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Genetic potential of some elite turmeric genotypes in North Bengal

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Abstract
An investigation was carried out for three years (2019-20, 2020-21 and 2021-2022) in the university Research farm where the 30 turmeric genotypes were characterized according to DUS descriptors done by IISR (Indian Institute of Spices Research, Kozhikode, Kerala). Analysis of variance and GCV, PCV, heritability, genetic advance and genetic advance against mean were estimated as essential parameters of genetic potential of 30 genotypes to characterize and evaluate in terai region of West Bengal along with TCP-2 as local check and Prativa as national check. In case of analysis of variance of year wise performance, all the descriptors were found to have significant results in the pooled analysis of three years except number of mother rhizome, girth of mother rhizome, weight of secondary finger and length of secondary finger. In case genotype performance, all the genotypes were found to have significant results on descriptors in three years pooled data. In case of genotype and season interaction effect, all the descriptors were found to have significant results except number of shoots, number of leaves, girth of mother rhizome, weight of primary finger, weight of secondary finger, length of secondary and curcumin percentage. The high GCV along with high heritability, high percentage of genetic gain were found in rhizome parameters like weight of mother rhizome (WMR), curcumin content, weight of primary finger and weight of secondary finger. From the investigation, it can be concluded that, for effective selection, the characters like wt of mother rhizome (WMR), curcumin content, weight of primary finger and weight of secondary finger will be considered for future crop improvement programme due its high heritability and high to moderate genetic advance against mean and high GCV which determines that the characters are heritable in nature due to the action of additive genes and the variability of genotypes were high in nature, the characters are not influenced much by environmental effects.

Keywords: DUC descriptors, Genotypic coefficient of variation (GCV), Genetic advance against mean (GAM), Curcumin content, Wt of Mother rhizome, wt of secondary rhizome, Heritability

Introduction
Turmeric (*Curcuma longa* L.) is a plant of the Zingiberaceae family and comprises about 70 species (Smartt Simmonds 1992) [14]. It is a herbaceous plant belonging to the family Zingiberaceae, order *Scitamineae*, considered to have originated in the Indo - Malayan region (Purseglove 1968) [8]. Curcuma belongs to the tribe *Hedychium*. Taxonomy of the genus is quite confusing. A few studies on morphological and anatomical characterization of Curcuma species and turmeric varieties have been attempted, but not much has been done on molecular characterization except a few studies on isozyme polymorphism and identification of species based on 18S rRNA and trnK genes (Sashikumar 2005) [11]. The ecology of the species varies so much that their habitat ranges from sea level (sandy coastal habitat) to high altitude such as above 2000 m in the Western Ghats and Himalayas in India. The species such as *C. longa*, *C. zedoaria*, *C. amada* and *C. aromatica* are found predominantly in plains, *C. angustifolia*, *C. neilgherrensis*, *Cladogenesis*, *C. thalakaveriensis*, *C. pseudomontana* and *C. coriacea* etc. are confined to hills at 1000 – 2500 m altitude (Velayudhan *et al.*, 1999) [16]. The higher diversity is concentrated in India and Thailand (Hikmat UI Zaan *et al.*, 2011) [5]. Purseglove *et al.* (1981) [9] stated that the people of Malagasy believed in Malay – Polynesian connection in the origin of turmeric in that country. Burkill (1966) [4] believed that the crop spread to West Affrica in the 13th and to East Africa in the 17th centuries. It was introduced to Jamaica in 1783. India is the largest producer, consumer, exporter of turmeric in the world, with an annual production of about 1,190 thousand tonnes from an area of 233 thousands hectare and productivity of 5.11 tonnes / hectare (2013-2014).

There are many species of *Curcuma* that are related to turmeric *viz*., *C. amada* is endemic in South Asia, which is found wild in many parts of North East and in the hills of South India; *C. angustifolia* is native of India; *C. aromatica* distributed from China southwards to Srilanka; *C. caesia* is a native of northeast India; and *C. zedoaria* occurs mainly in the northeastern and west coastal regions of India, extending to the hills (Ravindran *et al*. 2007) [10]. The principle colouring components of turmeric rhizome is the curcumin (Cur-I) [1,7- bis (4-hydroxy-3-methoxyphenyl)-1,6-heptadiene-3,5-dione], while two other pigments demethoxycurcumin (Cur-II) [1-(4-hydroxyphenyl)-7-(4-hydroxy-3-methoxyphenyl)- 1,6-heptadiene-3,5 dione] and bisdemethoxycurcumin (Cur-III) [1,7-bis(4-hydroxyphenyl)-1,6-heptadiene-3,5-dione] are present in lesser extent (Jayprakasha *et al*., 2002) [6]. The major components were alpha-turmerone (53.4%), beta-turmerone (18.1%) and aromatic - turmerone (6.2%) in fresh rhizome and aromatic-turmerone (9.6%), alpha-santalene (7.8%) and alpha turmerone (6.5%) in dry rhizome. The significantly less amount of alpha- turmerone and beta-turmerone in dry rhizome could contribute to its low antioxidant activity as reported by Mittal *et al.* (2018) [7].

Materials and Methods

The present experimental investigation was carried out during the summer season 2019 – 2020, 2020 – 2021 and 2021-2022 at the experimental field comes under the University farm of Uttar Banga Krishi Viswavidyalaya, Pundibari, Cooch-Behar. The location of the field is 26° 19′ 86″ N latitude, 89° 23′ 53″ E longitude with an altitude of 43 m above the mean sea level. Specified operational practice where a fertilizer dose of N: P_2O_5: K_2O @ 120:60:60 (Kg/ha) were given in standard plot. The required amount of fertilizer were considered in terms of plot size and applied as Urea (46%N), SSP (16%P_2O_5) and MOP (60%K_2O). The experimental material comprised of 30 genotypes. Each rhizome bits weighing 20 gm were used. 750-800 gm healthy rhizomes per replication were taken to grow 40 plants in each replication. Completely dried rhizomes were pretreated with trichoderma solution @ 10 ml/per kg of rhizomes for 30 minutes.

Results and Discussion

The present investigation was carried out on thirty different turmeric genotypes collected from different parts of the country. Among these genotypes Pratibha was used as national check and TCP-2 was used as local check for this experiment. Characterization was done following the DUS descriptor. In this experiment, 20 quantitative traits were analysed during 3 cropping seasons. Bartlett test was done to confirm the homogeneity of 3 season's data for pooled ANOVA analysis. The results of Bartlett test revealed that among these 20 traits 18 traits had shown non-significant difference between 3 successive seasons. Therefore, Pooled ANOVA is possible for these traits. The present investigation was carried out on thirty different turmeric genotypes collected from different parts of the country. Among these genotypes Pratibha was used as national check and TCP-2 was used as local check for this experiment. Characterization was done following the DUS descriptor. In this experiment, 20 quantitative traits were analysed during 3 cropping seasons. Bartlett test was done to confirm the homogeneity of 3 season's data for pooled ANOVA analysis. The results of Bartlett test revealed that among these 20 traits selected for this investigation, 18 traits were found non-significant difference between 3 successive seasons (Table-1). Two traits (leaf spot PDI and Leaf Bloch PDI) were found significant in p-value (lesser than 0.05 and 0.01 at 5% and 1% level of significance) (Table-1) whereas in 18 quantitative characters, non-significant P value was found greater than 0.05 at 5% level and greater than 0.01 at 1% level of significance. Therefore, Pooled ANOVA is done in these 18 traits of characters in the evaluation and comparison of 30 genotypes among themselves and with national and local check varieties for these DUS descriptors and other rhizome characters. The analysis of diseases was done separately to evaluate and categorize the disease resistance among the 30 genotypes in this investigation (Table- 3).

Table 1: Comparison of EMS values of 3 seasons for homogeneity test

	PH	NS	NL	LL	LW	PL	LR	NMR	IP	DR
Year 1	253.01	0.20	0.12	60.32	1.54	6.88	1.07	0.12	0.01	1.47
Year 2	333.77	0.32	0.19	60.21	1.75	4.98	0.76	0.08	0.01	2.07
Year 3	196.36	0.28	0.12	35.97	0.90	3.63	0.75	0.11	0.01	1.74
chi^2	4.04	3.44	4.63	4.79	6.66	5.86	2.42	2.56	6.52	1.68
p	0.26	0.33	0.20	0.19	0.08	0.12	0.49	0.46	0.09	0.64

	WMR	GMR	WPF	WSF	LSF	CUR	CW	LS PDI	LB PDI	PY
Year 1	5.81	0.31	1.49	0.28	0.06	0.01	0.01	190.65	384.619	12.96
Year 2	8.96	0.37	1.48	0.34	0.08	0.01	0.01	280.28	40.10	20.18
Year 3	8.91	0.48	1.48	0.52	0.06	0.01	0.01	111.81	224.76	14.98
chi^2	3.37	2.65	0.00	5.78	1.41	2.44	6.14	11.76	61.82	2.99
p	0.34	0.45	1.00	0.12	0.70	0.49	0.10	0.008	0.00001	0.39

PH-Plant height (cm), **NS**-Number of shoots, **NL**-Number of leaves, **LL**-Leaf length (cm), **LW**-Leaf width (cm), **PL**-Petiole length (cm), **LR**-Length of rhizome (cm), **NMR**-Number of mother rhizome, **IP**-Internode pattern, **DR**-Dry recovery percentage, **WMR**-Weight of mother rhizome, **GMR**-Girth of mother rhizome, **WPF**-Weight of primary finger, **WSF**-Weight of secondary finger, **LSF**-length of secondary finger, **CUR**-Curcumin percentage, **LS PDI**-Leaf spot PDI, **LB PDI**-Leaf blotch PDI, **CW**-Clump weight (kg), **PY**-Projected yield (t/ha).

From the ANOVA table (Table: 2) it was comprehended that in between the seasons that is in each year all of the DUS characters except number of mother rhizome, girth of the mother rhizome, weight of the secondary rhizome and length of secondary rhizome are significantly different between themselves in 1% and 5% level of significance. All the characters performed differently in each year except these four characters. In genotypes, all the genotypes were found performed significantly different both in 5% and 1% level of significance.

Table 2: Analysis of variance for eighteen quantitative characters in turmeric (pooled)

Source	Df	PH	NS	NL	LL	LW	PL	LR	NMR	IP
Season	2	10286.2**	8.96***	1.67***	1819.7***	211.85***	950.23***	45.4***	0.02	0.66***
Genotype	29	2034.0**	0.86***	0.85***	240.8***	10.94***	50.89***	4.67***	0.30***	0.06***
Replication (with in environments)	6	1938.40***	0.34	0.22	461.26***	8.92***	42.59***	2.66**	0.14	0.01
G × S	58	590.20**	0.31	0.05	84.46**	3.99***	22.38***	3.24***	0.18**	0.05***
Error(pooled)	174	264.70	0.27	0.14	52.17	1.39	5.16	0.86	0.10	0.01

Source	Df	DR	WMR	GMR	WPF	WSF	LSF	CUR	CW	PY	WMR
Season	2	16.2***	240.04***	0.54	27.73***	0.99	0.16	0.12***	0.20**	87.73**	240.04***
Genotype	29	21.08***	1152.71***	12.39***	137.46***	12.51***	3.29***	9.17***	0.05**	161.90***	1152.71***
Replication (with in environments)	6	17.08***	9.05	1.17**	3.02	0.54	0.09	0.01	0.02**	19.70	9.05
G × S	58	4.68***	13.98**	0.26	1.51	0.29	0.08	0.01	0.01***	35.77***	13.98**
Error(pooled)	174	1.76	18.29	0.39	1.49	0.38	0.07	0.01	0.01	16.04	18.29

***, **,* Significant at 0.05%, 1% and 5% levels of probability, respectively

PH-Plant height (cm), **NS**-Number of shoots, **NL**-Number of leaves, **LL**-Leaf length (cm), **LW**-Leaf width (cm), **PL**-Petiole length (cm), **LR**-Length of rhizome (cm), **NMR**-Number of mother rhizome, **IP**-Internode pattern, **DR**-Dry recovery percentage, **WMR**-Weight of mother rhizome, **GMR**-Girth of mother rhizome, **WPF**-Weight of primary finger, **WSF**-Weight of secondary finger, **LSF**-length of secondary finger, **CUR**-Curcumin percentage, **LS PDI**-Leaf spot PDI, **LB PDI**-Leaf blotch PDI, **CW**-Clump weight (kg), **PY**-Projected yield (t/ha).

In genotype and environment interaction, all the characters except number of shoots (0.31), number of leaves (0.05),girth of mother rhizome (0.27), weight of primary finger (1.51), weight of secondary finger (0.29), length of secondary finger (0.08) and curcumin percentage (0.01) were found performed differently in 5% and 1% level of significance. It indicates that all the genotypes are significantly different but their performance was varied from year to year significantly. In performances of some of the characters and their interaction with the environment were found insignificant in some of the characters. In all of these characters which are found significantly different were found to have variability and exploitation of variability can be done in future crop improvement programme. The effect of rhizome parameters may not be considered for their individual performance.

In Table-3, the performances of individual genotypes were evaluated in genetical parameters which include genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic gain of the descriptors and other characters like leaf spot PDI and leaf Blotch PDI, curcumin percentage which were evaluated for their performances in this investigation. Weight of the mother rhizome (WMR), weight of primary finger (WPF), weight of secondary finger (WSF), length of secondary finger (LSF) and curcumin percentage were evaluated and found to have very high heritability and high percentage of genetic gain. It indicated that these characters were heritable and would not be influenced by environmental fluctuations. Similar results of high heritability coupled with high genetic gain were also reported by Aarthi *et al*. (2022) [1], Vinodhini *et al*. (2018) [16], Bahadur *et al*. (2016) [3] and Vamshi Krishna *et al*. (2018) [15] for these characters in turmeric genotypes in their investigation.

The GCV (%) and PCV (%) of weight of mother rhizome were (29.02) and (29.90) which was found due to environmental influence was higher compared to genetic effects of this character. According to Sivasubramanian and Menon (1973) [13] the values of both GCV and PCV is higher than 20% which was indicative of high variability although the higher percentage of PCV was due to more environmental influence on this character than sole genetic expression of this character. The difference between GCV% and PCV% was found to be not high enough and high heritability (94.16) and very high genetic advance as percentage of mean (58.00) were indicative of high influence of additive genes on this character although influence of environmental effects was there. This character was found heritable and could be considered for crop improvement programme.

Table 3: Phenotypic and genotypic coefficient of variation, heritability and genetic gain for 20 characters in turmeric. (Pooled Data Analysis 2019-22)

Characters	Grand Mean	Range		GCV (%)	PCV (%)	Heritability (%)	Genetic gain (%)
		Max	Min				
PH	127.29	152.83	106.79	11.02	16.87	42.62	14.81
NS	2.19	2.98	1.70	11.72	26.47	19.60	10.69
NL	8.19	8.82	7.37	3.41	5.76	35.01	4.16
LL	56.11	63.07	46.26	8.16	15.24	28.66	9.00
LW	13.29	15.13	10.65	7.76	11.79	43.21	10.50
PL	25.67	29.81	21.17	8.78	12.47	49.60	12.74
LR	8.17	9.67	6.66	7.97	13.86	33.04	9.43
NMR	1.29	1.60	1.00	11.32	27.51	16.92	9.59
IP	0.89	0.99	0.63	8.69	13.93	38.89	11.16
DR	26.78	28.81	22.48	5.47	7.38	55.02	8.36
WMR	38.87	58.57	19.41	29.02	29.90	94.16	58.00
GMR	11.66	13.74	8.86	9.91	11.25	77.51	17.97
WPF	13.77	22.00	5.33	28.23	29.59	91.05	55.50
WSF	4.12	7.45	1.89	28.15	31.86	78.07	51.24
LSF	3.95	5.53	2.32	15.17	16.55	84.00	28.64
CUR	2.26	4.34	0.82	44.67	44.83	99.27	91.68
LS PDI	46.06	61.67	22.26	23.04	38.03	36.69	28.74

LB PDI	31.32	68.70	10.52	56.78	73.70	59.35	90.11
CW	0.26	0.40	0.17	26.82	42.97	38.95	34.48
PY	10.81	19.46	5.73	37.25	52.55	50.26	54.40

PH-Plant height (cm), **NS**-Number of shoots, **NL**-Number of leaves, **LL**-Leaf length (cm), **LW**-Leaf width (cm), **PL**-Petiole length (cm), **LR**-Length of rhizome (cm), **NMR**-Number of mother rhizome, **IP**-Internode pattern, **DR**-Dry recovery percentage, **WMR**-Weight of mother rhizome, **GMR**-Girth of mother rhizome, **WPF**-Weight of primary finger, **WSF**-Weight of secondary finger, **LSF**-length of secondary finger, **CUR**-Curcumin percentage, **LS PDI**-Leaf spot PDI, **LB PDI**-Leaf blotch PDI, **CW**-Clump weight (kg), **PY**-Projected yield (t/ha).

Similar result was also reported by Athira *et al*. (2018) [2] and Sivakumar *et al*. (2021) [12]. Girth of mother rhizome (GMR) were also found to have high heritability (77.51) and medium genetic advance (17.97) which were indicative of heritability and medium additive gene effects of this character. High heritability for girth of mother rhizome was also reported by Aarthi *et al.* (2022) [1] and Vinodhini *et al*. (2018) [16] to corroborate the results for present investigation.

Range of GCV% (9.91) and PCV% (11.25) were reported low as the variability and range of values of this character was very low in this investigation. In case of weight of primary finger, GCV% (28.23) and PCV% (29.59) were found higher which was found to be indicative of high variability of this character among the genotypes although influence of environmental factors were found to be high, however, very high heritability (91.05) along with high genetic advance against mean (55.50) were found due to influence of high additive gene effects due to which, this character can be considered for future crop breeding programme. Similar results were also reported by Bahadur *et al*. (2016) [3], Vinodhini *et al*. (2018) [16] and Sivakumar *et al*. (2021) [12]. In other character like weight of secondary finger, GCV% (28.15) and PCV% (31.86) was found higher although influence of environmental factors was present, but very high heritability (78.07) and very high genetic advance (51.24) was also recorded. Effect of additive genes was higher in determining the heritability of this character generation after generation and should be chosen for crop improvement programme.

Length of the secondary finger was also important character to be recognized for selection as heritable character because of high heritability (84.0) and high genetic advance against mean (28.64) although was found to have medium range of PCV% (16.55) and GCV% (15.17) according to Sivasubramanian and Menon (1973) which was indicative of medium variability of characters among the genotype in this character. In another important character of curcumin%, very high range of GCV % (44.67) and PCV% (44.83) was reported which was indicative of very high variability among the genotypes of this character. High heritability (99.27%) along with extremely high genetic advance against mean (91.68) indicated very active additive gene effects in this character which is strongly heritable generation after generation. So this character should be considered for crop improvement programme. In case of both leaf spot PDI and leaf blotch PDI, high GCV (23.04) and PCV values (38.03) in leaf spot PDI and GCV (56.78) and PCV(73.70) in leaf blotch PDI indicative of high environmental influence on this character which showed exactly that the disease was found having environmental influence in these characters. Very high genetic gain in both the cases, leaf spot PDI (28.74) and (90.11) were indicative of additive effects of genetic gains which showed the effect of resistance, moderately resistance, susceptible and very susceptible genes were active generation after generation. These results also showed different capabilities of the turmeric genotypes for resistance against these diseases.

Conclusion

From the investigation, after the evaluation of different DUS descriptors along with effect leaf spot and leaf blotch disease parameters, it can be concluded that from the 30 genotypes investigated with 18 DUS characters and other quantitative characters, wt of the mother rhizome (WMR), girth of mother rhizome (GMR), wt of primary finger (WPF), wt of secondary finger (WSF), length of secondary finger (LSF) and curcumin percentage should be taken as important characters for consideration of crop improvement programme in future in this region.

Conflict of interest: The authors declared that there is no conflict of interest in this investigation.

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