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Evaluation of Genetic Variability in Mutants of Black Turmeric

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ABSTRACT: A study on mutagenic studies in black turmeric (*Curcuma caesia* Roxb.)" was carried out at College of Horticulture, Mudigere during the year 2021-22. Black turmeric is an underexploited medicinal plant of Zingiberaceae family. Since it is a vegetatively propagated crop, induction of mutation and isolation of desirable mutants are the means for producing genetic variability. Mutagens like gamma rays (10, 15, 20, 25, 30, 35 Gy), EMS (1, 1.25, 1.5 %) and colchicine (0.1, 0.2, 0.3 %) were used along with untreated control. The experiment was laid out in RCBD design with thirteen treatments and two replication. There was a slight difference between GCV and PCV for all the characters indicating they were least affected by the environment. High heritability coupled with high genetic advance over percent mean were observed for all the yield parameters which indicates that these traits are under the influence of additive gene action which can be improved through selection.

Keywords: Black turmeric, GCV, PCV, heritability, genetic advance over percent mean.

INTRODUCTION

Black turmeric (*Curcuma caesia*) is an important medicinal plant of Zingiberaceae family with bluish-black rhizome. It is an under- exploited plant which is having high medicinal value which can be used in the treatment of piles, bronchitis, asthma, impotency, cancer, epilepsy and fever *etc*. The central forest department of India has declared it as endangered species due to biopiracy (Venugopal *et al*., 2017). As it is a highly valuable medicinal plant, crop improvement is necessary for the generation of varieties with better performance. Since it is a vegetatively propagated crop, crop improvement is mainly confined to selection of better performing varieties among the existing population. Due to the lack of seed set, genetic improvement by other approaches such as hybridisation is challenging. Mutation breeding has been proven to be an effective tool in the improvement of vegetatively propagated crops by generating variability in the existing population. Understanding the genetic variation created by mutagenic treatment, estimating the heritability and expected genetic advance are crucial for improving the efficiency of selection on genetic improvement program of black turmeric. Considering these aspects, the present study was carried out to estimate the genetic variability among the mutagenic treatment groups in black turmeric.

MATERIALS AND METHODS

Healthy and disease free rhizomes of 15 to 20 g were treated with three different mutagens like gamma (10, 15, 20, 25, 30, 35 Gy), EMS (1, 1.25, 1.5 %) and colchicine (0.1, 0.2, 0.3 %). Gamma irradiation was carried out in IIHR, Bangalore. Rhizome pieces were dipped in EMS and colchicine for four and thirty hours respectively. After mutagenic treatment the rhizomes were sown in protrays along with control. It was transplanted to the field after one month at a spacing of 30 × 30 cm. The experimental design was RCBD with two replications. FYM and fertilizers were applied as per the recommendations. The other cultural practices like irrigation, weeding and plant protection operation were carried out as and when required. The statistical analysis was done according to the methods of Panse and Sukhatme (1967) for the analysis of variance, Burton and Devane (1953) for genetic coefficients of variation and Johnson *et al.* (1955) for heritability in broad sense, genetic advance and genetic advance over percent mean.

RESULTS AND DISCUSSION

The present study was conducted to assess variability among different treatment group for growth, yield and quality traits. Analysis of variance revealed that there were significant differences among the treatments for all the traits studied (Table 1).

In the present investigation, estimates of phenotypic coefficient of variation for all the growth parameters were in general slightly higher than the genotypic coefficient of variation indicating that the influence of environmental factors were narrow for all these traits (Table 2).

Table 1: Analysis of variance for different growth, yield and quality traits.

Sr. No.	Source of variation	Replication	Treatment	Error	S. Em±	CD @ 5%
	Degree of freedom	**2**	**13**	**26**		
1.	Plant height	1.03	144.44*	1.24	0.79	2.43
2.	Pseudostem girth	0.27	2.28*	0.69	0.59	1.81
3.	No. of tillers per clump	0.62	1.29*	0.29	0.38	1.18
4.	Number of leaves per clump	11.38	22.24*	3.98	1.41	4.35
5.	Number of primary fingers/clump	0.35	0.56*	0.03	0.13	0.40
6.	Number of secondary fingers/clump	14.18	6.14*	0.39	0.44	1.39
7.	Number of tertiary fingers/clump	2.08	6.09*	0.67	0.58	1.79
8.	Length of rhizome/clump	0.01	2.61*	0.27	0.37	1.13
9.	Width of rhizome/clump	13.85	4.5*	0.40	0.45	1.38
10.	Weight of mother rhizome	27.01	23.83*	2.27	1.07	3.28
11.	Girth of mother rhizome	0.86	4.84*	0.27	0.37	1.13
12.	Yield/plant	231.68	1990.46*	7.58	1.95	6.00
13.	Dry recovery (%)	9.63	3.23*	0.76	0.62	1.90
14.	Oleoresin (%)	0.35	1.49*	0.15	0.28	0.85
15.	Crude fibre (%)	0.01	0.53*	0.05	0.15	0.48
16.	Curcumin content (%)	0.00	0.01*	0.00	0.00	0.00
17.	Essential oil (%)	0.00	0.00*	0.00	0.01	0.02

Note: * indicate significance at 5 % level

Table 2: Estimation of mean, range and genetic parameters for growth, yield and quality traits in black turmeric (*Curcuma caesia*).

Sr. No.	Traits	Mean±S.Em	Range		V_g	V_p	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
			Min.	Max.							
1.	Plant height(cm)	59.11±0.79	43.35	71.80	71.60	72.84	14.32	14.44	98.30	17.28	29.24
2.	Pseudostem girth (cm)	7.42±0.59	5.86	9.36	0.79	1.49	11.99	16.42	53.34	1.34	18.04
3.	Number of tillers per clump	4.64±0.38	3.30	5.85	0.50	0.79	15.18	19.17	62.73	1.15	24.76
4.	Number of leaves per clump	20.37±1.41	14.40	25.30	9.13	13.11	14.83	17.78	69.63	5.19	25.50
5.	Number of primary fingers/clump	3.64±0.13	2.71	4.59	0.26	0.30	14.07	14.93	88.79	1.00	27.31
6.	Number of secondary fingers/clump	8.57±0.44	5.84	11.64	2.88	3.27	19.78	21.09	88.02	3.28	38.24
7.	Number of tertiary fingers/clump	9.58±0.58	7.02	13.22	2.71	3.38	17.19	19.21	80.14	3.04	31.71
8.	Length of rhizome/clump (cm)	9.47±0.37	7.18	11.06	1.17	1.44	11.41	12.67	81.16	2.01	21.18
9.	Width of rhizome/clump (cm)	11.28±0.45	9.01	14.41	2.09	2.50	12.83	14.01	83.87	2.73	24.21
10.	Weight of mother rhizome(g)	23.20±1.07	18.11	30.75	10.78	13.05	14.15	15.17	82.61	6.15	26.50
11.	Girth of mother rhizome (cm)	10.64±1.13	8.04	13.90	2.29	2.55	14.21	15.02	89.54	2.95	27.71
12.	Rhizome yield per plant (g)	100.34±1.95	42.67	130.03	991.44	999.02	31.38	31.50	99.24	64.62	64.40
13.	Dry recovery (%)	19.30±1.90	17.94	21.51	1..23	2.00	5.75	7.32	61.74	1.80	9.31
14.	Oleoresin content (%)	5.51±0.28	4.00	6.80	0.67	0.82	14.84	16.45	81.38	1.52	27.57
15.	Crude fibre content (%)	3.71±0.15	2.86	4.69	0.24	0.29	13.19	14.45	83.30	0.92	24.80
16.	Curcumin content (%)	0.007±0.00	0.006	0.008	0.00	0.00	7.97	8.92	79.78	0.00	14.67
17.	Essential oil content (%)	0.25±0.01	0.20	0.36	0.00	0.00	18.34	18.83	94.84	0.09	36.79

Note: DAT- Days After Transplanting
V_g- Genotypic variance
V_p- Phenotypic variance
GCV- Genotypic Coefficient of Variation
PCV- Phenotypic Coefficient of Variation
h^2- Broad sense heritability
GA- Genetic advance
GAM- Genetic advance over percent Mean

A low estimate of genotypic coefficient of variation and phenotypic coefficient of variation were observed for dry recovery (5.75 % and 7.32 % respectively) and curcumin content (7.97 % and 8.92 % respectively). The presence of low estimates of GCV and PCV showed that selection based on these characters would be ineffective. Lower GCV and PCV for these attributes indicate less variability.

A moderate estimate of GCV and PCV were observed for plant height (14.32 % and 14.44 % respectively), pseudostem girth (11.99 % and 16.42 % respectively), number of tillers per clump (15.18 % and 19.17 % respectively), number of leaves per clump (14.83 % and 17.78 % respectively), number of primary fingers per clump (14.07 % and 14.93 % respectively), number of tertiary fingers per clump(17.19 % and 19.21 % respectively), length of rhizome per clump (11.41% and 12.67% respectively), width of rhizome per clump (12.83 % and 14.01 % respectively), girth of mother rhizome (14.21 % and 15.02 % respectively), weight of mother rhizome (14.15 % and 15.17 % respectively), essential oil (18.34 % and 18.83 % respectively) and oleoresin content (14.84 % and 16.45 % respectively). This shows equal importance of additive and non-additive gene action in these traits. Moderate estimate of GCV and PCV values indicates that there is a reasonable scope for selection of these characters due to the presence of moderate genetic variability during yield improvement.

A high estimate of GCV and PCV were observed for rhizome yield per plant (31.38 % and 31.50 % respectively) and crude fibre content (13.19 % and PCV

14.45 % respectively). The occurrence of high estimates of GCV and PCV indicated that these characters allow a huge scope for the yield improvement through selection due to the presence of high genetic variability during yield improvement. These results are in accordance with Prajapati *et al.* (2014); Vinodhini *et al.* (2018) in turmeric.

High heritability was observed for the traits such as plant height (98.30 %), number of tillers per clump (62.73%), number of leaves per clump (69.63%), rhizome yield per plant (99.24%), number of primary fingers per clump (90.58 %), number of secondary fingers per clump (88.02%) , number tertiary fingers per clump (80.14%), rhizome length per clump (81.16%), rhizome width per clump (83.87%), girth of mother rhizome (89.54%), weight of mother rhizome (82.61%), essential oil (94.84%), oleoresin (81.38%), crude fibre (83.30%) and curcumin content (79.78%). High estimates of heritability for these traits indicates that these traits are less affected by environmental factors and thus there is a huge scope for genetic improvement of these characters through selection. A moderate heritability was observed for pseudostem girth. These findings are in accordance with the reports of Salimath *et al.* (2017); Venugopal *et al.* (2017); Vinodhini *et al.* (2018); Krishna *et al*. (2019) in turmeric.

High genetic advance over per cent mean were recorded for the characters *viz.*, plant height (29.24 %), number of tillers per clump (24.76 %), number of leaves per clump (25.50 %), rhizome yield per plant (64.40 %), number of primary fingers per clump (27.31 %), number of secondary fingers per clump (38.24 %), number of tertiary fingers per clump (31.71 %), rhizome length per clump (21.18 %), rhizome width per clump (24.21 %), girth of mother rhizome (27.71 %), weight of mother rhizome (26.50 %), essential oil (36.79 %), oleoresin (27.57 %) and crude fibre (24.80 %). Medium genetic advance over per cent mean were recorded for pseudostem girth (18.04 %) and curcumin content (14.67 %). Low genetic advance over per cent mean were observed for dry recovery (9.31 %). Vinodhini *et al.* (2018) and Maurya *et al.* (2018) recorded high genetic advance over per cent mean for all the growth parameters in turmeric.

High heritability coupled with high genetic advance over per cent mean were noticed for the characters such as plant height, number of leaves per clump, number of tillers per clump, rhizome yield per plant, number of primary fingers per clump, number of secondary fingers per clump, number tertiary fingers per clump, rhizome length per clump, rhizome width per clump, girth of mother rhizome and weight of mother rhizome, essential oil, oleoresin, crude fibre which indicates that these traits are under the influence of additive gene action which can be improved through selection. The estimate of high heritability coupled with moderate genetic advance over per cent mean was recorded for curcumin content. For dry recovery, high heritability coupled with low genetic advance over per cent mean was recorded which is attributable to non-additive gene action. Similar results were recorded by Vinodhini *et al.* (2018); Krishna *et al.* (2019) in turmeric.

CONCLUSION

Mutation treatment resulted in creation of variability in the existing black turmeric population. A moderate to high estimate of GCV and PCV were recorded for all the growth and yield parameters. High heritability coupled with high genetic advance over per cent mean were noticed for the all the yield parameters.

FUTURE SCOPE

Future studies to be carried out in identification of the desirable and stabile mutants in the next generations and molecular characterization of identified mutants

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Conflict of Interest. None.

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