Morphological Characterization and Quality Assessment of Cochin Ginger (*Zingiber officinale* Rosc.)

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Abstract

Cochin ginger, one of the finest traded ginger genotypes is popular in the middle east, Europe and United states of America due to its high Zingiberene (28 to 31 %), fibre, volatile oil content, greenish yellow core colour and flavour components. Due to replacement of this local ginger with other high yielding varieties, the cultivation of Cochin ginger over the years have almost vanished except in some areas. The present investigation was thus carried out to screen the local ginger types for identification of cochin ginger and their rejuvenation in the niche areas of Central Kerala. Twenty-five cochin ginger genotypes were evaluated in Thrissur Kerala during 2023-24. Morphological data recorded for the cochin ginger genotypes showed significant variation for the quantitative traits. Among the genotypes CG 47 (30.92 tonnes/ha) showed the highest rhizome yield followed by CG 46 (25.32 tonnes/ha), CG 27 (25.28 tonnes/ha) and CG 53 (24.36 tonnes/ha). These high yielding genotypes recorded zero incidence of rhizome rot disease and were found to be promising ones. Genotypic correlation coefficients showed a significant positive relationship between fresh rhizome yield and yield components viz., rhizome weight, vegetative traits such as plant height, number of tillers and leaf length. Based on selection index, ranking was done and genotypes CG 47, CG 44, CG 53 and CG 22 were found superior. These four genotypes were identified as ideal cochin ginger genotypes and may be further evaluated as multi-location trials for validation.

Key words: Cochin ginger, Characterization, Correlation, Zingiberene

Ginger (*Zingiber officinale* Rosc.) a widely used rhizomatous herb belongs to Zingiberaceae family. It is known for its diverse applications in the food, pharmaceutical, and cosmetic industries. Native to Southeast Asia, ginger is prized for its bioactive compounds, including gingerols, shogaols, and paradols, which contribute to its potent antioxidant, anti-inflammatory, and antimicrobial effects [1]. Recent studies have also highlighted ginger's role in managing metabolic syndromes, improving digestive health, and its potential in cancer prevention [2]. The increasing global demand for ginger reflects its economic and therapeutic significance.

Some of the tropical and subtropical countries where abundant ginger cultivation occurs are India, China, Nepal, Nigeria, Thailand. These countries are top five ginger producing countries [3]. India and China are presently leading in ginger cultivation. During 2021-22, ginger worth 8,3734.24 lakh rupees was exported from India [4]. The major ginger-producing states in India are Odisha, Kerala, Karnataka, Arunachal Pradesh, West Bengal, Sikkim, and Madhya Pradesh. Kerala ranks first in ginger production and contributes nearly one-third of total production of country [5].

The demand for a particular variety of ginger is influenced by its quality. India, the world's top ginger producer, offers the highest quality ginger [6]. Most of the local varieties are identified by the locale in which they are cultivated. Cochin ginger and Calicut ginger are the two important dry ginger type genotypes from Kerala with a niche in the international market. Cochin ginger is renowned for its quality in the global market viz., α-zingiberene content, β-sesquiphellandrene, camphene, fibre content etc. [7].

Cochin ginger (CG), cultivated in central Kerala, holds significant value in India's agricultural export market. However, the current lack of CG availability for export highlights the urgent need for research to improve its production. This study aims to identify high-yielding and high-quality CG genotypes. Once the optimal types are discovered, they can be widely multiplied in site-specific regions. Therefore, this research is crucial and could significantly boost the state's economy by encouraging farmers to cultivate these particular CG varieties.

MATERIALS AND METHODS

A field study was carried out at the Department of Plantation, Spices, Medicinal and Aromatic Crops, College of Agriculture, Vellanikkara, Kerala Agricultural University, Thrissur, from July 2023 to March 2024. Twenty-five CG

genotypes were gathered from districts in central Kerala viz., Idukki, Kottayam, Ernakulam, Wayanad, Palakkad, and Thrissur. One improved variety KAU Chithra, developed by Kerala Agricultural University were used as check variety to evaluate the growth and yield of the collected genotypes. The details of the genotype collection are provided in (Table 1).

The genotypes along with check were planted using a randomized block design (RBD) with two replications. Raised beds of 2 m x 1 m were prepared, and seed rhizomes were planted at 20 cm x 20 cm spacing with a plant population of 32 plants per bed. The crop management was done as per the the guidelines outlined in the "Package of Practices Recommendations: Crops" by Kerala Agricultural University, 2024 [8]. Morphological observations were recorded 150 days after planting, once the plants had fully emerged, and rhizome characteristics were noted after harvest. Stem, leaf, and rhizome colour analyses were conducted using the Royal Horticultural Society (RHS) colour chart.

The percentage disease index was calculated by scoring 50 random leaves on a scale of 0 to 4 [9]. Analysis of variance and other statistical evaluations were performed using GRAPES R-based software [10].

These differences may have also contributed to the variation observed in the yield. However, variation was not observed in terms of qualitative morphological traits viz., pseudostem colour and leaf colour. The reported pseudostem colour was strong yellow-green (RHS 144A), the dorsal leaf colour was moderate yellow-green (RHS 137C) and ventral leaf colour was moderate olive-green (RHS 137A). However, leaf orientation varied among the genotypes. Most of the genotypes were erect except CG 13, CG 29, CG 35 A, CG 39 and CG 49 which showed semi erect condition.

There was significant variation in qualitative rhizome characters, such as branching of rhizome, rhizome nature, and rhizome inner core colour. About 8 per cent of the genotypes displayed straight branching, while 11 per cent displayed zigzag and 81 per cent showed curved branching. Additionally, 81 per cent of the genotypes had plumpy rhizomes, remaining 19 per cent had slender ones. Based on the RHS colour chart, majority of the genotypes, except four genotypes, had inner core with a light greenish yellow colour, while the others showed brilliant greenish yellow. The inner core colour is crucial as it determines the colour of ginger powder.

Table 1 Details of the genotypes collected and used in this study

S. No.	Genotypes	Place of collection
1	CG 09	Wayanad
2	CG 13	Kottayam
3	CG 15	Palakkad
4	CG 20	Kottayam
5	CG 21	Kottayam
6	CG 22	Kottayam
7	CG 23	Kottayam
8	CG 26 A	Ernakulam
9	CG 27	Ernakulam
10	CG 29	Ernakulam
11	CG 31	Idukki
12	CG 32	Idukki
13	CG 35 A	Ernakulam
14	CG 35 B	Ernakulam
15	CG 39	Palakkad
16	CG 40	Wayanad
17	CG 41	Palakkad
18	CG 44	Idukki
19	CG 46	Idukki
20	CG 47	Idukki
21	CG 48	Idukki
22	CG 49	Ernakulam
23	CG 51	Idukki
24	CG 52	Idukki
25	CG 53	Idukki
26	Chithra	KAU, Thrissur

Table 2 Colour variations in genotypes as per the RHS colour chart

Genotype	Inner core colour
CG 09	Brilliant greenish yellow (6A)
CG 13	Brilliant greenish yellow (6B)
CG 15	Brilliant greenish yellow (5A)
CG 20	Brilliant greenish yellow (6B)
CG 21	Brilliant greenish yellow (3B)
CG 22	Light greenish yellow (3C)
CG 23	Brilliant greenish yellow (3B)
CG 26 A	Brilliant greenish yellow (3B)
CG 27	Brilliant greenish yellow (4A)
CG 29	Light greenish yellow (1C)
CG 31	Brilliant greenish yellow (5A)
CG 32	Light greenish yellow (5C)
CG 35 A	Brilliant greenish yellow (3B)
CG 35 B	Brilliant greenish yellow (2B)
CG 39	Brilliant greenish yellow (4A)
CG 40	Brilliant greenish yellow (4A)
CG 41	Brilliant greenish yellow (5B)
CG 44	Brilliant greenish yellow (5B)
CG 46	Light greenish yellow (4B)
CG 47	Brilliant greenish yellow (4A)
CG 48	Brilliant greenish yellow (4A)
CG 49	Brilliant greenish yellow (6A)
CG 51	Brilliant greenish yellow (6C)
CG 52	Brilliant yellow (11A)
CG 53	Brilliant greenish yellow (5A)
Chithra	Brilliant greenish yellow (5B)

RESULTS AND DISCUSSION

The notable variation observed for the morphological traits among the ginger genotypes suggests genetic differences.

Significant variation was observed among the genotypes for traits such as plant height, tiller diameter, number of tillers, number of leaves, leaf length, leaf width, and crop duration (Table 3). This variability in growth characteristics may be attributed to the genetic makeup of the genotypes.

Table 3 Quantitative morphological characters of cochin ginger genotypes

Genotypes	Plant height (cm)	Tiller diameter (cm)	Number of tillers	Number of leaves	Leaf length (cm)	Leaf width (cm)	Crop duration (days)
CG 09	45.3[hij]	0.70[ijk]	13.4[kl]	17.0[fghi]	18.3[e]	2.25	217.5[hijk]
CG 13	60.9[abcd]	0.85[a]	19.3[fg]	19.3[abcdef]	22.8[ab]	2.35	217.0[hijk]
CG 15	46.1[hij]	0.72[ghi]	24.9[d]	20.0[abcde]	21.4[abcd]	2.50	222.5[defghi]
CG 20	39.0[j]	0.65[lm]	18.1[gh]	16.0[i]	19.7[cd]	2.35	221.5[efghij]

Genotypes							
CG 21	63.1^{ab}	0.78^{cde}	27.2^{cd}	$18.7^{abcdefgh}$	23.2^{a}	2.55	218.0^{hijk}
CG 22	59.5^{abcde}	0.76^{cdef}	22.5^{e}	21.0^{ab}	21.6^{abcd}	2.50	220.5^{fghijk}
CG 23	51.4^{fgh}	0.67^{jkl}	16.8^{hi}	16.2^{hi}	20.5^{cd}	2.50	221.5^{efghij}
CG 26 A	56.4^{bcdef}	0.80^{bcd}	25.0^{d}	19.7^{abcde}	21.1^{bcd}	2.45	$223.5^{cdefghi}$
CG 27	51.4^{fgh}	0.79^{cd}	19.7^{fg}	$18.6^{bcdefgh}$	21.2^{abcd}	2.50	232.0^{abc}
CG 29	43.4^{ij}	0.66^{klm}	10.7^{m}	16.5^{fghi}	19.6^{cd}	2.50	213.5^{jk}
CG 31	48.4^{ghi}	0.78^{cde}	29.8^{b}	$18.4^{cdefghi}$	19.6^{cd}	2.50	231.0^{abcd}
CG 32	59.2^{abcde}	0.74^{efghi}	26.7^{cd}	16.2^{hi}	20.4^{cd}	2.25	232.5^{ab}
CG 35 A	57.8^{abcdef}	0.74^{efgh}	13.3^{kl}	20.3^{abcde}	22.1^{abc}	2.50	215.5^{ijk}
CG 35 B	58.1^{abcdef}	0.71^{hij}	16.3^{hij}	$18.9^{abcdefg}$	23.0^{ab}	2.65	216.0^{ijk}
CG 39	54.0^{defg}	0.67^{jkl}	14.3^{jk}	17.0^{fghi}	22.4^{abc}	2.50	118.0^{jk}
CG 40	54.2^{defg}	0.73^{fghi}	25.1^{d}	$18.3^{cdefghi}$	21.1^{bcd}	2.45	219.5^{ghijk}
CG 41	55.2^{cdefg}	0.77^{cdef}	11.2^{lm}	17.9^{efghi}	21.2^{abcd}	2.55	$223.5^{cdefghi}$
CG 44	62.6^{abc}	0.66^{klm}	38.2^{a}	20.7^{abcd}	22.0^{abc}	2.45	235.0^{a}
CG 46	59.9^{abcd}	0.76^{defg}	20.5^{ef}	20.8^{abc}	22.4^{abc}	2.60	218.5^{hijk}
CG 47	64.1^{a}	0.83^{ab}	21.4^{ef}	19.1^{abcdef}	22.1^{abc}	2.50	229.0^{abcdef}
CG 48	54.8^{defg}	0.62^{m}	29.7^{b}	19.3^{abcdef}	21.2^{abcd}	2.55	$225.5^{bcdefgh}$
CG 49	63.2^{ab}	0.73^{fghi}	15.1^{ijk}	17.8^{efghi}	20.4^{cd}	2.50	212.5^{k}
CG 51	52.2^{efgh}	0.79^{bcd}	20.1^{fg}	19.8^{abcde}	21.8^{abc}	2.55	215.5^{ijk}
CG 52	60.0^{abcd}	0.66^{klm}	28.8^{bc}	20.2^{abcde}	21.6^{abcd}	2.50	232.0^{abc}
CG 53	60.9^{abcd}	0.80^{bc}	29.5^{b}	21.2^{a}	22.8^{ab}	2.65	230.0^{abcde}
Chithra	61.2^{abcd}	0.64^{lm}	13.3^{kl}	18.2^{defghi}	21.5^{abcd}	2.60	$228.0^{abcdefg}$
SE(m)	2.59	0.01	0.77	0.88	0.70	0.10	2.98
CV (%)	6.62	2.69	5.16	6.66	4.67	5.74	1.89

Table 4 Quantitative rhizome characters of cochin ginger genotypes

Genotypes	Rhizome length (cm)	Rhizome width (cm)	Internodal length (cm)	Rhizome weight per plant (g)	Average rhizome yield (tonnes ha^{-1})	Dry recovery (%)	PDI (%)
CG 09	15.55^{klmn}	1.75^{gh}	0.97^{abcde}	122.0^{hi}	8.12^{ij}	19.95^{hijk}	49.1^{f} (44.48)
CG 13	14.15^{n}	1.99^{abcd}	0.85^{ghi}	71.80^{k}	4.40^{klmn}	29.28^{a}	52.7^{d} (46.54)
CG 15	19.60^{bcd}	2.03^{abcd}	0.94^{cdef}	144.0^{fg}	16.36^{e}	18.67^{jk}	0.00^{i} (4.06)
CG 20	14.40^{mn}	1.97^{abcde}	0.91^{defg}	106.8^{i}	7.52^{ijk}	19.83^{hijk}	47.8^{g} (43.73)
CG 21	19.50^{bcde}	2.08^{ab}	0.92^{cdefg}	222.0^{c}	21.68^{cd}	28.81^{ab}	0.00^{i} (4.06)
CG 22	19.75^{bc}	1.95^{bcdef}	0.99^{abcd}	303.5^{a}	23.64^{bcd}	24.82^{cdef}	0.00^{I} (4.06)
CG 23	12.30^{o}	1.37^{k}	0.79^{hij}	51.50^{lm}	2.84^{lmn}	18.68^{jk}	55.3^{c} (48.04)
CG 26 A	18.75^{bcdef}	2.00^{abcd}	0.91^{defg}	148.5^{f}	17.12^{e}	24.93^{cdef}	0.00^{I} (4.06)
CG 27	17.50^{fghi}	1.83^{efg}	1.03^{ab}	193.5^{d}	25.28^{b}	24.90^{cdef}	0.00^{I} (4.06)
CG 29	14.80^{lmn}	2.01^{abcd}	0.89^{efg}	53.20^{l}	1.08^{n}	22.93^{defgh}	64.2^{a} (53.24)
CG 31	18.10^{def}	1.61^{hi}	0.72^{j}	34.50^{m}	2.52^{mn}	17.63^{kl}	58.1^{b} (49.66)
CG 32	17.30^{fghij}	1.61^{hi}	0.89^{efg}	109.5^{i}	8.16^{ij}	15.01^{l}	45.6^{h} (42.47)
CG 35 A	16.50^{ghijk}	2.10^{a}	0.89^{efg}	157.0^{ef}	14.72^{ef}	25.85^{bcde}	38.2^{k} (38.17)
CG 35 B	17.70^{fghi}	1.89^{def}	0.96^{bcde}	104.0^{ij}	6.32^{ijkl}	22.00^{fghij}	49.1^{f} (44.48)
CG 39	18.00^{efg}	1.95^{bcdef}	1.00^{abc}	170.5^{e}	16.32^{e}	20.33^{ghijk}	0.00^{i} (4.06)

CG 40	15.45 klmn	1.81 fg	0.77 ij	128.5 gh	9.36 ghi	22.91 defgh	41.7j (40.22)
CG 41	14.90 lmn	1.92 cdef	0.98 abcd	69.00 kl	4.00 lmn	29.14 ab	52.7d (46.54)
CG 44	17.75 fgh	1.52 ij	0.96 bcde	113.5 hi	20.80 d	19.16 ijk	0.00 i (4.06)
CG 46	18.65 cdef	1.74 gh	1.00 abc	158.0 ef	25.32 b	27.09 abc	0.00 i (4.06)
CG 47	21.60 a	2.07 ab	1.05 a	249.5 b	30.92 a	24.75 cdef	0.00 i (4.06)
CG 48	18.10 def	1.42 jk	0.87 fgh	173.5 e	7.84 hi	24.95 cdef	47.8 g (43.73)
CG 49	16.15 ijkl	2.02 abcd	0.96 bcde	162.0 ef	14.36 ef	19.09 jk	38.2 k (38.17)
CG 51	15.80 jklm	1.95 bcdef	1.05 a	85.00 k	5.32 jklm	22.50 efghi	50.5 e (45.28)
CG 52	18.80 bcdef	1.39 jk	0.89 efg	118.5 hi	12.08 fgh	26.12 abcd	41.7 j (40.22)
CG 53	20.30 ab	2.04 abc	0.94 cdef	257.5 b	24.36 bc	27.89 abc	0.00 i (4.06)
Chithra	16.30 hijkl	1.74 gh	0.92 cdefg	86.50 jk	12.68 fg	23.62 defg	44.3 i (41.72)
SE(m)	0.53	0.04	0.03	6.23	0.30	1.16	0.11
CV (%)	4.40	3.71	4.54	6.38	12.78	7.13	0.56

Plant height ranged from 39.0 to 64.1 cm, highest plant height was reported in CG 47 (64.1 cm) on par with 12 other genotypes and lowest plant height was seen in CG 20 (39.0). These results align with findings of Balakumbahan and Joshua (2017) [11]. CG 13 attained maximum tiller diameter at 0.85 cm on par with CG 47 (0.83 cm) whereas minimum tiller diameter was recorded by CG 48 (0.62cm) on par with CG 44 and CG 20. CG 44 exhibited the highest number of tillers (38.2) and CG 53 had a greater number of leaves (21.2) on par with 13 other genotypes whereas lowest number of leaves were observed in CG 20 (16.0) on par with 10 others. CG 21 had the longest leaf length (23.2 cm) on par with 16 other genotypes and shortest leaves were observed in CG 09 (18.03 cm), though broadest leaves were attained by highest leaf width were found in CG 53 and CG 35B (2.65 cm). Duration of crops among the genotypes varied from 212.5 days to 235.0 days. The genotype CG 44 had the highest duration of crops, reaching 235.0 days, while the lowest crops duration of 212.5 days was recorded in genotype CG 49. These findings indicate that CG-47, CG-44, CG 53 and CG-22 were superior in terms of morphological traits.

Similarly, rhizome characteristics viz., rhizome length and width, number of primary and secondary rhizomes, weight of primary and secondary rhizomes, rhizome weight per plant, average rhizome yield, dry recovery and zingiberene also showed variation as observed for morphological traits (Table 4-5). These traits are key factors contributing to yield, as the rhizome is the economically valuable part of ginger. In this study, rhizome weight ranged widely from 34.5 g (CG 31) to 303.5 g (CG 22). Similar findings were reported by Ravi *et al.* [12], with a maximum rhizome weight of 360.2 g. In the current study, CG 47 attained the highest rhizome yield at 30.92 tonnes/ha, followed by CG 46 (25.32 tonnes/ha), CG 27 (25.28 tonnes/ha) and CG 53 (24.36 tonnes/ha). Highest zingiberene content observed in CG 52 on par with CG 46 which is followed by CG 13 and CG 47. With these outperforming others in yield aspects and showing the highest values in growth characteristics.

Table 5 Quantitative rhizome characters of cochin ginger genotypes

Genotypes	Number of primary	Number of secondary	Weight of primary (g)	Weight of secondary (g)	Zingiberene (%)
CG 09	4.4 cd	6.8 ghi	54.00 c	71.80 f	28.72 e
CG 13	3.6 fgh	5.0 lm	39.60 e	29.40 no	32.78 b
CG 15	3.8 efg	8.8 de	33.00 fgh	57.40 ghi	25.81 hi
CG 20	3.2 hij	4.9 lm	48.60 d	54.20 hi	27.38 f
CG 21	5.6 ab	10.9 b	71.60 a	83.90 de	26.86 fg
CG 22	5.4 b	10.6 b	40.00 e	94.60 c	23.76 kl
CG 23	3.1 ij	4.2 n	14.80 jk	10.40 p	24.96 ij
CG 26 A	4.0 def	6.3 ij	39.40 e	51.70 ijk	25.27 hi
CG 27	3.0 j	7.2 fg	38.10 ef	84.20 de	29.65 de
CG 29	3.1 ij	3.1 o	47.30 d	45.20 jkl	26.20 gh
CG 31	2.9 j	2.9 o	12.60 k	11.80 p	25.81 hi
CG 32	4.4 cd	7.1 fgh	18.10 j	25.70 o	23.23 kl
CG 35 A	3.5 ghi	5.0 lm	33.90 fg	29.20 no	21.30 m
CG 35 B	3.2 hij	5.3 kl	39.90 e	61.40 gh	22.99 l
CG 39	4.2 de	6.5 hi	76.80 a	62.50 g	24.93 ij

CG 40	4.4^{cd}	7.6^{f}	29.50^{ghi}	44.70^{kl}	29.18^{de}
CG 41	4.0^{def}	5.4^{kl}	46.70^{d}	43.20^{lm}	24.08^{jk}
CG 44	4.2^{de}	5.7^{jk}	25.00^{i}	35.90^{mn}	23.48^{kl}
CG 46	4.2^{de}	6.8^{ghi}	57.80^{bc}	82.20^{e}	35.83^{a}
CG 47	5.9^{a}	13.6^{a}	72.60^{a}	143.50^{a}	31.58^{c}
CG 48	4.7^{c}	5.3^{kl}	15.20^{jk}	26.20^{o}	29.24^{de}
CG 49	3.8^{efg}	9.4^{cd}	61.40^{b}	90.20^{cd}	24.06^{jk}
CG 51	3.9^{efg}	6.8^{ghi}	28.40^{hi}	33.00^{no}	29.85^{d}
CG 52	4.7^{c}	8.4^{e}	30.50^{gh}	62.20^{g}	35.90^{a}
CG 53	4.2^{de}	9.7^{c}	46.30^{d}	108.30^{b}	29.61^{de}
Chithra	2.8^{j}	4.5^{mn}	31.80^{gh}	52.60^{ij}	27.69^{f}
SE(m)	0.22	0.23	1.80	2.55	27.31
CV (%)	5.71	4.78	6.31	6.29	1.80

The percent disease index (PDI) indicates the susceptibility of genotypes to specific diseases. For rhizome rot, CG 29 showed the highest susceptibility with a PDI of 64.2 per cent, followed by CG 31 at 58.1 per cent. However, out of the 28 genotypes studied, 10 showed no signs of rhizome rot disease (Table 4). Similarly, a percent disease index (PDI) of 66.6 per cent was previously reported in a study of ginger somaclones [13].

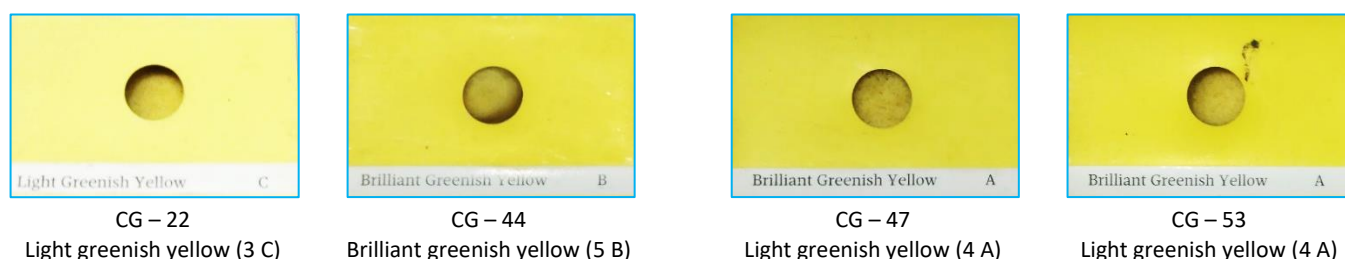| CG – 22	CG – 44	CG – 47	CG – 53
Light greenish yellow (3 C)	Brilliant greenish yellow (5 B)	Light greenish yellow (4 A)	Light greenish yellow (4 A)

Fig 1 Rhizome inner core colour of promising genotypes using RHS colour chart

Fig 2 Rhizomes of promising genotypes

Table 6 Pearson's correlation analysis of morphological characters

	No. of leaves	Leaf width	Leaf length	Plant height	Tiller diameter	No. of tillers plant^{-1}	Rhizome internode length	Rhizome width	Rhizome length	Rhizome weight	Crop duration	Average yield	Dry recovery
No. of leaves	1												
Leaf width	0.471*	1											
Leaf length	0.615***	0.574**	1										
Plant height	0.508**	0.317	0.684***	1									
Tiller diameter	0.355	0.018	0.334	0.324	1								
No. of tillers plant^{-1}	0.484*	-0.006	0.218	0.283	0.075	1							
Rhizome internode length	0.252	0.188	0.299	0.209	0.187	-0.224	1						
Rhizome width	0.114	0.115	0.269	0.014	0.52**	-0.386	0.401*	1					
Rhizome length	0.614***	0.334	0.441*	0.436*	0.29	0.52**	0.364	0.187	1				
Rhizome weight	0.482*	0.218	0.413*	0.424*	0.291	0.237	0.481*	0.37	0.726***	1			
Crop duration	0.258	-0.033	-0.165	0.099	0.173	0.38	-0.195	-0.248	0.052	-0.065	1		
Average yield	0.558**	0.261	0.478*	0.506**	0.319	0.311	0.557**	0.28	0.762***	0.847***	0.021	1	
Dry recovery	0.503**	0.428*	0.571**	0.395	0.407*	-0.076	0.211	0.322	0.193	0.343	0.096	0.303	1

***Correlation is significant at 0.001 level (two tailed)
**Correlation is significant at 0.01 level (two tailed)
*Correlation is significant at 0.05 level (two tailed)

Pearson's simple correlation analysis (Table 6) showed significant relationships between various traits in CG genotypes. In this study, average rhizome yield was significantly and positively correlated with rhizome weight (0.847***), rhizome length (0.762***), rhizome internodal length (0.557**), plant height (0.506**), number of leaves (0.558**) and leaf length (0.478*). This suggests that high-yielding varieties can be selected based on these morphological traits. Previous research also highlighted the importance of plant height, tiller diameter, number of tillers, number of leaves in selecting high-yielding genotypes due to their positive correlation with rhizome yield [14]. Similarly, other studies reported a positive correlation between rhizome weight, length, and width with rhizome yield [15]. On the other hand, rhizome weight was negatively correlated with crop duration.

CONCLUSION

The Cochin ginger (CG) genotypes examined in this study displayed significant variations in growth and yield traits. High genetic advance and variability were noted in factors contributing to yield, such as rhizome yield, rhizome weight per plant, length, width, and internodal length of the rhizome. These traits, along with plant height, number of leaves and the number of tillers, were found to be directly and significantly correlated with rhizome yield. Therefore, they can serve as important selection criteria for identifying superior genotypes. Genotypes like CG 47, CG 46, CG 27, and CG 53 are recommended for their superior yield characteristics. These genotypes also showed zero PDI of rhizome rot disease. Thus, these four genotypes hold potential for future genetic improvement and breeding programme. These genotypes should be evaluated further on basis of biochemical and molecular characterization. Multilocation trials may also be carried out for checking the stability of the genotype under different environment. Gene mapping is needed for these genotypes to determine their true genetic diversity. Since the high market value of ginger rhizomes is based on their quality, growers should take both the quality and the potential rhizome yield of each genotype into account when deciding which genotypes to cultivate.

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