipur.

Purkayastha S, Shrivastava R, Patel NB, Nag S and Perveen N. Genetics of spininess and petal color in safflower (*Carthamus tinctorious* L.) J. Agril. Issues 2016; 21(2) : 11-14.

Ramachandran M and Goud J V. Gene action for seed yield and it's components in safflower. Indian Journal of Genetics and Plant Breeding, 1982; 42(2): 213-220.

Saisanthosh K, Joseph Raju T, Kadirvel P, Keshavalu K, Razia S, Praduman Y and N Mukta. Correlations among seed traits: implications for breeding high oil yield in safflower (*Carthamus tinctorius* L.). J. of Oilseeds Res. 2018; 35(1) : 27-32.

Singh S. and Pawar I. S. 2005 Theory and application of biometrical genetics, 1st edition. CBS Press, Boca Raton, Florida, USA.