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Research Note

Genetic variability, correlation and path analysis in mango ginger (*Curcuma amada* ROXB.)

Raval Kalpesh*, R. K. Patel, Rajesh Panchal and K. G. Modha

Department of Genetics and Plant Breeding, N. M College of Agriculture, Navsari Agricultural University,
Navsari - 396 450
***E-Mail:** kalpeshraval655@gmail.com

Abstract

The present investigation was carried out at the Research Farm, Department of Genetics and Plant Breeding, Navsari Agricultural University, Navsari, Gujarat during the *kharif*, 2018. Twelve different quantitative characters related to rhizome yield were recorded and subjected for estimation of analysis of variance. The result revealed significant differences among the genotypes indicating presence of sufficient amount of variability in all the characters studied. Wide range of variation by virtue of exhibiting highly significant genotypic differences for all the twelve traits. The value of phenotypic coefficient of variation was recorded higher and closer to the respective genotypic coefficient of variation for majority of traits under study indicates less influence of environment. The magnitudes of genotypic correlations were higher as compared to the corresponding phenotypic correlations indicating that there was an inherent association between all the characters at genotypic level. Path coefficient analysis showed rhizome width, leaf width, mother rhizomes per plant, leaf length and leaves per plant exhibited positive direct effects on green rhizome yield per plant. Hence, priority should be given to these traits in mango ginger improvement programme.

Keywords: Correlation, Heritability, Mango ginger, Path analysis, Variability

Mango ginger (*Curcuma amada* Roxb., 2n = 42) is an important member of the genus *Curcuma* and is commonly known as mango ginger due to morphological resemblance of its aromatic rhizome with ginger (*Zingiber officinale*) and having raw unripe mango like aroma. The specific epithet *amada* is derived from Bengali meaning mango ginger referring to the rhizome having characteristic flavour of unripe mango. The crop is popular by many vernacular names like mango ginger in English, ama-haldi in Hindi, ambahaldar in Gujarati, karpuraharidra in Sanskrit, amada in Bengali, mavinakayi in Kannad, mangaiinji in Tamil, mamidiallamu in Telugu and manga inchi in Malayalam. The crop is found in wild as well as in cultivated forms and its distribution is confined to South-East Asia mainly India, Myanmar and Bangladesh. In India, it is under small scale cultivation in West Bengal, Gujarat, Uttar Pradesh, Kerala, Karnataka, Tamil Nadu and in the North-Eastern states. The crop originated in the Indo-Malayan region and distributed widely in the tropics from Asia to Africa and in Australia (Sasikumar, 2005). Out of 10 *Curcuma* species, two species *Curcuma amada* and *Curcuma zeodaria* are distributed throughout India in the wild and cultivated forms, whereas four species, *Curcuma aeruginosa, Curcuma brog, Curcuma caesia* and *Curcuma sylvatica* occurs in wild conditions and distributed throughout North-Eastern part of India. *Curcuma malabarica* and *Curcuma aromatic* occur in South India, while *Curcuma raktakanta* and *Curcuma harita* are distributed throughout Kerala (Velayudhan *et al*., 1999). Many species belonging to this genus having a significant value as medicines, dyes and spices (Islam, 2004).

Estimation of genetic variability in conjunction with heritability and genetic advance gives an idea about possible ways of improve the important traits. Studies on mango ginger with an objective of assessing their genetic variability and genetics of agronomic characters have been attempted only to a limited extent. Hence, the present experiment was designed with some objectives of analyzing the genetic variability and character association of *Curcuma amada* Roxb. on accessions collected from various areas of Gujarat state, so as to generate additional information and also to identify the best performing genotypes from them. This research will be helpful to the plant breeders to select highly efficient parents, which will add new germplasm base for future mango ginger breeding programmes to meet the ever-increasing demand of mango ginger for industrial and pharmaceutical uses.

The experimental materials comprised of thirty diverse genotypes of mango ginger **(Table 1)**, which were maintained at Research Farm, Department of Genetics and Plant Breeding, Navsari Agricultural University, Navsari. The experiment was laid out during *kharif*, 2018 in a Randomized Block Design with three replications. The planting was done on raised beds spaced row to row 45 cm with plant to plant distance of 30 cm creating a gross plot area of 201.5 m^2. All the recommended package of practices was adopted for raising a successful and healthy crop. Data was collected from five randomly selected plants, excluding the border ones, from each genotype of all the three replications. The average value of the traits of each genotype was used for statistical analysis.

The data recorded for all the characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978). Phenotypic and genotypic components of variance were estimated by applying the formula as suggested by Cochran and Cox (1959). Heritability in broad sense refers to the proportion of genetic variation to the total observed variance in the population. It was estimated as per the formula given by Allard (1960). Phenotypic and genotypic co-efficient of variation were calculated by using formulae suggested by Cockerham (1963). Analysis of covariance for all possible pairs of characters was carried out using the procedure of Panse and Sukhatme (1978). Path analysis suggested by Wright (1921) and Dewey and Lu (1959) was adopted for each genotype separately in order to partition the genotypic correlation between variables with rhizome yield into direct and indirect effects of those variables on yield.

The mean sums of squares of all the twelve studied characters of mango ginger are summarized in **(Table 2)**. The present experimental material showed a wide range of variation by virtue of exhibiting highly significant genotypic differences for all the twelve traits *viz*., for plant height, tillers per plant, leaves per plant, leaf length, leaf width, rhizome length, rhizome width, rhizome weight, mother rhizomes per plant, primary fingers per rhizome, secondary fingers per rhizome and green rhizome yield **(Table 3)**. The investigation showed ample amount of variability present in the germplasm with wide range of phenotypic variability and significant genotypic differences for all the traits. This suggests that there is ample scope to develop high green rhizome

Table 1. List of mango ginger germplasm used in the experiment

S. No.	Genotype	Source	S. No.	Genotype	Source
1	NVMG-1	NAU, Navsari	16	NVMG-16	NAU, Navsari
2	NVMG-2	NAU, Navsari	17	NVMG-17	NAU, Navsari
3	NVMG-3	NAU, Navsari	18	NVMG-18	NAU, Navsari
4	NVMG-4	NAU, Navsari	19	NVMG-19	NAU, Navsari
5	NVMG-5	NAU, Navsari	20	NVMG-20	NAU, Navsari
6	NVMG-6	NAU, Navsari	21	NVMG-21	NAU, Navsari
7	NVMG-7 (C)	NAU, Navsari	22	NVMG-22	NAU, Navsari
8	NVMG-8	NAU, Navsari	23	NVMG-23	NAU, Navsari
9	NVMG-9	NAU, Navsari	24	NVMG-24	NAU, Navsari
10	NVMG-10	NAU, Navsari	25	NVMG-25	NAU, Navsari
11	NVMG-11	NAU, Navsari	26	NVMG-26	NAU, Navsari
12	NVMG-12	NAU, Navsari	27	NVMG-27	NAU, Navsari
13	NVMG-13	NAU, Navsari	28	NVMG-28	NAU, Navsari
14	NVMG-14	NAU, Navsari	29	NVMG-29	NAU, Navsari
15	NVMG-15	NAU, Navsari	30	NVMG-30	NAU, Navsari

NVMG 7 (C): Check Variety

Table 2. Analysis of variance for different characters of mango ginger

Source of Variation	df	Plant height	Tillers per plant	Leaves per plant	Leaf length	Leaf width	Rhizome length
Replication	2	20.32	2.96	0.72	2.41	0.12	0.63
Genotype	29	3681.06**	6.20**	83.23**	104.23**	7.00**	17.53**
Error	58	54.24	1.10	5.66	5.55	1.00	1.28
S.Em ±		4.25	0.61	1.37	1.36	0.58	0.65
C.D. at 5%		12.04	1.72	3.89	3.85	1.63	1.85
C.D at 1%		16.02	2.29	5.17	5.12	2.17	2.46
CV%		9.35	10.78	9.45	8.56	9.54	9.65

Source of Variation	df	Rhizome width	Rhizome weight	Mother rhizomes per plant	Primary fingers per rhizome	Secondary fingers per rhizome	Green rhizome yield
Replication	2	1.97	0.001	0.13	1.65	0.23	1.96
Genotype	29	32.61**	0.012**	16.40*	65.20**	6.27**	82.04**
Error	58	2.10	0.001	0.80	6.46	1.12	4.77
S.Em ±		0.84	0.01	0.52	1.47	0.61	1.26
C.D. at 5%		2.37	0.04	1.47	4.15	1.73	3.57
C.D at 1%		3.15	0.06	1.95	5.53	2.31	4.75
CV%		9.59	9.51	9.80	9.40	9.62	14.14

* and ** indicates significance at 5% and 1% levels of probability, respectively

yielding materials, provided that the material is subjected to judicious clonal selection pressure.

The value of phenotypic coefficient of variation (PCV) **(Table 4)** was recorded higher and closer to the respective genotypic coefficient of variation (GCV) for majority of traits under study indicates less influence of environment. The higher magnitude of genotypic coefficient of variation was observed for plant height (44.16%), leaves per plant (20.20%), leaf length (20.85%), rhizome width (21.12%), rhizome weight (23.16%), mother rhizomes per plant (24.90%) and green rhizome yield (32.87%) indicated the inherent connection between genotypic and phenotypic expression of these traits, hence offers a better opportunity for improvement through clonal selection. Analogous results were also given by Singh *et al.* (2003), Chattopadhyay *et al.* (2004), Singh *et al.* (2008), Singh *et al.* (2012), Ravishanker *et al.* (2013), Prajapati *et al.* (2014), Bahadur *et al.* (2016) and Nandkangre *et al.* (2016) in ginger.

High estimates of heritability **(Table 4)** were observed for plant height (95.71%) followed by mother rhizomes per plant (86.59 %), leaf length (85.57%), rhizome weight (85.55%), green rhizome yield (84.39%), rhizome width (82.90%), leaves per plant (82.05%), rhizome length (80.91%), primary fingers per rhizome (75.19%) and leaf width (66.72%) suggesting the existence of sufficient heritable variation and so selection based on phenotypic value could be effective for isolating better types. The genetic advance in per cent was observed as high for plant height (89.00%) followed by green rhizome yield (62.20%) and mother rhizome per plant (47.73%). High heritability coupled with high genetic advance was found for plant height, tillers per plant, leaves per plant, leaf length, leaf width, rhizome length, rhizome width, rhizome weight, mother rhizomes per plant, primary fingers per rhizome and green rhizome yield indicated that these characters were governed by additive gene action. Hence, there are good chances of improvement of these traits through direct phenotypic clonal selection in the present materials. The above result was in resemblance with Singh *et al.* (2012), Ravishanker *et al.* (2013), Prajapati *et al.* (2014), Rajyalakshmi *et al.* (2014), Verma *et al.* (2014), Bahadur *et al.* (2016), Nandkangre *et al.* (2016), Salimath *et al.* (2017) and Veena *et al.* (2017) in turmeric.

All the traits revealed that genotypic correlations were higher as compared to corresponding phenotypic correlations for majority of the traits under study indicating that there was an inherent association between these characters at genotypic level **(Table 5).** Green rhizome yield showed positive and significant correlation with plant height (r_g = 0.887 and r_p= 0.783), leaves per plant (r_g = 0.621 and r_p= 0.512), leaf length (r_g = 0.570 and r_p= 0.453), leaf width (r_g = 0.753 and r_p= 0.549), rhizome length (r_g = 0.949 and r_p= 0.767), rhizome width (r_g = 0.999 and r_p= 0.802), rhizome weight (r_g = 0.927 and r_p= 0.766), primary fingers per rhizome (r_g = 0.420 and r_p= 0.345) and secondary fingers per rhizome

Table 3. Mean values of genotypes for different traits of mango ginger

S. No.	Genotypes	PH	TPP	LPP	LL	LW	RL	RWD	RWT	MRPP	PFPR	SFPR	GRY
1	NVMG-1	57.98	11.20	29.20	30.74	8.60	8.77	12.37	0.24	12.00	22.47	9.47	10.16
2	NVMG-2	53.81	9.43	22.53	28.29	8.99	8.27	12.11	0.20	9.40	17.93	11.33	10.66
3	NVMG-3	64.72	10.20	36.07	25.80	8.61	11.75	19.17	0.29	6.93	26.67	12.73	17.77
4	NVMG-4	56.80	9.47	19.47	32.29	10.39	11.40	13.00	0.22	12.13	31.73	10.13	11.39
5	NVMG-5	56.05	9.73	19.13	25.02	9.49	8.74	12.67	0.19	9.80	27.73	9.13	8.94
6	NVMG-6	58.04	9.87	24.20	30.33	9.66	10.55	14.34	0.25	11.80	26.33	9.33	13.78
7	NVMG-7	60.08	9.87	25.73	23.11	10.20	11.48	12.78	0.30	10.40	26.93	9.93	11.73
8	NVMG-8	191.86	7.60	30.27	37.55	11.53	16.04	24.66	0.46	4.47	30.47	14.60	30.83
9	NVMG-9	63.86	9.07	25.93	33.64	12.39	12.43	13.37	0.31	9.80	21.53	11.47	18.71
10	NVMG-10	83.10	8.27	21.00	23.52	11.43	12.11	14.49	0.23	8.27	21.87	9.67	14.53
11	NVMG-11	171.92	12.27	30.33	45.53	15.07	15.80	22.75	0.41	5.43	29.40	11.87	27.78
12	NVMG-12	54.23	9.60	18.53	30.60	9.89	8.87	12.48	0.24	10.20	22.20	9.67	10.41
13	NVMG-13	164.15	9.33	34.47	30.58	13.93	18.42	22.41	0.36	3.67	28.60	13.93	22.82
14	NVMG-14	60.65	10.27	19.20	23.10	9.84	9.13	13.38	0.22	10.20	21.60	9.20	11.99
15	NVMG-15	65.50	11.87	21.07	21.61	9.08	12.32	17.28	0.25	9.40	29.70	12.07	17.23
16	NVMG-16	75.96	8.80	20.20	21.92	11.12	11.37	12.46	0.20	6.40	22.20	10.60	10.81
17	NVMG-17	108.89	8.67	32.20	22.27	11.37	14.36	16.77	0.35	12.00	33.27	12.33	19.67
18	NVMG-18	73.77	11.33	23.53	22.90	10.25	12.06	12.79	0.21	7.30	25.27	9.60	12.66
19	NVMG-19	70.15	10.93	20.47	23.20	9.90	12.56	15.95	0.25	8.60	23.73	13.33	17.59
20	NVMG-20	68.95	12.93	30.07	32.50	9.43	12.62	15.26	0.20	10.60	32.40	11.53	18.11
21	NVMG-21	72.13	8.80	19.73	31.30	9.62	9.85	12.62	0.26	11.80	24.13	10.20	12.85
22	NVMG-22	73.43	8.27	21.00	20.97	8.52	8.98	13.43	0.25	10.60	25.60	11.53	11.36
23	NVMG-23	82.25	8.80	19.20	20.84	11.43	13.16	16.69	0.26	11.60	32.80	11.27	18.38
24	NVMG-24	66.84	12.13	30.40	31.89	12.11	13.51	15.23	0.28	8.00	22.80	11.80	17.35
25	NVMG-25	60.06	7.60	28.53	21.15	9.65	10.81	12.43	0.24	9.80	25.20	10.47	12.54
26	NVMG-26	77.03	7.47	25.80	34.07	10.53	12.92	15.02	0.30	10.00	33.90	12.20	18.43
27	NVMG-27	58.54	9.20	23.53	29.27	9.36	10.83	13.72	0.26	7.40	33.70	10.07	13.09
28	NVMG-28	65.95	9.20	23.53	22.07	10.27	8.70	12.72	0.20	7.80	32.40	9.47	10.20
29	NVMG-29	80.13	9.20	34.60	22.71	11.90	13.46	16.47	0.31	12.10	35.10	11.33	18.99
30	NVMG-30	65.19	11.27	25.40	26.40	9.73	10.24	14.13	0.26	6.80	23.70	10.53	12.47
Range	Minimum	53.81	7.47	18.83	20.84	8.52	8.27	12.11	0.19	3.67	17.93	9.13	8.94
	Maximum	191.86	12.93	36.07	45.53	15.07	18.42	24.66	0.46	12.13	35.10	14.60	30.83
	SED	6.01	0.86	1.94	1.92	0.82	0.92	1.18	0.02	0.73	2.08	0.86	1.78
	CD 5%	12.04	1.72	3.89	3.85	1.63	1.85	2.37	0.04	1.47	4.15	1.73	3.57
	CD 1%	16.02	2.29	5.17	5.12	2.17	2.46	3.15	0.06	1.95	5.53	2.31	4.75

PH = Plant height (cm)
TPP = Tillers per plant
LPP = Leaves per plant
LL = Leaf length (cm)
LW = Leaf width (cm)
RL = Rhizome length (cm)
RWD = Rhizome width (cm)
RWT = Rhizome weight (g)
MRPP = Mother rhizomes per plant
PFPR = Primary fingers per rhizome
SFPR = Secondary fingers per rhizome
GRY = Green rhizome yield (g)

(r_g = 0.915 and r_p= 0.652) at both genotypic and phenotypic level. These association of characters was in the desirable direction, thus, selection practiced for the improvement in one character will automatically result in the improvement of other even though direct selection for improvement has not made for the green rhizome yield. Similar result was found by Raveendra *et al.* (2001), Panja *et al.* (2002), Prasad *et al.* (2004), Tomar *et al.* (2005), Kumar *et al.* (2007), Rao *et al.* (2008), Ravishanker *et al.* (2013), Prajapati *et al.* (2014), Rajyalakshmi *et al.* (2014), Verma *et al.* (2014), Bahadur *et al.* (2016) in turmeric.

Table 4. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent of mean for different characters of mango ginger

S. No.	Characters	Mean	GCV %	PCV %	Heritability (%)	Genetic advance	Genetic advance (% of mean)
1	Plant height (cm)	78.73	44.16	45.14	95.71	70.07	89.00
2	Tillers per plant	9.75	13.36	17.16	60.58	2.09	21.42
3	Leaves per plant	25.18	20.20	22.30	82.05	9.49	37.69
4	Leaf length (cm)	27.51	20.85	22.54	85.57	10.93	39.73
5	Leaf width (cm)	10.48	13.50	16.53	66.72	2.38	22.72
6	Rhizome length (cm)	11.72	19.86	22.08	80.91	4.31	36.81
7	Rhizome width (cm)	15.10	21.12	23.20	82.90	5.98	39.62
8	Rhizome weight (g)	0.27	23.16	25.03	85.55	0.12	44.12
9	Mother rhizomes per plant	9.16	24.90	26.76	86.59	4.37	47.73
10	Primary fingers per rhizome	27.05	16.36	18.87	75.19	7.90	29.22
11	Secondary fingers per rhizome	11.03	11.88	15.28	60.41	2.10	19.02
12	Green rhizome yield (g)	15.44	32.87	35.78	84.39	9.60	62.20

Table 5. Genotypic (r_g) and phenotypic (r_p) correlations of green rhizome yield with other characters of mango ginger

Traits	r	PH	TPP	LPP	LL	LW	RL	RWD	RWT	MRPP	PFPR	SFPR	GRY
PH	r_g	**1.000**	-0.118	0.472**	0.506**	0.782**	0.828**	0.912**	0.860**	-0.634**	0.311**	0.737**	0.887**
	r_p	**1.000**	-0.093	0.433**	0.453**	0.607**	0.747**	0.830**	0.792**	-0.549**	0.252*	0.540**	0.783**
TPP	r_g		**1.000**	0.090	0.257*	0.023	0.053	0.058	-0.186	-0.098	-0.132	-0.109	0.031
	r_p		**1.000**	0.188	0.130	-0.030	-0.002	0.075	-0.125	-0.074	-0.098	0.003	0.025
LPP	r_g			**1.000**	0.306**	0.416**	0.634**	0.611**	0.623**	-0.298**	0.318**	0.611**	0.621**
	r_p			**1.000**	0.245*	0.286**	0.514**	0.519**	0.552**	-0.248*	0.287**	0.411**	0.512**
LL	r_g				**1.000**	0.489**	0.383**	0.471**	0.553**	-0.277**	0.089	0.312**	0.570**
	r_p				**1.000**	0.390**	0.324**	0.386**	0.475**	-0.249*	0.018	0.203	0.453**
LW	r_g					**1.000**	0.881**	0.653**	0.706**	-0.472**	0.211*	0.433**	0.753**
	r_p					**1.000**	0.625**	0.490**	0.519**	-0.359**	0.166	0.299**	0.549**
RL	r_g						**1.000**	0.883**	0.803**	-0.505**	0.458**	0.855**	0.949**
	r_p						**1.000**	0.754**	0.686**	-0.416**	0.360**	0.590**	0.767**
RWD	r_g							**1.000**	0.872**	-0.605**	0.419**	0.909**	0.999**
	r_p							**1.000**	0.751**	-0.509**	0.325**	0.626**	0.802**
RWT	r_g								**1.000**	-0.402**	0.348**	0.789**	0.927**
	r_p								**1.000**	-0.340**	0.283**	0.547**	0.766**
MRPP	r_g									**1.000**	0.093	-0.504**	-0.461**
	r_p									**1.000**	0.065	-0.363**	-0.409**
PFPR	r_g										**1.000**	0.301**	0.420**
	r_p										**1.000**	0.174	0.345**
SFPR	r_g											**1.000**	0.915**
	r_p											**1.000**	0.652**
GRY	r_g												**1.000**
	r_p												**1.000**

* and ** indicates significance at 5% and 1% levels of probability, respectively

PH = Plant height
TPP = Tillers per plant
LPP = Leaves per plant
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LW = Leaf width
RL = Rhizome length
RWD = Rhizome width
RWT = Rhizome weight
MRPP = Mother rhizomes per plant
PFPR = Primary fingers per rhizome
SFPR = Secondary fingers per rhizome
GRY = Green rhizome yield

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Table 6. Direct (diagonal) and indirect effect of eleven variables on green rhizome yield of mango ginger

Traits	PH	TPP	LPP	LL	LW	RL	RWD	RWT	MRPP	PFPR	SFPR
PH	**-4.934**	0.580	-2.329	-2.498	-3.860	-4.083	-4.501	-4.243	3.128	-1.535	-3.638
TPP	0.234	**-1.987**	-0.179	-0.511	-0.046	-0.106	-0.115	0.370	0.194	0.262	0.217
LPP	0.118	0.023	**0.249**	0.076	0.104	0.158	0.152	0.155	-0.074	0.079	0.152
LL	0.290	0.147	0.175	**0.573**	0.280	0.219	0.270	0.317	-0.159	0.051	0.178
LW	2.144	0.063	1.139	1.340	**2.740**	2.415	1.791	1.934	-1.295	0.578	1.188
RL	-1.589	-0.102	-1.217	-0.734	-1.692	**-1.920**	-1.695	-1.541	0.969	-0.879	-1.642
RWD	9.154	0.580	6.133	4.721	6.557	8.861	**10.035**	8.749	-6.071	4.200	9.122
RWT	-2.336	0.506	-1.692	-1.501	-1.916	-2.180	-2.368	**-2.716**	1.090	-0.946	-2.144
MRPP	-0.613	-0.094	-0.288	-0.268	-0.456	-0.488	-0.585	-0.388	**0.966**	0.090	-0.487
PFPR	-0.297	0.126	-0.303	-0.085	-0.201	-0.437	-0.399	-0.332	-0.089	**-0.954**	-0.287
SFPR	-1.286	0.190	-1.066	-0.543	-0.756	-1.491	-1.585	-1.376	0.879	-0.525	**-1.744**
Correlation coefficient	0.887**	0.031	0.621**	0.570**	0.753**	0.949**	0.999**	0.927**	-0.461**	0.420**	0.915**

** indicates significance 1% level
Residual = 0.358

PH = Plant height
TPP = Tillers per plant
LPP = Leaves per plant
LL = Leaf length
LW = Leaf width
RL = Rhizome length
RWD = Rhizome width
RWT = Rhizome weight
MRPP = Mother rhizomes per plant
PFPR = Primary fingers per rhizome
SFPR = Secondary fingers per rhizome
GRY = Green rhizome yield

Green rhizome yield per plant showed negative and significant correlation with mother rhizomes per plant at genotypic level and phenotypic level, while tillers per plant exhibited non-significant effect on green rhizome yield. Hence, direct weightage should not be given to these traits during improvement programme.

As per path coefficient analysis **(Table 6)**, the highest positive direct effect on green rhizome yield was exerted by rhizome width (10.035) followed by leaf width (2.740), mother rhizome per plant (0.966), leaf length (0.573) and leaves per plant (0.249) indicated that these traits may provide expected advance from selection for rhizome yield. The result was also in favor with Chattopadhyay *et al.* (2004), Kumar *et al.* (2007), Sharon *et al.* (2011) and Prajapati *et al.* (2014). Thus, these characters turned-out to be the major components of green rhizome yield. It also revealed that there was true relationship between these characters and green rhizome yield and hence direct selection of these characters could be highly rewarding in crop improvement programs.

There were some characters which exhibited the highest negative direct effect on green rhizome yield such as plant height (-4.934) followed by rhizome weight (-2.716), tillers per plant (-1.987), rhizome length (-1.920), secondary fingers per rhizome (-1.744) and primary fingers per rhizome (-0.954) but, they also exhibited positive indirect effect *via* other characters. Similar results were also observed by Prajapati *et al.* (2014), Verma *et al.* (2014), Bahadur *et al.* (2016) and Ravi *et al.* (2017) in ginger.

Mother rhizomes per plant exhibited positive direct effect with negative correlation at both genotypic and phenotypic level. Hence, it would be better to avoid direct selection for this character when rhizome yield is to be increased.

The final conclusion that can be obtained from the variability, correlations, path coefficient analysis is that rhizome width, rhizome length, rhizome weight, secondary fingers per rhizome, plant height, leaf width, leaves per plant, leaf length and primary fingers per rhizome are the most important component characters of green rhizome yield, hence these traits should be considered as selection criteria for green rhizome yield improvement in mango ginger.

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